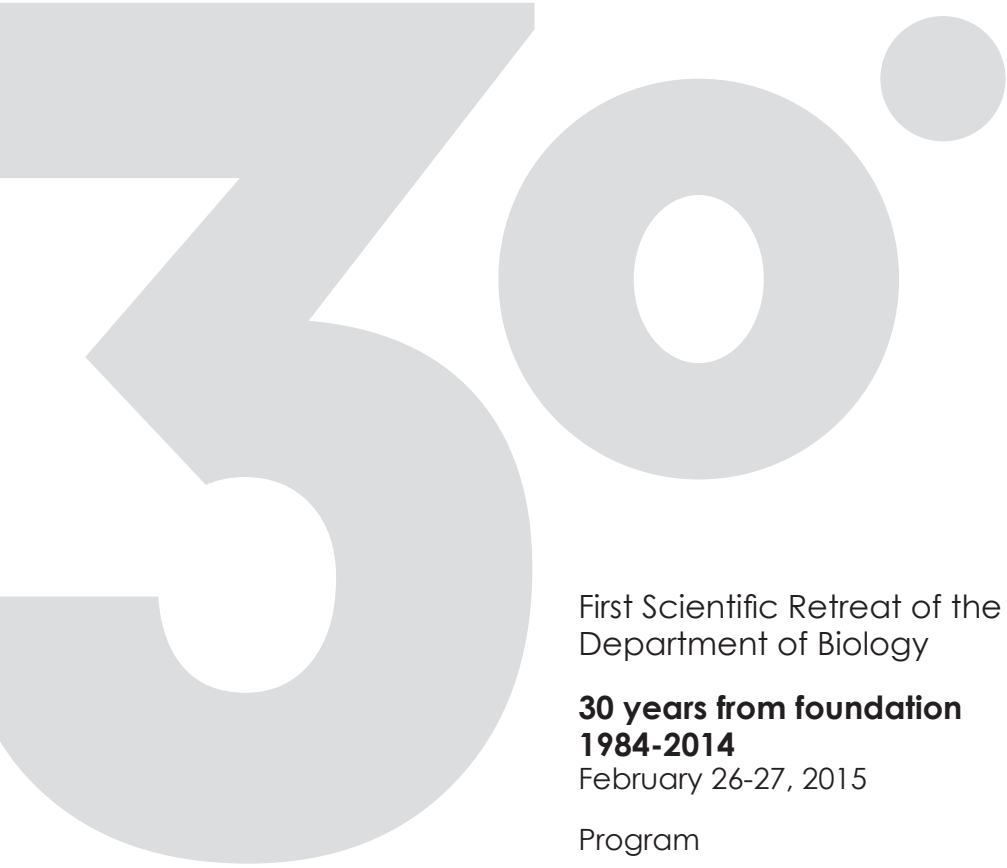


First Scientific Retreat of the Department of Biology

30 years from foundation
1984-2014
February 26-27, 2015

Program

Thursday, February 26

13.00 Registrazione, apertura
13.20 Saluto del Prof. Gerolamo Lanfranchi, Direttore del Dipartimento di Biologia
13.25 Proiezione
13.45 Saluto del Prof. Giuseppe Zaccaria, Magnifico Rettore dell'Università di Padova

Session 1 – Model organisms to study cell signalling - Chairman: Luca Scorrano

14.00 - 14.45 Conference
Massimo Zeviani, MRC Mitochondrial Biology Unit and University of Cambridge, UK
New mitochondrial disease genes and mechanisms

- 14.50 - 15.10 Presentation 1
  Tatiana Varanita
  The mitochondria shaping protein Optic Atrophy 1 counteracts cellular damage and controls metabolism in vivo
  Research Unit: Biochemistry, Biology and Physiopathology of Mitochondria
- 15.10 - 15.30 Presentation 2
  Luigi Leanza
  Selective killing of cancer cells by modulation of ion channels: from in vitro to in vivo models
  Research Unit: Biochemistry
- 15.30 - 15.50 Presentation 3
  Nicola Franchi
  Innate immunity in Tunicates
  Research Unit: Developmental Biology and Morphogenesis
- 15.50 - 16.10 Presentation 4
  Andrea Vettori
  Generation and application of transgenic reporter lines to study signaling pathway in zebrafish
  Research Unit: Regulative Biology and Translational Genetics
- 16.10 - 16.30 Presentation 5
  Gabriella Mazzotta
  Cryptochrome and the temporal control of visual plasticity in Drosophila melanogaster
  Research Unit: Neurogenetics and Chronobiology

16.30 - 17.00 coffee break

Session 2 – Evolution & Ecology - Chairman: Andrea Pilastro

- 17.00 - 17.20 Presentation 6
  Telmo Pievani
  Two kinds of exaptation
  Research Unit: Philosophy and History of Life Sciences
- 17.20 - 17.40 Presentation 7
  Clelia Gasparini
  Sex in the tank: what guppies can tell us about sexual selection and sexual conflict before and after mating
  Research Unit: Ecoetology and Evolutionary Biology
- 17.40 - 18.00 Presentation 8
  Leonardo Congiu
  Sturgeon conservation: from ex-situ planning to next-generation sequencing
  Research Unit: Molecular Ecology
- 18.00 - 18.20 Presentation 9
  Gianfranco Santovito
  New perspectives in the study of the antioxidant defences in Antarctic fish: the peroxiredoxins

Research Unit: Environmental Physiology and Experimental Zoology

- 18.20 - 18.40 Presentation 10
  Marco Munari
  Combined effects of seawater acidification and other stressors in marine bivalves at different stages of their life-history
  Research Unit: Marine Ecology
- 18.40 - 19.00 Presentation 11
  Maurizio G. Paoletti
  Sustainable use of biodiversity? Which food, which strategies to feed the 9 billion humans in 2050?
  Research Unit: Ecology of Biodiversity and Sustainability

19.00 - 19.30 drinks & snacks

Friday, February 27

Session 3 – Physiopathology & Molecular genetics - Chairman: Rodolfo Costa

- 08.30 - 08.50 Presentation 12
  Elena Stocco
  In vitro assessment of a novel composite scaffold for articular cartilage restoration
  Research Unit: Biology of Endothelial Cells and Regeneration
- 08.50 - 09.10 Presentation 13
  Elisa Palumbo
  Understanding DNA replication dynamics in the mammalian genome, and in loci specifically involved in genetic instability
  Research Unit: Cytogenetics and Molecular Genetics
- 09.10 - 09.30 Presentation 14
  Giovanni Vazza
  Deciphering the genetic landscape of Schizophrenia and Bipolar Disorder: genomic approaches on a population-based cohort.
  Research Unit: Human Molecular Genetics
- 09.30 - 09.50 Presentation 15
  Marco Bisaglia
  Dopamine and oxidative stress in Parkinson's disease: is an antioxidant therapy valuable?"
  Research Unit: Biophysics, Molecular and Cellular Physiology
- 09-50 - 10.10 Presentation 16
  Tommaso Pozzobon
  Angiogenesis in secondary syphilis: role of the bacterioferritin TpF1, antigen of Treponema pallidum
  Research Unit: General Pathology

10.10 - 10.40 coffee break

Session 4 – Genomics & Bioinformatics – Chairman: Giorgio Valle

10.45 - 11.30 Conference
Stefano Gustincich, Neurobiology sector, SISSA, Trieste
SINEUPS: a new functional class of natural and synthetic antisense long non-coding RNAs that activate translation

- 11.30 - 11.50 Presentation 17
  Francesco Filippini
  From bioinformatic design to regenerative medicine: enhanced neuronal differentiation combining biomimetic peptides and nanocomposite scaffolds
  Research Unit: Molecular Biology
- 11.50 - 12.10 Presentation 18
  Nicola Vitulo
  A deep survey of alternative splicing in grape

Research Unit: Genomics and Bioinformatics

- 12.10 – 12.30 Presentation 19
  Francesco Chemello
  MiRNA-mRNA network at single cell level reveal the role of specific miRNAs in the regulation of metabolism of muscle fibers
  Research Unit: Functional Genomics
- 12.30 - 12.50 Presentation 20
  Maddalena Mognato
  MicroRNAs in the cellular response to stress
  Research Unit: Cell Biology

13.00 - 14.00 lunch

Session 5 – Plant Sciences – Chairman: Giorgio Casadoro

14.15 - 15.00 Conference
Lucia Colombo, Department of Biosciences, University of Milano
From Ovule to Seed: the female contribution

- 15.00 - 15.20 Presentation 21
  Michela Zottini
  Organelles as critical players in plant cell communication network
  Research Unit: Plant Physiology and Molecular Biology
- 15.20 - 15.40 Presentation 22
  Alessandro Alboresi
  Molecular analysis of Nannochloropsis gaditana for the production of biofuels and high added value molecules
  Research Unit: Photosynthesis and Plant Biotechnology
- 15.40 - 16.00 Presentation 23
  Lorella Navazio
  Calcium-based communications in plant root endosymbioses: the microorganism perspective
  Research Unit: Plant Cell Biology
- 16.00 - 16.20 Presentation 24
  Livio Trainotti
  Molecular and hormonal regulation of fleshy fruit development and ripening
  Research Unit: Botany

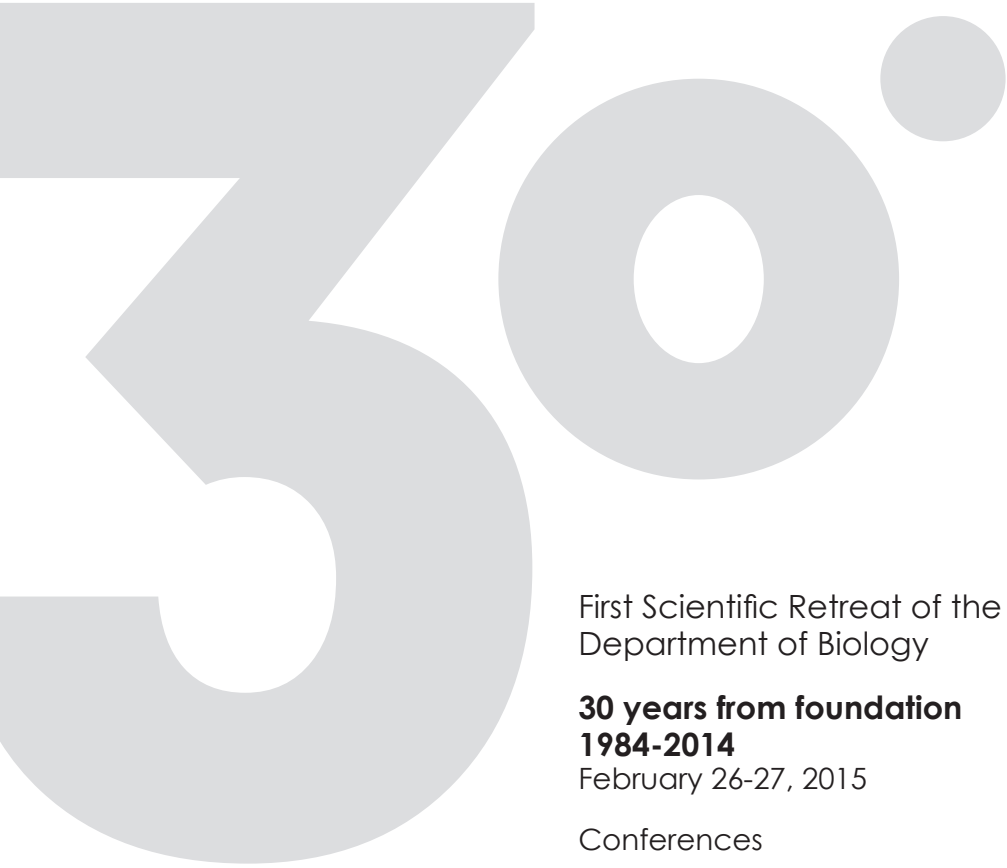
16.30 - 17.00 coffee break

Session 6 – Systematics & Phylogeny – Chairman: Alessandro Minelli

- 17.00 - 17.20 Presentation 25
  Katia Sciuto
  Barcoding P.A.T.H.S.: DNA barcodes for reference plant samples
  Research Unit: Biology and Systematics of Algae and Higher Plants
- 17.20 - 17.40 Presentation 26
  Moreno Clementi
  A multidisciplinary approach to the study of the collection of Roberto de Visiani (1800-1878), Praefectus of the botanical garden of Padova
  Research Unit: Palynology and Archaeobotany
- 17.40 - 18.00 Presentation 27
  Lucio Bonato
  Geophilomorph centipedes: diversity, phylogeny and evolution
  Research Unit: Evolutionary Biology of Arthropods

Concluding remarks

18.10 - 18.30 drinks & snacks



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Conferences

Massimo Zeviani, MRC Mitochondrial Biology Unit and University of Cambridge, UK
New mitochondrial disease genes and mechanisms

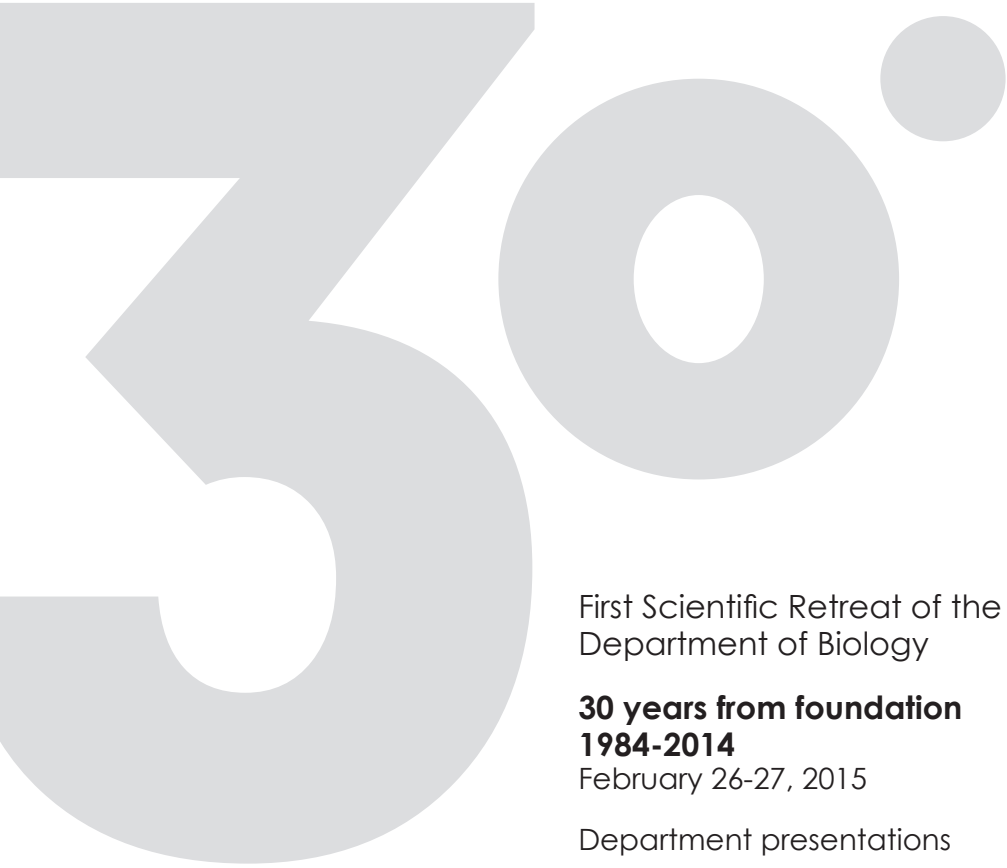
Abstract:
Mitochondria are the major source of ATP that is synthesized by the respiratory chain through the process of oxidative phosphorylation (OXPHOS), a complex biochemical process carried out through the dual control of physically separated, but functionally interrelated, genomes, nuclear and mitochondrial DNAs. The genetic and biochemical intricacy of mitochondrial bioenergetics explains the extreme heterogeneity of mitochondrial disorders, a group of highly invalidating human conditions, for which no effective treatment is nowadays available. In addition to bioenergetic failure, other mechanisms are probably predominant in the pathogenesis of specific syndromes, such as alterations of cellular redox status, the production of reactive oxygen species, compromised Ca2+ homeostasis, mitochondrial protein and organelle quality control, and mitochondrial pathways of apoptosis. By investigating selected families and patients, we have identified several new disease genes, each responsible of distinct defects of the respiratory chain, mtDNA metabolism, or both. Recently published and still unpublished findings will be presented and discussed. Structural analysis and the creation of ad hoc recombinant lines in yeast, flies, and mice have allowed us to dissect out the molecular consequences of the ablation or defects of some of these proteins, and their physical status in normal and disease conditions. These models have also been exploited to implement experimental therapeutic strategies, based on gene and cell replacement, or pharmacological control of mitochondrial biogenesis.

Stefano Gustincich, Neurobiology sector, SISSA, Trieste
SINEUPS: a new functional class of natural and synthetic antisense long non-coding RNAs that activate translation

Abstract:
ENCODE and FANTOM projects have been proving that the majority of the mammalian genome is transcribed generating a vast repertoire of transcripts that includes mRNAs, long non-coding RNA (lncRNA) and repetitive sequences, such as SINEs (short interspersed nuclear element) and LINE (long interspersed nuclear element).
Analyzing the non-coding part of the transcriptome, we have identified a group of natural and synthetic antisense non-coding RNAs that activate translation of their sense protein-encoding genes. These molecules have been named SINEUPs since their function requires the activity of an embedded inverted SINEB2 sequence to UP-regulate translation. SINEUPs are thus the first example of gene-specific inducers adding an unexpected layer to post-transcriptional gene regulation and providing a versatile tool to increase protein synthesis of potentially any gene of interest.

Lucia Colombo, Department of Biosciences, University of Milano
From Ovule to Seed: the female contribution

Abstract:
Ovule development is characterized by the transition from the sporophytic (diploid) to the gametophytic (haploid) phase and terminates in the formation of the seed. Therefore, the ovule can be considered the intermediate between the parental sporophyte and the next generation.
My group has in the past 15 years focused on the analysis of regulatory pathways that control the development of ovules. Interestingly, and somehow a bit unexpected, our study of key regulators that control ovule development have brought us to the identification of genes that are important for the fertilization process and those that control seed development. This intriguing female network of interactions will be presented during my presentation.



First Scientific Retreat of the Department of Biology

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Department presentations

Presentation 1

Tatiana Varanita

The mitochondria shaping protein Optic Atrophy 1 counteracts cellular damage and controls metabolism in vivo

Research Unit: Biochemistry, Biology and Physiopathology of Mitochondria

Abstract:
Mitochondrial morphology changes occur during apoptosis and autophagy, but whether they are relevant in vivo for tissue response to damage is unclear. Today we will discuss our recent results that place the inner mitochondrial membrane shaping protein Optic atrophy 1 (OPA1) at the crossroad between tissue damage, intermediate metabolism and adipogenesis. Targeted insertion of a transgenic single copy of Opa1 isoform 1 in a permissive X chromosome locus did not interfere with mouse development, but protected from muscular atrophy, ischemic heart and brain damage, as well as from hepatocellular apoptosis. Notably Opa1tg mice were leaner, displayed improved OGTT and IGTT and showed accumulation of beige fat. Moreover, the offspring from crosses of a constitutive knockout for the structural complex I component Ndufs4 (Ndufs4-/-), as well as of a muscle-specific conditional knockout for the complex IV assembly factor Cox15 (Cox15sm/sm) with Opa1 transgenic (Opa1tg) mice were clinically and biochemically improved. Conversely conditional inducible Opa1 skeletal muscle ablation resulted in muscular atrophy and elicited a systemic IGF-1 driven catabolic response. Our results indicate that the OPA1-dependent cristae remodeling pathway is a crucial, targetable determinant of metabolism and tissue damage in vivo.

Presentation 2

Luigi Leanza

Selective killing of cancer cells by modulation of ion channels: from in vitro to in vivo models

Research Unit: Biochemistry

Abstract:
Ion channels are emerging oncological targets. In particular, potassium-selective channels show a de-regulated expression in different tumor cells/tissues compared to healthy ones, representing thus possible targets for the development of new chemotherapeutic drugs. Furthermore, pharmacological targeting of ion channels in mitochondria proved to be a promising strategy, in accordance with the essential role of ion channels for the regulation of bioenergetics in these organelles and with the crucial role of mitochondria in apoptotic signaling.
Pharmacological inhibition of the a mitochondrial potassium channel (mtKv1.3) by membrane permeant blockers, Psora-4, PAP-1 and clofazimine, indeed triggered apoptotic cell death in different cancer cell lines, even in the absence of Bax and Bak, by inducing mitochondrial membrane potential depolarization, production of mitochondrial ROS and release of cytochrome c. Apoptosis upon incubation with the drugs did not occur when expression of Kv1.3 was downregulated by siRNA.
Importantly, the Kv1.3 inhibitor clofazimine, a drug already used in clinic to treat leprosy and autoimmune diseases, reduced melanoma volume up to 90% compared to the untreated mouse in an orthotopic mouse melanoma model. Furthermore, Psora-4, PAP-1 and clofazimine were able to selectively kill also primary Chronic Lymphocytic Leukemia B cells (B-CLL), without affecting normal blood cells of the same patients and independently of the currently used prognostic factors. An increased ROS production together with an increased Kv1.3 expression in B-CLL cells seems to account for the selective apoptosis-inducing ability of the drugs.
Recently, we obtained promising in vivo data also in a Pancreatic Ductal Adenocarcinoma (PDAC) mouse model: treatment of mice with clofazimine reduced PDAC tumor weight by 50%.
Since membrane permeant Kv1.3 inhibitors are characterized by poor water solubility, in order to increase their solubility as well as to increase their bioavailability, we have recently synthesized new PAP-1 derivatives. In vitro experiments using different cancer cell lines demonstrate the ability of these novel derivatives to kill tumor cells at significantly lower concentrations with respect to the precursor, still maintaining the specificity toward Kv1.3-expressing cells. The newly synthesized derivatives have been

tested also ex-vivo (B-CLL cells) and in vivo tumor models, yielding very promising results, i.-e. almost complete elimination of the tumor mass without affecting healthy tissues and the immune system.

Reference:

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Presentation 3

Nicola Franchi

Innate immunity in Tunicates

Research Unit: Developmental Biology and Morphogenesis

Abstract:

Our interest in the evolution of immunity led us to study the molecular mechanisms and the behaviour of immunocytes in invertebrates phylogenetically related to vertebrates. Our study aims to explain how animals, adapted to various environmental conditions, evolved different strategies to face non-self. We are also interested to understand how specific molecules of innate immunity changed their functions and structures in the evolution of chordates.

Tunicates are good model organisms for this kind of research as they are invertebrate chordates representing the sister group of vertebrates. Ascidians, in particular, share with vertebrates, many of the innate processes which anticipate the adaptive responses. In addition, lacking an adaptive immunity, they represent simple model organisms for the study of chordate innate immunity. Our recent investigations on tunicate immunity allowed us to describe the role of immunocytes in scavenging of reactive oxygen species and in toxic metals detoxification (Ferro et al., 2013; Franchi e Ballarin, 2013; Franchi et al., 2014a; 2011a), the immunomodulatory activity of soluble lectins (Franchi et al., 2011b) and the presence of a complement system much more complex than usually supposed for invertebrates (Franchi e Ballarin, 2014). Our results are interesting non only for basic general knowledge (Franchi et al., 2014b; 2013) but can suggest possible applications in the sanitary field.

References:
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Presentation 4

Andrea Vettori

Generation and application of transgenic reporter lines to study signalling pathway in zebrafish

Research Unit: Regulative Biology and Translational Genetics

Abstract:
In the last years, we have seen the emergence of different tools that have changed the face of biology from a simple modeling level to a more systematic science. The zebrafish embryo is one of the living models in which, after germline transformation with reporter protein-coding genes, specific fluorescent cell populations can be followed at single-cell resolution. Embryo and larval transparency, screening properties and transgenic manipulability, make zebrafish an ideal tool for analytical screenings and analysis of pathway reporters. For this reasons, we recently took advantage from these characteristics to developed a number of transgenic zebrafish transgenic lines specific for reporting the activity of signaling pathways such as Tgf-beta, Stat3, Hif-1 and Hippo. These genetically modified animals are individuals in which time lapse analysis, digital imaging quantification and genetic and pharmacological knock-down can be performed in specific times and/or tissues. In particular with these multifaceted genetic and cellular approaches we dissected in living embryos, specific molecular interactions between different signaling pathway, allowing us to identify previously unknown functions of this important regulators of embryonic development.

References:
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Presentation: 5
Gabriella Mazzotta
Cryptochrome and the temporal control of visual plasticity in Drosophila melanogaster
Research Unit: Neurogenetics and Chronobiology

Abstract:
Living organisms show daily rhythms in a wide variety of functions, from gene expression to physiology and behaviour. These rhythms are generated by timekeeping mechanisms that allow them to anticipate the cyclic fluctuations of the environment and not passively respond to them. In animals, the main circadian pacemaker is located in the brain and organizes the overall behavioural rhythms yet molecular oscillatory systems are present also in different peripheral tissues, where they temporally control the specific functions of these structures. One of such examples is the visual system, a highly developed structure that not only has evolved to match with organisms' needs, for example in terms of feeding habits and light environments, but has achieved a high plasticity in order to optimize the visual ability in the daily fluctuations of lighting conditions.
In Drosophila melanogaster a functional circadian clock in the visual system is important to control visual coding efficiency and optimize vision under different light intensity regimes. We have observed that the diurnal rhythmicity of two different visual behaviors, electroretinogram (ERG) and optomotor turning response, is no longer maintained in flies lacking the circadian photoreceptor Cryptochrome (dCRY) and the wild-type phenotype is rescued when dCRY is selectively expressed in the photoreceptor cells. dCRY interacts with the components of Drosophila visual cascade by binding INAD, the scaffolding protein that organizes the phototransduction complex, and we have hypothesized that this interaction could result in a circadian modulation of the activity of the visual cascade components. Moreover we have recently observed that dCRY interacts also with Bruchpilot (BRP), a scaffolding protein localized on the membrane of the presynaptic active zone of the lamina (the first optic neuropil of the fly's optic lobe). Both the formation of the presynaptic T-Bars and the BRP abundance at this structure show circadian variation, resulting in daily rhythms in the morphology and physiology of neurons, important in the visual plasticity. These results suggest that dCRY could modulate circadian plasticity in flies at two different levels: on the functionality of the visual cascade components and also on the morphology and physiology of the visual structures.

References:

- Mazzotta G, Rossi A, Leonardi E, Mason M, Bertolucci C, Caccin L, Spolaore B, Martin AJ, Schlichting M, Grebler R, Helfrich-Förster C, Mammi S, Costa R, Tosatto SC (2013) Fly cryptochrome and the visual system. Proc Natl Acad Sci USA 15, 6163-6168.

Presentation: 6
Telmo Pievani
Two kinds of exaptation
Research Unit: Philosophy and History of Life Sciences

Abstract:
Paleontologists Stephen J. Gould and Elisabeth Vrba introduced the term "ex-aptation" with the aim of improving and enlarging the scientific language available to researchers studying the evolution of any useful character, instead of calling it an "adaptation" by default. Exaptation is neither a "saltationist" nor an "anti-Darwinian" concept and, since 1982, has been adopted by many researchers in evolutionary and molecular biology, as well as particularly in human evolution. In our talk, we firstly analyze the meaning of the term "exaptation", the possible operationalization of this concept and we identify six ways to test "adaptive vs. exaptive" evolutionary hypotheses (Pievani T., E. Serrelli 2011). Then, we differentiate two kinds of exaptation: 1) functional shift, i.e. the re-use by natural selection of a structure with previously different functions; 2) functional co-optation from non-adaptive structures ("spandrels") (Pievani & Serrelli 2011, quoted by Barve & Wagner, in Nature, Aug. 2013, and by Tecumseh Fitch in 2012). Finally, we comment on the benefits of an "extended taxonomy of fitness" in studies concerning human evolution.

Specifically, we will focus on the issue of human language evolution, stressing out the major role of the exaptive mechanisms matched with a mosaic evolution model.

References:

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Presentation 7

Clelia Gasparini

Sex in the tank: what guppies can tell us about sexual selection and sexual conflict before and after mating

Research Unit: Ecoetology and Evolutionary Biology

Abstract:
Female sexual promiscuity is a widespread phenomenon in nature, yet the evolutionary consequences of the competition among males to fertilize the same batch of eggs have not been fully appreciated. These include specific adaptations in males and females which generate the potential for an evolutionary conflict between the sexes. Guppies (Poecilia reticulata) are small viviparous fish with internal fertilization which represent an ideal system to investigate these processes as male and female interactions can be analyzed in laboratory and natural conditions, and can be experimentally manipulated from the stage of mate choice to that of male and female sperm storage until fertilization.

References:

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Presentation 8

Leonardo Congiu

Sturgeon conservation: from ex-situ planning to next-generation sequencing

Research Unit: Molecular Ecology

Abstract:

The Research Unit of Molecular Ecology among various lines of research, is studying the conservation genetics of sturgeon, the animal group with the highest risk of extinction, as identified in the list produced by the International Union for the Conservation of Nature (IUCN). Studying these fishes leads to the possibility of exploring a variety of research themes, from basic research to the development of methods and protocols with strong applicative value. Some of the exploitable themes are: i) strategies for the management of residual genetic variability through the development of ex-situ crossing programs, ii) studies finalized to the reintroduction of locally extinct species, iii) the development of analytical protocols for the detection of poliploidity iv) the identification of acive transposable elements in the genome of these animals that can be considered as living fossils, v) the search and establishment of forensic markers also through next-geretation sequencing technologies.

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Presentation 9

Gianfranco Santovito

New perspectives in the study of the antioxidant defences in Antarctic fish: the peroxiredoxins

Research Unit: Environmental Physiology and Experimental Zoology

Abstract:
Peroxiredoxins (Prdxs) are a family of small (22 – 27 kDa) non-selenium peroxidases that are able to reduce hydrogen peroxide, organic hydroperoxides and peroxynitrite, thus representing a class of important antioxidant enzymes in many animal taxa. These enzymes protect cells against oxidative stress, acting together with other components, both enzymatic and non-enzymatic, of the antioxidant cell system. It is well known that this system is the first line of defense in cell protection against reactive oxygen species (ROS), which production can easily incremented in many physiological, pathological and environmental conditions. Antarctic marine environment is characterized by increased oxygen concentration, correlated to low temperature of waters (-1.9°C). In these conditions, ROS formation is favored and Antarctic organisms evolved an efficient antioxidant system.
In the present work we described the molecular characterization of five Prdx isoforms in *Trematomus bernacchii*, a teleost widely distributed in many areas of Antarctica, that plays a pivotal role in the Antarctic food chain. The obtained nucleotide and amino acid sequences were analyzed by multiple alignment comparison with orthologous sequences from other fish, and phylogenetic trees were build using the Bayesian inference and maximum likelihood methods. The expression of these genes in different tissues (liver, muscle, gills, spleen and heart) was studied by both biomolecular and biochemical approaches, also in relation to the expression of other antioxidant enzymes, such as superoxide dismutase and glutathione peroxidase.
The obtained results are the first data on Prdx of Antarctic fish, and represent a further contribution to the knowledge of antioxidant system evolution in the Antarctic teleost, animal evolved under a strong risk of oxidative stress.
In addition, these expression data represent the starting point for a research project, funded by the Italian Program for Antarctic Research (PNRA), which is aimed to investigate the physiological responses of these organisms to temperature changes, in a perspective of Global Warming. This project started with the XXIX Italian Antarctic Expedition (2013-2014) and involves two Italian universities (the University of Padova and the University of Calabria) and the IBP-CNR center of Naples.

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Presentation 10
Marco Munari
Combined effects of seawater acidification and other stressors in marine bivalves at different stages of their life-history
Research Unit: Marine Ecology

Abstract:
Increasing atmospheric concentration of CO_2, produced by human activities is responsible for the progressive acidification of oceans. Ocean acidification (OA) may influence the ability of marine organisms to produce calcareous structures, at the same time influencing physiological responses and growth. But OA is not the only stressor marine organisms have to face. OA could alter the susceptibility to changes in other environmental parameters (such as temperature and salinity) or to pollutants. During the last five years we have been studying the combined effect of OA and other stressors in marine bivalves at different stages of their life history. The exposure to different combinations of pH, temperature and salinity values influenced immune, biochemical and physiological parameters in the adults of *Mytilus galloprovincialis* and *Chamelea gallina* (Matozzo V et al 2012 and 2013, Chinellato et al 2010, Range P et al 2014), although the variation pattern varied depending on the species and the tissue analyzed. A long-term exposure to different pH values also demonstrated that OA affected the juveniles of the two species,

by altering their normal physiological rates, reducing survival and growth, and promoting severe shell damage (Chinellato et al 2010, Range P et al 2014). Overall, between the two species, *C. gallina* was less tolerant than *M. galloprovincialis* to the stress conditions considered.

To verify the hypothesis that OA alter marine organism susceptibility to pollutants, the combined effects of seawater CO_2-driven acidification and the emerging contaminant diclofenac (a non-steroidal anti-inflammatory drug) were investigated in *M. galloprovincialis* and in the clam *Ruditapes philippinarum*. In adult bivalves, immune and oxidative stress-related parameters showed to be influenced mostly by pH than diclofenac or their interaction (Munari M et al 2012). Conversely, in clam larvae, the most detrimental effects on survival and growth were observed under acidified condition in the presence of diclofenac. Our results highlighted the need for further research aimed to understand the effects of a variety of simultaneously occurring environmental stressors on the entire life-cycle of marine bivalves to develop predictive capabilities and response strategies.

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Presentation 11

Maurizio G. Paoletti

Sustainable use of biodiversity? Which food, which strategies to feed the 9 billion humans in 2050?

Research Unit: Ecology of Biodiversity and Sustainability

Abstract:

New Foodwebs? Or new more efficient strategies to afford a crowded world? Our research focus is biodiversity as the scarcely explored resource of the planet and the strategies matured in traditional societies to use non-conventional species. Bacteria, Fungi wild plants and small animals, especially invertebrates, are the innovative drivers of sustainability. At the same time the current foodwebs need a robust evaluation and control using appropriate bio-indicators.

Presentation 12

Elena Stocco

In vitro assessment of a novel composite scaffold for articular cartilage restoration

Research Unit: Biology of Endothelial Cells and Regeneration

Abstract:

Introduction. Cartilage lesions are generally believed to progress to severe forms of osteoarthritis

(Giovannini et al., Eur Cell Mater. 2010; Harris et al., J Bone Joint Surg Am. 2010), leading to pathologic changes in the joints with consequent pain, inflammation and functional disability (Farr et al., Open Orthop J. 2013; Yang et al., PLoS One 2013). The poor regenerative potential of cartilage and the unsatisfactory current clinical therapies have led to the search of strategies providing solutions to the treatment of focal defects (Archer et al., J Anat. 2006; Nesic et al., Adv Drug Deliv Rev. 2006). An emerging and promising field for the generation of tissue substitutes is tissue engineering: a composite scaffold, strong and bioactive, may represent an interesting solution to this problem. In this work we have investigated how to realize a scaffold able to sustain articular cartilage regeneration. We have combined mechanical properties of polyvinyl alcohol (PVA) hydrogel and bioactive features of extracellular matrix (ECM). In particular, our attention focused on the investigation of an alternative ECM tissue derived from the umbilical cord Wharton's jelly (W's J) in comparison with the more specific articular cartilage (AC) matrix.
Methods. Three different scaffold groups were investigated to analyse their ability in sustaining chondrocytes adhesion and proliferation: the PVA hydrogel alone, the PVA/W's J derived matrix; the PVA/AC derived matrix. Tissue samples were decellularized according to Meezan (Meezan et al., Life Sci. 1975) and homogenized in 10% acetic acid solution at 0 °C before lyophilisation. W's J and AC sections were stained with DAPI to ascertain complete decellularization and with Movat pentachromic and Masson trichromic kits to assess the maintenance of structural properties. Hydrated 16 and 25 wt % PVA hydrogel samples underwent tensile tests. PVA and PVA composite scaffold morphology before and after chondrocytes seeding was investigated by Scanning Electron Microscopy (SEM). Primary human chondrocytes were isolated from human cartilage by tissue digestion with 0.1% collagenase B and characterized by Reverse Transcription Polymerase Chain Reaction (RT-PCR) to evaluate the expression of specific cartilage mRNAs and by flow cytometry to identify cell specific immunophenotype. Chondrocytes from passage 1 were cultured on scaffolds (20,000 cells/cm2). After 24 hours, 7 and 14 days from seeding, cell proliferation was evaluated by MTT assay and SEM micrographs.
Results. The stretching and relaxation curves of two different PVA hydrogels (16% and 25% wt) were investigated. Stress values relative to a 100% elongation were equal to 0.35 MPa for 16% PVA and 0.5 MPa for 25% PVA. PVA 16 wt % hydrogel showed to be more elastic than 25 wt % one; it did not maintain the residual strain when subjected to tensile strength, revealing high elasticity.
According to SEM micrographs, PVA scaffolds show a quite homogenous porous distribution with pore size ranging from 4 to 10 mm. PVA/W's J and PVA/AC scaffolds have a different surface morphology: the first is quite regular, smooth and with convolution-like structures, the second has a more irregular spongy appearance. W's J and AC tissues were completely decellularized with 3 and 7 detergent-enzymatic cycles respectively; histological analysis showed that they both mainly consist of collagen fibers and mucus.
Freshly isolated chondrocytes demonstrated clear boundaries and distinct nuclei. At a subconfluence state, they showed the classic round or polygonal shape with small membrane extroflessions. RT-PCR showed that AC-derived cell populations are active in the transcription of typical chondrocyte mRNAs: collagen type II, IX and X, cartilage oligomeric matrix protein, aggrecan, SOX9, hyaluronan synthase. Flow cytometry evaluation demonstrated that cell specific immunophenotype is CD44+/CD73+/CD151+/CD49c+/CD49e+/CD49f-/ CD26-.
According to SEM and MTT assay, PVA did not sustain cell adhesion and proliferation. Twenty-four hours from seeding, colonization of PVA/ECM scaffolds was visible. A progressive increase of cell number was observable from day 7 to day 14 on PVA/ECM.
Conclusions. Decellularized W's J matrix is an attractive reservoir of macromolecules. It promotes chondrocyte adhesion, representing an idoneous biomimetic microenviroment even though its aspecific nature. Further investigations are necessary to evaluate the maintenance of chondrocyte phenotype grown upon PVA/W's J scaffolds.

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Presentation 13
Elisa Palumbo
Understanding DNA replication dynamics in the mammalian genome, and in loci specifically involved in genetic instability
Research Unit: Cytogenetics and Molecular Genetics

Abstract:
Mammalian genomes are replicated under a flexible program, implying cell-to-cell variability in origin usage and fork rates, and changes of the replication profiles according to the composition of nucleotide pool and to chromatin organization. It is well known that impairment of DNA replication may lead to genomic instability, but because many details of the regular process are still unravelled, identifying patterns corresponding to deregulated events and/or to cell response after replication stress is not immediate. To contribute to this subject, we evaluated genome-wide replication profiles (fork rates, organization of the replication clusters, fork dynamics) of different non-cancer human cells. Genomic regions with different replication timing and sequence stability were considered in single-locus analyses. Replication profiles were evaluated on stretched molecules. The replication timing of specific loci was defined by interphase FISH in asynchronous cell populations as well as in early-to-late S-phase fractions isolated by FACS sorting. Our results indicate the existence of both general and specific replication profiles among cell types and within the genome. Importantly, we demonstrated that several unexpected patterns consists in fact in normal replication features, which remain undetected when genomic methods are applied. Finally, replication forks progress at the same conditions in regions showing genomic instability, and in stable loci, however a differential use of replication origin and replication timing may be Associated to the inherent instability of these sequences.

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Presentation 14
Giovanni Vazza
Deciphering the genetic landscape of Schizophrenia and Bipolar Disorder: genomic approaches on a population-based cohort.
Research Unit: Human Molecular Genetics

Abstract:
Schizophrenia (SCZ) and Bipolar Disorder (BD) are neuropsychiatric disorders with a prevalence of 1% in the worldwide population. Despite an established heritability of about 80%, their genetic architecture is complex and still not completely clarified. Recently, extensive genome-wide association studies evidenced that common variants contribute to only half of the observed heritability, therefore attention has turned towards the identification of rare genetic factors especially in population and familial cases.
Since several years, we are studying a population sample of more than 250 SCZ and BD cases belonging to 37 large pedigrees all with a common ancestry. This allows us to hypothesize, on the one hand, a homogeneous genetic background and, on the other hand, the involvement of a small number of genetic susceptibility factors that should be shared among patients.
The presentation will highlight some recent results of our study and describe the genome-wide approaches used to identify genetic risk factors for SCZ and BD, which include mtDNA sequencing, linkage study, Copy Number Variants (CNVs) analysis, Identical By Descent (IBD) estimation and Whole-Exome Sequencing.

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Presentation 15

Marco Bisaglia

Dopamine and oxidative stress in Parkinson's disease: is an antioxidant therapy valuable?"

Research Unit: Biophysics, Molecular and Cellular Physiology

Abstract:
Parkinson's disease (PD), the second most common neurodegenerative disorder, is characterized by the preferential death of a subset of neurons in the mesencephalon that use dopamine as neurotransmitter for synaptic communication. Although PD is generally a sporadic neurological disorder, the discovery of monogenic, hereditable forms of the disease, representing 5–10% of all cases, has been very important in helping to partially delineate the molecular pathways that lead to this pathology. Oxidative damages and mitochondrial dysfunction are considered central in dopaminergic neurodegeneration. Oxidative stress occurs when the endogenous antioxidant systems are overcome by the generation of reactive oxygen species (ROS). A relevant source of oxidative stress, which could account for the selective degeneration of dopaminergic neurons, is the redox chemistry of dopamine (DA) that leads to the formation of ROS and reactive dopaminequinones (DAQs).
In the present communication, I will discuss the molecular mechanisms through which the oxidation product of dopamine could promote the selective loss of dopaminergic neurons observed in PD. Moreover, considering that most of, if not all, the intracellular ROS derive from superoxide anion, we evaluated the possibility to exploit the antioxidant properties of superoxide radical dismutating molecules, both endogenous and synthetic, as a tool to maintain cellular homeostasis of ROS. Our findings demonstrate that specific SOD-mimetic compounds can be effective in reducing toxicity Associated with oxidative stress and, likely, progression of the disease.

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Presentation 16

Tommaso Pozzobon

Angiogenesis in secondary syphilis: role of the bacterioferritin TpF1, antigen of Treponema pallidum

Research Unit: General Pathology

Abstract:
Syphilis is a chronic multisystem disorder caused by the spirochete Treponema pallidum. Cutaneous lesions of patients affected by secondary syphilis appear to be highly vascularised; moreover, the bacterium has been reported to activate the endothelium, thus suggesting the possibility that it may interact with endothelial cells promoting the formation of new blood vessels. Aim of this study was to verify whether TpF1, a bacterioferritin and major antigen of T. pallidum, endowed with immune modulant activity, activates endothelial cells favouring their organization in new vessels. We demonstrated that TpF1 stimulates the proliferation and migration of the cells as well as their assembly into micro capillary-like structures; this effect is mediated by the chemokine IL-8 that is expressed and released by endothelial cells exposed to the bacterial antigen, following the activation of the two transcription factors CREB and NF-κB. The ability of TpF1 in triggering angiogenesis was confirmed in vivo by injecting TpF1 in the vascular system of zebrafish larvae.
Collectively, these data support the idea that TpF1 has a crucial role in the pathogenesis of syphilis: indeed, by promoting the formation of new blood vessels, which are permeable in an early phase, it could contribute to the systemic dissemination of the bacterium.

Presentation: 17
Francesco Filippini
From bioinformatic design to regenerative medicine: enhanced neuronal differentiation combining biomimetic peptides and nanocomposite scaffolds
Research Unit: Molecular Biology

Abstract:
Carbon nanotubes are attractive candidates for the development of scaffolds able to support neuronal growth and differentiation thanks to their ability to conduct electrical stimuli, to interface with cells and to mimic the neural environment. We developed a biocompatible composite scaffold, consisting of multi-walled carbon nanotubes dispersed in a poly-L-lactic acid matrix able to support growth and differentiation of human neuronal cells. Moreover, to mimic guidance cues from the neural environment, we also designed synthetic peptides, derived from L1 and LINGO1 proteins. Such peptides could positively modulate neuronal differentiation, which is synergistically improved by the combination of the nanocomposite scaffold and the peptides, thus suggesting a prototype for the development of implants for long-term neuronal growth and differentiation.

References:
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Presentation: 18
Nicola Vitulo
A deep survey of alternative splicing in grape
Research Unit: Genomics and Bioinformatics

Abstract:
In this work we describe a detailed survey of alternative splicing (AS) in grape based on 124 SOLiD RNAseq analyses from different tissues, stress conditions and genotypes. We used the RNAseq data to update the existing grape gene prediction with 2,258 new coding genes and 3,336 putative long non-coding RNAs. Grape displays a marked AS tissue-specificity, while stress conditions produce splicing changes to a minor extent. Surprisingly, some distinctive splicing features were also observed between genotypes. This was further supported by the observation that the panel of Serine/Arginine-rich splicing factors show a few, but very marked differences between genotypes. The finding that a part the splicing machinery can change in closely related organisms can lead to some interesting hypotheses for evolutionary adaptation.

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Presentation: 19
Francesco Chemello
MiRNA-mRNA network at single cell level reveal the role of specific miRNAs in the regulation of metabolism of muscle fibers
Research Unit: Functional Genomics

Abstract:
Skeletal muscle, which performs important metabolic functions and allows movement, is the most abundant tissue of the human body. It consists of different cell types, but the motor units are myofibers that have different metabolisms depending on their performance in the process of contraction. The analysis of molecular processes that regulate the specificity of the different types of fibers was so far conducted using whole muscle enriched for different classes of myofibers. This approach does not allow to evaluate what is happening in the specific motor units of the muscle, and also brings in itself the problem of cells that do not participate in contraction (eg endothelial cells or immune system). The transcriptional analysis of the individual fibers has allowed the identification of genes regulated in function of the speed of contraction of the fibers themselves (Chemello et al. 2011). The regulation of gene expression can occur through mechanisms transcriptional or post-transcriptional. MicroRNAs operate according to the latter, and are becoming increasingly important in the processes of gene regulation. Thanks to a new protocol for sequencing (Biscontin at al. 2010), we have identified miRNAs expressed from single myofibers. The integration of transcript and miRNA expression data at sigle cell level, enabled us to discover the role of specific miRNA in the modulation of fiber metabolism. In particular, we have shown that miR-27-a is able to reduce the oxidative metabolism while miR-142-3p is able to induce the formation of lipids, a process that may have significant implications in the insulin-resistance and in amyotrophic lateral sclerosis.

References:
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Presentation 20
Maddalena Mognato
MicroRNAs in the cellular response to stress
Research Unit: Cell Biology

Abstract:
MicroRNAs are endogenous small noncoding RNAs (18–24 nt), acting as post-transcriptional modulators of gene expression, by interacting with 3'-untranslated regions (UTR) of target genes. The binding of miRNAs to complementary sequences in their target mRNAs may repress translation or induce degradation of mRNAs. Besides their physiological role in a variety of important biological processes, miRNAs mediate gene regulation also in response to cellular stress. Ionizing radiation (IR) and microgravity are two kinds of cellular stressors that may act alone or in combination. We analysed miRNA and gene expression profiles in human peripheral blood lymphocytes subjected to IR and/or microgravity. From an

integrated analysis of miRNA-mRNA we identified miRNAs targeting genes of DNA-Damage Response (DDR) and immunity. In vivo functional validation was performed to demonstrate selected miRNA-mRNA interactions. By this means we demonstrated that ATM, the main kinase in the DDR pathway, is directly targeted by miR-27a.

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Presentation 21

Michela Zottini

Organelles as critical players in plant cell communication network

Research Unit: Plant Physiology and Molecular Biology

Abstract:

Increasing evidence suggests that chloroplasts and mitochondria can be viewed as environmental sensors mediating cellular responses to external stimuli, resulting in short- and long-term responses. The coordinated activity of chloroplastic, mitochondrial and nuclear compartments is under a tight control of anterograde and retrograde regulatory pathways, implying the existence of signalling network apt to integrate nuclear and organellar gene expression. How signals are transduced from the organelles to the nucleus and integrated at the molecular level remains however unknown. Reactive Nitrogen and Oxygen. Species (RNS and ROS) and calcium are some of the signals suggested to be involved in the retrograde signalling. In order to unveil functional links among different organelles, the comparative monitoring of Ca2+ dynamics in plant cytosol, mitochondria (Loro et al. 2012), and chloroplasts/plastids (Loro et al. MS in preparation) in different experimental conditions, by employing the genetically encoded Ca2+ probe (Cameleon), has been carried out. Results on the inter-organellar calcium signalling in different cells, organs and entire plant will be presented, both in wild type and mutant Arabidopsis lines altered in the RS, such as whirly2 and alx8.

It has been proposed that the metabolic inter-dependence of various organelles might be mediated not only by the exchange of small signalling factors, but also by physical interactions among them. To address this topic, we have been working on AtFIS1A (Ruberti et al. 2014), a tail-anchored protein present on mitochondria, chloroplasts and peroxisomes and also on the dynamic protrusions generated from them. The latter could be a way to establish links between organelles, providing coordination in processes, as organelle fission or the maintenance of cell homeostasis.

References:

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Presentation 22

Alessandro Alboresi

Molecular analysis of Nannochloropsis gaditana for the production of biofuels and high added value molecules

Research Unit: Photosynthesis and Plant Biotechnology

Abstract:
Microalgae are considered promising next-generation feedstock for biofuels thanks to a high productivity per area and to the ability to grow on marginal land without competition with food crops. Solar radiation provides the energy supporting algae growth and lipid production and the available radiation must be exploited with the highest possible efficiency to optimize productivity and make their cultivation on a large scale economically competitive. Investigation of the molecular bases affecting light use efficiency is thus seminal to improve lipids/biomass productivity of algae industrial cultivation.
Algae in photobioreactors are growing in an artificial environment and experience conditions substantially different from the natural habitats where these organisms evolved. A prerequisite for optimization of algae cultivation is understanding how this artificial environment affects productivity, with a special focus on the influence of many parameters such as illumination regimes, light distribution in the culture, nutrient availability, CO2 supply.
We are dedicating special attention to the clarification of molecular basis controlling algae productivity, using as a model organism Nannochloropsis gaditana because of its remarkable ability to accumulate lipids. To this aim physiological, biochemical, transcriptomic and metabolomic approaches have been successfully run and their integration is exploited for a better understanding of the mechanisms underlying biomass and lipid production in Nannochloropsis species.
The information obtained is now being exploited for Nannochloropsis genetic modification, looking for the generation of new, more productive, strains. These will be employed for different biotechnological applications also going beyond biofuels like the production of chemicals or enzymes largely employed in green chemistry. For this aim, we developed resources to significantly enrich the molecular toolbox for N. gaditana and provide the algae research community with well-defined material and methods for the analysis of genes and proteins in vivo.

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Presentation 23

Lorella Navazio

Calcium-based communications in plant root endosymbioses: the microorganism perspective

Research Unit: Plant Cell Biology

Abstract:
In the rhizosphere plants engage in mutualistic associations with rhizobial bacteria and fungi belonging to the phylum Glomeromycota, leading to the nitrogen-fixing symbiosis and arbuscular mycorrhizal (AM) symbiosis, respectively. In both types of beneficial interactions, calcium has been firmly demon-

strated to play a pivotal role in initiating the symbiosis signalling pathway activated in host plants by diffusible microbial signals. On the other hand, the signalling systems of symbiotic microorganisms have been less investigated. By using aequorin-expressing rhizobial strains, we demonstrated that a transient intracellular Ca^{2+} change is an early necessary step in the flavonoid-NodD induction circuitry of the nodulation (*nod*) genes and that oligogalacturonides, pectic fragments of the plant cell wall generated upon bacterial entry into the host plant root, are involved as modulators of the flavonoid-induced *nod* gene expression. To analyse Ca^{2+}-mediated sensing mechanisms of AM fungi, a novel strategy based on the intracellular delivery of aequorin mediated by the cell-penetrating peptide TAT was used. Based on our findings, Ca^{2+} seems to be a common signalling system underlying the plant-microbe molecular dialogue in both types of plant root endosymbioses.

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Presentation: 24

Livio Trainotti

Molecular and hormonal regulation of fleshy fruit development and ripening

Research Unit: Botany

Abstract:

Fruits are structures useful in helping seed protection and dispersal. They can be either dry or fleshy, the latter being an important source of nutrients, vitamins and healthy molecules for animals and humans feeding on them. Fruit development and ripening has to cope with internal and environmental signals and transcriptomics tools have been developed in peach to unravel these networks. Light has been shed on an intricate relationship among several classes of transcription factors (TFs) and hormones, leading to the discovery that peptide hormones might be crucial in classical hormones' cross-talks like that between auxin and ethylene. These findings opened a new research line recently supported by UniPD. The functional characterization of peach genes in heterologous system is underway for several candidates and bHLH and MYB TFs, regulators of the production of the valuable anthocyanins, can exemplify the potential exploitation of these findings.

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Presentation 25

Katia Sciuto

Barcoding P.A.T.H.S.: DNA barcodes for reference plant samples

Research Unit: Biology and Systematics of Algae and Higher Plants

Abstract:
Better than a single line of research, Barcoding P.A.T.H.S. (Plant & Algal Type & Historical Specimens) is a complex project into which multiple lines of research are involved and from which many more lines may originate. As the first result, this project led to the creation of an online platform, whose core is a database of DNA sequences used as bar codes to unequivocally identify plant reference samples. This is the principle of DNA barcoding, a method increasingly used in various fields of applied research and which is spreading to more and more taxonomic groups. With "plant reference samples" we refer both to the samples type (i.e. the original samples used to describe existing species) and also to historical samples, the study of which has a considerable value, for example, in studies of phylogeography and in light of the recent climate changes.
The need of generating DNA barcodes from reference samples was created primarily by a problem we encountered during our research and also common to other researchers who use online sequence database, that is the presence of nucleotide sequences obtained from samples incorrectly identified at the species level. To solve this problem we started to compare the DNA sequences obtained from recently isolated samples with those of standard samples, especially preserved in historical collections.
The idea of bringing together in a database data derived from the application of DNA barcoding during our studies and make them easily accessible to the research community (the online platform is equipped with search tools, such as BLAST algorithm) was then transformed into a wider initiative, for all those who are studying plant reference samples with the technique of DNA barcoding. The web platform allows researchers wishing to join the project, to create an account to share their data. The realization of the platform Barcoding P.A.T.H.S. is thus at the same time a scientific result as well as a starting point for several, potential, future developments.

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Presentation 26

Moreno Clementi

A multidisciplinary approach to the study of the collection of Roberto de Visiani (1800-1878), praefectus of the botanical garden of Padova

Research Unit: Palynology and Archaeobotany

Abstract:
Samples stored in historical collections, in particular the original material that was used to describe new taxa, are landmarks for systematic botany. The lack of studies on the collections organized before the formulation of the modern principles of nomenclature, represents a major obstacle to the publication of taxonomy data, that are cornerstones of this discipline and central to the initiatives for environmental protection and conservation of biodiversity, exacerbating the taxonomic challenge. The same data are crucial for the diffusion and correct application of classification techniques based on molecular approaches (DNA-barcoding). The rediscovery of the collections is considered, therefore, a characteristic feature of the last twenty years of research in the field of systematic. The primary objective of these studies is to realize the typification of names. The research that will be presented focuses on the work of Roberto de Visiani, prefectus of the Botanical Garden of Padua from 1836 to 1878, whose work can be traced back more than 400 valid names, many of which are currently accepted but -almost always- not yet typified. The research is not focused, as usual, on a natural group of organisms, but on a single collection (Herbarium Dalmaticum) and all related materials, also unpublished (correspondence, manuscripts, etc.), with an approach that combines botanical, historical and geographical skills. With this research it is thus possible not only to perform extremely documented typifications, but also to produce at the same time skills, data and tools useful for other disciplines and for different fields of botany, while offering the opportunity to participate in international initiatives such as the Global Plants Initiative, the Biodiversity Heritage Library, the archive JStore Plant Science and the future archives of publications in the field of nomenclature, the creation of which is strongly recommended by the scientific community.

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Presentation 27

Lucio Bonato

Geophilomorpha centipedes: diversity, phylogeny and evolution

Research Unit: Evolutionary Biology of Arthropods

Abstract:

The Geophilomorpha is a group of terrestrial arthropods, specialized as predators in the interstitial soil and litter. The approximately 1,000 species currently known are an important component of many biotic communities of tropical and temperate regions, but are poorly studied. We conducted an analysis to reconstruct the phylogenetic relationships among the major clades of Geophilomorpha, using new morphological (acquired by light and electron microscopy) and molecular data, and employing methods of parsimony and maximum likelihood. The results of this analysis, though in some cases have confirmed the monophyletic nature of groups recognized by traditional taxonomy, in others have highlighted cases of homoplasy that reveal parallel or converging evolutionary processes of characters with potential adaptive value. This phylogeny is the basic information for a series of studies of comparative analysis, in part already underway, of ecology (trophic regime and intestinal symbiosis) and phenotypic evolution (in particular the metameric condition) of this group of animals.

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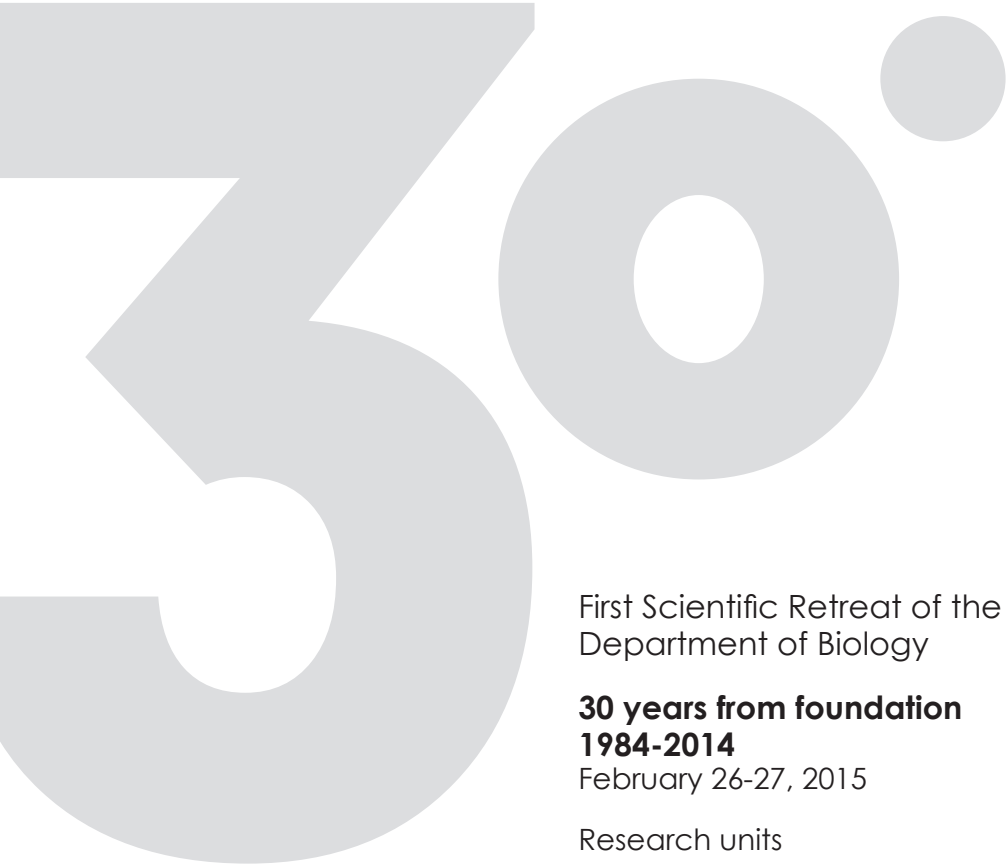

First Scientific Retreat of the Department of Biology

30 years from foundation
1984-2014
February 26-27, 2015

Research units

Research Unit: Biochemistry, Biology and Physiopathology of Mitochondria (Coordinator: Luca Scorrano)

Faculties: Laura Cendron, Paola Costantini, Luca Scorrano, Maria Eugenia Soriano Garcia Cuerva, Elena Ziviani

Research Fellows: Camilla Bean, Ruben Quintana Cabrera, Edith De Rosa, Marta Giacomello, Christina Glytsou, Sowmya Lakshminaranayan, Corrado Mauro, Domenico Migliorini, Deborah Naon, Alice Nardin, Lena Pernas, Aswin Pyakurel, Charlotte Quirin, Dijana Samardzcic, Claudia Savoia, Emilie Schrepfer, Martina Semenzato, Tatiana Varanita, Marta Zaninello

Research: The Unit investigates the role of mitochondrial shape in cell biochemistry. Our previous work changed classical tenets in the field of apoptosis and mitochondrial pathophysiology. Building on these findings, in the last 10 years the unit discovered that (i) an Opa1 dependent molecular staple holding cristae membranes tight is targeted during apoptosis (Cipolat et al, PNAS 2004; Frezza et al., Cell 2006; Cipolat et al., Cell 2006); (ii) Mitofusin (Mfn) 2 as the first molecular bridge between ER and mitochondria (deBrito&Scorrano, Nature 2008) and that Mfn deficiency leads to ER stress (Debattisti et al., J Cell Biol 2014); (iii) mitochondria change shape to control autophagy (Gomes et al., Nat Cell Biol 2011) and Mfn is a substrate of Parkin, mutated in Parkinson's disease (PD) during mitophagy (Ziviani et al., PNAS 2011); (iv) respiratory chain supercomplexes depend on cristae shape (Cogliati et al., Cell 2013) and mitochondrial morphology controls heart development (Kasahara et al., Science 2013). Using a combination of genetics, advanced imaging, cell physiology, electron tomography and structural biology the Unit dissects the role of mitochondria in genetic diseases (Scorrano, Soriano, Cendron, Costantini), mitophagy (Ziviani), PD (Ziviani), and cancer (Scorrano).

Research Unit: Biochemistry (Coordinator: Ildiko Szabo)

Faculties: Marisa Brini, Ildikò Szabò

Technicians: Anna Segalla

Research Fellows: Luca Carraretto, Tito Calì, Vanessa Checchetto, Sara De Bortoli, Valeria Elemer, Veronique Larosa, Luigi Leanza, Antonella Managò, Denis Ottolini, Enrico Teardo

Research: The Unit focusses on intracellular ion fluxes and ion homeostasis under physiological and pathological conditions, both in animals and plants. In particular, potassium and calcium fluxes across the mitochondrial inner membrane, the plasmamembrane and chloroplast/thylakoid membranes are the main topics. These ion fluxes are studied in the context of Parkinson disease, of X-Linked Congenital Cerebellar Ataxia and of different types of cancer including leukemias, melanoma and pancreas adenocarcinoma. Understanding of the molecular mechanisms by which ion channels/transporters impact on these diseases, might open the way to specific pharmacological intervention. In the plant kingdom, organellar ion fluxes are studied in the context of the regulation of photosynthetic efficiency and of inter-organellar cross-talk under abiotic stress. Most projects are carried out in collaborations with local and international groups, using state of the art techniques of cell biology, biochemistry, electrophysiology and plant physiology.

Research Unit: Developmental Biology and Morphogenesis (Coordinator: Loriano Ballarin)

Faculties: Loriano Ballarin, Francesca Cima, Luisa Dalla Valle, Lucia Manni

Technicians: Federico Caicci

Research Fellows: Francesca Ballin, Elisa Colletti, Nicola Franchi, Fabio Gasparini, Giacomo Meneghetti, Filippo Schiavon, Tatjana Skobo,

Research: The Unit concentrates its efforts on the study of the developmental biology of different model animals, such as ascidians, zebrafish and reptiles. In ascidians, the research is mainly focused on the colonial species /Botryllus schlosseri/ and regards sexual and asexual reproduction, development and evolution of nervous systems, angiogenesis, and innate immunity. In zebrafish, the study concerns the role of liposoluble hormones and maternal steroid receptor mRNAs in the epigenetic long-term modulation of development as well as the autophagic process. In reptiles,

investigations are addressed to the molecular, morphological and immunological analyses of the cornification process in the epidermis.

Research Unit: Regulative Biology and Translational Genetics (Coordinator: Francesco Argenton)

Faculties: Francesco Argenton, Natascia Tiso

Technicians: Luigi Pivotti

Research Fellows: Giorgia Busolin, Oliver Ek, Martina Milanetto, Margherita Peron, Andrea Vettori

Research:The Unit of Regulative Biology and Translational Genetics is mainly focused in using Zebrafish to model regulative mechanisms involved in normal and pathological development. The main focus of the lab is the Pancreas and its neoplastic development, however the Unit collaborates with many laboratories to dissect mitochondrial pathologies, dystrophy and other genetic diseases. To this aims the lab is to study mutant and transgenic fish lines in which a) cellular processes, such as proliferation, differentiation and movement, can be followed in vivo and b) regulatory pathway transduction crosswalks and cross regulations can be dissected. The main molecular biology, genetics and cell biology techniques used range from PCR, whole mount in situ hybridisation to genome editing, production of mutants and transgenics, their genotyping and characterisation, NGS analysis and in vivo confocal microscopy.

Research Unit: Neurogenetics and Chronobiology (Coordinator: Rodolfo Costa)

Faculties: Rodolfo Costa, Cristiano De Pittà, Gabriella Mazzotta, Federica Sandrelli, Mauro Zordan

Technicians: Paola Cisotto

Research Fellows: Gabriele Andreatta, Alberto Biscontin, Laura Caccin, Paola Cusumano, Samantha Corrà, Caterina Da Rè, Paolo Martini, Ottavia
omoli, Elena Sartori

Research: The Neurogenetics and Chronobiology Unit has an international reputation in the field of circadian chronobiology. Since many years, the research activity has concentrated in particular on the genetic, molecular and functional analysis of the circadian clock in the fruit-fly Drosophila melanogaster as well as in humans and in the Antarctic krill. More recently the research interest has been oriented also to the field of functional genomics, using Drosophila as a model to study orthologues of human genes mostly involved in mitochondrial disorders. The research unit combines complementary and synergistic expertise: Drosophila genetics, behavioural analyses, molecular and cellular biology, recombinant strategies based on targeted RNA knockdown and use of genome wide technologies for the analysis of gene expression (microarray and RNA-Seq).

Research Unit: Philosophy and History of Life Sciences (Coordinator: Telmo Pievani)

Faculties: Telmo Pievani

Research Fellows: Elena Canadelli, Andrea Parravicini, Francesco Suman

Research: The Research Unit in Philosophy and History of Biology works along several paths related to the progresses of the current scientific programme in evolutionary biology. Within the International project "The Hierarchy Group: Approaching Complex Systems in Evolutionary Biology", on the one hand the research is focused on the relationships between macro-evolutionary and ecological processes and the major aspects regarding hominin phylogeny; on the other hand, the research aims to analyze the historical developments and the conceptual structure of the multi-level approaches to evolution. The topic of the evolutionary interplay between selective pressures and developmental constraints is inquired in particular within the emergence of articulated language in human evolution, suggesting that a relaxation of selective pressures may have played a pivotal role. As regards the history of biology researches about Italian evolutionary biology in the Nineteenth Century are currently underway, in particular focusing on Umberto D'Ancona and on the role of zoological, anthropological and botanical collections of the University of Padua. The Research Unit is strongly involved in communication of science and museology as well, as demonstrated by the scientific editing of the exhibits at the "Garden of Biodiversity".

Research Unit: Ecoetology and Evolutionary Biology (Coordinator: Andrea Pilastro)

Faculties: Matteo Griggio, Alessandro Grapputo, Carlotta Mazzoldi, Andrea Pilastro, Maria Berica Rasotto

Research Fellows: Silvia Cattelan, Alessandro Devigili, Clelia Gasparini, Lisa Locatello, Federica Poli, Simone Pirrello, Andrea Riginella

Research: Our research interests encompass basic and applied topics in evolutionary biology of reproduction, in particular on sexual selection and sperm competition. Current research investigates the evolution of ejaculates and its interactions with sexual selection acting on secondary sexual characters involved in mate acquisition across difference mating systems in birds and fishes. These studies include the influence of sexual conflict in the evolution of mating strategies and parental care, and the effect of social interactions on the evolution of signals. From a more applied point of view, our research is developed along three main directions: the role of sexual selection in the adaptation to global warming and habitat degradation; the study of the evolution of life history traits in fish for the development of conservation strategies for the sustainable exploitation of these species; the study of the evolutionary processes associated with the invasion of alien species, using next generation sequencing and bioinformatic tools, to develop efficient control strategies.

Research Unit: Molecular Ecology (Coordinator: Lorenzo Zane)

Faculties: Leonardo Congiu, Lorenzo Zane

Research Fellows: Cecilia Agostini, Elisa Boscari, Chiara Caruso, Ilaria Anna Marino, Chiara Papetti, Marta Paterno, Josè Martin Pujolar, Michele Vidotto

Research: The research of the Molecular Ecology Unit is focused on non-model marine and freshwater species. Particular attention is devoted to endangered species and to species with relevant conservation and management features. The research activity includes markers development, both at the genomic and transcriptomic level, and their application in studies of molecular systematics, population genetics, ex situ and in situ conservation genetics, analyses of mating systems and inheritance patterns, species and hybrids identifications and forensic applications. The national and international visibility of our group is mainly due to the following general research areas: i) Estimation of genetic connectivity among marine populations, ii) Population genetics and molecular evolution of Antarctic organisms, iii) Genetics and conservation of sturgeons, iv) Development of molecular markers. Methodological approaches range from single locus genotyping to high throughput genome/transcriptome characterizations.

Research Unit: Environmental Physiology and Experimental Zoology (Coordinator: Olimpia Coppellotti)

Faculties: Olimpia Coppellotti, Laura Guidolin, Paola Irato, Gianfranco Santovito, Laura Tallandini

Technicians: Franco Cattalini

Research Fellows: Marta Bellio, Simone Bramuzzo, Monica Camerin, Daniele Codato, Stefania Del Piero, Michele Rosso, Elisa Stoppini, Nicola Tormen

Research: The research activity of the Environmental Physiology and Experimental Zoology Unit concerns the following topics:

- Structural and functional studies, also in environmental and evolutionary perspective, on physiological antioxidant defence systems in various organisms such as Antarctic fish and molluscs, tunicates, Drosophila and ciliated protozoa.
- Physiological and biochemical responses to xenobiotic agents in marine Invertebrates and in mammalian cell cultures: mechanisms of damage, oxidative stress – responsive elements and special detoxification abilities. Evaluation of possible environmental effects on biocoenosis and on human health.
- Bimodal cancer therapy implemented with functionalized photoactivatable nanoparticles electrostatically decorated with a porphyrinic photosensitizer and with a NO donor playing anticancer activity on different subcellular targets.
- Use of sunlight-activatable porphyrin formulates on larvae of Diptera vectors of pathogenic agents.
- Study of fossil microbial coenoses in amber from diverse geological periods.

- Sustainable use of natural resources as a strategic plan in the monitoring, defense and conservation of the biodiversity, of the species and habitats, also for the education and communication.

Research Unit: Marine Ecology (Coordinator: Maria Gabriella Marin)
Faculties: Monica Bressan, Maria Gabriella Marin, Valerio Matozzo
Technicians: Luciano Masiero
Research Fellows: Tihana Marceta, Ilaria Marisa, Marco Munari
Research: Main research activities of the Marine Ecology Unit focus on the evaluation of combined effects of environmental parameters (sea water temperature, salinity and pH), which are relevant in a global change scenario, and exposure to emerging contaminants (pharmaceuticals and nanoparticles) in several marine invertebrates, mostly bivalves. Using a multistressor approach in short-, medium- and long-term laboratory experiments, cellular, biochemical and physiological responses are assessed in various life stages of the studied organisms, from gametes to adults. At the same time, field surveys are carried out with the aim of evaluating the state of natural populations by measuring biomarker responses, as well as by studying reproductive cycle, larval settlement and size frequency distribution, thus obtaining information on anthropogenic pressures.

Research Unit: Ecology of Biodiversity and Sustainability (Coordinator: Maurizio G. Paoletti)
Faculties: Maurizio G. Paoletti, Renata Trevisan
Research Fellows: Leandro Dreon, Silvia Fusaro, Federico Gavinelli, Nicola Manno, Linda Sacchetti, Daniele Sommaggio, Fabio Stellin, Marina Zanardo
Research: the Unit is involved in different lines of research concerning the sustainable use of biodiversity, such as: Bio-indicators for sustainable use of agro-ecosystems and disturbed environments; Chitinase and human digestion of chitin, new interactions with nerve disorders; New food chains based on autolitothophic bacteria; Invertebrates (insects and minilivestock) for human food; Wild and semi-domesticated plants and local knowledge.

Research Unit: Biology of Endothelial Cells and Regeneration (Coordinator: Marcella Folin)
Faculties: Marcella Folin
Research Fellows: Silvia Barbon, Elena Stocco
Research: The poor regenerative potential of cartilage and the unsatisfactory current clinical therapies have led to the search of strategies providing solutions to the treatment of focal defects. An emerging and promising field for the generation of tissue substitutes is tissue engineering: a composite scaffold, strong and bioactive, may represent an interesting solution to this problem. We investigate how to realize a scaffold able to sustain articular cartilage regeneration. We combine mechanical properties of polyvinyl alcohol (PVA) hydrogel and bioactive features of extracellular matrix (ECM). In particular, our attention focuses on the investigation of an alternative ECM tissue derived from the umbilical cord Wharton's jelly (W's J) in comparison with the more specific articular cartilage (AC) matrix.

Research Unit: Cytogenetics and Molecular Genetics (Coordinator: Antonella Russo)
Faculties: Antonella Russo
Technicians: Alessandro Marinello
Research Fellows: Elisa Palumbo, Martina Stevanoni
Research: The research Unit investigates the mechanisms of genetic and chromosome instability in mammalian somatic and germ cells. At present, two projects are ongoing: the first is exploring common fragile site instability in mammalian germ cells and its potential involvement in human inherited disease and cancer. The second is focused on the relationship between chromosome instability and DNA replication.
Collaborations: Prof. Vera Bianchi, Dept. of Biology. Dr. Francesca Pacchierotti, Laboratory of Toxicology, Unit of Radiation Biology and Human Health, ENEA Casaccia, Rome. Dr. Annapaola Franchitto, Department of Environment and Primary Prevention, National Institute of Health (ISS) Rome. Dr. Marco Crescenzi, Department of Cell Biology and Neurosciences, National Institute of Health (ISS) Rome.

Research Unit: Human Molecular Genetics (Coordinator: Alessandra Rampazzo)

Faculties: Stefania Bortoluzzi, Gianluca Occhi, Alessandra Rampazzo, Giovanni Vazza, Libero Vitiello
Technicians: Maurizio Rosa
Research Fellows: Andrea Bisognin, Francesca Boaretto, Annagiulia Bonizzato, Martina Calore, Domenico Cieri, Alessandro Coppe, Marzia De Bortoli, Enrico Gaffo, Eva Galletta, Alessandra Lorenzon, Giulia Poloni, Claudia Saccoman, Cecilia Salvoro
Research: The research activity of the Human Molecular Genetics Unit is focused on the biological basis of Mendelian and multifactorial diseases. To this aim we use various approaches, ranging from genetic and genomic analyses (experimental and computational alike) to the use of in vitro and in vivo models. In particular, we study mutations and genomic variations involved in different inherited and multifactorial disorders, including tumors, both to elucidate their molecular pathogenesis and to provide medical diagnoses. These studies are carried out with in silico genome-wide approaches, which also involve the creation of specific bio-informatics tools, with in vitro cell culture models, both conventional and 3D, and with in vivo murine disease models, using both pre-existing strains and new transgenic animals created ad-hoc.

Research Unit: Biophysics, Molecular and Cellular Physiology (Coordinator: Mariano Beltramini)

Faculties: Mariano Beltramini, Marco Bisaglia, Luigi Bubacco, Elisa Greggio
Technicians: Paolo Di Muro, Vanni Ferrari
Research Fellows: Giulia Berti, Laura Civiero, Roberta Filograna, Adriano Gonnelli, Federico Lanciai, Sara Pizzato, Nicoletta Plotegher, Isabella Russo, Isabella Tessari
Research: The main scientific interest of the Biophysics and Molecular and Cell Physiology group is to understand how a number of brain processes are deregulated in Parkinson's disease (PD). Pathologically, PD is characterized by the loss of dopaminergic neurons in the substantia nigra pars compacta and the intracellular accumulation of the presynaptic protein alpha-synuclein (a-syn) into Lewy bodies of surviving cells. As the redox chemistry of dopamine is thought to play a major role in the neurodegenerative process, we are interested in understanding the molecular mechanisms through which the oxidation products of dopamine promote the selective loss of dopaminergic neurons observed in PD. Of note, we identified a-syn as robust target of dopamine-derived oxidation products, suggesting a direct link between dopamine chemistry and a-syn pathology. In the last fifteen years, monogenic forms of PD have been instrumental in providing mechanistic insights into the molecular pathways that lead to PD. To this regard, we are studying the cell-autonomous and non cell-autonomous nature of PD by reconstructing the molecular pathways of two major PD genes: a-syn and Leucine-rich repeat kinase 2 (LRRK2). In particular, we are exploring the role of LRRK2 in orchestrating neuronal cytoskeletal dynamics and synaptic vesicles trafficking by phosphorylation of key presynaptic proteins such as the ATPase NSF. A-syn also plays a central role in synaptic vesicle exocytosis, suggesting that impaired neurotransmitter release could arise as the first pathway compromised in PD and contribute to the early stage symptoms of the disease. Accumulating evidence also support a central role of inflammation in PD progression. To this regard, we are investigating the relationship between a-syn and LRRK2 as well as the contribution of neuronal oxidative stress in microglia activation. Overall, we propose a model where early presynaptic defects coupled with late microglia over-activation represent key events in PD pathogenesis.

Research Unit: General Pathology (Coordinator: Marina de Bernard)

Faculties: Marina De Bernard
Research Fellows: Gaia Codolo, Matteo Pagliari, Tommaso Pozzobon, Maria Amparo Vila Caballer
Research: The aim of the research carried out by the General Pathology Unit is to identify and characterize antigens produced by bacteria pathogenic to humans that possess immune-modulating properties, with the objective of expanding knowledge on the onset and progression of certain chronic and infectious diseases, like the pathologies incurred from infection by Helicobacter pylori (Hp) and syphilis, caused by the bacterium Treponema pallidum (Tp). More ambitious purpose of our research is to test the molecules we have characterized in murine models to evaluate the potential therapeutic applicability, for example in tumor therapy.

The main research lines of our unit are:
i) the characterization of vesicles released by immune cells and gastric epithelial cells following infection by Hp. The assessment of their potential impact on illnesses associated with Hp.
ii) the development of a novel formulation containing HP-NAP, an immune-modulating antigen produced by HP, able to counteract the growth of bladder cancer in mouse model. The search for the best system for administration of the therapeutic treatment and for its permanence in the bladder.
iii) the characterization of pro-angiogenic TpF1 antigen produced by Tp.

Research Unit: Molecular Biology (Coordinator: Pietro Benedetti)
Faculties: Pietro Benedetti, Francesco Filippini
Research Fellow: Adelaide Milani, Irene Righetto, Giorgia Scapin
Research: the laboratory coordinated by F. FIlippini integrates in silico and wet analyses to perform bioinformatic-driven characterization of protein domains and functional motifs. Research focuses in particular on the subcellular trafficking protein machinery and especially on the Longin domain and related domains. We also investigate on molecular players and cues driving neurite outgrowth and process elongation/gidance and set up a nanocomposite scaffold for regenerative medicine, that is able, in combination with biomimetic synthetic peptides, to support human neuronal differentiation. The laboratory coordinated by P. Benedetti is interested in the biological role of DNA Topology and DNA Topoisomerases. In particular it is focused on the role of DNA topology in genome stability. There are several diseases that seem to be originated by a non-functional DNA Topoisomerase. Topoisomerases are expressed throughout the developing and adult brain and are mutated in some individuals with autism spectrum disorder (ASD). However, how topoisomerases are mechanistically connected to ASD is unknown. We are planning to set up experiments in simplified biological system to address this question.

Research Unit: Genomics and Bioinformatics (Coordinator: Giorgio Valle)
Faculties: Stefano Campanaro, Giorgio Valle, Alessandro Vezzi
Technicians: Michela D'Angelo, Rosanna Zimbello
Research Fellows: Giovanni Birolo, Davide Campagna, Fabio De Pascale, Georgine Faulkner, Erica Feltrin, Claudio Forcato, Annarita Marrano, Chiara Rigobello, Riccardo Rosselli, Riccardo Schiavon, Robin Targon, Andrea Telatin, Nicola Vitulo
Research: The Research Unit of Genomics and Bioinformatics has been involved for many years in this research field either as coordinator or as participant in international projects. The current activities of our research group originate mostly from previous projects. For instance, many years ago we actively participated in the international yeast genome project and to the subsequent functional analysis; now one of the research lines is about genomics of yeast strains used in wine industry. Similarly, our group was the first in Italy to produce the full sequence of a bacterial genome and now a line of research is about microbial metagenomics. The main lines of research are currently directed in four directions:
1) Microbial genomics;
2) Functional genomics of muscle, aimed to clarify some aspects of muscle plasticity;
3) Plant genomics, to sequence and characterize genomes such as grape, tomato, olive and wheat;
4) Human genomics, in collaboration with different departments of Medicine, particularly towards personal genomics and epigenomics. Ourm group is also working at the CRIBI Biotechnology Centre of the University of Padua where it is responsible for the facilities and services of DNA sequencing and bioinformatics.

Research Unit: Functional Genomics (Coordinator: Gerolamo Lanfranchi)
Faculties: Stefano Cagnin, Gerolamo Lanfranchi, Paolo Laveder, Chiara Romualdi, Paola Venier
Technicians: Caterina Millino, Beniamina Pacchioni
Research Fellows: Enrico Alessio, Enrica Calura, Francesco Chemello, Stefania Domeneghetti, Marco Franzoi, Umberto Rosani, Gabriele Sales, Lucia Tombolan, Laura Varotto, Matteo Zampini
Research: The Research Unit of Functional Genomics is organized in three teams devoted to differ-

ent themes of functional genomics, using various animal models and experimental approaches.
The work team led by Paola Venier deals with functional genomics of bivalves and, more recently, aims to investigate the genetic/epigenetic basis of the differential susceptibility of bivalve species to infectious agents. Antimicrobial mussel peptides exemplify a group of molecules under study. Transcriptional and genomic analysis are currently performed in diverse biological models (malacoviruses, bivalves, fishes, human cells) with specific purposes.
The work team led by Chiara Romualdi is interested in the development of computational frameworks for genomic data integration and analysis. Specifically we are working on applicative and methodological approaches for the integration of different sources of genomic data (miRNAs and lincRNAs in particular) in the context of biological pathway and regulatory networks.
The work team led by Gerolamo Lanfranchi, who coordinates also the Unit, deals with the functional genomics of skeletal and heart muscle. The transcriptional signatures of muscle in different physiological conditions and dynamic variations are studied using an original single-cell approach in mouse and man. Pathological statuses of the muscle, such as atrophy/hypertrophy, inflammatory illness, dystrophies and tumours are also searched. The functional role of specific pathways and factors revealed by the genomic studies are then deepen using cell and molecular biology technologies. The team is also strictly collaborating with Venier and Romualdi groups for their projects.

Research Unit: Cell Biology (Coordinator: Vera Bianchi)
Faculties: Vera Bianchi, Lucia Celotti, Maddalena Mognato, Giovanna Pontarin, Chiara Rampazzo, Elena Reddi
Technicians: Paola Ferraro
Research Fellows: Francesca Moret, Elisa Franzolin
Research: Regulation of DNA precursors in mammalian cells: role of catabolic enzymes. Role of microRNAs in the DNA-Damage Response and their application as therapeutic agents to sensitize cancer cells to ionizing radiation. Nanomedicine and cancer. Toxicity of differently engineered and functionalized nanoparticles in human cells. Efficiency and targeted delivery of photo- and chemo-therapeutic agents to cancer cells in mono and combined therapies with different nano-platforms.

Research Unit: Plant Physiology and Molecular Biology (Coordinator: Fiorella Lo Schiavo)
Faculties: Fiorella Lo Schiavo, Michela Zottini
Technicians: Elisabetta Barizza
Research Fellows: Stefano D'Alessandro, Elide Formentin, Serena Golin, Bushra Ijaz, Giovanna Loro, Juri Nascimbeni, Cristina Sudiro
Research: Our research focuses on the study of signal transduction pathways triggered in plants by endogenous and exogenous stimuli. In particular, we carry on research projects analysing:
The signal dynamics of calcium, ROS and RNS acting in inter- and intra-cellular communication in physiological and stress conditions.
The role of mitochondria as key organelles in orchestrating the cellular response to stress.
Molecular mechanisms leading to tolerance and adaptation to environmental stress in crop plants, as rice and grapevine.

Research Unit: Photosynthesis and Plant Biotechnology (Coordinator: Tomas Morosinotto)
Faculties: Elisabetta Bergantino, Nicoletta La Rocca, Tomas Morosinotto
Technicians: Anna Segalla
Research Fellows: Pascal Albanese, Alessandro Alboresi, Alessandra Bellan, Elisa Beneventi, Caterina Gerotto, Laura Giaretta, Andrea Meneghesso, Mattia Niero, Giorgio Perin, Diana Simionato
Research: One of the main research focus of the research unit is the clarification of the mechanisms enabling photosynthetic organisms to convert light energy into biomass. Particular attention is dedicated to the understanding on how these processes are regulated in response to changes in environmental conditions and/or following adaptation to extreme environments like Antartica. A major part of the activity is also dedicated to the investigation of possible biotechnological applications of

photosynthetic organisms like the possibility of using algae or cyanobacteria for the production of biodiesel, high added value molecules or enzymes. In the latter case also other systems for heterologous expression are used to produce recombinant enzymes which can be used by the chemical industry to reduce the environmental impact of their production.

Research Unit: Plant Cell Biology (Coordinator: Barbara Baldan)
Faculties: Barbara Baldan, Lorella Navazio
Technicians: Stefania Marcato
Research Fellows: Enrico Baldan, Roberto Moscatiello, Sebastiano Nigris, Simone Sello, Alessandra Tondello, Filippo Giacomo Zanella
Research: The research activity deals with the plant cell biology field, with a special focus on beneficial plant-microbe interactions and calcium-mediated signaling in photosynthetic organisms. In particular, the involvement of calcium signals in the early stages of the nitrogen-fixing symbiosis and arbuscular mycorrhizal symbiosis is analyzed. Moreover, bacterial endophytes, living in inner tissues of grapevine and legumes, are identified and characterized. Microbial strains with plant growth promotion and/or biocontrol activities are selected to develop microbial consortia for potential application in improving crop productivity. Recent studies concern the analysis of the functional integration of plastids in the plant calcium signaling network.

Research Unit: Botany (Coordinator: Livio Trainotti)
Faculties: Giorgio Casadoro, Livio Trainotti
Technicians: Anna Pavanello
Research Fellows: Silvia Quaresmin, Francesca Resentini
Research: The research unit of Botany deals with the development and ripening of fleshy fruits. In particular, efforts are aimed at understanding:

- the seed-pericarp relationships and how they affect the progression of the development of the fruit, its ripening and its quality;
- the transcriptional and hormonal networks active at the transition from maturation to ripening in fruit;
- the transcriptional regulation that leads to the accumulation of anthocyanins in the peel and pulp of ripe fruit.

Researches are conducted in peach through transcriptomics experiments by means of microarray and RNAseq experiments to identify genes that are possibly at nodes of the regulatory networks. The function of candidate genes is evaluated in model systems such as tomato , tobacco and Arabidopsis .

Research Unit: Biology and Systematics of Algae and Higher Plants (Coordinator: Isabella Moro)
Faculties: Francesca Dalla Vecchia, Isabella Moro
Technicians: Luca Cesarotto, Emanuela Moschin
Research Fellows: Katia Sciuto, Marion Wolf
Research: In the last years, our research group has been involved in several projects regarding the identification and the characterization of plant organisms, using molecular techniques besides a more classical approach. The necessity of this type of studies arose both from purely systematic questions and on behalf of privates or public institutions. The organisms considered in our researches range from cyanobacteria and microalgae to seaweeds and, only recently, plants. The research lines carried out by our group are:
Cyanobacteria and microalgae from extreme environments
Effects of xenobiotics in algae and higher plants

- Alien seaweeds in the Mediterranean Sea.
- DNA Barcoding of Plant and Algal Type and Historical Specimens

Research Unit: Palynology and Archaeobotany (Coordinator: Antonella Miola)

Faculties: Antonella Miola

Technicians: Luca Cesarotto

Research Fellows: Moreno Clementi, Michele Maritan

Research: The research focus on Holocene sedimentary series from the North Adriatic coastal area (Altinum). We analyze plant macro and micro remains and non-pollen palynomorphs, to reconstruct the environmental history connected with the activities of prehistoric and Roman settlements in the area.

A different research topic concerns the herbarium collection and letters of Roberto de Visiani (praefectus of the Padova Botanical Garden 1836-1878). The multidisciplinary approach to the study of these documents aims to increase the value of the collections and share them with scientific community and public.

Research Unit: Evolutionary Biology of Arthropods (Coordinator: Giuseppe Fusco)

Faculties: Lucio Bonato, Giuseppe Fusco

Research Fellows: Francesca Bortolin, Sara Lefosse, Enrico Romanazzi

Research: The unit conducts research in the development, evolution and ecology of arthropods, with particular reference to the group of myriapods. There are three main research areas: i) taxonomy, phylogeny, phylogeography, and morphological evolution of centipedes, using both morphological and molecular data; ii) feeding ecology of geophilomorph centipedes, using techniques of DNA barcoding; iii) evolution of the post-embryonic development of some taxa of anamorphic arthropods, both living and fossils, with a particular focus on the processes of growth and segmentation.

Research Unit: Cell Proliferation (Coordinator: Maurizio David Baroni)

Faculties: Maurizio David Baroni

Research: Evaluation of the effects of Ras /cAMP pathway inhibitors in yeast with particular emphasis on some anti-inflammatory drugs (NSAIDs). Initially, the activity of individual molecules will be evaluated by measuring the effect on growth, cell cycle and response to stress of in vivo cultures of normal and mutant strains of Saccharomyces cerevisiae. A specific inhibition of Ras /cAMP pathway activity will be also tested at the biochemical level by measuring Ras2p-GTP levels and the activity of PKA. Based on the obtained in vivo results we will set up in vitro assays with purified proteins in order to study the mechanism of action of the above inhibitors.