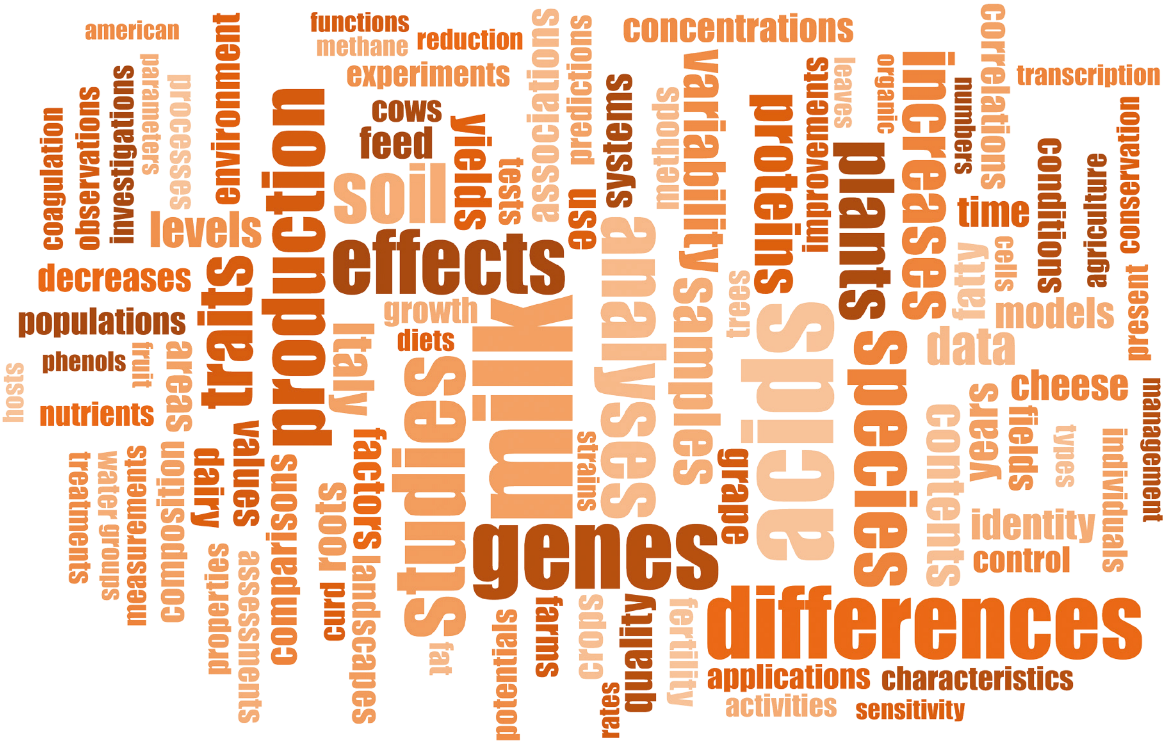
DAFNAE

RESEARCH YEARBOOK

2016



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RESEARCH YEARBOOK 2016

Edited by Alessandro Botton, Paolo Carletti, Martino Cassandro, Roberta Masin,
Mauro Penasa, Silvia Quaggiotti, Chiara Rizzi

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DEPARTMENT OF AGRONOMY FOOD NATURAL RESOURCES
ANIMALS AND ENVIRONMENT

RESEARCH YEARBOOK

2016

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INTRODUCTION

It is a great pleasure for me to introduce the 2016 edition of the Research Yearbook of the Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE) of the University of Padova. Following the three previous editions, it focuses on the top level scientific products of the Department and presents the abstracts of the peer-reviewed papers as retrieved from the Scopus database.

These publications represent only a part of the relevant deliverables of the wide research activity carried out within the Department. Indeed, an incredible number of other documents, such as book chapters, conference contributions, abstracts, reports, and fact sheets were also released.

Thank to this high scientific productivity, DAFNAE ranked for the second time, in the recent history of the national academic evaluation, as the top department in terms of quality of the research after the VQR 2004-2010 and VQR 2011-2014.

This great effort involved all the wide expertise present in the Department and was facilitated by the contribution of the technical staff and the enthusiastic participation of PhD students, postdocs, and grant holders that represent the freshest energy of the Department.

The research activity developed by DAFNAE has been accompanied by an impressive offer of undergraduate, MSc and PhD courses, in which the DAFNAE members can promptly transmit to the students the knowledges derived from their research activities, carried out both in field and lab.

I am very proud for the enthusiasm and the vitality of the Department and I am sure that this booklet will be a remarkable instrument to disseminate the research and innovation produced by DAFNAE.

I deeply thank all the colleagues who contributed with their papers, with a special acknowledgement to the group of editors who took care of this issue.

We are ready for the 2017 edition!

Maurizio Borin
Head
Department of Agronomy, Food,
Natural resources, Animals and Environment

RESEARCH PAPERS: STATISTICS AND COMMENTS

Also this year the moment to present the results of the DAFNAE research yearbook has arrived; this is a consolidated annual event on the production and quality of research and the strong collaboration and internationalization of the Department.

In the first edition of the yearbook, we predicted for the decade 2011-2020 an average number of documents per year published in peer review journals of 119, but also this year, we published a higher number of scientific documents as in the previous years 2012, 2013, 2014 and 2015 (151, 154, 123 and 150, respectively); in fact in the 2016 researchers of DAFNAE published 168 scientific articles.

The 168 scientific documents (+12% compared with 2015) produced a total of 1,237 pages (+11% compared with 2015), published in 99 (-13% compared with 2015) scientific journals. The present Research yearbook includes 148 scientific articles, 4 reviews, 14 conference papers, 1 note, and 1 letter. The Journal of Dairy Science (ranked in the first quartile, Q1, of its subject categories according to Scopus database), with 19 documents, has been the scientific journal most highly used by the researchers of DAFNAE in 2016, as in the previous two years. Other relevant scientific journals used, ranked in Q1 of the respective subject categories, were Agriculture, Ecosystems and Environment (6 documents), Frontiers in Plant Science (6 documents), Plos One (6 documents) and Scientific Reports (4 documents).

The number of papers published per researcher of DAFNAE in 2016 (69 researchers in total, considering 19 full professors, 25 associate professors, 15 researchers with a permanent position and 10 researchers with temporary position) averaged 2.43, with each document presenting an average of 5.9 co-authors with a minimum of 1 and a maximum of 21.

The high level of quality of the research published by researchers of DAFNAE is confirmed by the high number of scientific documents published in journals which ranked in the Q1 of the respective subject categories. Table 1 shows the frequency of scientific documents per quartile of the journal in which they have been published and for each of the 8 scientific categories considered in the yearbook; 67% (113 over 168 documents) of the published scientific documents were classified in Q1 using Scopus database.

Table 1. Frequency of scientific documents for quartile of ranking of the journals and for each scientific category (Scopus database).

Scientific category	Q1	Q2	Q3	Q4
Animal science	21	4	-	-
Genetics and genomics	12	3	-	1
Food science and technology	9	2	2	3
Plant science	16	3	1	3
Ecology and environmental science	13	4	-	2
Entomology	20	9	1	-

Agronomy and soil science	15	4	4	7
Microbiology	7	1	1	-
Total, n.	113	30	9	16
Total, %	67	18	5	10

The categories where all documents were published are reported in Table 2. The most prolific scientific categories, in absolute value, were: Agronomy and soil science (17.9% of total documents), Entomology (17.9%) and Animal science (14.9%).

The average number of authors per document ranged from 5.1 (Food science and technology) to 7.8 (Microbiology).

The quota of permanent research staff per document can be used as an indicator of the degree of self-sufficiency of the Department in the long period. Indeed, the total number of authors per document is based on the permanent and temporary research staff of the Department plus the external collaborations. In 2016, the average self-sufficiency degree of DAFNAE was 38% (37% in 2015), with a minimum of 26% (Plant science category) and a maximum of 45% (Animal science category).

These results are very interesting to valorize the temporary research staff and external collaborations of DAFNAE, to guarantee in the future this high scientific level of productivity.

Extensive and widespread National and International collaborations are guaranteed by 27 prestigious scientific research centers and universities located in Italy, and with research institutions of high scientific level, located in 25 countries of all the 5 continents.

Table 2. Frequency of scientific documents, average number of authors and average percentage of ownership per document, for scientific category (Scopus database).

Category	# of documents	% of total documents	% of documents with foreign co-authors	Average # of authors per document *	Average % of ownership per document **
Animal science	25	14.9	20.0	5.6 (min 3 – max 12)	45 (min 8 – max 100)
Genetics and genomics	16	9.5	37.5	5.7 (min 2 – max 9)	43 (min 11 – max 100)
Food science and technology	16	9.5	18.7	5.1 (min 3 – max 10)	41 (min 10 – max 75)
Plant science	23	13.7	52.2	7.7 (min 2 – max 15)	26 (min 7 – max 67)
Ecology and environmental science	19	11.3	15.8	5.4 (min 1 – max 21)	39 (min 5 – max 100)

Entomology	30	17.9	46.7	5.5 (min 2 – max 17)	33 (min 6 – max 80)
Agronomy and soil science	30	17.9	33.3	5.7 (min 2 – max 16)	44 (min 8 – max 100)
Microbiology	9	5.3	44.4	7.8 (min 5 – max 12)	31 (min 17 – max 60)
Total	168	100	33.6	5.95 (min 1 – max 21)	38 (min 5 – max 100)

* Total number of authors is based on permanent and temporary research staff of the Department plus the external collaborations.

** Ownership is considered counting the permanent research staff of University of Padova (researchers, associated professors and full professors) over the total number of authors per document.

In conclusion, the 2016 yearbook of DAFNAE aims to give a snapshot of the main research activities carried out in the 2016, with a special focus on the quality of the research documents, the role of the young collaborators and temporary staff on the total productivity, and the external collaborations.
This report would also act as an encouragment to strengthen the collaborative research in the next years. A special thank to all people who have worked at all levels to qualify the research activities of DAFNAE and a great thank to those who have allowed the realization of this edition.

Martino CASSANDRO

DAFNAE Research and Technical staff - 2017

Full Professors

Name	Surname	Phone	Email
GIANNI	BARCACCIA	0498272814	gianni.barcaccia@unipd.it
ANDREA	BATTISTI	0498272804	andrea.battisti@unipd.it
ANTONIO	BERTI	0498272828	antonio.berti@unipd.it
GIOVANNI	BITTANTE	3204347297	giovanni.bittante@unipd.it
MAURIZIO	BORIN	0498272838	maurizio.borin@unipd.it
SERGIO	CASELLA	0498272922	sergio.casella@unipd.it
MARTINO	CASSANDRO	0498272666	martino.cassandro@unipd.it
ANDREA	CURIONI	0498272624	andrea.curioni@unipd.it
CARLO	DUSO	0498272805	carlo.duso@unipd.it
LUIGI	GALLO	0498272657	luigi.gallo@unipd.it
MARGHERITA	LUCCHIN	0498272816	margherita.lucchin@unipd.it
ROBERTO	MANTOVANI	0498272661	roberto.mantovani@unipd.it
SERENELLA	NARDI	0498272911	serenella.nardi@unipd.it
MAURIZIO	RAMANZIN	0498272654	maurizio.ramanzin@unipd.it
PAOLO	SAMBO	0498272860	paolo.sambo@unipd.it
STEFANO	SCHIAVON	0498272644	stefano.schiavon@unipd.it
GEROLAMO	XICCATO	0498272639	gerolamo.xiccato@unipd.it
GIUSEPPE	ZANIN	0498272819	giuseppe.zanin@unipd.it

Associate Professors

Name	Surname	Phone	Email
MARINA	BASAGLIA	0498272921	marina.basaglia@unipd.it
STEFANO	BONA	0498272831	stefano.bona@unipd.it
CLAUDIO	BONGHI	0498272844	claudio.bonghi@unipd.it
ALESSIO	CECCHINATO	0498272646	alessio.cecchinato@unipd.it
GIUSEPPE	CONCHERI	3351012466	giuseppe.concheri@unipd.it
VIVIANA	CORICH	0498272925	viviana.corich@unipd.it

MASSIMO	DE MARCHI	0498272627	massimo.demarchi@unipd.it
MASSIMO	FACCOLI	0498272891	massimo.faccoli@unipd.it
ROSSELLA	GHISI	0498272910	rossella.ghisi@unipd.it
ALESSIO	GIACOMINI	0498272924	alessio.giacomini@unipd.it
ANNA	LANTE	0498272920	anna.lante@unipd.it
STEFANO	MACOLINO	0498272834	stefano.macolino@unipd.it
MARIO	MALAGOLI	0498272908	mario.malagoli@unipd.it
ANTONIO	MASI	0498272932	antonio.masi@unipd.it
ROBERTA	MASIN	0498272884	roberta.masin@unipd.it
FRANCESCO	MORARI	0498272857	francesco.morari@unipd.it
GABRIELLA	PASINI	0498272919	gabriella.pasini@unipd.it
MAURO	PENASA	0498272629	mauro.penasa@unipd.it
ANDREA	PITACCO	0498272848	andrea.pitacco@unipd.it
BENEDETTO	RUPERTI	0498272845	
MICHELA	SCHIAVON		michela.schiavon@unipd.it
MICHELE	SCOTTON	0498272833	michele.scotton@unipd.it
ANDREA	SQUARTINI	0498272923	squart@unipd.it
ENRICO	STURARO	0498272641	enrico.sturaro@unipd.it
FRANCO	TAGLIAPIETRA	0498272622	franco.tagliapietra@unipd.it
TEOFILO	VAMERALI	0498272861	teofilo.vamerali@unipd.it
SERENA	VAROTTO	0498272858	serena.varotto@unipd.it

Researchers with a permanent position

Name	Surname	Phone	Email
ALESSANDRO	BOTTON	0498272849	alessandro.botton@unipd.it
PAOLO	CARLETTI	0498272934	paolo.carletti@unipd.it
ANTONELLA	CRAPISI	0498272918	antonella.crapisi@unipd.it
CHIARA	DE FASSI NEGRELLI RIZZI	0498272625	chiara.rizzi@unipd.it
GIOVANNA	LOMOLINO	0498272917	giovanna.lomolino@unipd.it
LORENZO	MARINI	0498272807	lorenzo.marini@unipd.it

LUCA	MAZZON	0498272813	lmazzon@unipd.it
NICOLA	MORI	0498272802	nicola.mori@unipd.it
SILVIA	QUAGGIOTTI	0498272914	silvia.quaggiotti@unipd.it
RINA	VERDIGLIONE	0498272635	rina.verdiglione@unipd.it
SIMONE	VINCENZI		simone.vincenzi@unipd.it
GIAMPAOLO	ZANIN	0498272902	paolo.zanin@unipd.it

Researchers with a temporary position

Name	Surname	Type	Phone	Email
NICOLA	DAL FERRO	B	0498272818	nicola.dalferro@unipd.it
LORENZO	FAVARO	B	0498272800	lorenzo.favaro@unipd.it
MATTEO	MARANGON	B		matteo.marangon@unipd.it
ALBERTO	POZZEBON	B	0498272798	alberto.pozzebon@unipd.it
CRISTINA	SARTORI	B	0498272632	cristina.sartori@unipd.it
MARCO	BIROLO	A		marco.birolo@unipd.it
DAVID	CELETTI	A		david.celetti@unipd.it
GIULIO	GALLA	A		giulio.galla@unipd.it
FRANCO	MEGGIO	A	0498272863	franco.meggio@unipd.it
CARLO	NICOLETTO	A	049 8272826	carlo.nicoletto@unipd.it
DAVIDE	RASSATI	A		davide.rassati@unipd.it
PIERGIORGIO	STEVANATO	A	0498272938	stevanato@unipd.it
ALESSANDRO	VANNOZZI	A		alessandro.vannozzi@unipd.it

DAFNAE technical and administrative staff

Nome	Cognome	Telefono	Email
MATTIA	ARESU	0498272866	mattia.aresu@unipd.it
SARA	BACELLE	0498272881	sara.bacelle@unipd.it
LOREDANA	BALLIN	0498272930	loredana.ballin@unipd.it
ELISA	BARZON	0498272631	elisa.barzon@unipd.it
ALICE	BELLUCCO	0498272825	alice.belluco@unipd.it

LUISEL	BOLZONELLA	0498272940	luisel.bolzonella@unipd.it
MASSIMO	CAGNIN	0498272927	massimo.cagnin@unipd.it
CARLO	CAMAROTTO	0498272837	carlo.camarotto@unipd.it
VALERIO	CARDILLO	0498272843	valerio.cardillo@unipd.it
MILENA	CARLOT	0438453743	milena.carlot@unipd.it
LORENZO	CAROTTA	0498272577	lorenzo.carotta@unipd.it
ELISABETTA	CARRARO	0498272840	elisabetta.carraro@unipd.it
LUCA	CARRARO		luca.carraro@unipd.it
FLAVIODA	RONCH		flavio.daronch@unipd.it
CLAUDIA	DAL BUONO	0498272897	claudia.dalbuono@unipd.it
PATRIZIA	DALL'ARA	0498272801	patrizia.dallara@unipd.it
ROBERTO	DEGAN	0498272578	roberto.degan@unipd.it
FLAVIO	FACCHINELLI	0498272842	flavio.facchinelli@unipd.it
DONATELLA	FAGOTTO	0498272836	donatella.fagotto@unipd.it
VITTORIO	FERRARI	0498272852	vittorio.ferrari@unipd.it
DEBORAH	FRANCESCHI	0438453052	deborah.franceschi@unipd.it
LORENZO	GIORATO	0498272568	lorenzo.giorato@unipd.it
VALTER	GIRALDO	0498272568	valter.giraldo@unipd.it
LUCA	GRIGOLETTO	0498272678	luca.grigoletto@unipd.it
SIMONE	GUZZON	0498272815	simone.guzzon@unipd.it
LUCIANO	MAGRO	0498272672	luciano.magro@unipd.it
ADRIANO	MASSIGNAN	0498272578	adriano.massignan@unipd.it
KATIA	MILAN	0498272542	katia.milan@unipd.it
LAMARIKA	MOLINARI	0498272939	lamarika.molinari@unipd.it
ROSALBA	MORO	0498272617	rosalba.moro@unipd.it
PAOLO	PAOLUCCI	0498272809	paolo.paolucci@unipd.it
ALBERTO	PASIMENI	0498272649	alberto.pasimeni@unipd.it
DIEGO	PIZZEGHELLO	0498272915	diego.pizzeghello@unipd.it
VALENTINO	PIZZOCCHERO	0498272926	valentino.pizzocchero@unipd.it
RICCARDO	POLESE		riccardo.polese@unipd.it
ANGELA	RASORI	0498272843	angela.rasori@unipd.it

MARTINA	SALMASO	0498272664	martina.salmaso@unipd.it
SILVIA	SANTAGATA	0498272594	silvia.santagata@unipd.it
CATERINA	SIGOLO	0498272775	caterina.sigolo@unipd.it
ALBERTO	SIMONETTO	0498272568	alberto.simonetto@unipd.it
STEFANO	‘NETTI’TIOZZO	0498272663	stefano.tiozzo@unipd.it
ARCANGELA	TONO	0498272835	arcangela.tono@unipd.it
ANNA RITA	TRENTIN	0498272937	annarita.trentin@unipd.it
TIZIANA	TURRA	0498272671	tiziana.turra@unipd.it
MARA	VEGRO	0498272933	mara.vegro@unipd.it
STEFANIA	ZANNONI	0498272928	stefania.zannoni@unipd.it

Agronomy and soil science

Carbon budget of a temperate-climate vineyard-a green future for viticulture?

Meggio, F., Pitacco, A.

Department of Agronomy, Food, Natural Resources, Animals and Environment,
DAFNAE, University of Padova, Viale dell'Università 16, Legnaro (PD), Italy

Abstract

A common belief is that agricultural ecosystems cannot be net carbon sinks. Indeed, many technical inputs, heavy periodical harvests, and the repeated disturbances of upper soil layers, all contribute to a substantial loss both of the old and newly-synthesized organic matter. Perennial tree crops, however, are managed differently: they establish a permanent woody structure, stand undisturbed in the same field for decades, generate woody pruning debris, and are often grass-covered. We monitored the Net Ecosystem Exchange (NEE) by eddy covariance and the carbon partitioning in a temperate vineyard in northeastern Italy. A complete year budget confirms a substantial sink capacity of the system, with a NEE around 800 g C m^{-2} ha^{-1}, with grape harvest representing about 20-25% of it. Biometrical assessment of growth and partitioning show a good agreement with micrometeorological measurements and demonstrate a large input of organic matter into the soil. Temperate-climate vineyards seem to be good candidates to store carbon in agricultural systems. Management practices can be defined to preserve this storage, possibly contributing to the global carbon budget.

Keywords: Carbon allocation; Eddy covariance; Grapevine; Micrometeorology; Net ecosystem productivity

Acta Horticulturae

Volume 1112, Pages 455-459

Effectiveness of a zeolite-based fertilizer in reducing nutrient leaching in a recently sodded turfgrass

Macolino, S., Zanin, G.

Department of Agronomy, Food, Natural Resources, Animals and Environment,
University of Padova, Legnaro, PD, Italy

Abstract

A field study was performed to evaluate the effectiveness of a zeolite-containing fertilizer (Zeotech N) in reducing nutrient leaching in sodded turfgrass. Eighteen plots were established with sod established by a seed mixture comprised of 70% *Lolium perenne* and 30% *Poa pratensis*. The plots were sodded in April 2008 on a USGA sandy substrate amended with 20% peat (v/v). Zeotech N (12N-2.2P-6.7K + 2Fe) was compared with a mix of different conventional fertilizers which, all together, provided the same nutrient content of Zeotech N. The study was conducted in two temporal phases: a) In Study 1, Zeotech N and the conventional fertilizers were applied on 30 April, 28 May and 25 June 2008 at rate of 0 (control), 25 and 50 kg ha^{-1} nitrogen (N) as monthly applications of 0, 300 and 600 kg ha^{-1} N per year, respectively; b) In Study 2 the same fertilizers were applied on 30 July, 27 August and 24 September 2008 at a rate of 0, 50 and 100 kg ha^{-1} N (equivalent to 0, 600 and 1200 kg ha^{-1} N per year). Two suction lysimeters were installed in each plot to collect substrate solution at a depth of 40 cm. Turfgrass color was estimated weekly by visual ratings and vertical growth rate was determined by measuring turf height before mowing. Macronutrients leaching were determined through analysis of substrate solution collected by the suction lysimeters. It was found that turf growth and color were positively affected by the increase of fertilization rate. Treatments affected nutrient concentrations in substrate solution only in Study 2. Potassium and NO_3-N concentrations in the substrate solution were higher at the fertilization rate of 100 kg ha^{-1} N per month. Furthermore, at this fertilization rate, NO_3-N concentration was lower when Zeotech N fertilizer was used. s.

Keywords: Ammonium nitrogen; Conventional fertilizers; Macronutrients; Nitrate nitrogen; Phosphorus; Potassium; Turf color; Turf growth

Acta Horticulturae

Volume 1122, Pages 73-81

Seedling emergence and establishment of annual bluegrass (*Poa annua*) in turfgrasses of traditional and creeping perennial ryegrass cultivars

Masin, R., Macolino, S.

Department of Agronomy, Food, Natural Resources, Animals and Environment,
University of Padova, Viale dell'Università 16, Legnaro (PD), Italy

Abstract

Annual bluegrass is a cosmopolitan, cool-season grass that adapts to different environmental conditions. It is one of the main weeds of turfgrass, and its control is mainly achieved through chemical and cultural practices, although little importance is given to the competitive ability of turfgrass species or cultivars. A field study was performed in northeastern Italy from October 2012 to June 2014 to evaluate the competitive ability of selected perennial ryegrass cultivars to suppress emergence and establishment of annual bluegrass seedlings. Two creeping perennial ryegrasses ('CSI' and 'PPG-PR171') and two traditional cultivars ('Azimuth' and 'Presidio') were compared. In late autumn in both years, annual bluegrass was sown in a marked area (30 cm by 30 cm) in the turfgrass. Emerged seedlings were counted weekly, and emergence dynamics were modeled. In the second year, final density of annual bluegrass allowed to grow in turfgrass was also evaluated in summer. Results showed that both seedling emergence and density of annual bluegrass were significantly reduced by creeping perennial cultivars, supporting the hypothesis that these cultivars may reduce annual bluegrass establishment in turfgrass. Seedling emergence pattern of annual bluegrass did not differ in creeping and traditional cultivars of perennial ryegrass, suggesting the possibility of creating a general emergence model suitable in any turfgrass to help turfgrass managers in the control of this weed species.

Keywords: Competition; Emergence modeling; Grass weeds; Plant density; Plant morphology

Weed Technology

Volume 30, Issue 1, Pages 238-245

Organic input quality is more important than its quantity: C turnover coefficients in different cropping systems

Berti, A., Morari, F., Dal Ferro, N., Simonetti, G., Polese, R.

Department of Agronomy, Food, Natural Resources, Animals and the Environment,
Univ. of Padova-Viale dell'Università, Legnaro (PD), Italy

Abstract

Annual C input to soil is a major factor affecting soil organic carbon (SOC) dynamics. However different types of C-sources can have different behaviour, in relation to their chemical characteristics and how they interact with soil. Root-derived C, in particular, should be more efficient than other organic materials as a result of the physicochemical and biological characteristics of the surrounding environment, leading to a reduction in the C decomposition rate.To test this hypothesis, we considered a long-term experiment underway in Northern Italy since 1962, comparing permanent meadow and 6 different crop rotations over a wide range of nutrient inputs, in both organic and inorganic forms. C inputs from amendments were measured and those from crops were calculated using allometric functions and crop and residues yields. The time evolution of SOC was studied through a single-pool, first-order kinetic model, allowing the estimation of humification coefficients for residues, roots, farmyard manure and cattle slurries.The highest value of the humification coefficient was estimated for farmyard manure, which confirmed its high efficiency in stabilising SOC content. Root C presented a humification coefficient 1.9 times higher than above-ground plant materials while slurries were intermediate, with a humification coefficient roughly half that of farmyard manure and even lower that of roots.The quality of C input thus seems of fundamental importance for evaluating the sustainability of different cropping systems in terms of SOC dynamics.

Keywords: Crop residues; Humification coefficient; Long-term field experiment; Organic amendments; Roots; Soil organic carbon

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Disentangling the effects of conservation agriculture practices on the vertical distribution of soil organic carbon. Evidence of poor carbon sequestration in North- Eastern Italy

Piccoli, I.[a], Chiarini, F.[b], Carletti, P.[a], Furlan, L.[b], Lazzaro, B.[c], Nardi, S.[a], Berti, A.[a], Sartori, L.[d], Dalconi, M.C.[e], Morari, F.[a]

[a] DAFNAE Dept., University of Padova, Viale Dell'Università 16, Legnaro (PD), Italy
[b] Veneto Agricoltura, Settore Ricerca Agraria, Viale dell'Università 14, Legnaro (PD), Italy
[c] Regione del Veneto, Sezione Agroambiente, Settore Politiche Agroambientali, Via Torino 110, Mestre (VE), Italy
[d] TESAF Dept., University of Padova, Viale Dell'Università 16, Legnaro (PD), Italy
[e] Department of Geosciences, University of Padova, via G. Gradenigo 6, Padova, Italy

Abstract

Conservation agriculture is one of the agro-environment measures promoted by the Veneto Region (North-eastern Italy) to regulate and support many ecosystem services. This study compared conventional and conservation agriculture management systems in order to evaluate their effects on both SOC stocks and quality i.e. humic C and its molecular weight fractions, microbial C and N. The experiment was set up in 2010 on three farms in Veneto Region. In order to improve the monitoring procedures, a massive soil sampling programme was conducted in 2011 and 2014 in ca. 150 positions, considering the SOC stratification within a 0-50 cm profile.Results suggested that conservation agriculture practices affected SOC distribution rather than its total amount. The retention of crop residues on the soil surface and the absence of tillage operations drove SOC dynamics in the top layer (0-5 cm) of the conservation system, while residues incorporation with ploughing was responsible for SOC accumulation at the 30-50 cm depth in the conventional one. SOC stock variation in the conservation treatment was also influenced by root C input, which was identified as a major factor able to promote SOC accumulation in the 0-30 cm profile. The role of clay on SOC dynamics was not uniform in the three farms since it depended both on the clay amount and its mineral composition. The strong interactions existing between management systems and local soil conditions were also confirmed by the C quality analyses. This research did not demonstrate the benefits of conservation practices on SOC sequestration during the transition period. However, SOC sequestration is only one of the numerous ecosystem services provided by conservation practices. Some of these depend on the C content and quality in the top layers that, as demonstrated in our work, were strongly affected by the C stratification processes triggered by conservation agriculture

Keywords: Agro-environment measures; Carbon quality; Clay minerals; Conservation agriculture; Microbial biomass; No-tillage; Soil carbon sequestration; Soil organic carbon

Agriculture, Ecosystems and Environment

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Relationship between soil test phosphorus and phosphorus release to solution in three soils after long-term mineral and manure application

Pizzeghello, D., Berti, A., Nardi, S., Morari, F.

Dipartimento di Agronomia, Animali, Alimenti, Risorse Naturali e Ambiente (DAFNAE),
Università di Padova, Viale dell'Università 16, Padova, Legnaro, Italy

Abstract

Continued fertilizations have led to soil phosphorus (P) concentrations that exceed those required for optimal plant growth. In this study, P accumulation and leaching were investigated in 1-m profile of three reconstructed soils (sandy, SDY; clay, CLY; peaty, PTY) typical of the Po Valley (northern Italy) following long-term (44 years) farmyard manure and mineral applications and untreated. Soil test P was determined by extracting with ammonium oxalate (P_{Ox}), Mehlich-3 (P_{M3}) and Olsen (P_{Ols}) solutions, whereas soil P release was estimated by water extraction (P_{H2O}). Two single-point sorption indices ($PSI_{19.4}$ and PSI_{50}) were used to assess the P sorption capacity in these soils. The relationship between extractable P forms and water P was also modelled as a segmented line. Soil test P resulted as being affected by type of soil, treatment and depth. Farmyard manure increased the P forms by 7.7-fold that of untreated down to 50 cm in CLY and PTY, and 28-fold untreated down to 90 cm in SDY, thus indicating both accumulation and leaching of P. The P sorption indices were affected by type of soil, treatment and depth. P accumulation was also confirmed by increments of PSI_{50} in the manure-treated deeper layers, likely due to increased organic matter and/or precipitation and co-precipitation of P with carbonates in these soils. Although mineral fertilization also increased extractable P it was with lower magnitude than manure on P leaching and P sorption indices. From the segmented lines between P_{H2O} and extractable P, the presence of change points in CLY and PTY revealed P_{H2O} concentrations above the environmental threshold values. In the light-textured SDY soils, the low P sorption capacity and absence of change points evidenced high P leaching and potential contamination of surface and ground waters, in particular when manure was used.

Keywords: Carbonates; Change point; Fertilization; Sorption index

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Radicchio cultivation under different sprinkler irrigation systems

Bortolini, L.[a], Nicoletto, C.[b], Sambo, P.[b], Evans, M.R.[c]

[a] Department of Land, Environment, Agriculture and Forestry (TESAF), University of Padova, Viale dell'Università 16, Legnaro, Padova, Italy
[b] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, Legnaro, Padova, Italy
[c] Department of Horticulture, University of Arkansas, Fayetteville, AR, United States

Abstract

Gun sprinklers were commonly used in Italy to irrigate Radicchio. Although this high-pressure irrigation system allows large areas to be irrigated in a short time, it has some major disadvantages. Disadvantages include the impact of the drops on the soil and crop can be very strong, the high volume of water used tends to increase water use and runoff and water distribution uniformity is low. A 3-year experiment was conducted in North-East Italy in order to evaluate the possibility of using a mini-sprinkler irrigation system with low-volume application rates. The use of mini-sprinkler resulted in a higher distribution uniformity, higher Christiansen uniformity coefficient and a higher water use efficiency. Energy cost was also lower when the mini-sprinkler system was used for irrigation as compared to the irrigation gun system. Radicchio head weight and marketable yield were higher when plants were irrigated with the mini-sprinkler as compared to those irrigated with the irrigation gun. Therefore, the use of mini-sprinklers resulted in not only a reduction in water use and energy cost but also an increase in radicchio production.

Keywords: Chicory; Energy; Irrigation gun; Irrigation uniformity; Mini-sprinkler; Water use efficiency

Contemporary Engineering Sciences

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Use of organic fertilizers in nursery production of ornamental woody species

Zanin, G., Gobbi, V., Coletto, L., Passoni, M., Nicoletto, C., Ponchia, G., Sambo, P.

Dipartimento di Agronomia Animali Alimenti Risorse Naturali e Ambiente, University of Padova, Legnaro (PD), Italy

Abstract

In the nursery industry, fertilization technique is very important to obtain plants of good quality in the open field as well as in container production. Currently, because of a scarcity of manure, mineral fertilizers are widely used. This leads to a depletion of the soil in terms of soil organic matter, which involves a reduction in the overall fertility. In this trial, the effectiveness of two organic fertilizers (pelleted manure and compost), compared to a mineral complex fertilizer, was tested in field nursery cultivation *of Ligustrum vulgare* L. and *Carpinus betulus* L. Different fertilizer amounts were used in order to apply 150 kg ha^{-1} of N. In the two-year trial, plant height and width were monitored and, at the end of the second year, their fresh and dry weights were measured along with other biometric evaluations. Root growth was assessed by means of auger sampling and the soil organic matter concentration was determined at the beginning and end of the experiment. In the first year, a higher vegetative growth of plants fertilized with pelleted manure was obtained in both species. In the second year *L. vulgare* showed minimal differences among treatments in terms of plant growth. In *C. betulus*, at the end of the second year, more growth was obtained in plants fertilized with pelleted manure and compost. A minimal effect of the treatments was observed on root growth and organic matter concentration in the soil.

Keywords: *Carpinus betulus*; Compost; *Ligustrum vulgare*; Mineral fertilizer; Pelleted manure

Acta Horticulturae

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An overview on long-term agro-ecosystem experiments: Present situation and future potential

Berti, A.[a], Marta, A.D.[b], Mazzoncini, M.[c], Tei, F.[d]

[a] Department of Agronomy, Food Natural Resources Animals and the Environment, University of Padova, Viale dell'Università, 16, Legnaro, PD, Italy
[b] Department of Agrifood Production and Environmental Sciences, University of Florence, Piazzale delle Cascine 18, Firenze, Italy
[c] Department of Agriculture, Food and Environment, University of Pisa, Via del Borghetto, 80, Pisa, Italy
[d] University of Perugia, Department of Agricultural, Food and Environmental Sciences, Borgo XX Giugno 74, Perugia, Italy

Abstract

Modern Long Term Agricultural experiments (LTAE) have a long history initiated when modern agricultural science was just at its beginning. After about 180 years from the start of the first of the classical Rothamsted experiments in 1843, these experiments still maintains a consistent appeal for researchers and the interest on LTAEs is growing, as shown by the increasing number of papers dealing with long-term effect of agricultural practices, frequently considering topics, such as sustainability, environmental quality, species-adaptation impacts, that were never envisioned by the founders of classical LTAEs. However, these experiments have numerous constraints and weakness that have to be clearly understood and evaluated when using the data, especially for up-scaling or modelling purposes. Nevertheless, in our vision, the strengths and the opportunities of LTAEs are still overwhelming, particularly if connected in networks allowing a standardisation of procedures and facilitating the access to data and to the experiments of researchers external to the institution hosting the LTAE.

Keywords: Agriculture; Long-term research; Sustainability

European Journal of Agronomy

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Spatial interpolation quality assessment for soil sensor transect datasets

Scudiero, E.[a], Corwin, D.L.[a], Morari, F.[b], Anderson, R.G.[a], Skaggs, T.H.[a]

[a] USDA-ARS, United States Salinity Laboratory, 450 West Big Springs Rd., Riverside, CA, United States
[b] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padua, Viale dell'Università 16, Legnaro, Italy

Abstract

Near-ground geophysical soil sensors provide valuable information for precision agriculture applications. Indeed, their readings can be used as proxy for many soil parameters. On-the-go soil sensor surveys are, typically, carried out intensively (e.g., every 2 m) over many parallel transects. Two types of soil sensors measurements are considered in this paper: apparent electrical conductivity (4 fields in California, USA) and reflectance (1 field in Italy). Two types of spatial interpolations are carried out, universal kriging (model-based) and inverse distance weighting (deterministic). Interpolation quality assessment is usually carried out using leave-one-out (loo) resampling. We show that loo resampling on transect sampling datasets returns overly-optimistic, low interpolation errors, because the left-out data point has values very close to that of its neighbors in the training dataset. This bias in the map quality assessment can be reduced by removing the closest neighbors of the validation observation from the training dataset, in a (spatial) h-block (SHB) fashion. The results indicate that, for soil sensor data acquired along parallel transects: (i) the SHB resampling is a useful tool to test the performance of interpolation techniques and (ii) the optimal (i.e., rendering the same errors of un-sampled locations between transects) SHB threshold distance (h.dist) for neighbor-exclusion is proportional to the semi-variogram range and partial sill. This procedure provides research scientists with an improved means of understanding the error of soil maps made by interpolating soil sensor measurements.

Keywords: Apparent electrical conductivity; H-block resampling; NDVI; On-the-go sensors; R; Spatial interpolation

Computers and Electronics in Agriculture

Volume 123, Pages 74-79

A survey of carbon sequestration potential of orchards and vineyards in Italy

Scandellari, F.[a]*, Caruso, G.*[b]*, Liguori, G.*[c]*, Meggio, F.*[d]*, Palese, A.M.*[e]*, Zanotelli, D.*[a]*, Celano, G.*[e]*, Gucci, R.*[b]*, Inglese, P.*[c]*, Pitacco, A.*[a]*, Tagliavini, M.*[a]

[a] Faculty of Science and Technologies, Free University of Bolzano-Bozen, Piazza Università 5, Bolzano, Italy
[b] Department of Agriculture, Food and Environment, University of Pisa, Via del Borghetto 80, Pisa, Italy
[c] Dipartimento Scienze Agrarie e Forestali (SAF), Viale delle Scienze, University of Palermo, Palermo, Italy
[d] Department of Agronomy Food Natural Resources Animals and Environment - DAFNAE, University of Padova, Agripolis, Viale dell'Università 16, Legnaro, Padova, Italy
[e] Dipartimento delle Culture Europee e del Mediterraneo: Architettura, Ambiente, Patrimoni culturali (DiCEM), University of Basilicata, Via San Rocco 3, Matera, Italy

Abstract

Orchards and vineyards are important land use types in Southern Europe. In spite of their potential to sequester atmospheric C and to mitigate climate change, relatively little is known regarding the influx and outflux of C in these systems. The aim of this work is to provide data on the C budget, including net primary production (NPP), C removal through production, and C sequestration potential for the vineyards and the main fruit tree species (apple, citrus, olive, and peach) grown in Italy. Standing biomass and NPP were measured, and net ecosystem exchange and net C balance assessed directly, through either eddy covariance technique, or considering NPP and heterotrophic respiration. Aboveground NPP ranged between 10 and 20 t ha^{-1} while, when directly assessed, belowground NPP was less than 20% of the total NPP. The C leaving the system through fruit production ranged between 2 and 3 t ha^{-1}. Mature fruit tree ecosystems had positive net ecosystem productivity (ranging from 4.30 in *Apple-2* to 7.5 t C ha^{-1} y^{-1} in *Grape-1*.) and net ecosystem carbon balance (ranging from 0.6 to 5.9 t C ha^{-1} y^{-1}), indicating the potential of these systems to store C.

Keywords: Apple; Carbon budget; Citrus; Grapevine; Net primary production; Olive; Peach

European Journal of Horticultural Science

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Degradation of soil fertility can cancel pollination benefits in sunflower

Tamburini, G., Berti, A., Morari, F., Marini, L.

DAFNAE, University of Padova, Viale dell'Università 16, Legnaro, Padua, Italy

Abstract

Pollination and soil fertility are important ecosystem services to agriculture but their relative roles and potential interactions are poorly understood. We explored the combined effects of pollination and soil fertility in sunflower using soils from a trial characterized by different long-term input management in order to recreate plausible levels of soil fertility. Pollinator exclusion was used as a proxy for a highly eroded pollination service. Pollination benefits to yield depended on soil fertility, i.e., insect pollination enhanced seed set and yield only under higher soil fertility indicating that limited nutrient availability may constrain pollination benefits. Our study provides evidence for interactions between above- and belowground ecosystem services, highlighting the crucial role of soil fertility in supporting agricultural production not only directly, but also indirectly through pollination. Management strategies aimed at enhancing pollination services might fail in increasing yield in landscapes characterized by high soil service degradation. Comprehensive knowledge about service interactions is therefore essential for the correct management of ecosystem services in agricultural landscapes.

Keywords: Agricultural intensification; Ecosystem services; Food security; Interactions; Nutrient availability

Oecologia

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Seeding time affects establishment of warm-season turfgrasses

Pornaro, C.[a], *Macolino, S.*[a], *Leinauer, B.*[b]

[a] Department of Agronomy Food Natural Resources Animals and Environment,
Legnaro, PD, Italy
[b] Department of Extension Plant Sciences, Las Cruces, NM, United States

Abstract

Seashore paspalum (*Paspalum vaginatum* Swartz) is a warm-season, salttolerant grass species. It is considered suitable to subtropical climates and is being increasingly used for turf purposes in the Mediterranean countries of Europe. Several studies have reported on the performance of mature seashore paspalum stands under Mediterranean conditions; however, little information is available regarding establishment from seed. The objective of this study was to investigate the effect of seeding time and rate on the germination and speed of establishment of Sea Spray seashore paspalum in comparison to Riviera and Sovereign bermudagrass [*Cynodon dactylon* (L.) Pers.]. A field trial was conducted at the experimental farm of Padova University (Italy) from January to August 2006. The cultivars were planted and compared at three seeding dates (24 January, 27 February, and 18 April) and two seeding rates (2.5 and 5.0 g m.2). Percentage of green coverage was evaluated weekly using digital image analysis. Sea Spray and both bermudagrasses reached full coverage earlier when seeded in winter (January and February) than in spring (April). Furthermore, compared with bermudagrasses, seashore paspalum needed approximately 16 additional days to establish, reaching 75% cover on 4 July.

Keywords: Dormant seeding; Germination; Green coverage; Growing degree days; Seeding rate; Warm-season grasses

Acta Horticulturae

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Effect of injection depth of digestate liquid fraction on soil carbon dioxide emission and maize biomass production

Maucieri, C.[a], Barbera, A.C.[b], Borin, M.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padua, Legnaro, PD, Italy
[b] Department of Agriculture, Food and Environment, University of Catania, Catania, Italy

Abstract

The aim of this study was to evaluate, in open field conditions, the effect of injection depth of digestate liquid fraction (10 cm, 25 cm and 35 cm) in clay loam soil, on CO_2 emission. An un-amended soil was considered as control. The study was performed in 2014 on a farm located in Terrasa Padovana, Veneto region (Italy) distributing digestate before maize sowing. Digestate injection determined a high soil CO_2 emission in the first hour after application, followed by a progressive reduction in as early as 24 h, reaching significantly lower values, similar to those measured in the un-amended control, after 48 h. Gas emissions measured 1 h after digestate application decreased as injection depth increased with significantly higher emission values in the 10 cm treatment (median value 23.7 g CO_2 m^{-2} h^{-1}) than in the 35 cm one (median value 2.5 g CO_2 m^{-2} h^{-1}). In the 3 days between digestate distribution and maize sowing, soil CO2 emission was significantly higher in the amended treatments than un-amended one, with median values of 1.53 g CO_2 m^{-2} h^{-1} and 0.46 g CO_2 m^{-2} h^{-1} respectively. During maize growing season, no significant soil CO_2 emission difference was monitored among treatments, with a median value of 0.33 g CO_2 m^{-2} h^{-1}. Digestate application significantly improved maize aboveground dry biomass with an average yield of 22.0 Mg ha^{-1} and 16.2 Mg ha^{-1} in amended and un-amended plots, respectively, due to the different amount of nutrients supplied.

Keywords: Digestate use; Maize biomass yield; Soil CO_2 emission; Soil digestate injection

Italian Journal of Agronomy

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Spent mushroom substrate as organic fertilizer: Vegetable organic trials

Gobbi, V., Bonato, S., Nicoletto, C., Zanin, G.

Department of Agronomy, Food, Natural Resources, Animals and Environment,
University of Padova, Padova, Italy

Abstract

The fast dynamics of vegetable production, characterized by rapid cropping successions, species with very different cultural requirements, intensity of soil cultivation and scarcity of manure, lead to a progressive depletion of the soil and a reduction of the overall fertility. The effect of different nitrogen sources on lettuce and leek production was evaluated in this experiment. The nitrogen mineral fertilizer for each crop was partially or completely replaced by spent mushroom substrate (SMS). A factorial combination of four fertilization treatments and three different types of SMS were arranged in a completely randomized blocks design. The four treatments were: unfertilized control (T0), mineral control (TMIN, 100% mineral fertilizer), T50 (50% SMS and 50% mineral fertilizer) and T100 (100% SMS). The three types of SMS were straw + poultry manure (SP), horse manure + poultry manure (HP) and straw + poultry manure + horse manure (SPH). Plants were harvested at marketable size, and samplings were carried out in order to evaluate morphological and dimensional traits for both crops considered. Nitrogen concentration, and anion and cation content were also considered. No statistically significant differences were recorded among treatments for marketable yields. A small increase in salt content was also recorded when mineral fertilizers were used. In general, SMS was demonstrated to be a suitable replacement for mineral fertilizers. Cultivation with SMS as soil amendment and fertilizer seemed to have generally positive effects on lettuce and leek performance, showing yields comparable to those with mineral fertilization.

Keywords: Leek; Lettuce; Macronutrient; Organic matter; Vegetables

Acta Horticulturae

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Spatial variability of soil micronutrients (Cu, Fe, Zn & Mn) and population dynamic of mycoflora in potato fields of CKNP region Gilgit-Baltistan Pakistan

Hussain, A.[a], *Awan, M.S.*[a], *Ali, S.*[a], *Khan, S.W.*[a], *Morari, F.*[b], *Ali, S.*[c]

[a] Department of Agriculture and Food Technology, Karakoram International University, Gilgit Baltistan, Pakistan
[b] Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Agripolis, 16, Legnaro (Padova), Italy
[c] Department of Chemistry, Karakoram International University, Gilgit Baltistan, Pakistan

Abstract

The main aim of current study was to explore the spatial variability of micronutrients (Cu, Fe, Zn & Mn) and mycoflora in a potato growing valleys of CKNP region, Gilgit-Baltistan, Pakistan. Ninety sixty soil samples were collected by a random sampling technique using Global Positioning System (GPS). In general, soils of survey valleys are loamy or silty loam with slightly alkaline pH and low to medium organic matter. Geographic Information System (GIS) was applied for micronutrients mapping of the analyzed data obtained from laboratory test. Results indicated that micronutrients (Cu, Fe and Mn) were found high except Zn. The Zinc concentration was low in 57.29% samples, medium in 30.20% samples and high in 12.50% samples respectively. The GIS mapping of soil micronutrients can be used in precision farming studies with the application of fertilizers and this approach is also proposed for the evaluation of sustainable soil management practices. The observed spatial variability of micronutrients helps potato growers in crop management decisions to increase productivity and improve farmer's livelihood. Knowledge and conservation of soil mycoflora is essential for sustainable agriculture development. In the current study a total number of thirteen mycoflora species were isolated from the composite soil sample of four valleys. The valley wise population per gram of soil was recorded as 24x10^{-6} in Bagrote, 18x10^{-6} in Haramosh, 15x10^{-6} in Hoper and 26x10^{-6} in Shigar valley. The most dominant among them were *Aspergillus flavus*, *Mucor species*, *Rhizopus stolonifer*, *Penicillium species* and *Alternaria alternate*.

Keywords: Micronutrients; Mycoflora; Potato fields; Soil fertility; Spatial variability

Pakistan Journal of Agricultural Sciences

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Organic by-product substrate components and biodegradable pots in the production of *Pelargonium* x*hortorum* Bailey and *Euphorbia pulcherrima* L.

Zanin, G., Coletto, L., Passoni, M., Nicoletto, C., Bonato, S., Ponchia, G., Sambo, P.

Dipartimento di Agronomia, Animali, Alimenti, Risorse Naturali e Ambiente, University of Padova, Legnaro (PD), Italy

Abstract

The need to reduce peatland exploitation has increased demand for materials that can at least partially replace peat in root substrate mixes. In this study four substrates containing 10% perlite, or 10, 30 and 50% rice hulls (RH) (the rest being white peat) were evaluated alone or amended with 20% of the anaerobic digested residues of fruit and wine distillery stillage wastes (ADR). Substrates were analyzed physically and chemically and used to grow *Euphorbia pulcherrima* L. 'Red Fox Cosmo Red' and *Pelargonium* x*hortorum* Bailey 'Green Aida Red'. A compostable RH pot was also evaluated as an alternative to the conventional plastic one. Substrates containing 10% RH were very similar to the one containing 10% perlite, while substrates with 50% RH had higher pH, total pore space, air-filled porosity and nitrate nitrogen and potassium concentrations and lower electrical conductivity, water holding capacity, bulk density and ammonium nitrogen concentrations compared to the 10% RH substrate. The addition of ADR reduced organic matter concentration and increased pH, electrical conductivity, bulk density, and almost all nutrient concentrations. For both species growth with 10% RH substrates was similar to that with 10% perlite. However, while in poinsettia, only 50% RH gave worse performances than 10% perlite, in zonal geranium, growth was already poorer with 30% RH. ADR reduced poinsettia growth in general, while root growth of zonal geranium was improved. RH pots affected root dry weight, which significantly decreased in zonal geranium.

Keywords: Anaerobic digested residues; Chemical characteristics; Compostable pot; Physical characteristics; Rice hulls

Acta Horticulturae

Volume 1112, Pages 371-378

Morphological and dimensional traits in vegetables: Raised bed vs. flat soil

Nicoletto, C., Gobbi, V., Zanin, G., Sambo, P.

Department of Agronomy, Food, Natural Resources, Animals and Environment,
University of Padova, Padova, Italy

Abstract

The quick dynamics of the vegetable production sector, characterized by rapid cropping successions and species with very different cultural needs, usually results in intensive soil tillage and management. These processes are necessary to ensure the best conditions for the crop and adequate development throughout the crop cycle from sowing, or transplanting, to harvest. Different types of soil tillage are often used in the creation of raised seed-or transplant beds. The reported experiment was aimed at evaluating the effect of raised beds, in comparison to traditional soil management, on the morpho-dimensional traits of different vegetable species. Seven vegetable crops were considered: lettuce, zucchini, green beans, rocket salad, variegated-leaved Italian chicory, long-stemmed Italian chicory and chard, transplanted and seeded in raised beds and on flat soil. At marketable size the crops were harvested and sampled in order to evaluate morphological and dimensional characteristics specific for each crop including the root system. Results showed the positive effect of raised beds, especially for transplanted crops (lettuce and zucchini), which increased yield by more than 15% in the first case. Direct sown crops were more variable. Positive results for raised bed were recorded for rocket salad, with a weight gain of the aerial part higher than 50%; whereas green bean did not respond significantly to soil tillage. The tillage effect was also significant on root system dimensions that, in the case of beds, was generally higher compared to the flat soil.

Keywords: Chard; Chicory; Green bean; Lettuce; Rocket salad; Root; Soil tillage; Zucchini

Acta Horticulturae

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Nano to macro pore structure changes induced by long-term residue management in three different soils

Pituello, C., Dal Ferro, N., Simonetti, G., Berti, A., Morari, F.

Dipartimento di Agronomia, Animali, Alimenti, Risorse Naturali e Ambiente, Viale dell'Università 16, Padova, Italy

Abstract

The use of crop residues for bioenergy production has gathered much attention in recent years. For this reason, the potential detrimental effects on soil quality caused by their removal need to be carefully evaluated before this practice becomes widely used. Data from a long-term field experiment on residue management in three contrasting soils (clay, sandy-loam and sandy) were analysed in order to understand crop residue effects on soil organic carbon stocks. In addition, since soil structure is known to be a sensitive descriptor of soil quality, different techniques were combined to investigate a wide range of pore sizes (from 0.25 nm to 2.5 mm) and pore morphology.Forty-three years of crop residue incorporation led to a significant increase in the organic carbon content of the three soils. The clay and sandy-loam soils were the most effective in retaining organic carbon as they exhibited the highest absolute increases. The sandy soil showed a residue-induced increase in organic carbon content, indicating that some protection mechanisms may act in the long term even in soils with a scarce ability to protect organic carbon from degradation. Residues modified the soil structure, inducing an increase in total pore volume as measured by the core method, although their effect was not found in all pore size classes. Residues decreased mesoporosity (30-75 m), while their effect on macropores (>75. m) was in terms of shape, increasing the irregular and elongated pores rather than their size frequency. The results thus showed a limited overall effect of residues on soil structure. However, even minor pore network changes could affect other important soil properties such as water movement, solute transport and gas exchanges.

Keywords: Long-term experiment; Soil organic carbon; Soil pore architecture; X-ray microtomography

Agriculture, Ecosystems and Environment

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Outcomes from a long-term study on crop residue effects on plant yield and nitrogen use efficiency in contrasting soils

Pituello, C., Polese, R., Morari, F., Berti, A.

Dipartimento di Agronomia, Animali, Alimenti, Risorse Naturali e Ambiente, Viale dell'Università 16, Padova, Italy

Abstract

The use of crop residues to increase crop yield and NUE is still a matter of debate since studies in different climates and soil types have led to inconclusive results and this could be partly explained by the numerous and complex factors that affect the residue-derived N cycle in field conditions. Given this complexity, long-term field experiments appear to be the more suitable tools to investigate these dynamics and develop effective management practices. In this paper, we hypothesized that residue incorporation affects crop yield and NUE, both through a direct nutritional effect given by residue decomposition and an indirect influence on soil physical and biological properties related to the input of organic carbon. We used data from a long-term field experiment started in 1970 in North-eastern Italy to evaluate the effects of crop residue incorporation on the productivity and nitrogen use efficiency of different crops (i.e., maize, winter wheat, sugarbeet, tomato and potato) in three contrasting soil types: a Fluvi-Calcaric Cambisol, a Gleyi-Vertic Chernozem and a Calcaric Arenosol. The results showed that incorporation of residues seems to have different effects depending on crop and soil type. For potato and tomato and, to a lesser extent, for sugarbeet, residues can improve crop productivity, while the effects on cereals seem to be lower. Regarding soil type, residues are proportionally more effective in sandy and sandy-loam soils, both through a direct nutritional effect and, possibly, an improvement of soil characteristics. Anyway the residue effect is relatively low, with modest increments of biomass in the most fertile soils and their effect can be compensated by N fertilization. The use of residues as organic amendment or their re-use in other processes (e.g., as a source of bioenergy) therefore has to be carefully analysed considering both the energy and C balances and the positive effects on soil productivity.

Keywords: Crop residues; Crop yield; Field experiments; Long-term; Nitrogen use efficiency

European Journal of Agronomy

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Seasonal changes in carbohydrate and protein content of seeded bermudagrasses and their effect on spring green-up

Schiavon, M.[a], Macolino, S.[a], Leinauer, B.[b], Ziliotto, U.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals, and Environment, University of Padova, Legnaro (PD), Italy
[b] Department of Extension Plant Sciences, New Mexico State University, LasCruces, NM, United States

Abstract

The widespread use of warm-season turfgrasses in transition zones of Europe, such as northern Italy, has been hampered by the long dormancy periods. To encourage the conversion from cool- to warm-season grasses, research is needed to identify cultivars that exhibit early spring green-up. A 2-year study was conducted at the agricultural experimental farm of Padova University from November 2006 to October 2008 to compare water-soluble carbohydrate and protein content in stolons of four bermudagrass [*Cynodon dactylon* (L.) Pers.] cultivars and determine their effect on spring green-up. Samples of 'La Paloma', 'NuMex Sahara', 'Princess 77' and 'Yukon' were collected monthly, and water-soluble carbohydrates (WSC) and crude protein (CP) content of stolons were measured. Dry weight values of WSC and CP for each cultivar were regressed against days needed to reach 80 % green cover in spring (D80). 'Yukon' exhibited the highest rhizome dry weight and WSC content during the winter months and was the fastest to reach 80 % green cover. Conversely, 'Princess 77' was the slowest cultivar to green-up in both years. Regression analysis revealed a stronger relationship between D80 and WSC than between CP content and D80.

Keywords: Crude protein; Days to reach 80% green cover; Transition zone; Warm-season grasses; Water-soluble carbohydrates

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On the spatial variability of soil hydraulic properties in a Holocene coastal farmland

Bevington, J.[ab]*, Piragnolo, D.*[b]*, Teatini, P.*[c]*, Vellidis, G.*[d]*, Morari, F.*[b]

[a] College of Engineering, University of Georgia, Athens, GA, United States
[b] Dipartimento Agronomia Animali Alimenti Risorse Naturali e Ambiente, Agripolis, Universitá Di Padova, Viale Dell'Università, Legnaro, Pd, Italy
[c] Dipartimento di Ingegneria Civile, Edile e Ambientale, Universitá Di Padova, Via Marzolo, Padova, Italy
[d] Department of Crop and Soil Sciences, University of Georgia, Tifton, GA, United States

Abstract

Understanding water movement in the vadose zone is critical for accurate climate and crop modeling, precision agriculture, soil-atmosphere gas exchanges, and contamination mitigation. A major reason for the difficulty of performing effective hydraulic measurements is because they are scale dependent due to the inherent heterogeneity of the soil. A better understanding of the spatial variability and underlying processes responsible for this variability could lead to a more accurate modeling. The goal of this study is to investigate the scale dependencies of soil hydraulic properties. Factorial kriging analysis (FKA) is a geostatistical technique which identifies scale dependent spatial relationships and common sources of variability. FKA was applied on a number of soil properties acquired from samples collected at 4 depths ranging from 8 to 68. cm in a 20.8. ha field in the Po River delta. The farmland is characterized by the presence of paleo-channel structures and highly heterogeneous soil. Texture, bulk density, K_s (saturated hydraulic conductivity), and the van Genuchten-Mualem parameters α (inverse of air entry), n (shape parameter), θ_r (residual water content), and θ_s (saturated water content) were included in the analysis. Two nested spherical models with ranges around 105. m and 235. m plus nugget fit the experimental variograms and cross-variograms best. Regionalized correlation coefficients and regionalized PCA revealed many strong, scale dependent relationships which were not obvious from descriptive statistics, such as the effect of interaction between texture and bulk density on n and K_s, and the stronger influence of bulk density than texture on Ks. The first principal components (PCs) of the regionalized PCA explained the majority of the variability and the second PCs were rarely informative. The spatial distributions of the first PCs resembled bulk density at short scale and the paleo-channels and texture at long scale. The decoupling of bulk density and texture is likely caused by differences in soil structure. The influence of the short scale PCs is greater than the long scale PCs near the surface but becomes less important as depth increases. This suggests that depth plays an important role and should be considered more often in spatial analysis.

Keywords: Factorial kriging analysis; Mualem model; Pedotransfer function; Spatial variability; Unsaturated hydraulic conductivity; Van Genuchten model; Water retention curve

Geoderma

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Performance of various cool-season turfgrasses as influenced by simulated traffic in northeastern Italy

Pornaro, C.[a], Barolo, E.[b], Rimi, F.[ac], Macolino, S.[a], Richardson, M.[d]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Italy
[b] Agricultural Research Council (CRA SCS), Verona, Italy
[c] Sakata Seed America Inc., Morgan Hill, CA, United States
[d] Department of Horticulture, University of Arkansas, Fayetteville, AR, United States

Abstract

Warm-season grasses are known to be more wear tolerant than cool-season grasses, but in northern Italy the latter are generally preferred for ornamental turfgrasses and athletics fields. The Po River valley, in the North of Italy, is a typical transition zone where species and cultivar selection play a very important role in establishing successful turfgrasses with high stress tolerance, including foot traffic. The aim of this research was to evaluate the traffic tolerance and adaptation of 25 cultivars of three coolseason turfgrass species to transitional growing conditions of Italy. A study was conducted over a two-year period at the experimental farm of Padova University in Legnaro. The species studied were tall fescue (*Lolium arundinaceum*), kentucky bluegrass (*Poa pratensis*), and perennial ryegrass (*Lolium perenne*). Simulated traffic was applied using a Brinkman traffic simulator at a level equivalent to one soccer game per week. Turfgrass quality and density were assessed every week using a 1 to 9 visual scale during traffic treatments each year. Furthermore, turfgrass canopy height was measured weekly for calculating daily vertical growth rate (mm d-1) in spring, summer, and autumn. Trafficked plots exhibited lower quality than nontrafficked, primarily as a result of decline in turf density. The effect of traffic on density was more evident in the second year wherein all species exhibited ratings lower than 5.0. Traffic did not affect turf growth for perennial ryegrass and tall fescue, while a drastic decrease in growth rate in the second year of study was observed for kentucky bluegrass. Perennial ryegrass had lower density than tall fescue and kentucky bluegrass, especially in summer and autumn of the first year when it showed ratings lower than 6.0. Different responses occurred among kentucky bluegrass cultivars, while perennial ryegrass and tall fescue cultivars responded similarly. Results indicated a high quality and environmental adaptability of 'Rhambler SRP' tall fescue. Among kentucky bluegrass cultivars, 'Mystere' displayed the best wear tolerance with a decrease of density from 5.5 to 4.3 only during the second year. Perennial ryegrass cultivars were similarly affected by traffic, except for 'Yorktown III' which showed the lower performance in both traffic and non-traffic conditions reaching a turf density rating lower than 5.0 in both years of study.

Keywords: Cultivar; Transition zone; Turf density; Turf quality; Turf vertical growth; Wear tolerance

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Sorghum biomass production for energy purpose using treated urban wastewater and different fertilization in a mediterranean environment

Maucieri, C.[ab], Cavallaro, V.[c], Caruso, C.[ab], Borin, M.[b], Milani, M.[a], Barbera, A.C.[a]

[a] Department of Agriculture, Food and Environment (Di3A), University of Catania, Via Valdisavoia 5, Catania, Italy
[b] Department of Agronomy, Food, Natural Resources, Animals and Environment, DAFNAE, University of Padua, Agripolis Campus, Viale dell'Università 16, 35020 Legnaro, Italy
[c] Consiglio Nazionale delle Ricerche-Istituto per la Valorizzazione del Legno e delle Specie Arboree (IVALSA), Via Gaifami 18, 95123 Catania, Italy

Abstract

With the aim at enhancing the sustainability of biomass production in the Mediterranean area, this paper analyzes, for the first time, the production of sorghum (*Sorghum bicolor* (L.) Moench) biomass for bioenergy production using urban treated wastewaters and bio-fertilization. For this purpose, the effects on biomass production of three different fertilizations (no-nitrogen control, biofertilizer, and mineral ammonium nitrate), four levels of constructed wetland (CW) wastewater restitutions (0%, 33%, 66% and 100%) of crop evapotranspiration (ETc) and three harvesting dates (at full plant maturity, at the initial senescence stage, and at the post-senescence stage) were evaluated in a two year trial. For bio-fertilization, a commercial product based on arbuscular mycorrhizal fungi was used. Mineral nitrogen (N) fertilization significantly increased dry biomass (+22.8% in the first year and +16.8% in the second year) compared to the control (95.9 and 188.2 g plant^{-1}, respectively). The lowest and highest biomass production, in 2008 and 2009, was found at 0% (67.1 and 118.2 g plant^{-1}) and 100% (139.2 and 297.4 g plant^{-1}) ETc restitutions. In both years, the first harvest gave the highest biomass yield (124.3 g plant^{-1} in the first year and 321.3 g plant^{-1} in the second), followed by the second and the third one. The results showed that in Mediterranean areas, constructed wetlands treated wastewaters, when complying with the European restrictions for their use in agriculture, may represent an important tool to enhance and stabilize the biomass of energy crops by recycling scarce quality water and nutrients otherwise lost in the environment.

Keywords: Arbuscular mycorrhizal fungi; Biomass production; Constructed wetland; Sorghum bicolor (L.) Moench; Wastewater

Agriculture (Switzerland)

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Crambe abyssinica a non-food crop with potential for the Mediterranean climate: Insights on productive performances and root growth

Zanetti, F.[a], Scordia, D.[b], Vamerali, T.[c], Copani, V.[b], Dal Cortivo, C.[c], Mosca, G.[c]

[a] DipSA-Department of Agricultural Sciences, University of Bologna, Viale G. Fanin 44, Bologna, Italy
[b] Di3A-Dipartimento di Agricoltura, Alimentazione e Ambiente, University of Catania, Via Valdisavoia 5, Catania, Italy
[c] DAFNAE-Department of Agronomy, Food, Natural Resources, Animals and the Environment, University of Padova, Viale dell'Università 16, Legnaro, Padova, Italy

Abstract

Within a framework of renewed interest in crambe (*Crambe abyssinica* Hochst ex R.E. Fries) sourcing raw materials for the bio-based industry, the adaptability and productive performances of this oil crop have been evaluated under contrasting Mediterranean environments (i.e., a fertile site in the northern part of Po valley vs. a semi-arid site of southern Sicily) during two consecutive growing seasons, aiming at its possible stable introduction in this area. The trial set in northern Italy compared three commercial varieties of crambe (Galactica, Nebula and Mario) in spring sowing, while in southern Italy only the var. Mario was tested with autumn sowing. Regardless of location and variety, thermal time for maturity was quite stable (1200–1400 °C), and the crop provided satisfactory seed yields (grand mean 2.29 Mg hulled seeds ha^{-1}), with average oil content of ~400 g kg^{-1} (on dehulled seeds) and ~52% of erucic acid. Significantly higher seed and oil yields were reached in northern than in southern Italy. Furthermore, crambe thermal use efficiency (THUE) was also higher in the north than in the south, possibly due to better environmental adaptability of the crop. The limited intraspecific variability within crambe was confirmed, with better productive performances showed by the domestic selection Mario. Promising traits were revealed in Nebula, showing greater seed weight, root length density and area, and thinner roots, although the root growth of crambe was generally modest compared with modern high erucic acid rapeseed hybrids. Available crambe varieties could be efficiently included in crop rotations across a wide range of environments within the Mediterranean basin. The short growth cycle represents an outstanding added value for this species, allowing the avoidance of prolonged drought and heat stress typical of late spring/early summer months under the Mediterranean climate. However, increased yields are needed to meet the market requests; nonetheless, the little genetic variability suggests that there is large scope for future breeding improvements, maybe exploiting advanced techniques to improve the existing genetic resources.

Keywords: Industrial oils; Mediterranean environments; Root length density; Thermal time; THUE; Yield potential

Industrial Crops and Products

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Barcoding *Eophila crodabepis* sp. nov. (Annelida, Oligochaeta, Lumbricidae), a large stripy earthworm from alpine foothills of northeastern Italy similar to *Eophila tellinii* (Rosa, 1888)

Paoletti, M.G.[a], Blakemore, R.J.[b], Csuzdi, C.[c], Dorigo, L.[d], Dreon, A.L.[a], Gavinelli, F.[a], Lazzarini, F.[a], Manno, N.[a], Moretto, E.[e], Porco, D.[f], Ruzzier, E.[g], Toniello, V.[h], Squartini, A.[i], Concheri, G.[i], Zanardo, M.[i], Alba-Tercedor, J.[l]

[a] Università degli Studi di Padova, Dipartimento di Biologia, Padova, Italy
[b] Hanyang University, College of Natural Science, Seoul, South Korea
[c] Eszterházy Károly College, Department of Zoology, Eger, Hungary
[d] Museo Friulano di Storia Naturale, Udine, Italy
[e] ESAPOLIS, Padova, Italy
[f] Université de Rouen, Laboratoire ECODIV, Mont Saint Aignan Cedex, France
[g] Natural History Museum, Department of Life Science, London, United Kingdom
[h] Federazione Speleologica Veneta-G.S. C.A.I., Laboratorio di Biospeleologia di Villa Papadopoli, Vittorio Veneto, Italy
[i] Università degli Studi di Padova, Dipartimento di Agronomia, Animali, Alimenti, Risorse Naturali e Ambiente, DAFNAE, Padova, Italy
[l] Universidad de Granada, Departamento de Zoología, Facultad de Ciencias, Granada, Spain

Abstract

A new Italian earthworm morphologically close to the similarly large and anecic *Eophila tellinii* (Rosa, 1888) is described. Distribution of *Eophila crodabepis* sp. nov. extends over 750 km^2 from East to West on the Asiago Plateau and Vittorio Veneto Hills, from North to South on mounts Belluno Prealps (Praderadego and Cesen), Asiago, Grappa and onto the Montello foothills. This range abuts that of Eophila tellinii in northern Friuli Venezia Giulia region. Known localities of both *E. tellinii* and *E. crodabepis* sp. nov. are mapped. mtDNA barcoding definitively separates the new western species from classical *Eophila tellinii* (Rosa, 1888).

PLoS ONE

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Assessment of the natural endophytic association between *Rhizobium* and wheat and its ability to increase wheat production in the Nile delta

Yanni, Y.G.[a], Dazzo, F.B.[b], Squartini, A.[c], Zanardo, M.[c], Zidan, M.I.[d], Elsadany, A.E.Y.[a]

[a] Department of Microbiology, Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt
[b] Department of Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI, United States
[c] Department of Agronomy, Food, Animals, Natural Resources and Environment DAFNAE, University of Padova, Viale dell'Universita' 16, Legnaro, Italy
[d] Department of Plant NutritionSakha Agricultural Research Station, Kafr El-Sheikh, Egypt

Abstract

Aim of the research: This study examined whether rhizobia naturally associate with wheat (*Triticum aestivum*) and can enhance its production. Methods: Field-grown, surface-sterilized, macerated wheat roots were inoculated on legume roots to isolate rhizobial endophytes. Nodule occupants were purified, genotypically differentiated, and tested gnotobiotically for legume symbiotic effectiveness and wheat growth-promotion. Biofertilizer performance of 13 selected strains was evaluated on 8 wheat varieties in 24 field experiments in 10 counties of the Kafr El-Sheikh governorate in the Egypt Nile delta. Results: Only inoculated clover (*Trifolium alexandrinum*) produced root nodules hosting *Rhizobium leguminosarum* bv. trifolii. Some were symbiotically effective on clover and promoted wheat growth under gnotobiotic conditions. Inoculation significantly increased wheat grain yield in 21, 23, and 20 field experiments under N-application of 60, 120, and 180 kg N/ha, respectively, with corresponding increases of 9.2, 18.9, and 22.5% higher grain yield over the mean of farmers' yields using the same varieties in adjacent fields. Unlike the harvest indices, straw yield and agronomic fertilizer N-use efficiency benefitted from inoculation. Rhizobial mixed-strain inocula frequently outperformed single-strain inocula. Inoculation did not adversely affect endomycorrhizal infection of field-grown wheat roots. Conclusion: Rhizobium naturally develops an endophytic association with wheat. Selected biofertilizer strains can enhance wheat production with acceptable input/output economy.

Keywords: Biofertilizer; Endophyte; Plant growth-promoting rhizobacterium; Rhizobium; Wheat

Plant and Soil

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Dynamics of soil prokaryotes catalyzing nitrification and denitrification in response to different fertilizers in a greenhouse experiment with *Cynodon dactylon*

Zanardo, M.[a], Rosselli, R.[b], Meneghesso, A.[c], Sablok, G.[d], Stevanato, P.[a], Altissimo, A.[e], Perserico, L.[e], Dezuani, V.[e], Concheri, G.[a], Schloter, M.[f], Squartini, A.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment – DAFNAE, University of Padova, Viale dell'Università 16, Legnaro, PD, Italy
[b] División de Microbiología, Universidad Miguel Hernández, Apartado 18, San Juan de Alicante, Alicante, Spain
[c] Department of Biology, University of Padova, Viale G. Colombo 3, Padova, Italy
[d] Plant Functional Biology and Climate Change Cluster (C3), University of Technology, PO Box 123 Broadway, Sydney, NSW, Australi
[e] Landlab Studio Associato, Via Quintarello 12A, Quinto Vicentino, VI, Italy
[f] Research Unit for Environmental Genomics, Helmholtz Zentrum München, Ingolstädter Landstraße 1, Neuherberg, Germany

Abstract

Organic fertilizers are of high interest in agriculture as they promise a retarded release of the nitrogen to soil, which improves uptake efficiency by plants and reduces negative impacts like the formation of nitrate by nitrifiers or N_2O by denitrifying microorganisms. In this study we tested the effects of seven different commercially available organic fertilizers of plant-, animal-, or microbial origin in a two-month greenhouse trial, using the perennial grass *Cynodon dactylon* in pots and monitoring effects on plant growth as well as on the abundance of prokaryotic nitrifiers and denitrifiers by realtime PCR. In most cases a single application of the fertilizers induced plant growth but did not increase the abundance of nitrifiers and denitrifiers. In contrast a repeated application stimulated, in addition to plant growth, also the increase of the two functional groups studied and a faster mobilization of nitrogen from the different fertilizers. Upon analyzing total bacterial DNA extracted from soil *nirK* abundance was found responsive to plant presence. Bacterial *amoA* and *nosZ* gene copies were significantly positively correlated with plant growth and cumulative dry weight at harvest. The latter was responsive as early as 9 days after fertilizer supplementation.

Keywords: Crop yield; *Cynodon dactylon*; Denitrification; Nitrification; Organic fertilization; Real Time PCR

European Journal of Soil Biology

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Sugar beet yield and processing quality in relation to nitrogen content and microbiological diversity of deep soil layer

Stevanato, P., Squartini, A., Concheri, G., Saccomani, M.

DAFNAE, Dipartimento di Agronomia Animali Alimenti Risorse Naturali e Ambiente,
Università degli Studi di Padova, viale dell'Università 16, Legnaro, PD, Italy

Abstract

The aim of this study was to estimate the effects of different soil factors on sugar beet yield and processing quality. The parameters investigated included: (i) nitrogen (N) availability; (ii) overall microbial diversity and (iii) abundance of bacterial genes involved in key functions of the N cycle. These traits have been evaluated throughout the entire soil layer (0–2.5 m) explored by the sugar beet root system. Soil samples were taken from two nearby sites (A and B) in the Eastern Po Valley, Italy. At each site, three soil profiles were sampled every 0.5 m and the main soil physical and chemical characteristics were evaluated. ARISA (Amplified Ribosomal Intergenic Spacer Analysis) and Real Time PCR analyses were performed on genomic DNA extracted from soil samples for the estimation of microbial diversity and the quantitative presence of genes for ammonium monooxygenase (*amoA-Archaea*) and nitrite reductase (*nirK*). To assess the root length density, observations were made by means of minirhizotrons. At site B profile, organic matter as high as 13 % and min-N around 28 mg kg^{-1} were found between 2 and 2.5 m depth. Sugar beets harvested at this site showed less sugar content and processing quality than at site A (soil similar to B but without deep N accumulation). Soil collected below 0.5 m displayed a more species-rich composition of microbial communities than in the upper layer. The presence of *amoA* (nitrification) and *nirK* (denitrification) genes was found in all layers explored (down to a depth of 2.5 m). These findings highlight the contribution of the deep layers to key processes of the soil N cycle and its availability for deep-rooted crops. The usefulness of sampling soil to the depth reached by the roots to assess N fertilizer requirements is discussed.

Keywords: Microbial diversity; Nitrogen; Processing quality; Soil fertility; Sugar beet yield

Sugar Tech

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The Pignola-Abriola section (southern Apennines, Italy): a new GSSP candidate for the base of the Rhaetian Stage

Rigo, M.[a], Bertinelli, A.[c], Concheri, G.[d], Gattolin, G.[ae], Godfrey, L.[g], Katz, M.E.[g], Maron, M.[a], Mietto, P.[a], Muttoni, G.[h], Sproviери, M.[i], Stellin, F.[d], Zaffani, M.[a]

[a] Department of Geosciences, University of Padova, via Gradenigo 6, Padova, Italy
[b] IGG-CNR, Via G Gradenigo 6, Padova, Italy
[c] Department of Physics and Geology, University of Perugia, via Pascoli, Perugia, Italy
[d] Department of Agronomy Food Natural Resources Animals and Environment, University of Padova, Viale dell'Università 16, Legnaro, Padova, Italy
[e] ENI E&P division, via Emilia 1, San Donato Milanese, Italy
[f] Department Earth and Planetary Sciences, Rutgers University, Piscataway, NJ, United States
[g] Department of Earth and Environmental Sciences, Rensselaer Polytechnic Institute, 110 8th St., Troy, NY, United States
[h] Department of Earth Sciences 'Ardito Desio', University of Milano, via Mangiagalli 34, Milan, Italy
[i] IAMC-CNR, Via del Mare 3, Torretta Granitola, Trapani, Italy

Abstract

The base of the Rhaetian stage (Norian/Rhaetian boundary, NRB) is still awaiting formal designation by the International Commission on Stratigraphy. At present, only the 4.30-m-thick Steinbergkogel section (Austria) has been proposed as GSSP (Global Stratotype Section and Point) candidate for the base of the Rhaetian. Here we present data from the 63-m-thick Pignola-Abriola section (Southern Apennines, Italy) that we consider an alternative candidate for the Rhaetian GSSP. The Pignola-Abriola basinal section, represented by hemipelagic–pelagic carbonate successions belonging to the Lagonegro Basin, matches all the requirements for a GSSP: 1, it is well exposed with minimal structural deformation; 2, it is rich in age diagnostic fossils (e.g. conodonts and radiolarians); 3, it yields a geochemical record suitable for correlation (e.g. $\delta^{13}C_{org/carb}$); and 4, it has a robust magnetostratigraphy and is correlated with the Newark APTS for age approximation of the NRB and additional Rhaetian bioevents. In the Pignola-Abriola section, we opt to place the NRB at the 44.4 metre level, coincident with a prominent negative shift of ca. 6‰ of the $\delta^{13}C_{org}$. This level is located 50 cm below the FAD of conodont *Misikella posthernsteini* s.s within the radiolarian *Proparvicingula moniliformis* Zone. Both the negative δ13Corg shift and the FAD of *Misikella posthernsteini* occur within Pignola-Abriola magnetozone MPA-5r, at ~205.7 Ma, according to magnetostratigraphical correlation to the Newark APTS. We also illustrate the coeval Mt. Volturino stratigraphical section deposited below the calcite compensation depth (CCD) within the same Lagonegro Basin and characterized by a detailed radiolarian biostratigraphy and strong $\delta^{13}C_{org}$ negative shift around the NRB.

Keywords: Conodonts; GSSP; Late Triassic; Magnetostratigraphy; Radiolarians; Rhaetian; Stable isotopes

Lethaia

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Animal science

Influence of main dietary chemical constituents on the *in vitro* gas and methane production in diets for dairy cows

Maccarana, L.[a], Cattani, M.[a], Tagliapietra, F.[b], Bailoni, L.[a], Schiavon, S.[b]

[a] Department of Comparative Biomedicine and Food Science (BCA), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy
[b] Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), Viale dell'Università 16, 35020 Legnaro (PD), Italy

Abstract

Background: Modification of chemical composition of diets fed to dairy cows might be a good strategy to reduce methane (CH_4) production in the rumen. Notable reductions of CH_4 production compared to conventional high-roughages rations were more frequently observed for very concentrated diets or when fat supplements were used. In these cases, the reduction in the gas emission was mainly a consequence of an overall impairment of rumen function with a reduction of fiber digestibility. These strategies do not always comply with feeding standards used in intensive dairy farms and they are usually not applied owing to the risks of negative health and economic consequences. Thus, the present study evaluated the effects of seven commercial diets with contents of neutral detergent fiber (NDF), protein and lipids ranging 325 to 435 g/kg DM, 115 to 194 g/kg DM, and 26 to 61 g/kg DM, respectively, on *in vitro* degradability, gas (GP), and CH_4 production.

Results: In this experiment, changes in the dietary content of NDF, crude protein (CP) and lipids were always obtained at the expense or in favor of starch. A decreased of the dietary NDF content increased NDF (NDFd) and true DM (TDMd) degradability, and increased CH_4 production per g of incubated DM ($P < 0.001$), but not that per g of TDMd. An increase of the dietary CP level did not change in vitro NDFd and TDMd, decreased GP per g of incubated DM ($P < 0.001$), but CH_4 production per g of TDMd was not affected. An increased dietary lipid content reduced NDFd, TDMd, and GP per g of incubated DM, but it had no consequence on CH_4 production per g of TDMd.

Conclusions: It was concluded that, under commercial conditions, changes in dietary composition would produce small or negligible alterations of CH_4 production per unit of TDMd, but greater differences in GP and CH_4 production would be expected when these amounts are expressed per unit of DM intake. The use of TDMd as a standardizing parameter is proposed to account for possible difference in DM intake and productivity.

Keywords: Dairy cows; Dietary manipulation; Gas production; *In vitro* techniques; Methane production

Journal of Animal Science and Biotechnology

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A preliminary investigation of the role of the transcription co-activators YAP/TAZ of the Hippo signalling pathway in canine and feline mammary tumours

Beffagna, G.[a], Sacchetto, R.[a], Cavicchioli, L.[a], Sammarco, A.[a], Mainenti, M.[a], Ferro, S.[a], Trez, D.[a], Zulpo, M.[a], Michieletto, S.[b], Cecchinato, A.[c], Goldschmidt, M.[d], Zappulli, V.[a]

[a] Department of Comparative Biomedicine and Food Science, University of Padua, Viale dell'Università 16, 35020 Legnaro (PD), Italy
[b] Breast Surgery Unit, Veneto Institute of Oncology IOV - IRCCS, Via Gattamelata 64, 35128 Padua, Italy
[c] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy
[d] Laboratory of Pathology and Toxicology, Department of Pathobiology, University of Pennsylvania, 3900 Delancy Street, Philadelphia, PA 19104, USA

Abstract

Breast cancer is the most common cancer in women worldwide. Cancer metastases are responsible for the high mortality rate. A small but distinct subset of cells, cancer stem cells (CSCs), have the capacity to self-renew, initiate tumour formation, and develop metastases. The CSC content in human breast cancer correlates with the Hippo tumour suppressor signalling pathway. Specifically, the activity of YAP/TAZ, transcription co-activators of the Hippo pathway, sustains the self-renewal and tumour-initiation capacities of CSCs. Little is known about YAP/TAZ in canine and feline mammary tumours, which are very common tumours. The preliminary aim of the study was to investigate the expression of YAP/TAZ in canine and feline mammary tumours by Western blot and immunohistochemistry. Increased cytoplasmic and nuclear expression of YAP/TAZ was observed in all carcinomas compared to normal tissues, indicating neoplastic deregulation of the Hippo pathway. Nuclear expression significantly increased in grade III (high grade carcinomas) compared to grade I (low grade carcinomas) tumours, suggesting that YAP/TAZ play a role in the increased aggressiveness of these tumours. Moreover, different scoring systems for immunohistochemical analyses were compared and the H index and the Allred scores were the most significant. In conclusion, YAP/TAZ are expressed in aggressive canine and feline mammary tumours as reported in some human cancers. Further studies might better elucidate the role of the Hippo pathway in prognosis and as a target for new therapies. In addition, tumours in dogs and cats may be a useful model to study this pathway.

Keywords: Cancer stem cells; Immunohistochemistry; Mammary tumours; Scoring systems; Western blot

Veterinary Journal

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Environmental, morphological, and productive characterization of Sardinian goats and use of latent explanatory factors for population analysis

Vacca, G.M.[a], Paschino, P.[a], Dettori, M.L.[a], Bergamaschi, M.[b], Cipolat-Gotet, C.[b], Bittante, G.[b], Pazzola, M.[a]

[a] Department of Veterinary Medicine, University of Sassari, via Vienna, 2, 07100, Sassari, Italy
[b] Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, viale dell'Università, 16, 35020 Legnaro (PD), Italy

Abstract

Dairy goat farming is practiced worldwide, within a range of different farming systems. Here we investigated the effects of environmental factors and morphology on milk traits of the Sardinian goat population. Sardinian goats are currently reared in Sardinia (Italy) in a low-input context, similar to many goat farming systems, especially in developing countries. Milk and morphological traits from 1,050 Sardinian goats from 42 farms were recorded. We observed a high variability regarding morphological traits, such as coat color, ear length and direction, horn presence, and udder shape. Such variability derived partly from the unplanned repeated crossbreeding of the native Sardinian goats with exotic breeds, especially Maltese goats. The farms located in the mountains were characterized by the traditional farming system and the lowest percentage of crossbred goats. Explanatory factors analysis was used to summarize the interrelated measured milk variables. The explanatory factor related to fat, protein, and energy content of milk (the "Quality" latent variable) explained about 30% of the variance of the whole data set of measured milk traits followed by the "Hygiene" (19%), "Production" (19%), and "Acidity" (11%) factors. The "Quality" and "Hygiene" factors were not affected by any of the farm classification items, whereas "Production" and "Acidity" were affected only by altitude and size of herds, respectively, indicating the adaptation of the local goat population to different environmental conditions. The use of latent explanatory factor analysis allowed us to clearly explain the large variability of milk traits, revealing that the Sardinian goat population cannot be divided into subpopulations based on milk attitude. The factors, properly integrated with genetic data, may be useful tools in future selection programs.

Keywords: Autochthonous goat; Crossbreeding; Milk traits; Morphological traits

Journal of Animal Science

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Methodological factors affecting gas and methane production during in vitro rumen fermentation evaluated by meta-analysis approach

Maccarana, L.[a]*, Cattani, M.*[a]*, Tagliapietra, F.*[b]*, Schiavon, S.*[b]*, Bailoni, L.*[a]*,*
Mantovani, R.[b]

[a] Department of Comparative Biomedicine and Food Science (BCA), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy
[b] Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy

Abstract

Effects of some methodological factors on in vitro measures of gas production (GP, mL/g DM), CH_4 production (mL/g DM) and proportion (% CH_4 on total GP) were investigated by meta-analysis. These factors were considered: pressure in the GP equipment (0 = constant; 1 = increasing), incubation time (0 = 24; 1 ≥ 48 h), time of rumen fluid collection (0 = before feeding; 1 = after feeding of donor animals), donor species of rumen fluid (0 = sheep; 1 = bovine), presence of N in the buffer solution (0 = presence; 1 = absence), and ratio between amount of buffered rumen fluid and feed sample (BRF/FS; 0 = ≤ 130 mL/g DM; 1 = 130-140 mL/g DM; 2 = ≥ 140 mL/g DM). The NDF content of feed sample incubated (NDF) was considered as a continuous variable. From an initial database of 105 papers, 58 were discarded because one of the above-mentioned factors was not stated. After discarding 17 papers, the final dataset comprised 30 papers (339 observations). A preliminary mixed model analysis was carried out on experimental data considering the study as random factor. Variables adjusted for study effect were analyzed using a backward stepwise analysis including the above-mentioned variables. The analysis showed that the extension of incubation time and reduction of NDF increased GP and CH_4 values. Values of GP and CH_4 also increased when rumen fluid was collected after feeding compared to before feeding (+26.4 and +9.0 mL/g DM, for GP and CH_4), from bovine compared to sheep (+32.8 and +5.2 mL/g DM, for GP and CH_4), and when the buffer solution did not contain N (+24.7 and +6.7 mL/g DM for GP and CH_4). The increase of BRF/FS ratio enhanced GP and CH_4 production (+7.7 and +3.3 mL/g DM per each class of increase, respectively). In vitro techniques for measuring GP and CH_4 production are mostly used as screening methods, thus a full standardization of such techniques is not feasible. However, a greater harmonization of analytical procedures (i.e., a reduction in the number of available protocols) would be useful to facilitate comparison between results of different experiments.

Keywords: Experimental factors; Gas production; In vitro rumen fermentation, Meta-analysis, Methane production

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Effect of progressive reduction in crude protein and lysine of heavy pigs diets on some technological properties of green hams destined for PDO dry-cured ham production

Gallo, L.[a], *Dalla Bona, M.*[a], *Carraro, L.*[a], *Cecchinato, A.*[a], *Carnier, P.*[b], *Schiavon, S.*[a]

[a] Department of Agronomy Food Natural resources Animals and Environment,
University of Padova, Viale Università 16, 35020 Legnaro, PD, Italy
[b] Department of Comparative Biomedicine and Food Science, University of Padova,
Viale Università 16, Legnaro, PD, Italy

Abstract

In order to investigate the effects of dietary crude protein (CP) and lysine (Lys) content on some technological properties of green hams destined for Protected Designation of Origin (PDO) dry-cured ham, green hams visual appraisal scores, thickness, iodine number and fatty acid composition of subcutaneous fat, and ham weight losses during seasoning (SL) were assessed. The green hams were obtained from 233 pigs fed four diets containing 140 to 110 g/kg CP and 6.5 to 5.3 g/kg total Lys from 90 to 165 kg body weight. A reduction in dietary CP and Lys of up to 20% compared with conventional feeds led to a 15% increase in the thickness of the subcutaneous fat, a 5% decrease in linoleic and polyunsaturated fatty acids in subcutaneous fat and a 7% decrease in SL. A 20% reduction of CP and Lys in diets for finishing pigs has positive effects on the technological properties of green hams destined for PDO dry-cured ham production.

Keywords: Dry-cured ham; Green ham properties; Low-protein diets; Pig

Meat Science

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Potential influence of herd and animal factors on the yield of cheese and recovery of components from Sarda sheep milk, as determined by a laboratory bench-top model cheese-making

Cipolat-Gotet, C.[a], Cecchinato, A.[a], Pazzola, M.[b], Dettori, M.L.[b], Bittante, G.[a], Vacca, G.M.[b]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro, PD, Italy
[b] Department of Veterinary Medicine, University of Sassari, Via Vienna 2, 07100 Sassari, Italy

Abstract

Individual milk samples from 169 Sarda sheep were collected to characterise the cheese-making potential through the use of a laboratory bench-top model cheese-manufacturing procedure. As the milk samples were not standardised before processing, the data collected at laboratory level fully reflected the great variability of milk from individual animals. The average cheese yield traits of fresh cheese, cheese dry matter and water retained in cheese (as percentages of the milk processed) were 20.6%, 10.1% and 10.6%. The average milk fat and protein recoveries in the curd were 94.0% and 76.7%, respectively. The values for daily production of curd and curd dry matter per sheep were 0.41 kg d^{-1} and 0.20 kg d^{-1}, respectively. The cheese yield and cheese-related traits were mainly affected by the nutrient content of the milk and the individual effects of the stage of lactation and daily milk yield, respectively, but also by a large individual variation.

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Variable selection procedures before partial least squares regression enhance the accuracy of milk fatty acid composition predicted by mid-infrared spectroscopy

Gottardo, P.[a], Penasa, M.[a], Lopez-Villalobos, N.[b], De Marchi, M.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy
[b] Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Private Bag 11 222, Palmerston North, 4442, New Zealand

Abstract

Mid-infrared spectroscopy is a high-throughput technique that allows the prediction of milk quality traits on a large-scale. The accuracy of prediction achievable using partial least squares (PLS) regression is usually high for fatty acids (FA) that are more abundant in milk, whereas it decreases for FA that are present in low concentrations. Two variable selection methods, uninformative variable elimination or a genetic algorithm combined with PLS regression, were used in the present study to investigate their effect on the accuracy of prediction equations for milk FA profile expressed either as a concentration on total identified FA or a concentration in milk. For FA expressed on total identified FA, the coefficient of determination of cross-validation from PLS alone was low (0.25) for the prediction of polyunsaturated FA and medium (0.70) for saturated FA. The coefficient of determination increased to 0.54 and 0.95 for polyunsaturated and saturated FA, respectively, when FA were expressed on a milk basis and using PLS alone. Both algorithms before PLS regression improved the accuracy of prediction for FA, especially for FA that are usually difficult to predict; for example, the improvement with respect to the PLS regression ranged from 9 to 80%. In general, FA were better predicted when their concentrations were expressed on a milk basis. These results might favor the use of prediction equations in the dairy industry for genetic purposes and payment system.

Keywords: Genetic algorithm; Mid-infrared spectroscopy; Milk fatty acid; Variable selection

Journal of Dairy Science

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Predictive ability of mid-infrared spectroscopy for major mineral composition and coagulation traits of bovine milk by using the uninformative variable selection algorithm

Visentin, G., Penasa, M., Gottardo, P., Cassandro, M., De Marchi, M.

Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy

Abstract

Milk minerals and coagulation properties are important for both consumers and processors, and they can aid in increasing milk added value. However, large-scale monitoring of these traits is hampered by expensive and time-consuming reference analyses. The objective of the present study was to develop prediction models for major mineral contents (Ca, K, Mg, Na, and P) and milk coagulation properties (MCP: rennet coagulation time, curd-firming time, and curd firmness) using mid-infrared spectroscopy. Individual milk samples (n = 923) of Holstein-Friesian, Brown Swiss, Alpine Grey, and Simmental cows were collected from single-breed herds between January and December 2014. Reference analysis for the determination of both mineral contents and MCP was undertaken with standardized methods. For each milk sample, the mid-infrared spectrum in the range from 900 to 5,000 cm^{-1} was stored. Prediction models were calibrated using partial least squares regression coupled with a wavenumber selection technique called uninformative variable elimination, to improve model accuracy, and validated both internally and externally. The average reduction of wavenumbers used in partial least squares regression was 80%, which was accompanied by an average increment of 20% of the explained variance in external validation. The proportion of explained variance in external validation was about 70% for P, K, Ca, and Mg, and it was lower (40%) for Na. Milk coagulation properties prediction models explained between 54% (rennet coagulation time) and 56% (curd-firming time) of the total variance in external validation. The ratio of standard deviation of each trait to the respective root mean square error of prediction, which is an indicator of the predictive ability of an equation, suggested that the developed models might be effective for screening and collection of milk minerals and coagulation properties at the population level. Although prediction equations were not accurate enough to be proposed for analytic purposes, mid-infrared spectroscopy predictions could be evaluated as phenotypic information to genetically improve milk minerals and MCP on a large scale.

Keywords: Dairy cattle; Mid-infrared spectroscopy; Milk coagulation property; Milk mineral

Journal of Dairy Science

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Role of coenzyme Q and vitamin E on stallion semen motility evaluated both in frozen and cooled-stored semen

Rossi, M.[a], Falomo, M.E.[a], Mantovani, R.[b]

[a] Dipartimento di Medicina Animale Produzioni e Salute, University of Padova, Padova, Italy
[b] Dipartimento di Agronomia Animali Alimenti Risorse Naturali e Ambiente, University of Padova, Padova, Italy

Abstract

Several studies reveal that coenzyme Q (CoQ) and vitamin E (Vit. E) act against oxidative deterioration, and that CoQ restores the active and antioxidant form of Vit. E. These two antioxidants, acting against lipid peroxidation, seem to be able to improve motility parameters of spermatozoa. The objective of this study is to evaluate the addition of CoQ and Vit. E to semen extender for equine spermatozoa in order to evaluate possible effects on semen motility. First, immediately after collection, semen samples were diluted with 1mM of CoQ and 1mM of CoQ plus 1mM of Vit. E and prepared for frozen storage in liquid nitrogen. After thawing (37° C/30 s), samples were maintained at 37° C and subjected to analysis after 0, 2 and 4 h for motility parameters with CASA (Computer-Assisted Sperm Analysis) method. In a second experiment, after the collection, semen samples were diluted with 1mM of CoQ, in presence or absence of seminal plasma where Vit. E is normally present, and prepared for cooled storage at 4° C. The effects on motility parameters were determined with CASA at 0, 24, 31 and 48 h after collection. During the analysis, samples were kept at 4° C. The CASA variables were examined with a mixed linear model. No improvement ($p > .05$) in motility parameters results from the addition of CoQ and Vit. E in frozen or cooled-stored equine semen when compared to control group.

Keywords: α-tocopherol; Coenzyme Q; Equine semen; Oxidative stress; Vitamin E

Italian Journal of Animal Science

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Phenotypic characterisation of milk technological traits, protein fractions, and major mineral and fatty acid composition of Burlina cattle breed

Niero, G., Visentin, G., Ton, S., De Marchi, M., Penasa, M., Cassandro, M.

Dipartimento di Agronomia, Animali, Alimenti, Risorse Naturali e Ambiente, University of Padova, Padova, Italy

Abstract

The aim of the present study was to characterise milk of Burlina local cattle breed for traits of technological and nutritional relevance, such as milk coagulation properties (MCP), and protein, major mineral and fatty acid (FA) composition. Burlina is mainly reared in mountain areas of Veneto Region (Italy) and it has been inserted in conservation plans aiming to avoid biodiversity loss and marginal pasture areas abandonment. Eighty-one individual milk samples were collected in four farms. Milk coagulation properties were determined using Formagraph, and protein, mineral and FA composition were analysed in high performance liquid chromatography, inductively coupled plasma optical emission spectrometry and gas chromatography, respectively. Results evidenced good protein percentage (3.38%) and considerable casein content (28.89 mg/mL), as well as a desirable FA profile, with ω-6 to ω-3 ratio of 4.04. Somatic cell score, averaging 3.13, is a trait that should be enhanced through the improvement of farm management. This would have positive effects on MCP. Among milk minerals, the most and less abundant were K (1493.53 mg/kg) and Mg (110.07 mg/kg), respectively. Overall, herd, parity and lactation stage explained moderate to low variation of the studied traits. Results of the present study could be useful to valorise Burlina local breed and preserve biodiversity in marginal areas.

Keywords: Casein; Fatty acid; Local breed; Milk coagulation property; Mineral

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Prediction of individual milk proteins including free amino acids in bovine milk using mid-infrared spectroscopy and their correlations with milk processing characteristics

McDermott, A.[ab], Visentin, G.[ab], De Marchi, M.[b], Berry, D.P.[a], Fenelon, M.A.[c], O'Connor, P.M.[c], Kenny, O.A.[c], McParland, S.[a]

[a] Teagasc Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork, Ireland
[b] Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy
[c] Teagasc, Food Research Centre, Moorepark, Fermoy, Co. Cork, Ireland

Abstract

The aim of this study was to evaluate the effectiveness of mid-infrared spectroscopy in predicting milk protein and free amino acid (FAA) composition in bovine milk. Milk samples were collected from 7 Irish research herds and represented cows from a range of breeds, parities, and stages of lactation. Mid-infrared spectral data in the range of 900 to 5,000 cm^{-1} were available for 730 milk samples; gold standard methods were used to quantify individual protein fractions and FAA of these samples with a view to predicting these gold standard protein fractions and FAA levels with available mid-infrared spectroscopy data. Separate prediction equations were developed for each trait using partial least squares regression; accuracy of prediction was assessed using both cross validation on a calibration data set (n = 400 to 591 samples) and external validation on an independent data set (n = 143 to 294 samples). The accuracy of prediction in external validation was the same irrespective of whether undertaken on the entire external validation data set or just within the Holstein-Friesian breed. The strongest coefficient of correlation obtained for protein fractions in external validation was 0.74, 0.69, and 0.67 for total casein, total β-lactoglobulin, and β-casein, respectively. Total proteins (i.e., total casein, total whey, and total lactoglobulin) were predicted with greater accuracy then their respective component traits; prediction accuracy using the infrared spectrum was superior to prediction using just milk protein concentration. Weak to moderate prediction accuracies were observed for FAA. The greatest coefficient of correlation in both cross validation and external validation was for Gly (0.75), indicating a moderate accuracy of prediction. Overall, the FAA prediction models overpredicted the gold standard values. Near-unity correlations existed between total casein and β-casein irrespective of whether the traits were based on the gold standard (0.92) or mid-infrared spectroscopy predictions (0.95). Weaker correlations among FAA were observed than the correlations among the protein fractions. Pearson correlations between gold standard protein fractions and the milk processing characteristics of rennet coagulation time, curd firming time, curd firmness, heat coagulating time, pH, and casein micelle size were weak to moderate and ranged from -0.48 (protein and pH) to 0.50 (total casein and a_{30}). Pearson correlations between gold standard FAA and these milk processing characteristics were also weak to moderate and ranged from -0.60 (Val and pH) to 0.49 (Val and K_{20}). Results from this study indicate that mid-infrared spectroscopy has the potential to predict protein fractions and some FAA in milk at a population level.

Keywords: Free amino acids; Mid-infrared spectroscopy; Milk quality; Protein fractions

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The influence of dietary nitrogen reduction and conjugated linoleic acid supply to dairy cows on fatty acids in milk and their transfer to ripened cheese

Schiavon, S., Cesaro, G., Cecchinato, A., Cipolat-Gotet, C., Tagliapietra, F., Bittante, G.

Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padua, Viale dell'Università 16, 35020 Legnaro (PD), Italy

Abstract

The aim of this study was to investigate the consequences of reducing the dietary crude protein content, with or without a supply of protected conjugated linoleic acid (CLA), on the milk fatty acid (FA) yield and recovery in 90 d ripened cheese. Twenty mid-lactation Friesian dairy cows were reared for 4 periods of 3 wk each in groups of 5, following a 4 x 4 Latin square design. Cows were fed 4 different rations, consisting of a combination of the 2 dietary crude protein levels [150 (CP15) or 123 (CP12) g of crude protein/kg of dry matter], with or without a conjugated linoleic acid supply (80 g/d, providing 5.57 and 5.40 g/d of C18:2 *cis*-9,*trans*-11 and C18:2 *trans*-10,*cis*-12, respectively). Milk yield was recorded. Twice in each period, milk samples were analyzed for protein, fat, and lactose content, and 10 L milk samples (pooled by group) were processed to produce 96 cheeses, which were ripened for 90 d. Milk and cheese fat were analyzed for their FA profiles. Milk and cheese FA were expressed as daily yields and relative proportions, and nutrient recoveries were computed. Dietary crude protein reduction had small or no effects on the yield and relative presence of FA in milk and cheese, except for a small increase in mid-chain branched saturated fatty acids. The CLA supply strongly reduced the yield of various categories of FA, and had major effects on short-chain FA of de novo synthesis, leading to changes in the relative proportions of the various FA in milk and cheese. The addition of CLA tended to reduce uniformly the recovery of all milk constituents and of short-, medium-, and long-chain FA groups, but we observed large differences among individual FA with apparent recoveries ranging between 640 and 1,710 g/kg. The highest recoveries were found for polyunsaturated long-chain FA, the lowest for saturated or monounsaturated short- or medium-chain FA. A notable rearrangement of these FA components, particularly the minor ones, took place during ripening.

Keywords: Cheese; Conjugated linoleic acid; Dietary protein; Fatty acid; Milk

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Short communication: Effects of pregnancy on milk yield, composition traits, and coagulation properties of Holstein cows

Penasa, M., De Marchi, M., Cassandro, M.

Department of Agronomy, Food, Natural Resources, Animals and Environment,
University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy

Abstract

The aim of this study was to investigate the effect of pregnancy stage on milk yield, composition traits, and milk coagulation properties in Italian Holstein cattle. The data set included 25,729 records from 3,995 first-parity cows calving between August 2010 and August 2013 in 167 herds. The traits analyzed were milk yield (kg/d), fat (%), protein (%), casein (%), and lactose (%) contents, pH, somatic cell score, rennet coagulation time (min), and curd firmness (mm). To better understand the effect of gestation on the aforementioned traits, each record was assigned to one of the following classes of pregnancy stage: (1) nonpregnant, (2) pregnant from 1 to 120 d, (3) pregnant from 121 to 210 d, and (4) pregnant from 211 to 310 d. Gestation stage significantly influenced all studied traits with the exception of somatic cell score. Milk production decreased and milk quality improved from the fourth month of pregnancy onward. For all traits, nonpregnant cows performed very similarly to cows in the first period of gestation. Rennet coagulation time and curd firmness were influenced by pregnancy stage, especially in the last weeks of gestation when milk had better coagulation characteristics; this information should be accounted for to adjust test-day records in genetic evaluation of milk coagulation properties.

Keywords: Holstein cow; Mid-infrared spectroscopy; Milk coagulation property; Pregnancy

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The nonlinear effect of somatic cell count on milk composition, coagulation properties, curd firmness modeling, cheese yield, and curd nutrient recovery

Bobbo, T., Cipolat-Gotet, C., Bittante, G., Cecchinato, A.

Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy

Abstract

The aim of this study was to investigate the relationships between somatic cell count (SCC) in milk and several milk technological traits at the individual cow level. In particular, we determined the effects of very low to very high SCC on traits related to (1) milk yield and composition; (2) coagulation properties, including the traditional milk coagulation properties (MCP) and the new curd firming model parameters; and (3) cheese yield and recovery of milk nutrients in the curd (or loss in the whey). Milk samples from 1,271 Brown Swiss cows from 85 herds were used. Nine coagulation traits were measured: 3 traditional MCP [rennet coagulation time (RCT, min), curd firming rate (k_{20}, min), and curd firmness after 30 min (a_{30}, mm)] and 6 new curd firming and syneresis traits [potential asymptotic curd firmness at infinite time (CF_P, mm), curd firming instant rate constant (k_{CF}, % x min^{-1}), syneresis instant rate constant (k_{SR}, % x min^{-1}), rennet coagulation time estimated using the equation (RCT_{eq}, min), maximum curd firmness achieved within 45 min (CF_{max}, mm), and time at achievement of CF_{max} (t_{max}, min)]. The observed cheese-making traits included 3 cheese yield traits (%CY_{CURD}, %CY_{SOLIDS}, and %CY_{WATER}, which represented the weights of curd, total solids, and water, respectively, as a percentage of the weight of the processed milk) and 4 nutrient recoveries in the curd (REC_{FAT}, $REC_{PROTEIN}$, REC_{SOLIDS}, and REC_{ENERGY}, which each represented the percentage ratio between the nutrient in the curd and milk). Data were analyzed using a linear mixed model with the fixed effects of days in milk, parity, and somatic cell score (SCS), and the random effect of herd-date. Somatic cell score had strong influences on casein number and lactose, and also affected pH; these were traits characterized by a quadratic pattern of the data. The results also showed a negative linear relationship between SCS and milk yield. Somatic cell score influenced almost all of the tested coagulation traits (both traditional and modeled), with the exceptions of k_{20}, CF_P, and k_{SR}. Gelation was delayed when the SCS decreased (slightly) and when it increased (strongly) with respect to a value of 2, as confirmed by the quadratic patterns observed for both RCT and RCT_{eq}. The SCS effect on a_{30} showed a quadratic pattern almost opposite to that observed for RCT. With respect to the CF_t parameters, k_{CF} decreased linearly as SCS increased, resulting in a linear decrease of CF_{max} and a quadratic pattern for t_{max}. Milk SCS attained significance for %CY_{CURD}, %CY_{WATER}, and $REC_{PROTEIN}$. As the SCS increased beyond 3, we observed a progressive quadratic decrease of the water retained in the curd (%CY_{WATER}), which caused a parallel decrease in %CY_{CURD}. With respect to $REC_{PROTEIN}$, the negative effect of SCS was almost linear. Recovery of fat and (consequently) REC_{ENERGY} was characterized by a more evident quadratic trend, with the most favorable values associated with an intermediate SCS. Together, our results confirmed that high SCS has a negative effect on milk composition and technological traits, highlighting the nonlinear trends of some traits across the different classes of SCS. Moreover, we report that a very low SCS has a negative effect on some technological traits of milk.

Keywords: Cheese yield; Curd firming; Milk coagulation property; Somatic cell count; Whey loss

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The 9-MilCA method as a rapid, partly automated protocol for simultaneously recording milk coagulation, curd firming, syneresis, cheese yield, and curd nutrients recovery or whey loss

Cipolat-Gotet, C., Cecchinato, A., Stocco, G., Bittante, G.

Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova (Padua), viale dell'Università 16, 35020 Legnaro, Italy

Abstract

The aim of this study was to propose and test a new laboratory cheesemaking procedure [9-mL milk cheesemaking assessment (9-MilCA)], which records 15 traits related to milk coagulation, curd firming, syneresis, cheese yield, and curd nutrients recovery or whey loss. This procedure involves instruments found in many laboratories (i.e., heaters and lacto-dynamographs), with an easy modification of the sample rack for the insertion of 10-mL glass tubes. Four trials were carried out to test the 9-MilCA procedure. The first trial compared 8 coagulation and curd firming traits obtained using regular or modified sample racks to process milk samples from 60 cows belonging to 5 breeds and 3 farms (480 tests). The obtained patterns exhibited significant but irrelevant between-procedure differences, with better repeatability seen for 9-MilCA. The second trial tested the reproducibility and repeatability of the 7 cheesemaking traits obtained using the 9-MilCA procedure on individual samples from 60 cows tested in duplicate in 2 instruments (232 tests). The method yielded very repeatable outcomes for all 7 tested cheese yield and nutrient recovery traits (repeatability >98%), with the exception of the fresh cheese yield (84%), which was affected by the lower repeatability (67%) of the water retained in the curd. In the third trial (96 tests), we found that using centrifugation in place of curd cooking and draining (as adopted in several published studies) reduced the efficiency of whey separation, overestimated all traits, and worsened the repeatability. The fourth trial compared 9-MilCA with a more complex model cheese-manufacturing process that mimics industry practices, using 1,500-mL milk samples (72 cows, 216 tests). The average results obtained from 9-MilCA were similar to those obtained from the model cheeses, with between-method correlations ranging from 78 to 99%, except for the water retained in the curd (r = 54%). Our results indicate that new 9-MilCA method is a powerful research tool that allows the rapid, inexpensive, and partly automated analysis processing 40 samples per day with 2 replicates each, using 1 lacto-dynamograph, 2 heaters, and 3 modified sample racks, and yields a complete picture of the cheesemaking process (e.g., milk gelation, curd firming, syneresis, and whey expulsion) as well as the cheese yield and the efficiency of energy or nutrients retention in the cheese or loss in the whey.

Keywords: Cheese yield; Cheesemaking; Laboratory procedure; Milk coagulation properties; Milk nutrients recovery in the curd

Journal of Dairy Science

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***Short communication*: Variations in major mineral contents of Mediterranean buffalo milk and application of Fourier-transform infrared spectroscopy for their prediction**

Stocco, G.[a], Cipolat-Gotet, C.[a], Bonfatti, V.[b], Schiavon, S.[a], Bittante, G.[a], Cecchinato, A.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, viale dell'Università 16 - 35020 Legnaro (PD), Italy
[b] Department of Comparative Biomedicine and Food Science (BCA), University of Padova, viale dell'Università 16 - 35020 Legnaro (PD), Italy

Abstract

The aims of this study were (1) to assess variability in the major mineral components of buffalo milk, (2) to estimate the effect of certain environmental sources of variation on the major minerals during lactation, and (3) to investigate the possibility of using Fourier-transform infrared (FTIR) spectroscopy as an indirect, noninvasive tool for routine prediction of the mineral content of buffalo milk. A total of 173 buffaloes reared in 5 herds were sampled once during the morning milking. Milk samples were analyzed for Ca, P, K, and Mg contents within 3 h of sample collection using inductively coupled plasma optical emission spectrometry. A Milkoscan FT2 (Foss, Hillerød, Denmark) was used to acquire milk spectra over the spectral range from 5,000 to 900 wavenumber/cm. Prediction models were built using a partial least square approach, and cross-validation was used to assess the prediction accuracy of FTIR. Prediction models were validated using a 4-fold random cross-validation, thus dividing the calibration-test set in 4 folds, using one of them to check the results (prediction models) and the remaining 3 to develop the calibration models. Buffalo milk minerals averaged 162, 117, 86, and 14.4 mg/dL of milk for Ca, P, K, and Mg, respectively. Herd and days in milk were the most important sources of variation in the traits investigated. Parity slightly affected only Ca content. Coefficients of determination of cross-validation between the FTIR-predicted and the measured values were 0.71, 0.70, and 0.72 for Ca, Mg, and P, respectively, whereas prediction accuracy was lower for K (0.55). Our findings reveal FTIR to be an unsuitable tool when milk mineral content needs to be predicted with high accuracy. Predictions may play a role as indicator traits in selective breeding (if the additive genetic correlation between FTIR predictions and measures of milk minerals is high enough) or in monitoring the milk of buffalo populations for dairy industry purposes.

Keywords: Buffalo milk; Fourier-transform infrared spectroscopy; Mineral content

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Effectiveness of mid-infrared spectroscopy to predict the color of bovine milk and the relationship between milk color and traditional milk quality traits

McDermott, A.[ab], Visentin, G.[ab], McParland, S.[a], Berry, D.P.[a], Fenelon, M.A.[c], De Marchi, M.[b]

[a] Teagasc Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork, Ireland
[b] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy
[c] Teagasc, Food Research Centre, Moorepark, Fermoy, Co. Cork, Ireland

Abstract

The color of milk affects the subsequent color features of the resulting dairy products; milk color is also related to milk fat concentration. The objective of the present study was to quantify the ability of mid-infrared spectroscopy (MIRS) to predict color-related traits in milk samples and to estimate the correlations between these color-related characteristics and traditional milk quality traits. Mid-infrared spectral data were available on 601 milk samples from 529 cows, all of which had corresponding gold standard milk color measures determined using a Chroma Meter (Konica Minolta Sensing Europe, Nieuwegein, the Netherlands); milk color was expressed using the CIELAB uniform color space. Separate prediction equations were developed for each of the 3 color parameters (L* = lightness, a* = greenness, b* = yellowness) using partial least squares regression. Accuracy of prediction was determined using both cross validation on a calibration data set (n = 422 to 457 samples) and external validation on a data set of 144 to 152 samples. Moderate accuracy of prediction was achieved for the b* index (coefficient of correlation for external validation = 0.72), although poor predictive ability was obtained for both a* and L* indices (coefficient of correlation for external validation of 0.30 and 0.55, respectively). The linear regression coefficient of the gold standard values on the respective MIRS-predicted values of a*, L*, and b* was 0.81, 0.88, and 0.96, respectively; only the regression coefficient on L* was different from 1. The mean bias of prediction (i.e., the average difference between the MIRS-predicted values and gold standard values in external validation) was not different from zero for any of 3 parameters evaluated. A moderate correlation (0.56) existed between the MIRS-predicted L* and b* indices, both of which were weakly correlated with the a* index. Milk fat, protein, and casein were moderately correlated with both the gold standard and MIRS-predicted values for b*. Results from the present study indicate that MIRS data provides an efficient, low-cost screening method to determine the b* color of milk at a population level.

Keywords: Cow milk; Fourier transform infrared; Grazing system; Yellowness

Journal of Dairy Science

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Effect of feed restriction programs and slaughter age on digestive efficiency, growth performance and body composition of growing rabbits

Birolo, M.[a], Trocino, A.[a], Zuffellato, A.[b], Xiccato, G.[c]

[a] Department of Comparative Biomedicine and Food Science (BCA), University of Padova, Viale dell'Università 16, I-35020 Legnaro, Padova, Italy
[b] A.I.A. Agricola Italiana Alimentare S.p.A., Piazzale Apollinare Veronesi 1, I-37036 San Martino Buon Albergo, Verona, Italy
[c] Department of Agronomy Food Natural Resources Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, I-35020 Legnaro, Padova, Italy

Abstract

The effects of the feeding system (*ad libitum vs.* restricted) and the restriction programs (daily *vs.* weekly base) were evaluated on 300 commercial crossbred rabbits housed individually from weaning (37 d) until slaughter (at 73 d and 80 d of age). During the first three weeks, restricted rabbits received from 85% to 100% of the *ad libitum* intake according to two feeding curves with daily (+4 g/d; D group) or weekly increments (+22 g/week on average; W group). In the restriction period, the feeding system affected CTTAD of crude protein (+2.4% in restricted compared *ad libitum* rabbits; $P < 0.01$). After restriction, dry matter ($P = 0.10$), ether extract ($P = 0.03$) and ADF ($P = 0.05$) CTTAD were lower in previously restricted rabbits compared to those always fed *ad libitum*. During the first period, feed restriction reduced daily weight gain (-7.5%; $P < 0.01$), feed intake (-7.1%; $P < 0.001$), empty body lipid (-12.7%; $P = 0.03$) and energy (-5.2%; $P < 0.01$) contents compared to *ad libitum* feeding. In the second period, previously restricted rabbits showed higher daily weight gain (+8.7%; $P = 0.02$), lower feed conversion (-6.0%; $P = 0.03$), besides higher empty body lipid (+16.0%; $P < 0.01$) and energy (+6.6%; $P < 0.01$) contents compared to rabbits fed *ad libitum*. In the whole trial, feed restriction reduced mortality (20.7% *vs.* 8.7%; $P < 0.01$) and tended ($P < 0.10$) to reduce feed intake (142 *vs.* 139 g/d), feed conversion (3.10 *vs.* 3.05) as well as N retention (53.6 g *vs.* 51.9 g). The restriction program had no effects during the restriction period. In the re-feeding period, rabbits submitted to the week–by–week restriction exhibited higher weight gain ($P < 0.01$) and feed intake ($P = 0.02$) and lower feed conversion ($P = 0.01$) compared to those restricted on a daily base. In the whole trial, W rabbits showed higher feed consumption ($P = 0.04$) and N excretion ($P = 0.05$) than D rabbits. A later slaughter age increased final live weight (+8%; $P < 0.001$) and feed conversion (+11%; $P < 0.001$), dressing out percentages, dissectible fat, and hind leg muscle to bone ratio, empty body lipid (+13%; $P = 0.02$) and energy contents (+4.2%; $P = 0.03$), besides body N retention (+11%) and excretion (+32%) ($P < 0.001$). In conclusion, regardless from the restriction program, a mild feed restriction (93% of *ad libitum*) during the first period improved rabbit health status and reduced environmental pollution in the fattening sector without impairing growth performance, slaughter results and carcass traits.

Keywords: Carcass quality; Digestive health; Feed restriction; Nitrogen excretion; Nutrient digestibility

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Short communication: Selecting the most informative mid-infrared spectra wavenumbers to improve the accuracy of prediction models for detailed milk protein content

Niero, G., Penasa, M., Gottardo, P., Cassandro, M., De Marchi, M.

Department of Agronomy, Food, Natural resources, Animals and Environment,
University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy

Abstract

The objective of this study was to investigate the ability of mid-infrared spectroscopy (MIRS) to predict protein fraction contents of bovine milk samples by applying uninformative variable elimination (UVE) procedure to select the most informative wavenumber variables before partial least squares (PLS) analysis. Reference values (= 114) of protein fractions were measured using reversed-phase HPLC and spectra were acquired through MilkoScan FT6000 (Foss Electric A/S, Hillerød, Denmark). Prediction models were built using the full data set and tested with a leave-one-out cross-validation. Compared with MIRS models developed using standard PLS, the UVE procedure reduced the number of wavenumber variables to be analyzed through PLS regression and improved the accuracy of prediction by 6.0 to 66.7%. Good predictions were obtained for total protein, total casein (CN), and α-CN, which included α_{S1}- and α_{S2}-CN; moderately accurate predictions were observed for κ-CN and total whey protein; and unsatisfactory results were obtained for κ-CN, α-lactalbumin, and β-lactoglobulin. Results indicated that UVE combined with PLS is a valid approach to enhance the accuracy of MIRS prediction models for milk protein fractions.

Keywords: Fourier transform infrared spectroscopy; Milk protein fraction; Partial least squares regression; Uninformative variable elimination

Journal of Dairy Science

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Transhumance of dairy cows to highland summer pastures interacts with breed to influence body condition, milk yield and quality

Zendri, F., Ramanzin, M., Bittante, G., Sturaro, E.

Dipartimento di Agronomia Animali Alimenti Risorse Naturali e Ambiente, University of Padova, Legnaro (PD), Italy

Abstract

This paper aimed at testing the differences of adaptability of bovine dairy, dual purpose and local breeds during the summer transhumance to highland pastures (summer farms), evaluating temporal variations of body condition and of milk yield and quality. Data were from 799 dairy cows of specialised (Holstein Friesian and Brown Swiss), dual purpose (Simmental) and local (mostly Rendena and Alpine Grey) breeds, and were collected before and after the transhumance in 109 permanent dairy farms, and during transhumance in 15 summer farms of the Autonomous Province of Trento, north-eastern Italy. Body Condition Score (BCS), milk production and quality (fat, protein, casein, lactose, urea, SCS) were analysed for the fixed effects of breed, parity, days in milk, month, supplementary concentrate level, and for the random effects of summer farm and individual cow. Body condition score was influenced by transhumance to summer farms, with low values in July and a recovery at the end of the period. This pattern was particularly marked in the specialised breeds. Similarly, also milk production declined, especially for Holstein Friesian and Brown Swiss, so that towards the end of transhumance all breeds had similar milk productions. Returning to permanent farms did not compensate the specialised breeds for the production loss experienced at the beginning of the grazing season. In conclusion, local and dual purpose breeds adapt better than specialised breeds to the summer pastures, and this results into an important reduction of their productive gaps (with lower variations of milk quality) and in maintaining body fat reserves.

Keywords: Dairy cow; Milk yield and quality; Mountain; Summer pasture

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Dose-response and inclusion effects of pure natural extracts and synthetic compounds on *in vitro* methane production

Cattani, M.[a], Maccarana, L.[a], Rossi, G.[b], Tagliapietra, F.[b], Schiavon, S.[b], Bailoni, L.[a]

[a] Department of Comparative Biomedicine and Food Science (BCA), University of Padova, Viale dell'Università 16, 35020, Legnaro, PD, Italy
[b] Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020, Legnaro, PD, Italy

Abstract

This study explored the effects of one ionophore compound (monensin) and four pure extracts (limonene, allyl sulfide, cinnamaldehyde, and eugenol) on *in vitro* rumen fermentation and methane (CH_4) production of a commercial diet for dairy cows. Four consecutive incubations at 24 h were conducted using an automated gas production (GP) system, where gas was vented at fixed pressure. Bottles (317 ml) were filled with 1.0 ± 0.010 g of diet and 150 ml of buffered rumen fluid. Additives were added at two dosages: 0.015 (low) or 0.030 mg/g of diet (high) for monensin, 3 (low) or 30 mg/g of diet (high) for the pure extracts. In each incubation, eleven treatments were tested in 3 replications: a control (CTR; bottles without additive), plus 5 additives x 2 dosages. Twelve bottles (3/run), containing only the buffered rumen fluid, were included as blanks. At the end of each incubation, gas samples were collected from bottle headspace and analyzed for CH_4. The proportion of CH_4 lost with venting was calculated. Fermentation fluids were analyzed for aNDF (NDFd) and true DM (TDMd) degradability, ammonia N, and VFA. Data were analyzed using a model considering the treatment as fixed factor and run as a random factor. Additives were ineffective at the low dosage. Compared to CTR, the high dosage of monensin reduced NDFd (-17%), TDMd (-3%), and CH_4 produced per g of truly degraded DM (-19%). Acetate was reduced (-13%) in favor of propionate (+25%), but the total VFA production did not change. Compared to CTR, the high dosage of limonene reduced NDFd (-66%), TDMd (-14%), GP (-25%) and CH_4 production (-34%) per g of truly degraded DM, and the total production of VFA (-25%), acetate (-31%), and propionate (-13%) ($P < 0.001$ for all). The high dosage of allyl sulfide did not influence NDFd and TDMd, reduced GP (-14%) and CH_4 production (-32%) per g of truly degraded DM, the total VFA (-12%) and acetate production (-24%), but increased that of propionate (+15%). The high dosage of cinnamaldehyde did not influence NDFd, TDMd or the total VFA production, reduced GP (-10%), CH_4 production (-12%) per g of truly degraded DM and acetate production (-14%), but increased that of propionate (+9%). The high dosage of eugenol reduced only NDFd (-18%) and TDMd (-3%). In conclusion, the most promising results were observed for the high dosage of cinnamaldehyde, as in vitro CH_4 production was reduced without effects on degradability and VFA production. However, these effects should be confirmed using dosages and experimental conditions proper of *in vivo* trials.

Keywords: Dose-response; Gas production; Inclusion effects; Methane production; Pure natural extracts

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Growth performance, carcass traits and meat quality of growing pigs on different feeding regimes slaughtered at 145 kg BW

Dalla Bona, M., Schiavon, S., Carraro, L., Gallo, L.

Dipartimento di Agronomia Animali Alimenti Risorse Naturali e Ambiente, University of Padova, Legnaro, Italy

Abstract

This study investigated the effects of feeding regime on growth performance, carcass traits and meat quality of pigs slaughtered at around 145 kg BW. A total of 96 barrows housed in eight pens were allotted to three groups in each pen. One group was fed *ad libitum* (AL) and the others were fed according to two quasi AL feeding regimes adjusting feed allowances with increasing BW. At slaughterhouse, the weights of the main lean and fat cuts were recorded, and a sample of *longissimus lumborum* (LL) was taken for physical and chemical analyses. Average daily gain (ADG) approached 940 g d^{-1}, and gain to feed ratio (G:F) was close to 0.38. Compared with the AL-feeding regime, the feed restriction reduced the pigs' ADG (-3.5%), feed intake (-7.4%) and carcass weight (-3%) ($p < 0.01$), but improved their G:F (+4%, $p < 0.01$). Feeding regime did not affect meat quality traits and exerted only minor effects on the weight of primal cuts and on the fatty acid composition of the intramuscular fat of the LL. However, AL-fed pigs tended to yield heavier fat cuts and showed a greater proportion of saturated fatty acid in the LL when compared to restricted feed barrows. In conclusion, moderate restriction in the feeding of medium–heavy pigs seems advisable, as it improves feed efficiency and could cut feed costs compared with the AL-feeding regime without affecting carcass and meat characteristics.

Keywords: Carcass quality; Feeding regime; Growth performance; Meat quality; Medium-heavy pigs

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Environmental impact of a cereal-based intensive beef fattening system according to a partial Life Cycle Assessment approach

Berton, M.[a], *Cesaro, G.*[a], *Gallo, L.*[a], *Pirlo, G.*[b], *Ramanzin, M.*[a], *Tagliapietra, F.*[a], *Sturaro, E.*[a]

[a] Department of Agronomy, Food, Natural resources, Animals and Environment, University of Padova, Viale dell'Università 16, Legnaro, 35020 Padova, Italy
[b] Fodder and Dairy Production Research Centre, Council for Agriculture Research and Economics, Via Porcellasco 7, 26100 Cremona, Italy

Abstract

This study investigated the environmental impact of the intensive beef fattening sector in North-Eastern Italy. A partial Life Cycle Assessment method was used with the boundaries of the system set from the arrival of stock calves, mainly born and raised in French suckler cow-calf systems, to the sale of finished young bulls and heifers to the slaughterhouses. One kg of body weight gained (BWG) was taken as the functional unit. This study examined 327 batches (groups of animals homogeneous for sex, genotype, origin, fattening farm and finishing period, 63±32 heads of average size) fattened by 16 farms. Data on animal performance were recorded for each batch. Diet composition and feed intake were collected for each beef category (combination of genotype and sex) within farms. On- and off-farm feed production data and materials used were recorded for each farm. Impact categories regarded (mean values and standard deviation per kg BWG are provided between brackets): global warming potential (8.4±1.6 kg CO_2-eq), acidification potential (197±32 g SO_2-eq), eutrophication potential (65±12 g PO_4-eq), cumulative energy demand (62±16 MJ), and land occupation (8.9±1.7 m^2/year). The contribution to global warming, acidification, and eutrophication potentials was greater for the on-farm than off-farm activities, whereas the opposite pattern was found for cumulative energy demand and land occupation. When referred to the whole production system, adding the global warming potential of French suckler cow-calf systems taken from the literature to those found in the present study for the fattening period, the resulting GHG emission was comparable to those reported for other suckler cow-based beef chain systems. The impact category values obtained for each batch were analysed with a linear mixed model which included the effects of farm (random effect), beef category, season of arrival in the fattening farm, and body weight class at the start of the fattening period within beef category. Beef category greatly affected all impact categories and variation across farms was notable. In conclusion, the beef fattening system taken into account was characterized by an overall global warming potential similar to, or slightly lower than, those reported for other beef systems, due to its productive efficiency, but showed a high energy demand, due to the relevance of off-farm activities. Different impact categories evidenced notable variation among farms, suggesting that there is potential for decreasing impacts through appropriate and specific management procedures of herds and farms.

Keywords: Beef fattening; Environmental impact; Life Cycle Assessment

Livestock Science

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The influence of different sample preparation procedures on the determination of fatty acid profiles of beef subcutaneous fat, liver and muscle by gas chromatography

Schiavon, S.[a], Pellattiero, E.[a], Cecchinato, A.[a], Tagliapietra, F.[a], Dannenberger, D.[b], Nuernberg, K.[b], Nuernberg, G.[b], Bittante, G.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padua, 35020 Legnaro, PD, Italy
[b] Leibniz Institute for Farm Animal Biology, Institutes of Muscle Biology and Growth, and Genetics and Biometry, 18196 Dummerstorf, Germany

Abstract

Three sample preparation procedures for producing a solution of fatty acid methyl esters (FAME) from the liver, subcutaneous fat and muscle of 9 bulls were compared. Fat was extracted from fresh samples using solvents under ambient (Folch) or high temperature and pressure (ASE) conditions. As an alternative to Folch, a one-step procedure carried out on freeze-dried samples (Jenkins) was used to produce FAME solutions. All methods involved mild acid-base transmethylation and in each case 9 samples of each tissue type were analyzed in duplicate, resulting in the quantification of 77 FAs. Equal amounts of total FAs were extracted with the different methods. The effect of the method on the FA profile was low in fat, intermediate in liver, and high in muscle. Compared with Folch, ASE resulted in higher saturated and monounsaturated FAs and fewer polyunsaturated FAs (PUFAs), and a lower relative incidence of conjugated linoleic acids (CLA) in muscle (>25%) and liver (17%). Jenkins had a smaller influence than Folch on PUFAs, and caused only a weak reduction in CLA (<3.4%). ASE tended to cause greater oxidation of PUFAs and unacceptable alterations to CLAs compared with Folch. The Jenkins procedure is a valid alternative to Folch when freeze-drying of samples is appropriate.

Keywords: Beef; *Bos taurus*; Conjugated linoleic acids; Fat extraction methods; Fatty acids; Food analysis; Food composition; Tissues

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Multivariate factor analysis of detailed milk fatty acid profile: Effects of dairy system, feeding, herd, parity, and stage of lactation

Mele, M.[a], *Macciotta, N.P.P.*[b], *Cecchinato, A.*[c], *Conte, G.*[a], *Schiavon, S.*[c], *Bittante, G.*[c]

[a] Dipartimento di Scienze Agrarie, Alimentari, Agro-ambientali, Università di Pisa, Via del Borghetto, 80, 56124 Pisa, Italy
[b] Dipartimento di Agraria, Sezione Scienze Zootecniche, Università di Sassari, Via de Nicola 9, 07100 Sassari, Italy
[c] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro, Padova, Italy

Abstract

We investigated the potential of using multivariate factor analysis to extract metabolic information from data on the quantity and quality of milk produced under different management systems. We collected data from individual milk samples taken from 1,158 Brown Swiss cows farmed in 85 traditional or modern herds in Trento Province (Italy). Factor analysis was carried out on 47 individual fatty acids, milk yield, and 5 compositional milk traits (fat, protein, casein, and lactose contents, somatic cell score). According to a previous study on multivariate factor analysis, a variable was considered to be associated with a specific factor if the absolute value of its correlation with the factor was ≥ 0.60. The extracted factors were representative of the following 12 groups of fatty acids or functions: de novo fatty acids, branched fatty acid-milk yield, biohydrogenation, long-chain fatty acids, desaturation, short-chain fatty acids, milk protein and fat contents, odd fatty acids, conjugated linoleic acids, linoleic acid, udder health, and vaccelenic acid. Only 5 fatty acids showed small correlations with these groups. Factor analysis suggested the existence of differences in the metabolic pathways for de novo short- and medium-chain fatty acids and Δ^9-desaturase products. An ANOVA of factor scores highlighted significant effects of the dairy farming system (traditional or modern), season, herd/date, parity, and days in milk. Factor behavior across levels of fixed factors was consistent with current knowledge. For example, compared with cows farmed in modern herds, those in traditional herds had higher scores for branched fatty acids, which were inversely associated with milk yield; primiparous cows had lower scores than older cows for de novo fatty acids, probably due to a larger contribution of lipids mobilized from body depots on milk fat yield. The statistical approach allowed us to reduce a large number of variables to a few latent factors with biological meaning and able to represent groups of fatty acids with a common origin and function. Multivariate factor analysis would therefore be a valuable tool for studying the influence of different production environments and individual animal factors on milk fatty acid composition, and for developing nutritional strategies able to manipulate the milk fatty acid profile according to consumer demand.

Keywords: Brown Swiss; Factor analysis; Fatty acids; Milk fat

Journal of Dairy Science

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Ecology and environmental science

The METCRAX II field experiment: a study of downslope windstorm-type flows in Arizona's meteor crater

Lehner, M.[a], Whiteman, C.D.[a], Hoch, S.W.[a], Crosmsman, E.T.[a], Jeglum, M.E.[a], Cherukuru, N.W.[b], Calhoun, R.[b], Adler, B.[c], Kalthoff, N.[c], Rotunno, R.[d], Horst, T.W.[d], Semmmmer, S.[d], Brown, W.O.[d], Oncley, S.P.[d], Vogt, R.[e], Grudzielanek, A.M.[f], Cermak, J.[f], Fonteyne N.J.[f], Bernhofer, C.[g], Pitacco, A.[h], Klein, P.[i]

[a] Department of Atmospheric Sciences, University of Utah, 135 S 1460 E, Rm 819, Salt Lake City, UT, United States
[b] Arizona State University, Tempe, AZ, United States
[c] Karlsruhe Institute of Technology, Karlsruhe, Germany
[d] National Center for Atmospheric Research, Boulder, CO, United States
[e] University of Basel, Basel, Switzerland
[f] Ruhr-Universität Bochum, Bochum, Germany
[g] Technische Universität Dresden, Dresden, Germany
[h] University of Padova, Padova, Italy
[i] University of Oklahoma, Norman, OK, United States

Abstract

The second Meteor Crater Experiment (METCRAX II) was conducted in October 2013 at Arizona's Meteor Crater. The experiment was designed to investigate nighttime downslope windstorm type flows that form regularly above the inner southwest sidewall of the 1.2-km diameter crater as a southwesterly mesoscale katabatic flow cascades over the crater rim. The objective of METCRAX II is to determine the causes of these strong, intermittent, and turbulent inflows that bring warm-air intrusions into the southwest part of the crater. This article provides an overview of the scientific goals of the experiment; summarizes the measurements, the crater topography, and the synoptic meteorology of the study period; and presents initial analysis results.

Bulletin of the American Meteorological Society

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Treatment performance and greenhouse gas emission of a pilot hybrid constructed wetland system treating digestate liquid fraction

Maucieri, C.[a], Mietto, A.[a], Barbera, A.C.[b], Borin, M.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment – DAFNAE, University of Padova, Agripolis Campus, Viale dell'Università 16, PD, Legnaro, Italy
[b] Department of Agriculture, Food and Environment – Di3A, University of Catania, Via Valdisavoia 5, Catania, Italy

Abstract

A pilot hybrid constructed wetland (subsurface flow line (SSL, 15 m^2) + floating treatment wetland line (FTWL, 90 m2)) treating digestate liquid fraction (DLF) in northeast Italy was monitored to determine its depuration efficiency in treating COD, total nitrogen (TN), ammonia nitrogen (NH_4-N), nitrate nitrogen (NO_3-N), total phosphorus (TP) and orthophosphate (PO_4-P). CO_2, CH_4, and N_2O emissions were also measured in SSL beds. The system was fed with diluted DLF (0.7 m^3 day^{-1}) containing high COD (4580–6000 mg L^{-1}) and TN (378.0–657.5 mg L^{-1}). Removal efficiency was 57.9% for COD, 64.6% for TN, 65.1% for NH_4-N, 35.6% for NO_3-N, 49.2% for TP, 45.1% for PO_4-P in SSL and of 89.2% for COD, 90.0% for TN, 89.0% for NH_4-N, 93.8% for NO_3-N, 50.3% for TP, 49.9% for PO_4-P in FTWL. SSL showed a higher areal load reduction than FTWL. The carbon emitted (CO_2-C + CH_4-C) was always below 100% of C removed from digestate as COD, showing that during monitored periods SSL acted as C sink. The results indicate that the set-up composed by a sequence of vertical subsurface, horizontal subsurface and floating wetland represent a valid solution as secondary treatment for DLF.

Keywords: *Arundo donax* L.; Floating treatment wetland; Horizontal subsurface flow constructed wetland; *Phragmites australis* (Cav.) Trin. ex Steud; Vertical subsurface flow constructed wetland

Ecological Engineering

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A simplified process of swine slurry treatment by primary filtration and *Haematococcus pluvialis* culture to produce low cost astaxanthin

Ledda, C.[a]*, Tamiazzo, J.*[b]*, Borin, M.*[b]*, Adani, F.*[ca]

[a] Gruppo Ricicla - DiSAA, Università degli Studi di Milano, Biomass and Bioenergy Lab., Parco Tecnologico Padano, Via Einstein, Loc. C.na Codazza, Lodi, Italy
[b] DAFNAE, Università degli Studi di Padova, Via dell'Università 16, Legnaro, Italy
[c] Gruppo Ricicla - DiSAA, Università degli Studi di Milano, Soil and Env. Lab, Via Celoria 2, Milano, Italy

Abstract

A simplified process for treating swine slurry through primary filtration and subsequent depuration of the filtrate with the astaxanthin-rich microalga *Haematococcus pluvialis* is proposed. The first step comprises a low-cost filtration system capable of reducing 66% of ammonia, 7% of phosphorus and 19% of chemical oxygen demand, and increasing the concentration of nitrate, being this useful for subsequent growth of the algae. The second step comprises the discontinuous cultivation of *H. pluvialis* in diluted filtered slurry. The optimal dilution was researched by testing undiluted and 2, 4 and 8-fold diluted filtrate. This step led to a drastic reduction in macro and micronutrients concentration (up to 99% for NO_3-N and NH_4-N, 98% for TP and 26% for chemical oxygen demand). After *H. pluvialis* growth the accumulation of astaxanthin took place for 14 d in nutrient-deprived conditions: an astaxanthin accumulation of 1.27% on a dry weight basis was measured. These results indicate the possibility to couple low-cost filtration and microalgae production to recover nutrients from swine wastewaters and to add value by producing valuable astaxanthin for the feed market or for an on-farm utilization as feed addictive.

Keywords: Astaxanthin; Filtration; *Haematococcus pluvialis*; Nutrient removal; Swine slurry

Ecological Engineering

Volume 90, Pages 244-250

Soil management shapes ecosystem service provision and trade-offs in agricultural landscapes

Tamburini, G.[a], De Simone, S.[b], Sigura, M.[b], Boscutti, F.[b], Marini, L.[a]

[a] DAFNAE-Entomology, University of Padova, viale dell'Universitá 16, Legnaro, Padova, Italy
[b] Department of Agricultural and Environmental Science, University of Udine, via delle Scienze 206, Udine, Italy

Abstract

Agroecosystems are principally managed to maximize food provisioning even if they receive a large array of supporting and regulating ecosystem services (ESs). Hence, comprehensive studies investigating the effects of local management and landscape composition on the provision of and trade-offs between multiple ESs are urgently needed. We explored the effects of conservation tillage, nitrogen fertilization and landscape composition on six ESs (crop production, disease control, soil fertility, water quality regulation, weed and pest control) in winter cereals. Conservation tillage enhanced soil fertility and pest control, decreased water quality regulation and weed control, without affecting crop production and disease control. Fertilization only influenced crop production by increasing grain yield. Landscape intensification reduced the provision of disease and pest control. We also found tillage and landscape composition to interactively affect water quality regulation and weed control. Under N fertilization, conventional tillage resulted in more trade-offs between ESs than conservation tillage. Our results demonstrate that soil management and landscape composition affect the provision of several ESs and that soil management potentially shapes the trade-offs between them.

Keywords: Agriculture intensification; Conservation tillage; Crop yield; Nitrogen fertilization; Pest control; Soil fertility

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Phytoremediation opportunities with alimurgic species in metal-contaminated environments

Bandiera, M., Dal Cortivo, C., Barion, G., Mosca, G., Vamerali, T.

Department of Agronomy, Food, Natural Resources, Animals and Environment,
University of Padova, Viale dell'Università 16, Legnaro-Padova, Italy

Abstract

Alimurgic species are edible wild plants growing spontaneously as invasive weeds in natural grassland and farmed fields. Growing interest in biodiversity conservation projects suggests deeper study of the multifunctional roles they can play in metal uptake for phytoremediation and their food safety when cultivated in polluted land. In this study, the responses of the tap-rooted perennial species *Cichorium intybu*s L., *Sonchus oleracerus* L., *Taraxacum officinale* Web., *Tragopogon porrifolius* L. and *Rumex acetosa* L. were studied in artificially-highly Cd-Co-Cu-Pb-Zn-contaminated soil in a pot-scale trial, and those of *T. officinale* and *R. acetosa* in critical open environments (i.e., landfill, ditch sediments, and sides of highly-trafficked roads). Germination was not inhibited, and all species showed appreciable growth, despite considerable increases in tissue metal rates. Substantial growth impairments were observed in *C. intybus*, *T. officinale* and *T. porrifolius*; *R. acetosa* and *S. oleracerus* were only marginally affected. Zn was generally well translocated and reached a high leaf concentration, especially in *T. officinale* (~600 mg · kg^{-1} dry weight, DW), a result which can be exploited for phytoremediation purposes. The elevated Cd translocation also suggested applications to phytoextraction, particularly with *C. intybus*, in which leaf Cd reached ~16 mg · kg^{-1} DW. The generally high root retention of Pb and Cu may allow their phytostabilisation in the medium-term in no-tillage systems, together with significant reductions in metal leaching compared with bare soil. In open systems, critical soil Pb and Zn were associated with heavily trafficked roadsides, although this was only seldom reflected in shoot metal accumulation. It is concluded that a community of alimurgic species can serve to establish an efficient, long-lasting vegetation cover applied for phytoremediation and reduction of soil metal movements in degraded environments. However, their food use is not recommended, since leaf Cd and Pb may exceed EU safety thresholds.

Keywords: Alimurgic species; Food safety; Phytoremediation; Tap-rooted plants; Trace elements

Sustainability (Switzerland)

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Conservation tillage mitigates the negative effect of landscape simplification on biological control

Tamburini, G.[a], De Simone, S.[b], Sigura, M.[b], Boscutti, F.[b], Marini, L.[a]

[a] DAFNAE-Entomology, University of Padova, viale dell'Universitá 16, Legnaro, Padova, Italy
[b] Department of Agricultural and Environmental Science, University of Udine, via delle Scienze 206, Udine, Italy

Abstract

Biological pest control is a key ecosystem service, and it depends on multiple factors acting from the local to the landscape scale. However, the effects of soil management on biological control and its potential interaction with landscape are still poorly understood. In a field exclusion experiment, we explored the relative effect of tillage system (conservation vs. conventional tillage) on aphid biological control in 15 pairs of winter cereal fields (barley and wheat) selected along a gradient of landscape complexity. We sampled the abundance of the main natural enemy guilds, and we evaluated their relative contribution to aphid predation and parasitism. Conservation tillage was found to support more abundant predator communities and higher aphid predation (16% higher than in the fields managed under conventional tillage). In particular, both the abundance and the aphid predation of vegetation- and ground-dwelling arthropods were increased under conservation tillage conditions. Conservation tillage also increased the parasitism rate of aphids. A high proportion of semi-natural habitats in the landscape enhanced both aphid parasitism and predation by vegetation-dwelling organisms but only in the fields managed under conventional tillage. The better local habitat quality provided by conservation tillage may compensate for a low-quality landscape. Synthesis and applications. Our study stresses the importance of considering both soil management and landscape composition when planning strategies to maximize biological control services in agro-ecosystems, highlighting the role played by conservation tillage in supporting natural enemy communities. In simple landscapes, the adoption of conservation tillage will locally improve biological control provided by both predators and parasitoids mitigating the negative effects of landscape simplification. Moreover, considering the small scale at which both predation and parasitism responded to landscape composition, a successful strategy to improve biological control would be to establish a fine mosaic of crop and non-crop areas such as hedgerows, tree lines and small semi-natural habitat patches.

Keywords: Aphid; Ecosystem services; Landscape complexity; Natural enemies; Parasitoids; Pest control; Predation; Tillage intensity

Journal of Applied Ecology

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Biomethanation potential of wetland biomass in codigestion with pig slurry

Marchetti, R.[a], *Vasmara, C.*[a], *Florio, G.*[b], *Borin, M.*[b]

[a] Research Unit for Swine Husbandry, Consiglio per la Ricerca e la sperimentazione in agricoltura e l'analisi dell'economia agraria (CREA), San Cesario sul Panaro, Modena, Italy
[b] Department of Agronomy Food Natural Resources Animals Environment (DAFNAE), Padua University, Padua, Italy

Abstract

Constructed wetlands represent an increasingly expanding technology for treatment and reuse of poor quality waters and for the development of marginal areas. The exploitation of herbaceous biomass for biogas production may add further appeal to its adoption. Codigestion of lignocellulosic plant materials with pig slurry could meet the need for biomass hydration and possibly improve biogas yields. The objectives of this study were: (1) to evaluate the biomethanation potential of biomass from several species which are of interest for use in constructed wetlands, and its relationship with plant composition; (2) to evaluate the influence of codigestion of selected wetland species with pig slurry on methane production rate and yield. Biogas production was preliminarily measured in laboratory conditions using as substrates biomass samples belonging to 23 plant species coming from different environments. Eight of them were then tested for biogas production, alone or in codigestion with pig slurry (volatile solid ratio: 1/1). In monodigestion, CH_4 yields were on average 213 mL CH_4 g^{-1} volatile solids. Biogas production was positively related with N content and negatively with acid detergent fiber concentration and C to N ratio. The time for the joining of the maximum methane production was 25 % shorter and the amount of methane was 30 % higher for wetland biomass in codigestion with pig slurry than in monodigestion. The use of pig slurry as hydration medium for anaerobic digestion can improve the biomethanation potential of wetland biomass.

Keywords: Biomethanation; Constructed wetlands; Lignocellulosic biomass; Pig slurry

Waste and Biomass Valorization

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Mitigation of herbicide runoff as an ecosystem service from a constructed surface flow wetland

Pappalardo, S.E.[a], Otto, S.[b], Gasparini, V.[a], Zanin, G.[a], Borin, M.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Agripolis, Viale dell'Università 16, Legnaro, PD, Italy
[b] Institute of Agro-environmental and Forest Biology - CNR, Agripolis, Viale dell'Università 16, Legnaro, PD, Italy

Abstract

Ecosystem services provided by wetland systems presently play a pivotal role in intensive cropland as water purification from agricultural pollution. A field trial was conducted in 2014 to evaluate herbicide runoff reduction and retention using a 0.32 ha constructed surface flow wetland (CSFW) at the outlet of a 6 ha agricultural basin. To simulate an extreme pulse contamination, the CSFW was flooded with a runoff contaminated with metolachlor, and terbuthylazine and two other subsequent floods with pure water were applied 21 and 65 days later. Results show that the CSFW can reduce runoff concentration of metolachlor and terbuthylazine by a factor of 45–80 even in extreme flooding conditions. Herbicides retention in the CSFW was reversible, and the second and third floods mobilized 14–31 and 3.5–7.0% respectively, of the amount detected in the first flood. The CSFW performs a high buffer capacity for herbicides, capable to provide water purification service, protecting downstream surface water. Moreover, mitigation capacity of a CSFW for a heavy runoff from a 10 ha basin is 90% for every 50 m in length of a 15 m wide wetland. This confirms that the implementation of CSFWs in agro-systems can improve the sustainability of agricultural production.

Keywords: Artificial wetlands; Ecosystem services; Metolachlor; Sustainable agriculture; Terbuthylazine; Water purification

Hydrobiologia

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Vegetated ditches for the mitigation of pesticides runoff in the Po Valley

Otto, S.[a], Pappalardo, S.E.[b], Cardinali, A.[b], Masin, R.[b], Zanin, G.[b], Borin, M.[b]

[a] National Research Council, Institute of Agro-environmental and Forest Biology, Viale dell'Università 16, Legnaro (PD), Italy
[b] Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Viale dell'Università 16, Legnaro (PD), Italy

Abstract

In intensive agricultural systems runoff is one of the major potential diffuse pollution pathways for pesticides and poses a risk to surface water. Ditches are common in the Po Valley and can potentially provide runoff mitigation for the protection of watercourses. The effectiveness depends on ditch characteristics, so there is an urgent need for site-specific field trials. The use of a fugacity model (multimedia model) can allows recognition of the mitigation main processes. A field experiment was conducted in order to evaluate the mitigation capacity of a typical vegetated ditch, and results were compared with predictions by a fugacity model. To evaluate herbicide mitigation after an extreme runoff, the ditch was flooded with water containing mesotrione, S-metolachlor and terbuthylazine. Two other subsequent floods with uncontaminated water were applied 27 and 82 days later to evaluate herbicides release. Results show that the ditch can immediately reduce runoff concentration of herbicides by at least 50% even in extreme flooding conditions. The half-distances were about 250 m. As a general rule, a runoff of 1 mm from 5 ha is mitigated by 99% in 100 m of vegetated ditch. Herbicides retention in the vegetated ditch was reversible, and the second flood mobilized 0.03-0.2% of the previous one, with a concentration below the drinking water limit of 0.1 g L^{-1}. No herbicide was detected in the third flood, because the residual amount in the ditch was too low. Fugacity model results show that specific physical-chemical parameters may be used and a specific soil-sediment-plant compartment included for modelling herbicides behaviour in a vegetated ditch, and confirm that accumulation is low or negligible for herbicides with a half-life of 40 days or less. Shallow vegetated ditches can thus be included in a general agri-environment scheme for the mitigation of pesticides runoff together with wetlands and linear buffer strips. These structures are present in the landscape, and their environmental role can be exploited by proper management.

PLoS ONE

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Assessing the role of agri-environmental measures to enhance the environment in the Veneto Region, Italy, with a model-based approach

Dal Ferro, N.[a], Cocco, E.[a], Lazzaro, B.[b], Berti, A.[a], Morari, F.[a]

[a] Department of Agronomy, Food, Natural resources, Animals and Environment, Agripolis, University of Padova, Viale Dell'Università 16, Padova, Italy
[b] Veneto Region, Department of Agriculture and Rural Development, Sector Agri-environmental Policies, via Torino 110, Mestre, VE, Italy

Abstract

Many efforts have been made in Europe to improve the environmental quality of agro-ecosystems. Since the 2000s, agri-environmental measures (AEMs) have been financed and implemented in EU countries, although their beneficial effects are still questioned due to poorly targeted environmental issues and a lack of site-specific payments. Indeed, estimates of AEM outcomes at the territorial level require considerable efforts to consider simultaneously multiple environmental objectives with multiple targets. As a result, a DAYCENT model-GIS platform was developed that integrates multiple types of pedo-climatic and land management information. The aim was to provide a decision support system for spatially evaluating and selecting the best AEMs in terms of soil, water and air quality, when compared with a standard scenario without any adopted measure. Our modelled results showed that in the Veneto Region, north-eastern Italy, the AEMs applied from 2007 to 2013 improved the environmental value of the agro-ecosystems, especially in terms of soil and water quality. Continuous soil cover, reduction of soil disturbance through grasslands, conservation agriculture and cover crops were the best simulated strategies to increase soil organic matter content (+25%) and reduce nitrogen leaching (90%). These strategies were also able to sharply reduce soil water erosion (86%) and as a consequence P loss, in particular in the steep hilly and mountain areas, although their application to arable lands in those landscapes is still rare. In contrast, care should be taken in the long-term regarding an increase in P leaching, since predictions up to +0.15 kg ha^{-1} y^{-1} are reached compared to the standard scenario. Finally, greenhouse gas (GHG) emissions (N_2O and CH_4) were reduced mainly due to increased fertilisation efficiency. The proposed method can be a flexible decision support tool for a result-oriented and scientifically-based evaluation of AEMs that may help policy makers to evaluate the most effective measures for increasing the environmental value of agro-ecosystems.

Keywords: Agri-environmental measures; Decision support system; Environmental quality; Modelling; Nutrient cycling

Agriculture, Ecosystems and Environment

Volume 232, Pages 312-325

Assessing biochar ecotoxicology for soil amendment by root phytotoxicity bioassays

Visioli, G.[a], Conti, F.D.[a], Menta, C.[a], Bandiera, M.[b], Malcevschi, A.[a], Jones, D.L.[c], Vamerali, T.[b]

[a] Department of Life Sciences, University of Parma, Parco Area delle Scienze 11/A, Parma, Italy
[b] Department of Agronomy, Food, Natural Resources, Animals and the Environment, University of Padova, Padova, Italy
[c] School of the Environment, Natural Resources and Geography, Bangor University, Bangor, United Kingdom

Abstract

Soil amendment with biochar has been proposed as effective in improving agricultural land fertility and carbon sequestration, although the characterisation and certification of biochar quality are still crucial for widespread acceptance for agronomic purposes. We describe here the effects of four biochars (conifer and poplar wood, grape marc, wheat straw) at increasing application rates (0.5, 1, 2, 5, 10, 20, 50 % w/w) on both germination and root elongation of *Cucumis sativus* L., *Lepidium sativum* L. and *Sorghum saccharatum* Moench. The tested biochars varied in chemical properties, depending on the type and quality of the initial feedstock batch, polycyclic aromatic hydrocarbons (PAHs) being high in conifer and wheat straw, Cd in poplar and Cu in grape marc. We demonstrate that electrical conductivity and Cu negatively affected both germination and root elongation at 5 % rate biochar, together with Zn at 10 % and elevated pH at 20 %. In all species, germination was less sensitive than root elongation, strongly decreasing at very high rates of chars from grape marc (>10 %) and wheat straw (>50 %), whereas root length was already affected at 0.5 % of conifer and poplar in cucumber and sorghum, with marked impairment in all chars at >5 %. As a general interpretation, we propose here logarithmic model for robust root phytotoxicity in sorghum, based on biochar Zn content, which explains 66 % of variability over the whole dosage range tested. We conclude that metal contamination is a crucial quality parameter for biochar safety, and that root elongation represents a stable test for assessing phytotoxicity at recommended in-field amendment rates (<1–2 %).

Keywords: Biochar; Feedstock quality; Germination bioassay; Metal contamination; Root phytotoxicity

Environmental Monitoring and Assessment

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Establishing a semi-natural grassland: effects of harvesting time and sowing density on species composition and structure of a restored *Arrhenatherum elatius* meadow

Scotton, M.

Department of Agronomy, Food, Natural Resources, Animals and Environment,
University of Padova, Viale dell'Università 16, Legnaro, PD, Italy

Abstract

Species-rich semi-natural grasslands play an essential role in the conservation of European biodiversity. To restore them, existing grasslands may be used as a seed source. A key factor for successful restoration is the transfer of all species of the plant community to the site being restored. This approach, however, often poses practical problems due to variations in species phenology, so that only time-staggered harvesting allows the seeds of many species to be collected. Poor harvesting methods may reduce the number of species transferred from the donor to recipient site. The effects of harvesting at various time points by various methods were evaluated here in a restoration experiment on an ex-arable field in Northern Italy. Propagation materials from the first or second regrowth (or both) of a meadow dominated by *Arrhenatherum elatius* were collected by four harvesting methods. The materials were spread at the sowing density between 830 and 14360 seeds m^{-2}. Species composition and structure of the vegetation were examined during 6 years. Untransferred species were almost exclusively those not present at harvesting as mature seed. Compared with materials from one regrowth period, materials from both regrowth periods significantly increased the number of transferred species per plot (26.5 vs. 28.5, respectively) and the absolute transfer rate (64% vs. 75%). Higher sowing density yielded a greater number of positive than negative effects. It favored stable establishment of donor site species and significantly reduced the presence of weeds. Nonetheless, due to the initial dominance of species with high sowing density, evenness of the restored plots was lower than that at the donor site but increased with time, at least under low- and medium-sowing-density conditions. Multiple harvesting at time points when several species with mature seed are present increases the species transfer rate. Medium sowing density positively affects restoration development because it promotes the establishment of donor site species with lower sowing density, prevents species with the highest density from dominating the vegetation during the first few years, and reduces weed cover.

Keywords: Restoration; Semi-natural grassland; Sowing density; Species composition; Species richness; Vegetation structure

Agriculture, Ecosystems and Environment

Volume 220, Pages 35-44

Effect of water and salt stress on energy partitioning of two grapevine rootstock genotypes: a quantitative assessment

Meggio, F., Pitacco, A.

Department of Agronomy Food Natural Resources Animals and Environment - DAFNAE, University of Padova, Viale dell'Università 16, Legnaro, PD, Italy

Abstract

The ability of plants to adapt and/or acclimate to different environments is related to the plasticity and resilience of photosynthesis. This study aims at assessing the effects of salinity, drought and recovery on photosynthesis being either direct (stomatal limitations) or secondary (oxidative stress). Combined measurements of gas exchange and chlorophyll fluorescence enabled to quantify the absorbed energy used for net photosynthesis and that dissipated by photoprotective mechanisms. Measurements were performed under controlled conditions on leaves of susceptible (101.14) and new putative tolerant selection (M4) grapevine rootstocks in control and progressive drought and salt loading conditions. Leaves of 101.14 showed higher photosynthetic performances than the M4 in well-watered conditions. However, M4 showed a greater ability to tolerate increasing salt concentration and drought and an almost complete recovery after re-watering. Quenching analysis revealed the photoprotective thermal dissipation (NPQ) as the major responsible for the different stress responses among susceptible and tolerant rootstock studied.

Keywords: Drought; Fluorescence; NaCl stress; Photosynthesis; Photosystem II; Radiation; Rootstock; *Vitis*

Acta Horticulturae

Volume 1136, Pages 121-128

Do vineyards in contrasting landscapes contribute to conserve plant species of dry calcareous grasslands?

Nascimbene, J.[ab], Zottini, M.[c], Ivan, D.[c], Casagrande, V.[a], Marini, L.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and the Environment (DAFNAE), University of Padova, viale dell'Università 16, Legnaro, Padova, Italy
[b] Department of Life Sciences, University of Trieste, via Giorgieri 10, Trieste, Italy
[c] Department of Biology, University of Padova, via U. Bassi 58/B, Padova, Italy

Abstract

The increasing development of vineyards in Mediterranean areas worldwide is considered a major driver of conversion of several habitats of conservation concern, including calcareous dry grasslands that are targeted for biodiversity conservation by the European Union, according to Natura 2000 policies. Here, we aim at evaluating the potential of extensive vineyards located in contrasting landscapes (semi-natural vs crop-dominated) for providing suitable habitat conditions to plant species associated with dry grasslands. This study was carried out in one of the economically most important winemaking districts of Italy, characterized by a hilly landscape with steep slope vineyards. We compared plant communities of vineyards in contrasting landscapes with those of the remnants of dry grasslands. Our study demonstrates that landscape composition strongly affects local plant communities in vineyards, with a positive effect of semi-natural habitats bordering the cultivated areas. Our findings thus supply an additional tool for improving the effectiveness of viticultural landscapes for nature conservation. In particular, our results indicate that vineyards on steep slopes could provide moderate chance for the conservation of plant specialists inhabiting calcareous dry grasslands, depending on the landscape composition: vineyards embedded in semi-natural landscapes have more potential for conservation than those in crop-dominated landscapes. Our study also indicates that conservation efforts should aim at (a) decreasing the current management intensity that likely hampers the beneficial effects of semi-natural habitats in the surrounding landscape on local plant assemblages, and (b) strictly conserving the remnants of dry grasslands that are irreplaceable refugia for habitat specialists and species of conservation concern.

Keywords: Crop landscape; Plant conservation; Ruderal species; Semi-natural landscape; Specialist species; Species richness and composition

Science of the Total Environment

Volume 545-546, Pages 244-249

Environmental impact in floriculture: LCA approach at farm level

Bonaguro, J.E., Coletto, L., Samuele, B., Zanin, G., Sambo, P.

Dipartimento di Agronomia Animali Alimenti Risorse Naturali e Ambiente, University of Padova, Legnaro (PD), Italy

Abstract

The issue of sustainable floriculture and the continuous and increasing demand for environmentally-friendly products have produced, in recent years, several studies that tried to answer these requests. Simultaneously there is a need to meet the companies requirements for cost reduction and more attractive products. Nowadays, studies with an holistic approach to the problem, for example the evaluation of product's life cycle, are not very common. A complete study requires, in fact, a huge amount of data acquired throughout the investigation of a statistically significant sample of companies. The Life Cycle Assessment (LCA) methodology was first used to determine the environmental impact of industrial products. In the last decades its applications in the agricultural sector have increased, though studies on floriculture productions are still rare. In this study we performed the first Life Cycle Impact Assessment (LCIA) of three species, poinsettia (*Euphorbia pulcherrima* Willd.), zonal geranium (*Pelargonium xhortorum*) and cyclamen (*Cyclamen persicum* Mill.) and two type of containers, a traditional polypropylene pot and a compostable rice hulls pot. Life Cycle Inventory (LCI) data were sourced from interviews and published literature. The results showed that both type of pots are major contributor to the environmental impact of the assessed systems. Global Warming Potential (GWP) of plastic pot is mainly affected by the material used for its production, while rice hulls (RH) pot is only affected by transport process from the production site. The use of compostable RH pot could potentially be more sustainable, but to date its contribution is only slightly lower than the plastic one. Further assessments including end-of-life information, in particular for plastic materials, may lead to a better evaluation of the possible alternatives.

Keywords: Flower pots; LCI; LCIA; Rice hulls

Acta Horticulturae

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Thousand cankers disease in Europe: an overview

Montecchio, L.[a], Vettorazzo, M.[b], Faccoli, M.[c]

[a] Department of Land, Environment, Agriculture and Forestry (TeSAF), University of Padova, Viale dell'Università 16, Legnaro (PD), Italy
[b] Veneto Region, Depertment for Agriculture and Rural Development, Phytosanitary Service, Via Longhena 6, Marghera (VE), Italy
[c] Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, Legnaro (PD), Italy

Abstract

Walnut (*Juglans regia* L.) is traditionally present in most European countries as an ornamental tree, and in Southern Europe in particular it is grown for both fruit and wood. Since the 1980s, to supply the increasing demand for walnut timber, large areas of southern and central Europe, from France to Hungary, have been planted with black walnut (*Juglans nigra* L.) to provide wood for furniture production. The fungus *Geosmithia morbida* and its vector *Pityophthorus juglandis*, causing the thousand cankers disease of walnut in the USA in the last 2 decades, were recently reported in Europe (in Italy) on both walnut species. Thousand cankers disease can have a high negative impact on the landscape and economy of many agricultural and forest areas. Following a detailed pest risk analysis performed by EPPO in 2015, both organisms were included in the EPPO A2 List of pests recommended for regulation as quarantine pests. The main biological, epidemiological and monitoring aspects of thousand cankers disease and its status in Europe are reported.

EPPO Bulletin

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Lab-scale phytotreatment of old landfill leachate using different energy crops

Lavagnolo, M.C.[a], Malagoli, M.[b], Garbo, F.[a], Pivato, A.[a], Cossu, R.[a]

[a] Department of Industrial Engineering, University of Padova, via Lungargine Rovetta 8, Padova, Italy
[b] DAFNAE, University of Padova, viale dell'Università 16, Legnaro, PD, Italy

Abstract

Old landfill leachate was treated in lab-scale phytotreatment units using three oleaginous species: sunflower (H), soybean (S) and rapeseed (R). The specific objectives of this study were to identify the effects of plant species combinations with two different soil textures on the reduction of COD, total N (nitrogen) and total P (phosphorous); to identify the correlation between biomass growth and removal efficiency; to assess the potential of oily seeds for the production of biodiesel. The experimental test was carried out using 20 L volume pots installed in a greenhouse under different leachate percentages in the feeding and subsequent COD, N and P loads. Significant removal efficiencies were achieved: COD (> 80%), total N (> 70%) and total P (> 95%). Better performances were displayed by the clayey soil. Plants irrigated with leachate, when compared to control units fed only with water and nutrient solution (Hoagland solution), developed a larger plant mass. Sunflower was the best performing species.

Keywords: Leachate; Oleaginous crops; Phytotreatment; Renewable energy

Waste Management

Volume 55, Pages 265-275

Impact of dairy farming on butterfly diversity in Alpine summer pastures

Jerrentrup, J.S.[a], Klimek, S.[a], Marchiori, E.[b], Bittante, G.[b], Ramanzin, M.[b], Sturaro, E.[b], Marini, L.[b]

[a] Thünen Institute of Biodiversity, Bundesallee 50, Braunschweig, Germany
[b] University of Padova, DAFNAE, viale dell'Università 16, Padova, Italy

Abstract

The practice of transhumance of livestock herds to Alpine summer pasture has experienced pronounced changes over recent decades due to the general process of agricultural intensification in productive areas and abandonment of farming in marginal areas. Instead of moving lactating cows to summer pastures raising replacement heifers recently gained much importance. Here, we analysed the impact of these changes in dairy farming on butterfly diversity inhabiting Alpine summer pastures in the eastern Italian Alps. We sampled butterflies (Lepidoptera) in 16 Alpine summer pastures that were either grazed by lactating cows (n = 11) or replacement heifers (n = 5) at two distances from the farm building. Butterflies were classified according to their mobility. Our results showed a distance effect on total butterfly species richness only in pastures grazed by lactating cows indicating a stronger impact on vegetation structure and composition nearby the farm building. Abundance of butterflies was higher with increasing distance from the farm building. In contrast to mobile butterflies, sedentary species reacted more strongly to disturbance induced by grazing livestock. Moreover, butterfly composition differed slightly between pastures grazed by lactating cows and heifers. Our results indicate that the widespread adoption of heifer grazing induces a shift in butterfly diversity and composition likely caused by the different behaviour of grazing livestock. In order to benefit butterfly diversity in Alpine summer pastures, we suggest that future agri-environment schemes should provide extra support for summer farming of lactating cows.

Keywords: Agri-environment schemes; Agricultural intensification; Grazing; Mountain agriculture; Replacement heifers; Semi-natural grassland

Agriculture, Ecosystems and Environment

Volume 232, Pages 38-45

Entomology

First record of the Kuwana pine mealybug *Crisicoccus pini* (Kuwana) in Italy: A new threat to Italian pine forests?

Boselli, M.[a], *Pellizzari, G.*[b]

[a] Servizio Fitosanitario, Regione Emilia Romagna, Via di Saliceto, 81, Bologna, Italy
[b] Università di Padova, Dipartimento DAFNAE, Viale dell'Università 16, Legnaro, Italy

Abstract

The Asiatic Kuwana pine mealybug, *Crisicoccus pini* (Kuwana, 1902) (Hemiptera, Pseudococcidae), is reported in Italy for the first time. It was detected in September 2015 on maritime pine, Pinus pinaster, and stone pine, Pinus pinea, trees growing in the town of Cervia (Ravenna Province), Northern Italy. The mealybug has caused yellowing and decline of the pine trees. Pinus pinea is recorded here as a new host for C. pini.

Zootaxa

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Web-based automatic traps for early detection of alien wood-boring beetles

Rassati, D.[a]*, Faccoli, M.*[a]*, Chinellato, F.*[a]*, Hardwick, S.*[b]*, Suckling, D.M.*[c]*,*
Battisti, A.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Legnaro, Italy
[b] New Zealand and Better Border Biosecurity, AgResearch Limited, Lincoln, New Zealand
[c] New Zealand and Better Border Biosecurity, The New Zealand Institute for Plant & Food Research Limited, Lincoln, New Zealand

Abstract

The demand for automatic devices for remote monitoring of ecological variables is rapidly increasing because of the benefits of saving time, –reducing or avoiding direct field observations, solving logistical problems, and improving data consistency. In recent decades, remote cameras have been used mainly in plant studies and wildlife monitoring. Nevertheless, a few recent studies have focused on the possible use of cameras for detecting and monitoring insect occurrence and activity. Tools that can check insect traps remotely and automatically could be useful, for instance, for the early detection of invasive alien species at high-risk sites. Traps set up for the early detection of alien species are now common in many countries, but they must be frequently inspected, as specific actions should be taken immediately when a quarantine species is intercepted. The aims of the present study were to test the effectiveness of two camera models in monitoring bark and wood-boring beetles, and to explore their possible use for the early detection of alien bark and longhorn beetles at ports of entry. The devices presented in this paper show potential as tools for the remote checking of traps deployed for intercepting alien wood-boring beetles arriving at high-risk sites, as well as for the early detection of target species for which species-specific pheromones are available. Many camera integrated traps can be used simultaneously and independently in as many sites as needed, avoiding complex and expensive logistic organization. On-site checking of the trap is needed whenever a change of battery pack or lure is necessary, or when the collection of target insects is required. Our study suggests the applicability of camera-integrated traps for the monitoring and early detection of alien wood-boring beetles. The price of a camera is comparable to that of a medium-high range smart phone, to which the cost for the safe repository of the images on the internet has to be added. Given that the resources for monitoring and surveillance programs are often scarce, a decrease of the overall costs must be considered as the main achievement to reach in the next years. Further development may also consist of better integration of the camera in the trap, i.e., miniaturizing the camera components, and increased image quality and battery life.

Keywords: Bark beetles; BioCam; Biological invasions; Camera-integrated trap; Coleoptera; Exotic species; Longhorn beetles; RedEye; Remote monitoring; Surveillance; Trapping

Entomologia Experimentalis et Applicata

Volume 160, Issue 1, Pages 91-95s

Arbuscular mycorrhizal colonization in black poplar roots after defoliation by a non-native and a native insect

Zampieri, E.[a], Petrucco Toffolo, E.[b], Mello, A.[c], Giorcelli, A.[d], Faccoli, M.[b], Balestrini, R.[c], Gonthier, P.[a]

[a] Dipartimento di Scienze Agrarie, Forestali e Alimentari (DISAFA), Università di Torino, l.go Paolo Braccini 2, Grugliasco, TO, Italy
[b] Dipartimento di Agronomia, Animali, Alimenti, Risorse naturali e Ambiente Agripolis, Università di Padova, v.le dell'Università 16, Legnaro, PD, Italy
[c] Istituto per la Protezione Sostenibile delle Piante, CNR, SS Torino, v.le Mattioli 25, Torino, Italy
[d] CREA - Consiglio per la Ricerca in Agricoltura e l'Analisi dell'Economia Agraria, Unità di Ricerca per le Produzioni Legnose Fuori Foresta (CREA-PLF), str. Frassineto 35, Casale M.to, AL, Italy

Abstract

A major goal in ecology is to understand how interactions among organisms influence ecosystem services. This work compares the effects of two Lepidoptera defoliators, one non-native (*Hyphantria cunea*) and one native (*Lymantria dispar*) to Europe, on the colonization of black poplar (the *Populus nigra* clone "Jean Pourtet") roots by an arbuscular mycorrhizal (AM) symbiotic fungus (*Funneliformis mosseae*) in a pot experiment. The effects of defoliation have also been assessed on the expression of fungal and plant genes playing a role during symbiosis. Both control and defoliated poplars have shown a low level of mycorrhization. Additionally, neither the non-native nor the native insect seem to strongly affect the AM colonization, at least at the time of observation (eight days from the end of the defoliation). Concerning the gene expression analysis, our results suggest that defoliation does not influence neither the expression of genes coding for a fungal and a plant phosphate transporter nor that of a gene coding for a fungal ATPase, and that there were no differences between defoliation carried out by the non-native and the native insect.

Keywords: Arbuscular mycorrhizal symbiosis; Defoliators; Exotic; Gene expression; Poplar; QPCR

IForest

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Are *Phenacoccus solani* Ferris and *P. defectus Ferris* (Hemiptera: Pseudococcidae) distinct species?

Chatzidimitriou, E.[a]*, Simonato, M.*[a]*, Watson, G.W.*[b]*, Martinez-Sañudo, I.*[a]*,*
Tanaka, H.[c]*, Zhao, J.*[d]*, Pellizzari, G.*[a]

[a] University of Padova, Dipartimento di Agronomia, Animali, Alimenti, Risorse Naturali e Ambiente DAFNAE, viale dell'Università 16, Legnaro, Italy
[b] California Department of Food and Agriculture, Plant Pest Diagnostic Center, 3294 Meadowview Road, Sacramento, CA, United States
[c] Entomological Laboratory, Faculty of Agriculture, Ehime University, Tarumi 3-5-7, Matsuyama, Japan
[d] Institute of Plant Protection, Jiangsu Academy of Agricultural Sciences, Zhongling Street No. 50, Nanjing, China

Abstract

Among the Nearctic species of *Phenacoccus* (Hemiptera: Pseudococcidae), *Phenacoccus solani* Ferris and *P. defectus* Ferris are morphologically similar and it can be difficult to separate them on the basis of microscopic morphological characters of the adult female alone. In order to resolve their identity, a canonical variates morphological analysis of 199 specimens from different geographical origins and host plants and a molecular analysis of the COI and 28S genes were performed. The morphological analysis supported synonymy of the two species, as although the type specimens of the "species" are widely separated from each other in the canonical variates plot, they are all part of a continuous range of variation. The molecular analysis showed that *P. solani* and *P. defectus* are grouped in the same clade. On the basis of the morphological and molecular analyses, *P. defectus* is synonymized under the senior name *P. solani*, syn. n.

Keywords: Molecular analysis; Morphology; Multivariate analysis; Synonymy

Zootaxa

Volume 4093, Issue 4, Pages 539-551

Development of *Drosophila suzukii* at low temperatures in mountain areas

Tonina, L., Mori, N., Giomi, F., Battisti, A.

Department of Agronomy Food Natural resources Animals and Environment (DAFNAE),
University of Padova, Viale dell'Università, 16, Legnaro, PD, Italy

Abstract

As a fly tracking the availability of fruits along climatic gradients, *Drosophila suzukii* is deemed to be rather flexible in relation to environmental factors, among which temperature is a major player. We sampled potential wild host fruits of *D. suzukii* along two elevational gradients in mountain areas of north-eastern Italy, in order to measure fly performance in relation to temperature. In addition, we used a strong natural temperature gradient in an open-top cave, covering the lower range of temperatures known for *D. suzukii*, to deploy laboratory stock colonies to mimic conditions existing along elevational gradients. At least nine wild host species yielded adults of *D. suzukii* in the mountain area (*Daphne mezereum*, *Lonicera alpigena*, *Lonicera caerulea*, *Lonicera nigra*, *Lonicera xylosteum*, *Rubus caesius*, *Rubus saxatilis*, *Sambucus nigra*, and *Sambucus racemosa*) when the daily average temperature in the three preceding weeks was at least 11.1 °C. Similar results were obtained with the laboratory colonies reared on an artificial medium in the cave, where oviposition and development from egg to adult occurred at above 11.6 °C. Both values are lower than previously recorded lower thresholds for development at both constant and fluctuating temperatures. These findings indicate that *D. suzukii* performs well at low temperatures, suggesting that population buildup may occur even under these conditions, with likely consequences on crops and wild host reproduction.

Keywords: Fluctuating temperature; Host plant; Performance; Spotted wing *Drosophila*

Journal of Pest Science

Volume 89, Issue 3, Pages 667-678

High genetic diversity in the *Culex pipiens* complex from a West Nile Virus epidemic area in Southern Europe

Simonato, M.[a], Martinez-Sañudo, I.[a], Cavaletto, G.[a], Santoiemma, G.[a], Saltarin, A.[b], Mazzon, L.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals, and Environment (DAFNAE), University of Padua, Viale dell'Università 16, Legnaro, PD, Italy
[b] Istituto Tecnico Agrario O. Munerati, Via Capello 10, Sant'Apollinare, RO, Italy

Abstract

Background: The *Culex pipiens* complex includes the most widespread mosquito species in the world. *Cx. pipiens* is the primary vector of the West Nile Virus (WNV) in Europe and North America. Cases of WNV have been recorded in Italy since 1998. In particular, wet areas along the Po River are considered some of the most WNV affected areas in Italy. Here, we analyzed the genetic structure of ten *Cx. pipiens* populations collected in the last part of the Po River including the Delta area. Methods: We assessed the genetic variability of two mitochondrial markers, cytochrome oxidase 1 (COI) and 2 (COII), for a total of 1200 bp, and one nuclear marker, a fragment of acetylcholinesterase-2 (ace-2), 502 bp long. The effect of the landscape features was evaluated comparing haplotype and nucleotide diversity with the landscape composition. Results: The analysis showed a high genetic diversity in both COI and COII gene fragments mainly shared by the populations in the Delta area. The COI-COII network showed that the set of haplotypes found was grouped into three main supported lineages with the higher genetic variability gathered in two of the three lineages. By contrast, ace-2 fragment did not show the same differentiation, displaying alleles grouped in a single clade. Finally, a positive correlation between mitochondrial diversity and natural wetland areas was found. Conclusions: The high mitochondrial genetic diversity found in *Cx. pipiens* populations from the Po River Delta contrasts with the low variability of inland populations. The different patterns of genetic diversity found comparing mitochondrial and nuclear markers could be explained by factors such as differences in effective population size between markers, sex biased dispersal or lower fitness of dispersing females. Moreover, the correlation between genetic diversity and wetland areas is consistent with ecosystem stability and lack of insecticide pressure characteristic of this habitat. The mtDNA polymorphism found in the Po River Delta is even more interesting due to possible linkages between the mitochondrial lineages and different biting behaviors of the mosquitoes influencing their vector ability of arboviral infections.

Keywords: Acetylcholinesterase-2; *Culex pipiens* complex; Cytochrome oxidase; Genetic diversity; Mitochondrial DNA; Mosquitoes; Nuclear DNA; West Nile Virus

Parasites and Vectors

Volume 9, Article number 150

Prolonged pupal diapause drives population dynamics of the pine processionary moth (*Thaumetopoea pityocampa*) in an outbreak expansion area

Salman, M.H.R.[a]*, Hellrigl, K.*[b]*, Minerbi, S.*[c]*, Battisti, A.*[a]

[a] Department of Agronomy, Food, Natural Resources, Animals, and Environment (DAFNAE), University of Padua, Viale dell'Università 16, Legnaro, PD, Italy
[b] Via Wolkenstein 83, Bressanone/Brixen, Italy
[c] Forest Service of Bolzano/Bozen Province, Italy

Abstract

Due to its negative impact on tree growth and human health, pine processionary moth is a major concern for forest managers, especially in recent outbreak expansion areas. As some individuals have prolonged diapause for more than a single year, population dynamics of this species is hard to understand. To decipher the mechanism of prolonged diapause and its role in population dynamics, we started a pest surveillance program in 1999 in a pine processionary population in the southern-central Alps of northern Italy, a recent range expansion zone for the species. The 16-year study used a pheromone trap network and four large rearing cages. We found some individuals could diapause for up to a maximum of seven years. With few exceptions, prolonged pupal diapause increased and retrieval rate of moth in cages decreased with increasing elevation. Moreover, we found prolonged diapausing individuals to emerge in advance of non-diapausing individuals. This trait allowed us to infer the proportion of prolonged diapausing individuals caught in the pheromone traps. Prolonged diapause was responsible for maintaining high population density for eight years in spite of annual applications of the biocontrol agent *Bacillus thuringiensis kurstaki*. This sustained density relied on individuals from cohorts before the application of insecticide started, and from cohorts not completely suppressed by the insecticide applications.

Keywords: Alps; *Bacillus thuringiensis kurstaki*; Pheromone trap; *Pinus nigra*; Prolonged diapause; Range edge

Forest Ecology and Management

Volume 361, Pages 375-381

Forest health in a changing world: Effects of globalization and climate change on forest insect and pathogen impacts

Ramsfield, T.D.[a], Bentz, B.J.[b], Faccoli, M.[c], Jactel, H.[d], Brockerhoff, E.G.[e]

[a] Canadian Forest Service, Northern Forestry Centre, 5320-122 Street NW, Edmonton, AB, Canada
[b] USDA Forest Service, Rocky Mountain Research Station, 860 N. 1200 East, Logan, UT, United States
[c] Department of Agronomy, Animals and Environment, University of Padua, Viale dell'Università, Legnaro, PD, Italy
[d] INRA, BIOGECO, UMR1202, Cestas, France
[e] Scion (New Zealand Forest Research Institute), PO Box 29237, Christchurch, New Zealand
Better Border Biosecurity Collaboration, New Zealand

Abstract

Forests and trees throughout the world are increasingly affected by factors related to global change. Expanding international trade has facilitated invasions of numerous insects and pathogens into new regions. Many of these invasions have caused substantial forest damage, economic impacts and losses of ecosystem goods and services provided by trees. Climate change is already affecting the geographic distribution of host trees and their associated insects and pathogens, with anticipated increases in pest impacts by both native and invasive pests. Although climate change will benefit many forest insects, changes in thermal conditions may disrupt evolved life history traits and cause phenological mismatches. Individually, the threats posed to forest ecosystems by invasive pests and climate change are serious. Although interactions between these two drivers and their outcomes are poorly understood and hence difficult to predict, it is clear that the cumulative impacts on forest ecosystems will be exacerbated. Here we introduce and synthesize the information in this special issue of Forestry with articles that illustrate the impacts of invasions of insects and pathogens, climate change, forest management and their interactions, as well as methods to predict, assess and mitigate these impacts. Most of these contributions were presented at the XXIV IUFRO World Congress in 2014.

Keywords: Biological invasions; Climate change; Diagnostics; Forest resistance; Modelling; Risk

Forestry

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Transmission of grapevine Pinot gris virus by *Colomerus vitis* (Acari: Eriophyidae) to grapevine

Malagnini, V.[a], de Lillo, E.[b], Saldarelli, P.[c], Beber, R.[d], Duso, C.[f], Raiola, A.[e], Zanotelli, L.[a], Valenzano, D.[b], Giampetruzzi, A.[c], Morelli, M.[c], Ratti, C.[d], Causin, R.[e], Gualandri, V.[a]

[a] Unità di Protezione delle Piante e Biodiversità Agroforestale, Centro di Trasferimento Tecnologico, Fondazione Edmund Mach, via E. Mach, 1, San Michele all'Adige, TN, Italy
[b] Dipartimento di Scienze del Suolo, della Pianta e degli Alimenti, Università degli Studi di Bari "Aldo Moro", via G. Amendola, 165/A, Bari, Italy
[c] CNR Istituto per la Protezione Sostenibile delle Piante, via Amendola 122/D, Bari, Italy
[d] Laboratorio di Virologia e Fitoplasmologia, Università di Bologna, viale Fanin, 44, Bologna, Italy
[e] Dipartimento Territorio e Sistemi Agro-Forestali, Università di Padova, Viale dell'Università 16, Legnaro, Padova, Italy
[f] Dipartimento Agronomia Animali Alimenti Risorse Naturali e Ambiente, Università di Padova, Viale dell'Università 16, Legnaro, Padova, Italy

Abstract

Grapevine Pinot gris virus (GPGV) is a new virus reported in Europe and several other grape-growing countries. In an attempt to identify a vector for GPGV, samples of the eriophyid mite *Colomerus vitis* collected from buds and erinea in GPGV-infected vines were analysed by RT-PCR, using specific primers. Molecular analysis revealed the presence of GPGV in C. vitis. Transmission trials were conducted using *C. vitis* collected from GPGV-infected vines. Mites were able to transmit GPGV to healthy grapevines, suggesting that *C. vitis* is a potential vector of this virus.

Archives of Virology

Volume 161, Issue 9, Pages 2595-2599

Rapid on-site identification of the biocontrol agent of the Asian chestnut gall wasp

Colombari, F.[a], Villari, C.[ab], Simonato, M.[a], Cascone, P.[c], Ferracini, C.[d], Alma, A.[d], Guerrieri, E.[c], Battisti, A.[a]

[a] Department of Agronomy Food Natural resources Animals and Environment (DAFNAE), University of Padova, Legnaro, Italy
[b] Department of Plant Pathology, The Ohio State University, Columbus, OH, United States
[c] Institute for Sustainable Plant Protection, National Research Council of Italy, Portici, Italy
[d] Department of Agricultural, Forest and Food Sciences (DISAFA), University of Torino, Grugliasco, Italy

Abstract

In classical biocontrol programmes, a rapid and correct identification of the introduced antagonist is a key issue during both the release and establishment monitoring phases. It is often difficult to distinguish morphologically cryptic species or immature stages. An accurate diagnosis can now be provided by molecular diagnostic methods. Among the conventional and real-time PCR-based methods, loop-mediated isothermal amplification (LAMP) is a particularly suitable technique as it allows a rapid amplification of target DNA directly in the field. During the programme implemented in Italy against the Asian chestnut gall wasp (ACGW) *Dryocosmus kuriphilus*, we developed a real-time LAMP assay, combined with a simple DNA extraction method, for rapid in-field identification of larvae, pupae, and adults of the biocontrol agent, the parasitoid *Torymus sinensis*. Validation of the assay comprised adults as well as preimaginal stages of parasitoids obtained from ACGW galls collected from different localities. Results confirmed the effectiveness of the LAMP assay to rapidly and specifically identify the target parasitoid in the field. This assay will be a valuable tool for quick on-site checking of the parasitism rate.

Keywords: ACGW; Biocontrol; *Dryocosmus kuriphilus*; LAMP (loop-mediated isothermal amplification); Parasitism rate; *Torymus sinensis*

Biocontrol Science and Technology

Volume 26, Issue 9, Pages 1285-1297

Life history and geographical distribution of the walnut twig beetle, *Pityophthorus juglandis* (Coleoptera: Scolytinae), in southern Europe

Faccoli, M., Simonato, M., Rassati, D.

Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università, Legnaro, PD, Italy

Abstract

In September 2013, the walnut twig beetle (WTB) *Pityophthorus juglandis* Blackman, a species native to Mexico and south-western USA, was recorded for the first time in Europe, in northern Italy. The collected adults were found to be vector of the fungus *Geosmithia morbida* Kolaik, Freeland, Utley & Tisserat, an aggressive pathogen causing thousand cankers disease in walnut (*Juglans* spp.). To determine the geographical distribution of the WTB and the main aspects of biology, phenology and voltinism, an intensive survey of the main walnut plantations near the site of the first finding was conducted in 2014. The beetles began to fly with a mean air temperature of about 18°C (mid-May) and continued until late October. Two partially overlapping generations occurred, with the second taking place in late September. The WTB was found in 14 of the 27 monitored walnut plantations. The infested sites were spread over four different non-contiguous administrative provinces belonging to two regions (Veneto and Lombardy) of northern Italy. The most distant infested plantations were about 130 km apart along a west–east gradient, and about 70 km along a north–south gradient. In this respect, the distribution area of the WTB in northern Italy may be prudently estimated at about 4200 km2. Molecular analysis of the collected individuals showed no genetic differences among the six sampled *P. juglandis* populations, suggesting that a few individuals might have arrived in Italy through a single introduction event and then spread over the territory. Given the quick mortality of infested walnuts and the wide distribution area, eradication strategies appear unrealistic. Possible strategies of biological control or local chemical treatments must be investigated.

Keywords: Alien species; Bark beetles; Biological invasions; Forest pest; Monitoring; Thousand cankers disease

Journal of Applied Entomology

Volume 140, Issue 9, Pages 697-705

Spread of the introduced biocontrol agent *Torymus sinensis* in north-eastern Italy: dispersal through active flight or assisted by wind?

Colombari, F., Battisti, A.

Department of Agronomy Food Natural Resources Animals and Environment (DAFNAE), University of Padova - Agripolis, Via dell'Università 16, Legnaro, PD, Italy

Abstract

In successful classical biological control, natural enemies can provide enduring pest suppression if they reproduce and disperse without continued human management. To explain the efficient control exerted on the Asian chestnut gall wasp *Dryocosmus kuriphilus* Yasumatsu (Hymenoptera: Cynipidae) by the parasitoid *Torymus sinensis* Kamijo (Hymenoptera: Torymidae), it is required that the latter has the capacity to track the range expansion of its host. In the present study, we hypothesized that the distribution of infested patches and the prevailing wind directions would interactively influence and accelerate the spread of the parasitoid. It emerged that the spread capability of *T. sinensis* is high and likely affected by a combination of short- and long-distance flights (stratified dispersal). In particular, the ability to disperse long distances represents a successful trait of the parasitoid because the natural dispersal of its host is high and frequently aided by unintentional human-mediated transportation.

Keywords: Cynipidae; *Dryocosmus kuriphilus*; Hymenoptera; Torymidae; *Torymus sinensis*; Wind

BioControl

Volume 61, Issue 2, Pages 127-139

Two newly introduced tropical bark and ambrosia beetles (Coleoptera: Curculionidae, Scolytinae) damaging figs (*Ficus carica*) in southern Italy

Faccoli, M.[a]*, Campo, G.*[b]*, Perrotta, G.*[c]*, Rassati, D.*[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padua, Viale dell’Università 16, Legnaro (PD), Italy
[b] Regione Siciliana, Assessorato Dell’Agricoltura, Dello Sviluppo Rurale e della Pesca Mediterranea, Servizio 9, Laboratorio di Difesa Fitosanitaria, Via Sclafani, 34, Acireale (CT), Italy
[c] Regione Siciliana, Assessorato Dell’Agricoltura, Dello Sviluppo Rurale e della Pesca Mediterranea, Servizio 18, Ufficio Servizio per Il Territorio di Siracusa, Via S. Giovanni alle Catacombe, 7, Siracusa (SR), Italy

Abstract

In summer 2014, the bark beetle *Hypocryphalus scabricollis* (Eichhoff) and the ambrosia beetle *Xyleborus bispinatus* Eichhoff, species new to Italy and Europe, respectively, were found for the first time in south-eastern Sicily (Italy). Large infestations of the two species were recorded in many plantations of common fig (*Ficus carica* L.) both in 2014 and 2015. Data concerning insect characteristics, taxonomy, and distribution are briefly reported.

Keywords: Biological invasions; Exotic species; *Hypocryphalus scabricollis*; New records; Scolytids; *Xyleborus bispinatus*

Zootaxa

Volume 4138, Issue 1, Pages 189-194

Morphological and molecular identification of *Anagrus 'atomus'* group (hymenoptera: Mymaridae) individuals from different geographic areas and plant hosts in Europe

Zanolli, P.[a], *Martini, M.*[a], *Mazzon, L.*[b], *Pavan, F.*[a]

[a] Department of Agricultural, Food, Environmental and Animal Sciences, University of Udine, Via delle Scienze 206, Udine, Italy
[b] Department of Agronomy Food Natural Resources Animals and Environment, University of Padua, Agripolis, Viale dell'Università 16, Legnaro (Padova), Italy

Abstract

Morphological identification and molecular study on the COI gene were simultaneously conducted on *Anagrus* Haliday '*atomus*' group individuals collected in the field in Italy or supplied from a UK biofactory. Females were morphologically identified as *A. atomus* L. and *A. parvus* Soyka *sensu* Viggiani (=*A. ustulatus sensu* Chiappini). Alignment of COI gene sequences from this study permitted recognition of a total of 34 haplotypes. Phylogenetic and network analyses of molecular data not only confirmed that *A. atomus* is a species distinct from *A. parvus*, but also suggested that two species may be included within morphologically identified *A. parvus*. Different geographical distribution and frequency of haplotypes were also evidenced. For males considered in this study, morphometric analyses revealed a character that could be useful to discriminate *A. atomus* from *A. parvus*. Both species were found in vineyards and surrounding vegetation, confirming the potential role of spontaneous vegetation as a source of parasitoids for leafhopper control in vineyards.

Keywords: COI gene; Identification; Molecular analysis; Morphometry; Mymaridae

Journal of Insect Science

Volume 16, Issue 1, Article number 38

Bark and ambrosia beetles show different invasion patterns in the USA

Rassati, D.[a], Faccoli, M.[a], Haack, R.A.[b], Rabaglia, R.J.[b], Petrucco Toffolo, E.[a], Battisti, A.[a], Marini, L.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals, and Environment (DAFNAE), University of Padua, Legnaro (PD), Italy
[b] USDA Forest Service, Northern Research Station, Lansing, MI, United States; USDA Forest Service, Forest Health Protection, Washington, DC, United States

Abstract

Non-native bark and ambrosia beetles represent a threat to forests worldwide. Their invasion patterns are, however, still unclear. Here we investigated first, if the spread of nonnative bark and ambrosia beetles is a gradual or a discontinuous process; second, which are the main correlates of their community structure; third, whether those correlates correspond to those of native species. We used data on species distribution of non-native and native scolytines in the continental 48 USA states. These data were analyzed through a beta-diversity index, partitioned into species richness differences and species replacement, using Mantel correlograms and non-metric multidimensional scaling (NMDS) ordination for identifying spatial patterns, and regression on distance matrices to test the association of climate (temperature, rainfall), forest (cover area, composition), geographical (distance), and human-related (import) variables with -diversity components. For both non-native bark and ambrosia beetles, -diversity was mainly composed of species richness difference than species replacement. For non-native bark beetles, a discontinuous invasion process composed of long distance jumps or multiple introduction events was apparent. Species richness differences were primarily correlated with differences in import values while temperature was the main correlate of species replacement. For non-native ambrosia beetles, a more continuous invasion process was apparent, with the pool of non-native species arriving in the coastal areas that tended to be filtered as they spread to interior portions of the continental USA. Species richness differences were mainly correlated with differences in rainfall among states, while rainfall and temperature were the main correlates of species replacement. Our study suggests that the different ecology of bark and ambrosia beetles influences their invasion process in new environments. The lower dependency that bark beetles have on climate allowed them to potentially colonize more areas within the USA, while non-native ambrosia beetles, being dependent on rainfall, are typically filtered by the environment.

PLoS ONE

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Investigating Biological Control Agents for Controlling Invasive Populations of the Mealybug *Pseudococcus comstocki* in France

Malausa, T.[a], Delaunay, M.[a], Fleisch, A.[a], Groussier-Bout, G.[a], Warot, S.[a], Crochard, D.[a], Guerrieri, E.[b], Delvare, G.[c], Pellizzari, G.[d], Kaydan, M.B.[e], Al-Khateeb, N.[f], Germain, J.-F.[g], Brancaccio, L.[a], Le Goff, I.[a], Bessac, M.[a], Ris, N.[a], Kreiter, P.[a]

[a] INRA, Univ. Nice Sophia Antipolis, CNRS, UMR 1355-7254 Institut Sophia Agrobiotech, 06900, Sophia Antipolis, France
[b] Istituto per la Protezione Sostenibile delle Piante, Consiglio Nazionale delle Ricerche, Via Università 133, 80055 Portici, Napoli, Italy
[c] CIRAD, UMR CBGP INRA CIRAD Montpellier Supagro, 755 avenue du Campus Agropolis, CS 30016, 34988, Montferrier-sur-Lez Cedex, France
[d] Università di Padova, Dipartimento Agronomia, Animali, Alimenti, Risorse naturali e Ambiente, Viale dell'Università 16, 35020, Legnaro, Italy
[e] Imamoglu Vocational School, Çukurova University, Adana, 01330, Turkey
[f] Lattakia Center for Rearing Natural Enemies, Lattakia, Syria
[g] ANSES, Laboratoire de la Santé des Végétaux, Unité d'entomologie et Plantes Invasives 755 avenue du Campus Agropolis, CS 30016, Montferrier-sur-Lez, France

Abstract

Pseudococcus comstocki (Hemiptera: Pseudococcidae) is a mealybug species native to Eastern Asia and present as an invasive pest in northern Italy and southern France since the start of the century. It infests apple and pear trees, grapevines and some ornamental trees. Biocontrol programmes against this pest proved successful in central Asia and North America in the second half of the 20th century. In this study, we investigated possible biocontrol agents against P. comstocki, with the aim of developing a biocontrol programme in France. We carried out systematic DNA-barcoding at each step in the search for a specialist parasitoid. First we characterised the French target populations of *P. comstocki*. We then identified the parasitoids attacking *P. comstocki* in France. Finally, we searched for foreign mealybug populations identified a priori as *P. comstocki* and surveyed their hymenopteran parasitoids. Three mealybug species (*P. comstocki*, *P. viburni* and *P. cryptus*) were identified during the survey, together with at least 16 different parasitoid taxa. We selected candidate biological control agent populations for use against P. comstocki in France, from the species *Allotropa burrelli* (Hymenoptera: Platygastridae) and *Acerophagus malinus* (Hymenoptera: Encyrtidae). The coupling of molecular and morphological characterisation for both pests and natural enemies facilitated the programme development and the rejection of unsuitable or generalist parasitoids.

PloS ONE

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Vineyard colonization by *Hyalesthes obsoletus* (Hemiptera: Cixiidae) induced by stinging nettle cut along surrounding ditches

Mori, N.[a], Pozzebon, A.[a], Duso, C.[a], Reggiani, N.[b], Pavan, F.[c]

[a] Department of Agronomy, Food, Natural Resources, Animals, Environment (DAFNAE), University of Padova, Viale dell'Università, 16, Legnaro (Padova), Italy
[b] Consorzio Fitosanitario Provinciale di Modena, Via Santi 14, Direzionale Cialdini, Modena, Italy
[c] Department of Agricultural and Environmental Science, University of Udine, Via delle Scienze 206, Udine, Italy

Abstract

Stinging nettle (*Urtica dioica* L.) is the most important host plant for both phytoplasma associated with Bois noir disease of the grapevine and its vector *Hyalesthes obsoletus* Signoret (Hemiptera: Cixiidae). Vector abundance in vineyards is favored by stinging nettle growing in surrounding areas. Nettle control by herbicides or cutting can reduce vector population in vineyards. However, chemical weeding can cause environmental problems. Many authors suggest that stinging nettle control applied during *H. obsoletus* flight could force adults to migrate into vineyards. We evaluate if cutting of nettle growing along ditches during adult flight favors vineyard colonization by *H. obsoletus*. Three different weed management regimes ("no cuts, " "one cut" just before the beginning of adult flight, and "frequent cuts" over the whole vegetative season) were applied to the herbaceous vegetation in ditches bordering two vineyards. The flight dynamics of *H. obsoletus* were recorded by placing yellow sticky traps on the vegetation along the ditches and at different positions in the vineyards. Frequent stinging nettle cuts (compared with a single cut) in surrounding areas favored the dispersion of vectors inside the vineyards. Stinging nettle control should be based on an integration of a single herbicide application before *H. obsoletus* emergence followed by frequent cuts to minimize negative side effects of chemical weeding. In organic viticulture, a frequent-cuts strategy should avoid cuts during *H. obsoletus* flight period, at least in the first year of adoption.

Keywords: Bois noir; Integrated weed management; Urtica dioica; Vector control

Journal of Economic Entomology

Volume 109, Issue 1, Pages 49-56

Analysis of costs and benefits of Asian longhorned beetle eradication in Italy

Faccoli, M.[a], *Gatto, P.*[b]

[a] Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padua, Agripolis - Viale dell'Universita 16, Legnaro, PD, Italy
[b] Department of Land, Agriculture and Forestry (TESAF), University of Padua, Agripolis - Viale dell'Universita 16, Legnaro, PD, Italy

Abstract

The Asian longhorned beetle (ALB), *Anoplophora glabripennis* (Coleoptera: Cerambycidae), is one of the most harmful invasive species in Europe and North America, causing enormous economic damage to broadleaved trees growing in urban parks and gardens. As a quarantine species, everywhere it has been introduced ALB has led to the application of expensive eradication programmes often associated with additional indirect costs due to the loss of ornamental value connected with the presence of trees in urban areas. The aims of this article are to quantify the impact of ALB in terms of tree mortality and their ornamental value during the first year eradication of an infestation in Northern Italy, and to perform an economic assessment of the eradication programme vs inaction. During the first year of eradication 367 ALB infested trees were removed from the infestation area at a total cost of about €48 000, comprising scientific advice (21 per cent), tree survey (38 per cent) and plant removal (41 per cent). The ornamental value of the infested trees was assessed at about €850 per tree. The ALB eradication programme allowed a reduction of 52 per cent of the damage expected in the following year, corresponding to an ornamental value of about €300 000. The ornamental value of the saved trees was 6 times higher than the costs for their protection.

Forestry

Volume 89, Issue 3, Pages 301-309

Host preference and host colonization of the Asian long-horned beetle, *Anoplophora glabripennis* (Coleoptera Cerambycidae), in Southern Europe

Faccoli, M., Favaro, R.

Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padua, Agripolis - Viale dell'Universita 16, Legnaro, PD, Italy

Abstract

The Asian long-horned beetle (ALB), *Anoplophora glabripennis* (Motschulsky), is a highly polyphagous invasive pest with a broad range of host species, but showing relevant differences between infestation areas. Host preference and host colonization (female fecundity, egg and larval survival) were assessed in a population in Northern Italy by choice and no-choice experiments conducted in both field and laboratory conditions. During 5 years of field observations, ALB was found to infest seven genera of trees: *Acer*, *Aesculus*, *Betula*, *Populus*, *Prunus*, *Salix* and *Ulmus*. However, *Acer*, *Betula*, *Ulmus* and *Salix* resulted to be the preferred hosts corresponding to 97.5% (1112) of the 1140 infested trees. In both laboratory and field trials carried out on these four host genera, no-choice experiments recorded the highest host colonization of *A. glabripennis* on *Acer* trees, with the highest number of laid eggs and the lowest egg and larval mortality. *Ulmus* and *Salix* showed a lower number of laid eggs during laboratory choice test, but egg and larval mortality had mean values similar to *Acer*. On the contrary, despite the high number of *Betula* trees felled during the eradication plan carried out in the infestation area, this tree species showed the lowest beetle suitability in terms of number of laid eggs and insect survival. An overestimation of the number of infested *Betula* occurring during the tree survey may explain the discordance between high number of infested *Betula* and low beetle suitability. Instead, the large number of infested *Acer* recorded in the field was probably due to the high abundance of these trees occurring in parks and gardens within the infestation area and to the low adult dispersal of *A. glabripennis*. Overall, results from this study confirm that host species affects both beetle colonization and breeding performance. The study shows ALB host preference and host suitability varying between tree species, suggesting an ALB acceptance even of sub-optimal hosts.

Keywords: ALB; Choice; No-choice; Oviposition; Survival

Bulletin of Entomological Research

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Egg mortality in the cedar processionary moth, *Thaumetopoea bonjeani* (Lepidoptera: Notodontidae), in an outbreak area of Algeria

Rahim, N.[a], *Chakali, G.*[a], *Battisti, A.*[b]

[a] Département de Zoologie Agricole et Forestière, École Nationale Supérieure Agronomique (ENSA), Algiers, Algeria
[b] DAFNAE-Entomology, University of Padova, Padova, Italy

Abstract

The cedar processionary moth, *Thaumetopoea bonjeani* (Lepidoptera: Notodontidae), is one of the most serious pests of *Cedrus atlantica* in north-western Africa (Algeria and Morocco). We report on *T. bonjeani* egg mortality and the diversity and abundance of parasitoids associated with its eggs in the area of Djurdjura Mountain (Tala-Guilef, Algeria). For this goal, 223 egg batches were collected from *C. atlantica* over two cohorts (2012 and 2013). The average number of eggs per egg batch increased from 143 in 2012 to 171 in 2013, while the egg mortality decreased from 47.4% and 23.9%, respectively, possibly because of a dilution effect. The most important factors of egg mortality were parasitoids and predators, with hymenopteran egg parasitoids killing from 12.1% to 34.9%, and predators from 5.2% to 7.4% of the eggs. The pattern of egg parasitism was driven largely by *Ooencyrtus pityocampae*, accounting for about 94% of the total parasitoids, followed by *Baryscapus servadeii* and *Trichogramma embryophagum*. An hyperparasitoid *Chartocerus* sp. was collected for the first time from eggs of *Thaumetopoea* species. As the two major egg parasitoids are shared with the pine processionary moth *Thaumetopoea pityocampa* in the same area, it is likely that parasitoid abundance may depend on the occurrence of both hosts.

Keywords: Algeria; *Cedrus atlantica*; Egg mortality; Parasitoids; Predators; *Thaumetopoea bonjeani*

Biocontrol Science and Technology

Volume 26, Issue 6, Pages 849-860

Spillover of tachinids and hoverflies from different field margins

Inclán, D.J.[ab], Dainese, M.[ac], Cerretti, P.[ad], Paniccia, D.[d], Marini, L.[a]

[a] DAFNAE-Entomology, University of Padova, Viale dell'Università 16, Legnaro, Padova, Italy
[b] Museo Ecuatoriano de Ciencias Naturales del Instituto Nacional de Biodiversidad, Sección Invertebrados, Rumipamba 341 y Av. de los Shyris, Quito, Ecuador
[c] Department of Land, Environment, Agriculture and Forestry, University of Padova, Viale dell'Università 16, Legnaro, Padova, Italy
[d] Department of Biology and Biotechnology Charles Darwin, Sapienza University of Rome, Piazzale A. Moro 5, Rome, Italy; Via Colle 13, Frosinone, Italy

Abstract

The introduction and conservation of field margins have been proposed as an intervention to counteract the decline in farmland biodiversity. However, how these margins can affect the movement of species and individuals (i.e. spillover) of natural enemies between field margins and crop is still unclear. In this work, we investigated the spillover of two different groups of natural enemies: tachinids (Diptera: Tachinidae) and aphidophagous hoverflies (Diptera: Syrphidae). For comparison we also investigated the response of non-aphidophagous hoverflies. We examined the spillover from two types of field margin (grass margin vs. hedgerow + grass margin) to adjacent maize fields located in landscapes with different proportion of arable land. The spillover of natural enemies was affected by the field margins, but the response varied between insect groups. The spillover of tachinids was higher from the grass margin than from hedgerows, suggesting that the spillover of this group may be related to the low contrast between the vegetation structure of the margin and the crop. In contrast to tachinids, the abundance of aphidophagous hoverflies was higher toward the center of the crop field, independently of the type of field margin. The spillover of non-aphidophagous hoverflies was not affected by the type of field margin. These species were only affected by the landscape composition as their species richness and abundance were higher in landscapes with low amounts of arable land. Measures focusing on the creation and management of field margins need to consider the local contrast between field margins and crops in relation to the life-history traits of different taxa.

Keywords: Agri-environment schemes; Agricultural intensification; Hedgerows; Natural enemies; Parasitoids; Species movement

Basic and Applied Ecology

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Habitat and climatic preferences drive invasions of non-native ambrosia beetles in deciduous temperate forests

Rassati, D., Faccoli, M., Battisti, A., Marini, L.

Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università, 16, Legnaro, PD, Italy

Abstract

The introduction of non-native ambrosia beetles can cause severe damage in forest ecosystems. Understanding the environmental drivers affecting their invasion at the local scale is of utmost importance to enhancing management strategies. Our objectives were: (1) to determine the influence of forest composition, forest structure, and climate on invasion success of non-native ambrosia beetles in deciduous temperate forests, and (2) to test the effect of host tree species on colonization success by non-native ambrosia beetles. In 2013, we sampled 25 forest stands located in North-East Italy belonging to three forest types dominated respectively by hop hornbeam, chestnut, and beech. Both ethanol-baited traps and trap-logs of five tree species (hop hornbeam, chestnut, beech, manna ash, and black locust) were used to sample non-native and native ambrosia beetle communities. We found a clear effect of forest composition on non-native species richness and activity-density, as measured in ethanol-baited traps, both of which were higher in chestnut-dominated forests. Furthermore, we found a positive effect of temperature on both the number of trapped non-native species and their activity-density, with cold temperatures limiting beetle spread in high-elevation forests. Only *Xylosandrus germanus* successfully colonized the trap-logs. The number of colonized logs was higher for chestnut and in chestnut-dominated forests. Both trapping and log-baiting indicated that chestnut-dominated forests were at greater risk of invasion than hop hornbeam- and beech-dominated forests. Given the economic and ecological importance of chestnut, ambrosia beetle communities present in chestnut-dominated forests should be monitored to determine where protective measures must be taken.

Keywords: Alien species; Colonization success; Monitoring; Pests; Scolytinae; Temperature

Biological Invasions

Volume 18, Issue 10, Pages 2809-2821

Native and introduced parasitoids in the biocontrol of *Dryocosmus kuriphilus* in Veneto (Italy)

Colombari, F., Battisti, A.

Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Agripolis, Legnaro, Italy

Abstract

The invasive gallmaker *Dryocosmus kuriphilus* is a threat to chestnut stands and it is necessary to control it in order to maintain a satisfactory nut yield. A preliminary evaluation of the native natural enemies emerging from the galls, mainly parasitoids associated with native cynipid gallmakers, revealed that they were not able to contain the pest. Consequently, a classical biological control programme using *Torymus sinensis* started in 2010, with almost 500 releases being made in 6 years. The parasitoid achieved a satisfactory level of control of the pest over a period of time shorter than expected based on literature related to other countries. The success in the study area might be explained by specific traits intrinsic to *T. sinensis*, such as its high spread capability via stratified dispersal (i.e. a combination of short- and long-distance flights), together with a large availability of host galls and limited competition with other parasitoids.

EPPO Bulletin

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The invasive mealybug *Paracoccus burnerae* expands its range: New distribution and host-plant records

Masten Milek, T.[a], Pellizzari, G.[b]

[a] Institute for Plant Protection, Croatian Centre for Agriculture, Food and Rural Affairs,
Svetošimunska 25, Zagreb, Croatia
[b] Dipartimento di Agronomia, Animali, Alimenti, Risorse Naturali e Ambiente, DAFNAE,
University of Padova, Viale dell'Università 16, Legnaro, Italy

Abstract

The invasive mealybug *Paracoccus burnerae* (Brain) (Hemiptera Pseudococcidae) is recorded from Gran Canaria (Canary Islands) and Yemen for the first time. Comments on the present world distribution of this polyphagous species and new host-plant records are also provided.

Keywords: Canary Islands; Coccomorpha; Distribution; Host-plants; Pseudococcidae; Yemen

Bulletin of Insectology

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Non-crop plants used as hosts by *Drosophila suzukii* in Europe

Kenis, M.[a], Tonina, L.[b], Eschen, R.[a], van der Sluis, B.[c], Sancassani, M.[b], Mori, N.[b], Haye, T.[a], Helsen, H.[a]

[a] CABI, Delémont, Switzerland
[b] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Legnaro, PD, Italy
[c] Applied Plant Research, Wageningen University & Research, Zetten, Netherlands

Abstract

The invasive spotted wing drosophila *Drosophila suzukii*, a fruit fly of Asian origin, is a major pest of a wide variety of berry and stone fruits in Europe. One of the characteristics of this fly is its wide host range. A better knowledge of its host range outside cultivated areas is essential to develop sustainable integrated pest management strategies. Field surveys were carried out during two years in Italy, the Netherlands and Switzerland. Fruits of 165 potential host plant species were collected, including mostly wild and ornamental plants. Over 24,000 *D. suzukii* adults emerged from 84 plant species belonging to 19 families, 38 of which being non-native. Forty-two plants were reported for the first time as hosts of *D. suzukii*. The highest infestations were found in fruits of the genera *Cornus*, *Prunus*, *Rubus*, *Sambucus* and *Vaccinium* as well as in *Ficus carica*, *Frangula alnus*, *Phytolacca americana* and *Taxus baccata*. Based on these data, management methods are suggested. Ornamental and hedge plants in the vicinity of fruit crops and orchards can be selected according to their susceptibility to *D. suzukii*. However, the widespread availability and abundance of non-crop hosts and the lack of efficient native parasitoids suggest the need for an area-wide control approach.

Keywords: Fruit fly; Host range; Invasive species; Spotted wing drosophila

Journal of Pest Science

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Relative infestation level and sensitivity of grapevine cultivars to the leafhopper empoasca vitis (Hemiptera: Cicadellidae)

Fornasiero, D.[a], Pavan, F.[b], Pozzebon, A.[a], Picotti, P.[b], Duso, C.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals, Environment (DAFNAE), University of Padua, Viale dell'Università , 16, Agripolis, Legnaro, Padova, Italy
[b] Department of Agricultural and Environmental Science (DISA), University of Udine, Via delle Scienze, 206, Udine, Italy

Abstract

The leafhopper *Empoasca vitis* (Gö the) (Hemiptera: Cicadellidae) feeds on veins of grapevine leaves, mainly on the phloem, causing physiological injury, color change and drying of leaf margins, yield and sugar content reduction. The relative infestation level (i.e., the probability that a plant is attacked by herbivores) of *E. vitis* on different grapevine cultivars and their sensitivity (i.e., the incidence of symptoms expression in response to herbivore feeding or other stimuli) to this pest were studied over four years in two vineyards located in northeastern Italy. Some cultivars (e.g., Carménère and Sauvignon Blanc) were usually more infested than others (e.g., Cabernet Sauvignon and Pinot Gris) , although some differences were observed among years and sites. The sensitivity varied among cultivars, i.e., some of them showed more symptoms than expected on the basis of infestation levels (e.g., Carménère and Merlot) , in contrast with others (e.g., Rhine Riesling and Chardonnay) . Information obtained can be used within the framework of integrated pest management in vineyards. Action thresholds should differ on the basis of sensitivity. Sampling must first be carried out on the most susceptible cultivar and, if the action threshold is exceeded, it should be extended to the remaining cultivars based on their decreasing relative infestation level.

Keywords: Action threshold; *Empoasca vitis*; Grape; Infestation level; Sensitivity

Journal of Economic Entomology

Volume 109, Issue 1, Pages 416-425

A little further south: Host range and genetics of the Northern pine processionary moth, *Thaumetopoea pinivora* (Lepidoptera: Notodontidae) at the southern edge of its distribution

Hódar, J.A.[a], Cassel-Lundhagen, A.[b], Battisti, A.[c], Larsson, S.[b]

[a] Departamento de Ecología, Facultad de Ciencias, Universidad de Granada, Granada, Spain
[b] Department of Ecology, Swedish University of Agricultural Sciences, Box 7044, Uppsala, Sweden
[c] DAFNAE-Entomologia, Agripolis, Universitá di Padova, Via Romea 16, Legnaro, Italy

Abstract

The Northern pine processionary moth, *Thaumetopoea pinivora* (Treitschke, 1834) shows a highly scattered distribution with fragmented populations across Europe. A previous study exploring the postglacial history of *T. pinivora* defined it as a cold-tolerant relict species and concluded that a progressive reduction of suitable habitats after the postglacial expansion from refugia in the southern Iberian peninsula best explained the distribution and genetic structure of populations of this species. However, recent records, both by us and others, challenge this view. Surprisingly, some of the newly found populations from southern Spain use black pine, *Pinus nigra* J.F. Arnold as a host plant despite the fact that the typical host of the species, Scots pine, *Pinus sylvestris* L. occurs in the area. We provide genetic data for one of these recently found southern populations where the larvae feed on *P. nigra*, and compare this with previously published data on individuals collected on *P. sylvestris*. This data reveals that populations from different host trees are no more genetically differentiated than populations sharing the same host plant. The findings of a wider diet breadth open the way to widen the search for the still unidentified glacial refugium of *T. pinivora*, and as such may contribute to a better understanding about how the species has spread across Europe.

Keywords: Deforestation; Genetic diversity; Host shift; Lepidoptera; Marginal woodlands; Notodontidae; Relict populations; Thaumetopoea pinivora

European Journal of Entomology

Volume 113, Issue 1, Pages 200-206

Bacterial communities associated with invasive populations of *Bactrocera dorsalis* (Diptera: Tephritidae) in China

Liu, L.J.[a], Martinez-Sañudo, I.[b], Mazzon, L.[b], Prabhakar, C.S.[ac], Girolami, V.[b], Deng, Y.L.[d], Dai, Y.[a], Li, Z.H.[a]

[a] Department of Entomology, College of Plant Protection, China Agricultural University, Beijing, China
[b] Dipartimento di Agronomia Ambientale e Produzioni Vegetali, Università di Padova - Agripolis, Viale Dell'Università, Legnaro, Padova, Italy
[c] Department of Entomology, Bihar Agricultural University, Sabour- Bhagalpur, Bihar, India
[d] Xishuangbanna Entry-Exit Inspection and Quarantine Bureau, Xishuangbanna, Yunnan, China

Abstract

The oriental fruit fly *Bactrocera dorsalis* (Hendel) is a destructive insect pest of a wide range of fruits and vegetables. This pest is an invasive species and is currently distributed in some provinces of China. To recover the symbiotic bacteria of *B. dorsalis* from different invasion regions in China, we researched the bacterial diversity of this fruit fly among one laboratory colony (Guangdong, China) and 15 wild populations (14 sites in China and one site in Thailand) using DNA-based approaches. The construction of 16S rRNA gene libraries allowed the identification of 24 operational taxonomic units of associated bacteria at the 3% distance level, and these were affiliated with 3 phyla, 5 families, and 13 genera. The higher bacterial diversity was recovered in wild populations compared with the laboratory colony and in samples from early term invasion regions compared with samples from late term invasion regions. Moreover, *Klebsiella pneumoniae* and *Providencia* sp. were two of the most frequently recovered bacteria, present in flies collected from three different regions in China where *B. dorsalis* is invasive. This study for the first time provides a systemic investigation of the symbiotic bacteria of *B. dorsalis* from different invasion regions in China.

Keywords: Bacteria diversity; Bactrocera dorsalis; Invasion population; Laboratory colony; Wild population

Bulletin of Entomological Research

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Genetic differentiation of the pine processionary moth at the southern edge of its range: contrasting patterns between mitochondrial and nuclear markers

El Mokhefi, M.[a]*, Kerdelhué, C.*[b]*, Burban, C.*[c]*, Battisti, A.*[d]*, Chakali, G.*[a]*,*
Simonato, M.[d]

[a] Département de Zoologie Agricole et Forestière, Ecole Nationale Supérieure Agronomique, El-Harrach, Algiers, Algeria
[b] INRA, UMR CBGP, Montferrier-sur-Lez, France
[c] BIOGECO, INRA, Univ. Bordeaux, Cestas, France
[d] Department of Agronomy, Food, Natural Resources, Animals, & Environment (DAFNAE), University of Padua, Viale dell'Università 16, Legnaro (PD), Italy

Abstract

The pine processionary moth (*Thaumetopoea pityocampa*) is an important pest of coniferous forests at the southern edge of its range in Maghreb. Based on mitochondrial markers, a strong genetic differentiation was previously found in this species between western (*pityocampa* clade) and eastern Maghreb populations (ENA clade), with the contact zone between the clades located in Algeria. We focused on the moth range in Algeria, using both mitochondrial (a 648 bp fragment of the tRNA-cox2) and nuclear (11 microsatellite loci) markers. A further analysis using a shorter mtDNA fragment and the same microsatellite loci was carried out on a transect in the contact zone between the mitochondrial clades. Mitochondrial diversity showed a strong geographical structure and a well-defined contact zone between the two clades. In particular, in the *pityocampa* clade, two inner subclades were found whereas ENA did not show any further structure. Microsatellite analysis outlined a different pattern of differentiation, with two main groups not overlapping with the mitochondrial clades. The inconsistency between mitochondrial and nuclear markers is probably explained by sex-biased dispersal and recent afforestation efforts that have bridged isolated populations.

Keywords: Algeria; *Cedrus*; Insects; Maghreb; phylogeography; *Pinus*

Ecology and Evolution

Volume 6, Issue 13, Pages 4274-4288

Tree colonization by the Asian longhorn beetle, *Anoplophora glabripennis* (Coleoptera: Cerambycidae): Effect of habitat and tree suitability

Faccoli, M., Favaro, R., Concheri, G., Squartini, A., Battisti, A.

Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, Legnaro (PD), Italy

Abstract

Tree colonization and feeding activity of the invasive wood-borer Asian longhorn beetle (*Anoplophora glabripennis*), an Asian pest introduced into North America and Europe, was studied in a newly invaded area in Italy. The hypothesis being tested was that the reproductive success of the insect depend on habitat type and tree suitability. Adult beetles were caged on branches of host and nonhost species, in both urban and forest habitats. Two months later, number and size of feeding patches on plant tissues, eggs laid, and surviving larvae were assessed. Bark concentration of C and N was also measured from the same trees. Results indicated that the mean area of plant tissues consumed by adult feeding was significantly larger on trees growing in forest than in urban habitat, although within the same habitat there were no differences between susceptible and nonsusceptible trees. ALB tree colonization, in terms of number of eggs laid and young larvae survival, was not affected by habitat while it was higher on susceptible trees. Although trees growing in forests had a lower nitrogen concentration, they allowed colonization rates similar to those of trees growing in the urban habitat. Hence, the amount of carbon and nitrogen did not fully explain tree suitability or habitat selection. We suggest compensatory feeding as a potential mechanism that might explain this peculiar situation, as supported by a more intensive feeding activity recorded on trees in the forest. Suitability of different trees may be due to other factors, such as secondary chemical compounds.

Keywords: Asian longhorn beetle performance; Breeding; Feeding; Forest; Nonhost; Urban

Insect Science

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Conservation tillage reduces the negative impact of urbanisation on carabid communities

Tamburini, G.[a], Pevere, I.[a], Fornasini, N.[a], De Simone, S.[b], Sigura, M.[b], Boscutti, F.[b], Marini, L.[a]

[a] DAFNAE-Entomology, University of Padova, Legnaro, Padova, Italy
[b] Department of Agricultural and Environmental Science, University of Udine, Udine, Italy

Abstract

Urban sprawl has been widely recognised as major cause of biodiversity decline across multiple taxonomic levels. Nevertheless, comprehensive studies investigating the effects of landscape urbanisation and farming practices on arthropod biodiversity in agroecosystems are still scarce. We explored the combined effect of urbanisation in the landscape and tillage management (conservation vs. conventional tillage) on predatory carabid beetle communities (Coleoptera: Carabidae) in 10 pairs of winter cereal fields in the agricultural landscape of Udine province (north-east Italy). Urbanisation (at 750 m scale) strongly decreased carabid activity density, species richness, functional richness and increased functional divergence. We, however, found an interaction between tillage system and the proportion of urban areas in the landscape, i.e., the negative effects of urbanisation on carabid communities were more evident in the fields managed under conventional tillage, while conservation tillage supported more diverse (both taxonomically and ecologically) and abundant beetle communities also in highly urbanised landscapes. We also found that different functional groups differently responded to tillage management. The better local habitat quality provided by conservation tillage may mitigate the negative effects of urbanisation on carabid communities. Our study stresses the importance of considering both local management and landscape composition when planning strategies to support farmland biodiversity.

Keywords: Agricultural intensification; Biodiversity; Carabidae; Functional diversity; Ground beetles; Soil management

Insect Conservation and Diversity

Volume 9, Issue 5, Pages 438-445

Food science and technology

Effect of postharvest temperature and packaging on qualitative traits in strawberry

Nicoletto, C., Bonato, S., Santagata, S., Zanin, G., Sambo, P.

Department of Agronomy, Food, Natural Resources, Animals and Environment,
University of Padova, Padova, Italy

Abstract

Strawberry has antioxidant and nutraceutical properties beneficial for human health and is appreciated by the consumer. As part of the many issues that distinguish this fruit, the postharvest management turns out to be one of the most important in terms of both shelf-life and quality/nutritional product properties. In this paper, several parameters were evaluated in strawberry to understand how they are influenced by innovative packaging and different storage temperatures. Strawberries 'Elsanta', were stored unpackaged or packaged in polypropylene bags (PP) with different numbers of microperforations (MP) (0 or 6 MP) and stored at three different temperatures (4, 10 or 18°C). Dry matter, pH, titratable acidity, electrical conductivity, sugars, color, Vitamin C, antioxidant capacity, total phenols, flavonoids and phenolic acids were evaluated. Oxygen (O_2) and CO_2 concentrations were also monitored. Conservation at a temperature of 4°C gave the best result, maintaining the quality characteristic and especially reducing the respiration rate and decay. Temperature, if combined with MP packaging, stabilized gas exchange increasing shelf-life. The packaging with 6 MP, coupled to an appropriate temperature of 4°C, allowed the extension of the shelf-life by five days reducing the dehydration of the product by 50% and retaining the qualitative properties.

Keywords: Antioxidant; Phenolic acids; Phenols; Storage; Sugars; Vitamin C

Acta Horticulturae

Volume 1120, Pages 303-310

Antioxidant characterization of different Italian broccoli landraces [Caracterização antioxidante de diferentes variedades crioulas de brócolis Italiano]

Nicoletto, C.[a], Santagata, S.[a], Pino, S.[b], Sambo, P.[a]

[a] University of Padova, Legnaro, Italy
[b] Institute of Genetics and Agricultural Research 'N. Strampelli', Lonigo (VI), Italy

Abstract

The *Brassicaceae* plants are among the most consumed vegetables in the world. They feature a large biodiversity, in which landraces and primitive cultivars still play a major role on the cultivation systems of many countries. Brassicas and especially broccoli are closely linked to antioxidant compounds that play a key role for human health. This experiment aimed to characterize some Italian unknown broccoli landraces from the antioxidant point of view. Five landraces named BF, BF4, BFT, BB and BS were evaluated. The total antioxidant properties of broccoli were significantly different among ecotypes and the higher values were recorded in BS and BF4. Total phenols showed the higher values in BF4 and concerning the ascorbic acid content found in the different ecotypes results can be summarized in three groups: the first one is represented by BB with higher values, the second one by BF4 and BS and then BF and BFT. BB represented the lower amount of hydroxycinnamic acids, whereas BF4 showed quite higher sulforaphane content (+95%) than other cultivars. The high content of phenolic acids, vitamin C and antioxidant compounds make these broccoli landraces, still little known, an important natural source of dietary antioxidant.

Keywords: Antioxidant activity; *Brassica oleracea* var. *italica*; Hydroxycinnamic acids; Sulforaphane; Total phenols; Vitamin C

Horticultura Brasileira

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The quality of 'Oxheart' tomato: agronomic, chemical and sensory analysis

Bellaio, G.[a], *Carnevale, E.*[a], *Bona, S.*[a], *Tosini, F.*[b]

[a] Department of Agronomy Food Natural Resources Animals Environment, University of Padua, Viale dell'Università 16, Legnaro (PD), Italy
[b] Veneto Agricoltura, Centro Sperimentale Ortofloricolo 'Po di Tramontana', via Moceniga, 7, Rosolina (RO), Italy

Abstract

The tomato (*Lycopersicon esculentum* Mill.) is one of the most common vegetables in the world and in Italy it represents a significant part of the total agricultural production. The 'Oxheart' tomato has a slightly ribbed pear-shape, and can be of different colors from green to pink or red, depending on the state of ripeness. It is characterized by floury pulp and it is available almost all year round. The aim of the study was to compare from a sensory point of view the grafted varieties with the non-grafted ones and their berries derived from different types of maturation (matured on the plant or in cold storage). Samples were divided into two groups: the tomatoes ripened on the plant and collected at optimal ripeness and the tomatoes collected when they start to become red and then aged in cold storage (4°C). These in turn are divided into the three types of graft: variety Profitto not grafted (or ungrafted), variety Profitto grafted on Beaufort and variety Profitto grafted on Big Power. Finally, an attempt was made to determine whether or not it is possible to predict, using chemical parameters, the responses of the panelists for the sensory analysis. The test results showed that the difference between grafted and non-grafted variety was not great, because only a few parameters showed different behaviour depending on rootstock. The sensory analysis showed that the difference between berries derived from the two different types of aging is very strong and is perceived by the consumer. The interaction between type of graft and type of maturation was not very relevant from a sensory point of view, so it was concluded that that 'Oxheart' tomato quality is improved if the fruit ripened on plant compared to stored at 4°C, whether or not grafted.

Keywords: Antioxidant activity; Carotenoids; Grafting; Panel test; Phenolic acids; Preference; Sugar

Acta Horticulturae

Volume 1123, Pages 193-198

The use of polyphenol oxidase activity to identify a potential raisin variety

Lante, A., Tinello, F., Lomolino, G.

Department of Agronomy, Food, Natural Resources, Animals and Environment – DAFNAE Agripolis, University of Padova, Legnaro, Italy

Abstract

The biochemical characterization of polyphenol oxidase (PPO) in the white grape Bianchetta Trevigiana is addressed in this research to fulfil the requirement for raisin varieties with high concentrations of phenolic compounds and low PPO activity not only to avoid enzymatic browning but also for maintaining the nutritional value of raisins. Spectrophotometric assays and electrophoresis were used to study this ancient variety exhibiting low PPO activity (only cathecolase activity) which reached at the low pH value of grape berry and was about 15% of the maximum enzymatic activity measured. In addition, the visualization of the active isoforms of grape PPO after 2-DE separation of proteins was a key step for further studies using MALDI-TOF-MS and bioinformatic tools. Based on the thermal inactivation profiles, heating treatment at 70°C may be considered a way to inhibit Bianchetta Trevigiana PPO activity by preserving also its high phenolic content. Therefore PPO characterization may be proposed as a marker for identifying potential high value raisin varieties.

Keywords: Antioxidants; Bianchetta Trevigiana; Phenolic compounds; Polyphenol oxidase; Raisin

Food Biotechnology

Volume 30, Issue 2, Pages 98-109

Setup of a procedure for cider proteins recovery and quantification

Mainente, F.[ab] , *Rizzi, C.*[b], *Zoccatelli, G.*[b], *Chignola, R.*[b], *Simonato, B.*[b],
Pasini, G.[a]

[a] Department of Agronomy Food Natural Resources Animals and Environment,
University of Padova, Agripolis, Viale dell'Università, 16, 35020 Legnaro, Padova, Italy
[b] Department of Biotechnology, University of Verona, Verona, Italy

Abstract

Cider contains low amount of proteins that, nonetheless, can affect its stability, foam formation and potential allergenicity. At present, scarce information is available on cider proteins, probably due to the lack of methods for their recovery and analysis. The aim of the present study was to set up a method for recovering and quantifying cider proteins. To this purpose, the proteins from 13 Italian commercial ciders were recovered by dialysis, gel filtration, trichloroacetic acid/acetone (TCA/acetone) and potassium dodecyl sulfate (KDS) precipitation. The protein content of the samples was then determined by bicinchoninic acid (BCA), Bradford and *o*-phthaldialdehyde (OPA) assays. The results were compared to quantitative data obtained by densitometry of electrophoretic gels. The most reliable protocol resulted in the KDS method followed by OPA assay. KDS, in addition, allowed also to separate proteins from glycocompounds. KDS/OPA is the method of choice for cider proteins precipitation and quantification.

Keywords: Cider; KDS; *o*-Phthaldialdehyde (OPA) assay; Proteins quantification; Proteins recovery

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Microbial dynamics during shelf-life of industrial Ricotta cheese and identification of a *Bacillus* strain as a cause of a pink discolouration

Sattin, E.[a], *Andreani, N.A.*[b], *Carraro, L.*[b], *Fasolato, L.*[b], *Balzan, S.*[b], *Novelli, E.*[b], *Squartini, A.*[c], *Telatin, A.*[a], *Simionati, B.*[a], *Cardazzo, B.*[b]

[a] BMR Genomics, Via Redipuglia 21a, Padova, Italy
[b] Department of Comparative Biomedicine and Food Science, University of Padova, Viale dell'Università, 16, Legnaro, 35020, Padova, Italy
[c] Department of Agronomy, Food, Natural Resources, Animals, Environment (DAFNAE), University of Padova, Viale dell'Università, 16, Legnaro, 35020, Padova, Italy

Abstract

Dairy products are perishable and have to be preserved from spoilage during the food chain to achieve the desired shelf-life. Ricotta is a typical Italian soft dairy food produced by heat coagulation of whey proteins and is considered to be a light and healthy product. The shelf-life of Ricotta could be extended, as required by the international food trade market; however, heat resistant microflora causes spoilage and poses issues regarding the safety of the product. Next-generation sequencing (NGS) applied to the Ricotta samples defined the composition of the microbial community in-depth during the shelf-life. The analysis demonstrated the predominance of spore-forming bacteria throughout the shelf-life, mostly belonging to *Bacillus*, *Paenibacillus* and *Clostridium* genera. A strain involved in spoilage and causing a pink discolouration of Ricotta was isolated and characterised as *Bacillus mycoides/weihenstephanensis*. This is the first report of a food discolouration caused by a toxigenic strain belonging to the *Bacillus cereus* group that resulted the predominant strain in the community of the defective ricotta. These results suggest that the processing of raw materials to eliminate spores and residual microflora could be essential for improving the quality and the safety of the product and to extend the shelf-life of industrial Ricotta.

Keywords: Microbial community; Pink discolouration; Ricotta; Shelf-life; Spore forming bacteria

Food Microbiology

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UV-A light treatment for controlling enzymatic browning of fresh-cut fruits

Lante, A.[a], Tinello, F.[a], Nicoletto, M.[b]

[a] Department of Agronomy, Food, Natural Resources, Animals, and Environment - DAFNAE Agripolis, University of Padova, Viale Universita', 16, 35020 Legnaro (PD), Italy
[b] Istituto Nazionale di Fisica Nucleare, Sezione di Padova - INFN, Via Marzolo 8, 35131 Padova, Italy

Abstract

Enzymatic browning is critical in the preservation of the quality and the shelf-life of fresh-cut fruits. Non-thermal technologies such as UV radiation are emerging for controlling polyphenol oxidase (PPO) activity, the main agent responsible for browning. After determining the best operational conditions of a UV LED illuminator ($2.43 \cdot 10^{-3}$ Wm^{-2} irradiance), the anti-browning effect of UV-A light (390 nm) treatment at 25°C over increasing time periods up to 60 min was assessed on fresh-cut apples and pears. Color variation (ΔE) and its percent reduction ($\%R\Delta E$) were measured using a colorimeter and the greatest effect was observed in apples which showed higher $\%R\Delta E$ values than pears (58% vs 25% after 60 min exposure, respectively). Anti-browning was found to be related to irradiance, exposure time and the fruit cultivar. Overall this study confirmed UV-A LED technology as an eco-friendly alternative to traditional approaches for reducing browning of minimally processed products.

Industrial relevance: Treatment of fresh-cut products with UV-A LED is not only easy and inexpensive to produce but also presents few hazards for humans. Moreover, the use of LED light sources brings many advantages such as energy savings, device durability, low environmental impact, high luminous efficiency and little thermal effect. UV-A LED technology has great potential to meet the demands of the food industry in the processing of fresh-cut fruits and vegetables. In addition it could also be considered a pre-treatment of fruits and vegetables being processed for the production of snacks.

Keywords: Color; Enzymatic browning; Fresh-cut fruits; Polyphenol oxidase; UV-A light

Innovative Food Science and Emerging Technologies

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Hidden exogenous proteins in wine: Problems, methods of detection and related legislation - a review

Rizzi, C.[ab], *Mainente, F.*[ab], *Pasini, G.*[b], *Simonato, B.*[a]

[a] Department of Biotechnology, University of Verona, Verona, Italy
[b] Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Legnaro (PD), Italy

Abstract

Fining agents are commonly used in the winemaking process to clarify and stabilise wines. They have different origins (animal, vegetal or mineral) and are added to wines in order to remove specifically undesirable compounds that are discarded. Fining agents should not be present in the final product but their possible persistence, as well as other exogenous residual proteins such as the enzymes utilised in winemaking, cannot be excluded for sure. The principal concern about the presence of exogenous residual proteins is the health of allergic subjects. Nevertheless, the respect of religious creed or other practice of living of the consumer must be considered as well. In the present review we itemise the proteins used in winemaking and possible drawbacks of their permanence in the final products and the related risks, depict the status of the art of the studies performed about the detection of exogenous proteins, and describe the wine labelling laws adopted in different countries to avoid the drawbacks associated with these hidden substances.

Keywords: Allergy; Fining proteins; Food ethics; Residual protein detection; Technological enzymes; Wine labelling laws

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Quantification of whey proteins by reversed phase-HPLC and effectiveness of mid-infrared spectroscopy for their rapid prediction in sweet whey

Sturaro, A., De Marchi, M., Masi, A., Cassandro, M.

Department of Agronomy, Food, Natural Resources, Animals, and Environment
(DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy

Abstract

In the dairy industry, membrane filtration is used to reduce the amount of whey waste and, simultaneously, to recover whey proteins (WP). The composition of WP can strongly affect the filtration treatment of whey, and rapid determination of WP fractions would be of interest for dairy producers to monitor WP recovery. This study aimed to develop mid-infrared spectroscopy (MIRS) prediction models for the rapid quantification of protein in sweet whey, using a validated rapid reversed phase (RP)-HPLC as a reference method. Quantified WP included α-lactalbumin (α-LA), β-lactoglobulin (β-LG) A and B, bovine serum albumin, caseinomacropeptides, and proteose peptone. Validation of RP-HPLC was performed by calculating the relative standard deviation (RSD) in repeatability and reproducibility tests for WP retention time and peak areas. Samples of liquid whey (n = 187) were analyzed by RP-HPLC and scanned through MIRS to collect spectral information (900 to 4,000 cm^{-1}); statistical analysis was carried out through partial least squares regression and random cross-validation procedure. Retention times in RP-HPLC method were stable (RSD between 0.03 and 0.80%), whereas the RSD of peak area (from 0.25 to 8.48%) was affected by WP relative abundance. Higher coefficients of determination in validation for MIRS model were obtained for protein fractions present in whey in large amounts, such as β-LG (0.58), total identified WP (0.58), and α-LA (0.56). Results of this study suggest that MIRS is an easy method for rapid quantification of detail protein in sweet whey, even if better resolution was achieved with the method based on RP-HPLC. The prediction of WP in sweet whey by MIRS might be used for screening and for classifying sweet whey according to its total and individual WP contents.

Keywords: Mid-infrared spectroscopy; Reversed phase (RP)-HPLC; Whey protein quantification

Journal of Dairy Science

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Potential use of *scotta*, the by-product of the ricotta cheese manufacturing process, for the production of fermented drinks

Maragkoudakis, P., Vendramin, V., Bovo, B., Treu, L., Corich, V., Giacomini, A.

Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, viale dell'Università 16, 35020 Legnaro (PD), Italy

Abstract

In the present work, the use of scotta as substrate for bacterial fermentation was studied with the objective of obtaining a drink from transformation of this by-product. Scotta retains most of the lactose of the milk and it is normally colonized by a natural microbiota. A treatment was devised to reduce the autochthonous microbial populations in order to reduce competition towards the inoculated bacterial strains. Nine lactic acid bacteria (LAB) were assessed for their capability to develop in scotta. They evidenced different behaviors regarding growth rate, acidification capability and nitrogen consumption. A co-inoculum of three LAB, namely a *Streptococcus thermophilus*, a *Lactobacillus delbrueckii* subsp. *bulgaricus* and a *Lb. acidophilus* strains, chosen among those giving the best performances in single-strain fermentation trials, gave abundant (close to 10^9 cfu/ml) and balanced growth and lowered pH to 4·2, a value similar to that of yogurt. These results show that scotta may have potential as a substrate for bacterial growth for the production of a fermented drink. Further studies are needed to optimize the organoleptic aspects of the final product.

Keywords: Fermentation; Lactic acid bacteria; Lactobacillus; Microbiota; Streptococcus

Journal of Dairy Research

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Phenolic substances, flavor compounds, and textural properties of three native Romanian wine grape varieties

Urcan, D.E.[a], Lung, M.-L.[a], Giacosa, S.[b], Torchio, F.[b], Ferrandino, A.[b], Vincenzi, S.[c], Rió Segade, S.[b], Pop, N.[a], Rolle, L.[b]

[a] University of Agricultural Sciences and Veterinary Medicine, Cluj-Napoca, Romania
[b] University of Turin, Dipartimento di Scienze Agrarie, Forestali e Alimentari, Largo Paolo Braccini 2, Grugliasco (TO), Italy
[c] University of Padova, Centro Interdipartimentale per la Ricerca in Viticoltura Ed Enologia, Legnaro, Italy

Abstract

In this work, the chemical compositions and texture characteristics of three native Romanian wine grape varieties (Fetească regală, Fetească albă, and Fetească neagra) were studied. We assessed the distinct characteristics directly linked to their phenolic compositions, volatile profiles, and mechanical properties and compared these characteristics with those of Pinot noir grapes. The effect of the growing zone was also evaluated. Various spectrophotometric indices directly related to the phenolic compositions of berry skins and seeds were determined. The detailed phenolic compositions (anthocyanins, hydroxycinnamoyl tartaric acids, and stilbenes) of the skins were determined using high-performance liquid chromatography methods. Free and bound volatile compounds in the berries were quantified by gas chromatography/mass spectrometry. The textural properties of the skins and seeds were measured by instrumental texture analysis. The results showed high diversity among the varieties and zones that affected the enological potential. Among the white varieties, Fetească albă grapes could be less susceptible to browning as a consequence of their lower *trans*-caffeoyltartaric acid concentration, whereas Fetească regală grapes from Cluj had the highest concentrations of total free and bound volatile compounds, particularly terpenes and norisoprenoids. Among the red varieties, Fetească neagră was identified as a promising variety to be exploited in the future for its particular phenolic characteristics, particularly those grapes grown in Mica. Nevertheless, Fetească neagră grapes grown in Cluj had the highest total glycosidically bound terpene concentrations. Finally, differences in the mechanical and/or acoustic properties of the skins and seeds could strongly influence the kinetics and completeness of phenolic compound extractions.

Keywords: Anthocyanins; Hydroxycinnamoyl tartaric acids; Romanian wine grape varieties; Stilbenes; Texture properties; Volatile compounds

International Journal of Food Properties

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Study of elements concentrations of European seabass (*Dicentrarchus labrax*) fillets after cooking on steel, cast iron, teflon, aluminum and ceramic pots

Lomolino, G., Crapisi, A., Cagnin, M.

Department of Agronomy, Food, Natural Resources, Animals, and Environment -
DAFNAE Università degli Studi di Padova, Agripolis, Viale dell'Università, 35020
Legnaro, Padova, Italy

Abstract

Some elements and metals (Al, Ca, Cr, Cu, Fe, Mn, Ni, Pb, Se, Sr, Zn, P) were analyzed in European seabass (*Dicentrarchus labrax*), by comparing the concentration in raw and in the cooked fish. In particular, the cooking of European seabass was carried out on pots made of five different materials (cast iron, aluminum, steel, teflon and ceramic), commonly used in gastronomy. By measuring mineral elements and metals content of the fish before and after cooking on the 5 materials, there is an increase in elements which is due not only to water loss but also by the release of the materials upon contact with the surface of the pots. Among the analyzed elements the exception is represented by Cr, Se and Fe which decrease with cooking, while Pb remains unvaried. The use of 2 model solutions, made of water and water and vinegar, demonstrates that the used cooking materials are not inert to the leaching/release of elements that could be found in the processed fish.

Keywords: Cooking materials; Inductively coupled plasma optical emission spectrometry (ICP-OES); Metals; Seabass; Seafood

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Essential amino acids: master regulators of nutrition and environmental footprint?

Tessari, P.[a], Lante, A.[b], Mosca, G.[b]

[a] Dept. of Medicine, University of Padova, Italy
[b] Dept. of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Italy

Abstract

The environmental footprint of animal food production is considered several-fold greater than that of crops cultivation. Therefore, the choice between animal and vegetarian diets may have a relevant environmental impact. In such comparisons however, an often neglected issue is the nutritional value of foods. Previous estimates of nutrients' environmental footprint had predominantly been based on either food raw weight or caloric content, not in respect to human requirements. Essential amino acids (EAAs) are key parameters in food quality assessment. We re-evaluated here the environmental footprint (expressed both as land use for production and as Green House Gas Emission (GHGE), of some animal and vegetal foods, titrated to provide EAAs amounts in respect to human requirements. Production of high-quality animal proteins, in amounts sufficient to match the Recommended Daily Allowances of all the EAAs, would require a land use and a GHGE approximately equal, greater or smaller (by only ±1-fold), than that necessary to produce vegetal proteins, except for soybeans, that exhibited the smallest footprint. This new analysis downsizes the common concept of a large advantage, in respect to environmental footprint, of crops vs. animal foods production, when human requirements of EAAs are used for reference.

Scientific Reports

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Food supply chain - sustainability in small milk industry

Beux, S.[a], *Viagi, A.*[b], *Panizzolo, R.*[c], *Cassandro, M.*[c], *Waszczynskyj, N.*[a]

[a] Federal University of Paraná, Curitiba, Paraná, Brazil
[b] University of Taubaté, Taubaté, São Paulo, Brazil
[c] University of Padova, Padua, Veneto, Italy

Abstract

Farming is very important for the development of a country economy and, in Brazil, cattle (meat and milk) is one of the most important sectors of this segment. This paper aims to develop a conceptual framework to identify the key characteristics of the Short Food Supply Chain and, moreover, propose a model for the implementation of sustainability in the sector of small milk producers and dairy products. The research presents data from small producers located in Paraná, Brazil and utilizes the better condition of Italian producers in the Veneto region as a benchmarking to identify opportunities for improvement by adopting the concept of Short Food Supply Chain. The conclusion of the analysis showed that there are significant gains for small farmers with the adoption of the proposed model because it solves several issues that currently hinder the development of the sector.

Keywords: Milk; Production; Supply chain; Sustainability

IFIP Advances in Information and Communication Technology

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Cheesemaking in highland pastures: Milk technological properties, cream, cheese and ricotta yields, milk nutrients recovery, and products composition

Bergamaschi, M.[a], Cipolat-Gotet, C[a]., Stocco, G.[a], Valorz, C.[b], Bazzoli, I.[b], Sturaro, E.[a], Ramanzin, M.[a], Bittante, G.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy
[b] Breeders Federation of Trento Province, via delle Bettine, 40, 38100 Trento, Italy

Abstract

Summer transhumance of dairy cows to high Alpine pastures is still practiced in many mountainous areas. It is important for many permanent dairy farms because the use of highland pastures increases milk production and high-priced typical local dairy products often boost farm income. As traditional cheese- and ricotta-making procedures in Alpine pastures are central to this dairy system, the objective of this study was to characterize the quality and efficiency of products and their relationships with the quality and availability of grass during the grazing season. The milk from 148 cows from 12 permanent farms reared on a temporary farm located in Alpine pastures was processed every 2 wk during the summer (7 cheesemakings from late June to early September). During each processing, 11 dairy products (4 types of milk, 2 by-products, 3 fresh products, and 2 ripened cheeses) were sampled and analyzed. In addition, 8 samples of fresh forage from the pasture used by the cows were collected and analyzed. At the beginning of the pasture season the cows were at 233 ± 90 d in milk, 2.4 ± 1.7 parities, and produced 23.6 ± 5.7 kg/d of milk. The milk yield decreased with the move from permanent to temporary farms and during the entire summer transhumance, but partly recovered after the cows returned to the permanent farms. Similar trends were observed for the daily yields of fat, protein, casein, lactose, and energy, as we found no large variations in the quality of the milk, with the exception of the first period of Alpine pasture. The somatic cell counts of milk increased during transhumance, but this resulted from a concentration of cells in a lower quantity of milk rather than an increase in the total number of cells ejected daily from the udder. We noted a quadratic trend in availability of forage (fresh and dry matter weight per hectare), with a maximum in late July. The quality of forage also varied during the summer with a worsening of chemical composition. The evening milk (before and after natural creaming), the whole morning milk, and the mixed vat milk had different chemical compositions, traditional coagulation properties, and curd-firming modeling parameters. These variations over the pasture season were similar to the residual variations with respect to chemical composition, and much lower with respect to coagulation and curd-firming traits. Much larger variations were noted in cream, cheese, and ricotta yields, as well as in nutrient recoveries in curd during the pasture season. The protein content of forage was correlated with some of the coagulation and curd-firming traits, the ether extract of forage was positively correlated with milk fat content and cheese yields, and fiber fractions of forage were unfavorably correlated with some of the chemical and technological traits. Traditional cheese- and ricotta-making procedures showed average cream, cheese, and ricotta yields of 6.3, 14.2, and 4.9%, respectively, and an overall recovery of almost 100% of milk fat, 88% of milk protein, and 60% of total milk solids.

Keywords: Cheese manufacture; Cow; Milk; Transhumance

Journal of Dairy Science

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Effects of dairy factory, milk casein content and titratable acidity on coagulation properties in Trentingrana dairy industry

Penasa, M.[a], *Toffanin, V.*[a], *Cologna, N.*[b], *Cassandro, M.*[a], *De Marchi, M.*[a]

[a] Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy
[b] Trentingrana - Consorzio dei Caseifici Sociali Trentini s.c.a., Via Bregenz 18, 38121 Trento, Italy

Abstract

The objective of the present study was to investigate the effect of environmental factors, milk casein content and titratable acidity on milk coagulation properties (MCP) of samples routinely collected in the Trento province (northeast Italy) under field conditions. Rennet coagulation time (RCT, min), curd-firming time (k_{20}, min) and curd firmness (a_{30}, mm) were determined by Formagraph on 14 971 samples from 635 herds associated to 17 dairy factories. Besides MCP, fat, protein, and casein percentages, titratable acidity (TA), and somatic cell and bacterial counts were available. A standardised index of milk aptitude to coagulate (IAC) was derived using information of RCT and a_{30}. An analysis of variance was conducted on MCP and IAC using a fixed effects linear model. Approximately 3% of milk samples did not form a curd within the testing time (30 min) and k_{20} was missing for 26% of milks. The percentage of samples without information on k_{20} largely differed among dairy factories (1·7-20·9%). Significant differences were estimated between the best and the worst dairy factory for RCT (-2 min), k_{20} (-1·2 min), a_{30} (+3·4 mm) and IAC (+2·6 points). Milk casein content and TA were important factors in explaining the variation of MCP and IAC, supporting the central role of these two traits on technological properties. The Trento province is heterogeneous in terms of dairy systems and this could explain the differences among dairy factories.

Keywords: Casein content; Dairy industry; Milk coagulation property; Titratable acidity

Journal of Dairy Research

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Genetics and genomics

DNA barcoding as a molecular tool to track down mislabeling and food piracy

Barcaccia, G., Lucchin, M., Cassandro, M.

Laboratorio di Genomica, LabGEN c/o DAFNAE-Università di Padova, Via Università 16, Legnaro, Italy

Abstract

DNA barcoding is a molecular technology that allows the identification of any biological species by amplifying, sequencing and querying the information from genic and/or intergenic standardized target regions belonging to the extranuclear genomes. Although these sequences represent a small fraction of the total DNA of a cell, both chloroplast and mitochondrial barcodes chosen for identifying plant and animal species, respectively, have shown sufficient nucleotide diversity to assess the taxonomic identity of the vast majority of organisms used in agriculture. Consequently, cpDNA and mtDNA barcoding protocols are being used more and more in the food industry and food supply chains for food labeling, not only to support food safety but also to uncover food piracy in freshly commercialized and technologically processed products. Since the extranuclear genomes are present in many copies within each cell, this technology is being more easily exploited to recover information even in degraded samples or transformed materials deriving from crop varieties and livestock species. The strong standardization that characterizes protocols used worldwide for DNA barcoding makes this technology particularly suitable for routine analyses required by agencies to safeguard food safety and quality. Here we conduct a critical review of the potentials of DNA barcoding for food labeling along with the main findings in the area of food piracy, with particular reference to agrifood and livestock foodstuffs.

Keywords: cpDNA barcoding; Foodstuffs; Genetic traceability; mtDNA barcoding

Diversity

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Genome-wide characterization of maize small RNA loci and their regulation in the required to maintain repression6-1 (Rmr6-1) mutant and long-term abiotic stresses

Lunardon, A.[ab], Forestan, C.[a], Farinati, S.[a], Axtell, M.J.[b], Varotto, S.[a]

[a] Department of Agronomy, Animals, Food, Natural Resources and Environment,
University of Padova, Agripolis Viale dell'Università 16, Legnaro, PD, Italy
[b] Department of Biology and Huck Institutes of the Life Sciences, Penn State University,
University Park, PA, United States

Abstract

Endogenous small RNAs (sRNAs) contribute to gene regulation and genome homeostasis, but their activities and functions are incompletely known. The maize genome has a high number of transposable elements (TEs; almost 85%), some of which spawn abundant sRNAs. We performed sRNA and total RNA sequencing from control and abiotically stressed B73 wild-type plants and rmr6-1 mutants. RMR6 encodes the largest subunit of the RNA polymerase IV complex and is responsible for accumulation of most 24-nucleotide (nt) small interfering RNAs (siRNAs). We identified novel MIRNA loci and verified miR399 target conservation in maize. RMR6-dependent 23-24 nt siRNA loci were specifically enriched in the upstream region of the most highly expressed genes. Most genes misregulated in rmr6-1 did not show a significant correlation with loss of flanking siRNAs, but we identified one gene supporting existing models of direct gene regulation by TE-derived siRNAs. Long-term drought correlated with changes of miRNA and sRNA accumulation, in particular inducing down-regulation of a set of sRNA loci in the wild-typeleaf.

Keywords: 3' Untranslated Regions; DNA-Directed RNA Polymerases; MicroRNAs; Plant proteins; Plant RNA; Small interfering RNA; Small untranslated RNA

Plant Physiology

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A systems-oriented analysis of the grapevine R2R3-MYB transcription factor family uncovers new insights into the regulation of stilbene accumulation

Wong, D.C.J.[a], Schlechter, R.[b], Vannozzi, A.[c], Höll, J.[d], Hmmam, I.[c], Bogs, J.[ef],
Tornielli, G.B.[g], Castellarin, S.D.[a], Matus, J.T.[h]

[a] Wine Research Centre, University of British Columbia, Vancouver, BC, Canada
[b] Department of Biology, ETH Zurich, Zurich, Switzerland
[c] Department of Agronomy, Food, Natural Resources, Animals, and Environment, University of Padova, Legnaro, Padova, Italy
[d] Centre for Organismal Studies Heidelberg, University of Heidelberg, Heidelberg, Germany
[e] Dienstleistungszentrum Laendlicher Raum Rheinpfalz, Viticulture and Enology Group, Breitenweg 71, Neustadt/W, Germany
[f] Fachhochschule Bingen, Berlinstr. 109, Bingen-am-Rhein, Germany
[g] Department of Biotechnology, University of Verona, Verona, Italy
[h] Center for Research in Agricultural Genomics CSIC-IRTA-UAB-UB, Barcelona, Spain

Abstract

R2R3-MYB transcription factors (TFs) belong to a large and functionally diverse protein superfamily in plants. In this study, we explore the evolution and function of this family in grapevine (*Vitis vinifera* L.), a high-value fruit crop. We identified and manually curated 134 genes using RNA-Seq data, and named them systematically according to the Super-Nomenclature Committee. We identified novel genes, splicing variants and grapevine/woody-specific duplicated subgroups, suggesting possible neo- and sub-functionalization events. Regulatory network analysis ascribed biological functions to uncharacterized genes and validated those of known genes (e.g. secondary cell wall biogenesis and flavonoid biosynthesis). A comprehensive analysis of different MYB binding motifs in the promoters of co-expressed genes predicted grape R2R3-MYB binding preferences and supported evidence for putative downstream targets. Enrichment of cis-regulatory motifs for diverse TFs reinforced the notion of transcriptional coordination and interaction between MYBs and other regulators. Analysis of the network of Subgroup 2 showed that the resveratrol-related VviMYB14 and VviMYB15 share common co-expressed STILBENE SYNTHASE genes with the uncharacterized VviMYB13. These regulators have distinct expression patterns within organs and in response to biotic and abiotic stresses, suggesting a pivotal role of VviMYB13 in regulating stilbene accumulation in vegetative tissues and under biotic stress conditions.

Keywords: Cell wall; Radiation; Ripening; Stress; Wine

DNA Research

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Genetic identity of common buckwheat *(Fagopyrum esculentum* Moench) landraces locally cultivated in the Alps

Barcaccia, G.[a], *Volpato, M.*[a], *Gentili, R.*[b], *Abeli, T.*[c], *Galla, G.*[a], *Orsenigo, S.*[d], *Citterio, S.*[b], *Sgorbati, S.*[b], *Rossi, G.*[c]

[a] Laboratory of Plant Genetics and Breeding, DAFNAE, University of Padova, Campus of Agripolis, Legnaro, Italy
[b] Department of Earth and Environmental Sciences, University of Milano - Bicocca, Piazza della Scienza 1, Milan, Italy
[c] Department of Earth and Environmental Sciences, University of Pavia, Via S. Epifanio 14, Pavia, Italy
[d] Department of Agricultural and Environmental Sciences - Production, Landscape, Agroenergy, University of Milan, Via Celoria 2, Milan, Italy

Abstract

The conservation of landraces in Europe is challenging because very often they have already disappeared or cannot be properly identified, which in turn prevents any possibility for their utilization. This work deals with the collection of molecular and historical data to identify and study the original landraces of common buckwheat (*Fagopyrum esculentum* Moench), locally cultivated in Northern Italy (Valtellina) and to date surviving among other commercial varieties, recently introduced in the same areas of the Alps. As plant materials of *F. esculentum*, we analyzed a number of Italian accessions along with two foreign accessions from Poland and Nepal, for a total of 174 individuals. Molecular investigations were based on a set of eight nuclear SSR marker loci. The mean observed heterozygosity over all accessions was equal to Ho = 0.466, being significantly lower than the expected heterozygosity (He = 0.764). A major finding was the recognition of a marked inbreeding rate (Fit = 0.387) and a reduced fixation index (Fst = 0.061), indicating that most genetic variation is found within populations. A significant overall gene flow among accessions was found (Nm = 3.846). Results indicated that only two of the examined accessions, the so-called "Nustran" and "Curunin", could be considered, authentic Valtellina landraces. On the basis of results, we successfully developed a multi-locus marker system and identified a number of co-dominant marker alleles suitable for genetic traceability and authenticity certification of a "Nustran" and a "Curunin" autochthonous landraces of Valtellina and its food derivatives (i.e., Pizzoccheri, Polenta taragna).

Keywords: Agrobiodiversity conservation; Autochthonous landraces; *Fagopyrum esculentum*; Food traceability; Genetic diversity; Microsatellites

Genetic Resources and Crop Evolution

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Current advances in genomics and breeding of leaf chicory (*Cichorium intybus* L.)

Barcaccia, G., Ghedina, A., Lucchin, M.

Laboratory of Plant Genetics and Breeding, DAFNAE-School of Agriculture, University of Padova, Campus of Agripolis, Viale dell'Università, 16, Legnaro, PD, Italy

Abstract

This review gives an overview of agricultural topics on a non-model species, in other words, leaf chicory. Often classified as a minor crop, "Radicchio", the Italian name of leaf chicory, is assuming a very important role at both a local and national level, as it characterizes a high proportion of the agricultural income of suited areas. Botanical classification along the genus Cichorium is reported and a detailed description of the most important cultivated biotypes typical of northern Italy is presented. A special consideration is reserved to breeding aspects, from molecular marker-assisted selection to the implementation of the first genome draft and leaf transcriptomes. Sexual barriers, for example, self-incompatibility or male-sterility, are described in great detail with the aim to be utilized for breeding purposes. The main aspects of seed production are also critically presented. In conclusion, the present work is a sort of handbook to better understand this orphan crop and it is mainly directed to breeders and seed producers dealing with leaf chicory.

Keywords: Cultivated varieties; Marker-assisted breeding; Population genetics; Radicchio

Agriculture (Switzerland)

Volume 6, Issue 4, Article number 50

Effects of candidate gene polymorphisms on the detailed fatty acids profile determined by gas chromatography in bovine milk

Pegolo, S.[a], Cecchinato, A.[a], Mele, M.[b], Conte, G.[b], Schiavon, S.[a], Bittante, G.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, Legnaro, Padova, Italy
[b] Department of Agriculture, Food and Environment, Università di Pisa, Via del Borghetto, 80, Pisa, Italy

Abstract

Association analyses between candidate genes and bovine milk fatty acids can improve our understanding of genetic variation in milk fatty acid profiles and reveal potential opportunities to tailor milk fat composition through selection strategies. In this work, we investigated the association of 51 single nucleotide polymorphisms (SNP) selected from 37 candidate genes using a functional and positional approach, with 47 fatty acids, 9 fatty acid groups, and 5 9-desaturation indices in milk samples from Brown Swiss cows. Individual milk samples were collected from 1,158 Italian Brown Swiss cows, and gas chromatography was used to obtain detailed milk fatty acid compositions. A GoldenGate assay system (Illumina, San Diego, CA) was used to perform genotype 96 selected SNP located in 54 genes across 22 chromosomes. In total, 51 polymorphic SNP in 37 candidate genes were retained for the association analysis. A Bayesian linear animal model was used to estimate the contribution of each SNP. A total of 129 tests indicated relevant additive effects between a given SNP and a single fatty acid trait; 38 SNP belonging to 30 genes were relevant for a total of 57 fatty acid traits. Most of the studied fatty acid traits (~81%) were relevantly associated with multiple SNP. Relevantly associated SNP were mainly found in genes related to fat metabolism, linked to or contained in previously identified quantitative trait loci for fat yield or content, or associated with genes previously identified in association analyses with milk fatty acid profiles in other cow breeds. The most representative candidate genes were LEP, PRL, STAT5A, CCL3, ACACA, GHR, ADRB2, LPIN1, STAT1, FABP4, and CSN2. In particular, relevant associations with SNP located on bovine chromosome 19 (BTA19) were found. Two candidate genes on BTA19 (CCL3 and ACACA) were relevantly associated with de novo short- and medium-chain fatty acids, likely explaining the high heritability values found for these fatty acids (with the exception of C6:0). Two additional genes on BTA19 (CCL2 and GH1) showed associations with saturated and branched-chain fatty acids. Our findings provide basic information on genes and SNP affecting the milk fatty acid composition of dairy cows. These results may support the possibility of using genetic selection to modify milk fatty acid profiles to promote beneficial health-related effects.

Keywords: Association analyses; Candidate genes; Milk fatty acids; Single nucleotide polymorphism

Journal of Dairy Science

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From cow to cheese: genetic parameters of the flavour fingerprint of cheese investigated by direct-injection mass spectrometry (PTR-ToF-MS)

Bergamaschi, M.[a], Cecchinato, A.[a], Biasioli, F.[b], Gasperi, F.[b], Martin, B.[c], Bittante, G.[a]

[a] Department of Agronomy Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, Legnaro PD, Italy
[b] Department of Food Quality and Nutrition, Research and Innovation Centre, Fondazione Edmund Mach (FEM), Via E. Mach 1, San Michele all'Adige TN, Italy
[c] INRA, UMR Herbivores, Saint-Genès Champanelle, France; Clermont Université, BP 10448 VetAgro Sup, Clermont-Ferrand, France

Abstract

Background: Volatile organic compounds determine important quality traits in cheese. The aim of this work was to infer genetic parameters of the profile of volatile compounds in cheese as revealed by direct-injection mass spectrometry of the headspace gas from model cheeses that were produced from milk samples from individual cows.

Methods: A total of 1075 model cheeses were produced using raw whole-milk samples that were collected from individual Brown Swiss cows. Single spectrometry peaks and a combination of these peaks obtained by principal component analysis (PCA) were analysed. Using a Bayesian approach, we estimated genetic parameters for 240 individual spectrometry peaks and for the first ten principal components (PC) extracted from them.

Results: Our results show that there is some genetic variability in the volatile compound fingerprint of these model cheeses. Most peaks were characterized by a substantial heritability and for about one quarter of the peaks, heritability (up to 21.6%) was higher than that of the best PC. Intra-herd heritability of the PC ranged from 3.6 to 10.2% and was similar to heritabilities estimated for milk fat, specific fatty acids, somatic cell count and some coagulation parameters in the same population. We also calculated phenotypic correlations between PC (around zero as expected), the corresponding genetic correlations (from -0.79 to 0.86) and correlations between herds and sampling-processing dates (from -0.88 to 0.66), which confirmed that there is a relationship between cheese flavour and the dairy system in which cows are reared.

Conclusions: This work reveals the existence of a link between the cow's genetic background and the profile of volatile compounds in cheese. Analysis of the relationships between the volatile organic compound (VOC) content and the sensory characteristics of cheese as perceived by the consumer, and of the genetic basis of these relationships could generate new knowledge that would open up the possibility of controlling and improving the sensory properties of cheese through genetic selection of cows. More detailed investigations are necessary to connect

VOC with the sensory properties of cheese and gain a better understanding of the significance of these new phenotypes.

Genetics Selection Evolution

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Genome-wide association of coagulation properties, curd firmness modeling, protein percentage, and acidity in milk from Brown Swiss cows

Dadousis, C.[a], Biffani, S.[b], Cipolat-Gotet, C.[a], Nicolazzi, E.L.[c], Rossoni, A.[d],
Santus, E.[d], Bittante, G.[a], Cecchinato, A.[a]

[a] Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, Legnaro, Italy
[b] Istituto di Biologia e Biotecnologia Agraria (IBBA), Consiglio Nazionale delle Ricerche (CNR), Via Einstein-Loc. Cascina Codazza, Lodi, Italy
[c] Bioinformatics core, Parco Tecnologico Padano, Via Einstein-Loc. Cascina Codazza, Lodi, Italy
[d] Italian Brown Breeders Association, Loc. Ferlina 204, Bussolengo, Italy

Abstract

Cheese production is increasing in many countries, and a desire toward genetic selection for milk coagulation properties in dairy cattle breeding exists. However, measurements of individual cheesemaking properties are hampered by high costs and labor, whereas traditional single-point milk coagulation properties (MCP) are sometimes criticized. Nevertheless, new modeling of the entire curd firmness and syneresis process (CF_t equation) offers new insight into the cheesemaking process. Moreover, identification of genomic regions regulating milk cheesemaking properties might enhance direct selection of individuals in breeding programs based on cheese ability rather than related milk components. Therefore, the objective of this study was to perform genome-wide association studies to identify genomic regions linked to traditional MCP and new CF_t parameters, milk acidity (pH), and milk protein percentage. Milk and DNA samples from 1,043 Italian Brown Swiss cows were used. Milk pH and 3 MCP traits were grouped together to represent the MCP set. Four CF_t equation parameters, 2 derived traits, and protein percentage were considered as the second group of traits (CF_t set). Animals were genotyped with the Illumina SNP50 BeadChip v.2 (Illumina Inc., San Diego, CA). Multitrait animal models were used to estimate variance components. For genome-wide association studies, the genome-wide association using mixed model and regression-genomic control approach was used. In total, 106 significant marker traits associations and 66 single nucleotide polymorphisms were identified on 12 chromosomes (1, 6, 9, 11, 13, 15, 16, 19, 20, 23, 26, and 28). Sharp peaks were detected at 84 to 88 Mbp on *Bos taurus* autosome (BTA) 6, with a peak at 87.4 Mbp in the region harboring the casein genes. Evidence of quantitative trait loci at 82.6 and 88.4 Mbp on the same chromosome was found. All chromosomes but BTA6, BTA11, and BTA28 were associated with only one trait. Only BTA6 was in common between MCP and CF_t sets. The new CF_t traits reinforced the support of MCP signals and provided with additional information on genomic regions that might be involved in regulation of the coagulation process of bovine milk.

Keywords: Curd firmness; Dairy cattle; Genome-wide association study; Milk coagulation

Journal of Dairy Science

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Variations at regulatory regions of the milk protein genes are associated with milk traits and coagulation properties in the Sarda sheep

Noce, A.[ab], Pazzola, M.[a], Dettori, M.L.[a], Amills, M.[b], Castelló, A.[b], Cecchinato, A.[c], Bittante, G.[c], Vacca, G.M.[a]

[a] Department of Veterinary Medicine, University of Sassari, Via Vienna 2, Sassari, Italy
[b] Department of Animal Genetics, Center for Research in Agricultural Genomics (CSIC-IRTA-UAB-UB), Campus Universitat Autònoma de Barcelona, Bellaterra, Spain
[c] Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, viale dell'Università 16, Legnaro, PD, Italy

Abstract

Regulatory variation at the ovine casein genes could have important effects on the composition and coagulation properties of milk. Herewith, we have partially resequenced the promoters and the 3'-UTR of the four casein genes in 25 Sarda sheep. Alignment of these sequences allowed us to identify a total of 29 SNPs. This level of polymorphism (one SNP every 250 bp) is remarkably high if compared with SNP densities estimated in human genic regions (approximately one SNP per bp). The 29 SNPs identified in our resequencing experiment, plus three previously reported SNPs mapping to the *lactalbumin*, *alpha* (*LALBA*) and β-*lactoglobulin* (*BLG*, also known as *progestagen-associated endometrial protein, PAEP*) genes, were genotyped with a multiplex TaqMan Open Array Real-Time PCR assay in 760 Sarda sheep with records for milk composition and coagulation properties. Association analysis revealed the existence of significant associations of *CSN1S2* and *CSN3* genotypes with milk protein and casein contents. Moreover, genotypes at *CSN1S1* were significantly associated with rennet coagulation time, curd firming time and curd firmness, whereas *CSN2* was associated with curd firming time. These results suggest that SNPs mapping to the promoters and 3'-UTRs of ovine casein genes may exert regulatory effects on gene expression and that they could be used for improving sheep milk quality and technological traits at the population level through marker assisted selection.

Keywords: Association analysis; Haplotypes; Milk coagulation properties; Sarda sheep breed; Single nucleotide polymorphism

Animal Genetics

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Transcriptomic changes in liver of young bulls caused by diets low in mineral and protein contents and supplemented with n-3 fatty acids and conjugated linoleic acid

Pegolo, S.[a], Cecchinato, A.[a], Mach, N.[b], Babbucci, M.[c], Pauletto, M.[c], Bargelloni, L.[c], Schiavon, S.[a], Bittante, G.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Legnaro, Padova, Italy
[b] Animal Genetics and Integrative Biology Unit (GABI), INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France
[c] Department of Comparative Biomedicine and Food Science, University of Padova, Legnaro, Padova, Italy

Abstract

The aim of the present study was to identify transcriptional modifications and regulatory networks accounting for physiological and metabolic responses to specific nutrients in the liver of young Belgian Blue x Holstein bulls using RNA-sequencing. A larger trial has been carried out in which animals were fed with different diets: 1] a conventional diet; 2] a low-protein/ low-mineral diet (low-impact diet) and 3] a diet enriched in n-3 fatty acids (FAs), conjugated linoleic acid (CLA) and vitamin E (nutraceutical diet). The initial hypothesis was that the administration of low-impact and nutraceutical diets might influence the transcriptional profiles in bovine liver and the resultant nutrient fluxes, which are essential for optimal liver function and nutrient interconversion. Results showed that the nutraceutical diet significantly reduced subcutaneous fat covering *in vivo* and liver pH. Dietary treatments did not affect overall liver fat content, but significantly modified the liver profile of 33 FA traits (out of the total 89 identified by gas-chromatography). In bulls fed nutraceutical diet, the percentage of n-3 and CLA FAs increased around 2.5-fold compared with the other diets, whereas the ratio of n6/n3 decreased 2.5-fold. Liver transcriptomic analyses revealed a total of 198 differentially expressed genes (DEGs) when comparing low-impact, nutraceutical and conventional diets, with the nutraceutical diet showing the greatest effects on liver transcriptome. Functional analyses using ClueGo and Ingenuity Pathway Analysis evidenced that DEGs in bovine liver were variously involved in energy reserve metabolic process, glutathione metabolism, and carbohydrate and lipid metabolism. Modifications in feeding strategies affected key transcription factors regulating the expression of several genes involved in fatty acid metabolism, e.g. insulin-induced gene 1, insulin receptor substrate 2, and RAR-related orphan receptor C. This study provides noteworthy insights into the molecular changes occurring as a result of nutrient variation in diets (aimed at reducing the environmental impact and improving human health) and broadens our understanding of the relationship between nutrients variation and phenotypic effects.

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Genetic and environmental relationships of detailed milk fatty acids profile determined by gas chromatography in Brown Swiss cows

Pegolo, S.[a], Cecchinato, A.[a], Casellas, J.[b], Conte, G.[c], Mele, M.[c], Schiavon, S.[a], Bittante, G.[a]

[a] Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, Legnaro, Padova, Italy
[b] Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Spain
[c] Department of Agricolture, Food and Environment, Università di Pisa, Via del Borghetto, 80, Pisa, Italy

Abstract

The aim of this study was to characterize the profile of 47 fatty acids, including conjugated linoleic acid (CLA), 13 fatty acid groups, and 5 Δ^9-desaturation indices in milk samples from Brown Swiss cows. The genetic variation was assessed and the statistical relevance of the genetic background for each trait was evaluated using the Bayes factor test. The additive genetic, herd-date, and residual relationships were also estimated among all single fatty acids and groups of fatty acids. Individual milk samples were collected from 1,158 Italian Brown Swiss cows and a detailed analysis of fat percentages and milk fatty acid compositions was performed by gas chromatography. Bayesian animal models were used for (co)variance components estimation. Exploitable genetic variation was observed for most of the de novo synthesized fatty acids and saturated fatty acids, except for C4:0 and C6:0, whereas long-chain fatty acids and unsaturated fatty acids (including CLA) were mainly influenced by herd-date effects. Herd-date effect explained large portions of the total phenotypic variance for C18:2 *cis*-9,*cis*-12 (0.668), C18:3 *cis*-9,*cis*-12,*cis*-15 (0.631), and the biohydrogenation and elongation products of these fatty acids. The desaturation ratios showed higher heritability estimates than the individual fatty acids, except for CLA desaturation index (0.098). Among the medium-chain fatty acids, C12:0 had greater heritability than C14:0 (0.243 vs. 0.097, respectively). Both C14:0 and C16:0 showed negative additive genetic correlations with the main monounsaturated and polyunsaturated fatty acids of milk fat, suggesting that their synthesis in the mammary gland may be influenced by the presence of unsaturated fatty acids. No correlation was observed between C4:0 and the other short-chain fatty acids (except for C6:0), confirming the independence of C4:0 from de novo mammary fatty acid synthesis. Among the genetic correlations dealing with potentially beneficial fatty acids, C18:0 was positively correlated with vaccenic and rumenic acids and negatively with linoleic acid. Finally, fatty acids C6:0 through C14:0 showed relevant correlations due to unknown environmental effects, suggesting the potential existence of genetic variances in micro-environmental sensitivity. This study allowed us to acquire new knowledge about the genetic and the environmental relationships among fatty acids. Likewise, the existence of genetic variation for most of de novo synthetized fatty acids and saturated fatty acids was also observed.

Overall, these results provide useful information to combine feeding with genetic selection strategies for obtaining a desirable milk fatty acids profile, depending on the origin of fatty acids in milk.

Keywords: Bayes factor; Brown Swiss; Fatty acids; Genetic parameters; 9-desaturation index

Journal of Dairy Science

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Genetic and environmental relationships of different measures of individual cheese yield and curd nutrients recovery with coagulation properties of bovine milk

Cecchinato, A., Bittante, G.

Department of Agronomy, Food Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, Legnaro (PD), Italy

Abstract

The aim of this study was to elucidate the relationships between various cheesemaking-related traits, namely the well-known traditional milk coagulation properties (MCP), the new curd firming and syneresis traits, the cheese yield, and the curd nutrient recoveries or whey losses (all measured at the individual level). Data were obtained from 1,167 Brown Swiss cows reared in 85 herds. A 2-milk sample was collected once from each animal and assessed for 10 phenotypes related to changes in curd firmness (CF) over time, plus 7 cheesemaking traits. The CF-related traits included 4 traditional single-point lactodynamographic properties [rennet coagulation time (RCT, min); time to a CF of 20 mm, min; and the CF 30 and 45 min after rennet addition (a_{30} and a_{45}, respectively)], 4 parameters used to model the 360 CF data recorded over time for each milk sample [the potential asymptotic CF at infinite time (CF_P, mm); the CF instant rate constant, % x min^{-1}; the syneresis instant rate constant, % x min^{-1}; and the RCT obtained from modeling individual samples], and 2 traits calculated from individual equations [the maximum CF(CF_{max}, mm); and the time at CF_{max}, min]. The cheesemaking traits included 3 cheese yield traits (weights of the fresh curd, curd solids and curd moisture as percent of the weights of the processed milk) and 4 milk nutrient recoveries in the curd (calculated as the percent ratios between a given nutrient in the curd versus that in the processed milk). Bayesian methodology-based multivariate analyses were used to estimate the phenotypic, additive genetic, herd/date, and residual relationships between the aforementioned traits, whereas statistical inferences were based on the marginal posterior distributions of the parameters of concern. The a_{45}, CF_P, and CF_{max} traits were genetically associated with all of the percent cheese yield traits (the additive genetic correlations varied from 0.752 to 0.855 for a_{45}; 0.496 to 0.583 for CF_P; and 0.750 to 0.801 for CFmax) and the nutrient recovery traits (additive genetic correlations varied from 0.296 to 0.901 for a_{45}; 0.428 to 0.697 for CF_P; and 0.412 to 0.941 for CF_{max}). Moreover, the nutrient recoveries for fat, solids, and energy exhibited large additive genetic correlations with the other coagulation and curd firming traits. In particular, recovery of protein and fat were found to be powerful instruments for understanding the relationships between milk technological properties and cheese quantity or quality. We observed only weak genetic relationships with the milk quality and MCP traits, suggesting that the highly heritable trait of protein recovery should perhaps be included as a genetic index when seeking to improve cheesemaking efficiency at the population level. In contrast, we found that fat recovery exhibited moderate genetic variation and could be improved through the CF over time traits, especially using those recorded during the late phase of the curd firming process. Moreover, our results demonstrated that the traditional MCP have limited relevance for predicting individual cheese yield. Therefore, their use for this purpose in the dairy industry and breeding programs seems questionable.

Keywords: Cheese yield; Curd firming; Genetic correlations; Milk coagulation; Whey losses

Journal of Dairy Science

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Estimation of economic values for milk coagulation properties in Italian Holstein-Friesian cattle

Cassandro, M.[a], Pretto, D.[b], Lopez-Villalobos, N.[c], De Marchi, M.[a], Penasa, M.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Viale dell'Università 16, Legnaro (PD), Italy
[b] Institute of Veterinary Medicine and Animal Sciences, Estonian University of Life Sciences, Kreutzwaldi 1, Tartu, Estonia
[c] Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Private Bag 11-222, Palmerston North, New Zealand

Abstract

The economic values (EV) of production traits, rennet coagulation time (RCT, min), and curd firmness (a_{30}, mm) were derived for Italian Holstein-Friesian dairy cattle, based on the Grana Padano cheese industry. Three different sets of EV for RCT and a_{30} were estimated, assuming +2.5% (scenario 1), +5% (scenario 2), and +10% (scenario 3) increment in cheese yield due to the effect of milk coagulation properties (MCP). A model was developed to simulate the transformation of milk into Grana Padano cheese. The EV of RCT and a_{30} were €2.213, €4.426, and €8.852/min, and €0.877, €1.755, and €3.509/mm for scenarios 1, 2, and 3, respectively. Relative emphasis of traits in the breeding objectives of the Italian Holstein-Friesian dairy cattle population should account for the effect of MCP on cheese yield. Economic values for milk components and MCP were affected by changes of dairy products, whereas variations of feed prices did not influence EV of RCT and a_{30}.

Keywords: Economic value; Italian Holstein-Friesian cattle; Milk coagulation property; Milk production

Journal of Dairy Science

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Contribution of microsatellites markers in the clarification of the origin, genetic risk factors, and implications for conservation of Tunisian native sheep breeds

Ben Sassi-Zaidy, Y.[ab]*, Maretto, F.*[b]*, Charfi-Cheikhrouha, F.*[a]*, Mohamed-Brahmi, A.*[c]*, Cassandro, M.*[b]

[a] UR 11ES11 Bio-Ecologie et Systématique Evolutive, Université de Tunis El Manar, Tunis, Tunisia
[b] Department of Agronomy, Food Natural Resources Animals and Environment, University of Padova, Legnaro, Italy
[c] Laboratoire d'Appui à la Durabilité des Systèmes de Production Agricole dans la Région du Nord-Ouest, Département de la Production Animale, Ecole Supérieure d'Agriculture du Kef Boulifa, Le Kef, Tunisia

Abstract

The genetic diversity and genetic relationship of the two main groups of African sheep, thin-tailed and fat-tailed sheep, represented by the indigenous Tunisian sheep breeds "Barbarine" (BAR, fat-tailed) and "Queue Fine de l'Ouest" (QFO, thin-tailed) were investigated. The genotypes of 110 animals belonging to these two breeds and their crossbreed (CRO) were assessed using 17 microsatellite markers. The results showed high levels of genetic diversity and a total of 256 alleles were identified in the whole population. The mean values of observed and expected heterozygosity were 0.719 and 0.789, respectively, and the mean allelic richness estimate was 10.89. The average F_{IS} (0.112) and F_{IT} (0.118) values over all loci indicated a notable level of inbreeding within the whole population. However, the F_{ST} value (0.007) showed a low level of genetic differentiation between these two native breeds. The high level of both gene flow and molecular coancestry coefficient detected between the two breeds and their CRO revealed an old miscegenation between the BAR and QFO breeds. The clustering analysis performed with the STRUCTURE software confirmed gene flow between these two breeds. Results arising from this study provide evidence regarding the genetic structure and variability of the two main local sheep breeds, and the implications of their actual management, which indicates the need for an urgent conservation strategy in order to prevent significant gene flow and preserve the remaining breed specificity for future generations.

Keywords: Genetic variability; Microsatellite markers; Population structure; Tunisian indigenous sheep

Genetics and Molecular Research

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Comparison of genetic diversity of Turkish and Italian local chicken breeds for further conservation strategies

Özdemir, D.[a], Maretto, F.[b], Cassandro, M.[b]

[a] Teknik Bilimler Meslek Yüksekokulu, Akdeniz Universitesi, Antalya, Turkey
[b] Dept of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Legnaro (PD), Italy

Abstract

The present study was conducted to estimate and compare the intra and inter genetic variability and population structure of 8 Mediterranean chicken populations based on two Turkish (Denizli and Gerze) and 6 Italian (Ermellinata di Rovigo, Padovana, Pèpoi, Polverara, Robusta Lionata and Robusta Maculata) local chicken breeds, using 19 microsatellite markers. A total of 171 alleles were found across 19 microsatellite loci with a mean number of 9 alleles per locus. The breeds were highly differentiated with an average FST of 0.328. Global FIS values (0.277) indicated that non-random mating occurred in both Turkish and Italian chicken breeds. The mean number of alleles across breeds was 4.11. Observed heterozygosity was lower than HE for all breeds and it was in the range of 0.235 (Pèpoi) to 0.421 (Ermellinata di Rovigo). Genetic distance (DC) between pairs of breeds ranged from 0.307 (Padovana and Polverara) to 0.716 (Gerze and Ermellinata di Rovigo), with average DC across breeds ranging from 0.451 (Padovana) to 0.687 (Gerze). The most probable structure clustering of the 8 chicken populations was at K = 10. While Turkish breeds showed no substructures within breeds and were observed to be distinct homogenous genetic populations, subgroups were observed mainly in Italian chicken breeds corresponding to the different ecotypes present in these breeds. The information resulting from this study may be used as an initial guideline to design further investigations for development of sustainable genetic improvement and conservation programs for Turkish and Italian chicken genetic resources.

Keywords: Genetic diversity; Genetics; Italian chicken; Microsatellite; Population structure; Preservation; Turkish chicken

European Poultry Science

Volume 80

Genetic correlations between type and test-day milk yield in small dual-purpose cattle populations: The Aosta Red Pied breed as a case study

Mazza, S., Guzzo, N., Sartori, C., Mantovani, R.

Department of Agronomy, Food, Natural Resources, Animals and Environment,
University of Padova, Viale dell'Università 16, Legnaro, PD, Italy

Abstract

This study aimed at estimating the relationships between linear type traits and milk production in the dual-purpose Aosta Red Pied (ARP) cattle breed, by expressing type traits as factor scores with the same biological meaning of the individual traits. Factor analysis was applied to individual type traits for muscularity and udder of 32,275 first-parity ARP cows, obtaining 3 factor scores for individual muscularity (F1), udder side (F2), and udder conformation (F3). Data from 169,008 test-day records of milk, fat, and protein yield (kg), belonging to the first 3 lactations of 16,605 cows, were also analyzed. After obtaining genetic parameters for both morphological factors and milk production traits through a series of AIREML single-trait models, bivariate analyses were performed on a data set accounting for 201,283 records of 35,530 cows, to assess the phenotypic and genetic correlations among all factor scores and milk yield traits. The heritability estimates obtained proved to be moderate for both groups of traits, ranging from 0.132 (fat) to 0.314 (F1). Muscularity factor showed moderate and negative genetic correlations (r_a) with udder size (0.376) and udder conformation (0.214) factors. A low and negative r_a was found between udder factors. Strong and positive r_a were found among all the 3 milk production traits and F 0010 (r_a 0.597). Negative r_a with milk traits were obtained for both F 0005 and F3, ranging from 0.417 to 0.221. Phenotypic correlations were lower than the genetic ones, and sometimes close to zero. The antagonism between milk production and meat attitude traits suggests that great attention should be paid in assigning proper weight to the traits, comprising functional traits such as udder conformation, included in selection indices for the dual-purpose breed. The r_a obtained for factor scores are consistent with previous estimates for the corresponding individual type traits, and this confirms the possible use of factor analysis to improve type traits relevant to beef attitude.

Keywords: Dual-purpose cattle; Factor analysis; Genetic parameters; Test-day milk; Type traits

Journal of Dairy Science

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Microbiology

Aptitude of *Saccharomyces* yeasts to ferment unripe grapes harvested during cluster thinning for reducing alcohol content of wine

Bovo, B.[a], Nadai, C.[a], Vendramini, C.[a], Fernandes Lemos Junior, W.J.[a], Carlot, M.[ab], Skelin, A.[c], Giacomini, A.[ab], Corich, V.[ab]

[a] Department of Agronomy Food Natural resources Animals and Environment (DAFNAE), University of Padova, Legnaro, PD, Italy
[b] Interdepartmental Centre for Research in Viticulture and Enology (CIRVE), University of Padova, Conegliano, TV, Italy
[c] Department of Microbiology, Faculty of Agriculture, University of Zagreb, Zagreb, Croatia

Abstract

Among the viticultural techniques developed to obtain wine with reduced alcohol content, the use of unripe grapes with low sugar and high malic acid concentration, harvested at cluster thinning, was recently explored. So far, no studies have evaluated the fermentation performances of *Saccharomyces* in unripe grape musts, in terms of fermentation ability and reducing malic acid contents, to improve the quality of this low-alcohol beverage. In this work, we evaluated 24 *S. cerevisiae* strains isolated from Italian and Croatian vineyards with different fermentation aptitudes. Moreover, four *S. paradoxus* were considered, as previous works demonstrated that strains belonging to this species were able to degrade high malic acid amounts in standard musts. The industrial strain *S. cerevisiae* 71B was added as reference. Sugar and malic acid contents were modified in synthetic musts in order to understand the effect of their concentrations on alcoholic fermentation and malic acid degradation. *S. cerevisiae* fermentation performances improved when glucose concentration decreased and malic acid level increased. The conditions that simulate unripe grape must, i.e. low glucose and high malic acid content were found to enhance *S. cerevisiae* ability to degrade malic acid. On the contrary, *S. paradoxus* strains were able to degrade high amounts of malic acid only in conditions that resemble ripe grape must, i.e. high glucose and low malic acid concentration. In fermentation trials when low glucose concentrations were used, at high malic acid levels *S. cerevisiae* strains produced higher glycerol than at low malic acid condition. Malic acid degradation ability, tested on the best performing *S. cerevisiae* strains, was enhanced in fermentation trials when unripe grape must was used.

Keywords: Glycerol; Malic acid; *Saccharomyces cerevisiae*; *Saccharomyces paradoxus*; Unripe grape must

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Modeling quorum sensing trade-offs between bacterial cell density and system extension from open boundaries

Marenda, M.[a], Zanardo, M.[b], Trovato, A.[cd], Seno, F.[ce], Squartini, A.[b]

[a] SISSA, International School for Advanced Studies, via Bonomea 265, 34136 Trieste, Italy
[b] Department of Agronomy, Food, Natural Resources, Animals and Environment DAFNAE, Università di Padova, Viale dell'Università 16, 35020 Legnaro (Padova), Italy
[c] Department of Physics and Astronomy "Galileo Galilei", Università di Padova, Via Marzolo 8, 35131 Padova, Italy
[d] INFN, National Institute for Nuclear Physics, Sezione di Padova, Via Marzolo 8, 35131 Padova, Italy
[e] CNISM, National Interuniversity Consortium for the Physical Sciences of Matter, Unità di Padova, Via Marzolo 8, 35131 Padova, Italy

Abstract

Bacterial communities undergo collective behavioural switches upon producing and sensing diffusible signal molecules; a mechanism referred to as Quorum Sensing (QS). Exemplarily, biofilm organic matrices are built concertedly by bacteria in several environments. QS scope in bacterial ecology has been debated for over 20 years. Different perspectives counterpose the role of density reporter for populations to that of local environment diffusivity probe for individual cells. Here we devise a model system where tubes of different heights contain matrix-embedded producers and sensors. These tubes allow non-limiting signal diffusion from one open end, thereby showing that population spatial extension away from an open boundary can be a main critical factor in QS. Experimental data, successfully recapitulated by a comprehensive mathematical model, demonstrate how tube height can overtake the role of producer density in triggering sensor activation. The biotic degradation of the signal is found to play a major role and to be species-specific and entirely feedback-independent.

Scientific Reports

Volume 6, Article number 39142

Bacillus sp. strains to produce bio-hydrogen from the organic fraction of municipal solid waste

Shah, A.T.[ab], *Favaro, L.*[a], *Alibardi, L.*[c], *Cagnin, L.*[a], *Sandon, A.*[d], *Cossu, R.*[c], *Casella, S.*[a], *Basaglia, M.*[a]

[a] Department of Agronomy Food Natural resources Animals and Environment, University of Padova, Viale dell'Università 16, 35020 Legnaro, PD, Italy
[b] Fermentation Technology Group, Industrial Biotechnology Division, National Institute for Biotechnology and Genetic Engineering (NIBGE), 38000 Faisalabad, Pakistan
[c] Department of Industrial Engineering, University of Padova, Via Gradenigo 6/a, 35131 Padova, Italy
[d] Department of Civil, Environmental and Architectural Engineering, University of Padova, via Marzolo 9, 35131 Padova, Italy

Abstract

Bio-hydrogen, obtained by fermentation of organic residues, is considered a promising source of renewable energy. However, the industrial scale H_2 production from organic waste is far to be realized as technical and economical limitations have still to be solved. Low H_2 yields and lack of industrially robust microbes are the major limiting factors. To look for bacteria with both interesting hydrogen fermentative traits and proper robustness, granular sludge from a brewery full scale Upflow Anaerobic Sludge Blanket (UASB) digester was selected as trove of microbes processing complex substrates. One hundred and twenty bacterial strains, previously isolated from heat-treated granular sludge and genetically identified by 16S rDNA sequencing, were screened for extracellular hydrolytic enzymes on cellulose, hemicellulose, starch, pectin, lipids, protein. The most interesting hydrolytic strains were assessed for their H_2 production from glucose and soluble starch. Two *Bacillus* sp. strains, namely F2.5 and F2.8, exhibited high H_2 yields and were used as pure culture to convert Organic Fraction of Municipal Solid Waste (OFMSW) into hydrogen. The strains produced up to 61 mL of H_2 per grams of volatile solids and could be considered as good candidates towards the development of industrially relevant H_2-producing inoculants. This is the first successful application of pure microbial cultures in bio-hydrogen production from OFMSW.

Keywords: *Bacillus* sp.; Bio-hydrogen; Dark fermentation; Organic fraction of municipal solid waste; Pure cultures; Strain selection

Applied Energy

Volume 176, Pages 116-124

Antiradical and antimicrobial properties of fermented red chicory (*Cichorium intybus* L.) by-products

Kagkli, D.M., Corich, V., Bovo, B., Lante, A., Giacomini, A.

Department of Agronomy, Food, Natural Resources, Animals and the Environment (DAFNAE), University of Padova, viale dell'Università 16, Legnaro, Padova 35020, Italy

Abstract

Discarded leaves of red chicory (Radicchio "Rosso di Chioggia" IGP) were fermented with one *Saccharomyces* yeast and four lactic acid bacteria chosen on the basis of their ability to grow on plant material without any need of supplements. Antiradical and antimicrobial activities of the resulting products were assessed. Among the strains tested, *Lactobacillus plantarum* and *L. hilgardii* gave the best performances and also provided fermented substrates with antiradical and antimicrobial activities. In particular the latter compounds were found only in fermented samples, confirming that the choice of appropriate microorganisms for fermentation could be useful when the aim is to target specific functional foods starting from by-products or waste material.

Keywords: Antimicrobial activity; Antioxidant/antiradical activity; By-products; *Cichorium intybus*; Fermentation; Functional food

Annals of Microbiology

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Different mechanisms of resistance modulate sulfite tolerance in wine yeasts

Nadai, C.[a], *Treu, L.*[a], *Campanaro, S.*[b], *Giacomini, A.*[ac], *Corich, V.*[ac]

[a] Department of Agronomy Food Natural resources Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro, PD, Italy
[b] Department of Biology, University of Padova, Via U. Bassi 58/b, 35121 Padova, Italy
[c] Interdepartmental Centre for Research in Viticulture and Enology (CIRVE), University of Padova, Via XXVIII Aprile 14, 31015 Conegliano, TV, Italy

Abstract

From a technological point of view, yeast resistance to sulfite is of great interest and represents an important technological character for winemaking. Several mechanisms are involved, and strain-dependent strategies to obtain SO_2 resistance can deeply influence wine quality, although this choice is less relevant in determining the technological performance of the strain during fermentation. In this study, to better understand the strain-specific mechanisms of resistance, 11 *Saccharomyces cerevisiae* strains, whose genomes have been previously sequenced, were selected. Their attitude towards sulfites, in terms of resistance and production, was evaluated, and RNA-sequencing of four selected strains was performed during fermentation process in synthetic grape must in the presence of SO_2. Results demonstrated that at molecular level, the physical effect of SO_2 triggered multiple stress responses in the cell and high tolerance to general enological stressing condition increased SO_2 resistance. Adaptation mechanism due to high basal gene expression level rather than specific gene induction in the presence of sulfite seemed to be responsible in modulating strain resistance. This mechanism involved higher basal gene expression level of specific cell wall proteins, enzymes for lipid biosynthesis, and enzymes directly involved in SO_2 assimilation pathway and efflux.

Keywords: Antioxidant; Fermentation; RNA-seq; *Saccharomyces cerevisiae*; Stress response; Sulfur dioxide resistance

Applied Microbiology and Biotechnology

Volume 100, Issue 2, Pages 797-813

Biocontrol ability and action mechanism of *Starmerella bacillaris* (synonym *Candida zemplinina*) isolated from wine musts against gray mold disease agent *Botrytis cinerea* on grape and their effects on alcoholic fermentation

Lemos, W.J., Jr.[a], Bovo, B.[ab], Nadai, C.[ab], Crosato, G.[ab], Carlot, M.[ab], Favaron, F.[c], Giacomini, A.[ab], Corich, V.[ab]

[a] Department of Agronomy Food Natural Resources Animals and Environment, University of Padova, Legnaro, Italy
[b] Interdepartmental Centre for Research in Viticulture and Enology, University of Padova, Conegliano, Italy
[c] Department of Land Environment Agriculture and Forestry, University of Padova, Legnaro, Italy

Abstract

Gray mold is one of the most important diseases of grapevine in temperate climates. This plant pathogen affects plant growth and reduces wine quality. The use of yeasts as biocontrol agents to apply in the vineyard have been investigated in recent years as an alternative to agrochemicals. In this work, fermenting musts obtained from overripe grape berries, therefore more susceptible to infection by fungal pathogens such as *Botrytis cinerea*, were considered for the selection of yeasts carrying antifungal activity. Thirty-six isolates were identified as *Starmerella bacillaris*, a species recently proven to be of enological interest. Among them 14 different strains were studied and antifungal activity against *B. cinerea* was demonstrated, for the first time, to be present in *S. bacillaris* species. The production of volatile organic compounds (VOCs), tested *in vitro*, was found to be the main responsible of *S. bacillaris* antifungal effects. All the strains were able to reduce *B. cinerea* decay on wounded grape berries artificially inoculated with gray mold. The colonization level of wound was very high reaching, after 5 days, a concentration of 106 cells per ml of grape juice obtained after berry crushing. At this cell concentration *S. bacillaris* strains were used to ferment synthetic and natural musts. The sequential yeast inoculation, performed by adding *S. cerevisiae* 48 h after *S. bacillaris*, was needed to complete sugar consumption and determined a significant increase in glicerol content and a reduction of ethanol and acetic acid concentrations. The high wound colonization ability, found in this work, together with the propensity to colonize grape berry and the interesting enological traits possessed by the selected *S. bacillaris* strains allow the use of this yeast as biocontrol agent on vine and grape berries with possible positive effects on must fermentation, although the presence of *S. cerevisiae* is needed to complete the fermentation process. This work introduces new possibilities in wine yeast selection programs in order to identify innovative wine yeasts that are simultaneously antifungal agents in vineyards and alternative wine starters for grape must fermentation and open new perspective to a more integrated strategy for increasing wine quality.

Keywords: Antifungal activity; Fermentation; Glicerol; Grape must; Lytic enzymes; SAU-PCR; VOCs

Frontiers in Microbiology

Volume 7, Article number 1249

A novel FTIR-based approach to evaluate the interactions between lignocellulosic inhibitory compounds and their effect on yeast metabolism

Favaro, L.[a], Corte, L.[b], Roscini, L.[b], Cagnin, L.[a], Tiecco, M.[c], Colabella, C.[b], Berti, A.[a], Basaglia, M.[a], Cardinali, G.[bc], Casella, S.[a]

[a] Department of Agronomy Food Natural Resources Animals and Environment (DAFNAE), University of Padova, Agripolis, Italy
[b] Department of Pharmaceutical Sciences-Microbiology, University of Perugia, Borgo XX Giugno, 74, I-06121 Perugia, Italy
[c] CEMIN, Centre of Excellence on Nanostructured Innovative Materials, Department of Chemistry, Biology and Biotechnology, University of Perugia, Italy

Abstract

Inhibitors commonly found in lignocellulosic hydrolysates impair yeast metabolism and growth, reducing the productivity of the overall bioethanol production process. FTIR spectroscopy was used to analyze the metabolomic alterations induced by acetic and formic acid, furfural and 5-hydroxymethyl-2-furaldehyde (HMF) on yeast metabolism, using three *Saccharomyces cerevisiae* strains with different sensitivities. IR spectrum alterations were summarized with synthetic descriptors to rapidly visualize the kinds of molecules displaying the more intense reactions and to evaluate the type of interaction between inhibitors in a mixture, at concentrations close to those found at the industrial scale. The four inhibitors induced different levels of mortality and metabolomic changes. The metabolomic response was proportional to the different strain resistance level, further supporting their original classification. Inhibitor mixtures severely hindered the cell viability with the exception of the lowest concentration tested, which was partially biocidal. Furthermore, for the first time, this study revealed antagonistic interactions exerted by inhibitor mixtures on microbial metabolism, closely strain- and dose-dependent. This confirms that yeast strain resistance to single inhibitors cannot be used to predict behaviour on exposure to mixtures. This finding is worth further studies to explain the underlying antagonistic mechanism and to support the selection of highly tolerant strains.

RSC Advances

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Characterization of lipopeptides produced by *Bacillus licheniformis* using liquid chromatography with accurate tandem mass spectrometry

Favaro, G.[a], Bogialli, S.[a], Di Gangi, I.M.[a], Nigris, S.[b], Baldan, E.[b], Squartini, A.[c], Pastore, P.[a], Baldan, B.[a]

[a] Department of Chemical Sciences, University of Padova, via Marzolo 1, 35131 Padova, Italy
[b] Department of Biology, University of Padova, via Ugo Bassi 58/B, 35131 Padova, Italy
[c] Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy

Abstract

Rationale: The plant endophyte *Bacillus licheniformis*, isolated from leaves of *Vitis vinifera*, was studied to individuate and characterize the presence of bioactive lipopeptides having amino acidic structures.

Methods: Crude extracts of liquid cultures were analyzed by ultra-high-performance liquid chromatography (UHPLC) coupled to a quadrupole time-of-flight (QTOF) mass analyzer. Chromatographic conditions were optimized in order to obtain an efficient separation of the different isobaric lipopeptides, avoiding merged fragmentations of co-eluted isomeric compounds and reducing possible cross-talk phenomena. Composition of the amino acids was outlined through the interpretation of the fragmentation behavior in tandem high-resolution mass spectrometry (HRMS/MS) mode, which showed both common-class and peculiar fragment ions. Both $[M + H]^+$ and $[M + Na]^+$ precursor ions were fragmented in order to differentiate some isobaric amino acids, i.e. Leu/Ile. Neutral losses characteristic of the *iso* acyl chain were also evidenced.

Results: More than 90 compounds belonging to the classes of surfactins and lichenysins, known as biosurfactant molecules, were detected. Sequential LC/HRMS/MS analysis was used to identify linear and cyclic lipopeptides, and to single out the presence of a large number of isomers not previously reported. Some critical issues related to the simultaneous selection of different compounds by the quadrupole filter were highlighted and partially solved, leading to tentative assignments of several structures. Linear lichenysins are described here for the first time.

Conclusions: The approach was proved to be useful for the characterization of non-target lipopeptides, and proposes a rationale MS experimental scheme aimed to investigate the difference in amino acid sequence and/or in the acyl chain of the various congeners, when standards are not available. Results expanded the knowledge about production of linear and cyclic bioactive compounds from *Bacillus licheniformis*, clarifying the structures of isomeric forms, and enabling the use of selected endophytes to produce fungicides for eco-friendly biocontrol.

Rapid Communications in Mass Spectrometry

Volume 30, Issue 20, Pages 2237-2252

Direct 16S rRNA-seq from bacterial communities: a PCR-independent approach to simultaneously assess microbial diversity and functional activity potential of each taxon

Rosselli, R.[a], Romoli, O.[a], Vitulo, N.[b], Vezzi, A.[a], Campanaro, S.[a], de Pascale, F.[a], Schiavon, R.[a], Tiarca, M.[c], Poletto, F.[c], Concheri, G.[d], Valle, G.[a], Squartini, A.[d]

[a] Department of Biology, University of Padova, Padova, Italy
[b] Department of Biotechnology, University of Verona, Verona 37134, Italy
[c] RWL Water/Eurotec WTT, Water Treatment Technologies, S.r.l., Padova, Italy
[d] Department of Agronomy, Food, Natural Resources, Animals and Environment, DAFNAE, University of Padova, Legnaro (Padova), Italy

Abstract

The analysis of environmental microbial communities has largely relied on a PCR-dependent amplification of genes entailing species identity as 16S rRNA. This approach is susceptible to biases depending on the level of primer matching in different species. Moreover, possible yet-to-discover taxa whose rRNA could differ enough from known ones would not be revealed. DNA-based methods moreover do not provide information on the actual physiological relevance of each taxon within an environment and are affected by the variable number of rRNA operons in different genomes. To overcome these drawbacks we propose an approach of direct sequencing of 16S ribosomal RNA without any primer- or PCR-dependent step. The method was tested on a microbial community developing in an anammox bioreactor sampled at different time-points. A conventional PCR-based amplicon pyrosequencing was run in parallel. The community resulting from direct rRNA sequencing was highly consistent with the known biochemical processes operative in the reactor. As direct rRNA-seq is based not only on taxon abundance but also on physiological activity, no comparison between its results and those from PCR-based approaches can be applied. The novel principle is in this respect proposed not as an alternative but rather as a complementary methodology in microbial community studies.

Scientific Reports

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Plant science

Estimation of cotyledon isoflavone abundance by a grey luminance-based model in variously hilum-coloured soybean varieties

Barion, G., Mosca, G., Vamerali, T.

Department of Agronomy, Food, Natural Resources, Animals and the Environment,
University of Padova, Viale dell'Università 16, Legnaro, Padova, Italy

Abstract

Background: The nutraceutical uses of soybean (*Glycine max* L. Merr.) have received increasing attention in recent years, due to the therapeutic effects of high seed isoflavone concentrations against heart disease, cancer and menopausal symptoms.

Results: We found a close correlation between seed isoflavone abundance and hilum colour in a set of 17 contrasting soybean varieties. Image analysis of the hilum grey level pattern allowed us to identify a power model which approximates total cotyledon isoflavone concentrations (TCIC) at 65–71% by the normalised modal grey level. Higher TCIC levels were assigned to darker hilum varieties and vice versa within a variety-dependent response. Optimisation of the algorithm required correction for a few specific varieties falling in the intermediate 1.1–1.5 mg g^{-1} TCIC range, which were over-estimated by the model, perhaps due to variations in hilar optical properties related to the geometric features of both hilum and seed.

Conclusions: In view of its easy, low-cost detection, seed hilum colour is a useful phenotypic trait in soybean for rapid evaluation of isoflavone abundance in food uses and for improving specific nutraceutical breeding programmes.

Keywords: Hilum grey luminance; Image analysis; Isoflavone prediction; Soybean varieties

Journal of the Science of Food and Agriculture

Volume 96, Issue 12, Pages 4126-4134

Old apple (*Malus domestica* L. Borkh) varieties with hypoallergenic properties: an integrated approach for studying apple allergenicity

Vegro, M.[a]*, Eccher, G.*[a]*, Populin, F.*[a]*, Sorgato, C.*[a]*, Savazzini, F.*[b]*, Pagliarani, G.*[b]*,*
Tartarini, S.[b]*, Pasini, G.*[a]*, Curioni, A.*[a]*, Antico, A.*[c]*, Botton, A.*[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment -
DAFNAE Agripolis, University of Padova, Viale dell'università 16,
Legnaro (Padova), Italy
[b] Department of Agricultural Science, University of Bologna, Viale Fanin 46,
Bologna, Italy
[c] Allergy Unit, Ospedale Civile Srl, Via Guido Tonello 5, Volta Mantovana
(Mantova), Italy

Abstract

Freshly consumed apples (*Malus domestica* L. Borkh) can cause allergic reactions because of the presence of four classes of allergens. Knowledge of the genetic factors affecting the allergenic potential of apples would provide important information for the selection of hypoallergenic genotypes, which can be combined with the adoption of new agronomical practices to produce fruits with a reduced amount of allergens. In the present research, a multiple analytical approach was adopted to characterize the allergenic potential of 24 apple varieties released at different ages (pre- and post-green revolution). A specific workflow was set up including protein quantification by means of polyclonal antibodies, immunological analyses with sera of allergic subjects, enzymatic assays, clinical assessments on allergic patients, and gene expression assays on fruit samples. Taken as a whole, the results indicate that most of the less allergenic genotypes were found among those deriving from selection processes carried out prior to the so-called "green revolution".

Keywords: Gene expression studies; *Malus domestica*; Polyclonal antibodies; Prick-by-prick tests

Journal of Agricultural and Food Chemistry

Volume 64, Issue 48, Pages 9224-9236

Grapevine rootstocks differentially affect the rate of ripening and modulate auxin-related genes in cabernet sauvignon berries

Corso, M.[ab], Vannozzi, A.[ab], Ziliotto, F.[a], Zouine, M.[c], Maza, E.[c], Nicolato, T.[a], Vitulo, N.[d], Meggio, F.[ab], Valle, G.[d], Bouzayen, M.[c], Müller, M.[e], Munné-Bosch, S.[e], Lucchin, M.[ab], Bonghi, C.[ab]

[a] Department of Agronomy, Food, Natural resources, Animals and Environment, University of Padova Agripolis, Legnaro, Italy
[b] Centro Interdipartimentale per la Ricerca in Viticoltura e Enologia, University of Padova, Conegliano, Italy
[c] Genomics and Biotechnology of Fruit Laboratory, Institut National Polytechnique de Toulouse, Toulouse, France
[d] Centro di Ricerca Interdipartimentale per le Biotecnologie Innovative, University of Padova, Padova, Italy
[e] Department of Vegetal Biology, University of Barcelona, Barcelona, Spain

Abstract

In modern viticulture, grafting commercial grapevine varieties on interspecific rootstocks is a common practice required for conferring resistance to many biotic and abiotic stresses. Nevertheless, the use of rootstocks to gain these essential traits is also known to impact grape berry development and quality, although the underlying mechanisms are still poorly understood. In grape berries, the onset of ripening (véraison) is regulated by a complex network of mobile signals including hormones such as auxins, ethylene, abscisic acid, and brassinosteroids. Recently, a new rootstock, designated M4, was selected based on its enhanced tolerance to water stress and medium vigor. This study investigates the effect of M4 on Cabernet Sauvignon (CS) berry development in comparison to the commercial 1103P rootstock. Physical and biochemical parameters showed that the ripening rate of CS berries is faster when grafted onto M4. A multifactorial analysis performed on mRNA-Seq data obtained from skin and pulp of berries grown in both graft combinations revealed that genes controlling auxin action (ARF and Aux/IAA) represent one of main categories affected by the rootstock genotype. Considering that the level of auxin tightly regulates the transcription of these genes, we investigated the behavior of the main gene families involved in auxin biosynthesis and conjugation. Molecular and biochemical analyses confirmed a link between the rate of berry development and the modulation of auxin metabolism. Moreover, the data indicate that this phenomenon appears to be particularly pronounced in skin tissue in comparison to the flesh.

Keywords: Auxin conjugation; Fruit development; Grapevine; Polyphenols biosynthesis; Transcriptional program

Frontiers in Plant Science

Volume 7, Article number 69

Comparative analysis of genes involved in iron homeostasis in grapevine rootstocks characterized by contrasting tolerance to iron chlorosis

Vannozzi, A.[ab], Corso, M.[ab], Zen, I.[a], Bonghi, C.[a], Lucchin, M.[ab], Donnini, S.[c], Zocchi, G.[c]

[a] Università di Padova, Dipartimento di Agronomia Animali Alimenti Risorse Naturali e Ambiente (DAFNAE), Agripolis, Viale dell'Università 16, Legnaro, Italy
[b] Centro Interdipartimentale per la Ricerca in Viticoltura ed Enologia (CIRVE), Via XXVIII Aprile 14, Conegliano, TV, Italy
[c] Università di Milano, Dipartimento di Scienze Agrarie e Ambientali (DISAA), Via G. Celoria 2, Milano, Italy

Abstract

Iron chlorosis is an important nutritional disease that affects orchards and vineyards reducing quality and yield production. In soil, high calcareous conditions affect pH, raising it to sub-alkaline and alkaline levels and maintaining iron in an insoluble form as Fe3+. Chlorotic plants show abnormal photosynthesis and yellowing shoots. Nowadays the most used protection against iron chlorosis is grafting the cultivars of economic interest on tolerant rootstocks. Genetic improvement of fruit trees plays an important role on the selection of iron chlorosis resistant rootstocks using breeding techniques. In grapevine, this selection is based on breeding cultivars belonging to the V. vinifera species with non-vinifera ones (i.e., wild American species). In grapevine, iron uptake and homeostasis are controlled by a mechanism known as "Strategy I", characteristic of non-graminaceous plants and based on a system of iron reduction, soil acidification and transporters-mediated uptake. In this study, main Strategy I-genes involved in iron uptake were identified and analysed in two grapevine rootstocks characterized by different levels of tolerance and susceptibility to iron chlorosis. Expression analyses on selected genes under different iron-availability conditions revealed important differences which could explain the different degree of tolerance observed in the two genotypes under study.

Keywords: Flavonoids; Grapevine; Iron chlorosis; Resistance; Rootstocks; Transcriptome

Acta Horticulturae

Volume 1136, Pages 169-176

Transcriptome pathways in leaf and root of grapevine genotypes with contrasting drought tolerance

Corso, M.[a], *Vannozzi, A.*[a], *Maza, E.*[b], *Vitulo, N.*[c], *Meggio, F.*[a], *Bouzayen, M.*[b],
Valle, G.[c], *Bonghi, C.*[a], *Lucchin, M.*[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment, DAFNAE, University of Padova, Agripolis - Legnaro, Padova, Italy
[b] Genomics and Biotechnology of Fruit (GBF) Laboratory, Institut National Polytechnique de Toulouse, Avenue de l'Agrobiopole, Castanet-Tolosan Cedex (Toulouse), France
[c] CRIBI, University of Padova, viale G. Colombo 3, Padova, Italy

Abstract

Most of the world's wine-producing regions are subjected to seasonal drought, and, in the light of the dramatic climate-change events occurring in recent years, the selection of resistant rootstocks is becoming a crucial factor for the development of sustainable agricultural models to ensure optimal grape berry development and ripening. In this study, roots and leaves of 101.14 (drought-susceptible) and M4 (drought-tolerant) rootstocks were sampled in progressive drought and mRNA-seq profiles were evaluated. Physiological characterization indicated that only M4 was able to maintain high leaf transpiration and net assimilation rates under severe stress conditions. Statistical analyses, carried out on mRNA-seq data, highlighted that "treatment" (water stress) and "genotype" (rootstock-genotype) seem to be the main variables explaining differential gene expression in roots and leaves tissues, respectively. Upon water-stress, roots and leaves of the tolerant genotype M4 exhibit a higher induction of stilbenes (i.e., STS) and flavonoids (e.g., CHS, F3H, FLS) biosynthetic genes. Moreover, the higher expression of STS genes in M4 is coupled with an up-regulation of WRKYs transcription factors. STS genes promoter regions, extracted from whole genome of M4 and 101.14, highlighted a higher number of W-BOX cis elements (binding site for WRKYs) in the tolerant genotype.

Keywords: Flavonoids; mRNA-seq; Stilbenes; Vitis; Water stress; WRKY

Acta Horticulturae

Volume 1136, Pages 161-168

Stress-induced and epigenetic-mediated maize transcriptome regulation study by means of transcriptome reannotation and differential expression analysis

Forestan, C.[a], *Aiese Cigliano, R.*[b], *Farinati, S.*[a], *Lunardon, A.*[c], *Sanseverino, W.*[b], *Varotto, S.*[a]

[a] Department of Agronomy, Animals, Food, Natural Resources and Environment, University of Padova, Viale dell'Università 16, Legnaro (PD), Italy
[b] Sequentia Biotech SL, Calle Comte D'Urgell, 240, Barcelona, Spain
[c] Department of Biology, Huc Institutes of Life Sciences, Penn State University, University Park, PA, United States

Abstract

Plant's response and adaptation to abiotic stresses involve sophisticated genetic and epigenetic regulatory systems. To obtain a global view of molecular response to osmotic stresses, including the non-coding portion of genome, we conducted a total leaf transcriptome analysis on maize plants subjected to prolonged drought and salt stresses. Stress application to both B73 wild type and the epiregulator mutant rpd1-1/rmr6 allowed dissection of the epigenetic component of stress response. Coupling total RNA-Seq and transcriptome re-assembly we annotated thousands of new maize transcripts, together with 13,387 lncRNAs that may play critical roles in regulating gene expression. Differential expression analysis revealed hundreds of genes modulated by long-term stress application, including also many lncRNAs and transposons specifically induced by stresses. The amplitude and dynamic of the stress-modulated gene sets are very different between B73 and rpd1-1/rmr6 mutant plants, as result of stress-like effect on genome regulation caused by the mutation itself, which activates many stress-related genes even in control condition. The analyzed extensive set of total RNA-Seq data, together with the improvement of the transcriptome and the identification of the non-coding portion of the transcriptome give a revealing insight into the genetic and epigenetic mechanism responsible for maize molecular response to abiotic stresses.

Keywords: Plants genetics; Plant stress responses

Scientific Reports

Volume 6, Article number 30446

Preliminary studies on sensory, instrumental and chemical evaluation of dried goji (*Lycium barbarum* L.) berries

Bellaio, G., Carnevale, E., Bona, S.

Department Agronomy Food Natural Resources Animals Environment, University of Padua, Via dell'Universitá, 16, Italy

Abstract

Six commercial brands of dried goji (*Lycium barbarum* L.) berries were evaluated for their sensory, physical and chemical parameters. A quantitative descriptive analysis (QDA with 18 attributes) was undertaken and consumer preferences determined. Sensory assessments were supported with physical measurements of appearance and texture. Chemical parameters included: Total phenolic content, some phenolic acids (chlorogenic, caffeic, p-cumaric, ferulic and sinapic acids), antioxidant activity and ascorbic acid content. The berries were analyzed for their mineral elements (Ca, Cr, Fe, Ge, K, Na, P, Se, Zn) content. The main aim of this work was to assess differences between dried goji berries brands available in the Italian market and to relate them with the data available in the literature. Berries showed few differences in sensory, instrumental and chemical parameters, and those uncovered mainly related to visual, dimensional and texture descriptors (sensory analysis). Dried goji berries were not particularly appreciated by consumers and this suggests that they are bought for their advertised medicinal properties. For the most relevant compounds (e.g., phenolic acids, antioxidant molecules and elements), only a few variations were observed among brands. Dried goji berries showed to be an excellent source of antioxidants and mineral elements able to contribute in a relevant matter to the recommended daily intakes.

Keywords: Ascorbic acid; Panel test; Phenolic acids; Preference; Quality

Acta Horticulturae

Volume 1120, Pages 515-521

Inhibiting effect of shallow seed burial on grass weed emergence

Loddo, D.[a], Vasileiadis, V.P.[a], Masin, R.[b], Zuin, M.C.[a], Zanin, G.[b]

[a] Institute of Agro-Environmental and Forest Biology, CNR, Legnaro (PD), Italy
[b] Department of Agronomy, Food, Natural Resources, Animals and Environment,
University of Padova, Legnaro (PD), Italy

Abstract

The efficacy of superficial tillage as a sustainable tool to reduce the emergence of *Digitaria sanguinalis*, *Setaria viridis*, and *Sorghum halepense* was evaluated with field experiments. Seeds were buried at 1, 2, 5, and 10 cm of depth to simulate seed vertical distribution caused by autumn superficial tillage. Seedling emergence was monitored weekly for two years after sowing. The highest emergence was obtained in the first year after sowing and from 1 and 2 cm. *Sorghum halepense* was only slightly affected by seed burial, with 15% of emergence from 10 cm of depth, while *D. sanguinalis* was strongly affected, with 4% of emergence from 5 cm. The efficacy of superficial tillage as control tool could vary according to local weed flora.

Keywords: Conservation tillage; *Digitaria sanguinalis* (L.) scop; Seedling emergence; *Setaria viridis* (L.) beauv; *Sorghum halepense* (L.) pers; Weed control

Plant Protection Science

Volume 52, Issue 1, Pages 64-69

Transcript analysis and regulative events during flower development in olive (*Olea europaea* L.)

Alagna, F.[a], Cirilli, M.[b], Galla, G.[c], Carbone, F.[d], Daddiego, L.[d], Facella, P.[d], Lopez, L.[d], Colao, C.[b], Mariotti, R.[a], Cultrera, N.[a], Rossi, M.[a], Barcaccia, G.[c], Baldoni, L.[a], Muleo, R.[b], Perrotta, G.[d]

[a] Institute of Biosciences and Bioresources, National Research Council, Perugia, Italy
[b] Laboratory of Molecular Ecophysiology and Biotechnology of Woody Plants, Department of Agricultural and Forestry Science, University of Tuscia, Viterbo, Italy
[c] Laboratory of Plant Genetics and Genomics, DAFNAE, University of Padova, Legnaro, PD, Italy
[d] Italian National Agency for New Technologies, Energy and Sustainable Economic Development, TRISAIA Research Center, Rotondella, MT, Italy

Abstract

The identification and characterization of transcripts involved in flower organ development, plant reproduction and metabolism represent key steps in plant phenotypic and physiological pathways, and may generate high-quality transcript variants useful for the development of functional markers. This study was aimed at obtaining an extensive characterization of the olive flower transcripts, by providing sound information on the candidate MADS-box genes related to the ABC model of flower development and on the putative genetic and molecular determinants of ovary abortion and pollen-pistil interaction. The overall sequence data, obtained by pyrosequencing of four cDNA libraries from flowers at different developmental stages of three olive varieties with distinct reproductive features (Leccino, Frantoio and Dolce Agogia), included approximately 465,000 ESTs, which gave rise to more than 14,600 contigs and approximately 92,000 singletons. As many as 56,700 unigenes were successfully annotated and provided gene ontology insights into the structural organization and putative molecular function of sequenced transcripts and deduced proteins in the context of their corresponding biological processes. Differentially expressed genes with potential regulatory roles in biosynthetic pathways and metabolic networks during flower development were identified. The gene expression studies allowed us to select the candidate genes that play well-known molecular functions in a number of biosynthetic pathways and specific biological processes that affect olive reproduction. A sound understanding of gene functions and regulatory networks that characterize the olive flower is provided.

Keywords: Complementary DNA; Ttanscriptome; Messanger RNA

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Extreme hypoxic conditions induce selective molecular responses and metabolic reset in detached apple fruit

Cukrov, D.[a], Zermiani, M.[b], Brizzolara, S.[a], Cestaro, A.[c], Licausi, F.[a], Luchinat, C.[d], Santucci, C.[d], Tenori, L.[e], van Veen, H.[a], Zuccolo, A.[a], Ruperti, B.[b], Tonutti, P.[a]

[a] Istituto di Scienze della Vita, Scuola Superiore Sant'Anna, Pisa, Italy
[b] Dipartimento di Agronomia Animali Alimenti Risorse Naturalie Ambiente, University of Padova, Padova, Italy
[c] Centro Ricerca e Innovazione, Fondazione Edmund Mach di San Michele all'Adige, Trento, Italy
[d] CERM, University of Firenze, Firenze, Italy; Fondazione FiorGen Onlus, Firenze, Italy

Abstract

The ripening physiology of detached fruit is altered by low oxygen conditions with profound effects on quality parameters. To study hypoxia-related processes and regulatory mechanisms, apple (*Malus domestica*, cv Granny Smith) fruit, harvested at commercial ripening, were kept at 1°C under normoxic (control) and hypoxic (0.4 and 0.8 kPa oxygen) conditions for up to 60 days. NMR analyses of cortex tissue identified eight metabolites showing significantly different accumulations between samples, with ethanol and alanine displaying the most pronounced difference between hypoxic and normoxic treatments. A rapid up-regulation of alcohol dehydrogenase and pyruvate-related metabolism (lactate dehydrogenase, pyruvate decarboxylase, alanine aminotransferase) gene expression was detected under both hypoxic conditions with a more pronounced effect induced by the lowest (0.4 kPa) oxygen concentration. Both hypoxic conditions negatively affected ACC synthase and ACC oxidase transcript accumulation. Analysis of RNA-seq data of samples collected after 24 days of hypoxic treatment identified more than 1000 genes differentially expressed when comparing 0.4 vs. 0.8 kPa oxygen concentration samples. Genes involved in cell-wall, minor and major CHO, amino acid and secondary metabolisms, fermentation and glycolysis as well as genes involved in transport, defense responses, and oxidation-reduction appeared to be selectively affected by treatments. The lowest oxygen concentration induced a higher expression of transcription factors belonging to AUX/IAA, WRKY, HB, Zinc-finger families, while MADS box family genes were more expressed when apples were kept under 0.8 kPa oxygen. Out of the eight group VII ERF members present in apple genome, two genes showed a rapid up-regulation under hypoxia, and western blot analysis showed that apple MdRAP2.12 proteins were differentially accumulated in normoxic and hypoxic samples, with the highest level reached under 0.4 kPa oxygen. These data suggest that ripe apple tissues finely and specifically modulate sensing and regulatory mechanisms in response to different hypoxic stress conditions.

Keywords: Cortex; Ethylene-responsive factors; Low oxygen stress; *Malus domestica*; Metabolic profiling; Postharvest; Pyruvate metabolism; Storage

Frontiers in Plant Science

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The peach HECATE3-like gene *FLESHY* plays a double role during fruit development

Botton, A.[a], Rasori, A.[a], Ziliotto, F.[a], Moing, A.[bc], Maucourt, M.[cd], Bernillon, S.[bc], Deborde, C.[bc], Petterle, A.[a], Varotto, S.[a], Bonghi, C.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, viale dell'Università, 16, Agripolis, Legnaro, Italy
[b] UMR1332 Biologie du Fruit et Pathologie, INRA, 71 av Edouard Bourlaux, Villenave d'Ornon, France
[c] Plateforme Métabolome du Centre de Génomique Fonctionnelle Bordeaux, MetaboHUB, IBVM, Centre INRA Bordeaux, 71 av Edouard Bourlaux, Villenave d'Ornon, France
[d] UMR1332 Biologie du Fruit et Pathologie, University of Bordeaux, 71 av Edouard Bourlaux, Villenave d'Ornon, France

Abstract

Tight control of cell/tissue identity is essential for a correct and functional organ patterning, an important component of overall fruit development and eventual maturation and ripening. Despite many investigations regarding the molecular determinants of cell identity in fruits of different species, a useful model able to depict the regulatory networks governing this relevant part of fruit development is still missing. Here we described the peach fruit as a system to link the phenotype of a slow ripening (SR) selection to an altered transcriptional regulation of genes involved in determination of mesocarp cell identity providing insight toward molecular regulation of fruit tissue formation. Morpho-anatomical observations and metabolomics analyses performed during fruit development on the reference cultivar Fantasia, compared to SR, revealed that the mesocarp of SR maintained typical immaturity traits (e.g. small cell size, high amino acid contents and reduced sucrose) throughout development, along with a strong alteration of phenylpropanoid contents, resulting in accumulation of phenylalanine and lignin. These findings suggest that the SR mesocarp is phenotypically similar to a lignifying endocarp. To test this hypothesis, the expression of genes putatively involved in determination of drupe tissues identity was assessed. Among these, the peach HEC3-like gene *FLESHY* showed a strongly altered expression profile consistent with pit hardening and fruit ripening, generated at a post-transcriptional level. A double function for *FLESHY* in channelling the phenylpropanoid pathway to either lignin or flavour/aroma is suggested, along with its possible role in triggering auxin-ethylene cross talk at the start of ripening.

Keywords: Fruit patterning; Mesocarp identity; Metabolomics; MicroRNA; Phenylpropanoid pathway; Post-transcriptional regulation

Plant Molecular Biology

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Selenium biofortification in radish enhances nutritional quality via accumulation of methyl-selenocysteine and promotion of transcripts and metabolites related to glucosinolates, phenolics amino acids

Schiavon, M.[ab]*, Berto, C.*[c]*, Malagoli, M.*[a]*, Trentin, A.*[a]*, Sambo, P.*[a]*, Dall'Acqua, S.*[c]*, Pilon-Smits, E.A.H.*[b]

[a] Department of Agronomy, Food, Natural Resources, Animals and the Environment, University of Padova, Legnaro, Italy
[b] Biology Department, Colorado State University, Fort Collins, MS, United States
[c] Department of Pharmaceutical and Pharmacological Sciences, University of Padova, Padova, Italy

Abstract

Two selenium (Se) fertilization methods were tested for their effects on levels of anticarcinogenic selenocompounds in radish (*Raphanus sativus*), as well as other nutraceuticals. First, radish was grown on soil and foliar selenate applied 7 days before harvest at 0, 5, 10, and 20 mg Se per plant. Selenium levels were up to 1200 mg Se/kg DW in leaves and 120 mg Se/kg DW in roots. The thiols cysteine and glutathione were present at 2-3-fold higher levels in roots of Se treated plants, and total glucosinolate levels were 35% higher, due to increases in glucoraphanin. The only seleno-aminoacid detected in Se treated plants was Se-methyl-SeCys (100 mg/kg FW in leaves, 33 mg/kg FW in roots). The levels of phenolic aminoacids increased with selenate treatment, as did root total nitrogen and protein content, while the level of several polyphenols decreased. Second, radish was grown in hydroponics and supplied with 0, 5, 10, 20, or 40 μM selenate for 1 week. Selenate treatment led to a 20-30% increase in biomass. Selenium concentration was 242 mg Se/kg DW in leaves and 85 mg Se/kg DW in roots. Cysteine levels decreased with Se in leaves but increased in roots; glutatione levels decreased in both. Total glucosinolate levels in leaves decreased with Se treatment due to repression of genes involved in glucosinolates metabolism. Se-methyl-SeCys concentration ranged from 7-15 mg/kg FW. Aminoacid concentration increased with Se treatment in leaves but decreased in roots. Roots of Se treated plants contained elevated transcript levels of sulfate transporters (Sultr) and ATP sulfurylase, a key enzyme of S/Se assimilation. No effects on polyphenols were observed. In conclusion, Se biofortification of radish roots may be achieved via foliar spray or hydroponic supply. One to ten radishes could fulfill the daily human requirement (70 μg) after a single foliar spray of 5 mg selenate per plant or 1 week of 5-10 μM selenate supply in hydroponics. The radishes metabolized selenate to the anticarcinogenic compound Se-methyl-selenocysteine. Selenate treatment enhanced levels of other nutraceuticals in radish roots, including glucoraphanin. Therefore, Se biofortification can produce plants with superior health benefits.

Keywords: Fortification technologies; Glucosinolates; Nutritional quality enhancement; Radish (*Raphanus sativus* L.); Selenium

Frontiers in Plant Science

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PlantFuncSSR: Integrating first and next generation transcriptomics for mining of SSR-functional domains markers

Sablok, G.[a], Pérez-Pulido, A.J.[b], Do, T.[a], Seong, T.Y.[c], Casimiro-Soriguer, C.S.[b], La Porta, N.[def], Ralph, P.J.[a], Squartini, A.[g], Muñoz-Merida, A.[h], Harikrishna, J.A.[c]

[a] Plant Functional Biology and Climate Change Cluster (C3), University of Technology, Sydney, NSW, Australia
[b] Centro Andaluz de Biología del Desarrollo (CABD-CSIC), Universidad Pablo de Olavide, Sevilla, Spain
[c] Centre for Research in Biotechnology for Agriculture and Institute of Biological Sciences, Faculty of Science, University of Malaya, Kuala Lumpur, Malaysia
[d] Department of Sustainable Agro-Ecosystems and Bioresources, Research and Innovation Centre, Fondazione Edmund Mach, Trento, Italy
[e] Mount FOR Project Centre, European Forest Institute, Trento, Italy
[f] Consiglio Nazionale delle Ricerche, Istituto per la Valorizzazione del Legno e delle Specie Arboree, Florence, Italy
[g] Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Padova, Italy
[h] CIBIO Research Centre in Biodiversity and Genetic Resources, InBIO, Universidade do Porto, Vila do Conde, Portugal

Abstract

Analysis of repetitive DNA sequence content and divergence among the repetitive functional classes is a well-accepted approach for estimation of inter- and intrageneric differences in plant genomes. Among these elements, microsatellites, or Simple Sequence Repeats (SSRs), have been widely demonstrated as powerful genetic markers for species and varieties discrimination. We present PlantFuncSSRs platform having more than 364 plant species with more than 2 million functional SSRs. They are provided with detailed annotations for easy functional browsing of SSRs and with information on primer pairs and associated functional domains. PlantFuncSSRs can be leveraged to identify functional-based genic variability among the species of interest, which might be of particular interest in developing functional markers in plants. This comprehensive on-line portal unifies mining of SSRs from first and next generation sequencing datasets, corresponding primer pairs and associated in-depth functional annotation such as gene ontology annotation, gene interactions and its identification from reference protein databases. PlantFuncSSRs is freely accessible at: http://www. bioinfocabd.upo.es/plantssr.

Keywords: Functional domains markers; Gene ontology (GO); Inter-pro; NGS; Short tandem repeats (STRs)

Frontiers in Plant Science

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Drought stress in maize causes differential acclimation responses of glutathione and sulfur metabolism in leaves and roots

Ahmad, N.[ab]*, Malagoli, M.*[c]*, Wirtz, M.*[a]*, Hell, R.*[a]

[a] Heidelberg University, Centre for Organismal Studies Heidelberg, Im Neuenheimer Feld 360, Heidelberg, Germany
[b] University of Science and Technology Bannu, Bannu, Pakistan
[c] University of Padova, Department of Agronomy, Food, Natural Resources, Animals and Environment, Padova, Italy

Abstract

Background: Drought is the most important environmental stress that limits crop yield in a global warming world. Despite the compelling evidence of an important role of oxidized and reduced sulfur-containing compounds during the response of plants to drought stress (e.g. sulfate for stomata closure or glutathione for scavenging of reactive oxygen species), the assimilatory sulfate reduction pathway is almost not investigated at the molecular or at the whole plant level during drought. Results: In the present study, we elucidated the role of assimilatory sulfate reduction in roots and leaves of the staple crop maize after application of drought stress. The time-resolved dynamics of the adaption processes to the stress was analyzed in a physiological relevant situation -when prolonged drought caused significant oxidation stress but root growth should be maintained. The allocation of sulfate was significantly shifted to the roots upon drought and allowed for significant increase of thiols derived from sulfate assimilation in roots. This enabled roots to produce biomass, while leaf growth was stopped. Accumulation of harmful reactive oxygen species caused oxidation of the glutathione pool and decreased glutathione levels in leaves. Surprisingly, flux analysis using [35S]-sulfate demonstrated a significant down-regulation of sulfate assimilation and cysteine synthesis in leaves due to the substantial decrease of serine acetyltransferase activity. The insufficient cysteine supply caused depletion of glutathione pool in spite of significant transcriptional induction of glutathione synthesis limiting GSH1. Furthermore, drought impinges on transcription of membrane-localized sulfate transport systems in leaves and roots, which provides a potential molecular mechanism for the reallocation of sulfur upon prolonged water withdrawal. Conclusions: The study demonstrated a significant and organ-specific impact of drought upon sulfate assimilation. The sulfur metabolism related alterations at the transcriptional, metabolic and enzyme activity level are consistent with a promotion of root growth to search for water at the expense of leaf growth. The results provide evidence for the importance of antagonistic regulation of sulfur metabolism in leaves and roots to enable successful drought stress response at the whole plant level.

Keywords: Cysteine; Flux analysis; Glutathione synthesis; Reactive oxygen species; Sulfate assimilation; *Zea mays*

BMC Plant Biology

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Noisy beets: Impact of phenotyping errors on genomic predictions for binary traits in *Beta vulgaris*

Biscarini, F.[a], *Nazzicari, N.*[b], *Broccanello, C.*[c], *Stevanato, P.*[c], *Marini, S.*[d]

[a] PTP Science Park, Department of Bioinformatics and Biostatistics, Via Einstein - Loc. Cascina Codazza, Lodi, Italy
[b] Research Centre for Fodder Crops and Dairy Productions, Council for Agricultural Research and Economics (CREA), Lodi, Italy
[c] Università di Padova, DAFNE, Padua, Italy
[d] Kyoto University, Bioinformatics Center, Institute for Chemical Research, Kyoto, Japan

Abstract

Background: Noise (errors) in scientific data is endemic and may have a detrimental effect on statistical analyses and experimental results. The effects of noisy data have been assessed in genome-wide association studies for case-control experiments in human medicine. Little is known, however, on the impact of noisy data on genomic predictions, a widely used statistical application in plant and animal breeding. Results: In this study, the sensitivity to noise in the data of five classification methods (K-nearest neighbours-KNN, random forest-RF, ridge logistic regression-LR, and support vector machines with linear or radial basis function kernels) was investigated. A sugar beet population of 123 plants phenotyped for a binary trait and genotyped for 192 SNP (single nucleotide polymorphism) markers was used. Labels (0/1 phenotype) were randomly sampled to generate noise. From the base scenario without errors in the labels, increasing proportions of noisy labels-up to 50 %-were generated and introduced in the data. Conclusions: Local classification methods-KNN and RF-showed higher tolerance to noisy labels compared to methods that leverage global data properties-LR and the two SVM models. In particular, KNN outperformed all other classifiers with AUC (area under the ROC curve) higher than 0.95 up to 20 % noisy labels. The runner-up method, RF, had an AUC of 0.941 with 20 % noise.

Keywords: Binomial phenotype; Classification; Genomic predictions; K-nearest neighbours (KNN); Noisy data; Random forest (RF); Ridge logistic regression; Robustness to errors; Sugar beet; Support vector machines (SVM)

Plant Methods

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Leaf apoplastic proteome composition in UV-B treated *Arabidopsis thaliana* mutants impaired in extracellular glutathione degradation

Masi, A., Trentin, A.R., Arrigoni, G.

DAFNAE, University of Padova, Italy; Proteomic Center, University of Padova, Italy;
Department of Biomedical Sciences, University of Padova, Italy

Abstract

In plants, environmental perturbations often result in oxidative reactions in the apoplastic space, which are counteracted for by enzymatic and non-enzymatic antioxidative systems, including ascorbate and glutathione. However, the occurrence of the latter and its exact role in the extracellular space are not well documented. In Arabidopsis thaliana, the gamma-glutamyl transferase isoform GGT1 bound to the cell wall takes part in the so-called gamma-glutamyl cycle for extracellular glutathione degradation and recovery, and may be implicated in redox sensing and balance.In this work, oxidative conditions were imposed with UV-B radiation and studied in redox altered ggt1 mutants. Elevated UV-B has detrimental effects on plant metabolism, plasma membranes representing a major target for ROS generated by this harmful radiation. The response of ggt1 knockout Arabidopsis leaves to UV-B radiation was assessed by investigating changes in apoplastic protein composition. We then compared the expression changes resulting from the mutation and from the UV-B treatment. Rearrangements occurring in apoplastic protein composition suggest the involvement of hydrogen peroxide, which may ultimately act as a signal. Other important changes related to hormonal effects, cell wall remodeling, and redox activities are also reported. We argue that oxidative stress conditions imposed by UV-B and by disruption of the gamma-glutamyl cycle result in similar stress-induced responses, to some degree at least. Data shown here are associated with the article from Trentin et al. (2015) [1]; protein data have been deposited to the PRIDE database (Vizcaíno et al., 2014) [2] with identifier PXD001807.

Keywords: Apoplast; Environmental stress; Gamma-glutamyl transferase; Glutathione; Oxidative stress; ROS

Data in Brief

Volume 6, Pages 368-377

Plant biostimulants: Physiological responses induced by protein hydrolyzed-based products and humic substances in plant metabolism

Nardi, S., Pizzeghello, D., Schiavon, M., Ertani, A.

University of Padova, Dept. of Agronomy, Food, Natural Resources, Animal and
Environment, Viale dell'Università,16, Legnaro, PD, Italy

Abstract

In recent years, the use of biostimulants in sustainable agriculture has been growing. Biostimulants can be obtained from different organic materials and include humic substances (HS), complex organic materials, beneficial chemical elements, peptides and amino acids, inorganic salts, seaweed extracts, chitin and chitosan derivatives, antitranspirants, amino acids and other N-containing substances. The application of biostimulants to plants leads to higher content of nutrients in their tissue and positive metabolic changes. For these reasons, the development of new biostimulants has become a focus of scientific interest. Among their different functions, biostimulants influence plant growth and nitrogen metabolism, especially because of their content in hormones and other signalling molecules. A significant increase in root hair length and density is often observed in plants treated with biostimulants, suggesting that these substances induce a "nutrient acquisition response" that favors nutrient uptake in plants via an increase in the absorptive surface area. Furthermore, biostimulants positively influence the activity and gene expression of enzymes functioning in the primary and secondary plant metabolism. This article reviews the current literature on two main classes of biostimulants: humic substances and protein-based biostimulants. The characteristic of these biostimulants and their effects on plants are thoroughly described.

Keywords: Carbon metabolism; Hormones; Nitrogen metabolism; Phenylpropanoid pathway; Stress

Scientia Agricola

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Mixed nodule infection in *Sinorhizobium meliloti-Medicago sativa* symbiosis suggest the presence of cheating behavior

Checcucci, A.[a], Azzarello, E.[b], Bazzicalupo, M.[a], Galardini, M.[c], Lagomarsino, A.[d], Mancuso, S.[b], Marti, L.[b], Marzano, M.C.[b], Mocali, S.[d], Squartini, A.[e], Zanardo, M.[e], Mengoni, A.[a]

[a] Department of Biology, University of Florence, Florence, Italy
[b] Department of Agri-Food Production and Environmental Science, University of Florence, Florence, Italy
[c] European Molecular Biology Laboratory - European Bioinformatics Institute, Wellcome Trust Genome Campus, Cambridge, United Kingdom
[d] Consiglio per la Ricerca in Agricoltura e l'Analisi dell'Economia Agraria, Centro di Ricerca per l'Agrobiologia e la Pedologia, Florence, Italy
[e] Department of Agronomy, Food, Natural Resources, Animals and the Environment, University of Padua, Padova, Italy

Abstract

In the symbiosis between rhizobia and legumes, host plants can forms ymbiotic root nodules with multiple rhizobial strains, potentially showing different symbiotic performances in nitrogen fixation. Here, we investigated the presence of mixed nodules, containing rhizobia with different degrees of mutualisms, and evaluate their relative fitness in the *Sinorhizobium meliloti-Medicago sativa* model symbiosis. We used three *S. meliloti* strains, the mutualist strains Rm1021 and BL225C and the non-mutualist AK83. We performed competition experiments involving both in vitro and in vivo symbiotic assays with *M. sativa* host plants. We show the occurrence of a high number (from 27 to 100%) of mixed nodules with no negative effect on both nitrogen fixation and plant growth. The estimation of the relative fitness as non-mutualist/mutualist ratios in single nodules shows that in some nodules the non-mutualist strain efficiently colonized root nodules along with the mutualist ones. In conclusion, we can support the hypothesis that in *S. meliloti-M. sativa* symbiosis mixed nodules are formed and allow non-mutualist or less-mutualist bacterial partners to be less or not sanctioned by the host plant, hence allowing a potential form of cheating behavior to be present in the nitrogen fixing symbiosis.

Keywords: Cheating; Competition; *Medicago sativa*; Mixed nodules; *Sinorhizobium meliloti*; Symbiotic nitrogen fixation

Frontiers in Plant Science

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Proteomic changes induced by potassium deficiency and potassium substitution by sodium in sugar beet

Pi, Z.[ad], Stevanato, P.[b], Sun, F.[a], Yang, Y.[a], Sun, X.[a], Zhao, H.[a], Geng, G.[ac], Yu, L.[ac]

[a] Key Laboratory of Sugar Beet Genetic Breeding of Heilongjiang Province, Heilongjiang University, Room 410 Nongxue Building, Xuefu Road NO. 74, Nangang District, Harbin, Heilongjiang Province, China
[b] DAFNAE, Dipartimento di Agronomia, Animali, Alimenti, Risorse Naturali e Ambiente, Università degli Studi di Padova, Viale dell'Università 16, Legnaro, Padova, Italy
[c] Chinese Academy of Agricultural Science, Institute of Sugar Beet, Harbin, China
[d] Key Laboratory of Plant Resources and Beijing Botanical Garden, Institute of Botany, Chinese Academy of Sciences, Beijing, China

Abstract

In this study, sugar beets (*Beta vulgaris* L.) were grown at different K^+/Na^+ concentrations: mmol/L, 3/0 (control); 0.03/2.97 (K–Na replacement group; Trep); 0.03/0 (K deficiency group; Tdef) in order to investigate the effects of K^+ deficiency and replacement of K^+ by Na^+ on plant proteomics, and to explore the physiological processes influenced by Na^+ to compensate for a lack of K^+. After 22 days, fresh and dry weight as well as the $Na^+$and K^+ concentration were measured and changes in proteomics were tested by 2D gel electrophoresis. Interestingly, Na^+showed stimulation in growth of seedlings and hindrance of K^+ assimilation in Trep. Significant changes were also observed in 27 protein spots among the treatments. These are proteins involved in photosynthesis, cellular respiration, protein folding and degradation, stress and defense, other metabolisms, transcription related, and protein synthesis. A wide range of physiological processes, including light reaction, CO_2 assimilation, glycolysis, and tricaboxylic acid cycle, was impaired owing to K^+ starvation. Compensating for the effect of K^+ starvation, an increase in photosynthesis was also observed in Trep. However, we also found a limitation of cellular respiration by Na^+. Na^+ is therefore in some ways able to recover damage due to K deficiency at protein level, but cannot functionally replace K as an essential nutrient.

Keywords: K deficiency; K–Na replacement; Sugar beet; Two-dimensional electrophoresis

Journal of Plant Research

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Nitric oxide-mediated maize root apex responses to nitrate are regulated by auxin and strigolactones

Manoli, A.[a], Trevisan, S.[a], Voigt, B.[b], Yokawa, K.[bc], Baluška, F.[b], Quaggiotti, S.[a]

[a] Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padua, Padua, Italy
[b] Department of Plant Cell Biology, Institute of Cellular and Molecular Botany, University of Bonn, Bonn, Germany
[c] Department of Biological Sciences, Tokyo Metropolitan University, Tokyo, Japan

Abstract

Nitrate (NO_3^-) is a key element for crop production but its levels in agricultural soils are limited. Plants have developed mechanisms to cope with these NO_3^- fluctuations based on sensing nitrate at the root apex. Particularly, the transition zone (TZ) of root apex has been suggested as a signaling-response zone. This study dissects cellular and molecular mechanisms underlying NO_3^- resupply effects on primary root (PR) growth in maize, confirming nitric oxide (NO) as a putative modulator. Nitrate restoration induced PR elongation within the first 2 h, corresponding to a stimulation of cell elongation at the basal border of the TZ. Xyloglucans (XGs) immunolocalization together with Brefeldin A applications demonstrated that nitrate resupply induces XG accumulation. This effect was blocked by cPTIO (NO scavenger). Transcriptional analysis of ZmXET1 confirmed the stimulatory effect of nitrate on XGs accumulation in cells of the TZ. Immunolocalization analyses revealed a positive effect of nitrate resupply on auxin and PIN1 accumulation, but a transcriptional regulation of auxin biosynthesis/transport/signaling genes was excluded. Short-term nitrate treatment repressed the transcription of genes involved in strigolactones (SLs) biosynthesis and transport, mainly in the TZ. Enhancement of carotenoid cleavage dioxygenases (CCDs) transcription in presence of cPTIO indicated endogenous NO as a negative modulator of CCDs activity. Finally, treatment with the SLs-biosynthesis inhibitor (TIS108) restored the root growth in the nitrate-starved seedlings. Present report suggests that the NO-mediated root apex responses to nitrate are accomplished in cells of the TZ via integrative actions of auxin, NO and SLs.

Keywords: Auxin; Nitrate; Nitric oxide; Root; Strigolactones; Transition zone

Frontiers in Plant Science

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Digital PCR as New Approach to SNP Genotyping in Sugar Beet

Stevanato, P.[a], *Biscarini, F.*[b]

[a] DAFNAE, Dipartimento di Agronomia Animali Alimenti Risorse Naturali e Ambiente, Università degli Studi di Padova, viale dell'Università 16, Legnaro, PD, Italy
[b] FPTP, Fondazione Parco Tecnologico Padano, viale Einstein, Loc. Cascina Codazza, Lodi, Italy

Abstract

Real-time PCR (qPCR) allelic discrimination and high-resolution melting (HRM) methods are widely adopted for the detection of single nucleotide polymorphisms (SNP). Digital PCR (dPCR) is a new method recently proposed for the detection of low-frequency and/or rare SNP. The molecular marker SNP_BvBTC1 is used in sugar beet to distinguish between annual and biennial flowering plants. The CC genotype at this SNP locus is associated with biennial beets, while the CA and AA genotypes are typically found in annual beets. In this study, we compared the sensitivity of qPCR, HRM and dPCR in detecting the allele A from two pools of bulk beet DNA composed of 90 biennial + 10 annual plants (B1) and 99 biennial + 1 annual plant (B2), respectively. All annual plants were found to have the AA genotype. qPCR could not detect allele A in either the B1 or B2 pool and HRM detected allele A only at moderate frequencies (10 %), in the B1 pool. dPCR, on the contrary, was able to detect allele A in both pools. We therefore concluded that dPCR is a suitable method for the quantitation of SNP_BvBTC1 within bulked DNA samples of sugar beet.

Keywords: Digital PCR; DNA bulk samples; SNP genotyping; Sugar beet

Sugar Tech

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Proteomic analysis of a compatible interaction between sugarcane and *Sporisorium scitamineum*

Barnabas, L.[a], *Ashwin, N.M.R.*[a], *Kaverinathan, K.*[a], *Trentin, A.R.*[b], *Pivato, M.*[b], *Sundar, A.R.*[a], *Malathi, P.*[a], *Viswanathan, R.*[a], *Rosana, O.B.*[c], *Neethukrishna, K.*[c], *Carletti, P.*[b], *Arrigoni, G.*[de], *Masi, A.*[b], *Agrawal, G.K.*[fg], *Rakwal, R.*[fgh]

[a] Division of Crop Protection, ICAR-Sugarcane Breeding Institute, Indian Council of Agricultural Research, Coimbatore, India
[b] Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Padova, Italy
[c] Bioinformatics Center, ICAR-Indian Institute of Spices Research, Kozhikode, India
[d] Proteomics Center of Padova University, Padova, Italy
[e] Department of Biomedical Sciences, University of Padova, Padova, Italy
[f] Research Laboratory for Biotechnology and Biochemistry (RLABB), Kathmandu, Nepal
[g] GRADE (Global Research Arch for Developing Education) Academy Private Limited, Birgunj, Nepal
[h] Tsukuba International Academy for Sport Studies (TIAS), Faculty of Health and Sport Sciences, University of Tsukuba, Ibaraki, Japan

Abstract

Smut caused by *Sporisorium scitamineum* is one of the important diseases of sugarcane with global significance. Despite the intriguing nature of sugarcane, *S. scitamineum* interaction, several pertinent aspects remain unexplored. This study investigates the proteome level alterations occurring in the meristem of a *S. scitamineum* infected susceptible sugarcane cultivar at whip emergence stage. Differentially abundant proteins were identified by 2DE coupled with MALDI-TOF/TOF-MS. Comprehensively, 53 sugarcane proteins identified were related to defence, stress, metabolism, protein folding, energy, and cell division; in addition, a putative effector of *S. scitamineum*, chorismate mutase, was identified. Transcript expression vis-à-vis the activity of phenylalanine ammonia lyase was relatively higher in the infected meristem. Abundance of seven candidate proteins in 2D gel profiles was in correlation with its corresponding transcript expression levels as validated by qRT-PCR. Furthermore, this study has opened up new perspectives on the interaction between sugarcane and *S. scitamineum*.

Keywords: Compatible interaction; Plant proteomics; Smut; *Sporisorium scitamineum*; Sugarcane

Proteomics

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Biological activity of vegetal extracts containing phenols on plant metabolism

Ertani, A.[a], *Pizzeghello, D.*[a], *Francioso, O.*[b], *Tinti, A.*[c], *Nardi, S.*[a]

[a] Dipartimento di Agronomia, Animali, Alimenti, Risorse Naturali e Ambiente (DAFNAE), Università di Padova, Viale dell'Università 16, Legnaro (Padova), Italy
[b] Dipartimento di Scienze Agrarie, Università di Bologna, Viale Fanin 44, Bologna, Italy
[c] Dipartimento di Scienze Biomediche e Neuromotorie, Università di Bologna, Via Belmeloro 8/2, Bologna, Italy

Abstract

The influence of vegetal extracts derived from red grape, blueberry fruits and hawthorn leaves on *Zea mays* L. plant growth and the activity of phenylalanine ammonia-lyase (PAL), a key enzyme of the phenylpropanoid pathway, was investigated in laboratory experiments. The extracts were characterized using FT-IR and Raman spectroscopies in order to obtain a pattern of the main functional groups. In addition, phenols content was determined by HPLC, whereas the content of indoleacetic acid and isopentenyladenosine hormones was determined by ELISA test and the auxin and gibberellin-like activities by plant-bioassays. The treated maize revealed increased root and leaf biomass, chlorophyll and sugars content with respect to untreated plants. Hawthorn, red grape skin and blueberry at 1.0 mL/L induced high p-coumaric content values, whilst hawthorn also showed high amounts of gallic and p-hydroxybenzoic acids. PAL activity induced by hawthorn at 1.0 mL/L had the highest values (11.1-fold UNT) and was strongly and linearly related with the sum of leaf phenols. Our results suggest that these vegetal extracts contain more than one group of plant-promoting substances.

Keywords: Biostimulant; Hormone; Maize; Phenolic acid; Phenylpropanoid; Vegetal extract

Molecules

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IBAF - CNR

On-farm evaluation of inundative biological control of *Ostrinia nubilalis* (Lepidoptera: Crambidae) by *Trichogramma brassicae* (Hymenoptera: Trichogrammatidae) in three European maize-producing regions

Razinger, J.[a], Vasileiadis, V.P.[b], Giraud, M.[c], van Dijk, W.[d], Modic, S.[a], Sattin, M.[b], Urek, G.[a]

[a] Agricultural Institute of Slovenia, Ljubljana, Slovenia
[b] National Research Council (CNR), Institute of Agro-Environmental and Forest Biology, Legnaro, Padua, Italy
[c] InVivo AgroSolutions, Valbonne, France
[d] Applied Plant Research, Wageningen University, Lelystad, Netherlands

Abstract

Background: A 2 year study was conducted to evaluate the efficacy of biological control with optimally timed *Trichogramma brassicae* releases as an integrated pest management tool against the European corn borer (ECB), *Ostrinia nubilalis* (Hübner), in on-farm experiments (i.e. real field conditions) in three European regions with dissimilar geoclimatic conditions and ECB pressure and conventional management (i.e. insecticide treated and untreated).

Results: Biological control with Trichogramma (1) provided ECB protection comparable with conventional management, (2) in all cases maintained mycotoxin levels below the EU threshold for maize raw materials destined for food products, (3) was economically sustainable in southern France and northern Italy, but not in Slovenia where it resulted in a significant decrease in gross margin, mainly owing to the cost of Trichogramma product, and (4) enabled avoidance of detrimental environmental effects of lambda-cyhalothrin use in northern Italy.

Conclusions: Optimally timed mass release of *T. brassicae* could be considered a sustainable tool for IPM programmes against ECB in southern France and northern Italy. Better involvement of regional advisory services is needed for the successful dissemination and implementation of biological control. Subsidy schemes could also motivate farmers to adopt this IPM tool and compensate for high costs of Trichogramma product.

Keywords: Biological control; Economic sustainability; European corn borer; Integrated pest management; Mycotoxins; Pesticide risk reduction

Pest Management Science

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Farm-scale evaluation of herbicide band application integrated with inter-row mechanical weeding for maize production in four European regions

Vasileiadis, V.P.[a], van Dijk, W.[b], Verschwele, A.[c], Holb, I.J.[de], Vámos, A.[d], Urek, G.[f], Leskovšek, R.[f], Furlan, L.[g], Sattin, M.[a]

[a] National Research Council (CNR), Institute of Agro-Environmental and Forest Biology, Legnaro, PD, Italy
[b] Applied Plant Research, Wageningen University, Lelystad, Netherlands
[c] Julius Kühn-Institut, Federal Research Centre for Cultivated Plants, Braunschweig, Germany
[d] Faculty of Agricultural and Food Sciences and Environmental Management, University of Debrecen, Debrecen, Hungary
[e] Plant Protection Institute, Centre for Agricultural Research, Hungarian Academy of Sciences, Budapest, Hungary
[f] Agricultural Institute of Slovenia, Ljubljana, Slovenia
[g] Veneto Agricoltura, Legnaro, PD, Italy

Abstract

To promote integrated weed management (IWM) implementation in Europe, robust evidence on the sustainability of such tools and strategies is needed to motivate their adoption by stakeholders. This can only be achieved through assessing and validating them at real farm scale and using existing farm equipment, under diverse climatic and soil conditions representative of European agriculture. In 2013 and 2014, 12 on-farm experiments (i.e. real field conditions on commercial farms, with natural weed flora) were conducted in four important European grain maize-producing regions comparing the efficacy of herbicide band application integrated with inter-row mechanical weeding as a potential IWM tool with the conventional broadcast herbicide application (CON) used by the farms. The IWM tools tested were as follows: (i) early post-emergence herbicide band application combined with hoeing, followed by a second hoeing in southern Germany, (ii) early post-emergence herbicide band application followed by hoeing in eastern Hungary and central Slovenia and (iii) pre-emergence herbicide band application followed by hoeing in northern Italy. Herbicide band application integrated with hoeing provided good and partial weed control along and between maize rows respectively. No significant yield differences were detected between IWM and CON. IWM greatly reduced herbicide input and was economically sustainable over the duration of this study with no significant difference in gross margin compared with CON in all cases. This IWM tool could therefore be considered for implementation in European maize systems.

Keywords: Economic sustainability; Integrated weed management; IWM; Mechanical weeding; Pesticide risk reduction; *Zea mays*

Weed Research

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A “Stressed” alfalfa-based cropping system leads to the selection of quizalofop-Resistant Italian ryegrass (*Lolium perenne* ssp. multiflorum)

Collavo, A.[ac], *Panozzo, S.*[a], *Allegri, A.*[b], *Sattin, M.*[a]

[a] Institute of Agro-environmental and Forest Biology (IBAF)-CNR, Viale dell’Università 16, Legnaro (PD), Italy
[b] Consorzio Agrario Ravenna, via Madonna di Genova 39, Cotignola (RA), Italy
[c] Bayer CropScience AG, Industriepark Hoechst, H872, Frankfurt am Main, Germany

Abstract

Italian ryegrass populations investigated in this study were harvested in an alfalfa-based cropping system. In that system, the agronomic practices and chemical weed management, based on the use of aryloxyphenoxy-propionates herbicides (i.e., quizalofop ethyl ester), were optimized to obtain a dual seed-forage production. Five of seven populations tested were confirmed resistant to quizalofop ethyl ester with resistance indexes ranging from 4.5 to >209. Both target- and nontarget-site resistance mechanisms were most likely involved. Three allelic variants were detected (Ile-1781-Leu, Trp-2027-Cys, and Ile-2041-Asn) in four resistant populations, whereas no known mutations were found in one resistant population. The herbicide treatment on Italian ryegrass plants at different phenological stages suggested that to control regrowth, it is necessary to use two to five times the herbicide dose suitable for younger plants. This situation is encountered in fields when Italian ryegrass plants need to be controlled to maximize the alfalfa seed production, and it is comparable to using a sublethal herbicide dose, leading to the selection of herbicide-resistant biotypes. In such a situation, the cropping system is not sustainable, and integrated weed management should be implemented to deplete the soil weed seed bank and prevent new weed seed production.

Keywords: ACCase inhibitors; Cross-resistance; Herbicide efficacy; Herbicide resistance; Phenological stage; Target-site resistance mechanism

Weed Science

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Networking of integrated pest management: A powerful approach to address common challenges in agriculture

Lamichhane, J.R.[a], Aubertot, J.N.[b], Begg, G.[c], Birch, A.N.E.[c], Boonekamp, P.[d], Dachbrodt-Saaydeh, S.[e], Hansen, J.G.[f], Hovmøller, M.S.[g], Jensen, J.E.[h], Jørgensen, L.N.[g], Kiss, J.[i], Kudsk, P.[g], Moonen, A.C.[j], Rasplus, J.Y.[k], Sattin, M.[l], Streito, J.C.[m], Messéan, A.[a]

[a] INRA, UAR1240 ECO-INNOV, Avenue Lucien Brétignières, Thiverval Grignon, France
[b] INRA, UMR1248 AGIR, Castanet-Tolosan, France
[c] The James Hutton Institute, Invergowrie, Dundee, Scotland, United Kingdom
[d] Plant Research International, Wageningen University, Postbus 69, Wageningen, Netherlands
[e] Julius Kühn-Institut, Federal Research Centre for Cultivated Plants, Stahnsdorfer Damm 81, Kleinmachnow, Germany
[f] Department of Agroecology, Aarhus University, Foulum, Tjele, Denmark
[g] Department of Agroecology, Aarhus University, Flakkebjerg, Slagelse, Denmark
[h] SEGES, 15 Agro Food Park, Skejby, Aarhus N, Denmark
[i] Plant Protection Institute, Szent Istvan University, Pater K. Street 1, Gödöllö, Hungary
[j] Scuola Superiore Sant'Anna, Institute of Life Sciences, Land Lab, Via Santa Cecilia 3, Pisa, Italy
[k] INRA, UMR1062 CBGP, Montferrier-sur-Lez, France
[l] National Research Council, Institute of Agro-Environmental and Forest Biology, Agripolis, Padova, Legnaro, Italy
[m] INRA, CBGP, 755 avenue du Campus d'Agropolis, CS30016, Montferrier-Sur-Lez, France

Abstract

Integrated pest management (IPM) is facing both external and internal challenges. External challenges include increasing needs to manage pests (pathogens, animal pests and weeds) due to climate change, evolution of pesticide resistance as well as virulence matching host resistance. The complexity of designing effective pest management strategies, which rely less heavily on the use of conventional pesticides, is another external challenge. Internal challenges include organizational aspects such as decreasing trend in budget allocated to IPM research, increasing scarcity of human expertise, lack of knowledge transfer into practice and the communication gap both at country level and between countries, and lack of multi-, inter- and transdisciplinary IPM research. There is an increasing awareness that trans-national networking is one means to overcome such challenges and to address common priorities in agriculture. A large number of stakeholders (researchers, policy makers, growers and industries) are involved in the sector of crop protection, which needs to be coordinated through effective communications and dynamic collaboration to make any IPM strategy successful. Here we discuss a decade-long IPM networking experiences in Europe emphasizing how IPM research, implementation and adoption in Europe may benefit from a broader level networking.

Keywords: Common challengers; European networking; Knowledge transfer; Long-term experiments; Research priorities

Crop Protection

Volume 89, Pages 139-151

Transdisciplinary weed research: new leverage on challenging weed problems?

Jordan, N.[a], Schut, M.[bc], Graham, S.[d], Barney, J.N.[e], Childs, D.Z.[f], Christensen, S.[g], Cousens, R.D.[h], Davis, A.S.[i], Eizenberg, H.[j], Ervin, D.E.[k], Fernandez-Quintanilla, C.[l], Harrison, L.J.[m], Harsch, M.A.[n], Heijting, S.[o], Liebman, M.[p], Loddo, D.[q], Mirsky, S.B.[r], Riemens, M.[s], Neve, P.[t], Peltzer, D.A.[u], Renton, M.[v], Williams, M.[w], Recasens, J.[x], Sønderskov, M.[y]

[a] Agronomy and Plant Genetics Department, University of Minnesota, St. Paul, MN, United States
[b] Knowledge Technology and Innovation, Wageningen University, Wageningen, Netherlands
[c] International Institute of Tropical Agriculture (IITA), Kigali, Rwanda
[d] School of Social Sciences, The University of New South Wales, Sydney, NSW, Australia
[e] Department of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA, United States
[f] Department of Animal and Plant Sciences, University of Sheffield, Sheffield, United Kingdom
[g] Department of Plant and Environmental Sciences, University of Copenhagen, Frederiksberg C, Denmark
[h] School of BioSciences, The University of Melbourne, Melbourne, VIC, Australia
[i] Global Change and Photosynthesis Research Unit, USDA ARS, Urbana, IL, United States
[j] Department of Plant Pathology and Weed Research, Agricultural Research Organization (ARO), Newe Ya'ar Research Center, Ramat Yishay, Israel
[k] Institute for Sustainable Solutions, Portland State University, Portland, OR, United States
[l] CSIC-Institute of Agricultural Science, Madrid, Spain
[m] Environment Department, University of York, York, United Kingdom
[n] Department of Biology, University of Washington, Seattle, WA, United States
[o] Agrosystems Research, Wageningen University and Research Centre, Wageningen, Netherlands
[p] Department of Agronomy, Iowa State University, Ames, IA, United States
[q] Institute of Agro-environmental and Forest Biology, National Research Council, Legnaro, Italy
[r] Sustainable Agricultural Systems Laboratory, USDA-ARS, Beltsville, MD, United States
[s] Wageningen University and Research Centre – Applied Plant Research, Lelystad, Netherlands
[t] Agroecology, Rothamsted Research, Harpenden, Hertfordshire, United Kingdom
[u] Landcare Research – Ecosystems and Global Change, Lincoln, New Zealand
[v] School of Plant Biology, University of Western Australia, Crawley, WA, Australia
[w] Michael Williams & Associates Pty Ltd, Sydney, NSW, Australia
[x] Department of Horticulture, Botany and Landscaping, ETSEA, Universitat de Lleida – Agrotecnio, Lleida, Spain
[y] Agroecology, Aarhus University, Slagelse, Denmark

Abstract

Transdisciplinary weed research (TWR) is a promising path to more effective management of challenging weed problems. We define TWR as an integrated process of inquiry and action that addresses complex weed problems in the context of broader efforts to improve economic, environmental and social aspects of ecosystem sustainability. TWR seeks to integrate scholarly and practical knowledge across many stakeholder groups (e.g. scientists, private sector, farmers and extension officers) and levels (e.g. local, regional and landscape). Furthermore, TWR features democratic and iterative processes of decision-making and collective action that aims to align the interests, viewpoints and agendas of a wide range of stakeholders. The fundamental rationale for TWR is that many challenging weed problems (e.g. herbicide resistance or extensive plant invasions in natural areas) are better addressed systemically, as a part of broad-based efforts to advance ecosystem sustainability, rather than as isolated problems. Addressing challenging weed problems systemically can offer important new leverage on such problems, by creating new opportunities to manage their root causes and by improving complementarity between weed management and other activities. While promising, this approach is complicated by the multidimensional, multilevel, diversely defined and unpredictable nature of ecosystem sustainability. In practice, TWR can be undertaken as a cyclic process of (i) initial problem formulation, (ii) 'broadening' of the problem formulation and recruitment of stakeholder participants, (iii) deliberation, negotiation and design of an action agenda for systemic change, (iv) implementation action, (v) monitoring and assessment of outcomes and (vi) reformulation of the problem situation and renegotiation of further actions. Notably, 'purposive' disciplines (design, humanities and arts) have central, critical and recurrent roles in this process, as do integrative analyses of relevant multidimensional and multilevel factors, via multiple natural and social science disciplines. We exemplify this process in prospect and retrospect. Importantly TWR is not a replacement for current weed research; rather, the intent is to powerfully leverage current efforts.

Keywords: Agroecosystem processes; Crop protection; Ecosystem services; Interdisciplinary research; Multistakeholder processes; Systems research

Weed Research

Volume 56, Issue 5, Pages 345-358

Contribution of the seed microbiome to weed management

Müller-Stöver, D.[a], Nybroe O.[a], Baraibar, B.[bc], Loddo, D.[d], Eizenberg, H.[e], French, K.[f], Sønderskov, M.[g], Neve, P.[h], Peltzer, D.A.[i], Maczey, N.[j], Christensen, S.[a]

[a] Department of Plant & Environmental Sciences, University of Copenhagen, Frederiksberg, Denmark
[b] Plant Sciences Department, Pennsylvania State University, Pennsylvania, United States
[c] Department of Horticulture, Botany and Landscaping, University of Lleida, Lleida, Spain
[d] Institute of Agro-environmental and Forest Biology, National Research Council, Legnaro, Italy
[e] Department of Plant Pathology and Weed Research, Agricultural Research Organization (ARO), Newe Ya'ar Research Center, Ramat Yishay, Israel
[f] School of Biological Sciences, University of Wollongong, Wollongong, NSW, Australia
[g] Department of Agroecology, Aarhus University, Slagelse, Denmark
[h] Agroecology Department, Rothamsted Research, Harpenden, Hertfordshire, United Kingdom
[i] Landcare Research, Lincoln, New Zealand
[j] CABI, Egham, Surrey, United Kingdom

Abstract

Seed-attacking microorganisms have an undefined potential for management of the weed seedbank, either directly through inundative inoculation of soils with effective pathogenic strains, or indirectly by managing soils in a manner that promotes native seed-decaying microorganisms. However, research in this area is still limited and not consistently successful because of technological limitations in identifying the pathogens involved and their efficacy. We suggest that these limitations can now be overcome through application of new molecular techniques to identify the microorganisms interacting with weed seeds and to decipher their functionality. However, an interdisciplinary weed management approach that includes weed scientists, microbiologists, soil ecologists and molecular biologists is required to provide new insights into physical and chemical interactions between different seed species and microorganisms. Such insight is a prerequisite to identify the best candidate organisms to consider for seedbank management and to find ways to increase weed seed suppressive soil communities.

Keywords: Biological control; Microbiome; Plant-soil feedbacks; Seedbank; Soil microbial pathogens; Weed control

Weed Research

Volume 56, Issue 5, Pages 335-339

Emergence dynamics of barnyardgrass and jimsonweed from two depths when switching from conventional to reduced and no-till conditions

Vasileiadis, V.P.[a], *Froud-Williams, R.J.*[b], *Loddo, D.*[a], *Eleftherohorinos, I.G.*[c]

[a] National Research Council (CNR), Institute of Agro-Environmental and Forest Biology, Legnaro, PD, Italy
[b] University of Reading, School of Biological Sciences, Reading, United Kingdom
[c] Aristotle University of Thessaloniki, School of Agriculture, Thessaloniki, Greece

Abstract

A cylinder experiment was conducted in northern Greece during 2005 and 2006 to assess emergence dynamics of barnyardgrass (*Echinochloa crus-galli* (L.) Beauv.) and jimsonweed (*Datura stramonium* L.) in the case of a switch from conventional to conservation tillage systems (CT). Emergence was surveyed from two burial depths (5 and 10 cm) and with simulation of reduced tillage (i.e. by soil disturbance) and no-till conditions. Barnyardgrass emergence was significantly affected by burial depth, having greater emergence from 5 cm depth (96%) although even 78% of seedlings emerged from 10 cm depth after the two years of study. Emergence of barnyardgrass was stable across years from the different depths and tillage regimes. Jimsonweed seeds showed lower germination than barnyardgrass during the study period, whereas its emergence was significantly affected by soil disturbance having 41% compared to 28% without disturbance. A burial depth x soil disturbance interaction was also determined, which showed higher emergence from 10 cm depth with soil disturbance. Jimsonweed was found to have significantly higher emergence from 10 cm depth with soil disturbance in Year 2. Seasonal emergence timing of barnyardgrass did not vary between the different burial depth and soil disturbance regimes, as it started in April and lasted until end of May in both years. Jimsonweed showed a bimodal pattern, with first emergence starting end of April until mid-May and the second ranging from mid-June to mid-August from 10 cm burial depth and from mid-July to mid-August from 5 cm depth, irrespective of soil disturbance in both cases.

Keywords: Burial depth; Conservation tillage; Emergence timing; Soil disturbance; Soil seedbank

Spanish Journal of Agricultural Research

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Ecologically sustainable weed management: How do we get from proof-of-concept to adoption?

Liebman, M.[a], Baraibar, B.[b], Buckley, Y.[c], Childs, D.[d], Christensen, S.[e], Cousens, R.[f], Eizenberg, H.[g], Heijting, S.[h], Loddo, D.[i], Merotto, A.Jr.[j], Renton, M.[k], Riemens, M.[h]

[a] Department of Agronomy, Iowa State University, Ames, IA, United States
[b] Department of Horticulture, Botany and Landscaping, University of Lleida, Lleida, Spain
[c] School of Natural Sciences, Zoology, Trinity College Dublin, University of Dublin, Dublin 2, Ireland
[d] Department of Animal and Plant Sciences, University of Sheffield, Sheffield, United Kingdom
[e] Department of Plant and Environmental Sciences, University of Copenhagen, Copenhagen, Denmark
[f] School of Biosciences, University of Melbourne, Melbourne, Victoria, VIC, Australia
[g] Department of Plant Pathology and Weed Research, Newe Ya'ar Research Center, Agricultural Research Organization, Ramat Yishay, Israel
[h] Agrosystems Research, Wageningen UR, Wageningen, PB, Netherlands
[i] Institute of Agro-Environmental and Forest Biology, National Research Council, Legnaro, Italy
[j] Graduate Group in Plant Science, School of Agriculture, Federal University of Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil
[k] School of Plant Biology, Australian Herbicide Resistance Initiative and Institute of Agriculture, University of Western Australia, Crawley, WA, Australia

Abstract

Weed management is a critically important activity on both agricultural and non-agricultural lands, but it is faced with a daunting set of challenges: environmental damage caused by control practices, weed resistance to herbicides, accelerated rates of weed dispersal through global trade, and greater weed impacts due to changes in climate and land use. Broad-scale use of new approaches is needed if weed management is to be successful in the coming era. We examine three approaches likely to prove useful for addressing current and future challenges from weeds: diversifying weed management strategies with multiple complementary tactics, developing crop genotypes for enhanced weed suppression, and tailoring management strategies to better accommodate variability in weed spatial distributions. In all three cases, proof-of-concept has long been demonstrated and considerable scientific innovations have been made, but uptake by farmers and land managers has been extremely limited. Impediments to employing these and other ecologically based approaches include inadequate or inappropriate government policy instruments, a lack of market mechanisms, and a paucity of social infrastructure with which to influence learning, decision-making, and actions by farmers and land managers. We offer examples of how these impediments are being addressed in different parts of the world, but note that there is no clear formula for determining which sets of policies, market mechanisms, and educational activities will be effective in various locations. Implementing new approaches for weed management will require multidisciplinary teams comprised of scientists, engineers, economists, sociologists, educators, farmers, land managers, industry personnel, policy makers, and others willing to focus on weeds within whole farming systems and land management units.

Keywords: Diversified weed management strategies; Herbicide resistance; Multidisciplinary research; Outreach; Site-specific weed management; Weed ecology; Weed-suppressive crop genotypes

Ecological Applications

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DEGLI STUDI
DI PADOVA

This scientific report gives an overview of the research activity carried on during the fifth year of DAFNAE history, and of the wide and qualified collaboration with important research centers around the world in the sectors of agronomy, food, natural resources, animals and environment.
DAFNAE was inaugurated on 1st January 2012, following the re-organization of the Italian University system, in accordance with Italian law 240/2010.

The fourth research yearbook of DAFNAE collects the abstracts of the papers published in 2016 and indexed by Scopus. These abstracts were grouped into the following scientific categories:
Agronomy and soil science
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Ecology and environmental science
Entomology
Food science and technology
Genetics and genomics
Microbiology
Plant science
It offers a snapshot of DAFNAE research activity, that is mainly focused on the production and dissemination of basic and applied knowledge, to promote the quality of human life, the competitiveness of the agrifood sector, and the sustainable use of biotic and abiotic natural resources.

Prof. Maurizio Borin, head of DAFNAE (Department of Agronomy, Food, Natural resources, Animals and Environment), promoted the idea of publishing the DAFNAE annual yearbook as a tool to show and disseminate the level of the research activities of the Department.
All researchers of DAFNAE hope that this fourth edition will continue to propose their scientific activities in the territory and in the world.

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