DAFNAE

RESEARCH YEARBOOK

2017

PADOVA UP

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RESEARCH YEARBOOK 2017

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

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Contributions of the National Research Council (CNR) center in DAFNAE:

INTRODUCTION

The series of the Research Yearbook of the Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE) of the University of Padova continues!

I am extremely proud to welcome the 2017 edition, which, following the previous ones, 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 by the Department, which produces also an incredible number of books, chapters, conference contributions, abstracts, reports, and fact sheets.

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 research after the VQR 2004-2010 and VQR 2011-2014.

Moreover, in 2018 ANVUR assessed DAFNAE as one of the 180 Italian DEPARTMENTS of excellence. Following this achievement, DAFNAE was granted specific funds to improve its research activity for the next 5 years. In this frame, DAFNAE is developing an Excellence Center for Agriculture, Sustainability and Food – CASA – with the organisation of labs, facilities and interdisciplinary research groups.

In the past years DAFNAE also put a great deal of effort to recruit young researchers and one of the results is the increase of publications released in 2017 compared with previous years.

The research activity, carried out both in field and lab, involves faculties and staff, and is supported by the enthusiastic participation of PhD students, postdocs and grant holders.

The DAFNAE faculty members are involved in an impressive of undergraduate, MSc and PhD courses, in which they can promptly transmit to the students the knowledge derived from research.

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 present the 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 2018 edition!

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

RESEARCH PAPERS: STATISTICS AND COMMENTS

The DAFNAE research yearbook is a consolidated annual event on the production and quality of research and the grade of 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 (198) compared with the previous years (151, 154, 123, 150 and 168 in 2012, 2013, 2014, 2015 and 2016, respectively).
The 198 scientific documents (+18% compared with 2016) produced a total of 1,475 pages (+19% compared with 2016), published in 124 scientific journals (+25% compared with 2016). The present research yearbook includes 173 scientific articles, 15 reviews, 6 conference papers, 3 letters and 1 short survey. The Journal of Dairy Science, with 20 documents, has been the scientific journal most highly used by the researchers of DAFNAE, followed by Frontiers in Plant Science (7 documents), Acta Horticulturae (6 documents), Agriculturae Conspectus Scientificus and Scientific Reports (5 documents).
The average number of papers published per researcher of DAFNAE was 2.87.
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 first quartile (Q1) of the respective subject category. Table 1 shows the frequency of scientific documents per quartile of the journal in which they have been published and for each scientific category; 71% 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	18	6	2	2
Genetics and genomics	20	2	1	8
Food science and technology	18	3	4	2
Plant science	15	2	0	0
Ecology and environmental science	20	4	0	3
Entomology	15	4	3	0
Agronomy and soil science	23	4	3	1
Microbiology	11	2	0	0
Total, n.	140	27	13	16
Total, %	71	14	7	8

2 papers did not have information on quartile category.

The most prolific scientific categories were: Agronomy and soil science (15.7% of total documents), Genetics and genomics (15.7% of total documents) and Animal science (14.1% of total documents) (Table 2).
The average number of authors per document ranged from 5.7 (Food science and technology) to 7.6 (Agronomy and soil science), with a minimum of 2 and a maximum of 48 authors per document.
Impressive the number of national and international networks established by the research groups of DAFNAE, which are documented by collaborations with 32 prestigious scientific research centers and universities in Italy, and with international research institutions and universitis of high scientific level located in 36 countries of all the 5 continents.

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

Category	**# of documents**	**% of total documents**	**% of documents with foreign co-authors**	**Average # of authors per document**
Animal science	28	14.1	39.3	5.9 (min. 2 – max 14)
Genetics and genomics	31	15.7	77.4	6.9 (min. 3 – max 17)
Food science and technology	27	13.6	25.9	5.7 (min. 2 – max 9)
Plant science	17	8.6	61.1	6.1 (min. 2 – max 15)
Ecology and environmental science	27	13.6	53.6	5.8 (min. 2 – max 24)
Entomology	24	12.1	77.3	6.9 (min. 2 – max 16)
Agronomy and soil science	31	15.7	38.7	7.6 (min. 2 – max 48)
Microbiology	13	6.6	53.8	7.3 (min. 2 – max 13)
TOTAL	198	100	52.5	6.6 (min. 2 – max 48)

In conclusion, the 2017 yearbook of DAFNAE provides a snapshot of the main research activities carried out in the 2017, with a focus on the trend realized in the last 6 years of activity of the DAFNAE research community and 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 should act as an incite to enhance research collaborations 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 edition.

Martino CASSANDRO

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Agronomy and soil science

A critical review of plant protection tools for reducing pesticide use on grapevine and new perspectives for the implementation of IPM in viticulture

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Abstract

Several pests and diseases have grapevine as their favourite host and the vineyard as preferred environment, so an intensive pesticide schedule is usually required to meet qualitative and quantitative production standards. The need to prevent the negative impact of synthetic chemical pesticides on human health and the environment and the consumer expectations in term of chemical residues in food stimulated the research of innovative tools and methods for sustainable pest management. The research project PURE (www.pure-ipm.eu) was a Europe-wide framework, which demonstrated that several solutions are now available for the growers and evaluated several new alternatives that are under development or almost ready for being applied in practice. Although the use of resistant/tolerant varieties is not yet feasible in several traditional grape growing areas, at least part of the synthetic chemical pesticides can be substituted with biocontrol agents to control pests and pathogens and/or pheromone mating disruption, or the number of treatments can be reduced by the use of decision support systems, which identify the optimal timing for the applications. This review presents the state of the art and the perspectives in the field of grapevine protection tools and strategies.

Keywords: Fungicide; Herbicide; Insecticides; Integrated pest management

Crop Protection

Volume 97, Pages 70-84

Biostimulant effects of seed-applied sedaxane fungicide: Morphological and physiological changes in maize seedlings

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Abstract

Most crops are routinely protected against seed-born and soil-borne fungal pathogens through seed-applied fungicides. The recently released succinate dehydrogenase inhibitor (SDHI), sedaxane®, is a broad-spectrum fungicide, used particularly to control *Rhizoctonia* spp., but also has documented growth-enhancement effects on wheat. This study investigates the potential biostimulant effects of sedaxane and related physiological changes in disease-free maize seedlings (3-leaf stage) at increasing application doses (25, 75 and 150 g a.i. seed^{-1}) under controlled sterilized conditions. We show sedaxane to have significant auxin-like and gibberellin-like effects, which effect marked morphological and physiological changes according to an approximate saturation dose-response model. Maximum benefits were attained at the intermediate dose, which significantly increased root length (+60%), area (+45%) and forks (+51%), and reduced root diameter as compared to untreated controls. Sedaxane enhanced leaf and root glutamine synthetase (GS) activity resulting in greater protein accumulation, particularly in the above-ground compartment, while glutamate synthase (GOGAT) activity remained almost unchanged. Sedaxane also improved leaf phenylalanine ammonia-lyase (PAL) activity, which may be responsible for the increase in shoot antioxidant activity (phenolic acids), mainly represented by p-coumaric and caffeic acids. We conclude that, in addition to its protective effect, sedaxane can facilitate root establishment and intensify nitrogen and phenylpropanoid metabolism in young maize plants, and may be beneficial in overcoming biotic and abiotic stresses in early growth stages.

Keywords: Biostimulant; Hormone-like activity; Nitrogen metabolism; Phenolic acids; Root branching; Succinate dehydrogenase inhibitor (SDHI)

Frontiers in Plant Science

Volume 8, Article number 2072

Challenges of conservation agriculture practices on silty soils. Effects on soil pore and gas transport characteristics in North-eastern Italy

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Abstract

Soil air exchange is one of the most important soil functions that directly impacts on crop productivity and environment. Generally, conservation agriculture (CA) practices are expected to provide improved soil aeration but contrasting texture-related effects were found in the literature. The aim of this study was to evaluate the effect of CA practices on gas transport characteristics in the silty soils of the Veneto Region (North-Eastern Italy). In 2010, a field experiment comparing CA practices (no-tillage, cover crop and residues retention) to conventional intensive tillage (IT) system was established in four farms located in the Veneto low plain. In fall 2015, 144 undisturbed 100 cm^3 soil cores where collected at two different layers (3–6.5 cm and 20–23.5 cm) and analysed for air-filled porosity, air permeability, gas diffusivity and soil structure indices derived. Gas transport measurements highlighted low transmission properties of the silty soils independently from agronomic management. Both air permeability and relative gas diffusivity showed poor aerated conditions being generally <20 µm^2 and <0.005, respectively. CA treatments affected the transmission properties only in the coarsest soil studied causing a reduction of air permeability in the deeper layer and relative gas diffusivity in both layers. The CA-induced reduction was related to the tillage effect on soil bulk density and suggested that CA not only affected the air-filled porosity but also continuity and tortuosity characteristics. The poor structural stability of Veneto soils, particularly the poor soil organic carbon content, could prevent the exploitation of CA practices firstly on soil structure and in turn on gas exchanges. For these reasons further studies elucidating the mechanisms improving soil structural conditions for silty soils as those examined in this study are required.

Keywords: Air permeability; Air-filled porosity; Conservation agriculture; Gas diffusivity; No-tillage; Silty soils; Soil gas transport

Soil and Tillage Research

Volume 172, Pages 12-21

CO_2 emissions and maize biomass production using digestate liquid fraction in two soil texture types

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Abstract

The aim of this work was to evaluate the effects of soil texture and primary tillage type on soil CO_2 emission and maize biomass production after digestate liquid fraction (DLF) spreading. The study was conducted in 2014 in two open fields at Terrassa Padovana (farm 1) and Bovolenta (farm 2) in the Veneto Region of Italy. Soil CO_2 emission after digestate spreading was evaluated by comparing the effect of soil texture (sandy loam vs. clay loam) at farm 1 and the effect of long-term primary tillage management (>10 years) (ripping vs. plowing) in clay loam soil at farm 2. Unamended soil was considered the control at both farms. DLF was supplied before maize (*Zea mays* L.) sowing at a dose equal to 170 kg total nitrogen ha^{-1} using a splash-plate technique. DLF spreading determined a CO_2 emission peak 1 h after spreading at both farms, with median emission values of 8.93 and 4.35 g m^{-2} h^{-1}, respectively, from the sandy loam and clay loam soils at farm 1. At farm 2, primary tillage type did not exert a significant effect on CO_2 emission peak, with a median value of 5.85 g m^{-2} h^{-1}. About three days after DLF distribution, soil CO_2 fluxes were less than 1 g m^{-2} h^{-1}. The first soil harrowing and the first rainfall event after spreading determined significantly higher CO_2 emissions from amended plots than from unamended plots for a few hours. At farm 1, soil CO_2 emission during the maize growing season was significantly higher in the amended plots (+1.7 times) than in the unamended plots, which showed a median emission value of 0.29 g m^{-2} h^{-1}; soil texture and tillage exerted no significant influence. Maize yield at dough stage was not significantly influenced by DLF at farm 1, with 22.7 ±1.6 Mg ha^{-1} and 18.7 ±2.8 Mg ha^{-1} in the clay loam and sandy loam soils, respectively. At farm 2, the distribution of DLF increased maize biomass production by +17% with respect to the unamended treatment that produced 18.0 ±2.4 Mg ha^{-1}. Although the results reported in this article concern data from only one year, and further long-term experiments are needed to confirm our findings, they indicate that CO_2 emissions after digestate distribution are lower in a clay loam soil than in a sandy loam soil and are not affected by primary tillage type.

Keywords: Clay loam soil; Digestate splash-plate spreading; Plowing; Ripping; Sandy loam soil

Transactions of the ASABE

Volume 60, Issue 4, Pages 1325-1336

Conservation agriculture had a poor impact on the soil porosity of Veneto low-lying plain silty soils after a 5-year transition period

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Abstract

Conservation agriculture practices have been proposed as a set of techniques for improving soil structure properties and related ecosystem services. This study compared conservation agriculture (CA) practices (no-tillage, cover crop and residue retention) and conventional intensive tillage system in order to evaluate their effects on total porosity, pore size distribution, pore architecture and morphology. The experiment was set up in 2010 on four farms of the low-lying Veneto Region plain characterized by silty soils. Almost hundred soil samples were collected in 2015 at four depths down to 50-cm layer and investigated for porosity from micrometre (0.0074 m) to macrometre (2.5 mm) by coupling mercury intrusion porosimetry and X-ray computed microtomography (CT). Indices of soil morphology and architecture were derived by analysing 3D images and mercury intrusion porosimetry pore size curves. Results suggested that silty soils of Veneto plain are microstructured because much (82%) of the porosity ranged between 0.0074 and 30 m. CA practices positively influenced the ultramicroporosity class (0.1–5 μm) (1.86E-01 vs 1.67E-01 μm^3 μm^{-3}) that is strictly linked to soil organic carbon stabilization while no effects were observed in X-ray μCT porosity domain (>26 μm). Silty soils of Veneto plain showed a slow reaction to CA because of the poor aggregate stability and low soil organic carbon. However, the positive response of the ultramicropore fraction indicates that a virtuous cycle was initiated between soil organic carbon and porosity, hopefully leading to well-developed macropore systems and, in turn, enhanced soil functions and ecosystem services.

Keywords: Conservation agriculture; Mercury intrusion porosimetry; Pore morphology and architecture; Pore size distribution; X-ray computed microtomography

Land Degradation and Development

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Crop yield and energy use in organic and conventional farming: A case study in north-east Italy

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Abstract

The role played by organic farming as an alternative system to conventional farming is widely questioned, since conflicting results on crop yields sometimes greatly affect system efficiency. As a result, prolonged monitoring studies on organic (OF) and conventional farming (CF) systems are still required, especially in real-life farm conditions, in which the entire production process is quantified. In this context, this study reports crop yields (winter wheat, maize, soybean) and energy efficiency, over a 13-year monitoring period, on a farm in north-east Italy in which two sectors are farmed following OF and CF practices. Results showed that organic yields were always lower than conventional ones, averaging 69%, although their range varied greatly over the years (from 45% to 90%) and depended on crop type. Several management constraints had effects on the lower yields, especially reduced available nutrients and cropping season, but also the timings and types of tillage operations. By contrast, OF practices usually had positive effects on the environment, due to reduced energy input mainly fertilisation (-33.4% MJ ha^{-1} y^{-1}) and the generally higher productivity of invested energy ($E_{Out}E_{In}^{-1}$ = 4.53 in OF and 4.28 in CF); energy use differences per product unit were mainly equal. Other factors, such as local climate and soil variability, may have influenced system performance, but as the two experimental sites were located at a distance of 3.5 km from each other, the data reported here are still valuable, in that they represent the results of 13 years of monitoring, during which farm management played a major role. This case study, although conducted in two separate sites, did not highlight the best overall solution at farm level, it does indicate that the agricultural systems applied would be better suited for different situations and targets (e.g., productive, energetic, ecologic).

Keywords: Conventional farming; Energy use; Maize; Organic farming; Soybean; Winter wheat; Yield gap

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Distillery anaerobic digestion residues: A new opportunity for sweet potato fertilization

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Abstract

This paper represents an union point between two emerging issues: the productive potential derived from anaerobic digestion residues (ADRs) and the cultivation of sweet potato, an innovative species in Europe. The trial was carried out in open field condition in 2014 and 2015 comparing three fertilization treatments. ADRs were used to partially or completely substitute mineral N crop requirements: i) 50% N through ADRs and 50% N through mineral fertilizer (T50); ii) 75% N through ADRs and 25% N through mineral fertilizer (T75); iii) 100% N through ADRs (T100). Two controls treatments were also predisposed, one unfertilized (T0), and one with only mineral fertilization (TMIN). The highest significant aerial biomass yield (>57 t ha^{-1}) was showed by T75 whereas no differences were found among other treatments (46 t ha^{-1}). The highest significant marketable yield was showed by T75 and T100 (16 t ha^{-1}). The marketable yield showed the highest value in 2015 with almost 16 t ha^{-1} with an year effect on root size. During the experiment harvest index ranged from 20.5% (TMIN) to 26.9% (T100). The nitrogen agronomic efficiency was greatly lower (-59.1%) in 2014 as a result of the high rainfall amount compared to 2015. T75 treatment showed the highest nitrogen agronomic efficiency, apparent recovery efficiency and utilization efficiency. The highest content of nitrates in aerial biomass was detected in combination with the N organic treatments. The storage roots harvested in 2014 presented a higher concentration of glucose (+19.7%) and fructose (+29.4%) than that harvested in 2015. The concentration of glucose and fructose increased with the amount of nitrogen supplied with ADRs. The obtained results offer potentially useful data for producers order to demonstrate the usability of ADRs as an alternative to traditional mineral fertilization in sweet potato cultivation.

Keywords: Digestates; *Ipomoea batatas*; Nitrogen use efficiency; Quality; Sugars; Yield

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Effect of vegetative propagation materials on globe artichoke production in semi-arid developing countries: Agronomic, marketable and qualitative traits

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Abstract

In Tunisia, globe artichoke is mainly propagated by underground dormant axillary buds (ovoli), which are removed from the field in August during the quiescence period. The high cost of in vitro-plants and the absence of specialized nurseries were among the reasons for the rise of heterogeneity and spread of diseases. The aim was to help farmers to improve artichoke yield and quality by ameliorating their vegetative propagation technique with low cost methods. Three plant cuttings management methods were tested: summer ovoli (T0); spring offshoots nursery's cuttings forced to pass a vegetative rest period by stopping irrigation (T1); and offshoots nursery's cuttings not forced (T2). The cuttings management can affect both yield and qualitative traits of artichoke. T1 nursery plants produced the heaviest primary heads, 7% and 23% higher than T2 and T0, respectively. T1 plants exhibited the highest yield during the harvest season, with +17.7% and +12.2% compared to T0 and T2, respectively. T0 and T1 showed the highest total antioxidant capacity and inulin content; the propagation method also affected the short-chain sugars ratio. T1 is a viable and sustainable alternative to the traditional one that does not heavily impact on growing costs and improves yield and quality of artichoke.

Keywords: Antioxidant; Cuttings; *Cynara scolymus*; Fructans; Phenolic acids; Sugars; Yield

Agronomy

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Effects of digestate solid fraction fertilisation on yield and soil carbon dioxide emission in a horticulture succession

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Abstract

The aim of this study was to evaluate the agronomical and environmental effects of digestate solid fraction (DSF) used as fertiliser in a vegetable crop succession (green bean, savoy cabbage, cabbage and cauliflower) in Northeast Italy (45°20′ N; 11°57′ E). Three fertilisation treatments were tested using DSF to substitute 0% (Tmin), 50% (T50) and 100% (T100) optimal level of mineral nitrogen fertilisation. The experiment was carried out from 22nd May 2014 (green bean sowing) to 3rd June 2015 (cabbage harvest). Summer and spring crops did not show significantly different marketable yield among fertilisation treatments with an average value (±standard error) of 9.0±0.5, 9.9±1.2 and 51.3±6.4 Mg ha^{-1} for green bean, cauliflower and cabbage, respectively. Lower DSF fertilisation effect was monitored on winter crop (savoy cabbage) with a marketable yield reduction of -35.1% than mineral fertilisation (25.9 Mg ha^{-1}), whereas the T50 treatment was not significantly different compared to the two previous ones. Crop species significantly influenced the N use efficiencies with negative recovery and use efficiency indexes for the DSF fertilisation treatments. Soil CO2 emissions were not significantly influenced by fertilisation in all studied crops with median values always lower than 1 g m^{-2} h^{-1}.

Keywords: Cabbage; Cauliflower; Green bean; Nitrogen; Savoy cabbage

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Effects on water management and quality characteristics of ozone application in chicory forcing process: A pilot system

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Abstract

Agriculture is the largest user of world water resources, accounting for 70% of all consumption. Reducing water consumption and increasing water use efficiency in agriculture are two of the main challenges that need to be faced in the coming decades. Radicchio Rosso di Treviso Tardivo (RTT) is a vegetable that requires a water forcing process prior to final commercialization which presents a significant environmental impact due to the high water volumes used and then dispersed into the environment. The experiment was aimed at reducing the water use in the forcing process of RTT, by developing a pilot system with recycled water in a closed loop through ozone treatment. Concerning water quality, the redox potential value was higher in the ozonized system, whereas turbidity, pH and electrical conductivity of the ozonized system did not change significantly from the control. Yield and quality of plants obtained in the ozonized system did not significantly differ from the control plants except for the antioxidant activity that was higher in plants forced using the water treated with ozone. Our initial results suggest that the ozone treatment could be applied in the forcing process and is suitable for growers, saving up to 95% of water volumes normally used for this cultivation practice.

Keywords: Antioxidant; Bitter taste; *Cichorium intybus* L.; Guaianolides; Phenols; Radicchio; Rubifolium group; Sustainability; Water use efficiency

Agronomy

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Environment, agro-system and quality of food production in Italy

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Abstract

In the context of increasing attention towards sustainable and high quality food products, Italy plays a key role in Europe due to its embedded territorial vocation for locally produced food and alternative agriculture systems helping biodiversity and landscape preservation. Here, we report an overview of Italian agriculture by analysing organic farming (OF) and geographical indication (GI) systems and their contribution to the national agriculture. Land use data highlight that OF and GI contribute around 10% to the utilised agriculture area (UAA), with relevant distinctions in terms of regional distribution. While GIs are mostly in the north-central regions (8.5%), OF products are most frequent in the south and on the islands (5.0% of UAA). This trend was observed on the one hand in Trentino-South Tirol, Veneto and Friuli-Venezia Giulia (%UAA GI/%UAA OF>5.9), and on the other in Calabria, Basilicata and Sicily (%UAA GI/%UAA OF<0.1). Similarly, both systems are widespread in less-favoured areas in terms of agricultural intensification, providing support to preserve agro-systems and reduce land abandonment.

Keywords: Agricultural systems; Geographical indications; Land use; Organic farming

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Environmental and agronomic performance of fresh rice hulls used as growing medium component for *Cyclamen persicum* L. pot plants

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Abstract

The issue of environmental compatibility of some specialized agricultural sectors is becoming more appealing to both consumers and growers. Growing medium components that are non-renewable, or partly renewable, such as perlite and peat, are among the production factors which can be modified by growers in the short term. In this study a 'gate to gate' life cycle assessment was performed for a floral commodity, *Cyclamen persicum* Mill., grown in four different substrates formulated by blending expanded perlite (EP) (at 10% v/v) or fresh rice hulls (FRH) (10%, 30% and 50% v/v) with sphagnum peat. Results of the LCIA show that growing media components have a relevant share of impact for this production phase, along with greenhouse materials, plastic pots, fertilizer and plant protection products. Peat and EP replacement with a small amount of FRH can slightly improve the environmental performance for AD and GWP categories. Growth trials showed that substitution of EP with equal amount of FRH does not affect plant quality, but higher amounts increase water and fertilizer requirements not only reduces plant performance but also worsen the ecoprofile of the functional unit for most impact categories.

Keywords: *Cyclamen persicum*; Growing media; LCIA; Rice hulls

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Growth and quality responses of low-maintenance turfgrasses to trinexapac-ethyl

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Abstract

The positive effects of trinexapac-ethyl (TE) on turfgrass growth and tolerance to various types of stress could promote its use in low-input maintenance turfgrasses to reduce the expense associated with mowing. However, there is a general lack of information about TE effects in low maintenance turfgrasses, and especially when used in transition zone turfgrass mixtures. The objective of this study was to evaluate the response of three inter-specific turfgrass mixtures to three different application rates of TE under low maintenance conditions. A 2-year field study was conducted from April 2006 to July 2008 at the Agricultural Experimental Farm of the University of Padova (northern Italy, 45°20N, 11°57E, elevation 8 m). Visual turfgrass quality (1–9 scale) and clippings biomass production of three mixtures were evaluated seasonally under four TE treatments with rates representing 0, 0.5, 1.0 or 1.5x the rates indicated on label instructions. Based on both visual quality and biomass production, turfgrass responded differently to TE application depending on dominant species in the mixture. Furthermore, our results suggested that changes over time in turfgrass botanical composition influence visual quality and biomass production through the experimental period. The main effect of TE treatments occurred in biomass production while the effect on turfgrass quality was mainly associated with the two highest TE rates. Application at a rate lower than the labeled seems to be enough for reducing biomass production without affecting turfgrass quality or even, in some seasons, improving it. Finally, we found that the effect of TE seems to weaken over time as turfgrass maturity advances.

Keywords: Clipping biomass; Turfgrass mixtures; Vertical growth rate; Visual quality

Crop Protection

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Increased root growth and nitrogen accumulation in common wheat following PGPR inoculation: Assessment of plant-microbe interactions by ESEM

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Abstract

The use of plant growth-promoting rhizobacteria (PGPR) meets the current need to reduce nitrogen input in order to attain greater sustainability in the production of crops, particularly cereals. This study investigated whether a commercial bio-fertiliser containing a consortium of PGPR and N-fixing bacteria (*Azospirillum* spp., *Azoarcus* spp. and *Azorhizobium* spp.) affects shoot and root growth, N accumulation and grain yield in common wheat (*Triticum aestivum* L.). Trials were conducted in a fertile, silty loam soil, firstly in rhizoboxes, by applying bacteria either as a seed-coating inoculum or by foliar + soil spraying, and then in the field by spraying the canopy at the tillering stage with decreasing levels of N fertilisation (160, 120 and 80 kg ha^{-1}) in two consecutive years. Culm height, leaf chlorophyll content, nitrogen accumulation and yield were recorded above ground, while below ground Root Length Density (RLD) patterns were investigated by soil coring and image analysis at the flowering stage. Environmental Scanning Electron Microscope (ESEM) imaging revealed an excellent ability of bacteria to adhere to the surface of intact leaves and roots, and to colonise both leaf mesophyll and root vascular tissues in aseptic conditions. Bacteria increased the number of root tips and ramifications (+65% vs. non-inoculated controls) in sterilised rhizobox soil, regardless of the method of application, and the volumetric root length density in the open field with medium (+29%) and high (+11%) N supply, resulting in greater N accumulation (about +25 kg ha^{-1}). Although the N dose had clear positive effects, no significant variations in grain yield (only + 1–3% vs. non-inoculated controls) or other agronomic parameters could be ascribed to bacteria inoculation. The conclusion drawn is that the use of a combination of PGPR and N-fixing bacteria offers an opportunity to improve root growth in wheat and increase plant resilience to environmental stresses, and helps to reduce N losses from agricultural ecosystems thereby offering partial fertiliser savings within crop rotations.

Keywords: Bio-fertilisers; Common wheat; Endophytic bacteria; Nitrogen accumulation; Root growth; Vegetation indices

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Qualitative and quantitative response of soil organic carbon to 40 years of crop residue incorporation under contrasting nitrogen fertilisation regimes

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Abstract

Crop residue incorporation (RI) is recommended to increase soil organic carbon (SOC) stocks. However, the positive effect on SOC is often reported to be relatively low and alternative use of crop residues, e.g. as a bioenergy source, may be more climate smart. In this context, it is important to understand: (i) the response of SOC stocks to long-term crop residue incorporation; and (ii) the qualitative SOC change, in order to judge the sustainability of this measure. We investigated the effect of 40 years of RI combined with five different nitrogen (N) fertilisation levels on SOC stocks and five SOC fractions differing in turnover times on a clay loam soil in Padua, Italy. The average increase in SOC stock in the 0-30 cm soil layer was 3.1 Mg ha^{-1} or 6.8%, with no difference between N fertilisation rates. Retention coefficients of residues did not exceed 4% and decreased significantly with increasing N rate (R2 ≤ 0.49). The effect of RI was higher after 20 years (4.6 Mg ha^{-1}) than after 40 years, indicating that a new equilibrium has been reached and no further gains in SOC can be expected. Most (92%) of the total SOC was stored in the silt and clay fraction and 93% of the accumulated carbon was also found in this fraction, showing the importance of fine mineral particles for SOC storage, stabilisation and sequestration in arable soils. No change was detected in more labile fractions, indicating complete turnover of the annual residue-derived C in these fractions under a warm humid climate and in a highly base-saturated soil. The applied fractionation was thus useful to elucidate drivers and mechanisms of SOC formation and stabilisation. We conclude that residue incorporation is not a significant management practice affecting soil C storage in warm temperate climatic regions.

Keywords: Carbon sequestration; Soil fractionation; Straw incorporation

Soil Research

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Short-term effects of biochar and salinity on soil greenhouse gas emissions from a semi-arid Australian soil after re-wetting

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Abstract

Arid and semi-arid soils often show a pulse of soil greenhouse gas (GHG) emissions upon re-wetting – whether from irrigation water or rainfall. We used a laboratory incubation to elucidate interactions of salinity, biochar amendment, and simulated wetting intensity in emissions of carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O) in a semi-arid Australian soil. A factorial experimental design was used with three main factors: irrigation water salinity (using NaCl, control or ~ 0.9 dS m^{-1}, 5 dS m^{-1} and 10 dS m^{-1}), biochar amendment (0% and 5% by mass of Eucalyputs polybractea biochar) and soil moisture (25%, 50%, 75% and 100% of water-holding capacity, WHC – a proxy for wetting intensity after irrigation or rainfall). The strongest single regulating variable of rates of soil CO_2 emission was WHC (+ 171% increase between 25% and 100% WHC). Salinity reduced CO_2 emissions (relative to controls) by 19% at 5 dS m^{-1} and 28% at 10 dS m^{-1}. Soils amended with biochar produced less (10%) CO_2 emissions. All treatments showed negative CH_4 emissions (or CH_4 oxidation) that were only influenced by WHC. Soil N_2O emissions increased with salinity (+ 60%), while biochar additions reduced them slightly (12%). N_2O emissions were not influenced by WHC. Overall, results showed that biochar additions can mitigate some of the "pulse" effects of rainfall on emissions (~ 10% in term of global warming potential across all treatments).

Keywords: Biochar; Carbon dioxide; Methane; NaCl; Nitrous oxide; Water holding capacity

Geoderma

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Soil porosity in physically separated fractions and its role in SOC protection

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Abstract

Purpose: Processes that lead to soil organic carbon (SOC) protection depend on both soil porosity and structure organization, as well as chemical and biological properties. In particular, the soil micro-nano porosity <30 μm) regulates microorganism accessibility to the soil pore system and offers surfaces for organic carbon adsorption and intercalation into soil minerals. The aim of this work was to investigate how pore size distribution can selectively protect specific carbon pools in different aggregate size fractions, by considering the effects of long-term application of farmyard manure (FYM) and mineral (Min) fertilization. Materials and methods: Macroaggregates (250–2000 μm), microaggregates (53–250 μm), and silt–clay (<53 μm) fractions of three different soils (clayey, peaty, and sandy) were separated by wet sieving technique and then subjected to chemical and physical analysis. Sample porosity and pore size distribution were analyzed using mercury intrusion porosimetry (MIP), while SOC chemical structure was characterized by means of nuclear magnetic resonance (^{13}C cross-polarization–magic angle spinning nuclear magnetic resonance (CP MAS ^{13}C NMR)) and diffuse reflectance infrared Fourier transform (DRIFT) spectroscopies. Results and discussion: Results showed that FYM increased organic (OC) and humic carbon (HC) content compared to the Min fertilization and unfertilized soils. However, it caused a gradual decrease in O,N-alkyl C, and alkyl C of humic C from macroaggregate to silt–clay fractions, suggesting an advanced state of humic component degradation as revealed by CP MAS ^{13}C NMR, DRIFT analyses. MIP analysis showed a clear increase of micropores (5–30 μm) and cryptopores (0.0035–0.1 μm) from macroaggregate to silt–clay fractions, while minor differences were observed among the treatments. The application of principal component analysis to mineral soil fractions identified the formation of three main clusters, where (i) macroaggregates of clayey soil were mainly associated to cryptopores and OC and (ii) microaggregates and silt–clay fraction were mainly isolated by carbonyl C, ultramicropores, and total porosity. The third cluster was associated with medium and fine sand of the sand soil fraction as coupled with O,N-alkyl C, anomeric C, mesopores, and HC/OC ratio. Conclusions: Overall, this study indicates that pore size distribution may be a valuable indicator of soil capacity to sequester carbon, due to its direct influence on SOC linkages with soil aggregates and the positive effects against SOC decomposition phenomena. In this context, micropore- to nanopore-dominated structures (e.g., clayey soil) were able to protect OC compounds by interacting with mineral surfaces and intercalation with phyllosilicates, while meso/macropore-dominated structures (i.e., sandy soil) exhibited their low ability to protect the organic components.

Keywords: CP MAS ^{13}C NMR; DRIFT; Mercury intrusion porosimetry; MIP; Pore volume; Soil aggregate; Soil porosity; WSA

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Temporal variability of soil management effects on soil hydrological properties, runoff and erosion at the field scale in a hillslope vineyard, North-West Italy

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Abstract

Soil management in vineyard inter-rows has a great influence on soil hydraulic conductivity and bulk density, and, consequently, on runoff and soil erosion processes at the field scale. The maintenance of bare soil in vineyard inter-rows with tillage, as well as the tractor traffic, are known to expose the soil to compaction, reduction of soil water holding capacity and increase of runoff and erosion. The use of grass cover is one of the most common and effective practices in order to reduce such threats. It is therefore important to relate rainfall characteristics, soil properties and response in terms of runoff and soil erosion, from yearly to seasonal and to single event temporal scales. The objective of this work is to quantify the temporal variability of the effects of two different kind of inter-row management on soil hydrological properties, runoff and erosion in vineyards. For this reason two vineyard field-scale plots in the Alto Monferrato vine-growing area (Piedmont, NW Italy) were monitored in two years. The inter-rows were managed with conventional tillage (CT) and grass cover (GC), respectively. Fifteen series of infiltration tests were carried out during a 2-year period of observation (October 2012 to November 2014). In order to take into account the effect of tractors traffic, the tests were done on the track, and outside the track. Furthermore, a dataset of 29 rainfall-runoff events covering a wide range of topsoil characteristics was collected in the two plots, along with soil water content and runoff discharge monitoring, and determination of sediment yield in case of erosive events. An optical disdrometer installed in the plots provided also 1-min rainfall intensity data. In summer, just one month after tillage, CT soil showed very low hydraulic conductivity, so storms were able to cause Hortonian runoff and soil losses up to 5.7 Mg ha^{-1}. In autumn and winter very high saturation-excess runoff was observed in CT, that reached 83% of the precipitation. Runoff in the grass cover plot was mainly due to saturation of the topsoil, and the annual reduction of runoff in the GC plot was about 63%. Soil erosion up to 1.2 Mg ha^{-1} in a single event was observed in the GC vineyard in winter. In each year of observation, most of the erosion occurred during a single event, while the total annual erosion was up to 9 times higher in the CT treatment than in the GC.

Keywords: Soil hydrological properties; Soil management; Vineyards

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Turf quality and species dynamics in bermudagrass and kentucky bluegrass mixtures

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Abstract

Climatic changes and the need to reduce water consumption for irrigation have led to expanded use of warm-season turf species in transitional zones. Turf managers are often hesitant to use warm-season species because they undergo dormancy for a long period during the winter. Although this issue might be addressed by mixing cool- with warm-season species, there is a lack of information on the performance and dynamics of species succession in such turfgrass mixtures. A 2-yr investigation was conducted in Legnaro, Italy, and Fayetteville, AR, to test the turf quality and species succession in mixtures of various cultivars of bermudagrass (BG) [*Cynodon dactylon* (L.) Pers.] with Kentucky bluegrass (KBG) (*Poa pratensis* L.). Bermudagrass cultivars, Yukon and Veracruz, were seeded in June 2011 at 5 g m^{-2} and KBG cultivars Brooklawn, Mystere, and Nublue Plus were overseeded in September 2011 at 30 g m^{-2}. Across both studies, the frequency of BG in the mixture was generally higher for Yukon and ranged from 40 to 95%. However, the mixtures with Veracruz had superior turf quality in Legnaro from October 2012 to March 2013. The species succession was influenced by BG cultivars, whereas KBG cultivar had little effect on the rate of plant composition change. On the basis of these results, the choice of BG cultivar appears critical for establishing functional KBG and BG mixtures in transitional zones.

Keywords: *Cynodon dactylon*; Turfgrass; Turfgrass species

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Vegetable intercropping in a small-scale aquaponic system

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Abstract

This paper reports the results of the first study of an aquaponic system for Pangasianodon hypophthalmus production that uses *Lactuca sativa* L. (lettuce) and *Cichorium intybus* L. rubifolium group (red chicory) intercropping in the hydroponic section. The experiment was conducted in a greenhouse at the Zurich University of Applied Sciences, Wädenswil, Switzerland, using nine small-scale aquaponic systems (each approximately 400 L), with the nutrient film technique (NFT). The intercropping of vegetables did not influence the water temperature, pH, electric conductivity (EC), oxidation–reduction potential, nor O_2 content. Intercropping with red chicory increased the lettuce sugar content (+16.0% and +25.3% for glucose and fructose, respectively) and reduced the lettuce caffeic acid content (16.8%). In regards to bitter taste compounds (sesquiterpene lactones), intercropping reduced the concentrations of dihydro-lactucopicrin + lactucopicrin (42.0%) in lettuce, and dihydro-lactucopicrin + lactucopicrin (22.0%) and 8-deoxy–lactucin + dihydro-lactucopicrin oxalate (18.7%) in red chicory, whereas dihydro-lactucin content increased (+40.6%) in red chicory in regards to monoculture. A significantly higher organic nitrogen content was found in the lettuce (3.9%) than in the red chicory biomass (3.4%), following the intercropping treatment. Anion and cation contents in vegetables were affected by species (Cl^-, NO_3^-, PO_4^{3-}, SO_4^{2-}, and Ca^{2+}), intercropping (K^+ and Mg^{2+}), and species × intercropping interactions (NO_2^- and NH_4^+). Experimental treatments (monoculture vs intercropping and distance from NFT inlet) did not exert significant effects on leaf SPAD (index of relative chlorophyll content) values, whereas the red coloration of the plants increased from the inlet to the outlet of the NFT channel. Intercropping of lettuce and red chicory affected the typical taste of these vegetables by increasing the sweetness of lettuce and changing the ratio among bitter taste compounds in red chicory. These results suggest intercropping as a possible solution for improving vegetable quality in aquaponics. Although the results are interesting, they have been obtained in a relatively short period, thus investigations for longer periods are necessary to confirm these findings. Further studies are also needed to corroborate the positive effect of the presence of red chicory in the system on fish production parameters.

Keywords: *Cichorium intybus* L.; *Lactuca sativa* L.; Nutrient film technique; *Pangasianodon hypophthalmus*; Vegetables quality; Yield

Agronomy

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Year-round variability of field-saturated hydraulic conductivity and runoff in tilled and grassed vineyards

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Abstract

The soil management adopted in vineyard inter-rows has a great influence on soil hydraulic properties, and, consequently, on runoff at the field scale. Conventional management with tillage is adopted by vine-growers to improve the soil water recharge during winter. Nevertheless, this practice is known to increase runoff and soil erosion in steep areas, especially in mechanized vineyards, thus grass cover is adopted to reduce these negative impacts. The year-round values of field-saturated hydraulic conductivity and of the field-scale runoff were measured in vineyard plots from November, 2012 to March, 2016 in the Alto Monferrato vine-growing area (Piedmont, NW Italy). Field-saturated hydraulic conductivity values were obtained by 110 infiltration measurements. The tests were carried out by adopting the Simplified Falling Head methodology in two adjacent vineyards plots, where inter-rows were managed with conventional tillage (CT) and grass cover (GC), respectively. The runoff, the soil temperature and the soil water content in the two plots have also been recorded. As it was expected, the tillage increased the field-saturated hydraulic conductivity with respect to the plot with permanent grass cover. However, this effect was only temporary, since a decrease in field-saturated hydraulic conductivity was observed as a consequence of cumulative precipitation and tractor passages after the tillage operations. The field-saturated hydraulic conductivity ranged between 9 and 9119 mm h^{-1} in the tilled plot and between 4 and 1775 mm h^{-1} in the plot with grass cover. The response of the plots to precipitation events, in terms of runoff also varied considerably. Generally, during most of the events, the runoff in the tilled plot resulted higher (up to nearly 20 times) than in the grassed one. The grass cover was less effective in occasion of large precipitation events during the wet seasons than in other months.

Keywords: Conventional tillage; Cumulative precipitation; Infiltration measurements

Chemical Engineering Transactions

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Evaluation of compost and anaerobic digestion residues as a component of growing media for ornamental shrub production

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Abstract

For some decades, compost has been investigated as a partial substitute for peat in the preparation of pot growing media. Nevertheless, its use for the preparation of professional substrates still remains limited. Anaerobic digestion residues are agro-industrial by-products that have recently gained interest due to their potential as feedstock for growing media preparation. In this study, 8 growing media: peat blended with 4 rates (0, 15, 30 and 45% v/v) of green waste compost and two rates (0 and 20% v/v) of anaerobic digestion residues were evaluated. After physical and chemical characterization, the 8 media were used to grow rooted cuttings of Rosa 'Sweet Haze' and *Abelia* x *grandiflora* 'Prostata' in 15 cm diameter plastic containers. One year old abelia plants, grown in a peat-based media in 15 cm containers, were also re-cultivated in 19 cm containers using the prepared substrates. Results showed that increasing compost rates increased bulk density, pH and electrical conductivity, but reduced organic matter, total pore space and air filled porosity. Addition of anaerobic digestion residues limited the increase of these parameters. Response of plants differed according to species and, for abelia, type of cultivation. Roses grown in the substrates with compost were similar to those grown in peat media. On the contrary, abelia plants from cuttings were negatively affected by increasing rates of compost. However, addition of anaerobic digestion residues to the substrates improved plant growth. Plants of abelia repotted in 19 cm containers were less negatively affected by compost than abelia cultivated in 15 cm container and, in general, only at the highest rate, and growth was promoted by the addition of anaerobic digestion residues.

Keywords: *Abelia*×*grandiflora* 'Prostata'; Peat replacement; Rosa 'Sweet Haze'; Substrates

Acta Horticulturae

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Prospects for crowdsourced information on the geomorphic 'engineering' by the invasive Coypu (*Myocastor coypus*)

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Abstract

Among the most invasive species, the Coypu (*Myocastor coypus*) best exemplifies the widespread effect of alien species on ecosystems. Among the impacts, the induced erosion in riverbanks has an increasing economic and social importance. Despite its significance, this type of erosion is rarely quantified, and the available information is limited to local knowledge, grey literature, and maintenance reports. This research shows the potential of freely and instantly available Structure-from-Motion (SfM) photogrammetry to obtain crowdsourced information based on smartphone images. The results highlight how it is possible to provide a rough estimate of the damages with relatively low or null cost of application, and limited expert knowledge and expenditure of time, depending on the scale of analysis. The proposed technique provides a fresh approach to a known long-standing issue, offering a new source of information for farmers, researchers, wildlife managers, as well as for land managers and planners. The potential applications of such a technique and its unprecedented ease of use and very low cost offer effective tools for management plans and scientific research, providing a basis to relate eroded volumes to the functioning of the drainage system and the connected agroecosystem. The method would also enable the opportunity of participatory and opportunistic crowdsourced sensing. Further scientific research on the crowd-based data on erosion should encourage standardisation of data gathering and accessibility, together with a public involvement in information exchange, to generate a better understanding and awareness of erosion problems also for other fields of research.

Keywords: Coypu (*Myocastor coypus*); Crowdsourcing; Drainage channels; Erosion; Smartphone; Structure-from-Motion (SfM); Topography

Earth Surface Processes and Landforms

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Biostimulant activity of humic substances extracted from leonardites

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Abstract

Background and aims: Biostimulants are natural compounds that enhance plant growth and plant nutrient use efficiency. In this study, biostimulant effects of humic substances (HS) extracted from leonardites were analysed on the metabolism of maize plants grown in hydroponic conditions. Methods: HS extracted from four leonardites were tested for their auxin-like and gibberellin-like activities. Then, 11 day old maize seedlings were treated for 48 h with five concentrations (0, 0.1, 0.5, 1, and 10 mg C L1) of HS. After sampling, root growth and morphology, glutamine synthetase (GS) activity, glutamate synthase (GOGAT) activity, total protein content, soluble sugars content, phenylalanine ammonia-lyase (PAL) activity, soluble phenols, and free phenolic acids were analysed. Results: HS from leonardites had similar spectroscopic pattern, with small differences. The HS from the South Dakota lignite (HS_USA) had more carboxylic groups, whereas the three from Turkish mines had more aromatic and aliphatic structures. HS_USA best enhanced total root growth, root surface area, and proliferation of secondary roots. Plant nutrient use efficiency was enhanced by HS_4, HS_USA and HS_B, with increment of GS and GOGAT enzymes activity and total protein production. HS stimulated also PAL enzyme activity, followed by a higher production of total soluble phenols, p-hydroxybenzoic acid, p-coumarilic acid, and chlorogenic acid. Conclusion: This study found that, although the activity of the HS depended on the origin of the leonardite, these compounds can be attributed to the biostimulant products, eliciting plant growth, nitrogen metabolism, and accumulation of phenolic substances.

Keywords: Biostimulant; FT-IR; Glutamate synthase; Glutamine synthetase; Humic substances; Leonardite; Phenylalanine ammonia-lyase

Plant and Soil

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Chemical and biochemical properties of soils developed from different lithologies in Northwestern Spain (Galicia)

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Abstract

Physical and chemical soil properties are generally correlated with the parent material, as its composition may influence the pedogenetic processes, the content of nutrients, and the element biocycling. This research studied the chemical and biochemical properties of the A horizon from soils developed on different rocks like amphibolite, serpentinite, phyllite, and granite under a relatively similar climatic regime from Galicia (northwest Spain). In particular, the effect of the parent material on soil evolution, organic carbon sequestration, and the hormone-like activity of humic and fulvic acids were tested. Results indicated that all the soils were scarcely fertile because of low concentrations of available P, exchangeable Ca (except for the soils on serpentinite and phyllite), and exchangeable K, but sequestered relevant quantities of organic carbon. The scarce soil fertility was common to all soils independently of the parent material, and we attributed this similarity to the pedogenetic pressure induced by the climatic conditions. Also, the hormone-like activity of humic and fulvic acids, similar for all the soils, was probably due to pedogenesis. We hypothesized that the hormone-like activity of the humic substances helps growth and diffusion of vegetation in low fertile soils and, consequently, soil organic carbon sequestration too.

Keywords: Amphibolite; Auxin-like activity; Fulvic acids; Granite; Humic acids; Humic substances; Indoleacetic acid; Phyllite; Serpentinite

Forests

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Effects of moderate and high rates of biochar and compost on grapevine growth in a greenhouse experiment

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Abstract

Biochar is used as soil amendment and enhancer of plant growth, but the mechanisms involved in grapevine are not understood. In this study, the short-term effects of amendments were evaluated in a trial combining three substrates (biochar, compost, peat-based media) with three doses (30, 70, 100%) along a time sequence on 1-year-old bare root cuttings of grapevine. Amendments were analyzed for elemental composition. Soil pH, electrical conductivity (EC), chlorophyll (CHL), flavonoids (FL), anthocyans (ANT) and nitrogen balance index (NBI) were measured. Biochar differed from other amendments for stable C structures, where nutrients and lignin residues were high in compost. Biochar increased soil pH, whereas biochar plus compost mixture augmented EC. The amended plants had detrimental effects on root, true and lateral leaves. Nevertheless, at the lowest rate biochar increased the primary shoot and total scion to root biomass ratio. Among biochemicals, ANT and NBI were mostly affected by biochar, while compost gave only slight increments. Thus, although biochar rate was not adequate for the shedding in open field our results suggest that biochar might be useful in nursery when used at low dosages.

Keywords: Biostimulant; Primary shoot biomass; Stable C structures

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Rapid peat accumulation favours the occurrence of both fen and bog microbial communities within a Mediterranean, free-floating peat island

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Abstract

The unique environment of a 4m-thick, free-floating peat island within the Posta Fibreno lake (Central Italy) was analyzed using DNA-based techniques to assess bacterial and fungal community members identity and abundance. Two depths were sampled at 41 and 279 cm from the surface, the former corresponding to an emerged portion of Sphagnum residues accumulated less than 30 yrs ago, and the latter mainly consisting of silty peat belonging to the deeply submerged part of the island, dating back to 1520-1660 AD. The corresponding communities were very diverse, each of them dominated by a different member of the Delta-proteobacteria class for prokaryotes. Among Eukaryotes, Ascomycota prevailed in the shallow layer while Basidiomycota were abundant in the deep sample. The identity of taxa partitioning between acidic surface layer and neutral core is very reminiscent of the differences reported between bogs and fens respectively, supporting the view of Posta Fibreno as a relic transitional floating mire. Moreover, some microbial taxa show an unusual concurrent species convergence between this sub-Mediterranean site and far Nordic or circumpolar environments. This study represents the first report describing the biotic assemblages of such a peculiar environment, and provides some insights into the possible mechanisms of its evolution.

Keywords: Fungal community; Identity; Microbial community

Scientific Reports

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Humusica 1, article 4: Terrestrial humus systems and forms — Specific terms and diagnostic horizons

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Abstract

Knowledge of a little number of specific terms is necessary to investigate and describe humipedons. This “new vocabulary” allows individuating and circumscribing particular diagnostic horizons, which are the fundamental bricks of the humipedon. Few “components” defined by specific terms characterize a specific “humipedon horizon”; few “humipedon horizons” compose a given “humus form” and some similar “humus forms” are grouped in a functional “humus system”. In this article, specific terms and humus horizons are listed and explained one by one. Field difficulties are illustrated and resolved. The aim of the article is to present in a manner as simple as possible how to distinguish in the field the soil structures allowing a morpho-functional classification of terrestrial (aerated, not submerged) humipedons.

Keywords: Humic component; Humipedon; Humus; Humus classification; Humus diagnostic horizon; Humusica; Recognizable remains; Terrestrial humus; Zoogenically transformed material

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Humusica 1, article 5: Terrestrial humus systems and forms - Keys of classification of humus systems and forms

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Abstract

This article is an as simple as possible key of classification of terrestrial (aerobic, not submersed) topsoils (organic and organic-mineral series of soil horizons). Based on the introduction exposed in Humusica 1, article 1, and using vocabulary and definitions listed in article 4, a classification is proposed for better understanding the biological functioning of the soil, partially disclosing the process of litter digestion. Five types of terrestrial topsoils, called terrestrial humus systems, are described and illustrated with the help of photographs. Within each humus system, 3–4 humus forms are also revealed, corresponding to similar series of soil horizons generated in a relatively homogeneous environment whose range of ecological factors is not so large to overstep and cause the genesis of another different humus system. The article ends with a figure that shows the relationship between Tangel and Amphi humus systems, and a dichotomous key of classification that one can easily print and bring in the field for practicing humus classification.

Keywords: Humus; Humus classification; Humus forms; Humus systems; Humusica; Terrestrial humus forms

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Soil–root cross-talking: The role of humic substances

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Abstract

The biological activity of humic substances (HS) has been elucidated in the last 40 years. Growth enhancement from HS has been demonstrated in several plants in the laboratory and the field. Morphogenesis effects have also been investigated and include induction of lateral root formation and root hair initiation in intact plants and stimulation of root and shoot development in treated cell calluses. HS enhance nutrient use efficiency, aiding assimilation of both macro and microelements and promoting plant growth by the induction of carbon, nitrogen, and secondary metabolism. The review aims are to: (1) shed light on the mechanism by which plants "talk" with soil through humic substances, (2) elucidate the plant responses to the stimulatory effects of HS, the regulatory circuits that allow plants to cope with humus, and the feedback between plant community structures, and (3) show (in light of recent debate about the alkaline extraction of soil humic substances) the plant capability to acquire biologically active substances from soil. It will be shown that plants modify soils, creating and maintaining favorable habitats for growth and survival. Therefore, organic substances exuded by roots are not a wasteful loss of carbon and energy. They represent an evolved strategy by which plants "talk" to the soil. The mobilization of bioactive organic/humic substances from bulk soil or bulk humus is critical to plant and soil health.

Keywords: auxin; biological activity; IAA; ion uptake; plant metabolism; root exudates; root morphology

Journal of Plant Nutrition and Soil Science

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Mini review: Fruit residues as plant biostimulants for bio-based product recovery

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Abstract

The request of natural products has augmented in the last years due to the increase in intolerance and allergy reactions showed by humans versus pesticides and certain chemical compounds used in agriculture. In response to this demand, innovative methods and new natural matrices have been exploited to obtain products able to increase plant nutrients use efficiency. In this context, agro-industrial residues contain bioactive molecules, including antioxidants and phenols, which may be used by farmers to improve crop productivity. Phenols are ubiquitous in plants and are essential components of the human diet by virtue of their antioxidant properties. They may also act as positive growth regulators by modifying the root architecture and, consequently, the uptake of macronutrients, potassium especially. In order to understand their effects on the plant metabolic pathways, agro-industrial residues were supplied to maize plants and the activity of specific enzymes was evaluated. In this review, developments and improved understanding on fruit residues on primary and secondary plants metabolism are discussed.

Keywords: Antioxidants; Elicitors; Phenols; Phenylalanine ammonia lyase (PAL); *Zea mays*

AIMS Agriculture and Food

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Animal science

Aggressiveness in group-housed rabbit does: Influence of group size and pen characteristics

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Abstract

The aim of this work was to study how the group size and the number of doorways in a pen may influence the aggressive interactions throughout the reproductive cycle among does kept in a part-time group housing system. Thirty-two crossbred multiparous pregnant rabbit does were housed in individual modules (0.5 m^2) that were connected to form collective pens with two (P2) or four (P4) does (8 and 4 replications, respectively) by using one (D1) or two (D2) doorways. The females were maintained in stable groups from the start of the trial, 8 d before kindling (-8 d), until 2 d before kindling and from 18 d after kindling (+18 d) until weaning (31 d). The aggressive interactions were video recorded through 24 consecutive hours at -8 d and +18 d and at 21 d and 30 d after kindling. Aggressive behaviour at 21 d and 30 d after kindling was not analysed due to its scarce (total interactions per doe in 24 h: 0.02 events) and null occurrences, respectively. Then, data of the first hour after grouping at -8 d and +18 d were analysed by Bayesian inference, and the posterior distributions of the differences between group size, number of doorways and observation day were estimated. Does in P4 pens showed a higher frequency of boxing (1.63 vs. 0.50 events per doe) and chasing (1.00 vs. 0.28) than those in P2 pens (probability of relevance, Prob_R = 0.87). Does in D2 pens showed a higher frequency of attacking (2.00 vs. 0.46 events per doe), chasing (0.83 vs. 0.21), and mount attempts (0.38 vs. 0.08) than those in D1 pens (Prob_R 0.80–0.83). Aggressive interactions were higher at the first group formation (-8 d) than at regrouping (at +18 d) (10.5 vs. 6.25 events per doe; Prob_R = 0.69). In conclusion, aggression among does was affected by group size and pen characteristics and decreased throughout the reproductive cycle. Nevertheless, studies of more reproductive cycles and collective pens will be necessary to confirm the present results.

Keywords: Bayesian inference; Behaviour; Collective housing; Reproducing rabbit does

Applied Animal Behaviour Science

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Aging and veterinary care of cats, dogs, and horses through the records of three university veterinary hospitals

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Abstract

The present article examines over 63,000 medical records belonging to the Veterinary Hospitals of the Universities of Bologna, Torino, and Padova, all in Northern Italy, and relative to dogs (approximately 50,000), cats (approximately 12,000), and companion horses (slightly less than 1,000). The animals of the three species were divided into age classes and categorized per sex into males, females, and neutered individuals. The mean age at visit and the effects of age classes and category (analyzed *via* ANOVA) are presented and discussed. The data indicate that many animals are presented to the hospitals either in the early phases of their life (presumably for vaccination and, in cats and dogs, gonadectomy) or in the advanced age (over 10 years in dogs, over 15 years in cats, and over 17 years in horses). The records of very old individuals of the three species are also reported. On the whole, the results suggest that a growing population of mature to old domestic carnivores or companion horses reaches ages that were considered exceptional only a few years ago. The data also testify an evolution in the animal-owner relationship and a renewed respect for the value of life in companion domestic mammals.

Keywords: Aging; Animal gerontology; Animal hospital; Animal life span; Cat; Dog; Horse

Frontiers in Veterinary Science

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Associations between pathogen-specific cases of subclinical mastitis and milk yield, quality, protein composition, and cheese-making traits in dairy cows

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Abstract

The aim of this study was to investigate associations between pathogen-specific cases of subclinical mastitis and milk yield, quality, protein composition, and cheese-making traits. Forty-one multibreed herds were selected for the study, and composite milk samples were collected from 1,508 cows belonging to 3 specialized dairy breeds (Holstein Friesian, Brown Swiss, and Jersey) and 3 dual-purpose breeds of Alpine origin (Simmental, Rendena, and Grey Alpine). Milk composition [i.e., fat, protein, casein, lactose, pH, urea, and somatic cell count (SCC)] was analyzed, and separation of protein fractions was performed by reversed-phase high performance liquid chromatography. Eleven coagulation traits were measured: 5 traditional milk coagulation properties [time from rennet addition to milk gelation (RCT, min), curd-firming rate as the time to a curd firmness (CF) of 20 mm (k_{20}, min), and CF at 30, 45, and 60 min from rennet addition (a_{30}, a_{45}, and a_{60}, mm)], and 6 new curd firming and syneresis traits [potential asymptotical CF at an infinite time (CF_P, mm), curd-firming instant rate constant (k_{CF}, % x min^{-1}), curd syneresis instant rate constant (k_{SR}, % x min^{-1}), modeled RCT (RCT_{eq}, min), maximum CF value (CF_{max}, mm), and time at CF_{max} (t_{max}, min)]. We also measured 3 cheese yield traits, expressing the weights of total fresh curd ($\%CY_{CURD}$), dry matter ($\%CY_{SOLIDS}$), and water ($\%CY_{WATER}$) in the curd as percentages of the weight of the processed milk, and 4 nutrient recovery traits ($REC_{PROTEIN}$, REC_{FAT}, REC_{SOLIDS}, and REC_{ENERGY}), representing the percentage ratio between each nutrient in the curd and milk. Milk samples with SCC > 100,000 cells/mL were subjected to bacteriological examination. All samples were divided into 7 clusters of udder health (UH) status: healthy (cows with milk SCC < 100,000 cells/mL and uncultured); culture-negative samples with low, medium, or high SCC; and culture-positive samples divided into contagious, environmental, and opportunistic intramammary infection (IMI). Data were analyzed using a linear mixed model. Significant variations in the casein to protein ratio and lactose content were observed in all culture-positive samples and in culture-negative samples with medium to high SCC compared to normal milk. No differences were observed among contagious, environmental, and opportunistic pathogens, suggesting an effect of inflammation rather than infection. The greatest impairment in milk quantity and composition, clotting ability, and cheese production was observed in the 2 UH status groups with the highest milk SCC (i.e., contagious IMI and culture-negative samples with high SCC), revealing a discrepancy between the bacteriological results and inflammatory status, and thus confirming the importance of SCC as an indicator of udder health and milk quality.

Keywords: Cheese yield; Coagulation properties; Intramammary infection; Milk composition; Subclinical mastitis

Journal of Dairy Science

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Body traits, carcass characteristics and price of cull cows as affected by farm type, breed, age and calving to culling interval

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Abstract

Beef production from cull cows is an additional source of income for dairy farms and greatly contributes to red meat production, but the sources of variation of live animal characteristics and the carcass traits of cull cows have rarely been examined. This study investigated the effects of the farm type, breed, age at slaughter (AGE) and calving to culling interval (Calv_Cull) on the body traits and carcass characteristics of dairy and dual-purpose cull cows. Data from 555 cull cows from 182 herds belonging to five farm types, characterised by a combination of housing and feeding systems, were recorded and analysed. Dairy breeds, such as Holstein Friesian and Brown Swiss, and dual-purpose breeds (Simmental, Rendena) were included in the trait assessments. The day before slaughter, the cows were weighed and scored for body condition (BCS) and fleshiness, and then, their heart girth and wither height were measured. At the slaughterhouse, the carcass weight (CW), dressing percentage (DP), carcass conformation and fatness scores, carcass price per kg and carcass total value were obtained. On average, the cows were slaughtered at nearly 71±27 months of age, 285±187 days after the last calving; 615±95 kg BW; and provided a 257±51 kg CW. Nearly 50% of the cows fell within the BCS range of 2.75 to 3.50, and the carcasses were mostly graded in the lowest class of conformation and fatness scores. Cull cows from free-stall farms had a higher DP, carcass conformation score and price than those from traditional tie-stall farms. The breed influenced the AGE, live animal characteristics and carcass traits. Cows from dairy breeds were younger at slaughter, had a lower BCS and fleshiness, and greater body measurements, but a lower DP and carcass price than those from dual-purpose breeds, although differences between the breeds were found within both groups. The age of the cows at slaughter influenced the Calv_Cull and increased the BW, body measurements and CW, but not the fleshiness and fatness appreciation (both *in vivo* and *postmortem*) or carcass price. The increasing Calv_Cull improved the BW, BCS, fleshiness, CW and carcass conformation and fatness. In conclusion, the decision to cull dairy cows should also take into account the factors that affect their carcass value in regards to improving the carcass price of cows.

Keywords: Age at culling; Carcass traits; Cull cows; Dairy breeds; Farm systems

Animal

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Breed of cow and herd productivity affect milk composition and modeling of coagulation, curd firming, and syneresis

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Abstract

Milk coagulation properties (MCP) have been widely investigated in the past using milk collected from different cattle breeds and herds. However, to our knowledge, no previous studies have assessed MCP in individual milk samples from several multi-breed herds characterized by either high or low milk productivity, thereby allowing the effects of herd and cow breed to be evaluated independently. Multi-breed herds (n = 41) were classified into 2 categories based on milk productivity (high vs. low), defined according to the average milk net energy yielded daily by lactating cows. Milk samples were taken from 1,508 cows of 6 different breeds: 3 specialized dairy (Holstein-Friesian, Brown Swiss, Jersey) and 3 dual-purpose (Simmental, Rendena, Alpine Grey) breeds, and analyzed in duplicate (3,016 tests) using 2 lactodynamographs to obtain 240 curd firming (CF) measurements over 60 min (1 every 15 s) for each duplicate. The 5 traditional single-point MCP (RCT, k_{20}, a_{30}, a_{45}, and a_{60}) were yielded directly by the instrument from the available CF measures. All 240 CF measures of each replicate were also used to estimate 4 individual equation parameters: RCT estimated according to curd firm change over time modeling (RCT_{eq}), asymptotic potential curd firmness (CF_P), curd firming instant rate constant (k_{CF}), and syneresis instant rate constant (k_{SR}) and 2 derived traits: maximum curd firmness achieved within 45 min (CF_{max}) and time at achievement of CF_{max} (t_{max}) by curvilinear regression using a nonlinear procedure. Results showed that the effect of herd-date on traditional and modeled MCP was modest, ranging from 6.1% of total variance for k_{20} to 10.7% for RCT, whereas individual animal variance was the highest, ranging from 32.0% for t_{max} to 82.5% for RCT_{eq}. The repeatability of MCP was high (>80%) for all traits except those associated with the last part of the lactodynamographic curve (i.e., a_{60}, k_{SR}, k_{CF}, and t_{max}: 57 to 71%). Reproducibility, taking into account the effect of instrument, was equal to or slightly lower than repeatability. Milk samples collected in farms characterized by high productivity exhibited delayed coagulation (RCT_{eq}: 18.6 vs. 16.3 min) but greater potential curd firmness (CF_P: 76.8 vs. 71.9 mm) compared with milk samples collected from low-productivity herds. Parity and days in milk influenced almost all MCP. Large differences in all MCP traits were observed among breeds, both between specialized and dual-purpose breeds and within these 2 groups of breeds, even after adjusting for milk quality and yield. Milk quality and MCP of samples from Jersey cows, and coagulation time of samples from Rendena cows were better than in milk from Holstein-Friesian cows, and intermediate results were found with the other breeds of Alpine origin. The results of this study, taking into account the intrinsic limitation of this technique, show that the effects of breed on traditional and modeled MCP are much greater than the effects of herd productivity class, parity, and DIM. Moreover, the variance in individual animals is much greater than the variance in individual herds within herd productivity class. It seems that improvement in MCP depends more on genetics (e.g., breed, selection) than on environmental and management factors.

Keywords: Breed; Curd firming; Herd productivity; Milk coagulation; Syneresis

Journal of Dairy Science

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Comparison between automatic and conventional milking systems for milk coagulation properties and fatty acid composition in commercial dairy herds

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Abstract

The aim of this study was to investigate the effect of milking dairy cows using conventional milking parlour (CMP) and automatic milking system (AMS) on milk coagulation properties and fatty acid (FA) composition. Milk coagulation traits were rennet coagulation time, curd-firming time and curd firmness. Data consisted of 10,476 individual milk samples collected from 918 Holstein-Friesian cows in 8 herds: four herds milked cows using a CMP and four using an AMS. A linear mixed model was used to investigate sources of variation for milk yield, traditional quality traits, coagulation properties and FA profile. On average, cows from AMS produced 1 kg/d more milk than cows from CMP. Rennet coagulation time was slightly longer (+1.2 min) and free FA content was greater (+0.16 mmol/100 g milk fat) in milk from cows milked in AMS than CMP. Overall, the milking system did not affect the FA concentration of milk. Results of the present study suggest that AMS can be adopted without detrimental effects on milk features.

Keywords: Fatty acid; Mid-infrared spectroscopy; Milk acidity; Milk technological trait; Milking system

Italian Journal of Animal Science

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Cow and environmental factors associated with protein fractions and free amino acids predicted using mid-infrared spectroscopy in bovine milk

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Abstract

The objective of the present study was to identify the factors associated with both the protein composition and free amino acid (FAA) composition of bovine milk predicted using mid-infrared spectroscopy. Milk samples were available from 7 research herds and 69 commercial herds. The spectral data from the research herds comprised 94,286 separate morning and evening milk samples; the spectral data from the commercial herds comprised 40,260 milk samples representing a composite sample of both the morning and evening milkings. Mid-infrared spectroscopy prediction models developed in a previous study were applied to all spectra. Factors associated with the predicted protein and FAA composition were quantified using linear mixed models. Factors considered in the model included the fixed effects of calendar month of the test, milking time (i.e., morning, evening, or both combined), parity (1, 2, 3, 4, 5, and ≥6), stage of lactation, the interaction between parity and stage of lactation, breed proportion of the cow (Friesian, Jersey, Norwegian Red, Montbéliarde, and other), and both the general heterosis and recombination coefficients of the cow. Contemporary group as well as both within- and across-lactation permanent environmental effects were included in all models as random effects. Total proteins (i.e., total casein, CN; total whey; and total β-lactoglobulin) and protein fractions (with the exception of α-lactalbumin) decreased postcalving until 36 to 65 days in milk and increased thereafter. After adjusting the statistical model for differences in crude protein content and milk yield separately, irrespective of stage of lactation, younger animals produced more total proteins (i.e., total CN, total whey, and total β-lactoglobulin) as well as more total FAA, Glu, and Asp than their older contemporaries. The concentration of all protein fractions (except β-CN) in milk was greatest in the evening milk, even after adjusting for differences in the crude protein content of the milk. Relative to a purebred Holstein cow, Jersey cows, on average, produced a greater concentration of all CN fractions but less total FAA, Glu, Gly, Asp, and Val in milk. Relative to their respective purebred parental average, first-cross cows produced more total CN and more β-CN. Results from the present study indicate that many cow-level factors, as well as other factors, are associated with protein composition and FAA composition of bovine milk.

Keywords: Free amino acid composition; Mid-infrared spectroscopy; Protein composition

Journal of Dairy Science

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Detailed fatty acid profile of milk, cheese, ricotta and by products, from cows grazing summer highland pastures

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Abstract

In this research two-dimensional GC was used to analyse, for the first time, the detailed fatty acid (FA) profiles of 11 dairy matrices: raw milk (evening whole, evening partially skimmed, morning whole, and vat milk), cream, fresh cheese, whey, ricotta, scotta, 6- and 12-month-ripened cheeses, obtained across artisanal cheese- and ricotta-making trials carried out during the summer period while cows were on highland pastures. Samples were collected during 7 cheese- and ricotta-making procedures carried out at 2-week intervals from bulk milk to study possible differences in the transfer and modification of FA. Compared with morning milk, evening milk had fewer de novo synthetised FA. The detailed FA profile of partially skimmed milk differed little from that of evening whole milk before skimming, but the cream obtained differed from partially skimmed milk and from fresh cheese in about half the FA, due mainly to higher contents of all de novo FA, and lower contents of *n*-3 and *n*-6 FA. Fresh cheese and whey had similar FA profiles. The ricotta manufacturing process affected the partition of FA between ricotta and scotta, the FA profile of the latter differing in terms of groups and individual FA from the former, whereas ricotta and fresh cheese had similar composition of FA. In general, there was an increase in medium-chain saturated FA, and a decrease in many polyunsaturated FA during the first 6 months of ripening, but not during the second 6 months. Two-dimensional GC yielded a very detailed and informative FA profile on all the 11 dairy products and by-products analysed.

Keywords: Cows' milk; Dairy product; Fatty acid; Pasture; Two-dimensional gas chromatography

Journal of Dairy Research

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Effect of age on the occurrence of muscle fiber degeneration associated with myopathies in broiler chickens submitted to feed restriction

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Abstract

To evaluate muscle fiber degeneration (MFD) associated with white striping and wooden breast, pectoralis major of 192 broilers differing for genotype (standard vs. high breast yield), gender, and feeding regime (ad libitum vs. restricted rate 80% from 13 to 21 d of age) were sampled at 14, 21, 28, 35, and 46 d of age for histological analyses by hematoxylin and eosin (H&E) staining to evaluate tissue morphology, Masson's trichrome to identify collagen presence, and Oil red and Nile blue for lipid presence. Microvessels (diameter ≤15 μm), nuclei positive to anti-cleaved lamin A and monoclonal proliferating cell nuclear antigen (PCNA) antisera were counted to assess apoptotic and regenerative processes, respectively. Significant differences were found according to feeding system, age, and their interactions. The frequency of chickens with MFD was higher with ad libitum than restricted feeding (75.0% vs. 62.5%; $P = 0.01$) and increased with age (18.8%, 28.1%, 75.1%, 96.9%, and 96.9% at 14, 21, 28, 35, and 46 d). However, at 14 d a similar frequency (18.8%) was found in all broilers; at 21 d, MFD occurred more in broilers fed ad libitum than in those under restriction (50.0% vs. 6.3%; $P < 0.01$); at 28 d differences were reduced (87.5% vs. 62.5%; $P = 0.10$) to disappear by 35 (100% and 93.8%) and 46 d (96.9% and 96.9%). The number of microvessels decreased with age (20.7 to 9.46; $P < 0.001$) and the number of nuclei positive to the anti-cleaved lamin A antibody increased. At histology, MFD at 46 d corresponded to loss of typical cross striations, massive necrotic process, degenerating fibers surrounded by inflammatory cells, scattered fibers in an abundant collagen-rich connective tissue, numerous adipose cells; necrotic fibers showed a high percentage of apoptotic nuclei, and regenerating fibers appeared positive to anti-PCNA antibody. In conclusion, MFD soon occurred after 2 wk of growth and increased dramatically within 28 d. Early feed restriction reduced MFD as long as animals were restricted, but no residual effect was recorded after re-alimentation.

Keywords: Apoptosis; Gender; Genotype; Histology; Myopathies

Poultry Science

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Effect of feed restriction and feeding plans on performance, slaughter traits and body composition of growing rabbits

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Abstract

Two feeding systems (L, *ad libitum vs.* R, feed restriction) were combined with 3 feeding plans (MM, MH, HH) to evaluate the effects on performance, slaughter results, body composition and nitrogen balance of 300 commercial crossbred rabbits kept individually from weaning to slaughter (34-70 d of age). The R rabbits were fed from 80% (first days on trial) to 100% (end of 3rd wk) of *ad libitum* intake, whereafter R rabbits had free access to feed. The 3 feeding plans were: MM plan, M diet with moderate digestible energy (DE) content, 10.6 MJ/kg, throughout the trial; HH plan, H diet with high DE content, 11.1 MJ/kg, throughout the trial; MH plan, M diet for the first 3 wk and H diet for the last 2 wk. Feed restriction did not affect nutrient digestibility, growth rate on the whole trial and slaughter results, but improved feed conversion (2.96 *vs.* 2.89 in L and R rabbits, respectively; $P<0.01$) and reduced N excretion (2.16 *vs.* 2.07 g excreted N/d, in L and R rabbits; $P<0.05$). At the end of the first period (55 d), R rabbits showed lower empty body protein, lipid, and gross energy gains than L rabbits, but differences disappeared within the end of the trial. The HH plan improved feed conversion (2.97 *vs.* 2.89 for MM *vs.* HH; $P<0.05$), but increased excreted N (2.03 *vs.* 2.17 g/d; $P<0.001$) in comparison with the MM plan due to the higher digestible protein/DE ratio of H diet, whereas the MH plan showed intermediate results. In conclusion, a moderate feed restriction during post weaning improved feed conversion and reduced N excretion without negative effects on growth or slaughter results. Moreover, N excretion was confirmed to depend largely on dietary nitrogen content.

Keywords: Body composition; Feed restriction; Feeding plans; Growth performance; Nitrogen excretion; Rabbit

World Rabbit Science

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Effect of genotype, gender, and feed restriction on slaughter results and meat quality of broiler chickens

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Abstract

Slaughter results and meat quality were evaluated in 768 broilers according to genotype (standard breast yield vs. high breast yield), gender, and feeding systems (*ad libitum* vs. feed restriction from 13 to 21 d of age). Standard-yield chickens had higher carcass weights (2358 g vs. 2319 g; $P < 0.001$) and hind legs proportion (31.1% vs. 30.6%; $P < 0.01$), and lower dressing out percentage (73.6% vs. 74.0%; $P < 0.01$) compared to high-yield birds, besides lower meat L* index (45.3 vs. 46.2; $P < 0.05$), higher final pH (5.89 vs. 5.85; $P < 0.05$) and thawing losses (10.5% vs. 9.43%; $P < 0.05$). Males showed higher carcass weight (+24%), dressing percentage (+0.7%), and hind leg yield (+4%) ($P < 0.001$) than females. Restricted birds had lower carcass weight (–2%; $P < 0.001$) and dressing percentage (-0.3%) ($P < 0.05$) than those always fed *ad libitum*. As what concerns meat quality, gender and feeding system affected only meat final pH, lower in *ad libitum* group than in restricted one and in females than males. In conclusions, slaughter results and carcass traits changed especially with genotype and gender, coherently with slaughter weight whereas meat quality was mostly affected by genotype.

Keywords: Broiler chickens; Feeding system; Gender; Genotype; Meat quality

Agriculturae Conspectus Scientificus

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Effect of growth rate on live performance, carcass and green thigh traits of finishing Italian heavy pigs

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Abstract

This study aimed at investigating the effects of growth rate (GR) on live performance, carcass and dressed green ham (DRHAM) traits of finishing heavy pigs managed in accordance with the regulations governing the production of Protected Denomination of Origin (PDO) dry-cured hams. Data were obtained from 233 crossbred pigs restrictively fed from 90 to 165 kg BW. Individual BW, daily feed intake, and weights of carcass and main cuts were recorded. Thighs were measured for subcutaneous fat thickness, analysed for fatty acid composition of subcutaneous fat, and dry-cured hams were weighed. Records were classified according to GR quartile, calculated using the residuals of a statistical model that included the effects of pen, sex and diet. Data were analysed using the same model with the addition of the effect of GR quartile. Average GR ranged from 578 in the first quartile to 748 g/d in the fourth. Final BW and weights of carcass, DRHAM and dry-cured ham increased as the GR quartile increased ($p < .01$). An increase in GR improved feed efficiency linearly ($p < .001$) and tended to increase the thickness of subcutaneous fat of DRHAM, whereas seasoning losses decreased linearly with increasing average GR. In conclusion, targeting the GR of finishing pigs at a minimum of 750 g/d and consequently increasing final BW to around 175–180 kg may be a way to improve feed efficiency and some quality traits of DRHAM.

Keywords: Carcass traits; Growth rate; Heavy pigs; Raw ham properties

Italian Journal of Animal Science

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Effect of THI on milk coagulation properties of Holstein-Friesian dairy cattle

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Abstract

The objective of this study was to evaluate the effect of temperature-humidity index (THI) on the milk coagulation properties of Holstein-Friesian dairy cattle from northeast part of Italy. A total of 592 individual milk samples from six dairy herds were evaluated. The milk coagulation properties traits analysed were milk rennet coagulation time and curd firmness, as well as the fat, protein, and casein contents, pH, milk aptitude to coagulate (IAC), and the somatic cell count. The THI was determined during the periods of sample collection. The THI results showed that values of up to 75 did not significantly change the IAC values; however, when the THI values were above 75, the IAC decreased significantly. The control of THI can be used to guarantee appropriate milk coagulation properties.

Keywords: Clotting; Curd firmness; Dairy cow; Heat stress

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Effects of ketosis status defined by FTIR spectroscopy on milk quality traits of first-lactation cows

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Abstract

The aim of the present study was to investigate the effect of ketosis status on milk yield and quality traits of Holstein Friesian cows. Individual milk samples (n = 15,674) of first-lactation cows from 5 to 60 days in milk (DIM) were collected during the official monthly test-day milk recording scheme and analysed for milk quality traits using Fourier transform infrared (FTIR) spectroscopy. Also, beta-hydroxybutyrate (BHB) was predicted by FTIR spectroscopy and used to classify records as normal, suspect or ketotic. Data were analysed with a linear mixed model including ketosis status, DIM and their interaction as fixed effects, and cow, herd-test-day and residual as random effects. Overall, ketotic cows exhibited the worst performance in terms of milk yield and quality compared to suspect and normal cows across the first 60 DIM. Results suggest that elevated milk BHB concentrations have a strong negative effect on milk yield and quality traits in early lactation.

Keywords: BHB; Dairy cow; Ketosis; Milk quality

Agriculturae Conspectus Scientificus

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Effects of total replacement of corn silage with sorghum silage on milk yield, composition, and quality

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Abstract

Background: In the last years, difficulties occurring in corn cultivation (i.e., groundwater shortages, mycotoxin contamination) have been forcing dairy farmers to consider alternative silages. Some experiments conducted on lactating cows have proven that the total replacement of corn silage with sorghum silage did not reduce milk yield. However, this kind of substitution involves supplementing sorghum-based diets with grains, to compensate for the lower starch content of sorghum silage compared to corn silage. Change of silage type and inclusion of starch sources in the diet would influence rumen fermentations, with possible effects on milk composition (i.e., fatty acid profile) and coagulation properties. A worsening of milk coagulation properties would have a negative economic impact in Italy, where most of the milk produced is processed into cheese. This study was designed to compare milk composition and quality, with emphasis on fatty acid profile and coagulation properties, in dairy cows fed two diets based on corn or sorghum silage.

Results: The sorghum diet reduced milk yield ($P = 0.043$) but not 4% fat corrected milk ($P = 0.85$). Feeding sorghum silage did not influence milk contents of protein ($P = 0.07$) and lactose ($P = 0.65$), and increased fat content ($P = 0.024$). No differences emerged for milk concentrations of saturated ($P = 0.61$) and monounsaturated fatty acids ($P = 0.50$), whereas polyunsaturated fatty acids were lower ($P < 0.001$) for the sorghum diet. Concentrations of n-6 ($P < 0.001$) and n-3 fatty acids ($P = 0.017$) were lower in milk of cows fed the sorghum diet. Milk coagulation properties did not differ between the two diets, except the “a30” (the curd firmness, expressed in mm, 30 min after rennet addition), that was lower ($P = 0.042$) for the sorghum diet.

Conclusions: Feeding a forage sorghum silage, properly supplemented with corn meal, as total replacement of corn silage maintained milk composition and did not influence negatively milk coagulation properties, which have a great economic relevance for the Italian dairy industry. Thus, silages obtained from forage sorghums could have a potential as substitute of corn silages in dairy cow diets.

Keywords: Dairy cows; Forage sorghum silage; Mean particle size; Milk coagulation properties; Milk fatty acid profile

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Environmental footprint of the integrated France–Italy beef production system assessed through a multi-indicator approach

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Abstract

This study aims to evaluate the environmental footprint of the integrated France–Italy beef production system (extensive grassland-based suckler cow-calf farms in France with intensive cereal-based fattening farms in northeastern Italy) using a multi-indicator approach, which combines environmental impact categories computed with a cradle-to-farm gate Life Cycle Assessment, and food-related indicators based on the conversion of gross energy and protein of feedstuffs into raw boneless beef. The system boundaries were set from the calves' birth to their sale to the slaughterhouse, including the herd management, on- and off-farm feed production and materials used on the farms. One kilogram of body weight (BW) sold was used as the functional unit. The study involved 73 Charolais batches (i.e., a group of animals homogeneous for age, finishing period and fattening farm), kept at 14 Italian farms. Data from 40 farms originating from the Charolais Network database (INRA) were used to characterize the French farm types, which were matched to the fattening batches according to the results of a cluster analysis. The impact categories assessed were as follows (mean ± SD per kg BW): global warming potential (GWP, 13.0 ± 0.7 kg CO_2-eq, reduced to 9.9 ± 0.7 kg CO_2-eq when considering the carbon sequestration due to French suckler cow-calf system permanent grassland), acidification potential (AP, 193 ± 13 g SO_2-eq), eutrophication potential (EP, 57 ± 4 g PO_4-eq), cumulative energy demand (CED, 36 ± 5 MJ), and land occupation (LO, 18.7 ± 0.8 m^2/year). The on-farm impacts outweighed those of the off-farm activities, except in the case of CED. On average, 41 MJ and 16.7 kg of dietary feed gross energy and protein were required to provide 1 MJ or 1 kg of protein of raw boneless beef, respectively, but nearly 85% and 80%, respectively, were derived from feedstuffs not suitable for human consumption. Emission-related (GWP, AP, EP) and resource utilization categories (CED, LO) were positively correlated. Food-related indicators showed positive correlations with emission-related indicators when the overall feedstuffs of the diet were considered but negative correlations when only the potentially human-edible portions of the beef diets were considered. In conclusion, the integration of the pasture-based France suckler cow-calf system with the cereal-based Italian fattening farms allows for the exploitation of the resources available, increasing the share of non-human-edible feedstuffs while maintaining good livestock productive efficiency. Combining indicators of impact categories with indicators of feed net supply may improve the assessment of the environmental footprint of livestock systems.

Keywords: Conversion efficiency; Environmental impact; Life Cycle Assessment; Livestock farming system; Multi-indicator approach

Agricultural Systems

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Environmental life cycle assessment of Italian mozzarella cheese: Hotspots and improvement opportunities

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Abstract

The present study investigated a cradle-to-grave life cycle assessment to estimate the environmental impacts associated with Italian mozzarella cheese consumption. The differences between mozzarella produced from raw milk and mozzarella produced from curd were studied, and differences in manufacturing processes have been emphasized in order to provide guidance for targeted improvements at this phase. Specifically, the third-largest Italian mozzarella producer was surveyed to collect site-specific manufacturing data. The Ecoinvent v3.2 database was used for secondary data, whereas SimaPro 8.1 was the modeling software. The inventory included inputs from farm activities to end of life disposal of wasted mozzarella and packaging. Additionally, plant-specific information was used to assign major inputs, such as electricity, natural gas, packaging, and chemicals to specific products; however, where disaggregated information was not provided, milk solids allocation was applied. Notably, loss of milk solids was accounted during the manufacture, moreover mozzarella waste and transport were considered during distribution, retail, and consumption phases. Feed production and animal emissions were the main drivers of raw milk production. Electricity and natural gas usage, packaging (cardboard and plastic), transport, wastewater treatment, and refrigerant loss affected the emissions from a farm gate-to-dairy plant gate perspective. Post-dairy plant gate effects were mainly determined by electricity usage for storage of mozzarella, transport of mozzarella, and waste treatment. The average emissions were 6.66 kg of CO_2 equivalents and 45.1 MJ of cumulative energy demand/kg of consumed mozzarella produced directly from raw milk, whereas mozzarella from purchased curd had larger emissions than mozzarella from raw milk due to added transport of curd from specialty manufacturing plants, as well as electricity usage from additional processes at the mozzarella plant that are required to process the curd into mozzarella. Normalization points to ecotoxicity as the impact category most significantly influenced by mozzarella consumption. From a farm gate-to-grave perspective, ecotoxicity and freshwater and marine eutrophication are the first and second largest contributors of mozzarella consumption to average European effects, respectively. To increase environmental sustainability, an improvement of efficiency for energy and packaging usage and transport activities is recommended in the post-farm gate mozzarella supply chain.

Keywords: Carbon footprint; Climate change; Dairy industry; Energy use

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Evaluation of behaviour in stabled draught horse foals fed diets with two protein levels

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Abstract

The present work is aimed at evaluating the behaviour of Italian Heavy Draught Horse (IHDH) foals reared in semi-covered stables and fed two isoenergetic total mixed rations with different dietary protein levels (13.2% and 10.6% of CP on dry matter). The study was prompted by the restrictions for nitrate emissions in farms of the European Nitrate Directive. One suggested solution is to reduce dietary protein while maintaining normal performance and welfare, but there is a lack of literature in studies of horses. The behaviours of 20 foals of 437±60 kg of BW, aged 379±37 days and stabled in four pens by sex (S) and diet (D) were video recorded and analysed to build a suitable ethogram including 18 behaviours in six categories: ingestion, resting, maintenance, movement, social activities, other. The percentage of the daily time spent in each behavioural category and single behaviours was analysed via a single traits GLM including S, D and their interaction. Daily activity was consistent with existing literature: foals spent about 33% of the day in ingestion activities and 41% in resting, whereas social interactions constituted 8% of the time and individual maintenance <2%. Concerning diet, foals fed high protein spent more time in movement (19.62±0.73% of day *v.* 10.45±0.73% in low-protein (LP) foals; $P \leq 0.001$), whereas the LP group increased resting (43.42±1.12% *v.* 38.02±1.12%; $P \leq 0.001$). No stereotypies were found, and daily activity followed the typical values for draught breeds for foals in both dietary groups, a result that suggests the maintenance of well-being after dietary protein reduction. This result, together with the findings of a companion study showing no changes in growth performances of foals, showed that a reduction of CP in foal diet is reconcilable with the maintenance of performance and welfare.

Keywords: Behaviour; Dietary protein; Draught horse; Foals; Video recording

Animal

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Factors affecting variations in the detailed fatty acid profile of Mediterranean buffalo milk determined by 2-dimensional gas chromatography

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Abstract

Buffalo milk is the world's second most widely produced milk, and increasing attention is being paid to its composition, particularly the fatty acid profile. The objectives of the present study were (1) to characterize the fatty acid composition of Mediterranean buffalo milk, and (2) to investigate potential sources of variation in the buffalo milk fatty acid profile. We determined the profile of 69 fatty acid traits in 272 individual samples of Mediterranean buffalo milk using gas chromatography. In total, 51 individual fatty acids were identified: 24 saturated fatty acids, 13 monounsaturated fatty acids, and 14 polyunsaturated fatty acids. The major individual fatty acids in buffalo milk were in the order 16:0, 18:1 *cis*-9, 14:0, and 18:0. Saturated fatty acids were the predominant fraction in buffalo milk fat (70.49%); monounsaturated and polyunsaturated fatty acids were at 25.95 and 3.54%, respectively. Adopting a classification based on carbon-chain length, we found that medium-chain fatty acids (11–16 carbons) represented the greater part (53.7%) of the fatty acid fraction of buffalo milk, whereas long-chain fatty acids (17–24 carbons) and short-chain fatty acids (4–10 carbons) accounted for 32.73 and 9.72%, respectively. The n-3 and n-6 fatty acids were 0.46 and 1.77%, respectively. The main conjugated linoleic acid, rumenic acid, represented 0.45% of total milk fatty acids. Herd/test date and stage of lactation were confirmed as important sources of variation in the fatty acid profile of buffalo milk. The percentages of short-chain and medium-chain fatty acids in buffalo milk increased in early lactation (+0.6 and +3.5%, respectively), whereas long-chain fatty acids decreased (-4.2%). The only exception to this pattern was butyric acid, which linearly decreased from the beginning of lactation, confirmation that its synthesis is independent of malonyl-CoA. These results seem to suggest that in early lactation the mobilization of energy reserves may have less influence on the fatty acid profile of buffalo milk than that of cow milk, probably due to a shorter and less severe period of negative energy balance. Parity affected the profiles of a few traits and had the most significant effects on branched-chain fatty acids. This work provided a detailed overview of the fatty acid profile in buffalo milk including also those fatty acids present in small concentrations, which may have beneficial effects for human health. Our results contributed also to increase the knowledge about the effects of some of the major factors affecting buffalo production traits and fatty acid concentrations in milk, and consequently its technological and nutritional properties.

Keywords: 2-dimensional gas chromatography; Mediterranean buffalo; Milk fatty acid; Sources of variation

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Factors associated with milk processing characteristics predicted by mid-infrared spectroscopy in a large database of dairy cows

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Abstract

Despite milk processing characteristics being important quality traits, little is known about the factors underlying their variability, due primarily to the resources required to measure these characteristics in a sufficiently large population. Cow milk coagulation properties (rennet coagulation time, curd-firming time, curd firmness 30 and 60 min after rennet addition), heat coagulation time, casein micelle size, and pH were generated from available mid-infrared spectroscopy prediction models. The prediction models were applied to 136,807 spectra collected from 9,824 Irish dairy cows from research and commercial herds. Sources of variation were investigated using linear mixed models that included the fixed effects of calendar month of test; milking time in the day; linear regressions on the proportion of Friesian, Jersey, Montbéliarde, Norwegian Red, and "other" breeds in the cow; coefficients of heterosis and of recombination loss; parity; stage of lactation; and the 2-way interaction parity × stage of lactation. Within- and across-parity cow effects, contemporary group, and a residual term were also included as random effects in the model. Supplementary analyses considered the inclusion of either test-day milk yield or milk protein concentration as fixed-effects covariates in the multiple regression models. Milk coagulation properties were most favorable (i.e., short rennet coagulation time and strong curd firmness) for cheese manufacturing in early lactation, concurrent with the lowest values of both pH and casein micelle size. Milk coagulation properties and pH deteriorated in mid lactation but improved toward the end of lactation. In direct contrast, heat coagulation time was more favorable in mid lactation and less suitable (i.e., shorter) for high temperature treatments in both early and late lactation. Relative to multiparous cows, primiparous cows, on average, yielded milk with shorter rennet coagulation time and longer heat coagulation time. Milk from the evening milking session had shorter rennet coagulation time and greater curd firmness, as well as lower heat coagulation time and lower pH compared with milk from the morning session. Jersey cows, on average, yielded milk more suitable for cheese production rather than for milk powder production. When protein concentration was included in the model, the improvement of milk coagulation properties toward the end of lactation was no longer apparent. Results from the present study may aid in decision-making for milk manufacturing, especially in countries characterized by a seasonal supply of fresh milk.

Keywords: Lactation; Milk processability; Milk quality; Seasonal variation

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Fatty acid composition of lamb liver, muscle, and adipose tissues in response to rumen-protected conjugated linoleic acid (CLA) supplementation is tissue dependent

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Abstract

The tissue-specific response to rumen-protected conjugated linoleic acid supply (rpCLA) of liver, two muscles, and three adipose tissues of heavy lambs was studied. Twenty-four lambs, 8 months old, divided into 4 groups of 6, were fed ad libitum on a ration supplemented without or with a mixture of rpCLA. Silica and hydrogenated soybean oil was the rpCLA coating matrix. The lambs were slaughtered at 11 months of age. Tissues were collected and analyzed for their FA profiles. The dietary rpCLA supplement had no influence on carcass fatness nor on the fat content of the liver and tissues and had little influence on the FA profiles of these tissues. In the adipose tissues, rpCLA increased the proportions of saturated FAs, 18:0 and 18:2*t*10*c*12, and decreased the proportions of monounsaturated FAs in the adipose tissues. In muscles, the effects were the opposite. The results suggest that Δ9 desaturase activity is inhibited by the rpCLA mixture in adipose tissues to a greater extent than in the other tissues.

Keywords: Adipose tissues; Conjugated linoleic acid; Lamb; Liver; Muscles

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Methodological considerations for the use of faecal nitrogen to assess diet quality in ungulates: The Alpine ibex as a case study

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Abstract

Faecal indices are used to describe spatiotemporal patterns of diet quality in wild herbivores, and near infrared spectroscopy methods (NIRS) distinctively reduce costs and labour compared to conventional chemical analyses. In this study we compared the prediction accuracy of faecal nitrogen (N), ash and fibrous fractions of a laboratory instrument (NIRS) with that of a lightweight portable instrument (VisNIRS) using faecal samples of Alpine ibex (*Capra ibex*). We then compared how different indices based on faecal N and fibrous fractions were able to detect the expected temporal trend and difference between sexes in diet quality, and verified whether the presumably lower accuracy of NIRS and VisNIRS (compared to wet chemistry) influenced the ability of indices to detect such trends. The laboratory NIRS was more accurate than the portable VisNIRS, especially for fibrous fractions. Predicted data from both instruments clearly identified the temporal trend identified by chemically analysed data, but only NIRS identified the small difference between sexes. Expressing faecal N as a proportion of organic matter (OM) or neutral detergent fibre (NDF) improved the power of the index as compared to expressing it as a proportion of dry matter (DM), irrespective of the method used to estimate the data. Faecal NDF contents followed the patterns expected from the variation of faecal N, while faecal acid detergent fibre (ADF) and especially lignin (ADL) followed contradictory patterns, which might be due to a selection of different forage sources rather than to changing quality of a homogenous forage source. We conclude that expressing faecal N as a proportion of OM is advised with wild herbivores faeces, where ash content can be biased by accidental soil contamination or ingestion. Faecal fibrous fractions are useful to complement faecal N and to avoid simplified interpretations of the results. For this purpose, NIRS methods can be extremely useful to predict multiple indices on large numbers of samples. VisNIRS portable instruments might be unable to detect subtle biological patterns in small numbers of samples. However, developing procedures for portable instruments outside laboratory facilities might further improve practicability, cost effectiveness, and, through allowing on-field predictions on large numbers of samples, power of statistical testing of diet quality indices.

Keywords: Alpine ibex; Diet quality; Faecal fibre; Faecal nitrogen; NIRS

Ecological Indicators

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Predicting herbivore faecal nitrogen using a multispecies near-infrared reflectance spectroscopy calibration

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Abstract

Optimal management of free-ranging herbivores requires the accurate assessment of an animal's nutritional status. For this purpose 'near-infrared reflectance spectroscopy' (NIRS) is very useful, especially when nutritional assessment is done through faecal indicators such as faecal nitrogen (FN). In order to perform an NIRS calibration, the default protocol recommends starting by generating an initial equation based on at least 50-75 samples from the given species. Although this protocol optimises prediction accuracy, it limits the use of NIRS with rare or endangered species where sample sizes are often small. To overcome this limitation we tested a single NIRS equation (i.e., multispecies calibration) to predict FN in herbivores. Firstly, we used five herbivore species with highly contrasting digestive physiologies to build monospecies and multispecies calibrations, namely horse, sheep, Pyrenean chamois, red deer and European rabbit. Secondly, the equation accuracy was evaluated by two procedures using: (1) an external validation with samples from the same species, which were not used in the calibration process; and (2) samples from different ungulate species, specifically Alpine ibex, domestic goat, European mouflon, roe deer and cattle. The multispecies equation was highly accurate in terms of the coefficient of determination for calibration $R^2 = 0.98$, standard error of validation SECV = 0.10, standard error of external validation SEP = 0.12, ratio of performance to deviation RPD = 5.3, and range error of prediction RER = 28.4. The accuracy of the multispecies equation to predict other herbivore species was also satisfactory ($R^2 > 0.86$, SEP < 0.27, RPD > 2.6, and RER > 8.1). Lastly, the agreement between multi- and monospecies calibrations was also confirmed by the Bland-Altman method. In conclusion, our single multispecies equation can be used

as a reliable, cost-effective, easy and powerful analytical method to assess FN in a wide range of herbivore species

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Prediction and repeatability of milk coagulation properties and curd-firming modeling parameters of ovine milk using Fourier-transform infrared spectroscopy and Bayesian models

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Abstract

The aim of this study was to apply Bayesian models to the Fourier-transform infrared spectroscopy spectra of individual sheep milk samples to derive calibration equations to predict traditional and modeled milk coagulation properties (MCP), and to assess the repeatability of MCP measures and their predictions. Data consisted of 1,002 individual milk samples collected from Sarda ewes reared in 22 farms in the region of Sardinia (Italy) for which MCP and modeled curd-firming parameters were available. Two milk samples were taken from 87 ewes and analyzed with the aim of estimating repeatability, whereas a single sample was taken from the other 915 ewes. Therefore, a total of 1,089 analyses were performed. For each sample, 2 spectra in the infrared region 5,011 to 925 cm^{-1} were available and averaged before data analysis. BayesB models were used to calibrate equations for each of the traits. Prediction accuracy was estimated for each trait and model using 20 replicates of a training-testing validation procedure. The repeatability of MCP measures and their predictions were also compared. The correlations between measured and predicted traits, in the external validation, were always higher than 0.5 (0.88 for rennet coagulation time). We confirmed that the most important element for finding the prediction accuracy is the repeatability of the gold standard analyses used for building calibration equations. Repeatability measures of the predicted traits were generally high (≥95%), even for those traits with moderate analytical repeatability. Our results show that Bayesian models applied to Fourier-transform infrared spectra are powerful tools for cheap and rapid prediction of important traits in ovine milk and, compared with other methods, could help in the interpretation of results.

Keywords: Bayesian; Curd-firming modeling; Fourier-transform infrared spectroscopy; Milk coagulation properties; Ovine milk

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Short communication: Association between udder health status and blood serum proteins in dairy cows

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Abstract

The aim of this study was to investigate the association between udder health (UH) status and blood serum proteins (i.e., total protein, albumin, globulin, and albumin-to-globulin ratio) in dairy cows. Blood and milk samples were collected from 1,508 cows of 6 different breeds (Holstein Friesian, Brown Swiss, Jersey, Simmental, Rendena, and Alpine Grey) that were housed in 41 multibreed herds. Bacteriological analysis was performed on milk samples with somatic cell count (SCC) >100,000 cells/mL and bacteria identification was confirmed by multiplex-PCR assays. Milk samples were grouped into 7 clusters of UH status: healthy (cows with milk SCC <100,000 cells/mL and not cultured); culture-negative samples with low, medium, or high SCC; and culture-positive samples with contagious, environmental, and opportunistic intramammary infections. Data of blood serum proteins were analyzed using a linear mixed model that included the fixed effects of stage of lactation, parity, breed, herd productivity (high or low production) and UH status, and the random effect of herd-date within herd productivity. Culture-negative samples with high milk SCC, which were most likely undergoing a strong inflammatory response and whose pathogens could not be isolated because they were engulfed by macrophages or because they had already cleared, and milk samples infected by contagious and environmental bacteria were associated with greater globulin concentrations (and lower albumin-to-globulin ratio) in blood. Variation in blood serum proteins seems to be associated with inflammatory status rather than infection, as serum globulin significantly increased in UH status groups with the highest milk SCC and no differences were observed among intramammary infections pathogens. Blood serum proteins can be a mammary gland inflammation indicator, but cannot be used to differentiate among different UH status groups.

Keywords: Blood serum proteins; Dairy cattle; Intramammary infection; Subclinical mastitis

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The use of near infrared spectroscopy to predict faecal indigestible and digestible fibre fractions in lactating dairy cattle

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Abstract

The objective of this study was to investigate the ability of faecal near infrared spectroscopy (FNIRS) to predict undigested neutral detergent fibre at 240 h of fermentation (uNDF240) and other fibre fractions in lactating dairy cattle faeces. A total of 130 faecal samples (600 g) were collected directly from the rectum of dairy cows randomly selected across the lactating groups of 6 herds located in northern Italy and fed grass/alfalfa hay forage based total mixed ration. Reference values were matched with FNIRS spectra. Prediction equations were developed for each trait using external validation. Our results showed that the calculated uNDF240 (DM basis) to ADL ratio in faeces averaged 2.84, ranging from 1.58 to 4.10. The similar ratio of acid detergent fibre (ADF) and uNDF240 to NDF (66–67%) indicated that potentially digestible NDF in faeces is mainly represented by hemicelluloses, whereas uNDF240 is mainly composed of lignin and cellulose. The coefficient of determination of external validation (R^2_V) of uNDF240 was 0.59 when expressed as percentage of DM and 0.36 when expressed as percentage of NDF, and the corresponding ratio performance deviation of external validation (RPD) values in validation were 1.52 and 1.26, respectively. Values of R^2_V ranged from 0.54 to 0.63 for fibre fractions and RPD in validation ranged from 1.45 (ADL, % DM) to 1.68 (ADF, % DM). Despite the low accuracy of the prediction models, this study contributes to the knowledge of the FNIRS application to uNDF240 and other fibre fractions in faeces. Further investigations with different diet composition should be addressed.

Keywords: Dairy cattle; Faeces; Infrared spectroscopy; uNDF

Livestock Science

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Variation in blood serum proteins and association with somatic cell count in dairy cattle from multi-breed herds

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Abstract

Blood serum proteins are significant indicators of animal health. Nevertheless, several factors should be considered to appropriately interpret their concentrations in blood. Therefore, the objectives of this study were (1) to assess the effect of herd productivity, breed, age and stage of lactation on serum proteins and (2) to investigate association between serum proteins and somatic cell count (SCC) in dairy cattle. Milk and blood samples were collected from 1508 cows of six different breeds (Holstein Friesian, Brown Swiss, Jersey, Simmental, Rendena and Alpine Grey) that were housed in 41 multi-breed herds. Milk samples were analyzed for composition and SCC, while blood samples were analyzed for serum proteins (i.e. total protein, albumin, globulin and albumin-to-globulin ratio (A:G)). Herds were classified as low or high production, according to the cow's average daily milk energy yield adjusted for breed, days in milk (DIM) and parity. Data were analyzed using a linear mixed model that included the fixed effects of DIM, parity, SCS, breed, herd productivity and the random effect of the herd-test date within productivity level. Cows in high producing herds (characterized also by greater use of concentrates in the diet) had greater serum albumin concentrations. Breed differences were reported for all traits, highlighting a possible genetic mechanism. The specialized breed Jersey and the two dual-purpose local breeds (Alpine Grey and Rendena) had the lowest globulin concentration and greatest A:G. Changes in serum proteins were observed through lactation. Total protein reached the highest concentration during the 4th month of lactation. Blood albumin increased with DIM following a quadratic pattern, while globulin decreased linearly. As a consequence, A:G increased linearly during lactation. Older cows had greater total protein and globulin concentrations, while albumin concentration seemed to be not particularly affected by age. A linear relationship between serum proteins and SCS was observed. High milk SCS was associated with greater total protein and globulin concentrations in blood. The rise in globulin concentration, together with a decrease in albumin concentrations, resulted in a decline in A:G as SCS of milk increased. In conclusion, such non-genetic factors must be considered to appropriately interpret serum proteins as potential animal welfare indicator and their evaluation represents an important first-step for future analysis based on the integration of metabolomics, genetic and genomic information for improving the robustness of dairy cows.

Keywords: Albumin; Dairy; Globulin; Serum total protein; Somatic cell count

Animal

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Variation of milk coagulation properties, cheese yield, and nutrients recovery in curd of cows of different breeds before, during and after transhumance to highland summer pastures

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Abstract

This paper aimed at evaluating the effect of summer transhumance to mountain pastures of dairy cows of different breeds on cheese-making ability of milk. Data were from 649 dairy cows of specialized (Holstein Friesian and Brown Swiss), dual purpose (Simmental) and local (mostly Rendena and Alpine Grey) breeds. The Fourier-Transform Infra-Red Spectra (FTIRS) of their milk samples were collected before and after transhumance in 109 permanent dairy farms, and during transhumance in 14 summer farms (with multi-breeds herds) of the Trento Province, north-eastern Italy. A variety of 18 traits describing milk coagulation, curd firming, cheese yield and nutrients recovery in curd/loss in whey were predicted on the basis of FTIRS collected at the individual cow level. Moving the cows to summer farms improved curd firming traits but reduced cheese yields because of an increase of water and fat lost in the whey. During summer grazing, most of cheese-making traits improved, often non-linearly. The milk from summer farms supplementing cows with more concentrates showed better curd firming and cheese yield, because of lower fat lost in the whey. The breed of cows affected almost all the traits with a worst cheese-making ability for milk samples of Holsteins through all the trial, and interacted with concentrate supplementation because increasing compound feed tended to improve cheese-making traits for all breed, with the exception of local breeds for coagulation time and of Brown Swiss for curd firming time. In general, summer transhumance caused a favourable effect on cheese-making aptitude of milk, even though with some difference according to parity, initial days in milk, breed and concentrate supplementation of cows.

Keywords: Cheese yield; Milk coagulation; Mountain; Summer pasture; Whey losses

Journal of Dairy Research

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Ecology and environmental science

Above- and belowground patterns in a subalpine grassland-shrub mosaic

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Abstract

Many mountain pastures consist of a mosaic of grassland and shrub communities. Ongoing changes in mountain agriculture have affected the balance between the two elements of the mosaic. In order to understand the consequences of these changes for ecosystem functioning, we studied patterns in vegetation, root structure and soil properties along transects of varying grassland-to-shrub proportions. Our hypothesis was that differences in the vegetation aboveground are accompanied by differences belowground, related to soil properties and depth. The research was conducted at a subalpine site in the Trentino region (South-eastern Alps), consisting of *Nardus stricta* grasslands alternating with shrub patches of *Rhododendron ferrugineum*. Our investigation showed that the composition of vegetation was mainly governed by *R. ferrugineum* cover and less by soil properties. Plant species richness peaked at low to intermediate degrees of shrub cover and composition between transects became more similar with increasing shrub cover. Where *R. ferrugineum* cover was higher, Hemicryptophytes caespitosae were replaced by Nano-phanerophytes with consequences for belowground structures. At increasing shrub cover, root length density decreased, especially in the top soil, while root weight density remained stable and C content increased insignificantly. We discuss that theses structural changes along the gradient of *R. ferrugineum* cover affect a number of ecosystem services. The presented evidence suggests that maintaining grasslands with a low cover of *R. ferrugineum* balances a number of services, namely plant species diversity, carbon stabilization in soil and the prevention of soil erosion.

Keywords: Diameter size distribution; Life forms; Plant species composition; Root length density; Root weight density

Plant Biosystems

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Above- and belowground insect herbivory modifies the response of a grassland plant community to nitrogen eutrophication

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Abstract

Understanding the role that species interactions play in determining the rate and direction of ecosystem change due to nitrogen (N) eutrophication is important for predicting the consequences of global change. Insects might play a major role in this context. They consume substantial amounts of plant biomass and can alter competitive interactions among plants, indirectly shaping plant community composition. Nitrogen eutrophication affects plant communities globally, but there is limited experimental evidence of how insect herbivory modifies plant community response to raised N levels. Even less is known about the roles of above-and belowground herbivory in shaping plant communities, and how the interaction between the two might modify a plant community's response to N eutrophication. We conducted a 3-yr field experiment where grassland plant communities were subjected to above-and belowground insect herbivory with and without N addition, in a full-factorial design. We found that herbivory modified plant community responses to N addition. Aboveground herbivory decreased aboveground plant community biomass by 21%, but only at elevated N. When combined, above-and belowground herbivory had a stronger negative effect on plant community biomass at ambient N (11% decrease) than at elevated N (4% decrease). In addition, herbivory shifted the functional composition of the plant community, and the magnitude of the shifts depended on the N level. The N and herbivory treatments synergistically conferred a competitive advantage to forbs, which benefited when both herbivory types were present at elevated N. Evenness among the plant species groups increased when aboveground herbivory was present, but N addition attenuated this increase. Our results demonstrate that a deeper understanding of how plant-herbivore interactions above and below ground shape the composition of a plant community is crucial for making reliable predictions about the ecological consequences of global change.

Keywords: *Agriotes spp*; *Chorthippus albomarginatus*; Community evenness; Global change; Mesocosm; Plant community composition; Root shoot ratio; Trophic interactions

Ecology

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Assessing the water-purification service in an integrated agricultural wetland within the Venetian Lagoon drainage system

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Abstract

Wetlands are a cornerstone of beneficial ecosystem services, especially in intensive agricultural landscapes characterised by nutrient loss, and shallow and surface water bodies. Water-purification services can trap 80-90% of the sediments and eliminate 70-90% of the entering nitrogen. An experimental wetland of 3.2 ha was created within the Venetian drainage system to control nutrient loss from croplands and protect surface water bodies. The aims of the present study were to assess the water-purification service by monitoring nutrient runoff and testing the adaptability of seven macrophyte species in a floating treatment wetland system. Results showed that median concentrations of total nitrogen were 2.43 ppm at the inlet and 1.79 ppm at the outlet, whereas after an extreme rainfall event, total nitrogen concentrations were 6.34 ppm at the inlet and 1.29 ppm at the outlet. Carex spp. adapted best to the floating wetlands (433.13gm^{-2} of biomass production), followed by Lythrum salicaria (210.32gm^{-2}). Carex spp. had the highest total nitrogen uptake (4.84gm^{-2}), mostly in roots (3.19gm^{-2}), followed by L. salicaria with 2.35gm^{-2}. Constructed wetlands could, therefore, play a crucial role in integrated agro-environmental management to control nutrient runoff from intensive cropping systems.

Keywords: Biodiversity; Ecosystem services; Macrophytes; Phytoremediation

Marine and Freshwater Research

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Climate drivers of bark beetle outbreak dynamics in Norway spruce forests

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Abstract

Bark beetles are among the most devastating biotic agents affecting forests globally and several species are expected to be favored by climate change. Given the potential interactions of insect outbreaks with other biotic and abiotic disturbances, and the potentially strong impact of changing disturbance regimes on forest resources, investigating climatic drivers of destructive bark beetle outbreaks is of paramount importance. We analyzed 17 time-series of the amount of wood damaged by *Ips typographus*, the most destructive pest of Norway spruce forests, collected across 8 European countries in the last three decades. We aimed to quantify the relative importance of key climate drivers in explaining timber loss dynamics, also testing for possible synergistic effects. Local outbreaks shared the same drivers, including increasing summer rainfall deficit and warm temperatures. Large availability of storm-felled trees in the previous year was also strongly related to an increase in timber loss, likely by providing an alternative source of breeding material. We did not find any positive synergy among outbreak drivers. On the contrary, the occurrence of large storms reduced the positive effect of warming temperatures and rainfall deficit. The large surplus of breeding material likely boosted *I. typographus* population size above the density threshold required to colonize and kill healthy trees irrespective of other climate triggers. Importantly, we found strong negative density dependence in *I. typographus* that may provide a mechanism for population decline after population eruptions. Generality in the effects of complex climatic events across different geographical areas suggests that the large-scale drivers can be used as early warning indicators of increasing local outbreak probability.

Ecography

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Effect of vegetative buffer strips on herbicide runoff from a nontilled soil

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Abstract

Buffer strips can reduce herbicide runoff from cultivated fields due to the ability of vegetation to impede the flow of surface runoff, promote infiltration, and adsorb herbicides. Conservation agriculture has many environmental advantages, but the transition phase from a conventional to a conservation system is a critical period, especially for surface runoff. In 2015, a field in Italy that was transitioning from conventional to conservation agriculture was tested to analyze the efficacy of different types of buffer strips in reducing the runoff of three herbicides compared with no-buffer plots. At each runoff event, water volume was measured and terbuthylazine, metolachlor, and mesotrione concentrations were determined. Buffer strips were able to reduce the number of runoff events by 63% to 83%. The runoff volumes were significantly reduced in the presence of buffer strips, whereas no differences were found between different types of buffer strips. Among herbicides, mesotrione was not detected in runoff water samples. The highest losses of terbuthylazine and metolachlor were from plots without buffer strips during the first three runoff events. All types of buffer strips significantly reduced the total losses of terbuthylazine and metolachlor in the monitored runoff events, with a reduction of more than 99%. This study confirmed that buffer strips are a very effective mitigation system against surface water pollution by herbicides, even in agronomic situations that promote runoff.

Keywords: Buffer strips; Herbicides; No tillage; Runoff

Soil Science

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Efficiency of mechanical seed harvesting for grassland restoration

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Abstract

Maintaining and re-creating species-rich semi-natural grasslands are important issues in current agricultural policy in Europe. The seed that is required for their establishment can be obtained through direct harvesting from semi-natural herbaceous vegetation. To test the efficiency of mechanical seed harvesting on donor *Arrhenatherion elatioris* grasslands, experiments were performed in northern Italy and eastern Czech Republic. Trials were organized with a randomized block design and involved harvesting as green hay (grass mowing and immediate collection), dry hay (grass mowing and collection after drying on the field), direct combining (grass cutting and threshing at the same combine passage) and seed stripping with pull-type equipment (seed removal without grass cutting with a brush harvester pulled by a tractor). Harvesting was carried out at the time of maximum ripe standing seed yield (SSY) in the first and second regrowth. The harvested materials were analysed for seed number and weight and compared with the SSY. The species composition and phenology were also surveyed. In all methods, the seed mixture obtained contained the species present as seed at harvest time and was correlated with SSY. However, with regard to the seed number collected, the harvesting efficiency changed in relation to species group (grasses or forbs), individual species, seed maturation and regrowth. The most efficient method was harvesting as green hay (efficiency of approximately 71% of SSY and seed mixture composition that was very highly correlated with SSY). The least efficient methods were direct combining (30% of SSY and negative selectivity against light or difficult to detach seeds, producing the highest mean 1000-seeds weight) and harvesting as dry hay (39% of SSY and a high sensitivity to seed maturation level). Seed stripping, operated with downward brush rotation at the leading edge, resulted in an intermediate efficiency (60% of SSY and a seed mixture composition highly correlated with SSY). The harvesting efficiency for seed number was higher at the first regrowth than the second one for both species groups and, especially at the second regrowth, higher for forbs than for grasses. Especially forb harvesting presented a problem with regard to the species number collected. The problem was, not due to harvesting inefficiency but rather for phenological reasons, as several forbs did not produce fertile stems at the first or second regrowth and some other early flowering species had already shed the seed at the harvesting time. These results improve our understanding of factors affecting the efficiency of mechanical harvesting and will help in the preparation of efficient harvesting programs.

Keywords: Combining; Green hay; Harvesting efficiency; Hay-making; Seed harvesting; Seed stripping; Semi-natural grasslands; Standing seed yield

Agriculture, Ecosystems and Environment

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High cover of hedgerows in the landscape supports multiple ecosystem services in Mediterranean cereal fields

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Abstract

Field-margin diversification through conservation and restoration of hedgerows is becoming a prominent intervention for promoting biodiversity and associated ecosystem services in intensive agricultural landscapes. However, how increasing cover of hedgerows in the landscape can affect ecosystem services has rarely been considered. Here, we assessed the effect of increased field-margin complexity at the local scale and increasing cover of hedgerows in the landscape on the provision of pest control, weed control and potential pollination. Locally, three types of field margin were compared as follows: (i) standard grass margin, (ii) simple hedgerow and (iii) complex hedgerow, along two independent gradients of hedgerow cover and arable land cover in the landscape. We performed an exclusion experiment to measure biological control of cereal aphids and assessed natural enemy and pest abundance in the field. We sampled plant weed communities and performed a phytometer experiment to test the effects of pollinators on plant reproductive success. At the local scale, planting a new hedgerow or improving its structural complexity and vegetation diversity did not enhance the delivery of ecosystem services in the neighbouring field. However, high cover of hedgerows in the landscape enhanced aphid parasitism (from 12 to 18%) and potential pollination (visitation rate and seed set increased up to 70%) irrespective of local margin quality. The cover of arable land in the landscape reduced the abundance of plant-dwelling predators and weed diversity, but did not affect the delivery of the investigated ecosystem services. Synthesis and applications. Our results highlight the key importance of the surrounding landscape context, rather than local factors, to the delivery of ecosystem services. This suggests a need for new policies that pay particular attention to the conservation of hedgerows at large scales for promoting multiple ecosystem services in agroecosystems. Specifically, hedgerows can serve to develop a network of ecological corridors that can facilitate the movement of beneficial organisms, such as pollinators and natural enemies in the agricultural matrix. Such interventions may be a 'low cost–high benefit solution', since farmers can create or conserve high-quality habitats taking little or no land from crop production and without the need to change their crop management.

Keywords: Aphid; Biological control; Ecosystem services; Field-margin diversification; Hedgerows; Landscape complexity; Natural enemies; Off-field interventions; Pollination; Weed control

Journal of Applied Ecology

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Human disturbance and upward expansion of plants in a warming climate

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Abstract

Climate change is expected to trigger an upward expansion of plants in mountain regions and, although there is strong evidence that many native species have already shifted their distributions to higher elevations, little is known regarding how fast non-native species might respond to climate change. By analysing 131,394 occurrence records of 1,334 plant species collected over 20 years in the European Alps, we found that non-natives are spreading upwards approximately twice as fast as natives. Whereas the spread of natives was enhanced by traits favouring longer dispersal distances, this was not the case for non-natives. This was due to the non-native species pool already being strongly biased towards species that had traits facilitating spread. A large proportion of native and non-native species seemed to be able to spread upwards faster than the current velocity of climate change. In particular, long-distance dispersal events and proximity to roads proved to be key drivers for the observed rapid spread. Our findings highlight that invasions by non-native species into native alpine communities are a potentially significant additional pressure on these vulnerable ecosystems that are already likely to suffer dramatic vegetation changes with ongoing warming and increasing human activity in mountain regions.

Nature Climate Change

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Landscape simplification weakens the association between terrestrial producer and consumer diversity in Europe

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Abstract

Land-use change is one of the primary drivers of species loss, yet little is known about its effect on other components of biodiversity that may be at risk. Here, we ask whether, and to what extent, landscape simplification, measured as the percentage of arable land in the landscape, disrupts the functional and phylogenetic association between primary producers and consumers. Across seven European regions, we inferred the potential associations (functional and phylogenetic) between host plants and butterflies in 561 seminatural grasslands. Local plant diversity showed a strong bottom-up effect on butterfly diversity in the most complex landscapes, but this effect disappeared in simple landscapes. The functional associations between plant and butterflies are, therefore, the results of processes that act not only locally but are also dependent on the surrounding landscape context. Similarly, landscape simplification reduced the phylogenetic congruence among host plants and butterflies indicating that closely related butterflies become more generalist in the resources used. These processes occurred without any detectable change in species richness of plants or butterflies along the gradient of arable land. The structural properties of ecosystems are experiencing substantial erosion, with potentially pervasive effects on ecosystem functions and future evolutionary trajectories. Loss of interacting species might trigger cascading extinction events and reduce the stability of trophic interactions, as well as influence the longer term resilience of ecosystem functions. This underscores a growing realization that species richness is a crude and insensitive metric and that both functional and phylogenetic associations, measured across multiple trophic levels, are likely to provide additional and deeper insights into the resilience of ecosystems and the functions they provide.

Keywords: Coevolution; Ecosystem resilience; Functional traits; Habitat loss; Herbivory; Host specialization; Land-use change; Phylogenetic diversity; Plant–insect interactions; Trophic associations

Global Change Biology

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Pollination benefits are maximized at intermediate nutrient levels

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Abstract

Yield production in flowering crops depends on both nutrient availability and pollination, but their relative roles and potential interactions are poorly understood. We measured pollination benefits to yield in sunflower, combining a gradient in insect pollination (0, 25, 50, 100%) with a continuous gradient in nitrogen (N) fertilization (from 0 to 150 kg N ha-1) in an experiment under realistic soil field conditions. We found that pollination benefits to yield were maximized at intermediate levels of N availability, bolstering yield by approximately 25% compared with complete pollinator exclusion. Interestingly, we found little decrease in yield when insect visits were reduced by 50%, indicating that the incremental contribution of pollination by insects to yield is greater when the baseline pollination service provision is very low. Our findings provide strong evidence for interactive, nonlinear effects of pollination and resource availability on seed production. Our results support ecological intensification as a promising strategy for sustainable management of agroecosystems. In particular, we found optimal level of pollination to potentially compensate for lower N applications.

Keywords: Agricultural intensification; Ecosystem services; Incremental contribution; Interactions; Nitrogen fertilization; Pollinators

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Topographical, soil, and water determinants of the Vallevecchia coastal dune-marsh system

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Abstract

Due to their low elevation range, coastal environments are extremely sensitive to rising sea levels resulting from climate change and other direct human impacts. Increased knowledge about site and vegetation characteristics can contribute to improving their conservation and restoration. A survey of 51 sampling areas and seven transects in the sand dune, salt marsh system of Vallevecchia (Caorle, Italy) was conducted, while taking into account the vegetation and certain important topographical, soil, and hydrological characteristics. The most important factors differentiating the presence of sand dunes and salt marsh vegetation were found to be soil electric conductivity (EC: threshold EC = 0.4 mS cm1) and site elevation (threshold + 0.70 cm a.s.l.). In psammophilous vegetation, the soil pH and EC decreased with elevation and the water table was composed of freshwater. A small amount of salt accumulation was found only at the white dune bottom. In salt marsh vegetation, the soils were flooded daily by high tides and were saline and alkaline at higher elevations, where less frequent tide flooding led to frequent soil drying and salt accumulation. The soil OM content of the salt marshes was highest due to the slow mineralization rate as a consequence of the high water content. The current low sediment transport from adjacent rivers was the cause of the regression of the central-eastern part of Vallevecchia, where the dunal system width and number of vegetation types decreased and the height and mean slope of the sea facing sides of the white dunes increased. The 60-cm local sea level rise predicted by 2100 will increase the salt marsh extent by 60%, which will be a disadvantage for the more rare non-saline retrodunal and psammophilous vegetation. Reactivating river sediment transport, reducing or eliminating the deep-rooted pine and Ammophila arenaria plantations and closing drainage ditches in the adjacent pinewoods can mitigate the negative impacts of sea level rise.

Keywords: Salt marsh; Saltwater; Sand dune; Soil salinity; Water table

Ecological Engineering

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Treatment performance and macrophytes growth in a restored hybrid constructed wetland for municipal wastewater treatment

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Abstract

This work evaluated depuration performance and macrophyte plants growth in a full-scale hybrid-constructed wetland (H-CW) (1000 population equivalent) treating municipal wastewater. The plant was activated in June 2010 after a restoration of an existent H-CW composed of a horizontal subsurface flow (HSSF) bed vegetated with evergreen xerophile species (*Prunus laurocerasus, Pittosporum* spp., *Elaeagnus angustifolia*), connected with a sedimentation pond vegetated with *Lemna* spp. To enhance the depuration performances, in both sections of the plant the original vegetation was removed and the HSSF bed was vegetated with *Phragmites australis*, whereas in the pond, a floating treatment wetland vegetated with *Iris pseudacorus* was installed. The depuration performance in treating total nitrogen (TN), nitrate nitrogen (NO_3-N), ammonia nitrogen (NH_4-N), total phosphorus (TP), orthophosphate (PO_4-P) and chemical oxygen demand (COD) was weekly monitored between August 2010 and August 2011. Results indicated median concentration abatements for the entire system of 74.3% for TN, 62.1% for NH_4-N, 77.7% for NO_3-N, 29.6% for TP, 37.4% for PO_4-P, and 46.7% for COD. In addition, at the end of the first growing season (June 2010–November 2010), good adaption to the system was detected for both *P. australis* and *I. pseudacorus*, which produced respectively 3.9 ± 2.2 kg $m^{-2}$and 3.7 ± 1.0 kg m^{-2} of above-ground dry biomass, with average above-ground N uptakes of 62.4 ± 35.6 g m^{-2} and 69.8 ± 19.0 g m^{-2} and average above-ground P uptakes of 4.6 ± 2.6 g m^{-2} and 7.8 ± 2.1 g m^{-2}. The results indicate that a H-CW composed of a sequence of HSSF bed and FTW represents an effective application for abating TN, NH_4-N, NO_3-N and COD concentrations from municipal wastewater.

Keywords: Floating treatment wetland; Horizontal subsurface flow wetland; *Iris pseudacorus* L.; *Phragmites australis* (Cav.) Trin. ex Steud.

Ecological Engineering

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Using Landsat Images and Spectral Mixture Analysis to Assess Drivers of 21-Year LULC Changes in Sudan

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Abstract

Landsat images acquired in 1987, 1999 and 2008 were selected to evaluate land use and land cover changes in three different ecological zones in the Republic of the Sudan: savannah (North Kordofan), semi-desert (River Nile) and desert (Northern State). Maps of soil, vegetation and non-photosynthetic material were built by spectral mixture analysis using endmembers spectra derived from images. Multitemporal comparison techniques were then applied to vegetation and soil maps to estimate the long-term land degradation/re-growth dynamics and to emphasize land cover variation over time and in space. Multitemporal comparisons have shown that site-specific interactions between natural processes, climate variation and human activity played a pivotal role in land use and land cover change. In savannah, human activities strongly affected degradation phenomena. Expansion of villages triggered a change in land use and mismanagement of the natural resources, mainly caused by deforestation to supply wood for domestic uses. The degradation then promoted sand encroachment and dune migration. On average, 48% of the total area was subjected to medium (25–50%) and high (50–75%) land degradation. Differently, climatic constraints drove increasing degradation processes in semi-desert and desert zones. The phenomenon was particularly severe in the desert zone. In each site, an inversion of the general trend was due to a land use change where forestry or agricultural projects were established, partly sustained in savannah by the positive rainfall trend of the last two decades. Site-specific strategies that take into account the interactions of the driving factors at local scale are thus necessary to combat land degradation.

Keywords: Change vector analysis; Landsat; LULC; Remote sensing; Spectral mixture analysis

Land Degradation and Development

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Carbon sequestration potential of Italian orchards and vineyards

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Abstract

From 2004 to 2012 carbon (C) fluxes between the soil-vegetation system and the atmosphere in apple, grape, olive and orange orchards planted in different Italian regions were measured. Above-ground net primary productivity (ANPP) ranged from 4 (olive) to 9 (apple) Mg C ha-1. Alley grass contribution to total ANPP significantly varied among the systems, reaching a maximum of 60% in vineyards. The harvest index ranged from 46% for apple, to 58% for orange, 60% for grape and 41% for olive, while abscised leaves accounted for 30% of ANPP, on average. Soil respiration fluxes ranged from 6 (orange) to 10 (grape) Mg C ha^{-1}. Results indicate the potential of these fruit crop to sequester atmospheric C.

Keywords: Apple; Net ecosystem productivity; Net primary productivity; Olive; Orange; Peach

Acta Horticulturae

Volume 1177, Pages 145-149

Evaluation of different establishment methods of sedum cuttings for summer vegetation of green roofs in Venetian Plain conditions

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Abstract

Sedum species are the most commonly used plants to vegetate green roofs because of their tolerance to extreme conditions. Despite the easier and faster establishment of sedums by plugs or mats, the direct spreading of cuttings is still an interesting cost-effective installation method, especially for large-scale roofs. To improve cutting establishment in the difficult conditions of the Venetian plain during summer, a three-way experimental design was set up on June 5, 2015. Rooted and unrooted cuttings of five Sedum species (*Sedum acre, S. album, S. reflexum, S. sexangulare and S. spurium*) were compared with and without ground cover with non-woven fabric (fabric) in the first four weeks after cutting spreading (WAS). Cuttings survival and plant growth was evaluated over 20 weeks: 4 WAS (at fabric removal), after 12 and 20 WAS. Plant growth was measured by means of growth index, and shoot and root dry weights. After 4 WAS sedum cuttings were negatively affected by covering with fabric as only 68.5% of cuttings had survived compared to 98.5% of the uncovered control. Shoot and root dry weights were also negatively affected by fabric cover. At the end of the study both the fabric cover and Sedum species affected plant survival. Uncovered treatment exhibited better survival compared to the fabric cover (71.5 vs. 60.5%) while *S. spurium* and *S. sexangulare* had only 50% survival compared to the over 80% survival for *S. acre*. The sedum cuttings of the fabric cover treatment recovered over time, providing similar growth as the uncovered treatment at the end of the experiment. *Sedum spurium* had the highest growth index, shoot and root dry weights and *S. album* growth was also good. Pre-rooted cuttings did not affect survival but favored aerial growth of *S. spurium* and *S. reflexum*.

Keywords: Non-woven fabric; Pre-rooted cuttings; Urban landscape

Acta Horticulturae

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The experimental and educational rain gardens of the Agripolis Campus (north-east Italy): Preliminary results on hydrological and plant behavior

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Abstract

In most urbanized areas stormwater runoff, flowing on impervious surfaces, can increase the risk of floods and overload of drainage systems. Landscape designers may contribute to the mitigation of the problem by incorporating appropriate solutions in the design of green spaces. Rain gardens are green infrastructures that can contribute to more sustainable urban development. Since 2011, an experiment has been carried out at the University of Padova with the aim to assess the use of rain gardens for a sustainable management of the stormwater runoff. Two circular rain gardens with herbaceous perennials, differently sized and equipped with TDR soil moisture sensors, were designed and built to intercept equal amounts of runoff draining from a building roof with an area of 215 m2. The experiment consisted of testing the capacity of intercepting runoff caused by storm of different magnitude, in measuring the dynamics of water in the topsoil after the rainfall events and in evaluating the growth and aesthetic quality of the different plant species used. Input and output water volumes were measured and actual ET was estimated using WUCOLS Landscape Coefficient Methods. Results of the preliminary phase showed that both the rain gardens were able to satisfactorily manage the roof runoff, which was taken off the urban drainage system, with a good aesthetic result.

Keywords: Hydrological behaviour; Infiltration; Outflow; Urban landscape; WUCOLS

Acta Horticulturae

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Combined effects of agrochemicals and ecosystem services on crop yield across Europe

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Abstract

Simultaneously enhancing ecosystem services provided by biodiversity below and above ground is recommended to reduce dependence on chemical pesticides and mineral fertilisers in agriculture. However, consequences for crop yield have been poorly evaluated. Above ground, increased landscape complexity is assumed to enhance biological pest control, whereas below ground, soil organic carbon is a proxy for several yield-supporting services. In a field experiment replicated in 114 fields across Europe, we found that fertilisation had the strongest positive effect on yield, but hindered simultaneous harnessing of below- and above-ground ecosystem services. We furthermore show that enhancing natural enemies and pest control through increasing landscape complexity can prove disappointing in fields with low soil services or in intensively cropped regions. Thus, understanding ecological interdependences between land use, ecosystem services and yield is necessary to promote more environmentally friendly farming by identifying situations where ecosystem services are maximised and agrochemical inputs can be reduced.

Keywords: Agricultural intensification; Biological pest control; Ecological intensification; Fertilisers; Insecticides; Landscape complexity; Soil organic carbon; Yield loss

Ecology Letters

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A review on the main affecting factors of greenhouse gases emission in constructed wetlands

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Abstract

Constructed wetlands (CWs) are natural-like systems for wastewater treatment capable to remove both pollutants and nutrients without additional energy demand. In these systems, gaseous compounds are released into the atmosphere through microbial processes. Among these gases carbon dioxide (CO_2), methane (CH_4) and nitrous oxide (N_2O) are the most dangerous because they act as greenhouse gases (GHGs) and are well known as contributory factors to cause global warming. In this paper we reviewed 224 scientific articles (from 1980 to 2016) from the literature in order to analyze the most important factors that drive the quantity and type of GHGs production and emission from different CWs systems. Wastewater flow and composition, hydroperiod, environmental conditions and plant presence and species used to vegetate CWs have been considered. CWs typologies influence GHGs fluxes with lower CH_4 emissions from subsurface flow CWs than free water surface (FWS) ones and higher N_2O emissions from vertical subsurface flow (VSSF) CWs than FWS ones. The inlet wastewater COD/N ratio of 5:1 has been found as the best ratio to obtain in the same time the lowest N_2O emission and the highest nitrogen removal in FWS CWs. The inlet wastewater C/N ratio of 5:1 allows to obtain the lowest CO_2 and CH_4 emissions in VSSF CW treatment. Intermittent CWs bed wastewater loading decreases CH_4 and promote CO_2 and N_2O emissions. Temperature is positively correlated with CO_2, CH_4 and N_2O emissions and solar radiation with CO_2 and CH_4 emissions. GHGs flux is affected by plant presence and species, and it is influenced both by the phenology and density of vegetation. Plant presence significantly increases the CO_2 emission respect to unvegetated condition in all CWs types, and increases N_2O and CH_4 emissions in VSSF CWs. Considering the HSSF CWs plant presence significantly reduce the CH_4 emissions. Plant species richness effect on CH_4 emission has been investigates in a limited number of papers with not unique results, probably due to the different plant species and number used by authors, which may have influenced the CWs microbial population and activity. Considering plant species *Zizania latifolia* determine significant higher CH_4 and N_2O emissions than *Phragmites australis*. No significant different CH_4 and N_2O emissions have been found between *P. australis* and *Typha latifolia*. Significant lower N_2O emissions determine the *T. angustifolia* than *P. australis*. Although plant presence, in some case, increases CW GHG emissions respect to unvegetated situation, the vegetation fixes atmospheric carbon by photosynthesis; as a consequence CWs act, in most cases, as sink of CO_2(eq).

Keywords: Carbon dioxide; Constructed wetlands; Methane; Nitrous oxide; Plant species; Wastewaters

Agricultural and Forest Meteorology

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Chromium in agricultural soils and crops: A review

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Abstract

The mobility and distribution of metals in the environment is related not only to their concentration but also to their availability in the environment. Most chromium (Cr) exists in oxidation states ranging from 0 to VI in soils but the most stable and common forms are Cr(0), Cr(III), and Cr(VI) species. Chromium can have positive and negative effects on health, according to the dose, exposure time, and its oxidation state. The last is highly soluble; mobile; and toxic to humans, animals, and plants. On the contrary, Cr(III) has relatively low toxicity and mobility and it is one of the micronutrients needed by humans. In addition, Cr(III) can be absorbed on the surface of clay minerals in precipitates or complexes. Thus, the approaches converting Cr(VI) to Cr(III) in soils and waters have received considerable attention. The Cr(III) compounds are sparingly soluble in water and may be found in water bodies as soluble Cr(III) complexes, while the Cr(VI) compounds are readily soluble in water. Chromium is absorbed by plants through carriers of essential ions such as sulfate. Chromium uptake, accumulation, and translocation, depend on its speciation. Chromium shortage can cause cardiac problems, metabolic dysfunctions, and diabetes. Symptoms of Cr toxicity in plants comprise decrease of germination, reduction of growth, inhibition of enzymatic activities, impairment of photosynthesis and oxidative imbalances. This review provides an overview of the chemical characteristics of Cr, its behavior in the environment, the relationships with plants and aspects of the use of fertilizers.

Keywords: Chromium; Agricultural soil; Anthropic pollution; Speciation

Water, Air, and Soil Pollution

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Different leachate phytotreatment systems using sunflowers

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Abstract

The use of energy crops in the treatment of wastewaters is of increasing interest, particularly in view of the widespread scarcity of water in many countries and the possibility of obtaining renewable fuels of vegetable origin. The aim of this study was to evaluate the feasibility of landfill leachate phytotreatment using sunflowers, particularly as seeds from this crop are suitable for use in biodiesel production. Two different irrigation systems were tested: vertical flow and horizontal subsurface flow, with or without effluent recirculation. Plants were grown in 130L rectangular tanks placed in a special climatic chamber. Leachate irrigated units were submitted to increasing nitrogen concentrations up to 372 mgN/L. Leachate was successfully tested as an alternative fertilizer for plants and was not found to inhibit biomass development. The experiment revealed good removal efficiencies for COD (>50%) up until flowering, while phosphorous removal invariably exceeded 60%. Nitrogen removal rates decreased over time in all experimental units, particularly in vertical flow tanks. In general, horizontal flow units showed the best performances in terms of contaminant removal capacity; the effluent recirculation procedure did not improve performance. Significant evapo-transpiration was observed, particularly in vertical flow units, promoting removal of up to 80% of the inlet irrigation volume.

Keywords: Horizontal sub-superficial flow; Landfill leachate; Phytotreatment; Sunflowers; Vertical flow

Waste Management

Volume 59, Pages 267-275

Land use affects the soil C sequestration in alpine environment, NE Italy

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Abstract

Soil carbon sequestration is strongly affected by soil properties, climate, and anthropogenic activities. Assessing these drivers is key to understanding the effect of land use on soil organic matter stabilization. We evaluated land use and soil depth influencing patterns of soil organic matter stabilization in three types of soil profiles located under the same pedogenetic matrix and alpine conditions but with different vegetation cover. The stock in soil organic carbon in the mean 0-20 cm layer increased from prairie (31.9 t ha^{-1}) to prairie in natural reforestation (42 t ha^{-1}) to forest (120 t ha^{-1}), corresponding to increments of 1.3-fold prairie, for prairie in natural reforestation, and of 3.8-fold prairie for forest. The forest showed the highest humic carbon (21.7 g kg^{-1}), which was 2.8 times greater than the prairie in natural reforestation and 4 times higher than the prairie. 13C-NMR spectroscopic measurements suggested a different C pattern. The prairie in natural reforestation and the prairie were characterized by a higher content in O,N-alkyl C with respect to the forest. Alkyl C and aromatic C in the prairie in natural reforestation and prairie did not show relevant differences while they decreased with respect to the forest. Carboxyl and phenolic C groups were markedly higher in forest and prairie than prairie in natural reforestation. Alkyl C, carboxyl C, and phenolic C prevailed in the Ah horizons whereas aromatic C and O,N-alkyl C were dominant in the B horizons. Overall, the marked distribution of O,N-alkyl C and alkyl C in humic substances (HS) indicates a low degree of humification. Nevertheless, in forest, the relatively high presence of aromatic C designated HS endowed with a relatively high humification degree. Thus, our results might suggest that in the alpine environment of NE Italy differences in soil organic matter (SOM) stocks and characteristics are affected by land use and anthropic activities.

Keywords: 13C-NMR; Alpine; Forest; Humic; Land use; Soil organic carbon

Forests

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Soil properties as indicators of treeline dynamics in relation to anthropogenic pressure and climate change

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Abstract

Mountain forests, treeline ecotones included, provide numerous ecosystem services. However, different drivers heavily impact the treeline areas, in particular anthropogenic pressure and climate change. Any change affecting the aboveground portion of terrestrial ecosystems automatically influences their belowground part, i.e. soil and soil organisms. Therefore, the focus of the present paper is on the soil resource that provides multiple ecosystem services, such as carbon storage, water filtration, food and biomass provisioning, biodiversity, maintenance, etc. Soil physical, chemical, and biological properties can be very helpful as indicators of ecosystem services in mountain regions. A selection and integration of appropriate indicators of soil quality is thus needed for soil monitoring and assessment in treeline areas. In this paper, results of case studies from mountain regions in Bulgaria, the Czech Republic, Italy, Romania, and Slovakia are presented. From these studies, it emerges that soil organic matter (content and quality), pH, and microbial parameters show significant changes in response to anthropogenic pressures and/or climate change. These indicators of soil quality, either in the short- or in the long-term, can thus be used as reliable and sensitive tools for monitoring actions. However, it is advisable to integrate this basic set with additional indicators that can be further selected in relation to specific conditions, such as geographical area, lithological substrate, land use, and management practices.

Keywords: Ecosystem services; Forest resilience; Mountains

Climate Research

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The Norian “chaotic carbon interval”: New clues from the ^{13}Corg record of the Lagonegro Basin (southern Italy)

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Abstract

A global carbon-isotope curve for the Late Triassic has the potential for global correlations and new insights on the complex and extreme environmental changes that took place in this time interval. We reconstruct the global ^{13}Corg profile for the late Norian, improving on sparse published data from North American successions that depict a “chaotic carbon-isotope interval” with rapid oscillations. In this context, we studied three sections outcropping in the Lagonegro Basin (southern Italy), originally located in the western Tethys. The carbon-isotope profiles show four negative excursions correlatable within the Lagonegro Basin. In particular, a negative shift close to the Norian/Rhaetian boundary (NRB) appears to correlate with that observed in the North American ^{13}Corg record, documenting the widespread occurrence of this carbon cycle perturbation. The ^{87}Sr/^{86}Sr and ^{187}Os/^{188}Os profiles suggest that this negative shift was possibly caused by emplacement of a large igneous province (LIP). The release of greenhouse gases (CO_2) to the atmosphere-ocean system is supported by the ^{12}C enrichment observed, as well as by the increase of atmospheric pCO_2 inferred by different models for the Norian/Rhaetian interval. The trigger of this strongly perturbed interval could thus be enhanced magmatic activity that could be ascribed to the Angayucham province (Alaska, North America), a large oceanic plateau active ca. 214 ± 7 Ma, which has an estimated volume comparable to the Wrangellia and the Central Atlantic Magmatic Province (CAMP) LIPs. In fact, these three Late Triassic igneous provinces may have caused extreme environmental and climate changes during the Late Triassic.

Geosphere

Volume 13, Issue 4, Pages 1-16

Use of oleaginous plants in phytotreatment of grey water and yellow water from source separation of sewage

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Abstract

Efficient and economic reuse of waste is one of the pillars of modern environmental engineering. In the field of domestic sewage management, source separation of yellow (urine), brown (faecal matter) and grey waters aims to recover the organic substances concentrated in brown water, the nutrients (nitrogen and phosphorous) in the urine and to ensure an easier treatment and recycling of grey waters. With the objective of emphasizing the potential of recovery of resources from sewage management, a lab-scale research study was carried out at the University of Padova in order to evaluate the performances of oleaginous plants (suitable for biodiesel production) in the phytotreatment of source separated yellow and grey waters. The plant species used were *Brassica napus* (rapeseed), *Glycine max* (soybean) and *Helianthus annuus* (sunflower). Phytotreatment tests were carried out using 20L pots. Different testing runs were performed at an increasing nitrogen concentration in the feedstock. The results proved that oleaginous species can conveniently be used for the phytotreatment of grey and yellow waters from source separation of domestic sewage, displaying high removal efficiencies of nutrients and organic substances (nitrogen > 80%; phosphorous > 90%; COD nearly 90%). No inhibition was registered in the growth of plants irrigated with different mixtures of yellow and grey waters, where the characteristics of the two streams were reciprocally and beneficially integrated.

Keywords: Decentralization; Energy crops; Grey water; Phytotreatment; Sewage; Source separation; Urine

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Possible developments for *ex situ* phytoremediation of contaminated sediments, in tropical and subtropical regions – Review

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Abstract

The growing problem of remediation of contaminated sediments dredged from harbor channels needs to be resolved by a cost effective and sustainable technology. Phytoremediation, by ex situ remediation plants, seems to have the potential to replace traditional methods in case of moderately contaminated sediments. On the other side, the need to mix sediments with soil and/or sand to allow an easier establishment of most employed species causes an increase of the volume of the processed substrate up to 30%. Moreover the majority of phytoremediating species are natives of temperate climate belt. Mangroves, with a special focus on the genus Avicennia – a salt secreting species – should represent an effective alternative in terms of adaptation to salty, anoxic sediments and an opportunity to develop ex situ phytoremediation plants in tropical and subtropical regions. The use of humic acid to increase root development, cell antioxidant activity and the potential attenuation of the "heavy metals exclusion strategy" to increase phytoextraction potentials of mangroves will be reviewed.

Keywords: Auxin; Avicennia; Humic acids; Peroxidase; ROS; Sediments

Chemosphere

Volume 182, Pages 707-719

Selenium accumulation and metabolism in algae

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Abstract

Selenium (Se) is an intriguing element because it is metabolically required by a variety of organisms, but it may induce toxicity at high doses. Algae primarily absorb selenium in the form of selenate or selenite using mechanisms similar to those reported in plants. However, while Se is needed by several species of microalgae, the essentiality of this element for plants has not been established yet. The study of Se uptake and accumulation strategies in micro- and macro-algae is of pivotal importance, as they represent potential vectors for Se movement in aquatic environments and Se at high levels may affect their growth causing a reduction in primary production. Some microalgae exhibit the capacity of efficiently converting Se to less harmful volatile compounds as a strategy to cope with Se toxicity. Therefore, they play a crucial role in Se-cycling through the ecosystem. On the other side, micro- or macro-algae enriched in Se may be used in Se biofortification programs aimed to improve Se content in human diet via supplementation of valuable food. Indeed, some organic forms of selenium (selenomethionine and methylselenocysteine) are known to act as anticarcinogenic compounds and exert a broad spectrum of beneficial effects in humans and other mammals. Here, we want to give an overview of the developments in the current understanding of Se uptake, accumulation and metabolism in algae, discussing potential ecotoxicological implications and nutritional aspects.

Keywords: Accumulation; Algae; Metabolism; Selenium; Toxicity; Uptake

Aquatic Toxicology

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Individual activity interacts with climate and habitat features in influencing GPS telemetry performance in an alpine herbivore

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Abstract

Global Positioning System (GPS) telemetry allows to monitor large herbivores in Alpine habitats that are difficult or impossible to access by humans. However, little is known about the factors influencing the performance of GPS telemetry in these habitats. We used stationary test collars and a data set of over 90000 attempted locations from 11 collared free-ranging Alpine ibex (*Capra ibex ibex*) females to quantify the loss of scheduled locations and accuracy of GPS telemetry at the high-elevation habitats of the Marmolada massif (eastern Italian Alps). In both tests the fix acquisition rates and proportions of 3D fixes averaged near 90%. After removing outliers, the estimated location error in stationary collar tests was within 10 m for 75% of 3D locations and within 20 m for 75% of 2D locations. In both tests, sky view determined by terrain morphology was the main habitat feature influencing the performance of GPS telemetry, while forest had only minor effects compared to open ground. Both fix acquisition rates and proportions of 3D fixes in free-ranging ibexes were lowest (close to 85%) in winter and highest (close to 95%) in summer, and exhibited contrasting seasonal diel patterns, being lowest during the night and highest at midday in winter, and lowest at midday and highest at dawn and dusk in summer. Fix acquisition rates and proportions of 3D fixes were positively influenced by individual activity, warm temperatures in winter, absence of precipitation in all seasons, and shallow snow depth in winter. These effects could explain the seasonal and diel patterns. The performance of GPS telemetry of large herbivores at Alpine habitats can be as good as or better than in forested habitats at low elevations. However, acquired locations underestimate inactive periods in sheltered habitats, especially in winter and in adverse weather conditions.

Keywords: Animal activity; *Capra ibex*; Fix accuracy; Fix acquisition rate; GPS telemetry

Hystrix

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Entomology

A total evidence phylogeny for the processionary moths of the genus *Thaumetopoea* (Lepidoptera: Notodontidae: *Thaumetopoeinae*)

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Abstract

Processionary moths belong to a group of about 100 species well known for their social behaviour and their urticating systems. The genus *Thaumetopoea* s.l. includes about 15 species and has been divided into three genera (*Helianthocampa*, *Thaumetopoea* s.s., and *Traumatocampa*) in the last revision, based on key morphological features of the adults and on the host plants of the larvae. We performed a total evidence approach to resolve the phylogeny of the genus *Thaumetopoea* s.l., analysing all valid taxa included in this group, plus a broad array of close relatives. *Thaumetopoea* was monophyletic and supported by several apomorphies. Further subclades corroborated by synapomorphies were identified. Our phylogeny suggests that *Thaumetopoea* must be regarded as a single genus. The mapping of key life history traits on the total evidence tree allowed us to sketch a plausible identikit of the *Thaumetopoea* ancestor and to track the evolution of the genus. The ancestor originated in the eastern Mediterranean area, and used broadleaved host plants. Subsequently, a switch to conifers occurred, just once, in a large subclade. The ancestor pupated in the soil, like several current species, but in a few taxa this trait was lost, together with the related morphological adaptations.

Keywords: Adaptation; Ancestry; Host plant; Life history trait; Morphology; Moth; Phylogeny; Social behavior

Cladistics

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An artificial diet for rearing three exotic longhorn beetles invasive to Europe

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Abstract

Anoplophora glabripennis, *Anoplophora chinensis* and *Psacothea hilaris hilaris* are three invasive exotic longhorn species (*Coleoptera Cerambycidae*) threatening native broadleaf trees in Europe and North America. Field studies on invasive species are somewhat difficult in the areas of introduction due to the application of eradication measures and the activation of quarantine protocols. Rearing these species in standard laboratory conditions would allow specific ecological and biological investigations to be conducted. In this paper, the rearing of these longhorn beetles has been tested on an artificial diet in laboratory conditions. The tested diet can be used to obtain viable healthy adults of each of the three studied species. *P. h. hilaris* had the best rearing performance with 74% of eggs producing new adults, while *A. chinensis* and *A. glabripennis* were poorer with 24.7% and 23.3%, respectively. The low percentage of emerging A. glabripennis and A. chinensis adults was due mainly to a high mortality of their first instar larvae not entering the diet. Moreover, A. chinensis and A. glabripennis had a mean development time, 60.06 and 37.29 weeks, respectively (including the chilling periods required for pupation), longer than P. h. hilaris (16.1 weeks). During development, larval moults varied according to species and within species ranging from 5-7 (*P. h. hilaris*), 6-11 (*A. chinensis*) and 7-8 (*A. glabripennis*) moults, respectively. Adults of *A. glabripennis* and *P. h. hilaris* reared on the diet were bigger than wild specimens collected from the same population, whereas *A. chinensis* adults were smaller. Adult survival was shorter in *A. glabripennis* (62.9 days) than in *P. h. hilaris* (119.3 days). According to the different performance of the three species, the rearing costs were about 2.0, 8.1 and 16.1 US dollars per adult beetle for *P. h. hilaris*, *A. glabripennis* and *A. chinensis*, respectively. A laboratory insect population has to be cost effective and self-sustainable over time, and the tested diet provided valuable results for the low-cost mass rearing of these invasive longhorn beetles.

Keywords: ALB; *Anoplophora chinensis*; *Anoplophora glabripennis*; CLB; Exotic species; Laboratory rearing; *Psacothea hilaris hilaris*; YLB

Bulletin of Insectology

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Attraction of *Halyomorpha halys* (Hemiptera: Pentatomidae) haplotypes in North America and Europe to baited traps

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Abstract

Halyomorpha halys is a global invasive species, native to Southeast Asia, that is threatening agriculture in invaded regions. Our objectives were to: 1) establish the attractiveness of semiochemical stimuli paired with field-deployed traps in Europe (Greece, Hungary, Italy, and Switzerland), compared with Maryland, USA, and 2) identify *H. halys* haplotypes recovered from traps at each location. We found qualitatively identical patterns of capture between sites located across Europe and in Maryland, USA. In both regions, captures of *H. halys* adults indicated a synergistic response to traps baited with the two component *H. halys* aggregation pheromone, and pheromone synergist, methyl (2E, 4E, 6Z)-decatrienoate when compared with either individually. Haplotype diversity in Europe based on trapped specimens was much greater than the USA, with five new haplotypes described here, probably indicating ongoing invasion and re-introduction of *H. halys*. By contrast, a single, previously identified haplotype was trapped in Maryland, USA, representing a single introduction. All *H. halys* haplotypes responded to each semiochemical in apparent proportion to their frequency in the overall population based on independently derived information from prior work. Taken together, these data suggest that pheromone-based technology will be of global utility for the monitoring of this important invasive species.

Scientific Reports

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Careful choice of insecticides in integrated pest management strategies against *Ostrinia nubilalis* (Hübner) in maize conserves *Orius* spp. in the field

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Abstract

A long-term field experiment was set up in April 2011 at Legnaro, Italy, within the European Project PURE, to evaluate two Integrated Pest Management (IPM) tools against conventional pest management in maize-based cropping systems (MBCS) that involved different crops every year. Three foliar insecticide treatments were applied against *Ostrinia nubilalis* (Hübner) in 2011 and 2014 when maize was present in the rotation. Lambda-cyhalothrin was applied as the conventional management (CON), while chlorantraniliprole and a biological insecticide containing *Bacillus thuringiensis* var. kurstaki were tested for IPM1 and IPM2, respectively. The minute pirate bug (Orius spp.) was the most abundant among the beneficial organisms and was considered as the indicator species to evaluate the impact of the insecticide treatments tested. Statistical analysis showed no significant difference in *Orius nymphs* (N), adults (A) and total population (N + A) before treatments, whereas after treatments Orius was significantly lower in the CON than in IPM in all cases. No differences in Orius population were determined between IPM1 and IPM2. The percentage reduction calculated in total Orius (N + A) after the three insecticide treatments ranged from 91% for CON, 18% for IPM1 to 4% for IPM2. The latter had a significantly higher number of plants broken below the ear, total number of broken plants and damaged ears by *O. nubilalis* compared to CON and IPM1, but no significant difference was determined between treatments in percentage ear surface damaged, being below 1% in all cases. Treatment with chlorantraniliprole did not affect Orius population confirming its selectivity towards this species, conserved Orius at the same level as *B. thuringiensis* var. kurstaki and had similar efficacy to the CON against *O. nubilalis*.

Keywords: Biopesticides; Conservative biological control; IPM; Maize; *Orius* spp.; *Ostrinia nubilalis*; Selectivity

Crop Protection

Volume 97, Pages 45-51

Cave hygropetric beetles and their feeding behaviour, a comparative study of *Cansiliella servadeii* and *Hadesia asamo* (Coleoptera, Leiodidae, Cholevinae, Leptodirini)

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Abstract

Several Leptodirini beetles (Leiodidae) are known to dwell in hygropetric habitats where films of water run down the cave walls, but observations of their behaviour are lacking. The ultra-specialised hygropetricolous beetles belonging to the genera *Cansiliella* and *Hadesia* are biogeographically and phylogenetically unrelated leptodirines. As the species of the former genus are known to be associated with the moonmilk deposits our study aimed to obtain data on their foraging behaviour, as well as to compare the feeding strategies of both genera. In situ monitoring of *C. servadeii* from the cave Grotta della Foos (Italy) and *H. asamo* from Bravenik Cave (Bosnia and Herzegovina), was complemented by video recordings to ensure accurate results. Mouthparts and tarsi of both species were examined using scanning electron microscopy and compared with *H. weiratheri* from Montenegro to evaluate potential morphological adaptations to the hygropetricolous ecological niches. The three species had significantly different mouthpart morphologies, likely due to differences in semi-aquatic feeding strategies and overall ecology. A series of new observations on site movement and feeding behaviour are presented, compared and discussed.

Keywords: Behaviour; Cave hygropetric; Coleoptera; Ecology; Moonmilk

Acta Carsologica

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Control of *Scaphoideus titanus* with natural products in organic vineyards

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Abstract

The leafhopper *Scaphoideus titanus* is the vector of '*Candidatus* Phytoplasma vitis', the causal agent of Flavescence dorée (FD) a key disease for European viticulture. In organic vineyards, the control of *S. titanus* reliesmostly on the use of pyrethrins that have suboptimal efficacy. During 2016, three field trials were conducted to evaluate the efficacy of kaolin, orange oil, insecticidal soap and spinosad against *S. titanus* nymphs, in comparison with pyrethrins. The activity of kaolin was evaluated also in the laboratory. In all field trials, kaolin had an efficacy against nymphs comparable to pyrethrins, while the other products were not effective. Laboratory results confirmed that kaolin increased nymph mortality. In organic vineyards, kaolin and pyrethrins are valuable tools in the management of FD. Nevertheless, their efficacy is lower compared to that of the synthetic insecticides used in conventional viticulture. Therefore, further research should be conducted in order to identify alternatives to synthetic insecticides for *S. titanus* control in the context of organic viticulture.

Keywords: Flavescence dorée; Kaolin; Natural substances; Organic viticulture; Pyrethrins; *Scaphoideus titanus*; Vector control

Insects

Volume 8, Issue 4, Article number 129

Density-dependence in the declining population of the monarch butterfly

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Abstract

The Eastern monarch butterfly population has significantly declined over the last two decades creating growing concerns around its conservation status. Here, we showed that the overwintering population exhibited a negative density-dependence (i.e. a negative effect on growth rate of the density in the previous year) and that, after accounting for the density effect, the population growth rate tended to decline over time. The negative time effect is probably linked to the host plant (i.e. milkweed) decline in North America. A negative density-dependence was also found in the time series of both egg density per host plant and adult density across North America suggesting the importance of a bottom-up, resource-driven regulation such as host plant limitation and/or of a top-down regulation through generalist natural enemies or diseases. The temporal stability of the density effect indicated that the negative density-dependence and the population decline are likely independent phenomena. One of the most common conclusions of previous research is that environmental stochasticity is the dominant key compounded driver of population dynamics. We showed that density dependence explained 37-50% of the total variation in growth rate in three independent datasets, indicating that several non-exclusive density-related mechanisms can be important in monarch population dynamics.

Scientific Reports

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Effects of elevation and aspect on the flight activity of two alien pine bark beetles (Coleoptera: Curculionidae, Scolytinae) in recently-harvested pine forests

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Abstract

Climate is an important driver of the establishment and impact of invasive alien species. Species transported to new regions can only invade those with a climate that meets their thermal requirements, but climate change is likely to alter the invasibility of recipient environments. Likewise, species are unlikely to reach pest status where climatic conditions are suboptimal. Here our objectives were to determine the relationship between climatic conditions and flight activity of two alien pine bark beetles (*Hylastes ater* and *Hylurgus ligniperda*) and to anticipate how climate change may affect the future distribution of these species. We used elevational gradients and slope aspect (north versus south-facing slopes), which are known to affect microclimates, to assess the effects on beetle flight across 18 locations in pine forests in the South Island, New Zealand. Using panel traps baited with alpha-pinene and ethanol we caught a total of 45,363 *H. ligniperda* and 6676 *H. ater*. Catches of both species decreased significantly and substantially with increasing elevation. Significantly more beetles were caught at north-facing than at south-facing sites towards the end of the flight season in autumn, leading to an extended flight period at northerly aspects. These results are important for pest management and the identification of 'areas of low pest prevalence' as a measure to reduce post-harvest infestations of logs destined for export. For example, during risk periods, logs could be harvested preferentially from stands with reduced flight activity (i.e., southerly aspects and higher elevations). Furthermore, such sites could be chosen to reduce post-harvest infestation risks during periods of temporary log storage at skid sites in the forest. Our findings are also important because climate change can be an important factor contributing to population expansion of bark beetles, and warmer temperatures could lead to increased flight activity and abundance, as well as enhanced suitability of sites that are currently less favourable.

Keywords: Alien species; Biological invasions; Climate change; *Hylastes ater*; *Hylurgus ligniperda*; Microclimate

Forest Ecology and Management

Volume 384, Pages 132-136

Efficacy and mode of action of Kaolin in the control of *Empoasca vitis* and *Zygina rhamni* (Hemiptera: Cicadellidae) in vineyards

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Abstract

During 2015, the influence of kaolin applications and bunch-zone leaf removal on the grapevine leafhoppers, *Empoasca vitis* (Göthe) and *Zygina rhamni* Ferrari, and their egg parasitoids (*Anagrus* spp.) was tested in four vineyards of northeastern Italy. The mode of action of kaolin on *E. vitis* nymphs was also investigated in the laboratory. In the treated plots, kaolin was applied at a rate of 2% w/v on two occasions separated by 5-6 d. In two vineyards, it was applied either on the whole canopy or the bunch zone at the beginning of the *E. vitis* second generation (preventive criterion), and in the other two vineyards, it was applied to the whole canopy at the peak of the E. vitis third generation (curative criterion). Both the preventive and curative kaolin applications caused a significant decrease in the populations of *E. vitis* and *Z. rhamni* nymphs. The effect of the preventive applications was persistent and was associated with reduced *E. vitis* leaf symptoms. Kaolin did not influence the activity of *Anagrus* spp. Bunch-zone leaf removal did not affect leafhopper populations. Laboratory experiments showed that inhibition of feeding was the main mode of action through which kaolin affected nymph populations. Based on these outcomes, kaolin could be a valuable alternative to synthetic insecticides in controlling grapevine leafhoppers.

Keywords: Anagrus; Feeding inhibition; Grapevine; Leaf removal; Leafhopper

Journal of Economic Entomology

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Environmental heterogeneity effects on predator and parasitoid insects vary across spatial scales and seasons: a multi-taxon approach

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Abstract

As predator and parasitoid insects depend on multiple resources for adult feeding and reproduction, environmental heterogeneity (EH) is expected to be a key driver of their species diversity. In temperate regions, the benefits of EH are expected to vary across spatial scales and seasons, depending on species life-history traits and temporal fluctuations in resources. We tested the importance of EH at multiple spatial scales on diversity and abundance of predator and parasitoid insects, and whether its effects changed across seasons. Insect sampling was carried out in highly fragmented landscapes in a Mediterranean region (Tuscany, Central Italy). We selected 18 semi-natural patches, embedded in an intensive agricultural matrix. For each patch, EH was measured at three spatial scales (micro, patch, and landscape). Five groups of predator and parasitoid insects were sampled 16 times with pan traps between March and November, 2012. EH at the landscape scale positively influenced the diversity of predator and parasitoid insects, while the effects at smaller spatial scales were less evident. The strength and the direction of EHdiversity relationship changed between groups and across seasons, indicating that the mechanisms by which EH affects predators and parasitoids are various and complex. Conservation strategies aimed at maximising the diversity of predators and parasitoids should focus more on increasing EH at the landscape scale than at the local scale.

Keywords: Habitat diversity; Habitat fragmentation; Landscape; Scale-dependence; Seasonality; Temporal dynamics

Insect Conservation and Diversity

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Fine-scale phylogeography of *Rana temporaria* (Anura: Ranidae) in a putative secondary contact zone in the southern Alps

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Abstract

The common frog (*Rana temporaria*) has been the focus of several broadscale phylogeographic studies, revealing a deep split between eastern and western European populations, most likely induced by the onset of the Pleistocene glaciations. However, the identification of glacial refugia, as well as the understanding of recolonization processes and their genetic legacy remain far from complete. A recent survey on Italian populations revealed a previously unrecognized Pleistocene refuge in the Italian peninsula and suggested the hypothesis of multiple separated microrefugia ('refugia-within refugia' model), but fine-scale studies required to confirm this hypothesis are lacking. We examined the phylogeographic structure of 54 common frog populations (540 individuals) by means of COI (cytochrome oxidase I) mitochondrial gene, focusing on a south-eastern Alpine region (Trentino, Italy) with an intensive sampling design. Phylogeographical reconstruction indicated the presence of three different COI lineages, exhibiting different levels of genetic diversity, and a contact zone in the eastern part of the region. Our data supported the scenario of multiple sub-refugia, probably located in the southern slopes of the Alpine chain, where the species survived the ice ages in fragmented populations. The recorded patterns are explained by the biogeographic peculiarity of the study region.

Keywords: Amphibians; Common frog; Genetic diversity; Glacial refugia; Mitochondrial DNA; Postglacial recolonization

Biological Journal of the Linnean Society

Volume 122, Issue 4, Pages 824-837

First report of the ambrosia beetle *Xylosandrus compactus* and associated fungi in the Mediterranean maquis in Italy, and new host–pest associations

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Abstract

In September 2016, a survey conducted in the Circeo National Park revealed an outbreak and serious damage caused by the black twig borer (*Xylosandrus compactus*) and its associated fungi in the Mediterranean maquis. Among the affected hosts, Quercus ilex, *Viburnum tinus*, *Ruscus aculeatus*, *Pistacia lentiscus*, *Laurus nobilis* and *Ceratonia siliqua*, showed flagging and wilting of branches and, in younger individuals, the death of the whole plant occurred. In total, 18 different fungal taxa were found associated with the insect. These included *Ambrosiella xylebori*, *Geosmithia pallida*, *Fusarium* spp., *Epicoccum nigrum* and *Bionectria* sp. This is the first report in Europe of *X. compactus* and associated ambrosia fungi in a natural environment.

EPPO Bulletin

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Fungal communities associated with bark and ambrosia beetles trapped at international harbours

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Abstract

Bark and ambrosia beetles (Coleoptera; Scolytinae) establish trophic relationships with fungi, which could be also agents of plant diseases. *Orthotomicus erosus* (Wollaston) and *Xyleborinus saxesenii* (Ratzeburg) are two species of Palaearctic origin that have been introduced in several countries around the world. Here, we investigated their associated fungal communities using individuals trapped at harbours in their native range, without strictly focusing on nutritional symbionts. Targeting the ITS2 region of the fungal rDNA through pyrosequencing, we retrieved taxa known to be agents of plant diseases, taxa never previously reported associated with these beetle species, and sequence clusters not linked to any known fungus. These findings underline that surveillance at harbours should be extended to the fungi associated with trapped bark and ambrosia beetles, taking into account their role as potential vectors of plant pathogens.

Keywords: ITS2; Metabarcoding; Ophiostomataceae; *Orthotomicus erosus*; Pyrosequencing; Scolytinae; *Xyleborinus saxesenii*

Fungal Ecology

Volume 28, Pages 44-52

Great molecular variation within the species *Phytoseius finitimus* (Acari: Phytoseiidae): Implications for diagnosis decision within the mite family phytoseiidae

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Abstract

Molecular markers are increasingly used for species identification and new taxa description. However, rules to determine frontiers between populations and species are not clear depending on taxa considered. For mites, few studies deal with molecular diagnoses, making associated decision' rules difficult. The present study focuses on a species of the predatory mite family Phytoseiidae (*Phytoseius finitimus*), considered for biological control of mites and small insect pests in fruit orchards and vineyards in the Mediterranean basin. This paper aims to elucidate the causes of great molecular variations and questions the occurrence of cryptic species. Molecular (12S rRNA, CytB mtDNA, ITSS) and morphological analyses were performed on four populations collected in Corsica and Italy in crops (vine and kiwi) and in an uncultivated environment (*Viburnum lantana*). Different methods for identifying species have been used (tree approaches, distances and ABGD algorithms). A reference database of distances within and between Phytoseiidae species has been elaborated to inform the present question and to assist with further diagnosis within Acari. Mitochondrial DNA analyses show that specimens from V. lantana were well separated from the three other populations with high genetic distances, suggesting the existence of a cryptic species. Molecular ITSS analyses coupled with morphological features show however that the four populations seem to belong to the same species. The great mitochondrial polymorphism is discussed in regards to: (i) genetic distances reported for Phytoseiidae species and (ii) potential biological differences between populations (cultivated versus uncultivated areas). This study clearly emphasizes the necessity of integrative taxonomy approaches for diagnosis decisions. Furthermore, based on the polymorphism herein detected, maximal intraspecific distances are proposed (9, 23 and 2.8% for 12S rRNA, CytB mtDNA and ITSS) for diagnosis decisions within Phytoseiidae. Further statistical analyses are however clearly required to determine statistical error for general and reliable decision making.

Keywords: Acari; Integrative taxonomy; Molecular taxonomy; Morphometrics; Species delineation

Acarologia

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New records of Iranian bark beetles (Coleoptera: Curculionidae, Scolytinae) and their host plants

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Abstract

Bark and ambrosia beetles from the subfamily Scolytinae are among the most important pests in forests of Northern Iran. During investigations conducted in 2013-2016 in different parts of northern forests, the species *Crypturgus cribrellus* Reitter, *Liparthrum bartschti* Mühl, *Scolytus varshalovitchi* Michalski, *Scolytus sulcifrons* Rey, *Scolytus triarmatus* (Eggers) and *Trypophloeus granulatus* (Ratzeburg) were recorded for the first time in Iran; Trypophloeus and Liparthrum were new genera for Iran. As new host plants we found *Zelkova* sp. for *Scolytus varshalovitchi*, *Michalski*, *Populus* sp. for *Liparthrum bartschti*, Mühl, *Alnus* sp. and *Pterocarya fraxinifolia* for *Taphrorychus lenkoranus* Reitter, *Pterocarya fraxinifolia* for *Ernoporicus caucasicus* (Lindemann), *Carpinus* sp. for *Pteleobius vittatus* (Fabricius), *Parrotia persica* for *Scolytus intricatus* (Ratzeburg), *Alnus* sp. and *Pterocarya fraxinifolia* for *Hypothenemus eruditus* (Westwood).

Keywords: Bark beetles; Forests; Iran; New hosts; New records

Zootaxa

Volume 4350, Issue 2, Pages 396-400

Reproductive biology of *Sclerodermus brevicornis*, a European parasitoid developing on three species of invasive longhorn beetles

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Abstract

The reproductive performance of *Sclerodermus brevicornis* (Kieffer), a bethylid wasp native to Europe, was evaluated on three species of factitious hosts. These are longhorn beetles which have recently invaded Europe from Asia: *Anoplophora glabripennis* (Motschulsky), *Anoplophora chinensis* (Forster) and *Psacothea hilaris hilaris* (Pascoe) (Coleoptera: Cerambycidae). *Sclerodermus brevicornis* attacked all three species, but offspring only developed to maturity on medium and large sized host larvae. Host species influenced the duration of parasitoid development and the number of offspring maturing, both were greatest on *A. glabripennis*, with up to 373 adult parasitoids emerging from a single host. The sex ratios of *S. brevicornis* broods were strongly female biased (ca. 9% males). We conclude that *S. brevicornis* has the potential to be efficiently mass-reared and actively deployed in the biological control of invasive longhorn beetles. Further progress should be encouraged by the successful use of other species of Sclerodermus against beetle pests in China.

Keywords: *Anoplophora* spp.; Bethylid wasp; Biological control; Exotic alien species; Maternal care; *Psacothea hilaris hilaris*; Rearing techniques

Biological Control

Volume 105, Pages 40-48

Soil pathogen-aphid interactions under differences in soil organic matter and mineral fertilizer

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Abstract

There is increasing evidence showing that microbes can influence plant-insect interactions. In addition, various studies have shown that aboveground pathogens can alter the interactions between plants and insects. However, little is known about the role of soil-borne pathogens in plant-insect interactions. It is also not known how environmental conditions, that steer the performance of soil-borne pathogens, might influence these microbe-plant-insect interactions. Here, we studied effects of the soil-borne pathogen *Rhizoctonia solani* on aphids (*Sitobion avenae*) using wheat (*Triticum aestivum*) as a host. In a greenhouse experiment, we tested how different levels of soil organic matter (SOM) and fertilizer addition influence the interactions between plants and aphids. To examine the influence of the existing soil microbiome on the pathogen effects, we used both unsterilized field soil and sterilized field soil. In unsterilized soil with low SOM content, *R. solani* addition had a negative effect on aphid biomass, whereas it enhanced aphid biomass in soil with high SOM content. In sterilized soil, however, aphid biomass was enhanced by *R. solani* addition and by high SOM content. Plant biomass was enhanced by fertilizer addition, but only when SOM content was low, or in the absence of *R. solani*. We conclude that belowground pathogens influence aphid performance and that the effect of soil pathogens on aphids can be more positive in the absence of a soil microbiome. This implies that experiments studying the effect of pathogens under sterile conditions might not represent realistic interactions. Moreover, pathogen-plant-aphid interactions can be more positive for aphids under high SOM conditions. We recommend that soil conditions should be taken into account in the study of microbe-plant-insect interactions.

Keywords: Aphid; Biomass; Carbon; Fertilizer

PLoS ONE

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First record of the Granulate Ambrosia Beetle, *Xylosandrus crassiusculus* (Coleoptera: Curculionidae, Scolytinae), in the Iberian Peninsula

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Abstract

The Granulate Ambrosia Beetle *Xylosandrus crassiusculus*, an alien species of Asian origin, was recorded for first time in the Iberian Peninsula. Many specimens were collected in October 2016 in the Valencia region (Spain) from infested carob trees. The species is included in the EPPO Alert List as causing serious damage in many Mediterranean regions. A key for the morphological identification of the Xylosandrus species occurring in Europe is also reported.

Keywords: Coleoptera; Curculionidae; Scolytinae

Zootaxa

Volume 4273, Issue 3, Pages 431-434

Aspidiotus bornmuelleri Lindinger, 1911, Rev. Comb. (Hemiptera: Coccomorpha: Diaspididae), a neglected endemic species from Macaronesia, with comments on the genus *Cryptophyllaspis*, and further notes on the scale insect fauna of Canary Islands, Spain

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Abstract

Cryptophyllaspis bornmuelleri (Lindinger) (Hemiptera: Diaspididae), an endemic plant-galling species from the Canary Islands, has been re-collected in Tenerife. The galls induced by this species on *Globularia salicina* leaves and the diaspidid adult female are redescribed and illustrated. Detailed study of the species has resulted in the combination *Aspidiotus bornmuelleri* Lindinger being revived, with *C. bornmuelleri* sunk as a junior synonym. Its taxonomic history, and comments on the genus *Cryptophyllaspis* and the other species pertaining to it, are reported. Further data on the scale insect fauna of Canary Islands are also presented.

Keywords: *Bambusaspis miliaris*; Galls; *Globularia salicina*; *Icerya seychellarum*; Redescription; *Voraspis nerii*

Zootaxa

Volume 4300, Issue 1, Pages 99-110

Effect of spray drift reduction techniques on pests and predatory mites in orchards and vineyards

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Abstract

Spray drift of pesticides has a negative impact on aquatic ecosystems and the environment, including damage to non-target organisms. Particularly, the drift of some insecticides can have detrimental effects on beneficial arthropods such as predatory mites. According to a recent EU Directive, the reduction of spray drift is required for a sustainable use of pesticides, yet without reduction of efficacy against pests. In this framework, eight field trials were conducted from 2012 to 2014 in two typical growing areas of Verona district (Northern Italy), four on apple orchards and four on vineyards. The aim of these trials was to evaluate, for two spray drift reduction techniques: 1) the spatial patterns of in-field droplets, 2) the efficacy against key pests on apple and grape (*Cydia pomonella* L. and *Lobesia botrana* Denis & Schiffermüller respectively), 3) the side effects on predatory mite populations. Four insecticides: chlorpyrifos, chlorpyrifos-methyl, methoxyfenozide and spinetoram, were applied with three different spraying techniques: high-drift nozzles (Albuz, ATR 80 yellow), low-drift nozzles (Albuz, TVI 80015 green), and high-drift nozzles with an anti-drift adjuvant (rapeseed oil). Results showed that the two spray drift reduction techniques effectively increased droplets amounts next to sprayer, reducing potential drift on both apple orchards and vineyards and were generally as effective as standard nozzles without additional side effects on beneficial arthropods. Results suggest that the use of spray drift reduction techniques such as low-drift nozzles and anti-drift adjuvants can be effective in managing key pests and also in decreasing the environmental impact of using insecticides.

Keywords: *Cydia pomonella*; *Lobesia botrana*; Low-drift nozzles; Oil-based anti-drift adjuvants; Phytoseidae

Crop Protection

Volume 98, Pages 283-292

Processionary moths and associated urtication risk: Global change-driven effects

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Abstract

Processionary moths carry urticating setae, which cause health problems in humans and other warm-blooded animals. The pine processionary moth *Thaumetopoea pityocampa* has responded to global change (climate warming and increased global trade) by extending its distribution range. The subfamily Thaumetopoeinae consists of approximately 100 species. An important question is whether other processionary moth species will similarly respond to these specific dimensions of global change and thus introduce health hazards into new areas. We describe, for the first time, how setae are distributed on different life stages (adult, larva) of major groups within the subfamily. Using the available data, we conclude that there is little evidence that processionary moths as a group will behave like *T. pityocampa* and expand their distributional range. The health problems caused by setae strongly relate to population density, which may, or may not, be connected to global change.

Keywords: Climate; Health; Notodontidae; Plant trade; Seta; Thaumetopoeinae

Annual Review of Entomology

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Proteome analysis of Urticating Setae from *Thaumetopoea pityocampa* (Lepidoptera: Notodontidae)

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Abstract

Thaumetopoea pityocampa (Denis & Schiffermüller) (Lepidoptera: Notodontidae) is harmful to conifer trees because of defoliation and to public health because of the release of urticating setae from the caterpillars. Contact with setae by humans and domestic animals induces dermatitis, usually localized to the exposed areas. Recent studies demonstrated the presence of a complex urticating mechanism where proteins present in the setae may play a role as activators of immune responses. Yet, limited information is available at present about the proteins occurring in the setae of *T. pityocampa*. Using a refined method for protein extraction from the setae, and a combination of liquid chromatography tandem-mass spectrometry (LC-MS/MS), de novo assembly of transcriptomic data, and sequence similarity searches, an extensive data set of 353 proteins was obtained. These were further categorized by molecular function, biological process, and cellular location. All the 353 proteins identified were found to match through BLAST search with at least one Lepidoptera sequence available in databases. We found the previously known allergens Tha p 1 and Tha p 2 described from *T. pityocampa*, as well as enzymes involved in chitin biosynthesis, one of the principal components of the setae, and serine proteases that were responsible for inflammatory and allergic reactions in other urticating Lepidoptera. This new proteomic database may allow for a better understanding of the complexity of allergenic reactions due to *T. pityocampa* and to other Lepidoptera sharing similar defense systems.

Keywords: Allergen; Caterpillar; Hair; Transcriptome

Journal of Medical Entomology

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Pest categorisation of *Gilpina hercyniae*

Jeger, M., Bragard, C., Caffier, D., Candresse, T., Chatzivassiliou, E., Dehnen-Schmutz, K., Gilioli, G., Jaques Miret, J.A., MacLeod, A., Navajas Navarro, M., Niere, B., Parnell, S., Potting, R., Rafoss, T., Rossi, V., Urek, G., Van Bruggen, A., Van der Werf, W., West, J., Winter, S., Battisti, A., Kertész, V., Aukhojee, M., Grégoire, J.-C.

EFSA PLH Panel (EFSA Panel on Plant Health)

Abstract

The Panel on Plant Health performed a pest categorisation of the Diprionid sawfly, *Gilpinia hercyniae* Hartig (Hymenoptera: Diprionidae), for the EU. *G. hercyniae* is a well-defined and distinguishable species, native to Europe but also present in North America, Japan, Mongolia, Korea and Pakistan, and recognised as a pest of spruce (*Picea* spp.). The pest is distributed in 19 Member States (MSs) of the EU. It is a quarantine pest listed in Annex IIB of Council Directive 2000/29/EC. Protected zones are in place in Greece, Ireland and the United Kingdom (Northern Ireland, Isle of Man and Jersey). Plants for planting of *Picea* spp. and soil and litter associated with *Picea* spp. are considered as pathways for this pest, which is also able to disperse by flight. The prepupae overwinter inside cocoons in the litter or in the foliage. In spring, the adults, mostly females emerge and lay 35–60 eggs per female in mature needles. The larvae feed on the mature needles through five instars. There are 1–3 generations per year; some of the prepupae undergo prolonged diapause for more than 1 year. The impact on *Picea abies* (= *excelsa*) is minimal, because only the needles of the previous years are attacked; however, outbreaks have occurred on non-native spruce, *Picea glauca* and *Picea sitchensis*. The pest is controlled everywhere by natural enemies, including nuclear polyedrosis viruses. The insects spread on plants for planting of *Picea* spp., with soil and litter associated with *Picea* spp., and by flight. The EU protected zones have a similar climate and similar host plants as the MS where *G. hercyniae* is established. All criteria assessed by EFSA for consideration as potential protected zone quarantine pest and as a potential regulated non-quarantine pest were met.

Keywords: Diprionidae; European spruce sawfly; European Union; Pest risk; Plant health; Plant pest; Quarantine

EFSA Journal

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Pest categorisation of *Cephalcia lariciphila*

Jeger, M., Bragard, C., Caffier, D., Candresse, T., Chatzivassiliou, E., Dehnen-Schmutz, K., Gilioli, G., Jaques Miret, J.A., MacLeod, A., Navajas Navarro, M., Niere, B., Parnell, S., Potting, R., Rafoss, T., Rossi, V., Urek, G., Van Bruggen, A., Van der Werf, W., West, J., Winter, S., Battisti, A., Kertész, V., Aukhojee, M., Grégoire, J.-C.

EFSA PLH Panel (EFSA Panel on Plant Health)

Abstract

The Panel on Plant health performed a pest categorisation of the larch web-spinning sawfly *Cephalcia lariciphila* (Hymenoptera: Pamphiliidae) for the EU. The insect has been reported in 11 EU Member States (MSs). It is a quarantine pest listed in Annex IIB of Council Directive 2000/29/EC. Protected zones are in place in Ireland and the UK (Northern Ireland, Isle of Man and Jersey). *C. lariciphila* can feed on all species of the genus *Larix*. There have been reported outbreaks in the Czech Republic, Germany, the Netherlands and the UK (England and Wales) in plantations of European larch (*Larix decidua*) and Japanese larch (*Larix kaempferi = Larix leptolepis*). *C. lariciphila* is absent in the protected zones. The pest can enter the protected zones by human-assisted spread or by natural spread from EU areas where the pest is present. Plants for planting are considered the most important pathway for the pest. The pest can establish in the protected zones because the climatic conditions are similar to those of the 11 MSs where *C. lariciphila* is established, and the pest's main host plants are present. The prepupae overwinter in the litter, the adults emerge during May–June, and each female lays 30–40 eggs in slits in mature needles. The larvae feed on the needles through four instars. There is one generation per year; some of the prepupae undergo prolonged diapause for more than 1 year. The impact where the pest occurs is mainly related to the loss of tree growth following defoliation, while tree mortality was locally observed only after repeated defoliation. However, impact is likely to be mitigated by local biological control agents. All criteria assessed by EFSA above for consideration as a potential protected zone quarantine pest and as a potential regulated non-quarantine pest were met.

Keywords: European Union; European web-spinning larch sawfly; Pamphiliidae; Pest risk; Plant health; Plant pest; Quarantine

EFSA Journal

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Food science and technology

Electrostatic and conventional spraying of alginate-based edible coating with natural antimicrobials for preserving fresh strawberry quality

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Abstract

Microbial contamination and mold growth are common causes of strawberry deterioration during storage. The growing need for extending shelf-life while enhancing the overall quality of perishable fruits has generated increasing interest in the development of novel preservation technologies. This study used electrostatic spraying (ES) technology as an innovative and efficient technique for the application of edible alginate coating enriched with carvacrol and methyl cinnamate (natural antimicrobials) on fresh strawberries. The efficiency of the electrostatic technology was compared to non-electrostatic (conventional) spray (NES) technology in terms of transfer efficiency and coating evenness. Furthermore, physicochemical and textural parameters (such as weight loss, visible decay, firmness, surface color, total soluble phenolic content, and antioxidant capacity) of ES and NES coated fruits were studied and compared to uncoated controls. ES technology demonstrated higher transfer efficiency and evenness than NES, which led to a significant reduction of visible decay over uncoated controls. The delay in microbial spoilage by ES (11 days) was greater than by NES (10 days) and uncoated strawberries (7 days). ES coating significantly inhibited strawberry decay with only 5.6 % of infected fruits, compared to 16.6 and 8.3 % for control and NES fruits after 13 days of storage, respectively. At the end of 13 days of storage, ES coating demonstrated superior performance on strawberry firmness, color retention, and weight loss reduction. Additionally, no differences were observed between uncoated and coated fruits with regard to their antioxidant and total soluble phenolics.

Keywords: Alginate coating; Carvacrol; Essential oils; Methyl cinnamate; Physicochemical parameters; Shelf-life

Food and Bioprocess Technology

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Selenium biofortification in *fragaria x ananassa*: Implications on strawberry fruits quality, content of bioactive health beneficial compounds and metabolomic profile

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Abstract

Selenium (Se) is an essential nutrient for humans, due to its antioxidant properties, whereas, to date, its essentiality to plants still remains to be demonstrated. Nevertheless, if added to the cultivation substrate, plants growth resulted enhanced. However, the concentration of Se in agricultural soils is very variable, ranging from 0.01 mg kg^{-1} up to 10 mg kg^{-1} in seleniferous areas. Therefore several studies have been performed aimed at bio-fortifying crops with Se and the approaches exploited were mainly based on the application of Se fertilizers. The aim of the present research was to assess the biofortification potential of Se in hydroponically grown strawberry fruits and its effects on qualitative parameters and nutraceutical compounds. The supplementation with Se did not negatively affect the growth and the yield of strawberries, and induced an accumulation of Se in fruits. Furthermore, the metabolomic analyses highlighted an increase in flavonoid and polyphenol compounds, which contributes to the organoleptic features and antioxidant capacity of fruits; in addition, an increase in the fruits sweetness also was detected in biofortified strawberries. In conclusion, based on our observations, strawberry plants seem a good target for Se biofortification, thus allowing the increase in the human intake of this essential micronutrient.

Keywords: Flavonoids; Fruit quality; Metabolomics/metabolite profiling; Phenolic compounds; Se biofortification; Strawberry

Frontiers in Plant Science

Volume 8, Article number 1887

Physiological responses of wine grape berries to postharvest ethylene treatments

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Abstract

The application of ethylene to harvested grapes affects wine composition mainly in terms of phenol concentration and aroma compound profiling. Microarray analysis performed on skins of wine grapes (*Vitis vinifera*, 'Sangiovese') treated, after harvest, with 1,000 ppm of ethylene for 36 h revealed no difference between control and treated samples in terms of flavonoid-related genes, thus supporting the hypothesis of an effect of exogenous ethylene on extractability during vinification rather than on increasing flavonoid biosynthesis. Changes in specific lipophilic compound concentration have been observed with antheraxanthin and violaxanthin accumulating in ethylene-treated berries and neoxanthin (and, at lesser extent, β-carotene) more abundant in control samples. A correlation network analysis based on transcript-metabolite data integration showed that antheraxanthin was strongly correlated ($|\rho|>0.90$) with SAMDC gene expression (direct) and β-carotene (inverse). Taking into account the relationships existing between carotenoids and abscisic acid (ABA) and considering that, in other plant species, SAMDC expression is induced by exogenous ABA, these results suggest that responses to exogenous ethylene in harvested grape berries are mediated by ABA. This hypothesis is also strengthened by the HORMONEMETER analysis performed on microarray data, pointing out a general correlation with ABA, indicating a positive action of the ethylene treatment upstream abscisic acid biosynthesis/metabolism possibly resulting in ABA concentration increase. Our data further confirm that the interplay between ABA and ethylene may represent a key physiological aspect impacting the final stages of grape berry development.

Keywords: Abscisic acid; Carotenoids; Correlative analysis; Hormonometer; Microarray; Secondary metabolism; *Vitis vinifera*

Acta Horticulturae

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A multifunctional bread rich in beta glucans and low in starch improves metabolic control in type 2 diabetes: A controlled trial

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Abstract

Design: Functional foods may be useful for people with diabetes. The soluble fibers beta glucans can modify starch digestion and improve postprandial glucose response. We analyzed the metabolic effects of a specifically designed 'functional' bread, low in starch, rich in fibers (7 g/100 g), with a beta glucan/starch ratio of (7.6:100, g/g), in people with type 2 diabetes mellitus. Methods: Clinical and metabolic data from two groups of age-, sex- and glycated hemoglobin-matched diabetic subjects, taking either the functional bread or regular white bread, over a roughly six-month observation period, were retrieved. Results: Bread intake did not change during the trial. The functional bread reduced glycated hemoglobin by ~0.5% (absolute units) vs. pre-treatment values ($p = 0.028$), and by ~0.6% vs. the control group ($p = 0.027$). Post-prandial and mean plasma glucose was decreased in the treatment group too. Body weight, blood pressure and plasma lipids did not change. The acceptance of the functional bread was good in the majority of subjects, except for taste. Conclusions: A starch-restricted, fiber-rich functional bread, with an increased beta glucan/starch ratio, improved long term metabolic control, and may be indicated in the dietary treatment of type 2 diabetes.

Keywords: Beta glucan; Fibers; Metabolic control; Plasma glucose; Starch

Nutrients

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Bee moth (*Galleria mellonella*) allergy: New insight from a case of monosensitization

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Abstract

We present a case of bee moth (*Galleria mellonella*, Gm) allergy which shows some new clinical and immunological features, including a skin late phase reaction (LPR). Prick-by-prick test with showed a strong positive reaction with living larvae and a challenge confirmed the result. Immunoblotting analysis showed IgE-binding to bands at 27, 45 and 40 KDa, but only a 20 KDa band was reveled in heat-treated larvae. Anti-human IgG1, IgG3 and IgG4 antibodies were used to detect the presence of patient's IgG binding to the larvae proteins in immunoblotting. Bands of 47 and 20 kDa in extracts of Gm were detected by anti-IgG1 and anti-IgG3 antibodies, whereas no IgG4 antibodies were found. Allergic sensitization to bee moth seems to be uncommon, but the matter is of great interest as eating insects starts to spread also in Western Countries and the risk of allergic reactions to insect proteins has been stressed in advisory reports. In the present case-study we have observed, for the first time, immediate and late hypersensitivity skin reactions to heat-treated Gm larvae and proved IgE-binding also to thermostable allergens. With the introduction of insects as foods for humans we should expect and take into consideration the risk of sensitization and systemic allergic reactions from the consumption of bee moth and other edible insects.

Annals of Allergy, Asthma and Immunology

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Can sensory analysis and e-noses support the assessment work behind DOC and DOCG wines?

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Abstract

Protected Denominations of Origin (PDO) DOC/DOCG labelling is a key factor in qualifying wines for premium positioning and requires a batch-level institutional approval based on chemical and physical analyses and a gustative assay by a commission of experts. The highly standardised products required by international markets requires a critical assessment of the quality of the process generating the assaying commission counsel so that well-known denominated wine products, hold and possibly expand, their market position. The present study was carried out to investigate the relations between electronic nose analysis and judge-based sensory analysis and the assaying commission counsel to address possible ways to ‘inject’ quality assurance tools and concepts in the pipeline of the ‘institutional filter’ of the Prosecco-area DOC/DOCG. Chemical analysis and of chemometrics proved good predictors of the assaying commission counsel, while significant deviations between the outcomes of the panel and commission evaluations. The role of the electronic nose detection and of chemical/physical analyses in helping resolve such discrepancies is discussed.

Chemical Engineering Transactions

Volume 57, Pages 1759-1764

Changes in texture analysis parameters of wine grape berries at two ripeness stages: A study on varietal effect

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Abstract

Ripening of grapes is associated with great modifications at both the chemical and physical level. The aim of this work was to describe the changes in physical-mechanical parameters associated to ripening of wine grape berries, as evaluated by texture analysis, in order to understand if these modifications are stable across cultivars, or they are cultivar-specific. Berries from 21 different cultivars were sorted by flotation in different saline solutions, separated in two ripening stages differentiated by the amount of sugars (183 and 217 g L^{-1}) and then analysed. Multivariate and univariate variations in texture analysis parameters were found, which were not constant across the studied grapevine varieties. However, a general behaviour was observed for skin weight, which had the largest variation between the two ripening stages. Other parameters showed significant differences between the ripening stages: skin thickness, berry gumminess, chewiness, and springiness, but the variation was not common to all cultivars. The work therefore evidenced the existence of cultivar-specific differences in the behaviour of physical-mechanical parameters between ripening stages.

Keywords: Berry ripening; Physical-mechanical properties; Skin weight; Texture analysis; *Vitis vinifera* L.; Wine grapes

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Characterization of chitinase isoforms from grape juice

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Abstract

Grape chitinases are recognized as being mainly responsible for protein haze formation in white wines. *Vitis vinifera* L. cv. Manzoni Bianco grape juice proteins were fractionated using anion exchange and hydrophobic interaction chromatographies. According to SDS-PAGE and zymography, six protein bands with chitinolytic activity were subjected to mass spectrometry (MALDI-TOF/TOF MS), which assigned all the bands to *Vitis vinifera* class IV chitinases. These grape chitinase isoforms showing different electrophoretic and chromatographic behaviours are likely to be also distinct in their functionality in wine. This could be relevant to understand the involvement of single chitinase components in wine hazing and to develop specific winemaking techniques for their removal from wine.

Keywords: Chitinase; Electrophoresis; Glycol chitin; Grape juice; Isoform; Mass spectrometry

Italian Journal of Food Science

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Chemical and sensory analysis of verjuice: an acidic food ingredient obtained from unripe grape berries

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Abstract

Verjuice is the unfermented juice obtained from unripe grape berries, typically thinned fruit that is normally discarded. Despite a long history of use as a food ingredient, verjuice does not have a recognized standard of identity nor is made by standardized methods. To assess the potential for production in the Veneto region of Italy, verjuice produced from six different winegrape varieties harvested at three different dates from bunch closure through early *veraison*, and stabilized using either sulphite or sorbate, was subjected to compositional and sensory analyses. pH was found to range from 2.6 to 2.9 while soluble solids (°Brix) ranged from 3.8 to 9.9. Acidity (g/L) ranged from 17.4 to 40.5 while color (A_{420}) varied from 0.04 to 0.50. With respect to sensory character, harvest date had no influence on aroma, but affected taste, whereas the type of preservative used had no effect on taste, but did affect aroma.

Industrial relevance. Unripe grape juice can be used as a food ingredient to provide acidity and flavor and may be suitable as an alternative to vinegar in salad dressings and other applications where the sensory character of acetic acid is unacceptable. Because it can be produced from thinned grapes, a currently unused by-product of winegrape growing, it represents a product of great interest to grape growers and to the food industry.

Keywords: Aroma; Descriptive sensory analysis; Taste; Unripe grape juice; Verjuice; Verjus

Innovative Food Science and Emerging Technologies

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Co-fermentation of onion and whey: A promising synbiotic combination

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Abstract

Juice from three different onion varieties was mixed with sweet whey and used as growth substrate for four lactic acid bacteria strains, isolated from agri-food by-products, to evaluate the possibility to exploit such substrates, known to be reach in bioactive molecules, as fermented drinks for human consumption. Results show good growth performance for *Lactobacillus fabifermentans*, *L. plantarum* and *Streptococcus macedonicus*. On the contrary *S. thermophilus* did not grow in the mixture while *S. macedonicus* did not develop in pure onion juice. After 48 h the overall sugar content decreased significantly. In particular, glucose was not utilized while inulin was completely preserved. Moreover, MS/MS analysis revealed the presence of the rare trisaccharide lactosucrose.

In the light of these considerations, the formulation obtained may be considered a potential synbiotic product with pleasant taste and beneficial effects for consumers and also an eco-friendly solution to convert an agro-food by-product into value added products.

Keywords: Functional food; *Lactobacillus*; Lactosucrose; Prebiotic; *Streptococcus*

Journal of Functional Foods

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Comparative study of sodium bentonite and sodium-activated bentonite fining during white wine fermentation: its effect on protein content, protein stability, lees volume, and volatile compounds

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Abstract

In this work, we compare the effect of the addition during fermentation of both sodium bentonite and sodium-activated bentonite on the protein content, protein stability, lees volume, and aroma compounds of a Sauvignon blanc wine. Protein unstable Sauvignon blanc juices were vinified with or without bentonite added at three different stages: before fermentation, early during fermentation, and towards the end of fermentation. Different addition doses of bentonite were used (*X*, *X* - 0.1, *X* - 0.2 g/L) according to protein instability of the grape juice (*X* = 1.7 and 2.7 g/L to sodium bentonite and sodium-activated bentonite, respectively). The wines stabilized with sodium-activated bentonite presented a higher content of volatile compounds and a lower volume of lees were produced than those treated with sodium bentonite, an effect that was greater when the fining treatment was done before the start of the fermentation.

Keywords: Activated bentonite; Lees; Protein stability; Sauvignon blanc; Sodium bentonite; Volatile compounds

European Food Research and Technology

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Evaluation of antibrowning and antioxidant activities in unripe grapes recovered during bunch thinning

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Abstract

Background and Aims: Research into new systems for controlling enzymatic browning in the agro-food industry has been focused on eco-friendly alternatives to conventional thermal treatments and traditional additives, which could impair the sensory, nutritional and health properties. The use of unripe grapes for reducing alcohol concentration and pH of wines has been previously reported; however, no studies have been made of the evaluation of unripe grapes as potential functional ingredients to control enzymatic browning and to enhance antioxidant properties of plant products.

Methods and Results: Unripe berries were collected in two seasons during bunch thinning of Barbera and Merlot vineyards. Merlot grapes, which had the highest antioxidant activity in the 2,2-diphenyl-1-picrylhydrazyl and ferric reducing ability of plasma assays, were also the most effective in preventing enzyme browning, as confirmed by spectrophotometric assays using commercial mushroom tyrosinase, by zymographic techniques on the isoforms isolated from some plant polyphenol oxidases and by in vivo trials on fresh-cut fruits and vegetables.

Conclusions: The juice of unripe grapes showed not only antibrowning but also antioxidant and whitening activities.

Significance: Unripe grapes discarded during bunch thinning of vineyards represent for the agro-food industry a significant source of bioactive compounds that are easy to produce and safe for human health, thus converting these agricultural wastes into value-added products.

Keywords: Antibrowning; Antioxidant; Bunch thinning; Colour; Polyphenol oxidase; Unripe grapes

Australian Journal of Grape and Wine Research

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Grape seed extract: the first protein-based fining agent endogenous to grapes

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Abstract

Background and Aims: There is a growing interest in finding alternative wine fining agents to replace potentially allergenic animal-derived and plant-derived proteins. In this context, the potential use of grape-derived fining agents would be beneficial as they would not introduce additional, potentially allergenic products to the finished wine. In this project, grape seed flour, a by-product of the grape oil seed industry, has been used to prepare a grape seed extract (GSE) for testing as a novel wine fining agent.

Methods and Results: The fining performance of GSE was compared with that of patatin, pea proteins, polyvinylpolypyrrolidone and potassium caseinate in a white and in a rosé wine, and of ovalbumin and gelatin in a red wine. Reduction of turbidity, effect on wine colour, the concentration of phenolic substances, browning potential and wine sensory attributes were determined. Grape seed extract was effective in decreasing white wine turbidity when compared to potassium caseinate. In red wine, GSE removed some anthocyanin and proanthocyanins, while wine colour was only slightly affected. The greatest GSE effect was observed on the sensory properties of the treated wines, as it strongly reduced the vegetal notes in the rosé wine and improved the overall taste of the red wine as a result of the reduction in both acidity and astringency.

Conclusions: Grape seed extract can be considered a valid allergen-free alternative to the most common wine fining agents.

Significance of the Study: Grape seed extract is the first effective fining agent endogenous to grapes, thus not attracting the legal restrictions concerning the presence of foreign substances.

Keywords: Astringency; Fining; Grape seed; Sensory analysis; Wine

Australian Journal of Grape and Wine Research

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Hen egg white lysozyme is a hidden allergen in Italian commercial ciders

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Abstract

Hen egg white lysozyme (HEWL) is an enzyme used in alcoholic fermentation for its ability to control the growth of Gram-positive and spoilage bacteria, without inhibiting yeast growth, and it allows a reduction in the use of sulphur dioxide. Nevertheless, considering the potential allergenicity of this protein, the presence of HEWL should be declared on the label of the final product. In this work, we analysed 18 commercial Italian ciders by LC-MS/MS and found traces of HEWL in 12 samples without label declaration. We used Western blot and enzyme-linked immunosorbent assay (ELISA) to verify the immunological activity of HEWL, and to quantify its content in the ciders. Two out of 18 samples were found to be positive both by immunoblot and ELISA. The results indicate the requirement of a more stringent control of commercial ciders and the need of label declaration for ciders treated with such compounds.

Keywords: Cider; ELISA; European Union Regulation; Hidden allergens; LC-MS/MS; Lysozyme; Western blot

Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment

Volume 34, Issue 2, Pages 145-151

Investigating the einkorn (*Triticum monococcum*) and common wheat (*Triticum aestivum*) bread crumb structure with X-ray microtomography: effects on rheological and sensory properties

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Abstract

Einkorn wheat (Tm, *Triticum monococcum* L.) has nutritional characteristics that clearly distinguish it from common wheat (Ta, *Triticum aestivum* L.) although its rheological dough properties may be less-performing. Therefore, to better understand the potential of Tm for human consumption and food preparation, we compared the quality of bread baked with ancient einkorn and common wheat leavened with brewer's yeast and sourdough. Results showed that Tm had generally higher firmness (21.6 N vs. 10.5 N), and lower (65.6% vs. 71.2%) and less homogeneous porosity than Ta. These results suggest a minor potential in bread-making regardless of the Tm high total protein content and underline a weaker gluten ability to expand and retain the fermentation gas. The selection of best-performing einkorn varieties and leavening agents (e.g. fresh sourdough) can lead to bread products with acceptable texture features, meeting consumer demand for organic, natural and ancient products.

Keywords: Bread; Einkorn; Texture analysis; X-ray microtomography

International Journal of Food Science and Technology

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Saccharomyces cerevisiae vineyard strains have different nitrogen requirements that affect their fermentation performances

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Abstract

In this work the fermentation performances of seven vineyard strains, together with the industrial strain EC1118, have been investigated at three differing yeast assimilable nitrogen (YAN) concentrations (300 mg N l^{-1}, 150 mg N l^{-1} and 70 mg N l^{-1}) in synthetic musts. The results indicated that the response to different nitrogen levels is strain dependent. Most of the strains showed a dramatic decrease of the fermentation at 70 mg N l^{-1} but no significant differences in CO_2 production were found when fermentations at 300 mg N l^{-1} and 150 mg N l^{-1} were compared. Only one among the vineyard strains showed a decrease of the fermentation when 150 mg N l^{-1} were present in the must. These results contribute to shed light on strain nitrogen requirements and offer new perspectives to manage the fermentation process during winemaking.

Significance and Impact of the Study: Selected vineyard *Saccharomyces cerevisiae* strains can improve the quality and the complexity of local wines. Wine quality is also influenced by nitrogen availability that modulates yeast fermentation activity. In this work, yeast nitrogen assimilation was evaluated to clarify the nitrogen requirements of vineyard strains. Most of the strains needed high nitrogen levels to express the best fermentation performances. The results obtained indicate the critical nitrogen levels. When the nitrogen concentration was above the critical level, the fermentation process increased, but if the level of nitrogen was further increased no effect on the fermentation was found.

Keywords: Beverages; Biotechnology; Environmental; Fermentation; Fermentation biotechnology

Letters in Applied Microbiology

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Spectroscopy reveals that ethyl esters interact with proteins in wine

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Abstract

Impairment of wine aroma after vinification is frequently associated to bentonite treatments and this can be the result of protein removal, as recently demonstrated for ethyl esters. To evaluate the existence of an interaction between wine proteins and ethyl esters, the effects induced by these fermentative aroma compounds on the secondary structure and stability of VVTL1, a Thaumatin-like protein purified from wine, was analyzed by Synchrotron Radiation Circular Dichroism (SRCD) spectroscopy. The secondary structure of wine VVTL1 was not strongly affected by the presence of selected ethyl esters. In contrast, VVTL1 stability was slightly increased by the addition of ethyl-octanoate, -decanoate and -dodecanoate, but decreased by ethyl-hexanoate. This indicates the existence of an interaction between VVTL1 and at least some aroma compounds produced during fermentation. The data suggest that proteins removal from wine by bentonite can result in indirect removal of at least some aroma compounds associated with them.

Keywords: Aroma; Ethyl esters; Proteins; Spectroscopy; SRCD; VVTL1; Wine

Food Chemistry

Volume 217, Pages 373-378

The smell of *terroir*! Olfactory discrimination between wines of different grape variety and different *terroir*

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Abstract

The French term '*terroir*' refers to the relationship between a particular wine and the specific place where it is produced. To date, no investigation has directly tested in an experimentally-controlled setting whether participants can detect different *terroirs* in wines, and if their level of expertise can modulate such performance. We investigated wine olfactory discrimination ability by using a computer-controlled olfactometer. Participants' ability to discriminate two wines only based on the olfactory features of their *terroir* (zone and vineyard), their variety (e.g., cabernet vs. merlot) or both was tested. Olfactory discrimination performance of both novices and wine-professionals reflected whether two wines differed by *terroir*, variety or both. Performance peaked when wines differed in both *terroir* and variety, with *terroir* being more easily discriminated than variety. These results, obtained by controlling for the first time the precision of the olfactory stimulation, provide insightful clues in understanding the wine appreciation process, specifically with respect to the perceptual aspects of *terroir*.

Keywords: Expertise; Olfactometer; Olfactory discrimination; Terroir; VeneTerroir project; Wine

Food Quality and Preference

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Characterization of major and trace minerals, fatty acid composition, and cholesterol content of Protected Designation of Origin cheeses

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Abstract

Cheese provides essential nutrients for human nutrition and health, such as minerals and fatty acids (FA). Its composition varies according to milk origin (e.g., species and breed), rearing conditions (e.g., feeding and management), and cheese-making technology (e.g., coagulation process, addition of salt, ripening period). In recent years, cheese production has increased worldwide. Italy is one of the main producers and exporters of cheese. This study aimed to describe mineral, FA, and cholesterol content of 133 samples from 18 commercial cheeses from 4 dairy species (buffalo, cow, goat, and sheep) and from 3 classes of moisture content (hard, <35% moisture; semi-hard, 35–45%; and soft, >45%). Mineral concentrations of cheese samples were determined by inductively coupled plasma optical emission spectrometry, and FA and cholesterol contents were determined by gas chromatography. Moisture and species had a significant effect on almost all traits: the highest levels of Na, Ca, and Fe were found in cheeses made from sheep milk; the greatest level of Cu was found in cow milk cheese, the lowest amount of K was found in buffalo milk cheese, and the lowest amount of Zn was found in goat cheeses. In all samples, Cr and Pb were not detected (below the level of detection). In general, total fat, protein, and minerals significantly increased when the moisture decreased. Buffalo and goat cheeses had the highest saturated FA content, and sheep cheeses showed the highest content of unsaturated and polyunsaturated FA, conjugated linoleic acid, and n-3 FA. Goat and sheep cheeses achieved higher proportions of minor FA than did cow and buffalo cheeses. Buffalo cheese exhibited the lowest cholesterol level. Our results confirm that cheese mineral content is mainly affected by the cheese-making process, whereas FA profile mainly reflects the FA composition of the source milk. This study allowed the characterization of mineral and FA composition and cholesterol content and revealed large variability among different commercial cheeses.

Keywords: Conjugated linoleic acid (CLA); Dairy products; Goat; Sheep

Journal of Dairy Science

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Development and validation of a near infrared spectrophotometric method to determine total antioxidant activity of milk

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Abstract

In the present study a spectrophotometric method for the determination of total antioxidant activity (TAA) based on ABTS assay was developed and validated on raw milk (RM), whole UHT milk (WUM), partially skimmed UHT milk (SUM), whole pasteurised milk (WM) and partially skimmed pasteurised milk (SM). The most suitable solvent for antioxidant extraction was 80% acetone. Regardless of the type of milk, the coefficient of determination from the linearity test was greater than 0.95. The limit of detection ranged from 0.74 to 6.07 μmol l^{-1} Trolox equivalents. Repeatability, calculated as relative standard deviation of twenty measurements within a day, and reproducibility, calculated as relative standard deviation of sixty measurements across three days, ranged from 1.24 to 4.04% and from 2.18 to 3.52%, respectively. Preservative added to RM had negligible effects on the TAA of milk. The greatest TAA was measured for SM followed by SUM, RM, WM and WUM.

Keywords: Free radical; Milk; Nutraceutical; Repeatability; Reproducibility; Spectrophotometer

Food Chemistry

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Milk coagulation properties and methods of detection

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Abstract

One of the most crucial steps in cheesemaking is the coagulation process, and knowledge of the parameters involved in the clotting process plays an important technological role in the dairy industry. Milk of different ruminant species vary in terms of their coagulation capacities because they are influenced by the milk composition and mainly by the milk protein genetic variants. The milk coagulation capacity can be measured by means of mechanical and/or optical devices, such as Lactodynamographic Analysis and Near-Infrared and Mid-Infrared Spectroscopy.

Keywords: Clotting; Curd firmness; Infrared spectroscopy; Lactodynamograph

Ciência Rural

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Prediction of minerals, fatty acid composition and cholesterol content of commercial cheeses by near infrared transmittance spectroscopy

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Abstract

Prediction models for the mineral, fatty acid (FA) and cholesterol contents of commercial European cheeses using near infrared transmittance spectroscopy were developed. Cheese samples (n = 145) were from different dairy species and ripening time. Sample spectra were matched with mineral, FA and cholesterol reference data to develop prediction models. Modified partial least squares regressions were validated through cross-validation procedure on the complete dataset (n = 145) and through external validation after dividing the data into calibration (74%) and external validation (26%) sets. Satisfactory models were developed for Ca, P, S, Mg and Zn, and for FA groups (saturated, unsaturated, monounsaturated and polyunsaturated FAs), major FAs (myristic, palmitic and oleic acids) and some minor FAs, whereas cholesterol content could not be predicted with adequate accuracy. Results of the present study are a precursor to at-line utilisation of prediction models for the most abundant cheese minerals and FAs at an industry level.

International Dairy Journal

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Prediction of sodium content in commercial processed meat products using near infrared spectroscopy

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Abstract

The present study evaluated the ability of near infrared transmittance (NIT) spectroscopy (FoodScan, 850–1050 nm) to predict sodium (Na) content in commercial processed meat products (*n* = 310) as intact and ground samples. Prediction models were built with all samples spectra and with spectra divided in 5 categories according to the manufacturing meat process. Sodium content (%) was determined using inductively coupled plasma optical emission spectrometry. Modified partial least squares regression for the overall samples showed satisfactory predictive ability for intact (coefficient of determination in cross-validation, R^2_{CV} = 0.93) and ground samples (R^2_{CV} = 0.95). Despite the low number of samples, good specific prediction models were developed for each commercial meat category. In conclusion, NIT is really promising for *at-line* application to predict Na in processed meat products which could help industry to accomplish the new labelling regulation.

Keywords: Bacon; Meat product; Near infrared spectroscopy; Salt; Sausage; Sodium

Meat Science

Volume 125, Pages 61-65

Short communication: Prediction of milk coagulation and acidity traits in Mediterranean buffalo milk using Fourier-transform mid-infrared spectroscopy

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Abstract

Milk coagulation and acidity traits are important factors to inform the cheesemaking process. Those traits have been deeply studied in bovine milk, whereas scarce information is available for buffalo milk. However, the dairy industry is interested in a method to determine milk coagulation and acidity features quickly and in a cost-effective manner, which could be provided by Fourier-transform mid-infrared (FT-MIR) spectroscopy. The aim of this study was to evaluate the potential of FT-MIR to predict coagulation and acidity traits of Mediterranean buffalo milk. A total of 654 records from 36 herds located in central Italy with information on milk yield, somatic cell score, milk chemical composition, milk acidity [pH, titratable acidity (TA)], and milk coagulation properties (rennet coagulation time, curd firming time, and curd firmness) were available for statistical analysis. Reference measures of milk acidity and coagulation properties were matched with milk spectral information, and FT-MIR prediction models were built using partial least squares regression. The data set was divided into a calibration set (75%) and a validation set (25%). The capacity of FT-MIR spectroscopy to correctly classify milk samples based on their renneting ability was evaluated by a canonical discriminant analysis. Average values for milk coagulation traits were 13.32 min, 3.24 min, and 39.27 mm for rennet coagulation time, curd firming time, and curd firmness, respectively. Milk acidity traits averaged 6.66 (pH) and 7.22 Soxhlet-Henkel degrees/100 mL (TA). All milk coagulation and acidity traits, except for pH, had high variability (17 to 46%). Prediction models of coagulation traits were moderately to scarcely accurate, whereas the coefficients of determination of external validation were 0.76 and 0.66 for pH and TA, respectively. Canonical discriminant analysis indicated that information on milk coagulating ability is present in the MIR spectra, and the model correctly classified as noncoagulating the 91.57 and 67.86% of milk samples in the calibration and validation sets, respectively. In conclusion, our results can be relevant to the dairy industry to classify buffalo milk samples before processing.

Keywords: Buffalo cheese; Mid-infrared spectrometry; Milk coagulation property; Milk quality

Journal of Dairy Science

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Technical note: At-line prediction of mineral composition of fresh cheeses using near-infrared technologies

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Abstract

Milk and dairy products are important sources of macro- and trace elements for human health. However, fresh cheeses usually have a lower mineral content than other cheeses, and this makes mineral prediction more difficult. Although mineral prediction in several food matrices using infrared spectroscopy has been reported in the literature, very little information is available for cheeses. The present study was aimed at developing near-infrared reflectance (NIR, 866–2,530 nm) and transmittance (NIT, 850–1,050 nm) spectroscopy models to predict the major mineral content of fresh cheeses. We analyzed samples of mozzarella (n = 130) and Stracchino (n = 118) using reference methods and NIR and NIT spectroscopy. We developed prediction models using partial least squares regression analysis, and subjected them to cross- and external validation. Average Na content was 0.15 and 0.22 g/100 g for mozzarella and Stracchino, respectively. The NIR and NIT spectroscopy performed similarly, with few exceptions. Nevertheless, none of the prediction models was accurate enough to replace the current reference analysis. The most accurate prediction model was for the Na content of mozzarella cheese using NIT spectroscopy (coefficient of determination of external validation = 0.75). We obtained the same accuracy of prediction for P in Stracchino cheese with both NIR and NIT spectroscopy. Our results confirmed that mineral content is difficult to predict using NIT and NIR spectroscopy.

Keywords: Mineral; Mozzarella cheese; Sodium; Stracchino cheese

Journal of Dairy Science

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Technical note: Feasibility of near infrared transmittance spectroscopy to predict cheese ripeness

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Abstract

The aim of the study was to evaluate the feasibility of near infrared (NIR) transmittance spectroscopy to predict cheese ripeness using the ratio of water-soluble nitrogen (WSN) to total nitrogen (TN) as an index of cheese maturity (WSN/TN). Fifty-two Protected Designation of Origin cow milk cheeses of 5 varieties (Asiago, Grana Padano, Montasio, Parmigiano Reggiano, and Piave) and different ripening times were available for laboratory and chemometric analyses. Reference measures of WSN and TN were matched with cheese spectral information obtained from ground samples by a NIR instrument that operated in transmittance mode for wavelengths from 850 to 1,050 nm. Prediction equations for WSN and TN were developed using (1) cross-validation on the whole data set and (2) external validation on a subset of the entire data. The WSN/TN was calculated as ratio of predicted WSN to predicted TN in cross-validation. The coefficients of determination for WSN and TN were >0.85 both in cross- and external validation. The high accuracy of the prediction equations for WSN and TN could facilitate implementation of NIR transmittance spectroscopy in the dairy industry to objectively, rapidly, and accurately monitor the ripeness of cheese through WSN/TN.

Keywords: Cheese quality; Chemometric; Ripening time; Water-soluble nitrogen

Journal of Dairy Science

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Use of mid-infrared spectroscopy to predict coagulation properties of buffalo milk

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Abstract

This study aimed to evaluate the feasibility of mid-infrared spectroscopy (MIRS) to predict rennet coagulation time (RCT), curd-firming time (k_{20}) and curd firmness (a_{30}) of buffalo milk. One hundred and sixteen milk samples were collected and analysed using both reference analysis and MIRS. Reference measures of RCT, k_{20} and a_{30} were matched with milk spectra information (5,000 to 900 cm^{-1} wavenumber) and prediction equations were developed for each trait using i) cross-validation on the whole dataset and ii) external validation on a subset of the entire data. The prediction models were evaluated through the coefficient of determination (R^2) and the residual predictive deviation (RPD). The most accurate prediction model was developed for RCT ($R^2 = 0.72$; RPD = 1.88) in cross-validation. Models developed for RCT and a_{30} allowed a quite satisfactory prediction of milk coagulation properties. Nevertheless, the accuracy was not enough to suggest their application in milk payment systems. Instead, they might be interesting for breeding purposes.

Keywords: Buffalo milk; Chemometrics; Formagraph; FTIR

Agriculturae Conspectus Scientificus

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Genetics and genomics

Developing a molecular identification assay of old landraces for the genetic authentication of typical agro-food products: The case study of the barley 'Agordino'

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Abstract

The orzo Agordino is a very old local variety of domesticated barley (*Hordeum vulgare* ssp. *distichum* L.) that is native to the Agordo District, Province of Belluno, and is widespread in the Veneto Region, Italy. Seeds of this landrace are widely used for the preparation of very famous dishes of the dolomitic culinary tradition such as barley soup, bakery products and local beer. Understanding the genetic diversity and identity of the Agordino barley landrace is a key step to establish conservation and valorisation strategies of this local variety and also to provide molecular traceability tools useful to ascertain the authenticity of its derivatives. The gene pool of the Agordino barley landrace was reconstructed using 60 phenotypically representative individual plants and its genotypic relationships with commercial varieties were investigated using 21 pure lines widely cultivated in the Veneto Region. For genomic DNA analysis, following an initial screening of 14 mapped microsatellite (SSR) loci, seven discriminant markers were selected on the basis of their genomic position across linkage groups and polymorphic marker alleles per locus. The genetic identity of the local barley landrace was determined by analysing all SSR markers in a single multi-locus PCR assay. Extent of genotypic variation within the Agordino barley landrace and the genotypic differentiation between the landrace individuals and the commercial varieties was determined. Then, as few as four highly informative SSR loci were selected and used to develop a molecular traceability system exploitable to verify the genetic authenticity of food products deriving from the Agordino landrace. This genetic authentication assay was validated using both DNA pools from individual Agordino barley plants and DNA samples from Agordino barley food products. On the whole, our data support the usefulness and robustness of this DNA-based diagnostic tool for the orzo Agordino identification, which could be rapidly and efficiently exploited to guarantee the authenticity of local varieties and the typicality of food products.

Keywords: Barley; Food authentication; Genotyping; Landraces; Microsatellites; Traceability

Food Technology and Biotechnology

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Elucidation of the genetic architecture of self-incompatibility in olive: Evolutionary consequences and perspectives for orchard management

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Abstract

The olive (*Olea europaea* L.) is a typical important perennial crop species for which the genetic determination and even functionality of self-incompatibility (SI) are still largely unresolved. It is still not known whether SI is under gametophytic or sporophytic genetic control, yet fruit production in orchards depends critically on successful ovule fertilization. We studied the genetic determination of SI in olive in light of recent discoveries in other genera of the Oleaceae family. Using intra- and interspecific stigma tests on 89 genotypes representative of species-wide olive diversity and the compatibility/incompatibility reactions of progeny plants from controlled crosses, we confirmed that *O. europaea* shares the same homomorphic diallelic self-incompatibility (DSI) system as the one recently identified in *Phillyrea angustifolia* and *Fraxinus ornus*. SI is sporophytic in olive. The incompatibility response differs between the two SI groups in terms of how far pollen tubes grow before growth is arrested within stigma tissues. As a consequence of this DSI system, the chance of cross-incompatibility between pairs of varieties in an orchard is high (50%) and fruit production may be limited by the availability of compatible pollen. The discovery of the DSI system in *O. europaea* will undoubtedly offer opportunities to optimize fruit production.

Keywords: Diallelic self-incompatibility system; Homomorphic system; *Olea europaea* L.; Oleaceae; Olive diversity; Plant mating systems; Sporophytic genetic control; Trans-generic conservation of SI functionality

Evolutionary Applications

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Maize RNA PolIV affects the expression of genes with nearby TE insertions and has a genome-wide repressive impact on transcription

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Abstract

Background: RNA-directed DNA methylation (RdDM) is a plant-specific epigenetic process that relies on the RNA polymerase IV (Pol IV) for the production of 24 nucleotide small interfering RNAs (siRNA) that guide the cytosine methylation and silencing of genes and transposons. *Zea mays RPD1/RMR6* gene encodes the largest subunit of Pol IV and is required for normal plant development, paramutation, transcriptional repression of certain transposable elements (TEs) and transcriptional regulation of specific alleles.
Results: In this study we applied a total RNA-Seq approach to compare the B73 and *rpd1/rmr6* leaf transcriptomes. Although previous studies indicated that loss of siRNAs production in RdDM mutants provokes a strong loss of CHH DNA methylation but not massive gene or TEs transcriptional activation in both Arabidopsis and maize, our total RNA-Seq analysis of *rpd1/rmr6* transcriptome reveals that loss of Pol IV activity causes a global increase in the transcribed fraction of the maize genome. Our results point to the genes with nearby TE insertions as being the most strongly affected by Pol IV-mediated gene silencing. TEs modulation of nearby gene expression is linked to alternative methylation profiles on gene flanking regions, and these profiles are strictly dependent on specific characteristics of the TE member inserted. Although Pol IV is essential for the biogenesis of siRNAs, the genes with associated siRNA loci are less affected by the *pol IV* mutation.
Conclusions: This deep and integrated analysis of gene expression, TEs distribution, smallRNA targeting and DNA methylation levels, reveals that loss of Pol IV activity globally affects genome regulation, pointing at TEs as modulator of nearby gene expression and indicating the existence of multiple level epigenetic silencing mechanisms. Our results also suggest a predominant role of the Pol IV-mediated RdDM pathway in genome dominance regulation, and subgenome stability and evolution in maize.

Keywords: RdDM; SiRNAs; Transcriptome analysis; Transposable elements; *Zea mays*

BMC Plant Biology

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Pistil transcriptome analysis to disclose genes and gene products related to aposporous apomixis in *Hypericum perforatum* L.

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Abstract

Unlike sexual reproduction, apomixis encompasses a number of reproductive strategies, which permit maternal genome inheritance without genetic recombination and syngamy. The key biological features of apomixis are the circumvention of meiosis (i.e., apomeiosis), the differentiation of unreduced embryo sacs and egg cells, and their autonomous development in functional embryos through parthenogenesis, and the formation of viable endosperm either via fertilization-independent means or following fertilization with a sperm cell. Despite the importance of apomixis for breeding of crop plants and although much research has been conducted to study this process, the genetic control of apomixis is still not well understood. *Hypericum perforatum* is becoming an attractive model system for the study of aposporous apomixis. Here we report results from a global gene expression analysis of *H. perforatum* pistils collected from sexual and aposporous plant accessions for the purpose of identifying genes, biological processes and molecular functions associated with the aposporous apomixis pathway. Across two developmental stages corresponding to the expression of aposporous apomeiosis and parthenogenesis in ovules, a total of 224 and 973 unigenes were found to be significantly up- and down-regulated with a fold change ≥ 2 in at least one comparison, respectively. Differentially expressed genes were enriched for multiple gene ontology (GO) terms, including cell cycle, DNA metabolic process, and single-organism cellular process. For molecular functions, the highest scores were recorded for GO terms associated with DNA binding, DNA (cytosine-5-)-methyltransferase activity and heterocyclic compound binding. As deregulation of single components of the sexual developmental pathway is believed to be a trigger of the apomictic reproductive program, all genes involved in sporogenesis, gametogenesis and response to hormonal stimuli were analyzed in great detail. Overall, our data suggest that phenotypic expression of apospory is concomitant with the modulation of key genes involved in the sexual reproductive pathway. Furthermore, based on gene annotation and co-expression, we underline a putative role of hormones and key actors playing in the RNA-directed DNA methylation pathway in regulating the developmental changes occurring during aposporous apomixis in *H. perforatum*.

Keywords: Aposporous apomixis; *Hypericum perforatum*; Microarray; Sexual reproduction

Frontiers in Plant Science

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Transcriptional characterization of a widely-used grapevine rootstock genotype under different iron-limited conditions

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Abstract

Iron chlorosis is a serious deficiency that affects orchards and vineyards reducing quality and yield production. Chlorotic plants show abnormal photosynthesis and yellowing shoots. In grapevine iron uptake and homeostasis are most likely controlled by a mechanism known as “Strategy I,” characteristic of non-graminaceous plants and based on a system of soil acidification, iron reduction and transporter-mediated uptake. Nowadays, grafting of varieties of economic interest on tolerant rootstocks is widely used practice against many biotic and abiotic stresses. Nevertheless, many interspecific rootstocks, and in particular those obtained by crossing exclusively *non-vinifera* genotypes, can show limited nutrient uptake and transport, in particular for what concerns iron. In the present study, 101.14, a commonly used rootstock characterized by susceptibility to iron chlorosis was subjected to both Fe-absence and Fe-limiting conditions. Grapevine plantlets were grown in control, Fe-deprived, and bicarbonate-supplemented hydroponic solutions. Whole transcriptome analyses, via mRNA-Seq, were performed on root apices of stressed and unstressed plants. Analysis of differentially expressed genes (DEGs) confirmed that Strategy I is the mechanism responsible for iron uptake in grapevine, since many orthologs genes to the *Arabidopsis* “ferrome” were differentially regulated in stressed plant. Molecular differences in the plant responses to Fe absence and presence of bicarbonate were also identified indicating the two treatments are able to induce response-mechanisms only partially overlapping. Finally, we measured the expression of a subset of genes differentially expressed in 101.14 (such as *IRT1*, *FERRITIN1*, *bHLH38/39*) or known to be fundamental in the “strategy I” mechanism (*AHA2* and *FRO2*) also in a tolerant rootstock (M1) finding important differences which could be responsible for the different degrees of tolerance observed.

Keywords: Ferrome; Micronutrients; mRNA-Seq; Strategy I; *Vitis*

Frontiers in Plant Science

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Venetian local corn (*Zea mays* L.) germplasm: Disclosing the genetic anatomy of old landraces suited for typical cornmeal mush production

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Abstract

Due to growing concern for the genetic erosion of local varieties, four of the main corn landraces historically grown in Veneto (Italy)-Sponcio, Marano, Biancoperla and Rosso Piave-were characterized in this work. A total of 197 phenotypically representative plants collected from field populations were genotyped at 10 SSR marker loci, which were regularly distributed across the 10 genetic linkage groups and were previously characterized for high polymorphism information content (PIC), on average equal to 0.5. The population structure analysis based on this marker set revealed that 144 individuals could be assigned with strong ancestry association (>90%) to four distinct clusters, corresponding to the landraces used in this study. The remaining 53 individuals, mainly from Sponcio and Marano, showed admixed ancestry. Among all possible pairwise comparisons of individual plants, these two landraces exhibited the highest mean genetic similarity (approximately 67%), as graphically confirmed through ordination analyses based on PCoA centroids and UPGMA trees. Our findings support the hypothesis of direct gene flow between Sponcio and Marano, likely promoted by the geographical proximity of these two landraces and their overlapping cultivation areas. Conversely, consistent with its production mainly confined to the eastern area of the region, Rosso Piave scored the lowest genetic similarity (<59%) to the other three landraces and firmly grouped (with average membership of 89%) in a separate cluster, forming a molecularly distinguishable gene pool. The elite inbred B73 used as tester line scored very low estimates of genetic similarity (on average <45%) with all the landraces. Finally, although Biancoperla was represented at K = 4 by a single subgroup with individual memberships higher than 80% in almost all cases (57 of 62), when analyzed with an additional level of population structure for K = 6, it appeared to be entirely (100%) constituted by individuals with admixed ancestry. This suggests that the current population could be the result of repeated hybridization events between the two accessions currently bred in Veneto. The genetic characterization of these heritage landraces should prove very useful for monitoring and preventing further genetic erosion and genetic introgression, thus preserving their gene pools, phenotypic identities and qualitative traits for the future.

Keywords: Barley; Biodiversity; Genetic erosion; Local varieties; Maize; Microsatellite; SSR; Veneto region

Diversity

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WRKY transcription factors and regulation of the stilbene biosynthetic pathway in grapevine: new insights and perspectives

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Abstract

Stilbene synthase (STS) is the key enzyme leading to the biosynthesis of resveratrol and belongs to the type III polyketide synthase super family, of which chalcone synthase (CHS) represents the archetypal enzyme. Recently we reported the identification and functional characterization of two grapevine MYB transcription factors (TFs) that appear to regulate the stilbene biosynthetic pathway. These TFs, designated *VvMYB14* and *VvMYB15*, strongly co-express with *VvSTS* genes under a range of stress-induced conditions and in developmentally regulated tissues. In transient gene reporter assays, these TFs were demonstrated to specifically activate the promoter of two *VvSTS* genes and the ectopic expression of *VvMYB15* in grapevine hairy roots resulted in *VvSTSs* increased expression and in the accumulation of piceid in planta. However, despite these significant advances, many questions remain to be answered regarding the grapevine biosynthetic pathway. Based on the notion that genes involved in similar or related processes may exhibit similar expression patterns over a range of experimental conditions, we performed a co-expression network analysis on different grapevine gene expression datasets in order to identify candidate TFs belonging to the WRKY family, possibly involved in the regulation of the stilbene biosynthetic pathway. These genes scored correlation values with *VvSTSs* even higher than those observed for *VvMYB14* and *VvMYB15*, and proved to be induced in response to the same biotic stresses found responsible for *VvSTS* induction.

Keywords: Gene co-expression; Network; Resveratrol; STS; *Vitis vinifera*

Acta Horticulturae

Volume 1188, Pages 1-8

The WRKY transcription factor family in model plants and crops

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Abstract

The WRKY gene family in flowering plants encodes a large group of transcription factors (TFs) that play essential roles in diverse stress responses, developmental, and physiological processes. In this review, we provided a comprehensive screenshot about the studies on WRKY TFs in model plants and in crops of economical relevance. Specifically, we discussed the history of discovery and functional characterization, classification, and evolutionary history, 3D structure and physiological functions of WRKY transcription factors. Based on the previous functional studies of WRKY genes in model plants such as *Arabidopsis* and rice, we summarized various roles of WRKY TFs in a broad range of biological processes as well as their degradation process. We also discussed the characterization and functional studies of WRKY TFs in important crops. Considering the rapid progress of high-throughput techniques, especially genomics and transcriptomics, which have been instrumental in advancing our understanding of the crop genomes, we comment one-by-one on the applications of a suite of new and high-throughput techniques to accelerate the studies of WRKY genes in crops.

Keywords: Environmental stress; Gene family; Growth and development; Transcription factor; WRKY

Critical Reviews in Plant Sciences

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Draft genome sequence of the nitrogen-fixing *Rhizobium sullae* type strain IS123^{T} focusing on the key genes for symbiosis with its host *Hedysarum coronarium* L.

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Abstract

The prominent feature of rhizobia is their molecular dialogue with plant hosts. Such interaction is enabled by the presence of a series of symbiotic genes encoding for the synthesis and export of signals triggering organogenetic and physiological responses in the plant. The genome of the *Rhizobium sullae* type strain IS123^{T} nodulating the legume *Hedysarum coronarium*, was sequenced and resulted in 317 scaffolds for a total assembled size of 7,889,576 bp. Its features were compared with those of genomes from rhizobia representing an increasing gradient of taxonomical distance, from a conspecific isolate (*Rhizobium sullae* WSM1592), to two congeneric cases (*Rhizobium leguminosarum* bv. *viciae* and *Rhizobium etli*) and up to different genera within the legume-nodulating taxa. The host plant is of agricultural importance, but, unlike the majority of other domesticated plant species, it is able to survive quite well in the wild. Data showed that that the type strain of *R. sullae*, isolated from a wild host specimen, is endowed with a richer array of symbiotic genes in comparison to other strains, species or genera of rhizobia that were rescued from domesticated plant ecotypes. The analysis revealed that the bacterium by itself is incapable of surviving in the extreme conditions that its host plant can tolerate. When exposed to drought or alkaline condition, the bacterium depends on its host to survive. Data are consistent with the view of the plant phenotype as the primary factor enabling symbiotic nitrogen fixing bacteria to survive in otherwise limiting environments.

Keywords: *Hedysarum coronarium*; Host-specific symbiotic adaptation; Nitrogen fixation; Nod genes; *Rhizobium sullae*; Root-nodule bacteria; *Sulla coronaria*; Type strain

Frontiers in Microbiology

Volume 8, Article number 1348

Draft genome sequence of the yeast *Starmerella bacillaris* (syn., *Candida zemplinina*) FRI751 isolated from fermenting must of dried Raboso grapes

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Abstract

Starmerella bacillaris is an ascomycetous yeast commonly present in enological environments. Here, we report the first draft genome sequence of *S. bacillaris* FRI751, which will facilitate the study of the characteristics of this interesting enological yeast.

Genome Announcements

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Molecular markers for improving control of soil-borne pathogen *Fusarium oxysporum* in sugar beet

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Abstract

Fusarium spp. cause severe damage in many agricultural crops, including sugar beet, with *Fusarium oxysporum* historically being considered as the most damaging of all species. Sugar beet needs to be protected from this class of soil-borne pathogens in order to ensure an optimal sugar yield in the field. Genetic control of the disease is crucial in managing these pathogens. Identification of single nucleotide polymorphism (SNP) markers linked to resistance can be a powerful tool for the introgression of valuable genes needed to develop *Fusarium*-resistant varieties. A candidate gene approach was carried out to identify SNP markers linked to putative *Fusarium* resistance sources in sugar beet. Five resistant analogue genes (RGAs) were screened by means of high resolution melting (HRM) analysis in a set of sugar beet lines, considered as resistant and susceptible to *Fusarium oxysporum*. HRM polymorphisms were observed in 80% of amplicons. Two HRM polymorphisms were significantly associated with *Fusarium* resistance ($P < 0.05$). The amplicons that showed association were sequenced and two SNPs were identified. The association was further validated on 96 susceptible and 96 resistant plants using competitive allele-specific PCR (KASPar) technology. The selected SNPs could be used for marker-assisted breeding of *Fusarium* resistance in sugar beet.

Keywords: HRM polymorphisms; KASPar technology; Resistant analogue genes (RGAs); Sanger sequencing; Sugar beet

Euphytica

Volume 213, Issue 3, Article number 71

Molecular progress in sugar beet breeding for resistance to biotic stresses in sub-arid conditions-current status and perspectives

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Abstract

The yield of sugar beet depends mainly on the effective protection to a number of pests and diseases affecting the crop. In the absence of actual methods of management, as in the case of viral diseases, the availability of genetic resistance sometimes allows the survival of the crop in the affected areas. Integration of molecular markers in conventional breeding procedures has provided a reliable means for improving the efficiency of selection methods. The present review summarizes the evolution, thanks to the application of molecular techniques, of traditional breeding for resistance to some biotic stresses in sub-arid environments.

Keywords: Biotic stress; Cyst nematode; Molecular breeding; Rhizoctonia root rot; Rhizomania; Root-knot nematode; Sugar beet

Journal of Crop Science and Biotechnology

Volume 20, Issue 2, Pages 99-105

Single nucleotide polymorphism markers linked to root elongation rate in sugar beet

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Abstract

The aim of this study was to identify single nucleotide polymorphism (SNP) markers genetically linked to root elongation rate (RER) in sugar beet (*Beta vulgaris* L.). A population of 244 F_3 individuals, obtained from the cross between lines L01 (a low RER) and L18 (a high RER), was phenotyped by measuring RER of 11-d-old seedlings grown in a hydroponic culture. Two DNA bulks of 50 F_3 individuals with extreme phenotypes were used for bulk segregant analysis by restriction-associated DNA sequencing. A total of 20 376 SNPs were identified. Single nucleotide polymorphisms were filtered to reduce the number of the false positive and mapped on candidate chromosomal regions of the *B. vulgaris* reference genome. One of the total of SNPs selected, SNP10139, was strongly linked to RER ($P < 0.01$). The pattern of association between the SNP10139 genotype and RER was also evaluated on a breeding line panel comprising 40 low and 40 high RER individuals with different allele frequencies between groups ($P < 0.01$). The SNP10139 sequence was mapped on the *B. vulgaris* peptide transporter (*PTR*) gene, a carrier that influences root elongation in *Arabidopsis thaliana*. Our results suggest that SNP10139 influence RER in sugar beet, and sequence information can be used in marker-assisted selection programs.

Keywords: Abiotic stresses; *Beta vulgaris*; Bulk segregant analysis; Restriction-associated DNA sequencing

Biologia Plantarum

Volume 61, Issue 1, Pages 48-54

Targeted next-generation sequencing identification of mutations in disease resistance gene analogs (RGAs) in wild and cultivated beets

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Abstract

Resistance gene analogs (RGAs) were searched bioinformatically in the sugar beet (*Beta vulgaris* L.) genome as potential candidates for improving resistance against different diseases. In the present study, Ion Torrent sequencing technology was used to identify mutations in 21 RGAs. The DNA samples of ninety-six individuals from six sea beets (*Beta vulgaris* L. subsp. *maritima*) and six sugar beet pollinators (eight individuals each) were used for the discovery of single-nucleotide polymorphisms (SNPs). Target amplicons of about 200 bp in length were designed with the Ion AmpliSeq Designer system in order to cover the DNA sequences of the RGAs. The number of SNPs ranged from 0 in four individuals to 278 in the pollinator R740 (which is resistant to rhizomania infection). Among different groups of beets, cytoplasmic male sterile lines had the highest number of SNPs (132) whereas the lowest number of SNPs belonged to O-types (95). The principal coordinates analysis (PCoA) showed that the polymorphisms inside the gene *Bv8_184910_pkon* (including the CCCTCC sequence) can effectively differentiate wild from cultivated beets, pointing at a possible mutation associated to rhizomania resistance that originated directly from cultivated beets. This is unlike other resistance sources that are introgressed from wild beets. This gene belongs to the receptor-like kinase (RLK) class of RGAs, and is associated to a hypothetical protein. In conclusion, this first report of using Ion Torrent sequencing technology in beet germplasm suggests that the identified sequence CCCTCC can be used in marker-assisted programs to differentiate wild from domestic beets and to identify other unknown disease resistance genes in beet.

Keywords: AmpliSeq; Disease resistance; Gene *Bv8_184910_pkon*; Ion Torrent sequencing; Mutation discovery; Rhizomania and nematodes; Single nucleotide polymorphism; Sugar beet

Genes

Volume 8, Issue 10, Article number 264

The complete genome sequence of *Trueperella pyogenes* UFV1 reveals a processing system involved in the quorum-sensing signal response

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Abstract

We present here the complete genome sequence of *Trueperella pyogenes* UFV1. The 2.3-Mbp genome contains an extremely interesting AI-2 transporter and processing system related to the quorum-sensing signal response. This specific feature is described in this species for the first time and might be responsible for a new pathogenic behavior.

Genome Announcements

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Whole-genome sequence of *Starmerella bacillaris* PAS13, a nonconventional enological yeast with antifungal activity

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Abstract

Starmerella bacillaris is a fermentative yeast commonly found in vineyards. Here, we present the draft genome sequence of *S. bacillaris* PAS13, a nonconventional enological yeast with a potential role as a biocontrol agent. This gene sequence will provide insights into the genetic basis of yeast activity against gray mold disease (*Botrytis cinerea*).

Genome Announcements

Volume 5, Issue 32, Article number e00788-17

Whole-genome sequences of three *Streptococcus macedonicus* strains isolated from Italian cheeses in the Veneto region

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Abstract

We report here the genome sequences of three *Streptococcus macedonicus* strains isolated from different cheeses in the Veneto region of Italy. The presented data aim at increasing the scarce genomic information available for this species, which is frequently encountered in fermented foods and appears to be a promising technological microorganism.

Genome Announcements

Volume 5, Issue 50, Article number e01358-17

Association of candidate gene polymorphisms with milk technological traits, yield, composition, and somatic cell score in Italian Holstein-Friesian sires

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Abstract

Advances in DNA-based marker technology have enabled the identification of genomic regions underlying complex phenotypic traits in livestock species. The incorporation of detected quantitative trait loci into genetic evaluation provides great potential to enhance selection accuracies, hence expediting the genetic improvement of economically important traits. The objective of the present study was to investigate 96 single nucleotide polymorphisms (SNP) located in 53 candidate genes previously reported to have effects on milk production and quality traits in a population of highly selected Holstein-Friesian bulls. A total of 423 semen samples were used to genotype the bulls through a custom oligo pool assay. Forty-five SNP in 32 genes were found to be associated with at least 1 of the tested traits. Most significant and favorable SNP trait associations were observed for polymorphisms located in *CCL3* and *AGPAT6* genes for fat yield (0.037 and 0.033 kg/d, respectively), *DGKG* gene for milk yield (0.698 kg/d), *PPARGC1A*, *CSN1S1*, and *AGPAT6* genes for fat percentage (0.127, 0.113, and 0.093%, respectively), *GHR* gene for protein (0.064%) and casein percentage (0.053%), and *TLR4* gene for fat (0.090%), protein (0.066%), and casein percentage (0.050%). Somatic cell score was favorably affected by *GHR* (0.095) and *POU1F1* (0.137), and interesting SNP-trait associations were observed for polymorphisms located in *CSN2*, *POU1F1*, and *AGPAT6* genes for rennet coagulation time (0.592, 0.558, and 0.462 min, respectively), and *GHR* and *CSN2* genes for curd firmness 30 min after rennet addition (1.264 and 1.183 mm, respectively). In addition to the influence of individual SNP, the effects of composite genotypes constructed by grouping SNP according to their individual effects on traits considered in the analysis were also examined. Favorable and significant effects on milk traits were observed for 2 composite genotypes, one including 10 SNP and the other 4 SNP. The former was associated with an increase of milk (0.075 kg/d), fat (0.097 kg/d), protein (0.083 kg/d), and casein yields (0.065 kg/d), and the latter was associated with an increase of fat (0.244%), protein (0.071%), and casein percentage (0.047%). Although further research is required to validate the identified SNP loci in other populations and breeds, our results can be considered as a preliminary foundation for further replication studies on gene-assisted selection programs.

Keywords: Candidate gene; Holstein bulls; Milk coagulation trait; Milk yield and composition; Somatic cell count

Journal of Dairy Science

Volume 100, Issue 9, Pages 7271-7281

Development and validation of a novel SNP panel for the genetic characterization of Italian chicken breeds by next-generation sequencing discovery and array genotyping

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Abstract

The aim of this study was to compare the intra and inter genetic variability and population structure of 7 indigenous chicken breeds of the Veneto region, through a novel panel of 64 SNP, each located in an exonic region and mostly on different chromosomes. A total of 753 blood samples from 7 local chicken breeds (Ermellinata di Rovigo, Millefiori di Lonigo, Polverara, Pepòi, Robusta Lionata, Robusta Maculata, and Padovana) was collected and analyzed. Two strains of Polverara (Nera and Bianca) and Padovana (Dorata and Camosciata) were included in the study. The observed heterozygosity ranged from 0.124 (Pèpoi) to 0.244 (Ermellinata di Rovigo), and the expected heterozygosity varied from 0.132 (Millefiori di Lonigo) to 0.300 (Ermellinata di Rovigo). Global F_{IS} results (0.114) indicated a low-medium inbreeding effect, with values ranging from 0.008 (Millefiori di Lonigo) to 0.223 (Ermellinata di Rovigo). Pairwise F_{ST} values (0.167) for all populations ranged from 0.020 (Polverara Nera and Polverara Bianca) to 0.193 (Robusta Lionata and Polverara Nera), indicating that the studied breeds were genetically highly differentiated. The software STRUCTURE was used to detect the presence of population substructures, and the most probable number of clusters (K) of the 10 chicken populations was at K = 8. The affiliation was successful in all Veneto chicken breeds. The present SNP marker results, compared with previous data obtained using microsatellites, provided a reliable estimate of genetic diversity within and between the studied breeds, and demonstrated the utility of the proposed panel as a rapid, efficient, and cost-effective tool for periodical monitoring of the genetic variability among poultry populations. In addition, the present SNP panel could represent a resource for a systematic approach with relevant impact on breeding program decisions and could turn out to be a reliable tool for genetic traceability of indigenous chicken meat. Adoption of a periodical monitoring system of genetic diversity is a fundamental tool in conservation actions and should increase the value of typical and niche products.

Keywords: Genetic diversity; Local chicken breed; Population structure; SNP

Poultry Science

Volume 96, Issue 11, Pages 3858-3866

Effects of crossbreeding of Holsteins cows with Montbéliarde and Swedish Red in first and second generation on cheese yield traits

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Abstract

Crossbreeding in dairy cattle may improve functional traits of crossbred cows, but few are known on its effect on cheese-making traits. This study investigated the effects of crossbreeding of Holstein (HO) cows with Montbéliarde (MO) and Swedish Red (SR) on milk composition, cheese yield (CY) and other cheese-making traits. Milk samples from 188 cows were collected on 3 dairy herds producing PDO cheeses. Herds are following a 3-way rotational breeding scheme, so that parts of the cows were purebred HO and the remaining were 1st (SR x HO; MO x HO) and 2nd generation [MO x (SR x HO); SR x (MO x HO)] crossbred cows. Milk samples were analyzed for assessing milk composition, CY, curd composition, and recovery of milk nutrients (REC) in curd. Cows yielded nearly 30.5 kg/d milk, with a fat and protein content of 4.5 and 3.8%, respectively, without any difference between purebred HO and crossbred cows. Milk coagulation time was influenced by breed combination ($P < 0.05$), but purebred HO performed similarly to crossbred cows. Milk yielded nearly 16.3% of curd, but again CY and curd composition were not affected by the breed combination. In conclusion, the crossbreeding scheme considered did not exert any negative effect on cheese-making properties of milk, and can be chosen even in farms specialized in PDO cheese production. Further studies with larger sample size are needed for obtaining more robust estimates and for evaluating the performance of the different breed combinations.

Keywords: Cheese-making traits; Crossbreeding; Holstein; Montbéliarde; Swedish Red

Agriculturae Conspectus Scientificus

Volume 82, Issue 3, Pages 241-244

Fatty acid composition of milk from Holstein-Friesian, Brown Swiss, Simmental and Alpine Grey cows predicted by mid-infrared spectroscopy

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Abstract

The aim of this study was to investigate the sources of variation of milk fatty acids (FA) routinely predicted by mid-infrared spectroscopy in Holstein-Friesian (HF), Brown Swiss (BS), Simmental (SI) and Alpine Grey (AG) cattle breeds. A linear mixed model was used to analyse the data which included 153,801 individual milk samples from 14,301 cows. Fixed effects included in the model were breed, month of sampling, year of sampling, stage of lactation, parity and first order interactions between them, and random effects were herd nested within breed, cow nested within breed and the residual error. Milk of AG cows exhibited the lowest content of saturated FA and the greatest content of unsaturated FA, whereas milk of BS had an opposite pattern. Holstein-Friesian and SI were intermediate between AG and BS breeds for all the FA except for total C18:1, which was the greatest in HF. Saturated FA, C14:0 and C16:0 increased from calving until 120 days in milk, whereas unsaturated FA and C18:1 decreased. First parity cows produced milk with lower concentration of *de novo* FA than multiparous animals. The greatest content of unsaturated FA and C18:1 was observed in summer, whereas saturated FA, C14:0, C16:0 and C18:0 decreased in summer and increased in winter. The differences in milk FA profile among breeds are useful for genetic selection and for feeding strategies.

Keywords: Cow milk; Fatty acid; Mid-infrared spectroscopy; Mountain area; Season

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Fertility traits of Holstein, Brown Swiss, Simmental, and Alpine Grey cows are differently affected by herd productivity and milk yield of individual cows

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Abstract

Milk yield has a strong effect on fertility, but it may vary across different herds and individual cows. Therefore, the aim of this study was to assess the effects of breed and its interaction with level of milk production at the herd level (Herd-L) and at a cow-within-herd level (Cow-L) on fertility traits in dairy cattle. Data were gathered from Holstein (n = 17,688), Brown Swiss (n = 32,697), Simmental (n = 27,791), and Alpine Grey (n = 13,689) cows in northeastern Italy. The analysis was based on records from the first 3 lactations in the years 2011 to 2014. A mixed model was fitted to establish milk production levels of the various herds (Herd-L) and individual cows (Cow-L) using milk as a response variable. The interval fertility traits were interval from calving to first service, interval from first service to conception, and number of days open. The success traits were nonreturn rate at 56 d after first service, pregnancy rate at first service, and the number of inseminations. The interval from calving to first service, interval from first service to conception, and number of days open were analyzed using a Cox's proportional hazards model. The nonreturn rate at 56 d after first service, pregnancy rate at first service, and the number of inseminations were analyzed using logistic regression. There was a strong interaction between breed and productivity class at both Herd-L and Cow-L on all traits. The effects of herd and cow productivity differed from each other and differed among breeds. The dual-purpose Simmental and Alpine Grey breeds had better fertility than the specialized Holstein and Brown Swiss dairy cows; this difference is only partly attributable to different milk yields. Greater herd productivity can result in higher fertility in cows, whereas higher milk yield of individual cows within a herd results in lower fertility. These effects at both Herd-L and Cow-L are curvilinear and are stronger in dual-purpose breeds, which was more evident from low to intermediate milk yield levels than from central to high productivity classes. Disentangling the effects of milk productivity on fertility at Herd-L and Cow-L and taking the nonlinearity of response into account could lead to better modeling of populations within breed. It could also help with management—for example, in precision dairy farming of dairy and dual-purpose cattle. Moreover, assessing the fertility of various breeds and their different responses to herd and individual productivity levels could be useful in devising more profitable crossbreeding programs in different dairy systems.

Keywords: Fertility; Genotype x environment; Milk production; Survival analysis

Journal of Dairy Science

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Genetic analysis of coagulation properties, curd firming modeling, milk yield, composition, and acidity in Sarda dairy sheep

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Abstract

Sheep milk is an important source of food, especially in Mediterranean countries, and is used in large part for cheese production. Milk technological traits are important for the sheep dairy industry, but research is lacking into the genetic variation of such traits. Therefore the aim of this study was to estimate the heritability of traditional milk coagulation properties and curd firmness modeled on time t (CF_t) parameters, and their genetic relationships with test-day milk yield, composition (fat, protein, and casein content), and acidity in Sarda dairy sheep. Milk samples from 1,121 Sarda ewes from 23 flocks were analyzed for 5 traditional coagulation properties by lactodynamographic tests conducted for up to 60 min: rennet coagulation time (min), curd-firming time (k_{20}, min), and 3 measures of curd firmness (a_{30}, a_{45}, and a_{60}, mm). The 240 curd firmness observations (1 every 15 s) from each milk sample were recorded, and 4 parameters for each individual sample equation were estimated: rennet coagulation time estimated from the equation (RCT_{eq}), the asymptotic potential curd firmness (CF_P), the curd firming instant rate constant (k_{CF}), and the syneresis instant rate constant (k_{SR}). Two other derived traits were also calculated (CF_{max}, the maximum curd firmness value; and t_{max}, the attainment time). Multivariate analyses using Bayesian methodology were performed to estimate the genetic relationships of milk coagulation properties and CF_t with the other traits; statistical inference was based on the marginal posterior distributions of the parameters of concern. The marginal posterior distribution of heritability estimates of milk yield (0.16 ± 0.07) and composition (0.21 ± 0.11 to 0.28 ± 0.10) of Sarda ewes was similar to those often obtained for bovine species. The heritability of rennet coagulation time as a single point trait was also similar to that frequently obtained for cow milk (0.19 ± 0.09), whereas the same trait calculated as an individual equation parameter exhibited larger genetic variation and a higher heritability estimate (0.32 ± 0.11). The other curd firming and syneresis traits, whether as traditional single point observations or as individual equation parameters and derived traits, were characterized by heritability estimates lower than for coagulation time and for the corresponding bovine milk traits (0.06 to 0.14). Phenotypic and additive genetic correlations among the 11 technological traits contribute to describing the interdependencies and meanings of different traits. The additive genetic relationships of these technological traits with the single test-day milk yield and composition were variable and showed milk yield to have unfavorable effects on all measures of curd firmness (a_{30}, a_{45}, a_{60}, CF_P, and CF_{max}) and t_{max}, but favorable effects on both instant rate constants (k_{CF} and k_{SR}). Milk fat content had a positive effect on curd firmness traits, especially on those obtained from CF_t equations, whereas the negative effects on both coagulation time traits were attributed to the milk protein and casein contents. Finally, in view of the estimated heritabilities and additive genetic correlations, enhancement of technological traits of sheep milk through selective breeding could be feasible in this population.

Keywords: Cheese-making; Curd-firming modeling; Heritability; Milk coagulation properties; Sheep milk

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Genetic and nongenetic factors associated with milk color in dairy cows

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Abstract

Milk color is one of the sensory properties that can influence consumer choice of one product over another and it influences the quality of processed dairy products. This study aims to quantify the cow-level genetic and nongenetic factors associated with bovine milk color traits. A total of 136,807 spectra from Irish commercial and research herds (with multiple breeds and crosses) were used. Milk lightness (L*), red-green index (a*), and yellow-blue index (b*) were predicted for individual milk samples using only the mid-infrared spectrum of the milk sample. Factors associated with milk color were breed, stage of lactation, parity, milking-time, udder health status, pasture grazing, and seasonal calving. (Co)variance components for L*, a*, and b* were estimated using random regressions on the additive genetic and within-lactation permanent environmental effects. Greater b* value (i.e., more yellow color) was evident in milk from Jersey cows. Milk L* increased consistently with stage of lactation, whereas a* increased until mid lactation to subsequently plateau. Milk b* deteriorated until 31 to 60 DIM, but then improved thereafter until the end of lactation. Relative to multiparous cows, milk yielded by primiparae was, on average, lighter (i.e., greater L*), more red (i.e., greater a*), and less yellow (i.e., lower b*). Milk from the morning milk session had lower L*, a*, and b*. Heritability estimates (±SE) for milk color varied between 0.15 ± 0.02 (30 DIM) and 0.46 ± 0.02 (210 DIM) for L*, between 0.09 ± 0.01 (30 DIM) and 0.15 ± 0.02 (305 DIM) for a*, and between 0.18 ± 0.02 (21 DIM) and 0.56 ± 0.03 (305 DIM) for b*. For all the 3 milk color features, the within-trait genetic correlations approached unity as the time intervals compared shortened and were generally <0.40 between the peripheries of the lactation. Strong positive genetic correlations existed between b* value and milk fat concentration, ranging from 0.82 ± 0.19 at 5 DIM to 0.96 ± 0.01 at 305 DIM and confirming the observed phenotypic correlation (0.64, SE = 0.01). Results of the present study suggest that breeding strategies for the enhancement of milk color traits could be implemented for dairy cattle populations. Such strategies, coupled with the knowledge of milk color traits variation due to nongenetic factors, may represent a tool for the dairy processors to reduce, if not eliminate, the use of artificial pigments during milk manufacturing.

Keywords: Commission Internationale d'Eclairage L*a*b*; Dairy industry; Genetic parameter; Mid-infrared spectroscopy; Milk color

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Genome-wide association and pathway-based analysis using latent variables related to milk protein composition and cheesemaking traits in dairy cattle

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Abstract

The aim of this study was to perform genome-wide associations (GWAS) and gene-set enrichment analyses with protein composition and cheesemaking-related latent variables (factors; F) in a cohort of 1,011 Italian Brown Swiss cows. Factor analysis was applied to identify latent structures of 26 phenotypes related to bovine milk quantity and quality, protein fractions [α_{S1}-, α_{S2}-, β-, and κ-casein (CN), β-lactoglobulin, and α-lactalbumin (α-LA)], coagulation and curd firming at time t (CF_t) measures, and cheese properties [cheese yield (%CY) and nutrients recovery in the curd] of individual cows. Ten orthogonal F were extracted, explaining 74% of the original variability. Factor $1_{\%CY}$ underlined the %CY characteristics, $F2_{CFt}$ was related to the CF_t process parameters, $F3_{Yield}$ was considered as descriptor of milk and solids yield, whereas $F4_{Cheese\ N}$ underscored the presence of nitrogenous compounds (N) into the cheese. Four more F were related to the milk caseins ($F5_{\alpha S1\text{-}\beta\text{-}CN}$, $F7_{\beta\text{-}\kappa\text{-}CN}$, $F8_{\alpha S2\text{-}CN}$, and $F9_{\alpha S1\text{-}CN\text{-}Ph}$) and 1 F was linked to the whey protein ($F10_{\alpha\text{-}LA}$); 1 F underlined the udder health status ($F6_{Udder\ health}$). All cows were genotyped with the Illumina BovineSNP50 Bead Chip v.2 (Illumina Inc., San Diego, CA). Single marker regression GWAS were fitted. Gene-set enrichment analysis was run on GWAS results, using the Gene Ontology and Kyoto Encyclopedia of Genes and Genomes pathway databases, to reveal ontologies or pathways associated with the F. All F but $F3_{Yield}$ showed significance in GWAS. Signals in 10 *Bos taurus* autosomes (BTA) were detected. High peaks on BTA6 (~87 Mbp) were found for $F7_{\beta\text{-}\kappa\text{-}CN}$, $F5_{\alpha S1\text{-}\beta\text{-}CN}$, and at the tail of BTA11 (~104 Mbp) for $F4_{Cheese\ N}$. Gene-set enrichment analyses showed significant results (false discovery rate at 5%) for $F8_{\alpha S2\text{-}CN}$, $F1_{\%CY}$, $F4_{Cheese\ N}$, and $F10_{\alpha\text{-}LA}$. For $F8_{\alpha S2\text{-}CN}$, 33 Gene Ontology terms and 3 Kyoto Encyclopedia of Genes and Genomes categories were enriched, including terms related to ion transport and homeostasis, neuron function or part, and GnRH signaling pathway. Our results support the feasibility of factor analysis as a dimension reduction technique in genomic studies and evidenced a potential key role of α_{S2}-CN in milk quality and composition.

Keywords: Cheesemaking; Factor analysis; Gene-set enrichment; GWAS; Milk protein

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Genome-wide association study for cheese yield and curd nutrient recovery in dairy cows

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Abstract

Cheese production and consumption are increasing in many countries worldwide. As a result, interest has increased in strategies for genetic selection of individuals for technological traits of milk related to cheese yield (CY) in dairy cattle breeding. However, little is known about the genetic background of a cow's ability to produce cheese. Recently, a relatively large panel (1,264 cows) of different measures of individual cow CY and milk nutrient and energy recoveries in the cheese (REC) became available. Genetic analyses showed considerable variation for CY and for aptitude to retain high proportions of fat, protein, and water in the coagulum. For the dairy industry, these characteristics are of major economic importance. Nevertheless, use of this knowledge in dairy breeding is hampered by high costs, intense labor requirement, and lack of appropriate technology. However, in the era of genomics, new possibilities are available for animal breeding and genetic improvement. For example, identification of genomic regions involved in cow CY might provide potential for marker-assisted selection. The objective of this study was to perform genome-wide association studies on different CY and REC measures. Milk and DNA samples from 1,152 Italian Brown Swiss cows were used. Three CY traits expressing the weight (wt) of fresh curd ($\%CY_{CURD}$), curd solids ($\%CY_{SOLIDS}$), and curd moisture ($\%CY_{WATER}$) as a percentage of weight of milk processed, and 4 REC (REC_{FAT}, $REC_{PROTEIN}$, REC_{SOLIDS}, and REC_{ENERGY}, calculated as the % ratio between the nutrient in curd and the corresponding nutrient in processed milk) were analyzed. Animals were genotyped with the Illumina BovineSNP50 Bead Chip v.2. Single marker regressions were fitted using the GenABEL R package (genome-wide association using mixed model and regression–genomic control). In total, 103 significant associations (88 single nucleotide polymorphisms) were identified in 10 chromosomes (2, 6, 9, 11, 12, 14, 18, 19, 27, 28). For REC_{FAT} and $REC_{PROTEIN}$, high significance peaks were identified in *Bos taurus* autosome (BTA) 6 and BTA11, respectively. Marker ARS-BFGL-NGS-104610 (~104.3 Mbp) was highly associated with $REC_{PROTEIN}$ and Hapmap52348-rs29024684 (~87.4 Mbp), closely located to the casein genes on BTA6, with REC_{FAT}. Genomic regions identified may enhance marker-assisted selection in bovine cheese breeding beyond the use of protein (casein) and fat contents, whereas new knowledge will help to unravel the genomic background of a cow's ability for cheese production.

Keywords: Cheese yield; Curd recovery; Dairy cattle; Genome-wide association study; Whey loss

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Pathway-based genome-wide association analysis of milk coagulation properties, curd firmness, cheese yield, and curd nutrient recovery in dairy cattle

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Abstract

It is becoming common to complement genome-wide association studies (GWAS) with gene-set enrichment analysis to deepen the understanding of the biological pathways affecting quantitative traits. Our objective was to conduct a gene ontology and pathway-based analysis to identify possible biological mechanisms involved in the regulation of bovine milk technological traits: coagulation properties, curd firmness modeling, individual cheese yield (CY), and milk nutrient recovery into the curd (REC) or whey loss traits. Results from 2 previous GWAS studies using 1,011 cows genotyped for 50k single nucleotide polymorphisms were used. Overall, the phenotypes analyzed consisted of 3 traditional milk coagulation property measures [RCT: rennet coagulation time defined as the time (min) from addition of enzyme to the beginning of coagulation; k_{20}: the interval (min) from RCT to the time at which a curd firmness of 20 mm is attained; a_{30}: a measure of the extent of curd firmness (mm) 30 min after coagulant addition], 6 curd firmness modeling traits [RCT_{eq}: RCT estimated through the CF equation (min); CF_P: potential asymptotic curd firmness (mm); k_{CF}: curd-firming rate constant (% x min^{-1}); k_{SR}: syneresis rate constant (% x min^{-1}); CF_{max}: maximum curd firmness (mm); and t_{max}: time to CF_{max} (min)], 3 individual CY-related traits expressing the weight of fresh curd ($\%CY_{CURD}$), curd solids ($\%CY_{SOLIDS}$), and curd moisture ($\%CY_{WATER}$) as a percentage of weight of milk processed and 4 milk nutrient and energy recoveries in the curd (REC_{FAT}, $REC_{PROTEIN}$, REC_{SOLIDS}, and REC_{ENERGY} calculated as the % ratio between the nutrient in curd and the corresponding nutrient in processed milk), milk pH, and protein percentage. Each trait was analyzed separately. In total, 13,269 annotated genes were used in the analysis. The Gene Ontology and Kyoto Encyclopedia of Genes and Genomes pathway databases were queried for enrichment analyses. Overall, 21 Gene Ontology and 17 Kyoto Encyclopedia of Genes and Genomes categories were significantly associated (false discovery rate at 5%) with 7 traits (RCT, RCT_{eq}, k_{CF}, $\%CY_{SOLIDS}$, REC_{FAT}, REC_{SOLIDS}, and REC_{ENERGY}), with some being in common between traits. The significantly enriched categories included calcium signaling pathway, salivary secretion, metabolic pathways, carbohydrate digestion and absorption, the tight junction and the phosphatidylinositol pathways, as well as pathways related to the bovine mammary gland health status, and contained a total of 150 genes spanning all chromosomes but 9, 20, and 27. This study provided new insights into the regulation of bovine milk coagulation and cheese ability that were not captured by the GWAS.

Keywords: Cow cheese ability; Gene-set enrichment; Genome-wide association; Milk coagulation and curd firmness; Pathway-based analysis

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Phenotypic and genetic aspects of milk freezing point in primiparous Holstein Friesian cows

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Abstract

Freezing point (FRP) of milk and its associations with milk traits have not been studied in Italian Holstein Friesian population yet. Moreover, in other countries, studies were based on small sample size. Therefore, the aim of the present paper was to investigate sources of variation of milk FRP, and to estimate its heritability and genetic correlations with milk yield and quality traits. An analysis of variance was carried out to identify sources of variation of FRP, and genetic parameters were assessed using test-day repeatability animal models on 37,331 records from 5,102 first-lactation cows in 435 herds. Only classes of days in milk and herd-test-date significantly affected FRP. Heritability and repeatability of FRP were low (0.12 and 0.23, respectively), and moderate genetic correlations of this trait with lactose percentage (-0.52), protein content (-0.32) and somatic cell score (0.29) were estimated. Despite low, heritability of FRP is comparable to that of other traits such as somatic cell score, suggesting that there is room for applying selection strategies to improve this trait, also exploiting its genetic relationships with other milk traits.

Keywords: Bovine milk; Freezing point; Genetic parameter; Lactose

Agriculturae Conspectus Scientificus

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Processing characteristics of dairy cow milk are moderately heritable

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Abstract

Milk processing attributes represent a group of milk quality traits that are important to the dairy industry to inform product portfolio. However, because of the resources required to routinely measure such quality traits, precise genetic parameter estimates from a large population of animals are lacking for these traits. Milk processing characteristics considered in the present study—rennet coagulation time, curd-firming time, curd firmness at 30 and 60 min after rennet addition, heat coagulation time, casein micelle size, and milk pH—were all estimated using mid-infrared spectroscopy prediction equations. Variance components for these traits were estimated using 136,807 test-day records from 5 to 305 d in milk (DIM) from 9,824 cows using random regressions to model the additive genetic and within-lactation permanent environmental variances. Heritability estimates ranged from 0.18 ± 0.01 (26 DIM) to 0.38 ± 0.02 (180 DIM) for rennet coagulation time; from 0.26 ± 0.02 (5 DIM) to 0.57 ± 0.02 (174 DIM) for curd-firming time; from 0.16 ± 0.01 (30 DIM) to 0.56 ± 0.02 (271 DIM) for curd firmness at 30 min; from 0.13 ± 0.01 (30 DIM) to 0.48 ± 0.02 (271 DIM) for curd firmness at 60 min; from 0.08 ± 0.01 (17 DIM) to 0.24 ± 0.01 (180 DIM) for heat coagulation time; from 0.23 ± 0.02 (30 DIM) to 0.43 ± 0.02 (261 DIM) for casein micelle size; and from 0.20 ± 0.01 (30 DIM) to 0.36 ± 0.02 (151 DIM) for milk pH. Within-trait genetic correlations across DIM weakened as the number of days between compared intervals increased but were mostly >0.4 except between the peripheries of the lactation. Eigenvalues and associated eigenfunctions of the additive genetic covariance matrix for all traits revealed that at least the 80% of the genetic variation among animals in lactation profiles was associated with the height of the lactation profile. Curd-firming time and curd firmness at 30 min were weakly to moderately genetically correlated with milk yield (from 0.33 ± 0.05 to 0.59 ± 0.05 for curd-firming time, and from −0.62 ± 0.03 to −0.21 ± 0.06 for curd firmness at 30 min). Milk protein concentration was strongly genetically correlated with curd firmness at 30 min (0.84 ± 0.02 to 0.94 ± 0.01) but only weakly genetically correlated with milk heat coagulation time (−0.27 ± 0.07 to 0.19 ± 0.06). Results from the present study indicate the existence of exploitable genetic variation for milk processing characteristics. Because of possible indirect deterioration in milk processing characteristics due to selection for greater milk yield, emphasis on milk processing characteristics is advised.

Keywords: Milk coagulation; Milk quality; Milk technological; Random regression; Spectrometry

Journal of Dairy Science

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SNP co-association and network analyses identify E2F3, KDM5A and BACH2 as key regulators of the bovine milk fatty acid profile

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Abstract

The fatty acid (FA) profile has a considerable impact on the nutritional and technological quality of milk and dairy products. The molecular mechanism underlying the regulation of fat metabolism in bovine mammary gland have been not completely elucidated. We conducted genome-wide association studies (GWAS) across 65 milk FAs and fat percentage in 1,152 Brown Swiss cows. In total, we identified 175 significant single nucleotide polymorphism (SNPs) spanning all chromosomes. Pathway analyses revealed that 12:0 was associated with the greatest number of overrepresented categories/pathways (e.g. mitogen-activated protein kinase (MAPK) activity and protein phosphorylation), suggesting that it might play an important biological role in controlling milk fat composition. An Associated Weight Matrix approach based on SNP co-associations predicted a network of 791 genes related to the milk FA profile, which were involved in several connected molecular pathways (e.g., MAPK, lipid metabolism and hormone signalling) and undetectable through standard GWAS. Analysis of transcription factors and their putative target genes within the network identified *BACH2*, *E2F3* and *KDM5A* as key regulators of milk FA metabolism. These findings contribute to increasing knowledge of FA metabolism and mammary gland functionality in dairy cows and may be useful in developing targeted breeding practices to improve milk quality.

Scientific Reports

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Fine mapping by composite genome-wide association analysis

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Abstract

Genome-wide association (GWA) studies play a key role in current genetics research, unravelling genomic regions linked to phenotypic traits of interest in multiple species. Nevertheless, the extent of linkage disequilibrium (LD) may provide confounding results when significant genetic markers span along several contiguous cM. In this study, we have adapted the composite interval mapping approach to the GWA framework (composite GWA), in order to evaluate the impact of including competing (possibly linked) genetic markers when testing for the additive allelic effect inherent to a given genetic marker. We tested model performance on simulated data sets under different scenarios (i.e., qualitative trait loci effects, LD between genetic markers and width of the genomic region involved in the analysis). Our results showed that the genomic region had a small impact on the number of competing single nucleotide polymorphisms (SNPs) as well as on the precision of the composite GWA analysis. A similar conclusion was derived from the preferable range of LD between the tested SNP and competing SNPs, although moderate-to-high LD seemed to attenuate the loss of statistical power. The composite GWA improved specificity and reduced the number of significant genetic markers. The composite GWA model contributes a novel point of view for GWA analyses where testing circumscribed to the genomic region flanking each SNP (delimited by the nearest competing SNPs) and conditioning on linked markers increases the precision to locate causal mutations, but possibly at the expense of power.

Genetics Research

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Microbiology

Bacteriocinogenic LAB strains for fermented meat preservation: Perspectives, challenges, and limitations

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Abstract

Over the last decades, much research has focused on lactic acid bacteria (LAB) bacteriocins because of their potential as biopreservatives and their action against the growth of spoilage microbes. Meat and fermented meat products are prone to microbial contamination, causing health risks, as well as economic losses in the meat industry. The use of bacteriocin-producing LAB starter or protective cultures is suitable for fermented meats. However, although bacteriocins can be produced during meat processing, their levels are usually much lower than those achieved during in vitro fermentations under optimal environmental conditions. Thus, the direct addition of a bacteriocin food additive would be desirable. Moreover, safety and technological characteristics of the bacteriocinogenic LAB must be considered before their widespread applications. This review describes the perspectives and challenges toward the complete disclosure of new bacteriocins as effective preservatives in the production of safe and "healthy" fermented meat products.

Keywords: Bacteriocins; Lactic acid bacteria; Meat; Preservation; Spoilage

Probiotics and Antimicrobial Proteins

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Comparative secretome analysis of *Colletotrichum falcatum* identifies a cerato-platanin protein (EPL1) as a potential pathogen-associated molecular pattern (PAMP) inducing systemic resistance in sugarcane

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Abstract

Colletotrichum falcatum, an intriguing hemibiotrophic fungal pathogen causes red rot, a devastating disease of sugarcane. Repeated in vitro subculturing of C. falcatum under dark condition alters morphology and reduces virulence of the culture. Hitherto, no information is available on this phenomenon at molecular level. In this study, the in vitro secretome of C. falcatum cultured under light and dark conditions was analyzed using 2-DE coupled with MALDI TOF/TOF MS. Comparative analysis identified nine differentially abundant proteins. Among them, seven proteins were less abundant in the dark-cultured C. falcatum, wherein only two protein species of a cerato-platanin protein called EPL1 (eliciting plant response-like protein) were found to be highly abundant. Transcriptional expression of candidate high abundant proteins was profiled during host-pathogen interaction using qRT-PCR. Comprehensively, this comparative secretome analysis identified five putative effectors, two pathogenicity-related proteins and one pathogen-associated molecular pattern (PAMP) of C. falcatum. Functional characterization of three distinct domains of the PAMP (EPL1) showed that the major cerato-platanin domain (EPL1 N1–92) is exclusively essential for inducing defense and hypersensitive response (HR) in sugarcane and tobacco, respectively. Further, priming with EPL1 N1–92 protein induced systemic resistance and significantly suppressed the red rot severity in sugarcane. BIOLOGICAL SIGNIFICANCE: Being the first secretomic investigation of C. falcatum, this study has identified five potential effectors, two pathogenicity-related proteins and a PAMP. Although many reports have highlighted the influence of light on pathogenicity, this study has established a direct link between light and expression of effectors, for the first time. This study has presented the influence of a novel N-terminal domain of EPL1 in physical and biological properties and established the functional role of major cerato-platanin domain of EPL1 as a potential elicitor inducing systemic resistance in sugarcane. Comprehensively, the study has identified proteins that putatively contribute to virulence of C. falcatum and for the first time, demonstrated the potential role of EPL1 in inducing PAMP-triggered immunity (PTI) in sugarcane.

Keywords: *Colletotrichum falcatum*; Effector; Pathogen-associated molecular pattern (PAMP); Secretome; Sugarcane; Systemic resistance

Journal of Proteomics

Volume 169, Pages 2-20

Differential sensitivity to infections and antimicrobial peptide-mediated immune response in four silkworm strains with different geographical origin

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Abstract

The domesticated silkworm *Bombyx mori* has an innate immune system, whose main effectors are the antimicrobial peptides (AMPs). Silkworm strains are commonly grouped into four geographical types (Japanese, Chinese, European and Tropical) and are generally characterised by a variable susceptibility to infections. To clarify the genetic and molecular mechanisms on which the different responses to infections are based, we exposed one silkworm strain for each geographical area to oral infections with the silkworm pathogens *Enterococcus mundtii* or *Serratia marcescens*. We detected a differential susceptibility to both bacteria, with the European strain displaying the lowest sensitivity to *E. mundtii* and the Indian one to *S. marcescens*. We found that all the strains were able to activate the AMP response against *E. mundtii*. However, the highest tolerance of the European strain appeared to be related to the specific composition of its AMP cocktail, containing more effective variants such as a peculiar Cecropin B6 isoform. The resistance of the Indian strain to *S. marcescens* seemed to be associated with its prompt capability to activate the systemic transcription of AMPs. These data suggest that *B. mori* strains with distinct genetic backgrounds employ different strategies to counteract bacterial infections, whose efficacy appears to be pathogen-dependent.

Scientific Reports

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Fast method for the determination of short-chain-length polyhydroxyalkanoates (scl-PHAs) in bacterial samples by In Vial-Thermolysis (IVT)

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Abstract

A new method based on the GC–MS analysis of thermolysis products obtained by treating bacterial samples at a high temperature (above 270 °C) has been developed. This method, here named "In-Vial-Thermolysis" (IVT), allowed for the simultaneous determination of short-chain-length polyhydroxyalkanoates (scl-PHA) content and composition. The method was applied to both single strains and microbial mixed cultures (MMC) fed with different carbon sources. The IVT procedure provided similar analytical performances compared to previous Py-GC–MS and Py-GC-FID methods, suggesting a similar application for PHA quantitation in bacterial cells. Results from the IVT procedure and the traditional methanolysis method were compared; the correlation between the two datasets was fit for the purpose, giving a R2 of 0.975. In search of further simplification, the rationale of IVT was exploited for the development of a "field method" based on the titration of thermolyzed samples with sodium hydrogen carbonate to quantify PHA inside bacterial cells. The accuracy of the IVT method was fit for the purpose. These results lead to the possibility for the on-line measurement of PHA productivity. Moreover, they allow for the fast and inexpensive quantification/characterization of PHA for biotechnological process control, as well as investigation over various bacterial communities and/or feeding strategies.

Keywords: Crotonic acid; Mixed microbial cultures (MMC); Polyhydroxyalkanoates; Thermolysis-GC–MS; Thermolysis-titration

New Biotechnology

Volume 39, Pages 29-35

Genome comparison and physiological characterization of eight *Streptococcus thermophilus* strains isolated from Italian dairy products

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Abstract

Eight *Streptococcus thermophilus* strains of dairy origin isolated in Italy were chosen to investigate autochthonous bacterial diversity in this important technological species. In the present study a comparative analysis of all the 17 *S.thermophilus* genomes publicly available was performed to identify the core and the variable genes, which vary among strains from 196 to 265. Additionally, correlation between the isolation site and the genetic distance was investigated at genomic level. Results highlight that the phylogenetic reconstruction differs from the geographical strain distribution. Moreover, strain M17PTZA496 has a genome of 2.15 Mbp, notably larger than that of the others, determined by lateral gene transfer (including phage-mediated incorporation) and duplication events. Important technological characters, such as growth kinetics, bacteriocin production, acidification kinetics and surface adhesion capability were studied in all the Italian strains. Results indicate a wide range of variability in adhesion properties that significantly clustered strains into four groups. Genomic differences among strains in relation to these characters were identified but a clear correlation between genotype and phenotype was not always found since most of the genomic modifications arise from single nucleotide polymorphisms. This research represents a step forward in the identification of strains-specific functions in *Streptococcus thermophilus* and it has also the potential to provide valuable information to predict strain specific behaviors in industrial processes.

Keywords: Bacterial biodiversity; Dairy products; Genome comparison; *Streptoccocus thermophilus*

Food Microbiology

Volume 63, Pages 47-57

In vitro fermentation of key dietary compounds with rumen fluid: A genome-centric perspective

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Abstract

The anaerobic decomposition of organic substrates leads to the generation of gases, such as methane, which can either be a valuable energy carrier in industrial applications or can be considered as a main greenhouse gas when it is naturally emitted. In this study we investigated in vitro the effect of dietary compounds, such as starch and proteins, on the microbial community present in the rumen fluid. High throughput shotgun sequencing, followed by metagenomic assembly and binning allowed the extraction of 18 genome bins. A composite bioinformatic analysis led to the prediction of metabolic pathways involved in the degradation of dietary compounds and in the biosynthesis of crucial products like propionate, methane and ammonia. The identification of genomes belonging to poorly characterized phyla such as *Thermoplasmata* and *Elusimicrobia* shed light on their putative role. The high abundance of methylotrophic archaea in the inoculum suggests a relevant role in methane production.

Keywords: Ammonia; Anaerobic digestion; Diets; Metagenomics; Methane; Methylotrophs

Science of the Total Environment

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In vitro secretomic analysis identifies putative pathogenicity-related proteins of *Sporisorium scitamineum* – The sugarcane smut fungus

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Abstract

Sporisorium scitamineum, the sugarcane smut pathogen, relies predominantly on its secretome to successfully colonise its host, in accordance with other related smut fungi. Considering the significance of deciphering its secretome, we have examined alterations in the *in vitro* secretome of *S. scitamineum* in response to synthetic and sugarcane meristem tissue–amended growth media, so as to identify host signal responsive secretory proteins. Secretory proteins that were differentially abundant and exclusively secreted in response to host extract media were identified by two-dimensional gel electrophoresis coupled with MALDI-TOF/TOF MS. Of the 16 differentially abundant and exclusively secreted proteins, nine proteins were identified. Among which, six were related to cell wall modification, morphogenesis, polysaccharide degradation, and carbohydrate metabolism. In planta gene expression profiling indicated that five *in vitro* secreted proteins were expressed in distinct patterns by *S. scitamineum* during different stages of infection with relatively higher expression at 1 day after inoculation, suggesting that these proteins could be aiding *S. scitamineum* at early time points in penetration and colonisation of sugarcane cells. The present study has provided insights into the alterations occurring in the secretome of *S. scitamineum* at *in vitro* conditions and has resulted in the identification of secretory proteins that are possibly associated with pathogenicity of the sugarcane smut fungus.

Keywords: CAZymes; Proteomics; Secretome; Sugarcane; Two-dimensional gel electrophoresis

Fungal Biology

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Necrotrophic fungal plant pathogens display different mechanisms to counteract grape chitinase and thaumatin-like protein

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Abstract

We characterized the ability of the necrotrophic plant pathogens *Botrytis cinerea*, *Sclerotinia sclerotiorum*, *Sclerotinia minor* and *Sclerotium rolfsii* to degrade or sequester two widespread plant PR proteins: a type IV chitinase and a thaumatin-like protein (TLP). A protein (150 μg mL^{-1}) extract from grape berries, containing about 58 and 68 μg mL^{-1} of TLP and chitinase, respectively, was added to the fungal cultures. The growth of the four fungi was not negatively affected by these proteins and, as determined by RP-HPLC, both TLP and chitinase were partially removed from the medium by the three ascomycetes fungi and almost completely by the basidiomycete *S. rolfsii*. Different levels of protease activity were secreted by fungi but these activities were ineffective against TLP and only partially active against chitinase. The cleavage of chitinase by *B. cinerea* protease generated a characteristic lower molecular size band on SDS-PAGE. To verify a possible absorption of TLP and chitinase by the fungal talli, mycelia were treated with β-1,3-glucanase. TLP and, to a lower extent, chitinase were released from mycelium of the three ascomycetes fungi but not from that of *S. rolfsii*. The treatment with β-1,3-glucanase of a mixture containing PR proteins and a purified preparation of the *S. rolfsii* glucan did not release TLP or chitinase. However, the two proteins were observed when the mixture was analyzed on SDS-PAGE. This result indicates a different type of binding of PR proteins with the glucan matrix of *S. rolfsii* in comparison to that of the three ascomycetes. As determined by RT-qPCR, one of the two examined putative glucan synthase genes of *S. rolfsii* was up-regulated following the administration of PR proteins, suggesting the formation of new glucan. Overall, in comparison to protease activity, the sequestering capacity of the fungal glucan matrix seems to play a major role in the fungal defense against the plant TLP and chitinase.

Keywords: *Botrytis cinerea*; Chitinases; Proteases; Thaumatins; β-glucans

Physiological and Molecular Plant Pathology

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Performance and stability of sewage sludge digestion under CO_2 enrichment: A pilot study

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Abstract

Carbon dioxide (CO_2) injection in anaerobic digestion has recently been proposed as an interesting possibility to boost methane (CH_4) recovery from sludge and organic waste by converting a greenhouse gas into a renewable resource. This research assessed the effects of exogenous CO_2 injection on performance and process stability of single-phase continuous anaerobic digesters. Two pilot scale reactors treating sewage sludge were operated for 130 days. One reactor was periodically injected with CO_2 while the other acted as control. Two injection frequencies and injection devices were tested. The results indicated that CO_2 enrichment allowed an increase in CH_4 production of *ca.* 12%, with a CH_4 production rate of 371 ± 100 L/(kgVS$_{fed}$·d) and a CH_4 concentration of *ca.* 60% when dissolved CO_2 levels inside the test reactor were increased up to 1.9-fold. Results also indicated an improvement in process resilience to temporary overloads and no impacts on stability parameters.

Keywords: Anaerobic digestion; Carbon dioxide utilisation; Pilot scale; Process stability; Sewage sludge

Bioresource Technology

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Production of bioethanol from multiple waste streams of rice milling

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Abstract

This work describes the feasibility of using rice milling by-products as feedstock for bioethanol. Starch-rich residues (rice bran, broken, unripe and discolored rice) were individually fermented (20% w/v) through Consolidated Bioprocessing by two industrial engineered yeast secreting fungal amylases. Rice husk (20% w/v), mainly composed by lignocellulose, was pre-treated at 55 C with alkaline peroxide, saccharified through optimized dosages of commercial enzymes (Cellic® CTec2) and fermented by the recombinant strains. Finally, a blend of all the rice by-products, formulated as a mixture (20% w/v) according to their proportions at milling plants, were co-processed to ethanol by optimized pre-treatment, saccharification and fermentation by amylolytic strains. Fermenting efficiency for each by-product was high (above 88% of the theoretical) and further confirmed on the blend of residues (nearly 52 g/L ethanol). These results demonstrated for the first time that the co-conversion of multiple waste streams is a promising option for second generation ethanol production.

Keywords: Alkaline peroxide pre-treatment; Consolidated bioprocessing; Enzymatic saccharification; Multiple waste streams co-fermentation; Rice milling by-products

Bioresource Technology

Volume 244, Pages 151-159

The geographic distribution of *Saccharomyces cerevisiae* isolates within three Italian neighboring winemaking regions reveals strong differences in yeast abundance, genetic diversity and industrial strain dissemination

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Abstract

In recent years the interest for natural fermentations has been re-evaluated in terms of increasing the wine terroir and managing more sustainable winemaking practices. Therefore, the level of yeast genetic variability and the abundance of *Saccharomyces cerevisiae* native populations in vineyard are becoming more and more crucial at both ecological and technological level. Among the factors that can influence the strain diversity, the commercial starter release that accidentally occur in the environment around the winery, has to be considered. In this study we led a wide scale investigation of *S. cerevisiae* genetic diversity and population structure in the vineyards of three neighboring winemaking regions of Protected Appellation of Origin, in North-East of Italy. Combining mtDNA RFLP and microsatellite markers analyses we evaluated 634 grape samples collected over 3 years. We could detect major differences in the presence of *S. cerevisiae* yeasts, according to the winemaking region. The population structures revealed specificities of yeast microbiota at vineyard scale, with a relative Appellation of Origin area homogeneity, and transition zones suggesting a geographic differentiation. Surprisingly, we found a widespread industrial yeast dissemination that was very high in the areas where the native yeast abundance was low. Although geographical distance is a key element involved in strain distribution, the high presence of industrial strains in vineyard reduced the differences between populations. This finding indicates that industrial yeast diffusion it is a real emergency and their presence strongly interferes with the natural yeast microbiota.

Keywords: Geographic distribution; Industrial wine yeasts; Microsatellite typing; mtDNA RFLP analysis; *Saccharomyces cerevisiae* native populations; Winemaking

Frontiers in Microbiology

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The role of nitrogen uptake on the competition ability of three vineyard *Saccharomyces cerevisiae* strains

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Abstract

Three vineyard strains of *Saccharomyces cerevisiae*, P301.4, P304.4 and P254.12, were assayed in comparison with a commercial industrial strain, QA23. The aim was to understand if nitrogen availability could influence strain competition ability during must fermentation. Pairwise-strain fermentations and co-fermentations with the simultaneous presence of the four strains were performed in synthetic musts at two nitrogen levels: control nitrogen condition (CNC) that assured the suitable assimilable nitrogen amount required by the yeast strains to complete the fermentation and low nitrogen condition (LNC) where nitrogen is present at very low level. Results suggested a strong involvement of nitrogen availability, as the frequency in must of the vineyard strains, respect to QA23, in LNC was always higher than that found in CNC. Moreover, in CNC only strain P304.4 reached the same strain frequency as QA23. P304.4 competition ability increased during the fermentation, indicating better performance when nitrogen availability was dropping down. P301.4 was the only strain sensitive to QA23 killer toxin. In CNC, when it was co-inoculated with the industrial strain QA23, P301.4 was never detected. In LNC, P301.4 after 12 h accounted for 10% of the total population. This percentage increased after 48 h (20%). Single-strain fermentations were also run in both conditions and the nitrogen metabolism further analyzed. Fermentation kinetics, ammonium and amino-acid consumptions and the expression of genes under nitrogen catabolite repression evidenced that vineyard yeasts, and particularly strain P304.4, had higher nitrogen assimilation rate than the commercial control. In conclusion, the high nitrogen assimilation rate seems to be an additional strategy that allowed vineyard yeasts successful competition during the growth in grape musts.

Keywords: Alcoholic fermentation; Autochthonous yeast; Killer toxin; Population dynamics; Wine

International Journal of Food Microbiology

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Microbial population dynamics in urban organic waste anaerobic co-digestion with mixed sludge during a change in feedstock composition and different hydraulic retention times

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Abstract

Microbial communities play an essential role in the biochemical pathways of anaerobic digestion processes. The correlations between microorganisms' relative abundance and anaerobic digestion process parameters were investigated, by considering the effect of different feedstock compositions and hydraulic retention times (HRTs). Shifts in microbial diversity and changes in microbial community richness were observed by changing feedstock composition from mono-digestion of mixed sludge to co-digestion of food waste, grass clippings and garden waste with mixed sludge at HRT of 30, 20, 15 and 10 days. Syntrophic acetate oxidation along with hydrogenotrophic methanogenesis, mediated by *Methanothermobacter*, was found to be the most prevalent methane formation pathway, with the only exception of 10 days' HRT, in which *Methanosarcina* was the most dominant archaea. Significantly, the degradation of complex organic polymers was found to be the most active process, performed by members of S1 (*Thermotogales*), *Thermonema* and *Lactobacillus* in a reactor fed with a high share of food waste. Conversely, *Thermacetogenium*, *Anaerobaculum*, Ruminococcaceae, Porphyromonadaceae and the lignocellulosic-degrading *Clostridium* were the significantly more abundant bacteria in the reactor fed with an increased share of lignocellulosic biomass in the form of grass clippings and garden waste. Finally, microbes belonging to *Coprothermobacter*, *Syntrophomonas* and *Clostridium* were correlated significantly with the specific methane yield obtained in both reactors.

Keywords: 16S rRNA; Anaerobic digestion; Methanogenesis; Microbial diversity; Urban organic waste

Water Research

Volume 118, Pages 261-271

Plant science

A grapevine TTG2-like WRKY transcription factor is involved in regulating vacuolar transport and flavonoid biosynthesis

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Abstract

A small set of TTG2-like homolog proteins from different species belonging to the WRKY family of transcription factors were shown to share a similar mechanism of action and to control partially conserved biochemical/developmental processes in their native species. In particular, by activating P-ATPases residing on the tonoplast, PH3 from *Petunia hybrida* promotes vacuolar acidification in petal epidermal cells whereas TTG2 from *Arabidopsis thaliana* enables the accumulation of proanthocyanidins in the seed coat. In this work we functionally characterized *VvWRKY26* identified as the closest grapevine homolog of *PhPH3* and *AtTTG2*. When constitutively expressed in petunia ph3 mutant, *VvWRKY26* can fulfill the PH3 function in the regulation of vacuolar pH and restores the wild type pigmentation phenotype. By a global correlation analysis of gene expression and by transient over-expression in Vitis vinifera, we showed transcriptomic relationships of *VvWRKY26* with many genes related to vacuolar acidification and transport in grapevine. Moreover, our results indicate an involvement in flavonoid pathway possibly restricted to the control of proanthocyanidin biosynthesis that is consistent with its expression pattern in grape berry tissues. Overall, the results show that, in addition to regulative mechanisms and biological roles shared with TTG2-like orthologs, *VvWRKY26* can play roles in fleshy fruit development that have not been previously reported in studies from dry fruit species. This study paves the way toward the comprehension of the regulatory network controlling vacuolar acidification and flavonoid accumulation mechanisms that contribute to the final berry quality traits in grapevine.

Keywords: Flavonoids; Grapevine; Petunia; Vacuolar acidification; WRKY

Frontiers in Plant Science

Volume 7, Article number 1979

Can alternating temperatures be used to estimate base temperature for seed germination?

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Abstract

Modelling weed seedling emergence pattern appears to be a promising approach in the development of effective weed management programmes based on the selection of optimal timing of control operations. Thermal and hydrothermal time models propose that seed germination rates are proportional to the amount by which temperature and water potential exceed threshold values for these environmental factors. Hence, base temperature for seed germination is a fundamental biological parameter for the prediction of weed emergence. A series of laboratory experiments were conducted to estimate base temperature in three weed species belonging to the Asteraceae family, predominant in conservation tillage fields in north-eastern Italy. The traditional method based on germination assays at constant temperatures was compared with a method based on assays at alternating temperatures. The latter might represent an alternative to the former for those species which do not germinate or only poorly under constant temperatures. Base temperature was estimated by regressing the reciprocal of the median germination time on temperature comparing two functions, a broken-stick and an exponential-type model. Both models showed good fit to all data in the whole temperature range and in almost all cases provided similar estimates of base temperature. The main result is that, for the weed species examined in this study, the use of alternating temperatures for base temperature estimation appears to be possible. However, further research is required to test if the use of germination assays performed at alternating temperatures can be a suitable method to estimate base temperature of species that have too low germination at constant temperatures.

Keywords: Alternating temperatures regimes; *Senecio vulgaris*; *Sonchus oleraceus*; *Taraxacum officinale*; Threshold temperature; Weed modelling

Weed Research

Volume 57, Issue 6, Pages 390-398

Combined effects of thinning and decline on fine root dynamics in a *Quercus robur* L. forest adjoining the Italian Pre-Alps

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Abstract

Aims Oak decline is a complex phenomenon, characterized by symptoms of canopy transparency, bark cracks and root biomass reduction. Root health status is one of the first stress indicators, and root turnover is a key process in plant adaptation to unfavourable conditions. In this study, the combined effects of decline and thinning were evaluated on fine root dynamics in an oak forest adjoining the Italian Pre-Alps by comparison of acute declining trees with non-declining trees, both with and without thinning treatment of surrounding trees. Methods Dynamics of volumetric root length density (RLDV) and tip density (RTDV), root tip density per unit length of root (RTDL), diameter, branching index (BI) and mycorrhizal colonization were monitored by soil coring over 2 years as possible descriptors of decline. Key Results At the beginning of the experiment, the relationship between canopy transparency and root status was weak, declining trees having slightly lower RLDV (-20 %) and RTDV (-11 %). After a 1 year lag, during which the parameters were almost unaffected, BI and RLDV, together with tip density, tip vitality and mycorrhizal colonization, became the descriptors most representative of both decline class and thinning. Thinning of declining trees increased RLDV (+12 %) and RTDV (+32 %), but reduced tip mycorrhizal colonization and vitality over time compared with non-thinned trees, whereas the opposite occurred in healthy trees, together with a marked decrease in branching. After thinning, there was an initial reduction in the structure of the ectomycorrhizal community, although recovery occurred about 10 months later, regardless of decline severity. Conclusions Decline causes losses of fine root length, and a moderate recovery can be achieved by thinning, allowing better soil exploration by oak roots. The close correlation between root vitality and mycorrhizal colonization and their deterioration after thinning indicates that decline does not benefit from reduced root competition, excluding the hypothesis of limited water and nutrient availability as a possible cause of the syndrome in this forest.

Keywords: Fine roots; Mycorrhizal colonization; Oak decline; *Quercus robur* L.; Root length and tip density; Thinning

Annals of Botany

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Controlling for genetic identity of varieties, pollen contamination and stigma receptivity is essential to characterize the self-incompatibility system of *Olea europaea* L

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Abstract

Bervillé et al. express concern about the existence of the diallelic self-incompatibility (DSI) system in *Olea europaea*, mainly because our model does not account for results from previous studies from their group that claimed to have documented asymmetry of the incompatibility response in reciprocal crosses. In this answer to their comment, we present original results based on reciprocal stigma tests that contradict conclusions from these studies. We show that, in our hands, not a single case of asymmetry was confirmed, endorsing that symmetry of incompatibility reactions seems to be the rule in Olive. We discuss three important aspects that were not taken into account in the studies cited in their comments and that can explain the discrepancy: (i) the vast uncertainty around the actual genetic identity of vernacular varieties, (ii) the risk of massive contamination associated with the pollination protocols that they used and (iii) the importance of checking for stigma receptivity in controlled crosses. These studies were thus poorly genetically controlled, and we stand by our original conclusion that Olive tree exhibits DSI.

Keywords: Diallelic self-incompatibility system; *Olea europaea* L.; Oleaceae; Paternity analysis; Plant mating systems; Symmetry in reciprocal crosses

Evolutionary Applications

Volume 10, Issue 9, Pages 860-866

Electrostatically stabilized hybrids of carbon and maghemite nanoparticles: Electrochemical study and application

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Abstract

Binary hybrids have been investigated for the past few decades due to the emerging properties of nanoparticle composites. Electrostatically stabilized core-shell nanostructures composed of surface active magnetic nanoparticles (SAMNs) and differently charged carbon nanomaterials display specific electrochemical properties. In this work, a set of binary hybrids that include a new class of magnetic nanoparticles is presented and the electrochemical features of the hybrids are reported. Gallic acid derived carbon dots (GA-CDs), PEG derived graphene dots (PEG-GDs), and quaternized carbon dots (Q-CDs) characterized by different charged groups were used for the preparation of different complexes with SAMNs. Thus, a set of six binary nanomaterials was obtained, and characterized by electrochemical impedance spectroscopy, cyclic voltammetry and chronoamperometry, demonstrating significant differences in the charge transfer resistance, capacitive current, electrochemical performance, and reversibility with respect to the isolated subunits. Among them, the combination of Q-CDs with an excess of SAMNs led to a Q-CD@SAMN hybrid, which displayed peculiar electrocatalytic properties attributable to the influence of the strong electrostatic interactions exerted by Q-CDs on the SAMN surface. Notwithstanding their small fraction (around 1% w/w), Q-CDs oriented the electrocatalysis of SAMNs toward the selective electro-oxidation of polyphenols at low applied potentials (+0.1 V vs. SCE). Finally, the Q-CD@SAMN hybrid was used for the development of a coulometric sensor for polyphenols, composed of a simple carbon paste electrode in a small volume electrochemical flow cell (1 μL), and used for the complete direct electro-oxidation of polyphenols from plant extracts.

Physical Chemistry Chemical Physics

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Fusarium oxysporum f. Sp. *melonis*-melon interaction: Effect of grafting combination on pathogen gene expression

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Abstract

This work is part of a comprehensive study addressed to gain new insights into *Fusarium oxysporum* f. sp. *melonis* (FOM)-melon interaction and understand molecular mechanisms of disease control by grafting. Grafting vegetable is primarily used to provide resistance to soilborne diseases. In this study, the effect on FOM race 1 and race 1,2 gene expression was investigated by quantitative PCR (qPCR), during infection of both resistant and susceptible grafted melon scion-rootstock combinations. Eleven fungal genes related to pathogenicity were considered. The expression of the selected genes varied according to race, susceptible or resistant interaction, and time clustering into six profiles. Classical infection related genes, including Zn-Cys transcription factor FOW2, xylanase, and its relative transcriptional activator were highly induced particularly in the resistant combination when infected by race 1,2 at any time point. In turn, ROS degrading catalase/peroxidase enzyme and actin binding protein were upregulated only at the early stage of infection, in both resistant and susceptible combinations. Genes such as E3 ubiquitin-protein ligase and UTP-glucose-1-phosphate uridylyl transferase showed significant differences between both FOM races in both grafting combinations. Whereas MADS-box transcription factor and acyl-CoA synthetase were essentially unmodulated in race 1, but induced in race 1,2. The only gene significantly dependent on fungal race, resistant/susceptible interaction, and time, was a histidine kinase. Temporal transcription profiles were consistent with the capacity of race 1,2 to grow in the resistant host without inducing wilting symptoms being race 1,2 host colonization independent from virulence. In general, single FOM gene transcription profiles showed no evident differences between rootstock and scion confirming at a molecular level that a melon grafted plant reacts to the pathogen as a single genotype ruled by the rootstock.

Keywords: *Cucumis melo* L; Fusarium wilt; Gene expression; Quantitative PCR; Virulence

European Journal of Plant Pathology

Volume 149, Issue 4, Pages 787-796

High-temperature effects on seed germination of fourteen Kentucky Bluegrass (*Poa pratensis* L.) cultivars

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Abstract

Kentucky bluegrass (*Poa pratensis* L.) is a perennial cool-season grass commonly used for sport and ornamental turfgrasses in transition zones. It is a rather difficult species to establish due to slow germination and the relatively moderate growth rate of seedlings. Early autumn is considered the best time for sowing Kentucky bluegrass in temperate regions. Spring sowing is not recommended as low soil moisture and high temperatures can have a negative impact on germination. However, unavoidable circumstances often force turfgrasses to be sown in spring with high probability of failure. The risk of failure may increase in the near future as a consequence of climate change, so more knowledge is required on the ability of Kentucky bluegrass cultivars to germinate at high temperatures. A laboratory study evaluated the germination response of fourteen cultivars selected among those most used in northern Italy. They were compared in a conditioning chamber under five regimes of alternating temperatures (20/30 °C, 23/33 °C, 26/36 °C, 29/39 °C, 32/42 °C). Germination was recorded weekly starting from sowing. The germination patterns were similar up to 26/36 °C. At 29/39 °C only five cultivars had a germination of over 50%. At the highest temperature regime none of the cultivars had more than 3% germination. It is concluded that only when very extreme high temperatures occur, growers need to pay attention to the choice of cultivars to avoid problems during the germination-emergence phase, but based on the climate change scenario this is likely to happen with greater frequency in the future.

Keywords: Climate change; Establishment; Germination pattern; Germination temperature; Turfgrass

Agronomy Research

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WinRHIZO technology for measuring morphological traits of bermudagrass stolons

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Abstract

WinRHIZO, a root-measuring system, may provide an alternative, reliable, and fast method to analyze stolon morphology of grass species. This study evaluated the possibility to use WinRHIZO technology to measure total length and average diameter of bermudagrass [*Cynodon dactylon* (L.) Pers.] stolons. The length and diameter of 70 stolons collected from four turftype cultivars and a wild bermudagrass were measured with a ruler (length) and caliper (diameter), and using WinRHIZO technology, a scanner-based image analysis system. The scanned length closely predicted the manually measured one and can be successfully used to determine stolon length in samples with a significant amount of biomass. WinRHIZO technology overestimated diameter values when the whole stolon was scanned, while the diameter prediction was more precise when nodes were removed and only internodes were measured.

Agronomy Journal

Volume 109, Issue 6, Pages 3007-3010

Rosaceae fruit development, ripening and post-harvest: An epigenetic perspective

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Abstract

Rosaceae is a family with an extraordinary spectrum of fruit types, including fleshy peach, apple, and strawberry that provide unique contributions to a healthy diet for consumers, and represent an excellent model for studying fruit patterning and development.In recent years, many efforts have been made to unravel regulatory mechanism underlying the hormonal, transcriptomic, proteomic and metabolomic changes occurring during Rosaceae fruit development.More recently, several studies on fleshy (tomato) and dry (Arabidopsis) fruit model have contributed to a better understanding of epigenetic mechanisms underlying important heritable crop traits, such as ripening and stress response.In this context and summing up the results obtained so far, this review aims to collect the available information on epigenetic mechanisms that may provide an additional level in gene transcription regulation, thus influencing and driving the entire Rosaceae fruit developmental process.The whole body of information suggests that Rosaceae fruit could become also a model for studying the epigenetic basis of economically important phenotypes, allowing for their more efficient exploitation in plant breeding.

Keywords: DNA methylation; Epigenetics; Fruit patterning; Histone modifications; Transcription factors; Transcriptional regulation

Frontiers in Plant Science

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Apoplastic gamma-glutamyl transferase activity encoded by GGT1 and GGT2 is important for vegetative and generative development

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Abstract

Gamma-glutamyl transferase (GGT; EC 2.3.2.2) is the only enzyme capable of degrading glutathione (GSH) in extra-cytosolic spaces. In plant cells, the GGT1 and GGT2 isoforms are located in the apoplast, bound respectively to the cell wall and the plasma membrane. GGT1 is expressed throughout plants, mainly in the leaves and vascular system, while GGT2 is more specifically expressed in seeds and trichomes, and weakly in roots. Their role in plant physiology remains to be clarified, however. Obtaining the *ggt1/ggt2* double mutant can offer more clues than the corresponding single mutants, and to prevent any compensatory expression between the two isoforms. In this work, *ggt1/ggt2* RNAi (RNA interference) lines were generated and characterized in the tissues where both isoforms are expressed. The seed yield was lower in the *ggt1/ggt2* RNAi plants due to the siliques being fewer in number and shorter in length, with no changes in thiols and sulfur compounds. Proline accumulation and delayed seed germination were seen in one line. There were also fewer trichomes (which contain high levels of GSH) in the RNAi lines than in the wild type, and the root elongation rate was slower. In conclusion, apoplastic GGT silencing induces a decrease in the number of organs with a high GSH demand (seeds and trichomes) as a result of resource reallocation to preserve integrity and composition.

Keywords: *Arabidopsis thaliana*; cysteine; Gamma-glutamyl transferase; Glutathione; RNA interference; Seed; Trichome

Plant Physiology and Biochemistry

Volume 115, Pages 44-56

mRNA-sequencing analysis reveals transcriptional changes in root of maize seedlings treated with two increasing concentrations of a new biostimulant

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Abstract

Biostimulants are a wide range of natural or synthetic products containing substances and/or microorganisms that can stimulate plant processes to improve nutrient uptake, nutrient efficiency, tolerance to abiotic stress, and crop quality (http://www.biostimulants.eu/, accessed September 27, 2017). The use of biostimulants is proposed as an advanced solution to face the demand for sustainable agriculture by ensuring optimal crop performances and better resilience to environment changes. The proposed approach is to predict and characterize the function of natural compounds as biostimulants. In this research, plant growth assessments and transcriptomic approaches are combined to investigate and understand the specific mode(s) of action of APR, a new product provided by the ILSA group (Arzignano, Vicenza). Maize seedlings (B73) were kept in a climatic chamber and grown in a solid medium to test the effects of two different combinations of the protein hydrolysate APR (A1 and A1/2). Data on root growth evidenced a significant enhancement of the dry weight of both roots and root/shoot ratio in response to APR. Transcriptomic profiles of lateral roots of maize seedlings treated with two increasing concentrations of APR were studied by mRNA-sequencing analysis (RNA-seq). Pairwise comparisons of the RNA-seq data identified a total of 1006 differentially expressed genes between treated and control plants. The two APR concentrations were demonstrated to affect the expression of genes involved in both common and specific pathways. On the basis of the putative function of the isolated differentially expressed genes, APR has been proposed to enhance plant response to adverse environmental conditions.

Keywords: Biostimulant; Gene expression; RNA-seq; Root; *Zea mays* L.

Journal of Agricultural and Food Chemistry

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Proteomic insight into the mitigation of wheat root drought stress by arbuscular mycorrhizae

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Abstract

Arbuscular mycorrhizal fungi (AMF) are plant growth promoters that ameliorate plant-water relations and the nutrient uptake of wheat. In this work, two cultivars of *Triticum* spp., a bread and a durum wheat, grown under drought stress and inoculated or not by AMF, are evaluated through a shotgun proteomic approach. The AMF association had beneficial effects as compared to non-mycorrhizal roots, in both bread and durum wheat. The beneficial symbiosis was confirmed by measuring morphological and physiological traits. In our work, we identified 50 statistically differential proteins in the bread wheat cultivar and 66 differential proteins in the durum wheat cultivar. The findings highlighted a modulation of proteins related to sugar metabolism, cell wall rearrangement, cytoskeletal organization and sulphur-containing proteins, as well as proteins related to plant stress responses. Among differentially expressed proteins both cultivars evidenced a decrease in sucrose:fructan 6-fructosyltransferas. In durum wheat oxylipin signalling pathway was involved with two proteins: increased 12-oxo-phytodienoic acid reductase and decreased jasmonate-induced protein, both related to the biosynthesis of jasmonic acid. Interactome analysis highlighted the possible involvement of ubiquitin although not evidenced among differentially expressed proteins. The AMF association helps wheat roots reducing the osmotic stress and maintaining cellular integrity. *Biological significance*: Drought is one of the major constraints that plants must face in some areas of the world, associated to climate change, negatively affecting the worldwide plant productivity. The adoption of innovative agronomic protocols may represent a winning strategy in facing this challenge. The arbuscular mycorrhizal fungi (AMF) inoculation may represent a natural and sustainable way to mitigate the negative effects due to drought in several crop, ameliorating plant growth and development. Studies on the proteomic responses specific to AMF in drought-stressed plants will help clarify how mycorrhization elicits plant growth, nutrient uptake, and stress-tolerance responses. Such studies also offer the potential to find biological markers and genetic targets to be used during breeding for new drought-resistant varieties.

Keywords: Drought stress; *Glomus mosseae*; Shotgun proteomics; Sustainable agriculture; *Triticum* spp

Journal of Proteomics

Volume 169, Pages 21-32

System analysis of metabolism and the transcriptome in *Arabidopsis thaliana* roots reveals differential co-regulation upon iron, sulfur and potassium deficiency

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Abstract

Deprivation of mineral nutrients causes significant retardation of plant growth. This retardation is associated with nutrient-specific and general stress-induced transcriptional responses. In this study, we adjusted the external supply of iron, potassium and sulfur to cause the same retardation of shoot growth. Nevertheless, limitation by individual nutrients resulted in specific morphological adaptations and distinct shifts within the root metabolite fingerprint. The metabolic shifts affected key metabolites of primary metabolism and the stress-related phytohormones, jasmonic, salicylic and abscisic acid. These phytohormone signatures contributed to specific nutrient deficiency-induced transcriptional regulation. Limitation by the micronutrient iron caused the strongest regulation and affected 18% of the root transcriptome. Only 130 genes were regulated by all nutrients. Specific co-regulation between the iron and sulfur metabolic routes upon iron or sulfur deficiency was observed. Interestingly, iron deficiency caused regulation of a different set of genes of the sulfur assimilation pathway compared with sulfur deficiency itself, which demonstrates the presence of specific signal-transduction systems for the cross-regulation of the pathways. Combined iron and sulfur starvation experiments demonstrated that a requirement for a specific nutrient can overrule this cross-regulation. The comparative metabolomics and transcriptomics approach used dissected general stress from nutrient-specific regulation in roots of Arabidopsis.

Plant Cell and Environment

Volume 40, Issue 1, Pages 95-107

The physiological and metabolic changes in sugar beet seedlings under different levels of salt stress

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Abstract

Salinity stress is a major limitation to global crop production. Sugar beet, one of the world's leading sugar crops, has stronger salt tolerant characteristics than other crops. To investigate the response to different levels of salt stress, sugar beet was grown hydroponically under 3 (control), 70, 140, 210 and 280 mM NaCl conditions. We found no differences in dry weight of the aerial part and leaf area between 70 mM NaCl and control conditions, although dry weight of the root and whole plant treated with 70 mM NaCl was lower than control seedlings. As salt concentrations increased, degree of growth arrest became obvious In addition, under salt stress, the highest concentrations of Na+ and Clwere detected in the tissue of petioles and old leaves. N and K contents in the tissue of leave, petiole and root decreased rapidly with the increase of NaCl concentrations. P content showed an increasing pattern in these tissues. The activities of antioxidant enzymes such as superoxide dismutase, catalase, ascorbate peroxidase and glutathione peroxidase showed increasing patterns with increase in salt concentrations. Moreover, osmoprotectants such as free amino acids and betaine increased in concentration as the external salinity increased. Two organic acids (malate and citrate) involved in tricarboxylic acid (TCA)-cycle exhibited increasing contents under salt stress. Lastly, we found that Rubisco activity was inhibited under salt stress. The activity of NADP-malic enzyme, NADP-malate dehydrogenase and phosphoenolpyruvate carboxylase showed a trend that first increased and then decreased. Their activities were highest with salinity at 140 mM NaCl. Our study has contributed to the understanding of the sugar beet physiological and metabolic response mechanisms under different degrees of salt stress.

Keywords: Osmotic stress; Photosynthesis; Reactive oxygen species; Salt stress; Sugar beet

Journal of Plant Research

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Transcriptome-wide identification of differentially expressed genes in *Solanum lycopersicon* L. In response to an Alfalfa-protein hydrolysate using microarrays

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Abstract

An alfalfa-based protein hydrolysate (EM) has been tested in tomato (*Solanum lycopersicon* L.) plants at two different concentrations (0.1 and 1 mL L^{-1}) to get insight on its efficacy as biostimulant in this species and to unravel possible metabolic targets and molecular mechanisms that may shed light on its mode of action. EM was efficient in promoting the fresh biomass and content in chlorophyll and soluble sugars of tomato plants, especially when it was applied at the concentration of 1 mL L^{-1}. This effect on plant productivity was likely related to the EM-dependent up-regulation of genes identified via microarray and involved in primary carbon and nitrogen metabolism, photosynthesis, nutrient uptake and developmental processes. EM also up-regulated a number of genes implied in the secondary metabolism that leads to the synthesis of compounds (phenols and terpenes) functioning in plant development and interaction with the environment. Concomitantly, phenol content was enhanced in EM-treated plants. Several new genes have been identified in tomato as potential targets of EM action, like those involved in detoxification processes from reactive oxygen species and xenobiotic (particularly glutathione/ascorbate cycle-related and ABC transporters), and defense against abiotic and biotic stress. The model hypothesized is that elicitors present in the EM formulation like auxins, phenolics, and amino acids, may trigger a signal transduction pathway via modulation of the intracellular levels of the hormones ethylene, jasmonic acid and abscissic acid, which then further prompt the activation of a cascade events requiring the presence and activity of many kinases and transcription factors to activate stress-related genes. The genes identified suggest these kinases and transcription factors as players involved in a complex crosstalk between biotic and abiotic stress signaling pathways. We conclude that EM acts as a biostimulant in tomato due to its capacity to stimulate plant productivity and up-regulate stress-related responses. Its use in agricultural practices may reduce the need of inorganic fertilizers and pesticides, thereby reducing the environmental impact of productive agriculture.

Keywords: Biostimulant; Defense; Hormones; Microarray; Phenols; Productivity; Signaling; Sugars

Frontiers in Plant Science

Volume 8, Article number 1159

Advances in proteomic technologies and their scope of application in understanding plant–pathogen interactions

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Abstract

Proteomics, one of the major tools of ‘omics’ is evolving phenomenally since the development and application of two-dimensional gel electrophoresis coupled with mass spectrometry at the end of twentieth century. However, the adoption and application of advanced proteomic technologies in understanding plant–pathogen interactions are far less, when compared to their application in other related fields of systems biology. Hence, this review is diligently focused on the advances in various proteomic approaches and their gamut of applications in different facets of phyto-pathoproteomics. Especially, the scope and application of proteomics in understanding fundamental concepts of plant–pathogen interactions such as identification of pathogenicity determinants (effector proteins), disease resistance proteins (resistance and pathogenesis-related proteins) and their regulation by post-translational modifications have been portrayed. This review, for the first time, presents a critical appraisal of various proteomic applications by assessing all phyto-pathoproteomics-related research publications that were published in peer-reviewed journals, during the period 2000–2016. This assessment has revealed the present status and contribution of proteomic applications in different categories of phyto-pathoproteomics, namely, cellular components, host–pathogen interactions, model and non-model plants, and utilization of different proteomic approaches. Comprehensively, the analysis highlights the burgeoning application of global proteome approaches in various crop diseases, and demand for acceleration in deploying advanced proteomic technologies to thoroughly comprehend the intricacies of complex and rapidly evolving plant–pathogen interactions.

Keywords: Global proteome analysis; Phyto-pathoproteomics; Plant–pathogen interactions; Targeted proteome analysis

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Common bean proteomics: Present status and future strategies

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Abstract

Common bean (*Phaseolus vulgaris* L.) is a legume of appreciable importance and usefulness worldwide to the human population providing food and feed. It is rich in high-quality protein, energy, fiber and micronutrients especially iron, zinc, and pro-vitamin A; and possesses potentially disease-preventing and health-promoting compounds. The recently published genome sequence of common bean is an important landmark in common bean research, opening new avenues for understanding its genetics in depth. This legume crop is affected by diverse biotic and abiotic stresses severely limiting its productivity. Looking at the trend of increasing world population and the need for food crops best suited to the health of humankind, the legumes will be in great demand, including the common bean mostly for its nutritive values. Hence the need for new research in understanding the biology of this crop brings us to utilize and apply high-throughput omics approaches. In this mini-review our focus will be on the need for proteomics studies in common bean, potential of proteomics for understanding genetic regulation under abiotic and biotic stresses and how proteogenomics will lead to nutritional improvement. We will also discuss future proteomics-based strategies that must be adopted to mine new genomic resources by identifying molecular switches regulating various biological processes.

Common bean is regarded as “grain of hope” for the poor, being rich in high-quality protein, energy, fiber and micronutrients (iron, zinc, pro-vitamin A); and possesses potentially disease-preventing and health-promoting compounds. Increasing world population and the need for food crops best suited to the health of humankind, puts legumes into great demand, which includes the common bean mostly. An important landmark in common bean research was the recent publication of its genome sequence, opening new avenues for understanding its genetics in depth. This legume crop is affected by diverse biotic and abiotic stresses severely limiting its productivity. Therefore, the need for new research in understanding the biology of this crop brings us to utilize and apply high-throughput omics approaches. Proteomics can be used to track all the candidate proteins/genes responsible for a biological process under specific conditions in a particular tissue. The potential of proteomics will not only help in determining the functions of a large number of genes in a single experiment but will also be a useful tool to mine new genes that can provide solution to various problems (abiotic stress, biotic stress, nutritional improvement, etc). We believe that a combined approach including breeding along with omics tools will lead towards attaining sustainability in legumes, including common bean.

Keywords: Common bean; Genomics; Markers; Proteogenomics; Proteomics

Journal of Proteomics

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IBAF - CNR

Diversity of methodologies to experiment Integrated Pest Management in arable cropping systems: Analysis and reflections based on a European network

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Abstract

Integrated Pest Management (IPM) aims to promote physical and biological regulation strategies that help farmers contain populations of pests (pathogens, animal pests and weeds) and to finally reduce the reliance on pesticides. It is based on the holistic combination of multiple management measures rather than on the sum of single methods, each of them having only small effects on pests reduction. Thus, to analyse the interactions between IPM measures and to evaluate the sustainability of their implementation, we require an approach considering the whole cropping system (CS), i.e. a functional entity whose complexity is more than the sum of its parts. A network of European experiments at the CS level was set up recently, and aimed at sharing data and expertise to enhance knowledge of IPM. Comparison of existing methodologies highlighted a diversity of CS designs and experimental layouts. We deduced that the concept of CS itself was viewed differently among scientists, and this affected experimental protocols. Other differences were related to the research context and objectives. Some experiments aimed to explore very innovative strategies and generated knowledge on both their effects on the agroecosystem and their ability to satisfy a set of performance targets, while others aimed to provide quickly adoptable solutions for local farmers in line with the current socio-economic constraints. In some research programmes, the experiment was part of the CS design process — and tested CS were regularly revised based on an continuous improvement loop — while in other cases CS were kept stable across years so as to enable the evaluation of their long-term cumulative effects. A critical aspect contributing to the diversity among CS experiments was the distinction between a factorial design of experimental CS and systemic approaches: factorial experiments allowed quantification of the effects of each IPM component regardless of the consistency between components defining the CS. In contrast, systemic approaches focused on the overall evaluation of CS designed with consideration of their consistency, hence maximising their ability to meet the objectives. Because CS experiments represent a huge investment in terms of economics and time, preliminary reflections of the relevance of the experimental strategy is of critical importance.

Keywords: Agroecology; Cropping system; Field experiment; Integrated pest management; SWOT analysis

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Sustainability of European winter wheat- and maize-based cropping systems: Economic, environmental and social ex-post assessment of conventional and IPM-based systems

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Abstract

In order to ensure higher sustainability of winter wheat and maize production in Europe, cropping systems featuring different levels of Integrated Pest Management (IPM) need to be tested in the field and validated for their sustainability before being adopted by farmers. However, the sustainability evaluation of cropping systems is difficult to perform effectively due to the complex economic, social and environmental dimensions of sustainability. Within the EU research project PURE, nine long-term experiments were conducted in various European regions from 2011 to 2014, comparing two IPM levels against the conventional system (CS) in winter wheat- and maize-based cropping systems. IPM1 encompassed some pesticide use in semi-diverse crop rotations while IPM2 favoured reduced- and non-chemical methods in diverse rotations. The modified DEXiPM (DEXi Pest Management) model for arable cropping systems was used for ex-post assessments to compare the economic, environmental and social sustainability of these systems. The assessments

showed that in six out of nine trials the CS was overall unsustainable because of low evaluation of the environmental sustainability that was mainly due to high pesticide use and simplified crop rotations where the choice of crops is primarily market-driven. In contrast, six IPM1 and five IPM2 systems could be classified as sustainable, achieving 'medium' or 'high' scores for all three sustainability dimensions. Differences in the socio-economic conditions across countries and/or climatic and soil conditions across experimental trials highlighted that IPM is based on general principles that must be adapted to address specific local conditions. Overall, IPM systems included more diverse crop rotations and practices compared to the CS, promoting IPM-based strategies with less pesticide use but also a reduced reliance on pesticides that could partially compensate for any yield reductions by the savings on pesticide and application costs. It is recommended that the results of the study should be disseminated to policy-makers, advisors and farmers and that their implementation should be considered on a regional level. Regional policies to encourage the adoption of more sustainable systems based on IPM principles, as well as better support by more closely involving the regional advisory services for the general implementation of IPM is further recommended. Ex-post analysis with DEXiPM also identified the constraints of the IPM1 and IPM2 systems evaluated as not sustainable. These were related to i) environmental issues for those IPM1 systems that still relied mainly on pesticide use and had less diverse crop rotations, and ii) economic issues for IPM2 systems, mainly due to the choice of less profitable crops in the rotation, as well as to yield penalties caused by the very low pesticide use or replacing pesticides with less effective non-chemical methods. The identification of these constraints is a valuable input to the local and regional discussion on how to adopt IPM and develop more sustainable cropping systems.

Crop Protection

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Risk assessment of soil-pest damage to grain maize in Europe within the framework of Integrated Pest Management

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Abstract

The management of soil-pests relies largely on conventional insecticides. Within the framework of the EU's PURE project, data were collected to assess the risk of soil-pest damage to grain maize in Europe in order to implement Integrated Pest Management (IPM) of soil-pests in a more practical and sustainable manner, thus optimizing the use of soil insecticides (in-furrow or as seed-dressing) at sowing. Plant density and soil-pest damage to maize seeds and/or plants during the growing season were determined in fields with no or some risk factors. Risk assessment on a sample of sixteen experimental sites (a total of 109.95 ha of maize) located in five European countries (Germany, Hungary, Italy, Slovenia and the Netherlands) from 2011 to 2014 showed a low risk of soil-pest damage to maize. In all fields, wireworms (Agriotes spp. larvae) caused 99.5%–100% of the plant damage, meaning that damage by other soil-pests was negligible. The fields studied were divided into two groups: those with no risk and those with risk factors. According to previous research, the risk factors were Agriotes brevis Candeze and Agriotes sordidus Illiger as prevalent damaging species, soil Organic Matter content over 5%, rotation including meadows and/or double crops, as well as surrounding landscape being mainly meadows, uncultivated grass and double crops, cover crops, and poor drainage. In the fields with no risk factors, wireworm plant damage (mainly holes in the collar causing central leaf wilting) never exceeded 15%, a threshold value for potential yield reduction. Furthermore, plant damage was much lower or even negligible in the vast majority of the fields (i.e. over 90% of fields had less than 5% wireworm damage to maize plants). Risk factors, such as rotation including meadows and/or double crops, led to the percentage of cultivated land with significant wireworm plant damage being even lower than predicted (8.7% instead of 14.7%) and almost 50% of that predicted for the whole sample (2.7% instead of 4.9%). In the few cases where plant damage was higher than 15%, yield was not affected when untreated strips were compared with strips treated with soil insecticides. In all trials, the soil insecticide Tefluthrin did not significantly increase the density of healthy maize plants or grain yield. In more than 99% of cases, no economic damage to maize by soil-pests was recorded. These results demonstrate that the occurrence of risk factors may increase the risk of wireworm damage to maize crops, while the probability of damage to a field with no risk factors is always very low (less than 1%). This highlights the importance of integrating risk assessment of soil-pest damage to maize into IPM strategies, which would include: i) an "area-wide" risk assessment evaluating the possible presence of risk factors, including click beetle population monitoring with pheromone traps, and ii) "complementary field monitoring" with bait traps where risk assessment has identified the presence of risk factors. In fields with no risk factors, treating maize with soil insecticides was found to be pointless. Therefore, IPM strategies in maize that include risk assessment of soil-pest damage may lead to a significant reduction in soil insecticides use and, consequently, to a reduction in environmental impact.

Keywords: Agriotes; Damage risk factors; IPM; Maize; Soil insecticides; Soil pests; Wireworms

Crop Protection

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Occurrence of different resistance mechanisms to acetolactate synthase inhibitors in European Sorghum halepense

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Abstract

Four Hungarian and two Italian Sorghum halepense populations harvested in maize fields were investigated to elucidate the levels and mechanisms underlying acetolactate synthase (ALS) inhibitors resistance. The two Italian populations were highly cross-resistant to all ALS inhibitors tested, and the variant ALS allele Leu574 was identified in most of the plants; no differences were observed when the plants were treated with herbicide plus malathion. This suggests that the main resistance mechanism is target-site mediated. The Hungarian populations proved to be controlled by imazamox, while they were resistant to sulfonylureas and bispyribac-Na. All Hungarian populations, but not all plants of population 12-49H, presented the variant allele Glu376. This is the first documented occurrence of the Asp-376-Glu substitution in *S. halepense*. ALS enzyme bioassay and treatment with malathion confirmed that at least in plants of two populations the resistance is very likely due to both target-site and enhanced metabolism of P450 enzymes.

Keywords: Enhanced metabolism; Herbicide resistance; Johnsongrass; Nicosulfuron; Target-site resistance

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A new ala-122-asn amino acid change confers decreased fitness to ALS-resistant *Echinochloa crus-galli*

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Abstract

Gene mutations conferring herbicide resistance may cause pleiotropic effects on plant fitness. Knowledge of these effects is important for managing the evolution of herbicide-resistant weeds. An *Echinochloa crus-gall*i population resistant to acetolactate synthase (ALS) herbicides was collected in a maize field in north-eastern Italy and the cross-resistance pattern, resistance mechanism and fitness costs associated to mutantresistant plants under field conditions in the presence or absence of intra-specific competition were determined. The study reports for the first time the Ala-122-Asn amino-acid change in the ALS gene that confers high levels of cross-resistance to all ALS inhibitors tested. Results of 3-year growth analysis showed that mutant resistant *E. crus-galli* plants had a delayed development in comparison with susceptible plants and this was registered in both competitive (3, 7, and 20 plants m^{-2}) and noncompetitive (spaced plants) situations. The number of panicles produced by resistant plants was also lower (about 40% fewer panicles) than susceptible plants under nointraspecific competition. Instead, with the increasing competition level, the difference in panicle production at harvest time decreased until it became negligible at 20 plants m^{-2}. Evaluation of total dry biomass as well as biomass allocation in vegetative parts did not highlight any difference between resistant and susceptible plants. Instead, panicle dry weight was higher in susceptible plants indicating that they allocated more biomass than resistant ones to the reproductive organs, especially in no-competition and in competition situations at lower plant densities. The different fitness between resistant and susceptible phenotypes suggests that keeping the infestation density as low as possible can increase the reproduction success of the susceptible phenotype and therefore contribute to lowering the ratio between resistant and susceptible alleles. If adequately embedded in a medium or long-term integrated weed management strategy, the presence of R plants with a fitness penalty provides an opportunity to minimize or reverse herbicide resistance evolution through the implementation of integrated weed management, i.e., all possible control tools available.

Keywords: Ala-122-Asn mutation; Barnyardgrass; Biomass allocation; Herbicide resistance management; Phenology; Seed production; Target-site resistance

Frontears in Plant Science

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Suitable reference genes for accurate gene expression analysis in *Papaver rhoeas* under 2,4-D herbicide stress

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Abstract

Resistance to 2,4-D (2,4-diclorophenoxyacetic acid) herbicide is increasing in various dicotyledonous weed species, including Papaver rhoeas, a weed infesting Southern European wheat crops. Non-target-site resistance to this herbicide is governed by a range of genes involved in herbicide stress response. To enable reliable measurement of gene expression levels in herbicide-resistant and susceptible plants it is necessary to normalize qPCR data using internal control genes with stable expression. In an attempt to find the best reference genes, the stability of seven candidate reference genes was assessed in plants resistant and susceptible to 2,4-D, subjected or not to herbicide stress. Using three statistical algorithms (geNorm, BestKeeper and NormFinder), the overall results revealed that glyceraldehyde-3-phosphate dehydrogenase, actin and ubiquitin were the most stable reference genes. The normalization expression levels of GH3 (indole-3-acetic acid amido synthetase) and GST3 (glutathione S-transferase) which are two genes up-regulated following 2,4-D treatment, were determined to verify the stability of these selected reference genes. A sudden increase in GH3 and GST3 expression was already detected 5 h after herbicide application, confirming their involvement in plant response to 2,4-D. The validation results confirmed the applicability and accuracy of these reference genes. This study identified and validated reference genes in the non-model weed species P. rhoeas and these will facilitate gene expression analysis studies aimed at identifying functional genes associated with non-target-site resistance.

Keywords: Auxinic herbicide; Gene expression; Herbicide resistance; RT-qPCR; Weed

Pesticide Biochemistry and Physiology

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DAFNAE
Department of Agronomy Food
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This scientific report gives an overview of the research activity carried on during the sixth 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 fifth research yearbook of DAFNAE collects the abstracts of the papers published in 2017 and indexed by Scopus. These abstracts were grouped into the following scientific categories:
Agronomy and soil science
Animal science
Ecology and environmental science
Entomology
Food science and technology
Genetics and genomics
Microbiology
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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 fifth edition will continue to propose their scientific activities in the territory and in the world.

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