

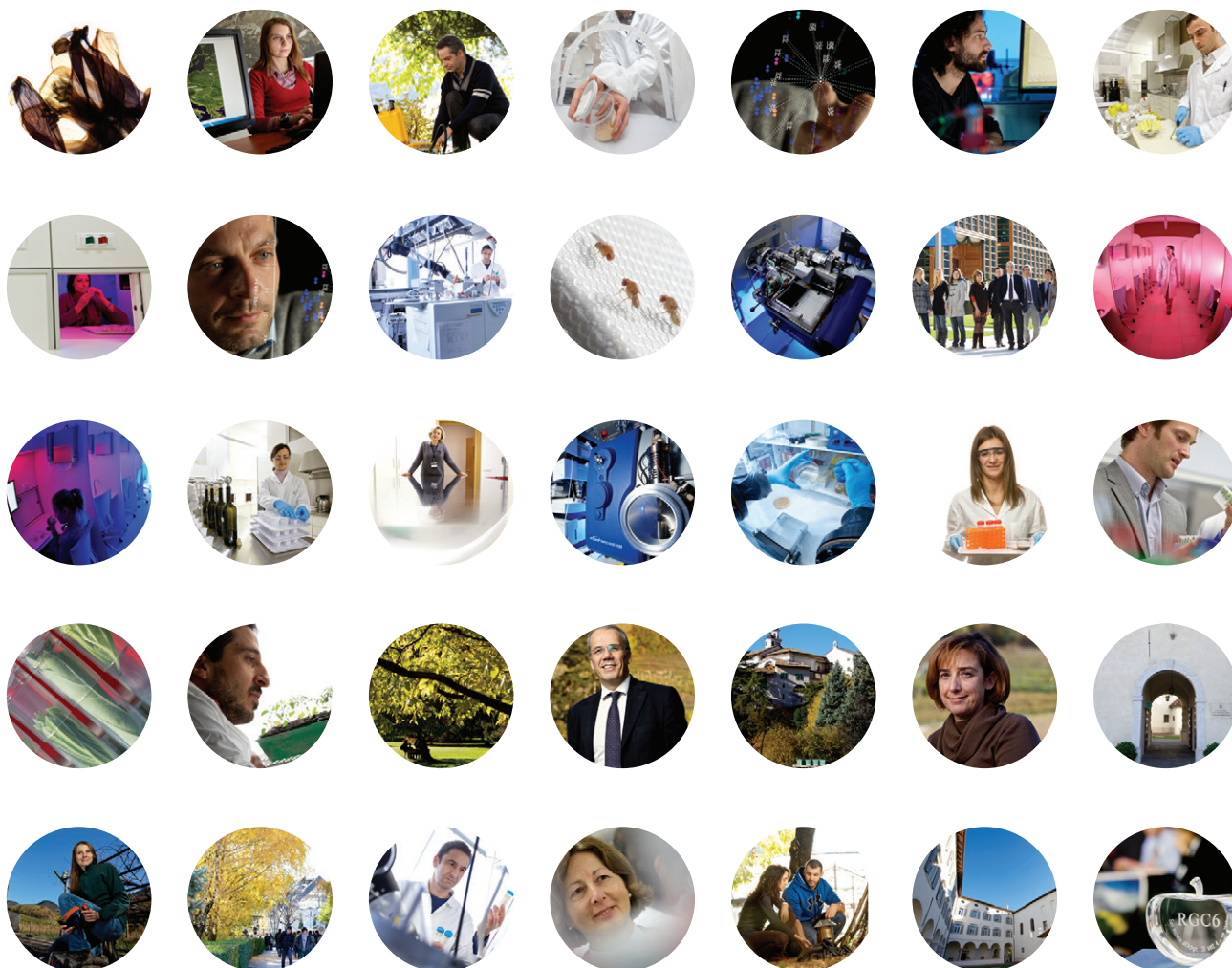


**RESEARCH
AND INNOVATION
CENTRE**

**FONDAZIONE
EDMUND MACH**

REPORT

11 / 12



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our world : at a glance

Preface



Alessandro Carlo
DINI
General Director of FEM

Francesco
SALAMINI
President of FEM

Roberto
VIOLA
Director of the Research and Innovation Centre

The intention of the Research and Innovation Centre (CRI) Report is to give a detailed account of our principal endeavours over the period 2011/12, to “open the doors of our laboratories” and to share our objectives, activities and achievements with our readers. To this end, we have broken with past tradition and have implemented a new presentation style which operates on two levels: the main text attempt to reach the non-expert, while some aspects are described in more detail to maintain the necessary “technical” dimension. With this approach we hope to reach the widest possible audience and to draw their attention to the tireless work of our staff of almost 300 people (including about 175 researchers), by clearly and effectively illustrating the activities they have carried out.

A few months after Nature Genetics published the news that the apple genome had been sequenced, 2011 opened with the announcement that another genome had been decoded with the scientific contribution of our researchers, that of wild strawberry. At the beginning of summer 2012, we also presented preliminary data on the genome sequence of *Drosophila suzukii*, a tiny fly that attacks soft fruit. Further international recognition of the prominent role played by CRI in the field of genomics came when we were given the task of organising the sixth edition of the International Rosaceae Genomics Conference (RGC6), which was held in autumn 2012. This conference was also an occasion for announcing the completion of the pear and raspberry genomes, in which, once again, we were actively involved.

A contributing factor to making all this possible is our infrastructure, comprising 2000 square metres of laboratories, offices and teaching facilities, over 200 square metres of greenhouses and 3000 square metres for experimentation associate with plant biotechnology. In addition, a centre for computational biology opened in 2012 with first-rate expertise in the field of bioinformatics and advanced statistics; we published around 130 scientific articles in high-impact journals; we have an education programme that, together with the International School of Research (FIRST), has attracted fresh, young talent to CRI from all over the world. These are, in my opinion, the essential components that make CRI an authority in the production of knowledge and in promoting innovation and concrete spin-offs for the Province and surrounding area.

My wish is that this Report will succeed in its intention of showcasing the work being carried out in the CRI laboratories and in so doing enable the Reader to appreciate our mission and the values with which we identify.

Roberto Viola
Director of the Research and Innovation Centre



Fondazione Edmund Mach

In order to improve agriculture in what was then southern Tyrol, on 12th January 1874 the Tyrolean Diet in Innsbruck approved the institution of an agricultural school to be located in the Augustinian monastery of San Michele all'Adige. The school opened in the autumn of that year with a programme established by its first director, Edmund Mach. He was an efficient organiser and from the very outset fervently supported the plan to turn the institute into an innovative organisation where teaching and research would together contribute to the development of agriculture in the region.

After the First World War, the Agricultural Institute of San Michele (IASMA) came under the control of the Italian government which in turn passed it over to the authority of the Autonomous Province of Trento.

In 1990 Provincial Law no. 28 formalised the transformation of IASMA into a functional agency of the Autonomous Province of Trento, in addition integrating the land services into the pre-existing structure based on training and research.

On 1st January 2008 the Institute's organisations and activities were transferred to a new legal body, the Edmund Mach Foundation (FEM-IASMA), a public agency under private law jurisdiction as provided by the law concerning reforms in research (P. Law no. 2, 14th August 2005).

The 3 centres that constituted IASMA were inherited by FEM and given a more flexible structure geared to the specific aims of Education and Training, Research and Innovation, and Technology Transfer, which became not just the new names for the centres but also described the most salient aspects of their respective missions.



Since 1st January 2009 FEM-IASMA's Experimental Centre has had a new organisational structure and is now known as the Research and Innovation Centre (CRI). Originally, it was organized in specialised research Areas covering the fields of Agriculture, Food and the Environment. In January 2011, a new organizational restructuring concerned the Centre, and resulted in a new arrangement based on a Research consortium (in participation with the National Research Council) and five Departments, which in turn are organized in Research Groups and Technological Platforms. CRI main research topics concern genetics and genomics of fruit plants, computational biology, agri-food and nutritional quality, biodiversity and molecular ecology, sustainable agro-ecosystems and bioresources.

Pioneering organisations, a young and dynamic environment, international researchers, collaborations with universities and institutions throughout the world, and the institution of high-level specialised training initiatives: all these together place the Centre in a global context, which encourages the exchange of ideas and the development of innovation and produces internationally-recognised results.

With this strong background, the CR&I occupies an authoritative position in knowledge acquisition and in fostering innovation and positive spillover effects for the region. These are indispensable requisites for stimulating the development of an economy which is increasingly knowledge-based and for supporting long-term, high-quality socio-economic growth.

The Research and Innovation Centre

FIRST

Title

The Fondazione Edmund Mach School of Research



FIRST is one of the many initiatives established by the Centre for Research and Innovation during the four years of its existence. It was launched in the spring of 2012 with the aim of bringing together under a single direction all the activities connected with the school of research at the Fondazione Edmund Mach.

The International Doctoral Programme in the Genomics and Physiology of Fruit Plants (GMPF) has expanded beyond its original agenda which was to focus on issues in the fields of genomics, informatics, functional genomics, proteomics and metabolomics, genetics, and the genetic improvement and molecular physiology of fruit tree species, and now also encompasses food and nutrition sciences, computational biology, environmental sciences, climatology and veterinary science.

The guiding principles of FIRST are applied research, an international working environment (the students, in fact, represent 24 countries and work in multi-cultural research groups) and state-of-the-art technology. The extensive network of international collaborations encourages student mobility and provides them with opportunities to develop their research at some of the world's most prominent laboratories. This fosters independence and the self-organisational skills that will prepare them to enter the world of scientific research.

It is in these very areas that CR&I provides the added value of a world-renowned research body with ten years' experience developed through a policy of orienting research to the demands of consumers and producers.

FIRST runs a twelve-month internal training course consisting of at least a pair of Summer or Winter Schools, specific Workshops, two seminars per month held by speakers of international standing, intensive courses in statistics and Italian for speakers of foreign languages, as well as a Journal Club and discussion forums on the progress of the various doctoral projects.

Almost ninety students, predominantly women (60%), are enrolled with FIRST, which awarded the first PhD titles in 2012.

our research : key subjects

part_1 Beyond the genome

part_2 Our natural capital

part_3 Food for life

BEYOND THE GENOME /

AFTER SEQUENCING
GENOMES OF PEAR,
STRAWBERRY,
RASPBERRY AND
OF *DROSOPHILA*
SUZUKI, WITH
METAGENOMICS
WE ARE ENTERING
NOW THE
ENVIRONMENT
THAT MORE
“INTIMATELY”
SURROUNDS US

part_1

Riccardo Velasco, Duccio Cavalieri

Going beyond the knowledge of genomes to enhance the biological complexity

GENOMES. With the advent of modern DNA sequencing technologies we now have access to the information encoded in the nucleotide sequences of many species of living organisms. In 2011 FEM sequenced the genomes of pear, strawberry and raspberry, thus obtaining crucial information for improving production and quality of these fruits. In the latter half of 2012 CRI-FEM also completed genome sequencing of the vinegar fly *Drosophila suzukii*, a parasite and serious threat to the cultivation of small fruits.

A question we are often asked is: why do we need to know the structure of genomes? For a scientist, the answer is simple: how can you even start to solve the problems of a system if you don't know the structure of the system? A mechanic is well aware how important it is to know the structure of the engine of the particular model of car that needs repairing in order to fix it. The difference is that while the car manufacturer can provide a construction diagram of the engine, when it comes to biological systems, scientists must first draw up the diagram by probing nature with the latest technologies.

BEYOND THE GENOMES. Despite promising initial breakthroughs, we still do not have sufficient knowledge of genome sequences to explain why we are healthy or why we get sick, how we can live longer, what makes plants resistant to pathogens or what gives them their particular aromatic properties. It is highly probable that many of the answers we are seeking are complex and depend on the function of many genes and their interaction with the environment. When we speak of "environment" we immediately think of the place where we live, the climate, pollution, food; but there is an environment that is much closer to us and far more "intimate", the importance of which we are only now beginning to understand. This environment is shaped by the microorganisms that are with us right from birth and which have been with us for thousands of years throughout our evolution. The development of metagenomic techniques and their application in the study of the microbial communities present in the human intestine, in foods, in the roots and bodies of plants, or in insect pathogens, is an area of research that promises to lead to a general understanding of how, using microorganisms, important biotechnological problems can be solved and how humans and plants can be kept healthy.

1.1

Title

What have we learned from the apple genome?

Two years ago, Fondazione Edmund Mach had the honour of leading an international team in the sequencing project of the apple genome (Velasco *et al.*, *Nature Genetics* 2012). The collaborative effort and synergies with other international institutions led to the completion of the project in a much shorter time than other similar initiatives that took place in the past. This work has cemented the Foundation's position as one of the top international institutes in the world working on plant **genomics**. This is also demonstrated by the Foundation's involvement in scientific initiatives of similar scope and relevance, such as the sequencing of the genome of strawberry (Shulaev *et al.*, *Nature Genetics*, 2012) and the genomes of raspberry and pear (rgc6.org) recently presented at the international Rosaceous Genomics Conference (Rosaceae is the botanical family of apple peach, strawberry, pear, plum, apricot, raspberry, rose and many others), which took place at the Palarotari di Mezzocorona the first week of October 2012.

In addition to these projects, the Foundation participates in European and national projects on the use of **genomic information**¹ in support of **genetic improvement**². A European project (www.fruitbreedomics.com) with the participation of 29 institutions from nine different countries, aims to develop **molecular markers**³ associated with innovative features of the apple species to produce new varieties that combine fruit quality with genetic resistance to major pathogens, with a lower environmental economic impact in their management.

The national project (www.projectager.it), led by FEM with the participation of five Italian universities and research institutes, is more focused on the health aspects of fruit consumption as well as fruit quality and aims to find correlations between molecular data (genes, proteins and metabolites of the apple fruit) and nutritional (in collaboration with UniTN and INRAN of Rome), allergenic (UniPd and UniBO), production (CRESO Cuneo and UniPd), and orchard management (UniBO and UNIUD) characteristics.

In both projects, re-sequencing data from many varieties with known pedigree have been used to associate the differences between the genomes of different varieties with the traits that characterize them in order to understand the biological basis underlying the characteristics of the fruit and their exploitation in orchard management, production and preservation of fruit, and genetic improvement.

Last but not least, the genome is being used for evolutionary studies of fruit trees and their domestication, and the exploitation of this knowledge through comparative genomics to identify common features within the same botanical family of the Rosaceae (Illa *et al.* *BMC Evol. Biology* 2011; Jung *et al.*, *BMC Genomics* 2012). These studies have revealed many interesting aspects about the origin of the chromosomal structure of the apple, strawberry, and peach genomes as well as common or unique characteristics that distinguish them. In the coming years, the basic knowledge gained will be vital to redirect the management of the plant and the production of innovative varieties needed to meet the challenges of the new millennium and the conception of a new fruit cultivation.

in short

One of the top
international institutes
working on plant genomics

More

Keywords

Michela Troggio, Dan Sargent, Fabrizio Costa, Riccardo Velasco

1 / Technologies used to exploit genome knowledge

Within the Fruitbreedomics project a high-density SNP chip has been developed from re-sequencing data of a set of cultivars, ancestors, and founders, representing the pedigrees of european apple breeding programs. 20,000 SNPs were included on the chip. They were uniformly distributed in the apple genome and to represent the genomes of all cultivars resequenced. The chip will provide unprecedented resolution for the discovery of marker-trait associations, investigation of genetic variation (neutral and functional), and will enable genomic selection in apple. The apple SNP-chip has been exploited by FEM scientists, in collaboration with colleagues, to develop the most comprehensive molecular map of the apple genome published to date. A map based on a cross between two closely related apple rootstock varieties was developed that contains a total of 2,856 molecular markers covering the genomes of both parental varieties.

Dan Sargent, Fabrizio Costa, Michela Troggio, Riccardo Velasco

2 / Genetic improvement

The availability of a diverse gene pool and information about the association of genes with morphological features is fundamental in satisfying present and future breeding needs. As such, a large apple collection containing 600 diverse apple varieties has been recently planted in the experimental orchard of FEM. These varieties are being characterised for a range of morphological characters of value for breeding, including disease resistance and fruit quality traits. In parallel, the varieties are being characterised with in excess of 20,000 molecular markers from across the genome using the apple SNP-chip. The data will be analyzed to associate the markers with specific phenotypes. The molecular markers will then be used to choose the best varieties for breeding the apples of the future.

Fabrizio Costa, Michela Troggio, Riccardo Velasco, Dan Sargent

3 / Molecular markers

Fruit quality plays a major role in the consumer's appreciation and is considered one of the most important priorities in apple breeding world-wide. However, quality is a complex character, controlled by many genes. The availability of the apple genome sequence is an unparalleled resource for understanding fruit quality. Together with the development of technologies to unravel phenotypic complexity, the genome allowed the identification of two regions involved in the regulation of two fundamental fruit quality traits; fruit texture (both mechanical and acoustic components) and aroma. The availability of the genome permitted the development of molecular markers for the breeding of new apples with superior fruit quality.

1.2

Title

The history of enzymatic families revealed by genome analysis

The emergence and evolution of **metabolic pathways**¹ was a crucial step in molecular and cellular evolution. In this process, plants and other organisms developed diverse chemical machineries for adapting to different environments, which led to the evolution of various groups of specialized metabolites selected for their endogenous biological function. The evolution of new genes/enzymes to synthesize novel secondary compounds in plants is an ongoing process and probably accounts for most of the differences in gene function among plant genomes. Although there are many substrates and products in **plant secondary metabolism**², there are only a few types of reaction. Repeated evolution is a special form of convergent evolution in which new enzymes with the same function evolve independently in separate plant lineages from a pool of related enzymes with similar but not identical functions. This appears to be common in secondary metabolism and may confound the assignment of gene function based on sequence information alone. In general, enzymes may be categorized as "generalist" or "specialist", although it is not apparent what purpose generalist enzymes serve. Specialist enzymes (i) are often essential, (ii) maintain higher metabolic flux, and (iii) require greater regulation of enzyme activity to control metabolic flux in dynamic environments than do generalist enzymes. Furthermore, these properties are conserved in Archaea and Eukarya.

In the post-genomic era the use of **phylogenetic analysis**³ to interpret chemical evolution and biosynthetic pathways is useful for understanding the formation of different enzymes and enzyme families at the molecular level. Several models have been proposed to explain their origin and their evolution in metabolic pathways. Network approaches combined with phylogenetic analysis of gene families (coding for proteins of the same family) have also been successfully used to study enzyme evolution in fully-sequenced genomes. Conservation of the type of chemical reaction catalysed by evolutionarily-related enzymes would seem to suggest that functional blocks of similar chemistry have evolved within metabolic networks. One possible explanation for

these observations is that the phenomenon of local evolution is likely to cause less global physiological disruption to metabolism than the evolution of enzymes from other enzymes distant from them in the metabolic network.

Thus, the emergence of metabolic pathways allowed primitive organisms to become increasingly less dependent on exogenous sources of organic compounds. Comparative analyses of genes and genomes from different organisms has revealed that during evolution different forces and molecular mechanisms may have driven the shaping of genomes and the emergence of new metabolic abilities. Among these gene elongations, gene and operon duplications have undoubtedly played a major role since they can lead to the (immediate) appearance of new genetic material that may, in turn, undergo evolutionary divergence giving rise to new genes coding for new metabolic abilities. Gene duplication has been invoked in the different accounts put forward to explain why and how the extant metabolic pathways have arisen and have been shaped. Analysis of completely sequenced genomes and directed evolution experiments strongly support the patchwork hypothesis, according to which metabolic pathways were assembled through the recruitment of primitive enzymes that were able to react with a wide range of chemically related substrates. However, analysis of the structure and organisation of genes belonging to ancient metabolic pathways, such as histidine biosynthesis and nitrogen fixation, suggest that other hypotheses, i.e. the retrograde hypothesis or the semi-enzymatic theory, may account for the emergence of certain metabolic routes.

in short

The evolution of new plant genes is an ongoing process and probably accounts for most of the differentiation in gene function among plant genomes

More

Keywords

1 / Identification and characterisation of early and late biosynthetic genes of the ellagitannin biosynthetic pathway in strawberry (*F. vesca*)

Ellagitannins are polyphenolic antioxidants found in certain fruits, nuts, trees, tea and medicinal plants. Our aim is to identify the biosynthetic genes which encode for the enzymes needed by the plant to produce these health-promoting metabolites. Putative shikimate dehydrogenase-encoding genes which synthesize the first step of the pathway were identified and are currently being characterised for the production of gallic acid. Genes encoding for putative galloyltransferases were also identified. These enzymes catalyse the reaction to pentagalloylglucose, the precursor of ellagitannins. Characterisation of these gene products using the outstanding metabolomics platform at FEM is in progress.

2 / Metabolism of raspberry antioxidants

Raspberries are rich in secondary metabolites with high antioxidant power, such as polyphenols, and are highly regarded for their health benefits. Several varieties, including yellow raspberries, were profiled for their content of several antioxidants, including phenolics (over 50 different compounds analysed), carotenoids and tocopherol. They were found to contain high amounts of tocopherols and carotenoids (mostly lutein and its esters), with some samples containing far more than others. Some raspberry varieties were also found to have unusual phenolic compositions, some richer than others in benzoic acids (Alpen Gold) or having different flavonol profiles (Heritage).

3 / Phylogenomics and evolution as a way of understanding protein function

The availability of several plant genomes provides the opportunity to obtain a broader view of the Family 1 UDP-glycosyltransferases (UGTs) in terms of its evolution and organisation. UGTs are known to glycosylate several classes of plant metabolites. A phylogeny reconstruction gave an insight into the evolution of this multigene family as plants adapted to life on land. The results of this study show that the family expanded during the transition from algae to vascular plants and that in higher plants the clustering of UGTs into phylogenetic groups appears to be conserved, although gene loss and gene gain events seem to have occurred. Interestingly, two new phylogenetic groups that are not present in *Arabidopsis* were discovered.

1.3

Title

Using genomics to study the evolutionary potential of wild plants

Since Charles Darwin's discovery that species evolve one from each other through natural selection, a central question in biology has been how natural diversity arises. With the additional discovery of Gregor Mendel's laws of genetic inheritance and of Watson and Crick's resolution of DNA structure, it became clear that the incredible richness of sizes, shapes, colors, and adaptations of plants that have kindled human curiosity for centuries, could in principle be understood by reading all the genetic information contained in plant DNA. However, with the exception of some major breakthroughs in the last few decades, the decoding of plant genetic information and, thus, the mechanistic explanation of plant biodiversity has remained a daunting task. Recently, the revolution in DNA sequencing technologies has permitted us, at unprecedented rates, to access the genetic information that controls all aspect of plants life , from their development to the way they cope with environmental stress and that allow to identify them with unprecedented accuracy (DNA barcoding¹). The complete decoding of all the genes (also called the genome) of a growing number of species has opened up new horizons for the study of plant natural genetic diversity. In fact, not only it is now possible to precisely reconstruct the degree of relatedness (molecular phylogeny²) of all existing plant species, but it is now even possible to read directly from their genes the traces left by natural selection during evolution. In other words, the application of next generation sequencing technologies allows us for the first time to identify the changes in plant genes that, among the hundreds of thousands of mutations that must have happened during millions of years of evolution, progressively created the amazing diversity that we can currently admire. Like a handful of needles in a huge haystack encompassing several million straws, these genetic variants allow the adaptation³ of some species to the extreme climate of the highest mountains, and of others to the highly competitive conditions of the understory, where the struggle for light makes the difference between life and death. Most importantly, however, the mechanistic understanding of how tiny differences in DNA sequences can make plant species so different will allow in the near future

to model how environmental conditions influence the distribution of plant species, a very relevant issue in the light of ongoing climate changes. By studying plant adaptation in wild species, we can also learn more about how to breed our domestic plants to cope with drought, global warming and new pathogens, exploiting the solutions devised in millions of years by natural selection. Ultimately, these approaches hold the promise to help us developing renewable and carbon-neutral sources of energy that are of paramount importance for sustainable development and to reduce climate change due to human activities (MAN_VIP project⁴).

in short

It is now possible
to read the traces
left by natural selection
during evolution directly
from plant genes

More

Keywords

Claudio Varotto

1 / DNA barcoding of wild plants

DNA sequencing represents a powerful approach to plant identification, as it can be carried out with little or no knowledge of the subtle morphological differences commonly used by botanists to distinguish different species. To improve standardization of the genetic approach to species identification, it has recently been proposed to use DNA sequences from two plant genes called *matK* and *rbcL*. Analogous to the barcodes that are used in supermarkets, these DNA "barcodes" will provide a unique identification of virtually any species from a certain region. This will allow, for instance, to quickly and reliably identify toxic plants and reduce poisoning risk.

Simone Fior e Claudio Varotto

2 / Investigating plant relatedness with molecular phylogenetics

Traditionally, the degree of relatedness among plant species has been determined by comparing differences in shape and color and assuming that morphologically similar species are more closely related. However, as similar shapes can often arise independently in unrelated species, this approach is relatively unreliable. On the contrary, the virtually unlimited number of molecular characters that can be recovered from DNA makes the reconstruction of evolutionary history and relationships (called phylogeny) of plant species much more precise. In particular, next generation sequencing allows to resolve plant phylogenies with unprecedented precision, and even help to identify new species.

Lino Ometto

3 / How Plants Adapt to Climate

Environmental stresses are important drivers of plant evolution. For example, species found at high altitudes respond to low temperatures and high solar radiation through specific morphological and physiological adaptations. To elucidate the genetic basis of these adaptive traits, we analyzed genome-wide patterns of molecular evolution in *Cardamine resedifolia*, which lives at high altitudes, and *C. impatiens*, found at low altitudes. The results revealed that genes involved in cold responses evolved particularly quickly only in *C. resedifolia*, consistent with their adaptive role in this high-altitude species.

Violeta Velikova e Claudio Varotto

4 / The MAN-VIP Project

The use of renewable and carbon-neutral sources of energy is of paramount importance for sustainable development and to combat climate change due to human activities. By means of next generation sequencing we are developing genomic resources for *Arundo donax* (the giant reed), an emerging model plant for biomass and bioethanol renewable production from marginal land. The MAN-VIP project aims to characterize the de-assimilative processes that cause net CO₂ loss in *Arundo* and use this knowledge to improve the overall productivity of this species.

1.4

Title

Solving the puzzle of plant genome structures with Bioinformatics

Plants have an extremely wide variety of shapes and sizes and as many ways of adapting to the most disparate of environments. The origin of this variability, as for all living organisms, resides in their DNA. Different plants will have equally different genomes. Take genome size, for example: *arabidopsis thaliana*, the first plant to have its genome sequenced, has 120 million nucleotides (Mbp), the grapevine genome 480 Mbp, apple 750 Mbp, strawberry 200 Mbp, while the maize genome is more or less the same size as the human genome (3 billion nucleotides). Decoding the complete genome sequence, i.e. identifying the entire sequence of nucleotides and their composition, is crucial to understanding how this variation arose.

DNA sequencing is a rapidly evolving technique yet **whole genome reading¹** is a goal that remains unattained; the average size of a "read" is currently around a few hundred nucleotides, far less than the millions of base pairs that make up a whole genome. To overcome this problem, the DNA is broken up into hundreds of thousands of pieces which are read and re-read tens of times. Iterative clustering of the pieces produces a "longer word", a process similar to putting together all the pieces from the same portion of a jig-saw puzzle, for example, all the blue sky pieces or all the green grass pieces. To assemble this puzzle in a reasonable amount of time, biologists use methods borrowed from computational science, such as computational linguistics, or from mathematics, such as graph theory.

Obtaining the sequence is only the first step towards **genome function²** analysis. The DNA sequence alone is almost meaningless, like a manual without commas, spaces and paragraph breaks: the information is there but it is barely readable. To continue with the metaphor of the puzzle. As it is being put together the picture begins to emerge and it becomes clear that certain details are especially useful in understanding the whole picture.

With respect to the genome, these details correspond to the coding regions, and these regions need to be decoded (using the genetic code) in order to reveal their **function³**.

Before they can be decoded, however, they need to be found. This is a highly complex task, since DNA is a puzzle with only four colours which are very similar to each other. It is rather like looking for a needle in a haystack.

In the last twenty years, the algorithms used in speech and face recognition have been successfully applied to gene prediction. Some of these algorithms are based on mathematical models built from known coding regions of the genome and then applied to unknown regions to see whether or not they are coding. Other approaches exploit genetic similarities between different plants, using knowledge of the coding regions of one genome to look for coding regions in the genome of another. These approaches also have recourse to mathematics and computer science which provide biologists with fast and reliable systems to compare genomes and identify common regions.

in short

To solve this puzzle, methods are borrowed from computational science, such as computational linguistics, or from mathematics, such as graph theory

More

Keywords

Luca Bianco

1 / Assembling in the right direction

Despite unceasing advances in sequencing techniques, the dimensions of genomes are far beyond the resolution of sequencers, which is why they are usually re-constructed from much smaller fragments in a process known as assembly. "Pair ends" are coupled sequences, which means they both come from a single DNA molecule a set distance apart and with a set orientation. Their role in assembly is crucial: rather like the corner-pieces of a jigsaw puzzle they have a fixed position that can be used as a point of reference to add the other sequences or to assess the correctness of a region already assembled.

Marco Moretto

2 / Assembling plant pathways

Photosynthesis and the accumulation of aromatic compounds are two examples of essential plant biochemical reactions that are continually taking place inside living cells and are known as pathways. The ability to distinguish which molecules belong to a specific pathway and how molecules interact is as fundamental as it is hard. It may be compared to attempting to follow a philosophical discourse during a rock concert. In order to ascertain what is important and what is background noise, researchers measure cellular activity and use methodologies borrowed from statistics and computer science to reconstruct complex molecular interactions.

Paolo Fontana

3 / The importance of ontologies in investigating genome function

Next-Generation Sequencing technologies have brought with them an exponential increase in the amount of sequence data generated. This in turn requires the development of efficient automatic functional annotation techniques to support and direct work in the laboratory. Structured vocabularies (ontologies), such as Gene Ontology, are especially useful for describing gene function and performing gene annotation computationally. Argot2 is a tool that was developed in our lab based on Gene Ontology. It efficiently annotates entire genomes and is currently one of the best functional prediction methods freely available.

1.5

Title

The other side of the genome: comparative metagenomics and the evolution of symbioses

When we think of microorganisms we often consider them as harmful. Since the formulation of Koch's postulates, which associated microbes with disease, these microscopic populations have been considered a curse, responsible for sickness and fatal diseases. More recently, we have come to realize how mistaken this view is and to understand the beneficial and essential role of microorganisms in our lives. Knowledge of the microscopic world gained through the development of modern DNA sequencing technologies has opened up new opportunities and allowed us to identify the microbes living in our gut, our food, in plants and soil, and to explain their functions.

The close symbiotic functional interaction between the cells of plants, insects and mammals and the cells of bacteria suggests that every multi-cell system should be considered a super-organism, its metabolic functions encoded both by the microbiome and genomes of the host. Several factors influence the composition of the microbiome, such as nutrients, environmental conditions and geographical location. Studies carried out by researchers at CRI-FEM have shown that the composition of the **intestinal microbiome**¹ in humans varies considerably according to state of health and weight, and across populations. This issue, which is discussed in greater detail in the section "food for life", may also be considered from a different perspective, by examining which microbes are found on food, fruit, plants and insects and which vectors carry these microbes to the various environments. A recent study led by Duccio Cavalieri demonstrated the importance of **hornets as vectors**² carrying these microbes around the different environments and into fermented beverages such as fruits. These recent discoveries indicate that preserving the diversity of regional microbiomes associated with traditional foods and diets is fundamental for maintaining product quality and consumer health as well as the natural balance between humans and the ecosystem..

The ability to sequence genomes of higher organisms, plants and bacteria has highlighted the importance of developing new skills bridging biology and bioinformatics. Comprehending the complexity

of the interaction between genomes and the environment involves a detailed process of comparison requiring **evolutionary analyses**³ of functions and gene networks. FEM researchers are perfecting the skills of using evolution as a means to study genomes and their functions. It is the only approach capable of bringing expertise in genomics to biotechnology and to the improvement of agriculture and food health with minimal environmental impact. These comparative and functional analyses will enable us to develop new strategies for innovation in agriculture which respect the distinctive features of alpine environments while maximizing their potential and give due consideration to the ecosystems associated with traditional food production.

in short

Preserving
the diversity of regional microbiomes
associated with traditional diets
is fundamental
for maintaining product quality
and consumer health

More

Keywords

Carlotta De Filippo

1 / How diet, evolution and geography shape metagenomes

Historically, the microbial ecosystem of the digestive tract was specific to a geographical area, much as the flora and fauna of different ecosystems are geographically distinct. Carlotta De Filippo and Kieran Thuy have recently shown that the intestinal microbiomes of African populations whose diet is high in fibre are dominated by bacteria of the genera *Prevotella* and *Xylanibacter* (De Filippo et al., PNAS 2010).. The combination of specific microbiomes and fibre enables large amounts of short-chain fatty acids, important components for healthy intestines, to be liberated. Our goal is to sample other human communities who have marginal contact with globalized food and draw attention to the potential of natural microbiomes.

Duccio Cavalieri

2 / Environmental and ecological metagenomics

Despite the fact that fermented beverages have been produced for more than two thousand years, the relationship between microbes and terroir is still unknown. A recent article in the journal PNAS (Stefanini et al., PNAS 2012) revealed that wine yeasts can survive winter in the gut of hornets and social wasps, the main vectors, therefore, of these microorganisms. It is a remarkable fact that in autumn the microbiomes of insect guts contains the same species found at the onset of wine fermentation. At the genomic level, the strains of hornet and grape and the types of wine from a given vineyard resemble each other, pointing to a typical microbial diversity. Social insects therefore play a crucial role in preserving the local biodiversity of fermented products, in symbiosis with the typical microbes of the area.

Vadim Goremykin

3 / Using evolution for interpreting genomes and metagenomes

The development of computational and evolutionary biology and bioinformatics has made it possible to transfer results from innovative "omics" research. Recent work by the Computational Biology Department on ontologies and metabolic pathways opens new opportunities to integrate genotype and phenotype information. We recently developed a method for discovering new genes that function as evolutionary molecular clocks in order to understand plants and bacterial evolution. In a similar vein, Vadim Goremykin and colleagues have developed a revolutionary algorithm aimed at removing artefacts in phylogeny reconstruction (Goremykin et al., 2012), thus improving classification of plants, bacteria and the highly diverse organisms populating natural ecosystems.

1.6

Title

Biostatistics and Data Management

Research in the field of life sciences is currently yielding more data than ever before. This is due not only to advances in high-throughput technologies, but also to analytical techniques which now provide far larger amounts of data than a few years ago. The result is that data analysis has become ever more important in transforming raw data into usable information. The mission of the Biostatistics and Data Management (BDM) group at FEM is to develop better algorithms and strategies for analysing complex data from all the FEM research areas. Our approach to obtaining these goals consists, on the one hand, in **advanced research in applied statistics**¹, and, on the other, in an extensive network of collaborations with experimental groups both within and outside FEM. At the same time, the group aims to bring experimentalists and data analysts closer together by organising a series of informal courses on statistics and data analysis at FEM. This not only allows researchers to carry out part of the data analysis themselves, but also serves to establish a common language and to stimulate exchange of ideas and expertise.

The scientific collaborations within FEM in the field of metabolomics are a good example of how practical scientific questions can stimulate fundamental research in statistics. The BDM group has been working closely with experimentalists to establish a completely **automatic data analysis pipeline for mass-spectrometry-based metabolomic data**², encompassing feature identification, quality control and annotation. This process will be finalized in 2013 and will include a web-based application allowing lab scientists to perform sophisticated analyses of highly complex data completely autonomously.

It should be noted that it is not sufficient to have a global measure of the abundance of metabolites in a plant sample. In many cases, knowledge of their spatial distribution in plant tissue is also essential for greater understanding of the biological processes involved. This cannot be achieved with the often destructive sample preparation methods, and therefore alternative methods, such as **mass-spectrometry imaging**³, are

required. With this technique a picture is made of the sample, but instead of recording a simple colour value for each pixel a complete mass spectrum is recorded, which provides a wealth of data with very little experimental pre-processing.

Another fruitful line of research has emerged in the field of food authentication, in collaboration with Stable-Isotope platform. Various statistical methods have been developed, validated and implemented to assess claims of origin for a range of foodstuffs, from tomatoes to cheese to wine, on the basis of chemical composition and stable-isotope ratios. Since the characteristics of the data differ according to the particular food under examination, different statistical techniques are required in each case.

The BDM group is well integrated into the FEM research structure and has several other ongoing scientific collaborations not mentioned here. These range from long-term, multi-person projects to half-hour consultation sessions, and include BDM outreach activities such as training courses and the development of web-based dedicated software tools. The connections between BDM and the rest of FEM will be further strengthened with the creation of the Department of Computational Biology.

in short

Managing large numbers:
automatic data analysis pipeline
for mass-spectrometry,
Imaging techniques,
statistical assessments
for food authentication

More

Keywords

Ron Wehrens

1 / Biomarker selection

Biomarker selection from new modern “omic” technologies has become extremely difficult due to the enormous number of variables involved. To deal with this problem, we have developed two meta-statistical methods which are able to select the variables showing the greatest differences between two groups of samples. The first applies “higher criticism”, a strategy for identifying suitable cut-off values for sets of statistical tests, to multivariate data and has been successfully tested in metabolomics applications. The second, “stability selection”, provides robust estimates of which variables differ between the two groups.

Matthias Scholz

2 / Automatic pipeline for analysing metabolomics data

An integrated system for efficient, automatic analysis of high-throughput metabolomics data is indispensable. We have set up a pipeline based on open-source software specifically addressing the needs of the Metabolomics Platform at FEM. The system deals with all stages in the analysis of MS-based metabolomics data, such as feature identification, quality control, matching and annotation. The pipeline runs on a Linux workstation and is accessible through a simple web interface.

Pietro Franceschi

3 / Imaging secondary metabolites in Golden Delicious apples

Polyphenols are an important class of secondary metabolites produced by plants. They play a fundamental role in plant biology and also have a high nutritional value due to their anti-oxidant properties. By combining state-of-the art mass spectrometry techniques with specific biostatistical algorithms we have been able to study the distribution of polyphenols in Golden Delicious apples. This integrated approach has allowed us to reconstruct a series of molecular images showing the distribution of different metabolites within different fruit tissues.

Highlights

Silvia Vezzulli, Claudio Moser

1 / Unravelling the origins of Pinot blanc and Pinot gris

The Pinot family of grape cultivars is an excellent system for studying the genetic bases of berry colour since it encompasses highly uniform genotypes (somatic variants) which differ with respect to berry skin colour. By studying the genetic make-up of the berry colour locus, located on chromosome 2, in different tissues of Pinot noir, Pinot gris and Pinot blanc, we identified and characterised a very large deletion in a single Pinot gris cell layer. This result sheds new light on the evolution of the Pinot family and shows that Pinot gris and Pinot blanc arose independently from the ancestral Pinot noir.

Fabrizio Costa

2 / Investigating fruit quality in the post-genomic era

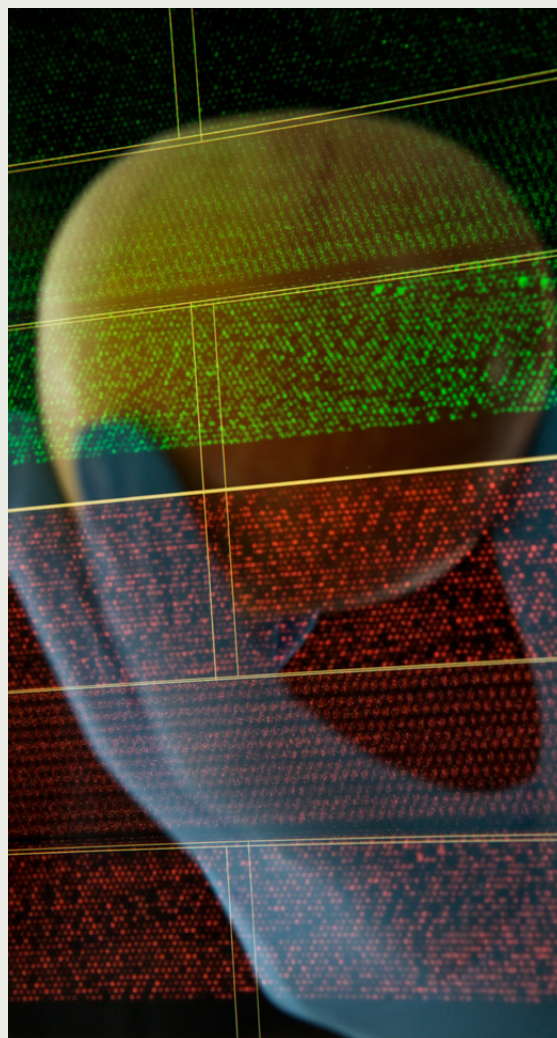
Fruit quality is generally represented by polygenic traits, and the information obtained from sequencing the genome is an invaluable tool for identifying them. Investigation of the apple genome has allowed us to target a polygalacturonase gene involved in the disassembly of the cell wall-middle lamella polysaccharide architecture. Full-length resequencing of the gene in an apple cultivar collection was carried out in order to detect the allelic variants. Association studies identified a set of haplotypes statistically associated to variations in fruit texture, which represent a valuable set of markers for assisted selection of fruit quality. A similar approach was employed to validate

another potential molecular marker associated to apple aroma, the second important aspect of fruit quality. These two cases highlight the importance of the apple genome as a tool for developing useful molecular markers suitable for selecting novel accessions characterised by superior fruit quality.

Fabrizio Costa

3 / Characterisation of the allelic pool present within a varietal collection as a potential new tool for assisted breeding in apple

The availability of a wide gene pool and association of their relative alleles to the various phenotypic features, are fundamental to meeting present and future needs in breeding. With this in mind, a large apple collection of both cultivated and wild species has been recently planted. Out of the entire collection, almost 600 accessions have so far been considered for complete, large-scale characterisation. The main goal of phenotyping is to analyse the variability of traits valuable for breeding, such as disease resistance (scab and powdery mildew) and fruit quality (texture, acid, sugar, aroma and fruit size). Molecular characterisation of the apple collection will be performed with SSR and SNP markers, the latter tested by 20K-SNP, targeted by resequencing the genomes of a few varieties of apple. Phenotypic and molecular data will be analysed in order to associate allelic variants to specific phenotypes. The molecular markers specifically associated to the trait of interest will then be used to characterise and choose the most suitable candidates for obtaining the desired ideotype.



Luca Cappellin

4 / Rapid, non-invasive characterisation of apple cultivars and clones

An urgent issue in technical management and plant patent applications is the characterisation of clones, and not only for apple, the aim of which is to identify the real properties which differentiate mutated individuals. Rapid, non-invasive fingerprinting provided by Proton Transfer Reaction Mass Spectrometry is a powerful tool for investigating the volatile compounds present in the apple metabolome. This technique may be used to find important differences in the profiles of volatile organic compound emissions of different clones of apple cultivars such as Fuji, Golden Delicious and Gala, as well as QTLs related to volatile compounds.



Giulia Malacarne, Michele Perazzoli

5 / New hypothesis concerning the evolution of the grapevine genome

One of the main research topics in the post-genomic era is the characterisation of the mechanisms that lead to the evolution of a genome. Our study, recently published in PLoS ONE, proposes a new evolutionary model for the origin of the grapevine genome which we hold to be derived from the union of two sub-genomes which evolved independently from a common ancestor. This hypothesis arose from *in silico* analysis of the mechanisms underlying the formation and evolution of NBS-resistance genes. Using this knowledge we are attempting to correlate the independent evolution of the two sub-genomes with phenotypic traits of interest.

Lisa Giacomelli, Claudio Moser

6 / Discovery of a family of grapevine genes involved in defence against pathogens

Bioinformatic analysis of the grapevine genome has led to identification of a family of defensin-like genes putatively encoding antimicrobial peptides. A subsequent molecular biology study led to characterisation of a few of the peptides produced by the plant, which are indeed active against the fungus *Botrytis cinerea*, the causal agent of grey rot. These peptides are highly expressed in grapevine inflorescence and seed, and may function as a natural antibiotic.

Floriana Marin, Alessandro Gretter, Natalja Nemceviute

7 / The Sixth Rosaceous Genomics Conference coordinated by FEM

The Sixth Rosaceous Genomics Conference (RGC6), organised by the Fondazione Edmund Mach, was held in Mezzocorona in the first week of October, 2012. The event's 10 sessions with oral and poster presentations addressed research topics related to the genetics, biology and genomics of Rosaceae, the botanical family of apple, pear, peach, apricot, plum, strawberry and raspberry. RGC6 was a valuable opportunity for leading experts in the field (more than 200 from around the world) to exchange ideas. It was also the occasion to announce successful sequencing of the genomes of pear and raspberry, carried out with contributions from FEM and a team from New Zealand and the USA.



Eugenio Aprea

8 / Rapid, non-invasive analysis of markers related to diet and liver disease using PTR-ToF-MS

We recently tested the potential of Proton Transfer Reaction - Time-of-Flight - Mass Spectrometry¹ to monitor through breath analysis the physiology state of awake rats affected by non-alcoholic steatohepatitis (NASH). Rats with NASH have the advantage of reducing the confounding factors induced by non-standardised dietary regimens and life-style. We found several reliable markers in the exhaled breath of rats, such as methanol, dimethyl sulphide, dimethyl sulphone and ammonia, which we were able to relate to the animals' physiological conditions and the influence of diet (high fat and administration of coffee).

9 / The genome of woodland strawberry (*Fragaria vesca*)

The woodland strawberry possesses many characteristics that make it attractive as a model for perennial plant research, one of which is a small, highly homozygous genome, relatively devoid of repetitive DNA. As such an international consortium, within which FEM scientists played a significant role, undertook to sequence the genome of the *F. vesca* variety 'Hawaii 4'. The genome was sequenced to a very high standard and was anchored to the reference map for the genus. It was the first plant genome to be sequenced using only short-read 'second generation' sequencing technology, and as such the project represents a milestone for plant genomics. The availability of the sequence of the woodland strawberry genome has accelerated research within the genus, enabling marker development, functional gene analysis and comparative genomics. The sequence, published in the journal Nature Genetics, is also helping to develop our understanding of the genome of the cultivated strawberry.

**10 /** Development of a high density SNP-based reference map for red raspberry

Advances in sequencing technology has meant that high throughput genotyping using re-sequencing is now possible for organisms for which no genome sequence is available. Using the protocol of Elshire et al (2011), FEM scientists in collaboration with colleagues in the USA developed a SNP-based linkage map of a red raspberry progeny composed of 6,912 markers which represents the most saturated linkage map developed to date for a Rosaceous species. Due to each of the SNP markers being sequence characterised, the linkage map is being used to assist in the assembly and anchoring of the red raspberry genome.

11 / International Meeting on *Drosophila suzukii* in Europe

On 2nd December 2011, more than 180 participants gathered in Trento for an international meeting on "*Drosophila suzukii*: new threat for European fruit production", organised by FEM. The meeting was a unique occasion to exchange information about the diffusion and impact of this new pest in Europe and to draw up strategies for the near future. The meeting was attended by researchers, producers and representatives of local institutions from several European countries. It became clear that a concerted, coordinated network is required, since *D. suzukii* is spreading rapidly throughout Europe and significant damage is being reported in most countries. The most recent advances in research on *D. suzukii* were presented at the meeting and the most important future research lines were identified.

12 / The *Drosophila suzukii* genome

A multidisciplinary team of CRI researchers coordinated by the Chemicla Ecology Lab of DASB have sequenced the genome of *D. suzukii*. The genome was presented to the media on 3rd July 2011 in the presence of the President of the Autonomous Province of Trentino, but was released to the scientific community immediately after sequencing in order to speed up international research and increase the chances of quickly finding practical control strategies. Analysis of the genome confirmed that *D. suzukii* undergoes reproductive diapause over winter and that it has genetically adapted to temperate, cold climates, such as Trentino's. The genes we have identified in the genome will serve various ongoing lines of research at CRI.

**13 /** First genome and microbiome survey of the European Lyme disease vector.

The GENOTICK project focussed on analysis of the *Ixodes ricinus* tick and was supported by a two-year Marie Curie Action/Outgoing Cofund Trentino fellowship coordinated by FEM (Dr. Giovanna Carpi). A synergetic combination of cutting-edge DNA sequencing technologies and a computational pipeline set up in collaboration with an international consortium of University Laboratories in North

America and Singapore yielded unprecedented results for a disease vector genome of such complexity and size. We were able to obtain the complete mitochondrial genomes of 23 ticks, a draft assembly of the nuclear genome, the discovery of 2 million genome-wide genetic markers (SNPs) and in-depth characterisation of the composition of the core tick microbiome. Overall, these results have provided the foundations for further study of the evolutionary history and genomic structure of populations of ticks, which will be crucial for future development of new parasite management strategies and disease control.

Lukasz Grzeskowiak

14/ "GRAPENET" - COST Action FA1003

The Applied Grapevine Genomics group is exploring grape variation and mobilization of adaptive traits for breeding under the COST action FA1003. Existing grape diversity has been reduced as a result of changes in viticulture and accelerated by the invasion of pests and the globalization of wine markets. At the same time, grape genetic resources in the area where vines have been domesticated (south-eastern Europe) contain undiscovered riches. Researchers in this Action group from eastern and western Europe are working together to develop strategies for phenotyping and for carrying out association studies in core collections in order to improve the quality of grape production.

Paolo Martinatti, Lara Giongo

15/ Strawberry Variety List Project (Mipaaf)

FEM-CRI has been involved in this initiative of the Italian Ministry of Agriculture and Forestry since 2009 with an Operational Unit in Pergine, which is now fully up and running with the establishment of several collection plantings. These allow monitoring of the vegetative-productive cycle of strawberry plants for production nurseries standardised for soilless cultivation. Advanced varieties and selections from the main national and international breeding programmes undergo qualitative and quantitative testing and results are compared with the other units operating in Italy. Each unit presents their results at national and international meetings, which are also an occasion to exchange ideas and knowledge in the field, allowing FEM to acquire and characterise new genetic material and providing incentives for local business innovation.

Lara Giongo

16/ Blueberry and raspberry breeding

The blueberry and raspberry breeding programmes at FEM are now starting to produce interesting advanced selections. They are complemented by genomics programmes directed at identifying the genes associated with various desirable traits with the ultimate aim of developing molecular markers. In an initial phase of the blueberry (*Vaccinium* spp.) programme, the objective was to expand the genetic base and the available gene pool. Through the selection of elite lines, both interspecific and intraspecific, it has been possible to obtain advanced

lines for fresh product and for various product uses. In the case of raspberry (*Rubus* spp.), attention has been focussed on producing lines of reflowering varieties with high quality fruit and elite lines from interspecific hybridization with various objectives.

Lara Giongo, Paolo Loretto, Paula Poncetta, Paolo Martinatti, Marco Fontanari, Marcella Grisenti, Matteo Ajelli, Fabrizio Costa, Dan Sargent

17/ Quality in small fruits and strawberry

Quality is what gives a particular variety of small fruits or strawberry its distinctive or identifying character and plays a crucial role in the enjoyment of the fruit. It has, in these species in particular, a strong influence on consumer acceptability and is also a powerful influence on the post-harvest phase and the intended product processing technique. In order to genetically improve quality it is necessary to obtain characterisation profiles that are as accurate and informative as possible of the various fruits, the various varieties and species, and the available germplasm. Throughout 2011, we acquired further information on the texture, in particular, of blueberry and strawberry as a fundamental trait, in addition to biochemical and organoleptic parameters, which are useful for optimal characterisation of fruit quality and for preparing the ground for the development of molecular markers.

Paula Poncetta, Lara Giongo

18/ Conservation and micropropagation of small fruits and strawberry

FEM holds a germplasm collection containing around 1,200 accessions of the genera *Rubus*, *Vaccinium*, *Ribes*, *Fragaria*, *Prunus* and other minor species. Traditional cultivars, advanced selections and wild selections are a valuable resource both for genetic improvement and for safeguarding genetic diversity. The germplasm collection serves the purposes of conservation and of plant breeding and the development of molecular markers, which are particularly useful in MAS. Different propagation and micropropagation techniques are tested and used for optimising germplasm maintenance and for continual implementation of specific genetic improvement protocols.

Paolo Martinatti, Paolo Zucchi, Lara Giongo

19/ Phenological modelling of the strawberry plant

The joint CRI-CCT study is part of a larger project which is analysing floral architecture and biology in order to understand the key factors involved in floral differentiation and the extrinsic factors of production potential in strawberry plants. The aim is to discover whether plants may be classified on the basis of their intrinsic morphological and physiological similarities. Subsequent establishment of environmental parameters and architectural analysis will allow for the building and implementation of predictive mathematical models of phenological intervals and critical phenological points. This will make it possible to manipulate plant vegetative-reproduction cycles.

OUR NATURAL CAPITAL /

**SINGLE FARMS
MUST BE VIEWED,
NOT SINGLY,
BUT AS PART
OF A REGIONAL
AGRO-ECOSYSTEM,
WITHIN A GLOBAL
COMMUNITY**

part_2

Ilaria Pertot, Heidi C. Hauffe

Biodiversity and sustainable development

Tomorrow's world depends on today's investments. With an ever-increasing human population and consumption of resources at record highs, the future for our fragile Earth depends on protection of the remaining natural environment and sustainable use of our bioresources. 'Sustainability' is based on one simple principle: the needs of the present must be met without compromising the well-being of future generations. Human populations must find a way to take into consideration environmental protection, the true value of natural resources being exploited, economic benefits of exploitation and social equality. Only a responsible use of resources can guarantee that our natural capital, including the water, air, and soil, as well as the millions of plants, animals and microorganisms that live and interact in these environments, will be inherited by future generations. Biodiversity is essential for the stability of ecosystems, the maintenance of human health, resistance against plant and animal pathogens, and resilience in the face of global change. High levels of biodiversity can also mitigate the effects of natural disasters and human disturbance. In addition, biodiversity adds hundreds of millions of euro to the global economy, in the form of 'ecosystem services', such as pollination, soil fertility and water quality. Biodiversity also represents an immense natural heritage, since myriads of organisms and their genetic material represent an almost inexhaustible source of new species for animal breeding, agriculture, forestry, biotechnology, the pharmaceutical industry and world trade. In effect, biodiversity contributes substantially to the sustainability of human activities.

The conservation of alpine biodiversity is of particularly high priority in Europe for its importance in maintaining ecosystem services and jobs. In the Autonomous Province of Trento not only agriculture, but also tourism is dependent on intact natural ecosystems; consequently, it is of crucial importance to preserve their integrity. Tourists choose to visit Trentino because this region offers many outdoor activities in a stunning natural landscape; they are attracted by 'ecotourism' and 'agritourism' that allow them to experience locally produced foods and traditional cuisine. Agriculture itself has also safeguarded the area for centuries, contributing to its conservation and improvement. The pressures of global markets and rapid economic and social changes could further exacerbate the indiscriminate use of resources and the environment. In fact, in the last few decades, genetic, species and ecosystem diversity is being reduced as never before, mainly as a result of global change and human disturbance or exploitation. These rapid changes have also been recorded in the animal, plant and microbial communities of the Alps. In order to grow sustainably and confront the vagaries of the market, it will be necessary to understand, measure and estimate the value of this biodiversity. But it will also be necessary to have a clear vision of the entire system. This means that single farms or vineyards must be viewed, not singly, but as part of a regional, of a global agro-ecosystem. Only detailed knowledge of ecosystems and how humans affect these will allow us to make responsible choices and sustainable exploitation of our natural capital.

2.1

Title

Conserving and utilizing grape biodiversity: the FEM germplasm collection

Knowing the extent and structure of genetic variation in germplasm collections is essential in order to conserve and utilize biodiversity in cultivated plants. Grapevine is one of the most economically important crops in this region and it has benefitted from investments in genomics with the aim of accelerating the exploitation of *Vitis* resources to develop new cultivars. However, although a large number of clonally propagated accessions are maintained in grape germplasm collections throughout the world, their use for crop improvement is limited by the scarcity of information on genetic diversity and population structure and detailed phenotypic assessments. More than 3,000 accessions of differing origins held in the FEM germplasm collection have been fingerprinted using SSR and SNP markers and phenotypically evaluated for phenological traits. This survey revealed that around half of the collection is redundant germplasm. Although there are a large number of putative duplicates and extensive clonal relationships among the accessions, there is also a high level of genetic variation, the average genetic diversity as quantified by expected heterozygosity being higher for SSR than for SNP loci. Accessions sharing the same SSR profile should undergo further morphological evaluation before being eliminated to reduce duplication. They may be **somatic variants**¹ and therefore of great interest for functional genomic studies.

In order to facilitate access to the collection's genetic diversity, molecular and phenotypic data were independently used to identify **core collections**². Comparison of the phenological and genetic core collections showed the latter to be more genetically diverse while both showed similar phenotypic variation.

Genome-wide germplasm characterisation using molecular markers provides reliable tools for detecting the presence of population stratification and kinship levels within the whole germplasm and genetic core collections. Analysis of the genetic structure has revealed several levels of stratification. The primary division was found to be between accessions of *V. vinifera* and non-*vinifera*, followed by the distinction between wild (*V. vinifera* ssp. *sylvestris*)

and domesticated (*V. vinifera* ssp. *sativa*) grapevine. Intra-specific subgroups representing different eco-geographic groups were detected within cultivated grapevine. A clear genetic stratification was also found within the core collections, showing that genetic structure should be taken into account when designing genetic association studies.

in short

The high genetic diversity found within the core collections shows that there is still a lot to discover about grape diversity



More

Keywords

Laura Costantini

1 / Somatic variants

Somatic variation results from genetic or epigenetic alterations which first take place in a single cell and then accumulate in one of the cell layers of a shoot. It represents an important source of phenotypic variation which can be easily established in vegetatively propagated plants, such as grapevine. This phenotypic variation is important for genetic improvement of the species through clonal selection as well as for functional analysis. Genotyping the FEM germplasm collection resulted in the identification of several somatic variants for vegetative, reproductive and berry quality traits, such as berry size, colour, metabolite and seed content, and ripening time.

Silvia Lorenzi, Paula Moreno-Sanz

2 / Core collections

The purpose of developing core collections is to provide a restricted, manageable set of accessions representing the variation among individuals in a large germplasm source. In our study we constructed genetic core collections designed to maximize allelic diversity among *V. vinifera* accessions based on 22 SSR markers. Fifty eight cultivars (core G-58) were sufficient to capture all the 274 alleles occurring in more than 0.5% of the samples analysed. The core G-58 was then used to assemble the final genetic core collection retaining 100% of the SSR diversity (362 alleles). The optimal size of this core was 110 individuals.

2.2

Title

Alpine Water Resources:
Ecological Research and Sustainable use

The biodiversity and water quality of lakes and rivers in alpine and subalpine regions are greatly influenced by human activities in the watershed and by climate change. Researchers from the Limnology and Stream Ecology Group and the Hydrochemistry Platform are investigating the resulting changes on ecosystems and populations and the impacts on water availability, and are developing mitigation measures and feasible restoration strategies.

The effects of altered flows and thermal regimes have been investigated in several rivers. The eco-hydraulic properties of the upper course of the Noce River are currently being assessed with the aim of drawing up restoration guidelines. Current and historical distributions of the native crayfish *Austropotamobius italicus-complex* and of the invasive *North American Orconectes limosus* have been mapped, and populations of native species are being investigated from a biomolecular perspective to support reintroduction projects. The biodiversity and biogeography of Italian and extra-European groundwater crustaceans has been investigated, resulting in new species and genera being described.

In 2012, Lake Tovel, which has been studied by San Michele since 1973, was officially included in the Italian LTER sites (Long Term Ecological Research) in the Montane Lake category. Current research is centred on climate change and its influence on the physical properties of the lake, cascading effects on lake plankton and on ecosystem functioning. Field research is backed up by physiological studies on psychrophilic algae and in particular how small temperature changes influence the composition of membrane lipids. Molecular techniques are being used to study hidden biodiversity in cryptic species in Tovel and in other regional lakes using the *rotifer*¹ *Synchaeta* as a model.

In Lake Garda and in other lakes south of the Alps, LTER investigations have found a strict connection between eutrophication, climatic fluctuations on an annual/decadal scale and the structure of planktonic communities. Recent studies have shown that

atmospheric modes of variability in the Mediterranean area (East Atlantic Pattern, Eastern Mediterranean Pattern) have a powerful impact on the development of toxic algal populations (*cyanobacteria*²). This impact was mediated by the mixing dynamics in the deepest layers and by subsequent fertilisation of the surface waters.

The diversity and concentrations of toxic metabolites produced by Cyanobacteria (blue-green algae) are assessed by Liquid Chromatography/Mass Spectrometry (LS/MS). These methods allow a large range of cyanotoxins to be detected, thus providing information regarding the negative impact of Cyanobacteria on the quality of water destined for drinking or recreational use. At the ecosystem level, these studies are backed up by research on the toxins transferred throughout the foodweb, including fish with a high commercial value (e.g. *Coregonus lavaretus*, *European white fish*).

Temporal extension of limnological records is often not sufficient to provide the long-term perspective necessary to address the combined effects of human stressors on lake ecosystems. Geo-chemical and biological proxies preserved in lake sediments represent a powerful tool for extending the time span of lake ecology reconstruction. Current research is investigating vulnerability and the sustainable use of large European lakes, the impact of melting *Alpine permafrost*³, and defining reference conditions for lakes in Trentino (e.g. Garda, and Ledro).

in short

Two lakes of Trentino
in the “Long Term Ecological Research”
network, eutrophication,
toxic cyanobacteria,
and the study of the past
by lake sediments

More

Keywords

Ulrike Obertegger, Giovanna Flaim

1 / Using the guild ratio to characterise pelagic rotifer communities

Rotifers, an important component of lake zooplankton, show a variety of trophic types (part of the eating apparatus). However, little is known about how this relates to community dynamics. Rotifers were classified into raptorial and microphagous species based on the functional aspect of food acquisition. In Lake Caldonazzo (I) and Lake Washington (USA) raptorial and microphagous species showed alternating dominance, while the later overlapped with their direct competitors, cladocerans. The guild ratio is an innovative approach to investigating community dynamics and highlights general principles of community assembly. This work was carried out in collaboration with Ripon College (USA).

Nico Salmaso, Shiva Shams, Jayant Ranjan, Adriano Boscaini, Leonardo Cerasino

2 / A multidisciplinary approach to studying the impact of anthropogenic activities and climate change on lacustrine ecosystems

The EULAKES (EU, Central Europe Programme) and LEDRO (PAT) projects are investigating the impact of toxic microalgae (cyanobacteria) in Lake Garda and Lake Ledro. Ecological studies aimed at identifying the factors favouring the development of cyanobacteria are being conducted in parallel with molecular studies focussed on the cryptodiversity of the dominant species (*Planktothrix rubescens*), and on the diversity of cyanotoxins and their impact on trophic webs. In the oligotrophic Lake Garda, preliminary results showed negligible transfer of cyanotoxins throughout the trophic webs. Since 2012, the study has also come within the framework of the CyanoCost project (EU, COST).

Monica Tolotti, Manuela Milan

3 / Permafrost and Alpine lakes

The Interreg Project IV Permaqua (2011-2014) is investigating the effects of progressive melting of the permafrost (widespread in the Alps above 2500 m) on biodiversity and the functionality of aquatic biocenoses in North and South Tyrol. Permafrost melt water may contain high concentrations of heavy metals (e.g. Ni, Al) which may be well above the limits for drinking water use. Paleolimnological investigations of Alpine lakes affected by permafrost will make it possible to reconstruct changes in hydrological dynamics and the effects of heavy metals in relation to climate variation on a centennial scale.



2.3

Title

Conserving genetic biodiversity

Biodiversity is a term of common usage, due to the increased interest in environmental issues. Public opinion generally perceives biodiversity as the number of different species that can be spotted in a certain geographical area. At Convention on Biological Diversity in 1992 in Rio, several countries agreed on what indeed biodiversity means. The biological diversity among all living organisms that occurs on three levels: genetic diversity, species diversity and ecosystem diversity. The latter two are macroscopic aspects: several different species in different habitats. Genetic diversity within species, on the other hand, is not visible to the naked eye. But its importance is immediately appreciated when we consider that all current species and ecosystems are the result of the long evolution path, started with the occurrence of Life on Earth, more than about 3,5 billion years ago. Thanks to Darwin before, and to the repeated scientific confirmation later, we know that evolution is possible only if there is genetic variability among the individuals of a species. The natural selection is indeed a choosing process and works directly on any individual hereditary material. Simplifying, we could say that a species evolves only if it has enough genetic diversity to cope with future environmental changes. Thus, putting genetic diversity into the definition of biodiversity, an important evaluation on the species' evolutionary potential is introduced. This raises relevant consequences when assigning priorities to nature conservation actions. In a time of resources paucity, genetic diversity assessment better drives our choices. In fact, we know that a population with reduced genetic variability is more threatened with the risks linked to inbreeding, such as the onset of hereditary diseases; moreover it is more exposed to the effects of genetic drift- the random variation in frequency of some variants of the hereditary material. If prolonged, these effects may trigger further reduction of diversity. The final outcome is that populations with reduced genetic variability, especially if isolated, can soon (evolutionarily speaking) become so small to risk extinction. To measure genetic diversity we have to read in the lab some DNA stretches from individuals of a species and/or population. Before this was possible only using discrete amount of biological

tissue- impossible to retrieve, for instance, without capturing the animal. Nowadays, DNA can be read starting from few hairs found on the ground, faeces, urine and tiny leaf fragments. Rare and elusive animals, [endangered plants](#)¹ can now be characterized at the genetic level, and in some case, thanks to the most recent technological innovations, also at the genomic level. Since years at CRI we perform studies aimed at [measuring and conserving the genetic biodiversity](#)² of wild flora and [fauna species](#)³ that can give us insights on mountain ecosystems, especially in light of climate and land use changes.

in short

A species
evolves only if
it has enough genetic diversity
to cope with future environmental
changes



More

Keywords

Claudio Varotto

1 / Trentino flora DNA repository

With the aim of providing a comprehensive reference for the identification of plant species from the region, in collaboration with the Museo Civico di Rovereto we collected several hundred plant species from Trentino and sequenced the genes *rbcL* and *matK* to be used as DNA "barcodes". Once completed this large reference dataset will constitute an invaluable resource for the conservation and management of plant species and potentially for the certification of several commercial products derived from wild plants.

Cristiano Vernesi

2 / ConGRESS- Conservation Genetic Resources for Effective Species Survival

CRI is one of the 14 partners of the three-year (2010-2013) EU FP7 project ConGRESS. With a series of web-based tools, we would like to present the capabilities of genetic analyses to all those involved in managing natural resources. Identifying species, studying connectivity, recognizing hybrids are just some instances where using genetics is crucial. ConGRESS aims at creating in Europe a community of researchers and conservation professionals able also to lobby so that genetic diversity estimation can be officially included in the EU policies.

Barbara Crestanello

3 / Tetraonid conservation

Tetraonids, ground-dwelling birds characteristic of the alpine ecosystem, are currently threatened by changes in landuse, climate and human disturbance. A careful and constant management is necessary to safeguard their presence. DNA extracted from feathers and droppings collected from lekking sites can be crucial to understanding more about these elusive creatures. Such 'conservation genetics' contributes decisively to knowledge of their population size, dispersal rate, and number of reproductive individuals, among others. The data we are now collecting on ptarmigan, black grouse, and capercaillie will be fundamental for the management and sustainable harvest of these species.

2.4

Title

Biodiversity and health

According to a definition of the World Health Organization, health is a “state of complete physical, mental and social well-being not only associated with the absence of disease or infirmity.” It is a condition that depends on the well-being and living conditions of every single living organism. As a result, human health, animal health, plant health and environmental health (ONE-Health) are closely interconnected, and each perturbation of one of them induce consequences of all the others. An example of this is provided by the relationship between biodiversity loss and human and animal health. Biodiversity in fact plays several important roles, as for example to mitigate the spread of infectious diseases. Many examples of this are provided by the pests of crop plants, but also in the case of pathogens of medical and veterinary relevance, the number of examples is growing. Over the last 50 years for example, the number of outbreaks of zoonotic micro-organisms (micro-organisms of animal origin which can also cause human diseases) have increased significantly and surprisingly within the more developed countries. Among them, diseases transmitted by rodents (Hantavirus, Harenavirus) and disease transmitted by vectors (tick, mosquitoes) provide the best examples. We are demonstrating for example, through the development of **epidemiological models¹** (see **highlight**) as some diseases have been able to greatly increase the incidence not only in Europe but also in Italy and Trentino. Among the diseases transmitted by the wood tick, as Lyme borreliosis and tick borne viral encephalitis (TBE) that we have studied in the past, we are now dealing with anaplasmosis, a disease that affects both pets, domestic animals (fever pasture) and humans and it is caused by *Anaplasma phagocytophilum*. This bacterium is widespread in ticks, but also in all domestic and wild animals that we are analyzing. Through **advanced studies in molecular biology²**, we are finding out that the genetic variability of this bacterium is very high, with different strains that are found for example in deer and roe deer (that we’re studying with innovative technological approaches; see project **BIO-LOGGING³**, see **highlight**), in wild rodents (see also **Project ROCOALPS⁴**, see **highlight**), in birds, in dogs and sheep. Our goal now is to analyze

the relationship between the genetic variability of this bacterium, the diversity and behavior of the tick key species (rodents and deer), and the hazard of infection for domestic animals and humans. Another group of diseases we are studying both at European and regional level are mosquito-borne diseases. Among them, the West Nile fever, caused by a virus (West Nile virus), is particularly worrying. The virus of African origin, is implicated in a series of outbreaks that are occurring with increasing frequency in many European regions, including northern Italy. In addition to humans, horses are particularly susceptible. The virus, transmitted mainly by infected mosquitoes, causes inflammation of the nervous system lead to serious and potentially fatal neurological disease. In Italy the disease has debilitated thousands of horses, with a significant mortality rate. As with many viral infections, there is specific cure for the disease but individual horses can be protected by vaccination. Moreover, a vaccine specifically for humans are currently under study. Our research projects in progress on this issue are co-financed by the European Union (project EDENext www.edenext.eu, project Eurowestnile www.eurowestnile.org) and the Autonomous province of Trento (Project ROCOALPS).

in short

Epidemiological models
to study the spread
of infectious diseases
from outbreaks
of zoonotic micro-organisms

More

Keywords

Roberto Rosà

1 / Epidemiological models

Models are mathematical descriptions of real processes. In particular, epidemiological models describe the spread of infectious diseases in human and animal populations. These models are helpful tools for answering specific epidemiological questions as well as building and testing various hypotheses. They may be used in planning, evaluating, and optimizing different prevention and control strategies. Epidemiological modelling can contribute to the design and analysis of empirical surveys, suggest crucial data that should be collected, identify trends, make general forecasts and estimate the uncertainty in such forecasts.

Giovanna Carpi

2 / Arthropod vector microbiome

Metagenomics is a rapidly growing field of research that aims at studying uncultured organisms and especially to identify the collective genomes of an organism's associated microbiota referred to as microbiome. Spurred by enormous advances in genomic technologies this field has been extended to the study of the microbiome of arthropod vectors of diseases such as ticks (GENOTICK project). Using metagenomics, we can understand the extent of taxonomical diversity of microbes, their functions, the complexity of their interactions and co-evolution with the host. The ultimate goal of this research field is to clarify how the microbiome affects the host phenotype and disease transmission dynamics.

Francesca Cagnacci, Federico Ossi

3 / Biologging: understanding animals and their environment

Biologging is a new field of research based on the collection of animal-borne information using multi-sensor devices worn by individual animals. As such, biologging is at the interface between information technology and several biological disciplines, such as physiology, behavioural sciences and ecology. FEM/CRI is at the forefront in biologging innovation: the DBEM/Animal Ecology group, in collaboration with the University of Trento (DISI) and Fondazione Bruno Kessler (ESU) is testing the application of Wireless Sensor Networks to animal-fitted devices, for detecting contact between animals as well as for the sensing of environmental variables.

Adam Konecny

4 / The ROCOALPS Project

The 3-years project "Rodent communities in a changing environment: implications for human health in the Alps" (ROCOALPS) aims to help our understanding of how the biodiversity of small mammal communities is affected by human disturbance, and how this in turn is related to the circulation of rodent-borne viruses. The ecological data used for modeling the disease dynamics has been obtained from fieldwork carried out in the most common habitats of Trentino (forest of different altitudes and disturbance levels) during 2011 and 2012. For this research, we live-trapped more than 1500 yellow-necked mice and bank voles; we counted the wood ticks and tapeworms they carried and we used genetic screening to check if they carried viruses transmissible to humans.

2.5

Title

Modelling for ecological and climate research

A central problem in spatial modelling is the **lack of high resolution maps¹** for remote areas, especially in complex terrain where ground surveys are usually sparsely and/or irregularly distributed.

This is particularly true for climate data because meteorological stations are often located only in agricultural or easily accessible areas. An alternative data source is remote sensing by satellite imagery, which involves specialized sensors mounted on satellites sending data such as surface temperature back to Earth. The prediction of weather data like temperature has a number of different **applications such as the estimate and prediction of the invasion of dangerous species²** or landscape suitability for viticulture.

Mapping and modeling ecosystems and their changes over time is a key issue in spatial ecology, biogeography and **environmental pollution research³**. Remote sensing has been acknowledged as one of the most powerful methods to map abiotic and **biotic components⁴** of ecosystems (including land cover, land use, vegetation, soils) and estimate their changes over time.

Because of the importance of remote sensing data and the complexity of its analysis, mathematical algorithms developed to analyse remotely sensed data must be constantly reviewed and improved by a large number of experts. In this view, the use of Free and Open Source Software (FOSS) is often used in this field to allow completely open and accurate science.

The increasing availability of ecological data through networks such as the Global Biodiversity Information Facility (GBIF, <http://www.gbif.org>) or the Data Observation Network for Earth (DataONE) federated data archive (<http://www.dataone.org>) makes it increasingly possible to test cutting-edge ecological theories, such as dark ("invisible") diversity, evolutionary paths and climate change scenarios. By using shared Free and Open Source Software for geographical analysis and spatial statistics guarantees high reproducibility and robustness of the modelling

procedures being carried out. Therefore, at CRI, the GIS and Remote Sensing Platform is engaged with the development of Free and Open Source algorithms for statistical computing and geographical analysis (e.g. <http://grass.osgeo.org>). This is achieved by focusing on the geostatistical analysis of geographical information layers, the creation and processing of indicators, and the production of ecological, landscape genetics, eco-epidemiological and physiological models. The group actively pursues the development of innovative methods and their implementation in a GIS framework including the analysis of proximal and remote sensing data and time-series.

in short

The increasing availability of "open" ecological data makes it increasingly possible to test cutting-edge ecological theories, such as evolutionary paths and climate change scenarios



More

Keywords

Emanuele Cordano e Emanuele Eccel

1 / Generating the weather for assessing climate

The reliability of models in projecting future climate scenarios is somehow ascertained just at the large scale, and with a low time resolution. On the other hand, daily series are often required for applications. For this reason, we developed a stochastic generator of temperature and rainfall series (a *"weather generator"*). The algorithm is based on autoregressive vector models, that maintain the meteorological consistency between the two phenomena and the space correlation among variables. The algorithm - an R library called RMAWGEN - was released as a free software under GNU licence.

Duccio Rocchini, Markus Neteler

2 / Estimating species distribution from space

Many predictive models have been developed for tracking animal and plant species in space and time by means of remotely sensed data. The GIS and Remote Sensing Platform focuses on measures of uncertainty of species distribution models, leading the task "Integrative analyses of distribution status and trends" in the FP7 project "EU BON - Building the European Biodiversity Observation Network", recently approved by the European Union.

Elena Gottardini, Fabiana Cristofolini, Antonella Cristofori

3 / Ozone

Ozone is a highly phytotoxic air pollutant. The knowledge of its levels and spatial distribution is necessary to assess the potential risk to vegetation. In the frame of the Ozone EFFORT project, potential risk maps, based on modelling of O₃ concentrations measured from 2007 to 2011 on a network of 20 forest sites, were developed for Trentino. Results showed a widespread exceedance of critical levels established for the protection of vegetation. Ozone-specific foliar symptoms were observed on some sensitive species but no effect was detected on health and growth of forest trees.

Monica Rinaldi, Ilaria Pertot

4 / Characterization of the geometry of grapevine from LIDAR datasets

To meet the request of the Directive 2009/128/EC on the reduction of use and risk of pesticides more accurate treatments against pests and diseases should be pursued. Measurements with LIDAR sensor to characterize the geometry of the grapevine and the Leaf Area Index in each growth stage can be used to adjust the flow rate and calculate the Tree Row Volume. Based on field trials we adjusted this relationship on Chardonnay. A fully automatic divergent laser scanner based on the measurement of time-of-flight with an accuracy of ± 15 mm in a single shoot measurement was used. Results showed that LIDAR is a powerful tool that helps to describe the volume and form canopy.

2.6

Title

Acting quickly against new pest and pathogen threats

The advent of the global economy has exposed local entities such as Trentino to the growing risk of pest and pathogen invasions. This is a major concern for plant health and poses a serious problems for fruit production.

Pests and pathogens are often introduced into new countries with the shipment of goods and on-going climatic change facilitates their establishment. Some pests are not yet present in Europe, but they nevertheless constitute a serious threat: where entry is not prevented, early detection and rapid identification of the most effective control measures should be enforced. These actions require a multidisciplinary approach and cooperative networking among invaded countries.

The most recent devastating example of pest invasion is that of *Drosophila suzukii*, a fruit fly endemic to South East Asia. It spread throughout Europe and America in just a few years and is now causing extensive economic damage to small fruits industries in Western countries. Most of the damage caused by *D. suzukii* is due to larvae feeding on the flesh of ripening fruit, but the physical damage to the fruit makes it vulnerable to secondary infections by fungi, yeasts and bacteria, which cause rapid deterioration and further losses. Apart from the obvious harvest loss, pre- and post-production costs increase (monitoring and chemical input, more intensive labour, greater fruit selection, reduced fruit shelf-life, reduced market appeal of contaminated areas). For these reasons and because efficient tools for monitoring and controlling this species are not yet available, growers are pushing for **immediate and efficient solutions¹**. Most of these fall into the category of Integrated Pest Management strategies: classic control methods, such as pesticides, are being integrated with more sustainable methods, such as trapping based on specific attractants and biocontrol using natural "parasites of the parasites".

Other pests/pathogens are present only in some of the EU member states or nearby countries. We are also tackling *Monilinia fructicola* species, whose dissemination may also be facilitated by *D. suzukii* and other Bactrocera flies. Accurate monitoring and the creation of a pipeline of fast actions in case of invasion play a key role in combatting these species.

Climate change and agricultural practices may increase the risk of new pest and pathogen invasions. As temperatures increase, many pathogens are predicted to spread into new geographical areas where they will come into contact with new potential hosts. Indeed, several aspects of the biology of an existing pest or pathogen may be directly influenced by environmental factors and/or human practices. *Rosellinia necatrix*, which causes white root rot disease in a large number of plant species, is an increasing concern in northern-eastern Italy given the potential losses in apple production that this pathogen could cause. *R. necatrix* is often present in **apple replant disease²**, as replanting with the same plant host species increases the risk of it taking hold.

Developing strategies against new invasive pests and pathogens is not straightforward. It relies on a detailed understanding of their biology, particularly the way they interact with the agro-ecosystem. This knowledge can be achieved only by taking a **multidisciplinary approach³** which encompasses fields from chemistry to genetics and is the first step in applying sanitation procedures and/or changing agronomic practices.

in short

A multidisciplinary approach,
from chemistry to genetics,
for innovation
in agronomic practices



More

Keywords

Valerio Mazzoni, Gianfranco Anfora

1 / Interfering with *Drosophila suzukii* communication

We are exploring different approaches which may provide management solutions to the increasing threat that *Drosophila suzukii* poses to European fruit production, with a particular focus on insect sensory ecology.

Identification of the most behaviourally-active volatiles emitted by *D. suzukii* host fruits might pave the way for the development of more selective and powerful attractants that could be used as part of strategies such as mass trapping, and attract and kill.

Deciphering the air- and substrate-borne signals that constitute the acoustic communication involved in *D. suzukii* mating behaviour may open up new perspectives in the field of alternative control methods, such as acoustic mating disruption.

Ilaria Pertot, Sandro Pastorelli, Daniele Prodorutti

2 / Apple replant disease

Specific apple replant disease (SARD) occurs when a new apple orchard is planted on land just removed from apple production. SARD severity may vary according to geographical location. Microorganisms are considered to be the main causal agents, since fumigation or the application of biocontrol agents (*Trichoderma* spp.) reduces severity, although nematodes and plant metabolites may also be involved. Some pathogens, such as *Rosellinia necatrix*, increase in severity in replanted apple orchards. In particular, we have demonstrated that the presence of apple wood residues in the soil greatly facilitates the growth of this fungus.

Omar Rota Stabelli, Gianfranco Anfora

3 / Model studies in *Drosophila*

Apart from its implications for agriculture, *D. suzukii* is an interesting model for studying the genetic/behavioural basis of ecological innovation. *D. suzukii* is closely related to *Drosophila melanogaster*, the most prominent animal model in biology, and there is, therefore, a plethora of analytical tools and genetic information we can use. We are carrying out comparative analyses which focus on the evolutionary history of *D. suzukii* and the repertoire of genes it uses to sense host fruits. The final goal is to find chemicals that bind to targeted key genes in order to facilitate field trapping. We are also considering using natural endosymbiotic parasites of *Drosophila* for genetic-based population disruption in the field.

2.7

Title

Preserving soil quality
for sustainable development

FAO states that “by 2050 the world’s population will reach 9.1 billion, 34 % higher than today. In order to feed this larger, more urban and richer population, food production must increase by 70 %”. Agriculture has so far been able to meet the rapidly growing global demand for food, feed and fibre, thanks to continuous growth in agricultural productivity. The mechanisation of agronomic practices, the availability of productive varieties, chemical pesticides and fertilizers have played a major role. A third of the increase in world cereal production in the 1970s and 1980s has been attributed to the increased use of fertilizers. However, monoculture and excessive use of chemical fertilizers and pesticides increase the risk of environmental pollution and often lead to a reduction in biodiversity and impoverished soil quality. Many soils throughout the world already show worrying signs of degradation.

Soil is one of our most important non-renewable natural resources¹. Moreover, it provides important nutrients and an anchor for plants and is a habitat for numerous macro- and microorganisms. The role microorganisms play in maintaining soil health is crucial: some form a symbiotic relationship with plant roots helping them to extract nutrients from the soil, others are important in breaking down organic matter and recycling nutrients. Cultivated soils are at higher risk of erosion than natural soils. Human-induced soil degradation has been on the rise over recent decades and most agricultural land, especially in developed countries, contains areas which have been degraded by erosion, salinization, compaction or compression, nutrient depletion, biological degradation or pollution. Soil degradation is the main factor responsible for reduced agricultural productivity. Some types of degradation are irreversible, but most of them can be prevented or reversed.

Soil is also the biggest carbon reservoir in the continental biosphere and soil respiration is the primary path through which CO₂ fixed by plants returns to the atmosphere. Currently, the main questions that scientists have yet to answer concern how much carbon a soil can sequester and store. Soil carbon sequestration capacity is rarely quantified in ecological

studies despite being a very important factor with the potential of reversing the carbon balance in an entire ecosystem. Ongoing research is also looking at ways to quantify the soil carbon sequestration potential in different ecosystems (forest and agriculture fields), or in land use change situations. Due to the very different timescales in turnover of organic matter in soil (from years to thousands of years) and vegetation (from months to hundreds of years) it’s not always easy to predict if a change in land use (e.g. colonisation of a pasture by the forest) will lead to accumulation or loss of carbon.

Soil biological processes² are extremely diverse and complex. The new culture-independent-molecular techniques for investigating microbial populations³ have opened up new perspectives in the study of the living component of soil. The isotopic techniques⁴ currently being developed will make it possible to quantify the heterotrophic and autotrophic components of soil respiration separately, a step forward in understanding if a soil is a carbon source or sink and therefore providing new approaches to mitigating the impact of climate change. A better understanding of the processes taking place in soil will lead to sustainable use of this precious resource and preservation of its quality.

in short

Understanding
the role of soil
in carbon sequestration
is of primary importance
for the mitigation
of climate change

More

Keywords

Mirco Rodeghiero

1 / Soil carbon reservoir

Soil organic matter is not only a the key component for sustainable soil fertility and productivity, it has also, in light of climate change, become increasingly important as the largest terrestrial carbon pool. At a global level, soil organic matter pools (estimated to a depth of 1 m) contain about 1580 Pg of carbon (Pg = 10¹⁵ g), while about 610 Pg are stored in the vegetation and about 750 Pg are present in the atmosphere. On an annual basis, global soil respiration is estimated at around 80 Pg carbon, roughly ten times the annual flux from fossil fuel combustion (7.2 Pg carbon), making it the largest source of carbon flux after photosynthesis.

Paola Elisa Corneo, Claudia Longa, Ilaria Pertot

2 / Understanding soil communities for improved soil management

The study of soil microbial communities through fingerprinting techniques advances understanding of the abiotic and biotic factors affecting microorganism dynamics. In particular, study of the total bacterial and fungal communities in vineyards has led to the soil chemical component being identified as one of the main factors affecting bulk soil communities, while microbial communities are mainly unaffected by seasonal changes. Investigation of different farming systems (biological and conventional) showed their microbial communities to have different structures.

Noemi Herrero, Michele Perazzolli, Ilaria Pertot

3 / Soil Population Transcriptome

Soil is a complex environment naturally populated by various microorganisms with beneficial or detrimental effects on plants. We applied metatranscriptomic analysis to an artificial soil ecosystem model in order to study functional and molecular interactions in microbial populations. We focussed in particular on transcriptional changes in the soil microbiome caused by the arrival of a root-rot agent (*Armillaria mellea*) and its antagonist (*Trichoderma atroviride*). Results from this analysis will help in understanding the soil system as a superorganism and the interplay between a pathogen and its antagonist in the equilibrium of the soil community.

Alberto Pellegrini, Federica Camin, Ilaria Pertot

4 / Studying trophic interactions between a plant pathogen and antagonistic microorganisms using a ¹³C - labelled compound and isotope ratio mass spectrometry

Different levels of trophic interactions take place in soil, but determining the relationships among microorganisms in a trophic chain is particularly difficult. Direct parasitism can be studied using microorganisms labelled with stable isotopes. A ¹³C isotope-labelled microorganism can be introduced into the environment and the ¹³C isotope can be detected in its parasites/ degraders by isotope ratio mass spectrometry (IRMS). We propose an innovative IRMS-based method for identifying trophic relationships (parasitism, degradation or assimilation products) in a tri-trophic system: ¹³C - labelled plant shoots (host) were parasitised by the fungus *Armillaria mellea* (pathogen), which in turn was hyperparasitised by the fungus *Trichoderma atroviride* (mycoparasite).



2.8

Title

FOXLAB

FoxLab is a joint research initiative between the Research and Innovation Centre (CRI) of the Edmund Mach Foundation (FEM) and five institutes of the National Research Council (CNR). It was the result of an accord jointly signed by Prof. Luciano Maiani, former President of CNR, Lorenzo Dellai, President of the Autonomous Province of Trento, and Prof. Francesco Salamini, President of FEM.

The main goal of FoxLab in the medium-term is to build a centre for forest research in Trentino that will become a benchmark for this field not just in Italy but also in Europe. To fulfil this ambitious objective, FoxLab has set up important national and international collaborations since its inauguration. These include:

- participation in the **AIRFORS Project**, financed by the European Union (7th Framework Programme, IAPP Industry-Academia Partnership and Pathways Programme, 2012 – 15), which has enabled FoxLab to enter into collaboration with an important Austrian aircraft company (Airborne Technologies, AT). The project is working on developing innovative solutions for monitoring forest areas using new airborne sensors. Its objective is to produce a bi-directional exchange between the company, who will be responsible for performing aerial surveys and training FoxLab personnel in the management of operational missions, and FoxLab researchers, who will transfer to the company advanced knowledge regarding implementation of innovative measurement systems and interpretation of observed data;

- active participation in the **European Projects ExpeER (Experimentation in Ecosystem Research) and Trees for Future (T4F)**. FoxLab manages the complex system of Transnational Access on behalf of a wide network of European researchers, enabling them to access key experimental sites focussing on the study of terrestrial ecosystems and a network of laboratories of excellence dealing with genetics, forest ecophysiology and wood technology;

- technical-scientific coordination of the **MOUNTFOR Project Centre**, an operational branch of the European

Forest Institute (EFI), which will be based at FEM in San Michele all'Adige and will be responsible for creating a focal point for advanced research on forest mountain systems. The main purpose of this initiative is to create an international network of collaboration in the field of forest research unprecedented in Italy. Alongside FoxLab, which will manage the operational centre, the Agricultural Research Council (CRA), operating under the supervision of the Ministry for Agriculture (MIPAF), the Universities of Molise and Tuscia, and the Free University of Bolzano (LUB) will participate in the project in collaboration with international partners of high standing.

- fulfilling the role of Italian focal point within the **ANAEE Project** (Analysis & Experimentation on Ecosystems). Coordinated by the Institut National de la Recherche Agronomique (INRA), the project will set up a highly advanced European network of research infrastructures over the next four years. FoxLab's role in ANAEE places it at the centre of an important venture for adapting and modernising the national network of agricultural, forestry and environmental experimentation. This important international collaboration will without doubt enhance the standing of researchers and management alike at FEM.

FoxLab is not, however, alone. Collaboration between researchers at CRI-FEM and CNR is having a strong multiplier effect in the production of **new knowledge**¹. To date, the work carried by FoxLab researchers has resulted in the publication of 12 articles in prestigious international peer-reviewed journals and many more are expected to be published over the coming months.

in short

An international network
of collaboration
in the field of forest research
unprecedented in Italy



More

Keywords

Franco Miglietta, Federico Carotenuto

1 / Terrestrial sources of biogenic material in the atmosphere: putting together a complex puzzle

It is now well known that microorganisms living on the leaves of plants are often transported through the atmosphere by wind gusts and turbulence. However, little attention has been paid to this phenomenon in the past as it was assumed that a microorganism passively transported in the atmosphere was basically inert, at least until its subsequent deposition onto another distant plant. But recent research has shown that this is not the case: bacterial and fungal proteins do, in fact, have a substantial effect while they are in the atmosphere, as these tiny particles can function as ice nuclei and, as a consequence, their presence in the air mass can trigger precipitation. Water vapour in the atmosphere requires condensation nuclei to form the core of ice droplets that subsequently grow to become snow, rain and hail. FoxLab is currently collaborating with their Austrian industrial partner, Airborne Technologies, the University of Innsbruck, and the University of Edinburgh, to develop a newly integrated system that will be able to collect biological material in the atmosphere, detect the occurrence of a range of microbial species, and calculate, on the basis of concurrent measurements of wind speed and turbulence, the back-trajectories of these materials to their original source. Other issues concern the contribution of specific forest types to these atmospheric feedbacks, and whether different land use types provide unexpected and crucial services to our society by triggering precipitation.

Highlights

1 /

Duccio Rocchini

Earth and Space Foundation prize

Duccio Rocchini is the first Italian researcher to receive an award from the Earth and Space Foundation, California, USA. Since 1994, these awards have been given to researchers from all over the world for the application of remote sensing data to the environment. Rocchini, who is a researcher in the GIS and Remote Sensing Platform, Department of Biodiversity and Molecular Ecology, has been acknowledged by the Earth and Space Foundation as the best researcher in the estimate of biodiversity by remote sensing field of research.

2 /

Markus Neteler

Book: GIS Open Source: GRASS GIS, Quantum GIS e SpatiaLite

Geographic information, with technologies related to satellite navigation, web maps and smartphones, has now become part of everyday life. This book introduces the reader to the use of Free and Open Source geographical software. In the first part, software installation on MS-Windows, Mac OSX, and Linux is shown. Subsequently, the most important features of well-known software like QGIS or GRASS GIS are introduced along with the use of relational database engines (SpatiaLite). Examples and applications are provided in the field of landscape analysis, geomorphology, hydrology and geology along with free online data resources.

3 /

Markus Neteler

Open Source

The DBEM-PGIS unit actively participates in the development of Open Source GIS software in long-term software development projects like GRASS GIS. This approach is considered to be perfectly in line with academic research due to the peer-review model applied to source code development. Open Source in general refers to software development method where the source code is maintained in a public repository with a group of developers, often volunteers, working on it. The aim is to receive quality software at lower cost which is flexible, interoperable (use of industrial standards for data exchange) and free of any vendor lock-in.

4 /

Roberto Zorer

Research visit in South Africa

ARC-Infruitec-Nietvoorbij and Stellenbosch University invited Dr. Roberto Zorer (DBEM-PGIS) for a research period during harvest in Stellenbosch, South Africa. The research focused on the impact of light distribution patterns in grapevine canopies as affected by row orientation. The aim is to produce a predictive model of canopy light patterns and berry temperature for different terroirs and cultivars, depending on the amount of direct sun received during the day, temperature and water availability. The research is part of approved research projects, financially supported by the Agricultural Research Council and the SA Wine Industry (Winetech).



5 /

Roberto Zorer

HarvAssist for PICA

This project aims to produce an integrated platform for the mapping of viticulture (PICA), that is, the study and characterization of the suitability of terrain for viticulture of the vineyards managed by 11 Trentino wineries. The web portal HarvAssist (<http://harvassist.fmach.it/pica/web>), developed in collaboration with CAVIT s.c., provides the characterization of about 30,000 vineyards, the management of pre-harvest data, and the forecast of the harvest in the current year, representing an innovative tool for the evaluation of viticulture for the entire Province of Trento.

Markus Neteler, Duccio Rocchini

6 / CRI among the giants in Biodiversity: The FP7 EU BON project for Biodiversity in Europe

The Department of Biodiversity and Molecular Ecology of CRI will participate to one of the most important projects on environment financed in 2012 by the European Union: the FP7 EU BON project, coordinated by the Museum für Naturkunde of Berlin. Duccio Rocchini, a researcher in the GIS and Remote Sensing Platform led by Markus Neteler, will coordinate a task group including the most prestigious European institutes such as the University of Cambridge and the London Natural History Museum. With a total budget of 11 millions euros, the project aims at integrating innovative methods for the analysis of European biodiversity data including approaches relying on satellite imagery.

Claudio Varotto

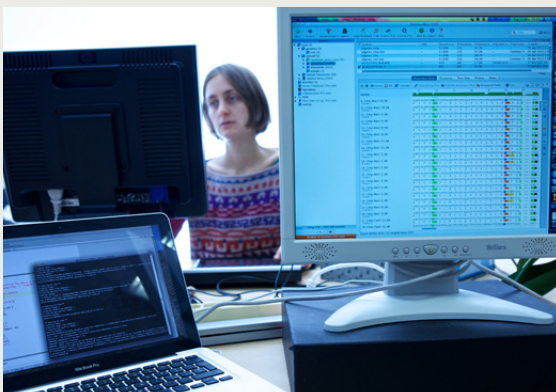
7 / Two novel plant species from Trentino and Friuli

Using genetic data from the *Brassica repanda* species complex, a group of morphologically similar taxa from southern Europe, we demonstrated that two *Brassica* taxa that only grow in a few localities of Trentino and Friuli are species new to science. We decided to rename these distinct species as *Brassica baldensis* and *Brassica glabrescens*. Our results show that 'cryptic' species (morphologically indistinguishable, but genetically distinct) could be more common than we think, as plants are still a poorly characterised component of alpine biodiversity.

Margherit Lega

8 / Conservation genetics in *Aquilegia thalictrifolia* (Ranunculaceae)

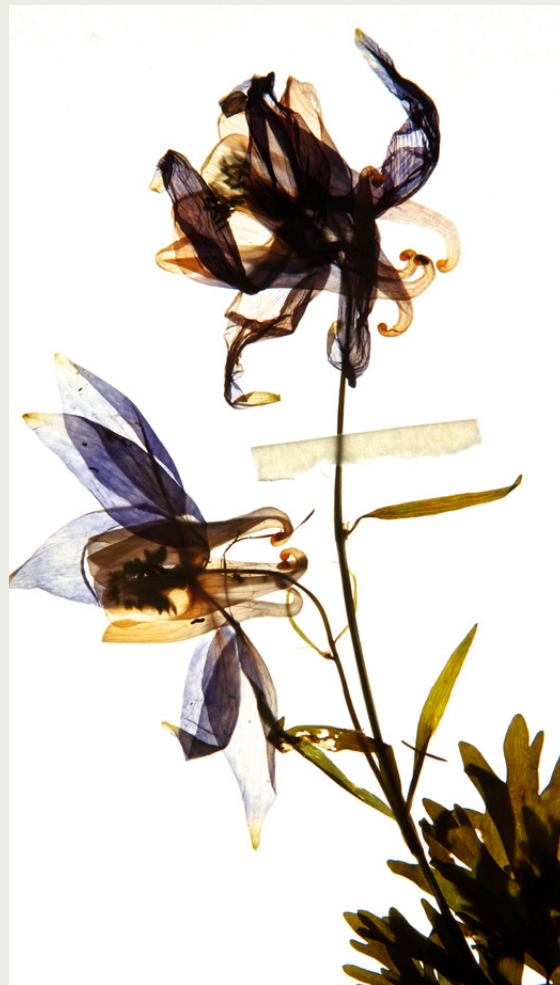
Aquilegia thalictrifolia is a rare plant growing only in the Tremalzo-Tombea mountains (Eastern Alps). This species has a very specific ecological niche characterised by well-drained calcareous bedrock, a habitat that may be endangered by global warming. Genetic analyses have demonstrated that existing populations have relatively high levels of genetic variation (important for future adaptation), but that they also appear to be isolated from one another (low pollen or seed exchange). Therefore, conservation should involve all of these populations to prevent losing an important component of the genetic variation of this species.



Simone Fior, Claudio Varotto

9 / *Aquilegia* phylogeny

Columbines (*Aquilegia* L.) are a genus of common ornamental plants that are being studied as models for plant-pollinator co-evolution and morphological novelties. Despite the imminent publication of its genome sequence, we still do not have a well-resolved phylogeny for *Aquilegia*. We used next-generation sequencing to determine the phylogeny of columbines round the world with unprecedented precision. This not only allowed us to reconstruct their evolutionary history but, most significantly, will also have important implications for the conservation of this group of attractive, commercially important plants.



Cristiano Vernesi

10 / Landscape genetics of holm oak from Lake Garda

Trentino populations of holm oak in the Garda lake area occur at the northernmost limit of the species distribution range. They are, therefore, important for conservation and evolutionary studies. From the analysis of 120 individuals it emerged that, despite being so geographically close, three genetically distinct groups can be identified. Each of them has medium-high genetic diversity if compared to that of central populations. The observed differentiation is correlated with climatic and ecological features such as soil depth, humidity, elevation and aspect. Biological Journal of Linnean Society (2012, 107, 458-467).

Luca Cornetti

11/ Conservation genetics of lizards and amphibians in Trentino

The toad *Bombina variegata* and the lizard *Zootoca vivipara* are vertebrate species, which live in the Province of Trento. They are only found in moist habitats, like swamps or peatbogs. Because of climate change and human activities, these ecosystems are now very rare, and many species that live in them can be considered endangered. Molecular genetic studies in the Conservation Genetics group in the Department of Biodiversity of Molecular Ecology at CRI have revealed the conservation status of these vertebrates. Our analyses have shown that some populations of both species suffer reduced genetic variability and do not move easily between populations. Therefore we will recommend that plans are made to carefully preserve the remaining populations of these two species in the Province.

Andreas Meraner, Andrea Gandolfi

12/ ABaTe project – Conservation Genetics of European Grayling and Italian Barbels

Many native species of Northern Adriatic freshwater fish are known to be threatened by the introduction of stocked species with which they interbreed. This 'genetic pollution' is particularly affecting European grayling (*Thymallus thymallus*) and Italian barbels (e.g. *Barbus plebejus*). The ABaTe project focuses on conservation status of both these endangered fish by determining the patterns and extent of introgression. Thus far, the genetic signatures of native and foreign populations have been identified and hybridization has been confirmed. These results provide a sound scientific basis for future conservation plans, aimed at impeding further loss of Northern Adriatic genetic biodiversity.

Francesca Cagnacci

13/ EURODEER workshop

Since 2009, FEM/CRI supports the EURODEER project (www.eurodeer.org), an initiative of collaborative science and data sharing to explore wildlife population responses (and specifically roe deer) along environmental gradients at the species distribution range. This collaboration has expanded rapidly, and currently involves 24 European research and wildlife management institutes. The III EURODEER meeting was hosted by FEM in 2012; the scientific sessions were preceded by a well-attended public meeting (The European roe deer: is it really a resilient species?), jointly organised by CRI and the CIF/AAFF, featuring international experts and a round table.

Francesca Cagnacci

14/ Wildlife Society awards for the CRI-edited "Challenges and opportunities of using GPS-based location data in animal ecology" Theme issue.

Several years ago, FEM/CRI organised a scientific workshop on the advent of GPS technology in animal ecology, with the participation of a selected

group of international experts. From the results presented at that meeting, a Theme Issue of the scientific journal *Philosophical Transactions of the Royal Society, B* (eds: F. Cagnacci, et al) was written. Two articles of this issue were awarded the "Wildlife Publications Award - Outstanding Article", for two consecutive years (2011 and 2012), assigned by The Wildlife Society of America, confirming the high scientific impact of this publication.



Roberto Rosà

15/ Impact of parasite on rock partridge

Rock partridge (*Alectoris graeca saxatilis*) are well known for their cyclic fluctuations in abundance while their total number are in steady decline in Trentino. We hypothesized that intestinal worms (helminths) may have an impact on these population dynamics. Host-parasite models predict higher parasite burden in cyclic than in non-cyclic populations. These predictions are well supported by multi-annual empirical findings in natural populations. Therefore, the effect of intestinal parasites on rock partridge populations should be considered when planning conservation strategies for this rare species in Trentino.



Heidi Hauffe

16/ Serological test developed for rodent borne-Ljungan virus

In the 2010 version of this Report, it was announced that the Ljungan virus, a rodent pathogen and candidate virus for several human diseases, was found in Italy for the first time by CRI researchers Hauffe et al. These samples were used in a collaboration with Finnish colleagues to develop a test that can be used to screen for the virus in blood sera samples, confirming that the virus can also infect humans, and establishing the presence of the virus in Finnish rodents for the first time. These results were announced at the recent Annual Meeting of the European Society for Clinical Virology (ESCV) in Spain.

Adam Konecny

17/ ROCOALPS results

Results from the ROCOALPS project indicate that small mammal diversity is much higher in forests at high altitude (1200 m a.s.l.) where both the yellow-necked mouse and bank vole is common, than in lowland forests (700 m a.s.l.) where only yellow-necked mice are found. In addition, rodents at high altitudes have more nematode worms. Rodent-borne zoonotic viruses were found in 3 species of rodent in all trapping areas, more commonly in yellow-necked mice than in bank voles.

Heidi Hauffe, Cristiano Vernesi

18/ Shrews survived LGM in eastern Alps

The last ice age (18000 years ago) had a profound effect on many alpine mammal species. Because the mitochondrial genome accumulates mutations slowly, analysis of its genetic variation is a common method for identifying areas of central Europe where species were able to survive (called 'glacial refugia'). A study of the most common shrew species in the Alps, published by Yannic et al and including several DBEM researchers (Hauffe, Vernesi), suggests that the *Sorex antinorii* was able to survive the last ice age not only in the Appennines, but also in a refugium in north-eastern Italy. Previous studies of alpine plants have also shown that the southern Alps including Trentino may have been an important area for species survival during the last glacial maximum.

Heidi Hauffe

19/ House mouse chromosomal diversity on Lake Garda

While many studies focus on the causes and consequences of biodiversity loss, studies of how new species are created are less well known. House mouse (*Mus musculus*) populations in Europe are divided into more than 100 'races' each of which has a different set of chromosome fusions. When races interbreed, their offspring are less fertile than the parents. Evolutionary theory predicts that races forming such 'hybrid zones' should cease interbreeding and become new species. Hauffe et al has studied this process in over the last 20 years in collaboration with colleagues from the UK (Oxford,

York) and USA (Cornell). She recently discovered a new hybrid zone along the western side of Lake Garda which is described in a scientific paper in Cytogenetic and Genome Research.

Fabiana Cristofolini, Amelia Caffarra, Antonella Cristofori, Fabio Zottele, Luca De Lucchi, Elena Gottardini

20/ Mapping the risk level of Betula pollen: the potential of phenological modelling

Knowing when and where significant concentrations of allergenic pollen occur in the air is useful for allergy sufferers. Phenological models may be a useful complement to standard aerobiological sampling. Taking a recently-developed phenological model for *Betula pubescens* (DORMPHOT), the predictors were spatialised and the phenological model applied and calibrated to the entire province of Trento. Pollen risk maps with high spatial and temporal resolution were developed for birch and visualised through a Web-GIS interface for effective communication of information. <http://pollenrisk.fem-environment.eu/>.

Ilaria Pertot

21/ Envirochange project throws light on climate change and agriculture in Trentino

The Envirochange project recently ended. One of its objectives was to investigate the degree of climate change and its impact on agriculture in Trentino and provide tools to counteract these effects. Increasing occurrences of pests and diseases and their impact on plant protection strategies used by growers, the appearance of invasive species and stress-related pathogens, and the increased risk of mycotoxin contamination of grapes are the most alarming aspects. The results can be seen in the e-conference on the web-site: www.envirochange.eu.



FOOD FOR LIFE /

**FOOD AND DRINKS
FROM TRENTINO:
THEIR QUALITY,
THE ANALYTICAL
KNOW-HOW
FOR THEIR
CONSERVATION,
THEIR EFFECTS
ON HUMAN HEALTH,
AND ON NATIVE
MICROFLORA**

part_3

Fulvio Mattivi, Duccio Cavalieri

More knowledge, less junk food

San Michele is contributing to the development of strategies for improving quality of life directed along the following five lines of research:

- investigating those compounds present in the principle agricultural products with a potentially positive effect on human health;
- enhancing food produced in Trentino and improving people's ability to maintain health through better food;
- investigating the role of microorganisms in improving the nutritional value and healthiness of food;
- the study of sensory properties, consumer behaviour and food production technologies;
- developing the enabling technologies needed to produce new knowledge and to support research in the agro-food sector, with particular emphasis on the creation of new products and consumer protection.

At the beginning of the new millennium, humans read for the first time the code containing the instructions for duplicating every cell in the body and for regulating life. Over the past five years, San Michele has acquired genomic information on grape, apple and strawberry, but despite the promises of these revolutionary discoveries, knowledge of the human genome sequence has not yet enabled us to explain why we are healthy or get sick, or how to live longer.

The answer needs to be sought in the enormous influence that the environment, and in particular food, has on human health. Many of the answers we are seeking are complex and depend on the function of many genes and how they interact with the environment. When we speak of **environment** we usually think of the place where we live, the climate and pollution. But there is an environment with which we are on more intimate terms, which is shaped by the microorganisms that are with us right from birth and which have been with us for thousands of years throughout our evolution: our **metagenome**. Viewed as an indispensable organ, the intestinal microbiota provides the host with advanced metabolic functions, protection against pathogens, education for the immune system and modulation of the gastrointestinal tract during development.

The way the consumption of food is evolving is certainly not guided by what is good, healthy and sustainable, but rather towards to an increase in so-called "junk food". It sells well, at the expense of high quality food, especially in times of crisis, it globalises eating behaviour and has low production quality standards. San Michele is using the knowledge acquired to understand how foods and their microorganisms can be used while maintaining the balance between them. Results are disseminated with the aim of increasing producer and consumer awareness.

3.1

Title

The benefits of resveratrol and its derivatives for healthy grapevine

Vitis vinifera L. is the most widespread cultivated grapevine and produces very high quality grapes popular with consumers as fresh fruit or transformed products. It is, however, very susceptible to fungal attack, the main grapevine fungal diseases being powdery mildew, caused by the ascomycete *Erysiphe necator*, and downy mildew, caused by the oomycete *Plasmopara viticola*. To combat these pathogens, farmers are requested to spray their vineyards with antifungal products whenever the weather conditions are favourable to the growth and spread of mycelia. This translates into around fifteen treatments per season. It is crucial to reduce this extensive use of chemicals in order to make viticulture environmentally sustainable in the long term.

At FEM-CRI we are developing various strategies aimed at sustainability, including establishing breeding programmes to transfer resistance traits present in *Vitis* wild species to the *V. vinifera* cultivars with the two-fold objective of maintaining quality and acquiring fungal resistance. A frequently observed defence mechanism in grapevine is the accumulation of stilbenoids upon pathogen elicitation. These are the main antimicrobial phenolic compounds derived from *trans*-resveratrol, and their toxicity is apparently related to their chemical structure.

Against this background, we have been investigating *P. viticola* resistance and **stilbenoid accumulation**¹ in a grapevine population generated by crossing Merzling, the resistance-bearing parent (a complex hybrid from *V. vinifera* x *V. rupestris* x *V. lincecumii*), with Teroldego, an autochthonous *V. vinifera* cultivar of Trentino. We have had some very interesting results which have recently been published in international scientific journals (see related Insights). Analysis of the population's response to artificial infection over a three year period enabled us to classify individuals into nine groups ranging from total resistance to total susceptibility, suggesting that this trait is controlled by few major genes. Interestingly, there were marked differences in the amount and type of stilbenoids accumulated in the leaves of individuals upon infection. In particular, there were high-producer

plants characterised by the presence of monomers of resveratrol, plus up to thirteen different oligomeric stilbenoids, nine of them identified for the first time in grapevine. These plants typically displayed resistance to fungal attack, strongly suggesting that the presence of stilbenoids contributes to the resistance response.

In order to select the genes associated to the resistance trait, the transcriptomes (the whole set of transcripts) of selected resistant and susceptible individuals were compared at different time points after fungal infection using a combination of AFLP-TP and microarray techniques. A group of 57 genes was found to be exclusively modulated in the resistant genotype, indicating their involvement in the grapevine-*P. viticola* incompatible interaction.

These **results**² highlight the important role of resveratrol and its derivatives in the response of grapevine to downy mildew, although further investigation is needed to compare the efficacy of different stilbenoids and to throw light on their action mechanisms.

Finally, it is worth noting that resveratrol, besides being beneficial to the plant, may also be beneficial to human health. For the time being, animal models provide compelling evidence for positive effects against cancer, diabetes, heart and neurodegenerative diseases and inflammation.

in short

Transferring resistance traits
present in *Vitis* wild species
to *V. vinifera*
for a more sustainable viticulture

More

Keywords

Giulia Malacarne, Claudio Moser

1 / Techniques and methods used in the study

Identification, quantification and structural characterisation of stilbenoids

HPLC-DAD-MS, High Performance Liquid Chromatography-Diode Array Detection-Mass Spectrometry, is used to perform metabolic analyses using liquid chromatography coupled to a photodiode array detector and mass spectrometer. **NMR**, Nuclear Magnetic Resonance, is a technique used in various fields of research. In biochemistry it is mainly used to characterise the structure of molecules.

Transcriptome analysis

AFLP-TP, Amplified Fragments Length Polymorphism-Transcripts Profiling, is used to analyse the transcriptome of an organism in the absence of knowledge of its sequence.

Microarray is a collection of microscopic DNA probes attached to a solid surface with high density and precise geometry and is used to analyse an organism's genome or transcriptome.

Giulia Malacarne, Claudio Moser

2 / Further readings

- Malacarne, G. et al. (2011) Resistance to *Plasmopara viticola* in a grapevine segregating population is associated with stilbenoid accumulation and with specific host transcriptional responses. *BMC Plant Biol*, 11:114.
- Mattivi F. et al. (2011) Profiling of resveratrol oligomers, important stress metabolites accumulating in the leaves of hybrid *V. vinifera* (Merzling x Teroldego) genotypes infected with *Plasmopara viticola*. *J Agric Food Chem*, 59:5364-5375.
- Vrhovsek U. et al. (2012) Profiling and accurate quantification of trans-resveratrol, trans-piceid, trans-pterostilbene and eleven viniferins induced by *Plasmopara viticola* in partially resistant grapevine leaves. *Aust J Grape Wine Res*, 18:11-19

3.2

Title

Traditional diets, whole plant and regional foods acting through the gut microbiota play a key role in human health

Diet is increasingly recognised as a key determinant of human health and disease. In fact, our high fat, high refined carbohydrate, energy rich but nutrient poor and largely sterile modern “Western-style” diet has been linked to chronic metabolic and autoimmune diseases like obesity, diabetes (type 1 and 2), certain cancers, allergy and inflammatory bowel disease. Interestingly, recent data, including studies carried out by the NN team, have shown that many of these diseases are associated with aberrant gut microbiota composition and activities. On the contrary, strong epidemiological data show that consumption of whole plant foods, especially fruits and whole grain cereals, and certain dairy products can reduce the risk of these chronic diet associated diseases. Food plants contain two classes of compounds most likely to contribute towards these health promoting activities, biologically active polyphenolic compounds and non-digestible carbohydrates or dietary fiber. Both of these plant food components interact closely with the human intestinal microbiota, shaping the microbial ecology of the gut and further, are themselves only made biologically available upon transformation by gut microorganisms. This raises the intriguing possibility that diet:microbiota interactions may play an important role in the pathobiology of chronic metabolic and autoimmune diseases.

The Nutrition and Nutrigenomics Group is investigating how these diet:microbiota interactions can be harnessed to modulate human disease risk. Using a combination of in vitro model systems and human dietary interventions, we are investigating how different whole plant foods (especially fruit), fiber fractions or plant polyphenolic extracts can modulate both the composition and activity of the gut microbiota. As described above, we form part of the local METAFODBOOK collaboration, and are investigating how to exploit the rich and biologically diverse microbiological heritage of Trentino [dairy](#)¹ and beverage fermentation industries to redress the lack of safe and immune-training encounters afforded by food passenger microorganisms, which are largely lacking from the modern Western style diet. Collaborating with colleagues locally at FEM and in

Trento (FBK and CiBIO), but also further afield in Italy, Europe and the United States, we are now unravelling how diet shapes [gut microbiota](#)² composition and its metabolic and immunological output in vivo and in model systems laying the foundations for improved whole plant and traditional foods. Our work draws on the ecological dimension of how we as humans have co-evolved along side our ancestral diets and foods, especially whole plant foods, and will help us design optimal nutritional strategies which can be applied at the population level to fight the spread of modern diet-associated chronic diseases.

in short

Applying optimal nutritional strategies
at the population level
to fight the spread
of modern diet-associated
chronic diseases



More

Keywords

Elena Franciosi e Lorenza Conterno

1 / Studies on the microbial diversity of Trentino dairy products

The Trentino region has a rich tradition in fermented dairy products, and our initial studies (TrentinoGut project) have identified bacteria from local cheeses with probiotic traits such as low pH and bile acid tolerance and the ability to inhibit important pathogenic microorganisms like *Escherichia coli*, and *Listeria monocytogenes*. Similarly, the FERMALGA project is providing amazing novel insight into the microbiology underpinning traditional Trentino artigianal or “malga” cheeses, enabling our team to catalogue and preserve an important component of the unique Trentino dairy microbiome and to develop technological solutions for sustaining this important local industry. A research highlight has been the successful application of metagenomics to characterise the successional development of the Trentin-Grana microbiota from high quality raw milk to final mature cheese product.

Carlotta De Filippo e Francesca Fava

2 / Metagenomics of gut microbiota

Collaborating with other colleagues at FEM, we are investigating how the same principles and technologies we apply to studying the human gut microbiota can be expanded to other species of relevance to the Trentino land based economies including cattle, fish and honey bees. For example, we have recently begun metagenomic studies into the architecture of the honey bee gut microbiota with the view towards both improving honey bee health, and therefore safeguarding their pollination duties and as a potential source of novel human functional foods.

3.3

Title

A holistic view of the chemistry behind wine micro-oxygenation

Exposing wine to excessive amounts of oxygen causes irreparable damage and leads to the production of off-flavours and bacterial spoilage. For centuries, wine quality referred to the quality of freshly-fermented grape juice, since the technology to preserve wine under anaerobic conditions was unavailable. The Egyptians used terracotta jars which could be hermetically sealed to store wine, probably the first true containers for fermented juices. Pasteur was the first to point out the importance of fine-tuning wine. The effect of oxygen on the sensorial quality of red wine is acknowledged to be hormetic, clearly positive at low levels and negative above a certain level.

In recent times, research has led to the development of modern techniques for controlling the amount of oxygen reaching the wine, and **wine micro-oxygenation**¹ is now a globally used treatment with considerable economic importance. A survey reported by Wine Business Monthly found that as many as 17% of the producers interviewed used this technique.

However, there is a pressing need to make this technology more efficient. One solution is to improve understanding of the chemical processes involved in order to develop sets of biomarkers that can be measured at appropriate levels, allowing us to gain control over the processes.

The aim of our work was to use an MS-based metabolomics experiment to measure changes to the **metabolic fingerprint**² of red wine brought about by micro-oxygenation. The oxygen doses adopted in the experiment were those typically used in wineries, and the levels of metals were within the limits usually present in wines, without any extreme values. The scale of the trials held at the Consorzio Tuscania winery was the largest ever used for such an experiment: 24,000 litres. Eight different procedural variations, four levels of oxygen addition and two levels of iron addition, were replicated three times in Sangiovese wine, before and after malolactic fermentation.

The results of this experiment have been recently published and are freely downloadable here:

<http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0037783>.

We believe the results of this experiment represent new knowledge of scientific importance for the following reasons:

- More than 250 known and 750 unknown compounds were monitored using the analytical method developed for this experiment.
- Data analysis using supervised and unsupervised multivariate methods highlighted most of the known candidate biomarkers (wine pigments and tannins), confirming the reliability of the untargeted experiment.
- Data analysis highlighted a large number of new metabolites which had not previously been considered as possible biomarkers for wine micro-oxygenation. Changes in the concentrations of primary metabolites such as arginine, proline, tryptophan and raffinose, and secondary metabolites such as succinic acid, xanthine, fatty acids, etc., correlated with oxygen dose and metal content. The candidate biomarkers which showed a biphasic effect in the presence of variable levels of oxygen should be further studied for a more comprehensive understanding of wine micro-oxygenation and to develop analytical tools able to provide winemakers with better control over the micro-oxygenation process.

This experiment highlights the feasibility of using unbiased, untargeted metabolomic fingerprinting to improve understanding of wine chemistry, thus filling a known research gap.

in short

More than 250 biomarkers detected
and described in the oxygenation
process of red wine,
and 750 unknown compounds monitored

More

Keywords

Fulvio Mattivi

1 / Micro-oxygenation

Micro-oxygenation is a practice consisting in the continuous addition of small amounts of oxygen to red wine in order to improve its colour, aroma and texture. The process increases fruity and spicy flavours, enhances the stability of red tones and decreases herbaceous aromas and wine astringency. Metals, such as iron or copper, play an important catalytic role, since they can act as electron donors when there is a small amount of oxygen present and an acid pH. The oxygen doses tested were those typically used in wineries. We avoided extreme values as these are inappropriate in the study of biphasic effects.

Panagiotis Arapitsas, Matthias Scholz

2 / Metabolomic fingerprinting

The purpose of **metabolomic fingerprinting** is to analyse as many metabolites and different classes of compound as possible in a single chromatographic run. Wines were directly injected into an Acquity UPLC using a reversed phase column coupled to a Synapt QTOF-MS via an electrospray ionization (ESI) interface. Raw data were processed using XCMS for feature extraction, grouping and alignment. Analysis of the chromatographic data revealed 8526 features in ESI positive mode and 5620 in ESI negative mode in the pre-MLF experiments, while in the post-MLF experiment, the number of features were 9135 and 8843, respectively.

3.4

Title

Advanced chemical methods for certifying the authenticity of Italian hard cheeses

To comply with European law (EC regulation No. 510/2006), geographical indications and designations of origin for agricultural products and foodstuffs must be protected against mislabelling. This is particularly important for Italian **PDO¹** (Protected Denomination of Origin) hard cheeses, such as Parmigiano Reggiano and Grana Padano, which have a yearly turnover of around 2.5 billion euros and can cost up to twice as much as non-PDO competitors. The market is therefore vulnerable to fraudulent use of PDO designations for non-PDO cheeses, especially in grated and shredded form where it is not possible to check the fire-marked trademark on the rind.

To protect consumers and honest producers from mislabelling fraud, objective and robust methods for differentiating between different types of hard cheese and for verifying the authenticity of marketed products need to be developed.

Of the available methods, measurement of the **stable isotope ratios of bioelements²** in combination with **mineral element³** content seems to be the one best suited to the task.

In collaboration with the Consortia for the protection of the two above-mentioned PDO cheeses and the Consulting and Services Centre of FEM, we analysed the isotopic ratios of hydrogen, carbon, nitrogen and sulphur and the content of 50 elements in 82 authentic samples of Parmigiano Reggiano, 203 of Grana Padano, and a total of 184 samples of non-PDO hard cheeses produced in Italy (Gran Biraghi/Valgrana), the Czech Republic (Gran Moravia), Lithuania (Goya/Dziugas), Germany (Reibekase), Austria, Latvia (Monterigo), Poland, France, Holland, China and the USA. The PDO cheeses were selected by the Consortia and cover all the traditional production areas indicated in the the specification, while the non-PDO cheeses are the main commercial competitors.

We found the isotopic and mineral compositions of Grana Padano and Parmigiano Reggiano to be significantly different from those of the competitors. Using **innovative statistical techniques⁴** it was possible

to create models (Camin et al., 2012) which combine the most significant analytical variables and which can be used as references in verifying authenticity. If the analytical results of the cheese do not comply with the model, it is considered not to be authentic.

The system can now also claim legal status. Firstly, stable isotope ratio analysis has been recognised by EU regulation as an official quality control technique and has been included in the specification of Grana Padano PDO cheese (EU Reg 584/2011). Secondly, the models and reference values of the PDO cheeses have been deposited at the Italian Ministry of Agriculture, Food and Forestry. Finally, the methods have been validated on the basis of results from an international collaborative study involving over 10 laboratories which analysed 7 pairs of cheeses in a double-blind study.

The system is now fully operative and can be used by official bodies and by Consortia for the protection and authenticity certification of hard cheeses on the market.

Combination of the two chemical methods has also been used to characterise other Italian PDO or traditional cheeses, such as Asiago, Fontina, Montasio, Spressa, Toma, Puzzone and Vezzena (Bontempo et al., 2011).

in short

A useful standard
for official food boards
and local Consortia
for authenticity certification



More

Keywords

Federica Camin

1 / PDO, Parmigiano Reggiano, Grana Padano

According to the 2011 ISMEA Report, there are over 1,000 indications and designations of origin in Europe, Italy having the greatest number (239). Total turnover is 6 billion euros in production and 10 billion euros in consumption. Grana Padano and Parmigiano Reggiano are the two biggest-selling certified Italian cheeses.

Federica Camin

2 / Stable isotope ratios of bioelements

These are $^2\text{H}/^1\text{H}$, $^{13}\text{C}/^{12}\text{C}$, $^{15}\text{N}/^{14}\text{N}$, $^{18}\text{O}/^{16}\text{O}$, $^{34}\text{S}/^{32}\text{S}$ and they are measured using an Isotope Ratio Mass Spectrometer. Where animal products are concerned, they are linked to the composition of the animal's diet and to the geographical (latitude, altitude, distance from the sea) and climatic (e.g. temperature, precipitation) characteristics of the area of origin.

Robert Larcher

3 / Mineral elements

These are measured using Inductively Coupled Plasma–Mass Spectrometry after acid digestion of cheese. Their presence in cheese depends on several factors, such as mobility and bioavailability in soils, absorption and storage in forages, animal intestinal absorption and mammary gland secretion, and the impact of technology and pollution in cheese production.

Ron Wehrens

4 / Statistical techniques

Multivariate statistical techniques can be used to discriminate between classes on the basis of selected analytical parameters. Significant results can be obtained from simple methods, such as linear discriminant analysis, but if there are large numbers of samples and variables more innovative techniques with greater discrimination capability, such as random forest, may be applied.

3.5

Title

Is it possible to measure the “perceivable” quality of apple?

Consumers' appreciation, and its health-giving properties and nutritional value are crucial factors influencing food choice. The quality of an apple, for example, can be directly evaluated by the consumer through sensory perception with additional information from context, external cues, and cognitive and emotional factors.

The sensory quality of apples relies on several genetic and agronomic factors that govern the characteristics of the fruit at the end of ripening and as they continue to evolve during post-harvest and shelf-life phases.

Shape and colour are the most salient properties perceived, and they strongly influence the consumer's choice and create expectations that affect judgment when the apple is tasted. Texture (i.e., mechanical and elastic properties) is a major cue for apple quality, as it is closely correlated with general fruit freshness. Furthermore, texture properties modulate the release of compounds responsible for chemosensory sensations: odours, flavours (i.e., taste and retronasal odours combined), and other sensations (e.g., astringency).

Eating quality is frequently measured by means of basic pomological descriptors, such as fruit shape, colour, soluble solid content, titratable acidity, or by using penetrometer measurements of hardness. Many studies have attempted to predict fruit eating quality using instrumental techniques, but there is little work on associating the measures obtained from them with sensory profiling carried out using a rigorous sensory methodology. Moreover, univariate correlations can often be unreliable due to interactions between sensory attributes.

Descriptive sensory analysis is the best way of providing a comprehensive and objective description of sensory perception, in both qualitative and quantitative terms. Human assessment should, therefore, be the key reference for calibrating instrumental analyses.

Thanks to the multidisciplinary skills of its researchers and the availability of a sensory laboratory with an internally-trained panel, FEM was able to begin **sensory characterisation¹** of several apple cultivars in 2010. A wide selection of cultivars, including those most commonly available on the Italian market, were analysed. Several new FEM genotypes were additionally included in the analysis in 2011.

In parallel with the analyses carried out by the panel, the apples were subject to instrumental profiling based on the physico-chemical parameters associated with the sensory descriptors appearance (colour), texture (mechanical and acoustic profiles), odour and flavour (basic composition and volatile metabolite profiling). The ultimate goal is to build **predictive models²** based on rapid instrumental characterisations that will provide reliable quantification of sensory attributes for the large sample sets necessary for genomic and metabolomics studies that could not otherwise be directly analysed due to the expense and time constraints of sensory methods. The preliminary results are positive and show that most of the textural properties examined and some of the odours and flavours can be predicted with instrumental measures.

Sensory characterisation was complemented by the study of the complex **multisensory interactions³** during apple consumption and by a **consumer test⁴** to assess the influence of intrinsic sensory attributes on preferences and the role of external information.

The sensory/instrumental approach presented here for defining and controlling perceivable apple quality is, therefore, a valuable tool for consumer-oriented genetic improvement of new apple accessions.

in short

Methods and models
for the quantification
of sensory attributes of apple

[More](#)

Keywords

Maria Laura Corollaro

1 / Sensory profiling

The sensory profiling of apple presented here is based on a quantitative descriptive analysis carried out by a panel of trained judges composed of FEM employees. The panel evaluated the apple samples according to a set of sensory attributes related to texture, odour, flavour and appearance. The method was validated by assessing the panel's degree of agreement and consistency, discriminant ability, and repeatability. Univariate and multivariate analyses were used to highlight differences between the cultivars and perceivable changes in fruit quality induced by pre- and post-harvest treatments or during shelf life, and to compare new genotypes with parentals.

Eugenio Aprea

2 / Predicting apple odours

About 20 apple cultivars were characterised by SPME-GC-MS² for volatile compounds and by a trained panel for sensory descriptors. Apples were grouped into 5 clusters according to specific volatiles and sensory descriptors. Predictive models were also built to predict apple odours from rapid headspace analysis. We found that different olfactory sensations were generated by the same volatile compounds but present in different proportions, thus the differences in perceived odours are due to the relative proportions rather than to the presence/absence of these compounds.

M. Luisa Demattè

3 / Multisensory interactions in texture perception

Our experience of food is multisensory because most of our senses are involved in the action of eating. To gain further insights into texture perception in apples, we asked a total of 63 volunteers to take part in a series of psychophysical tests. The results showed that manipulation of the sound produced while biting into an apple modifies not only its perceived crispness, a texture parameter based on purely auditory cues, but also its hardness, which is generally held to be based only on kinesthetic information.

Isabella Endrizzi

4 / Factors influencing consumer acceptability

A test involving 221 consumer participants was used to investigate the extent to which acceptability of some well-known apple varieties is affected by different degrees of crispness and taste (sweet and sour) and by extrinsic information, provided just before tasting, concerning the hypothetical content of fibre and antioxidants in the apple under evaluation. On average, significant effects were found for sensory factors, which positively influenced liking, while extrinsic factors seem not to have any effect except when different consumer groups were taken into account.

3.6

Title

The Volatile Compound Platform: a new approach to an old problem

Chemoreception was an important factor at the origin of life: communication and exploration of the environment occurred through the emission and detection of molecules dissolved in water. When living organisms colonised dry land, they relied on the small molecules that circulate freely in the air known as 'volatile compounds'.

Olfaction, our most ancient sense, is often taken for granted and little attention is paid to volatile compounds. However, they play a highly significant role in several fields of research in which FEM is involved: sensory quality of food, outdoor and indoor air quality, plant communication, and communication between plants and insects.

The most advanced techniques for identifying and quantifying volatile compounds require lengthy pre-treatment and chromatographic separation, making them slow and laborious.

The aim of the newly-established "Volatile Compound" platform, on the other hand, is to provide FEM with rapid and non-invasive methods based on direct-injection mass spectrometry. The platform has recently acquired a PTR-ToF-MS (Proton Transfer Reaction Time-of-Flight Mass Spectrometer), the first in Italy and one of the first in the world, which allows volatile compounds to be quantified much more rapidly and with greater sensitivity.

The experiments performed so far demonstrate the advantages of this new approach. On the one hand, it allows for non-destructive screening of large data sets, which is necessary when comparing large populations or when the same sample must be evaluated by different techniques to increase the efficiency of correlation analyses, for example, estimation of sensory attributes from rapid instrumental characterisation, identification of molecular markers related to volatile compounds, or [non-destructive classification](#)¹ of cultivars and clones. On the other hand, the technique is capable of fast, non-invasive monitoring allowing real time, on-line control of processes relevant to food science and technology, for example, quantification

of flavour compounds in exhaled breath during food consumption, so called [nose-space analysis](#)².

The Volatile Compound Platform also studies fundamental issues such as chemico-physical characterisation of [organo-sulphur compounds](#)³ and applications in other fields of interest to FEM: bioprocess monitoring (fermentation, [biodigestion](#)⁴), and breath analysis for diagnostics and metabolomics (Aprea: Highlights). In addition, recent studies have shown that plants appear to communicate with other plants and insects through the emission of volatile compounds. Direct-injection mass spectrometry is currently being employed in research in this area.

in short

Mass spectrometry
for a very sensitive, rapid,
and non-invasive quantification
of volatile compounds

More

Keywords

Josè Sanchez del Pulgar Rico

1 / Characterisation of Iberian Dry-Cured Ham by PTR-ToF-MS

Rapid PTR-ToF-MS analysis has been successfully used in **non-destructive classification of agro-industrial products** and, in particular, of dry-cured Iberian ham according to the pigs' diet during the fattening period, the most important factor affecting the quality of this expensive foodstuff. This work represents the first use in food science of the Switching Reagent Ion system, which improves the analytical capability of PTR-ToF-MS mainly due to the ability of NO⁺ ionization to detect aldehydes and ketons separately, both very important for the odour and flavour of dry-cured ham.

Andrea Romano

2 / Food-Consumer Interaction: new insights from nose-space analysis.

Studies in food-consumer interaction don't always take into account inter-individual differences. Direct-injection mass spectrometry (namely PTR-ToF-MS) provides a real-time "snapshot" of the volatile compounds released by food during tasting. This technique, commonly known as nose-space analysis, was used to assess reproducible inter-individual differences among coffee tasters. The ultimate goal is to provide further insights into the physiological basis of consumer sensitivity and preference with respect to coffee, and eventually to other foods.

Erna Schuhfried

3 / Chemico-physical characterisation of organo-sulphur compounds

Organo-sulphur compounds have been a particular focus of research, to which the University of Innsbruck has also contributed. These compounds are typically responsible for nauseating off-flavours in foods, but they also contribute to pleasant flavours in such products as wine, cheese and coffee. These compounds are therefore of great interest, yet due to their typically very low concentrations measuring them presents a considerable challenge. To support research in this area, important chemico-physical parameters of interest in PTR-MS applications have been quantified: Henry's law constant, fragmentation induced by protonation, and reaction mechanisms under humid conditions.

Davide Papurello

4 / Monitoring the biogas produced during anaerobic biodigestion of the organic fraction of municipal solid waste

In collaboration with Silvia Silvestri's team (FEM-CTT), SOFCpower spa and the Politecnico di Torino, we investigated the possibility of producing green energy from the organic fraction of municipal solid waste. The idea is to produce environmentally-friendly biogas from biowaste to generate power and heating. SOFC-type fuel cells can be harmed by volatile compounds co-generated in the biogas, for example, organo-sulphur, chlorine and siloxane compounds. PTR-MS allows these compounds to be investigated and monitored directly in the digester and the gas-cleaning section of the pilot plant.

Highlights



Federica Camin

1 / Potential isotopic and chemical markers for characterising organic fruits

Several isotopic ($^{13}\text{C}/^{12}\text{C}$, $^{15}\text{N}/^{14}\text{N}$, $^{18}\text{O}/^{16}\text{O}$, $^2\text{H}/^1\text{H}$, $^{34}\text{S}/^{32}\text{S}$) and chemico-physical parameters (pH, fruit weight, juice yield, titratable acidity, total soluble solids, skin resistance, flesh firmness, colorimetric characteristics, post-harvest weight loss, antioxidant activity, earliness index, total nitrogen, and the content of ascorbic acid, synephrine, anthocyanins, polyphenols, citric acid, malic acid, sucrose, glucose and fructose) were investigated as potential markers of organically cultivated oranges, clementines, strawberries and peaches. The $^{15}\text{N}/^{14}\text{N}$ ratio, ascorbic acid and total soluble solids were found to be the most significant variables.

Luana Bontempo

2 / Traceability throughout the production chain of Italian tomato products based on stable isotopes and mineral composition

The stable isotope ratios of H, C, N, O and S and the content of 50 minerals, nitrates, chlorides, sulphates and phosphates were measured in 320 samples of tomato and its derivatives (juice, purée and paste) in order to evaluate the possibility of tracing geographical origin. The tomato products were from three Italian regions (Piedmont, Emilia-Romagna, Apulia).

The method provided excellent discrimination between the tomatoes from the three regions. Irrespective of the type of processing, over 95% of the samples were correctly reclassified into the region of origin by cross-validation. The study was carried out in collaboration with the Consulting and Services Centre.



Valentina Catalano

3 / AGER-OENOLOGY: Geographical and genetic traceability in oenological products.

The network of foundations for the advancement of scientific research in the agro-food sector (AGER) has recently funded the project "New analytical methodologies for geographical and varietal traceability of oenological products" which will characterise high quality wines from Emilia Romagna and Trentino-Alto Adige. Our Research Centre will contribute to the project by carrying out stable isotopic studies and advanced metabolomic and genomic analyses.

Flavia Gasperi

4 / The contribution of research to promoting Trentingrana cheese

Collaboration between the Trentingrana Consortium and FEM researchers marks an important step towards developing a reliable tool for monitoring the quality of the main cheese produced in Trentino. The system is based on expert evaluation of sensory quality, the most important product characteristic driving consumer preference. Instrumental methods for measuring the physical and chemical parameters correlated with sensory characteristics are also being studied. A recent study on milk collection and Trentingrana quality confirms the validity of this dual approach.

Isabella Endrizzi

5 / New statistical tools for clustering consumer preferences

In consumer studies, understanding and classifying individual preferences in relation to the characteristics of the product and of the consumer is of prime importance. This type of information is essential for developing successful marketing strategies. In recent years, we have developed two new statistical tools to gain a better understanding of consumer choice. The first method1 is an algorithm that automatically clusters consumers while at the same time taking into account all the available information (preferences, product features and consumer background); the second2 is based on analysis of ANOVA residuals and allows individual differences to be investigated.

M. Luisa Demattè

6 / How different responses to odours can be!

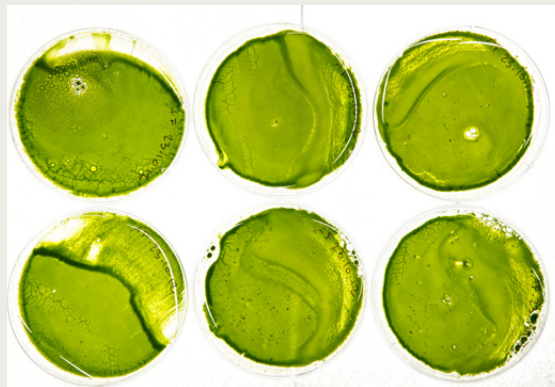
Naming an odour is a hard task for a human being and awareness of the chemosensory environment differs among individuals. Over 3 years, 171 volunteers participated in an experiment to identify a series of familiar odours and their performance was analysed as a function of personal and psycho-behavioural factors. We were able to demonstrate, for example, that women are more aware of odours than men, and that in general this awareness increases with age1. We also showed there to be a link between the reluctance to consume new or unusual foods (food neophobia) and the ability to correctly identify the name of an odour.



Ulrike Obertegger, Federica Camin, Giovanna Flaim

7 / Adaptation of a psychrophilic freshwater dinoflagellate to UVR

We investigated the physiological strategies adopted by *Borghiella dodgei* to cope with ambient levels of ultraviolet radiation (UVR) under cold conditions. The ability of *Borghiella* to adapt to UVR depends on a general increase in metabolic activity and efficient scavenging of oxygen radicals to mitigate or counteract damage. As climate changes, the combined effects of higher temperature and UVR on cold-adapted species will have repercussions on the whole food chain. This work was carried out in collaboration with the Bioorganic Chemistry Lab of the University of Trento.



Floriana Marin, Alessandro Gretter

8 / FEM brings the International Mass Spectrometry Conference to Trentino

In October 2013 FEM will be organising the 3rd edition of MS Food Days, an international event promoted by the Italian Chemistry Society (Mass Spectrometry Division) with the support of key players in the national food sector, such as Barilla and Illy coffee. The conference, which is expected to attract around 200 participants from agri-food research fields and industries, is a unique opportunity to address issues such as food quality and safety, traceability, and production technologies, all areas where mass spectrometry techniques are crucial. The prominent role played by FEM in scientific research in these areas was instrumental in the choice of Trentino as the venue for the third edition of the Conference.

our research : facts & figures

- part_1 FEM Campus
- part_2 Our International Network
- part_3 Research Projects
- part_4 Affiliations
- part_5 Editorial committees of scientific journals
- part_6 Prizes
- part_7 Thesis completed by FEM
- part_8 Articles published in scientific journals with Impact Factor
- part_9 Impact Factor Journal covers focussed on CRI research
- part_10 Organization chart / Staff data

FEM Campus



1 /

Student
residence

2 /

Wine cellar

3 /

12 /
13 /

Laboratories

4 /

Education
and Training
Building +
Library

5 /

FEM
Administration +
President's
office

6 /

Guest house
Maso
Kinderleit



7 /

Research and
Innovation
Building +
CRI Director's
office

8 /

Technology
Transfer
Building

9 /

Microvinification
cellar

10 /

Experimental
greenhouses

11 /

Research and
Knowledge
Building

14 /

Our International Network

128

EUROPE /

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15

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X

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- + California Academy of Sciences, Department of Vertebrate Zoology, **CA / USA**

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5

ASIA /

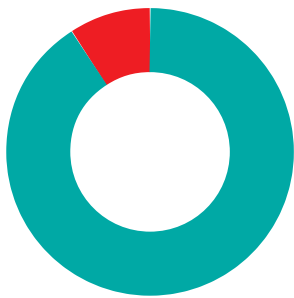
- + Centre for Biodiversity and Forest Studies, Madurai Kamaraj University, **Madurai / India**
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4

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- + CSIRO Plant Industry & Food Futures Flagship, **Adelaide / Australia**
- + Plant & Food Research Institute Oakland, **Auckland / New Zealand**
- + School of Agricultural and Wine Sciences, University of Wagga, **Wagga / Australia**
- + University of Newcastle, **New South Wales / Australia**
- + University of Otago, **Dunedin / New Zealand**

Research Projects



40 PROJECTS
funded by International Public Institutions

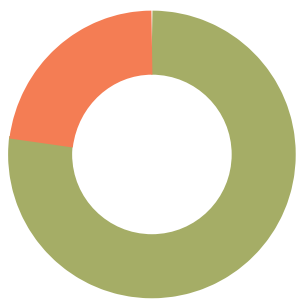
4 PROJECTS
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PUBLIC

26	4	2	1
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1	1	1	1
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1	1	1	1
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46	4	3	3	3
PROJECTS funded by / AUTONOMOUS PROVINCE OF TRENTO 32 of them are research lines funded by the Accordo di Programma	PROJECTS funded by / CARITRO FOUNDATION	PROJECTS funded by / MINISTRY FOR AGRICULTURAL AND FOREST POLICY	PROJECTS funded by / SICILY REGION	PROJECTS funded by / AGENZIA PROVINCIALE PER LA PROTEZIONE DELL'AMBIENTE (APPA)
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PROJECT funded by / PIEDMONT REGION	PROJECTS funded by / MINISTRY FOR RESEARCH AND HIGHER EDUCATION	PROJECTS funded by / MINISTRY FOR HEALTH	PROJECT funded by / AGENZIA PER L'AMBIENTE PROVINCIA DI BOLZANO	PROJECT funded by / UNIVERSITY OF SIENA
1		1	1	1
PROJECT funded by / CONSIGLIO NAZIONALE DELLE RICERCHE (CNR) - ISTITUTO PER LA VALORIZZAZIONE DEL LEGNO DELLE SPECIE ARBOREE (IVALSA)		PROJECT funded by / CONSORZIO DEL PARCO NAZIONALE DELLO STELVIO	PROJECT funded by / CAMERA DI COMMERCIO, INDUSTRIA ARTIGIANATO E AGRICOLTURA TRENTO	PROJECT funded by / VALLE DI SOLE COMMUNITY
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PROJECT funded by / CONSIGLIO DI RICERCA PER LA SPERIMENTAZIONE IN AGRICOLTURA - CENTRO DI RICERCA PER LA FRUTTICOLTURA (CRAFRU)		PROJECT funded by / AGER CONSORTIUM	PROJECT funded by / MUNICIPALITY OF TRENTO	

PRIVATE

2	1	1	1	1	1
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1	1	1	1	1	1
PROJECT funded by / DIAL SRL	PROJECT funded by / RAGAZZINI SRL	PROJECT funded by / TUSCANIA CONSORTIUM	PROJECT funded by / UNIONE ITALIANA VINI	PROJECT funded by / VITIS RAUSCEDO SCA	PROJECT funded by / PARMALAT RESEARCH CENTRE
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Affiliations



Society
Site
Member/s

A

American Association for the Advancement of Science (AAAS)

www.aaas.org

Azeddine Si-Ammour

American Geophysical Union

www.sites.agu.org

Emanuele Cordano

ASLO Association for the Sciences of Limnology and Oceanography

www.aslo.org/index.html

Nico Salmaso

Associazione Italiana di Agrometeorologia

www.agrometeorologia.it

Emanuele Eccel (member of the directive committee), Amelia Caffarra, Annalisa Di Piazza

Associazione Italiana di Oceanologia e Limnologia

www.aiol.info/home.htm

Giovanna Flaim, Monica Tolotti, Nico Salmaso (member of the directive committee), Leonardo Cerasino

Associazione italiana per l'informazione geografica libera

www.gfoss.it/drupal

Monica Fernanda Rinaldi

Associazione Teriologica Italiana

fauna.dipbsf.uninsubria.it

Francesca Cagnacci (elected member of the Counsel, 2010-2012 and 2012-2014).

E

Eco-Health Alliance

www.ecohealthalliance.org

Annapaola Rizzoli

European Chemoreception Research Organization

www.ecro-online.com

M. Luisa Demattè

European Geophysical Union

www.egu.eu

Annalisa Di Piazza

European Sensory Network

www.esn-network.com

Flavia Gasperi, Eugenio Aprea, Isabella Endrizzi, M. Luisa Demattè, Maria Laura Corollaro

European Society for Mathematical and Theoretical Biology (ESMTB)

www.esmtb.org

Roberto Rosà

European Society for Mathematical and Theoretical Biology (ESMTB)

www.esmtb.org

Roberto Rosà

G

German Botanical Society

www.deutsche-botanische-gesellschaft.de

Stefan Martens

Groupe Polyphenols

www.groupepolyphenols.com

Stefan Martens, Elisabete Carvalho

I

International Organisation for Biological Control of noxious animals and plants (IOBC)

www.iobc-wprs.org/about

Ilaria Pertot

International Biometrics Society

www.biometricsociety.org

Ron Wehrens, Pietro Franceschi

S

SIL International Society of Limnology

www.limnology.org

Nico Salmaso

Sociedad Latinoamericana en Percepción Remota y Sistemas de Información Espacial

www.selper.org

Monica Fernanda Rinaldi

Società Chimica Italiana

www.soc.chim.it

Leonardo Cerasino

Società di ortoflorofrutticoltura italiana- SOI

www.soihs.it

M. Stella Grando

Società Italiana di Biologia Evoluzionistica

www.sibe-iseb.it

Omar Rota Stabelli, Ulrike Obertegger

Società Italiana di Ecologia

www.ecologia.it

Nico Salmaso

Società Italiana di Genetica Agraria - SIGA

www.geneticagraria.it

M. Stella Grando, Riccardo Velasco, Claudio Moser

Società Italiana di Parassitologia (SOIPA)

www.soipa.it

Annapaola Rizzoli

Società Italiana di Patologia Vegetale

www.sipav.org

Nicola La Porta

T

The European Plant Science Organisation

www.epsoweb.org

Stefan Martens

The Systematics Association

www.systass.org

Omar Rota Stabelli

W

Wildlife Diseases Association (WDA USA)

www.wildlifedisease.org

Annapaola Rizzoli

Editorial committees of scientific journals



Journal
Site
Member/s

Advances in Oceanography and Limnology

www.tandfonline.com/toc/taol20/current

Nico Salmaso

Applied Vegetation Science, official journal of the International Association for Vegetation Science (IAVS)

eu.wiley.com/WileyCDA/WileyTitle/productCd-AVSC.html

Duccio Rocchini, Associate Editor

BMC Genomics

www.biomedcentral.com/bmcgenomics

Daniel James Sargent (Section Editor)

Bullettin of Faculty of Forestry della University of Belgrad

glasnik.sfb.bg.ac.rs/editorial_board.php

Nicola La Porta

Entomologia

Entomologia.pagepress.org

Gianfranco Anfora

Hystrix, the Italian Journal of Mammalogy

www.italian-journal-of-mammalogy.it/

Francesca Cagnacci

(elected member of the Editorial Committee)

International Journal of Parasitology:parasites and wildlife (Australia)

www.journals.elsevier.com/international-journal-for-parasitology-parasites-and-wildlife/

Annapaola Rizzoli

ISPRS International Journal of Geo-Information — Open Access Journal, Official journal of the International Society for Photogrammetry and Remoteensing

www.mdpi.com/journal/ijgi

Duccio Rocchini, Guest Editor

Italian Journal of Agrometeorology (field editor for "Phenology")

www.agrometeorologia.it/joomla/it/ija.html

Emanuele Eccel

Journal Geoinformatics FCE CTU, Prague

geoinformatics.fsv.cvut.cz/gwiki/Main_Page

Markus Neteler

Journal of Animal Biotelemetry

www.animalbiotelemetry.com/

Francesca Cagnacci

Journal of Limnology

www.jlimnol.it/index.php/jlimnol

Nico Salmaso

Journal of Vegetation Science, official journal of the International Association for Vegetation Science (IAVS)

eu.wiley.com/WileyCDA/WileyTitle/productCd-JVS.html

Duccio Rocchini, Associate Editor

Journal of Wildlife Diseases (USA)

www.jwildlifedis.org/

Annapaola Rizzoli

Mycology

www.tandf.co.uk/journals/TMYC

Nicola La Porta

Progress in Physical Geography, official journal of the Association of American geographers

ppg.sagepub.com/

Duccio Rocchini, Editorial Board

Recent Patents on Food, Nutrition & Agriculture

www.benthamscience.com/pfna/index.htm

Eugenio Aprea

The Open Agriculture Journal

www.benthamscience.com/open/toasj/index.htm

Eugenio Aprea

Phytopathologia mediterranea

www.fupress.net/index.php/pm

Ilaria Pertot

IOBC Bulletin

www.iobc-wprs.org/pub/index.html#bulletin

Ilaria Pertot

American Journal of Enology and Viticulture

ajevonline.org/

Riccardo Velasco

Plant Molecular Biology Reporter

www.springer.com/life+sciences/plant+sciences/journal/11105

Riccardo Velasco

Prizes

Prize
Institution
Name



Best Agrometeorological Paper 2012

Ass. It. di Agrometeorologia

Amelia Caffarra – Emanuele Eccel

Best Poster Prize

XXVth International Conference on Polyphenols, Florence, Italy

Antje Feller

FameLab 2012

Primo classificato alle selezioni di Trento

FameLab Italia

Emanuele Eccel

Premio Bagnaresi per miglior poster

SISEF – Società Italiana di Selvicoltura ed Ecologia Forestale

Elena Gottardini, Fabiana Cristofolini, Antonella Cristofori, M. Confalonieri, M. Ferretti

Premio giovani ricercatori

Società Italiana di Scienze Sensoriali

Nicola Pojer

Premio giovani ricercatori

Società Italiana di Scienze Sensoriali

Maria Laura Corollaro

Premio miglior poster SIGA 2011

Società Italiana di Genetica Agraria

Giulia Malacarne, Michele Perazzolli, Alessandro Cestaro, Lieven Sterck, Paolo Fontana, Yves Van de Peer, Roberto Viola, Riccardo Velasco, Francesco Salamini

Wildlife Publications Award 2012 / Outstanding Article

(Kie J.G., Matthiopoulos J., Fieberg J., Powell R.A., Cagnacci F., Mitchell M.S., Gaillard J.-M., Moorcroft P.R. 2010)

The Wildlife Society of America

Francesca Cagnacci

Norbert Gerbier-Mumm International Award 2012

World Meteorological Organization

Damiano Gianelle, Roberto Zampedri

Thesis completed by FEM



Name

University + Department

FEM Coordinator

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Leopold-Franzens Universität
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Gerardo Puopolo

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Mickael Malnoy

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Centro di Biologia Integrata
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Stefania Pilati

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Enologia
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Grando, Juri Battilana

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Costantini, M. Stella Grando

Valentini Chiara
Università di Trento
Dipartimento di Scienze e
Tecnologie biomolecolari
FEM Coordinator / M. Stella
Grando, Francesco Emanuelli

Articles published in scientific journals with **Impact Factor**

A / 27

<i>Agricultural and forest meteorology</i>	1
<i>Agriculture ecosystems & environment</i>	2
<i>Anaerobe</i>	1
<i>Analyst</i>	1
<i>Analytica chimica acta</i>	5
<i>Analytical & bioanalytical chemistry</i>	1
<i>Analytical & bioanalytical chemistry</i>	1
<i>Animal behaviour</i>	1
<i>Annals of microbiology</i>	3
<i>Annual review of phytopathology</i>	1
<i>Applied end environmental microbiology</i>	1
<i>Applied energy</i>	1
<i>Applied geography</i>	1
<i>Applied vegetation science</i>	1
<i>Aquatic sciences</i>	1
<i>Archives of virology</i>	2
<i>Arthropod-plant interactions</i>	1
<i>Australian journal of grape and wine research</i>	2

B / 27

<i>Behavioural brain research</i>	1
<i>Biocontrol science and technology</i>	1
<i>Biodiversity and conservation</i>	1
<i>Biogeosciences</i>	2
<i>Biological control</i>	2
<i>Biological journal of the Linnean society</i>	1
<i>Biology and fertility of soils</i>	1
<i>BMC Bioinformatics</i>	2
<i>BMC Evolutionary biology</i>	3
<i>BMC Genetics</i>	1
<i>BMC Genomics</i>	2
<i>BMC plant biology</i>	2
<i>Briefings in bioinformatics</i>	1
<i>British journal of nutrition</i>	3
<i>Bulletin of insectology</i>	4

C / 18

<i>Chemical physics</i>	1
<i>Chemical senses</i>	1
<i>Chemometrics and intelligent laboratory systems</i>	1
<i>Chemosensory perception</i>	1
<i>Chemosphere</i>	2
<i>Climate research</i>	4
<i>Community ecology</i>	2
<i>Computers & geosciences</i>	2
<i>Computers and electronics in agriculture</i>	1
<i>Crop protection</i>	1
<i>Cryptogamie algologie</i>	1
<i>Cytogenetic and genome research</i>	1

D / 2

<i>Diversity and distribution</i>	1
<i>Domestic animal endocrinology</i>	1

E / 32

<i>Ecohydrology</i>	2
<i>Ecological complexity</i>	1
<i>Ecological indicators</i>	4
<i>Ecology and Society</i>	1
<i>Environmental and experimental botany</i>	1
<i>Environmental management</i>	1
<i>Environmental modelling and software</i>	1
<i>Environmental pollution</i>	2
<i>Environmental research letters</i>	2
<i>Environmental science & technology</i>	1
<i>European biophysics journal</i>	1
<i>European biophysics journal with biophysics letters</i>	1

2011
2012*H* /₁₀

<i>European food research and technology</i>	1
<i>European journal of agronomy</i>	2
<i>European journal of cancer</i>	1
<i>European journal of forest research</i>	2
<i>European journal of lipid science and technology</i>	1
<i>European journal of nutrition</i>	3
<i>European journal of wildlife research</i>	1
<i>Evolutionary applications</i>	1
<i>Evolutionary biology</i>	1
<i>Experimental and applied acarology</i>	1

I /₂₀

<i>IEEE transactions on geoscience and remote sensing</i>	1
<i>Integrated environmental assessment and management</i>	1
<i>International dairy journal</i>	4
<i>International journal for parasitology</i>	2
<i>International journal of biometeorology</i>	2
<i>International journal of climatology</i>	1
<i>International journal of health geographics</i>	1
<i>International journal of mass spectrometry</i>	1
<i>International journal of obesity</i>	1
<i>International journal of remote sensing</i>	2
<i>Italian journal of animal science</i>	4

F /₁₇

<i>Food chemistry</i>	7
<i>Food control</i>	1
<i>Food microbiology</i>	2
<i>Food quality and preference</i>	2
<i>Forest ecology and management</i>	1
<i>Free radical biology and medicine</i>	1
<i>Freshwater biology</i>	3

J /₄₃*G* /₉

<i>Genes and nutrition</i>	1
<i>Genome biology and evolution</i>	1
<i>Genomics</i>	1
<i>Geoderma</i>	2
<i>Global biogeochemical cycles</i>	1
<i>Global change biology</i>	3

<i>Journal of agricultural and food chemistry</i>	8
<i>Journal of biogeography</i>	1
<i>Journal of cereal science</i>	1
<i>Journal of chemical ecology</i>	1
<i>Journal of chemometrics</i>	1
<i>Journal of chromatography</i>	2
<i>Journal of dairy science</i>	1
<i>Journal of economic entomology</i>	2
<i>Journal of environmental monitoring</i>	2
<i>Journal of experimental botany</i>	4

Articles published in scientific journals with **Impact Factor**

N /₉

<i>Journal of food composition and analysis</i>	3
<i>Journal of geophysical research</i>	2
<i>Journal of geophysical research-biogeosciences</i>	1
<i>Journal of limnology</i>	3
<i>Journal of mass spectrometry</i>	2
<i>Journal of natural products</i>	1
<i>Journal of paleolimnology</i>	1
<i>Journal of photogrammetry and remote sensing</i>	1
<i>Journal of phycology</i>	2
<i>Journal of proteome research</i>	1
<i>Journal of separation science</i>	1
<i>Journal of vector ecology</i>	1
<i>Journal of vegetation science</i>	1

<i>Natural product research</i>	1
<i>Nature genetics</i>	2
<i>Nature geoscience</i>	1
<i>Naturwissenschaften</i>	1
<i>Neural processing letters</i>	1
<i>New phytologist</i>	2
<i>Nucleic acid research</i>	1

O /₂

<i>Oikos</i>	2
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L /₃

<i>Landscape and urban planning</i>	1
<i>Landscape ecology</i>	1
<i>Letters in applied microbiology</i>	1

M /₁₀

<i>Metabolomics</i>	3
<i>Meteorological applications</i>	1
<i>Molecular biosystems</i>	1
<i>Molecular breeding</i>	3
<i>Molecular ecology</i>	1
<i>Molecular plant-microbe interactions</i>	1

P /₃₈

<i>Pest management science</i>	1
<i>Phycologia</i>	1
<i>Phytochemistry</i>	2
<i>Phytoparasitica</i>	1
<i>Phytopathology</i>	1
<i>Phytopatologia mediterranea</i>	2
<i>Planetary and space science</i>	1
<i>Plant and soil</i>	1
<i>Plant cell and environment</i>	1
<i>Plant cell, tissue, and organ culture</i>	1
<i>Plant growth regulation</i>	1
<i>Plant pathology</i>	1
<i>Plant physiology</i>	2
<i>Planta</i>	1
<i>PloS ONE</i>	14
<i>Postharvest biology and technology</i>	2
<i>Proceedings of the national academy of sciences</i>	2

2011

2012

<i>Proceedings of the Royal Society B. Biological sciences</i>	1
<i>Progress in physical geography</i>	1
<i>Proteomics</i>	1

R /₁₃

<i>Rapid communications in mass spectrometry</i>	5
<i>Remote sensing of environment</i>	3
<i>Review of palaeobotany and palynology</i>	1
<i>River research and applications</i>	3
<i>Russian journal of genetics</i>	1

S /₅

<i>Sensors</i>	2
<i>Sensors and actuators B: Chemical</i>	1
<i>South african journal of enology and viticulture</i>	1
<i>Systematic and applied microbiology</i>	1

T /₂₂

<i>Talanta</i>	1
<i>The plant journal</i>	2
<i>Theoretical and applied climatology</i>	1
<i>Theoretical and applied genetics</i>	1
<i>Theoretical ecology</i>	1
<i>Tr-AC trends in analytical chemistry</i>	2
<i>Tree genetics and genomes</i>	7
<i>Trees-structure and function</i>	1
<i>Trends in ecology and evolution</i>	1

<i>Veterinary parasitology</i>	1
<i>Virus research</i>	1
<i>Vitis</i>	3

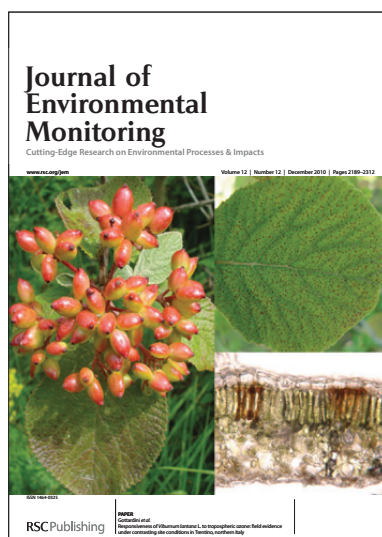
W /₁

<i>World journal of microbiology and biotechnology</i>	1
--	---

Z /₁₀

<i>ZooKeys</i>	1
<i>Zoologica scripta</i>	1
<i>Zoological studies</i>	1
<i>Zootaxa</i>	7

Impact Factor Journal covers focussed on CRI research



Journal of environmental monitoring Vol. 12, number 12, Dec 2010, ISSN 1464-0325

The cover of this issue refers to the effects of tropospheric ozone on vegetation. The research was led by FEM in collaboration with the University of Florence and Terra Data environmetrics.



Philosophical transactions of the Royal Society, vol. 365, no. 1550, ISSN 0962-8436

The cover of the Theme Issue pictures an African Wild dog (Lycaon pictus) pack at Mashatu Reserve, Botswana; the two interacting individuals wear GPS collars, a technology that has revolutionised animal ecology studies. The Theme issue is the outcome of a workshop organised by FEM, in cooperation with USA and Canada.



International Journal for Parasitology, Vol. 42, Issue 4, apr. 2012, ISSN 0020-7519

The cover of this issue pictures F10, GPS-GSM collar, and yearling (Capreolus capreolus) in Viote del Monte Bondone, Trento, Italy. Roe deer are feeding hosts for the tick Ixodes ricinus. The paper was funded by the FP6 European Project EDEN (FEM PI A. Rizzoli) and PAT project BECOCERWI (PI F. Cagnacci) and produced in cooperation with Slovakia and Finland.



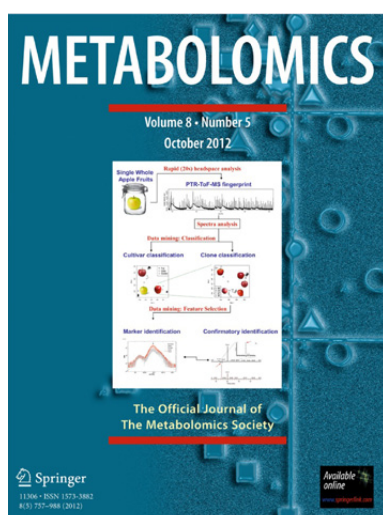
Nature Genetics, vol. 43, no. 2, Feb 2011

*This journal cover focusses on the results of an international effort to sequence the genome of the woodland strawberry, *Fragaria vesca*, in which FEM researchers played a significant role. The project was the first to sequence a nuclear genome using only second generation (short-read) sequencing technology*



Nature Genetics, vol. 42, no. 10, Oct 2010

The cover of this issue refers to the sequencing and analysis of the apple genome, cv. Golden Delicious. The project was led by FEM within an international collaboration with partners from USA, New Zealand, France, Italy, Belgium. Sequencing of the apple genome has increased a thousand-fold our knowledge of this important agricultural plant, in particular its nutritional properties, environmental impact, exploration of biodiversity, phylogenetic and evolutionary studies.



Metabolomics, vol. 8, no. 5, Oct 2012

The innovative methodological approach proposed by FEM for rapid characterization of apple by Direct Injection Mass Spectrometry has been recently published in "Metabolomics" and chosen for the cover of the October 2012 journal Issue.

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Magnago Pierluigi / **Reponsabile** the Rosaceae Breeding Technology Platform

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Sargent Daniel James / **Head of** Rosaceae Applied Genomics Research Group

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Paolini Mauro **
Pojer Elisa **

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Pedrotti Sonia *
Deromedi Marco *
Ress Lorena *

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Beckner **
Ahrar Mastaneh **
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Carafa Ilaria **
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Lotti Cesare **

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Criscuoli Irene **

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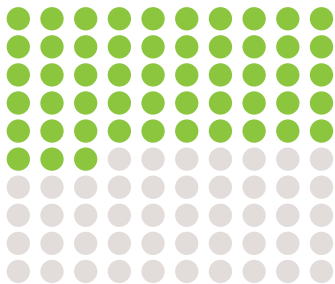
Rosà Paola **

Internships

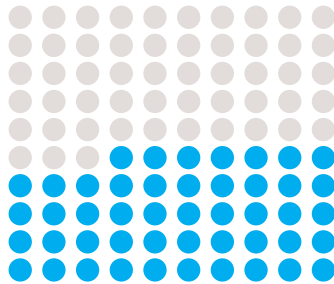
Baronti Silvia **
Genesio Lorenzo **
Martinez Cristina **
Vaccari Francesco Primo **

Staff Data

Male **53%** [161]



Female **47%** [140]

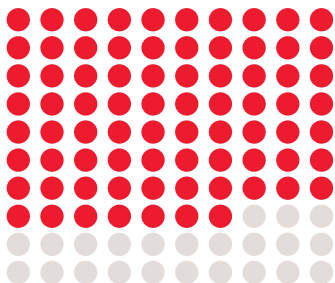


Permanent position **43%** [129]

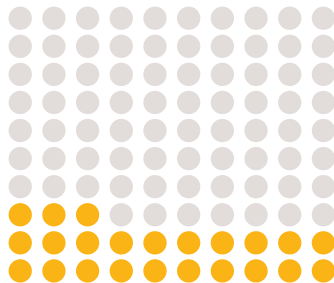
Temporary position **57%** [172]

Holding a PhD **44%** [131]

Italian **77%** [233]

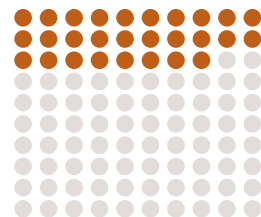


Foreign **23%** [68]

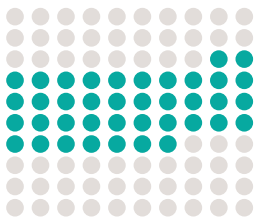


from **33**
different countries

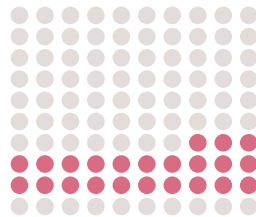
Less than 30 years old
28% [84]



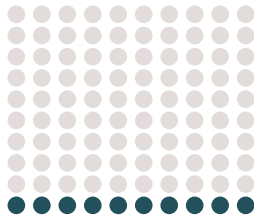
30 - 40 years old
39% [116]



41 - 50 years old
23% [70]



Over 50 years old
10% [31]



REPORT 2011 / 2013
Research and Innovation Centre
Fondazione Edmund Mach

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