

CURRICULUM BIOLOGIA E BIOTECNOLOGIE VEGETALI– Sede: Università degli Studi di Ferrara

Position with scholarship

Research title: *Light- and substrate-driven variations in microalgal metabolism to emphasize the production of antioxidant and anti-inflammatory molecules.*

Scientific Tutor: Dott.ssa Costanza Baldisserotto. **Co-tutor:** Prof.ssa Simonetta Pancaldi.

Microalgae are photosynthetic microorganisms recognized to produce a wide range of natural bioactive molecules (proteins, lipids, carotenoids, phenolic compounds, etc.), useful in biotechnological applications, for example as antioxidant, energetic, anti-inflammatory compounds. Light quality and quantity, together with organic carbon supply, are main parameters that influence microalgal biomass productivity and quality (Amaro et al., 2020; Baldisserotto et al., 2016, 2021; Xu and Harvey, 2019). The PhD program is aimed at emphasizing the production of bioactive molecules (anti-oxidative and anti-inflammatory) due to metabolic changes primarily induced by light variations or nutrient addition (mainly organic carbon-based) during the cultivation of the algae. Thus, biological responses of microalgae to light, also in combination with the supply of organic carbon sources, are main topics of the research. The illumination sources could be LED lights for the enrichment of white light with defined wavelength (e.g. blue and red).

The candidate will be asked to monitor algal cultures under different growth conditions to obtain information on biomass productivity and for fast screening of molecule classes, linked to antioxidant and anti-inflammatory activities. Concomitantly, within the screening study of bioactive compounds, microalgal extracts should be produced to assess the antioxidant activity using colorimetric tests (e.g. DPPH) and the anti-inflammatory properties in vitro (e.g. nitric oxide test) (Samarakoon et al., 2013; Goiris et al., 2015; Safarar et al., 2015). Furthermore, considering the relationships between photosynthetic activity and oxidative metabolism (Foyer 2018), photosynthetic properties of the algae will be studied for example through chlorophyll fluorimetry and biochemical studies of the thylakoid membranes (Kalaji et al., 2017; Giovanardi et al., 2017). For a better knowledge of antioxidant and anti-inflammatory properties, and in order to understand which compounds may be responsible for precise biological activities, the candidate will be given the opportunity to carry out collaborative research activities both within the University of Ferrara and/or in Italian or foreign Universities.

References

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CURRICULUM BIOLOGIA E BIOTECNOLOGIE VEGETALI. Sede: Università degli Studi di Ferrara

Position with scholarship

Research title: *Nuove strategie ecosostenibili per la lotta contro fitopatogeni delle piante*

Scientific Tutor: Dr Giovanni Bernacchia **Co-tutor:** Prof Chiara Scapoli.

Phytopathogenic insects attack crops causing significant losses in agriculture, not to mention the negative effects on the environment caused by chemical pesticides used to control infestations. Recent episodes of invasion of alien species in Europe (Marmorated stink bug and *Drosophila suzukii*) difficult to control with synthetic chemical pesticides have highlighted the limits and fragility of the current pest control strategies. In accordance with the recent EU directives, it becomes increasingly important to develop new methods to fight phytopathogens that are effective, specific and sustainable. The proposed research project will focus on two topics: the use of molecular technologies based on RNA interference to specifically fight pests and the use of plant extracts rich in monoterpenes (essential oils) as natural insecticides. These experiments will be applied to important pests such as marmorated stink bug and *Drosophila suzukii*.

On the RNAi front, we intend to study the silencing of different types of target genes in order to evaluate the negative effects on vitality and behavior of the marmorated stink bug at different stages of development. In parallel, we intend to compare different methods to deliver dsRNA to insects.

The study of different types of monoterpenes, essential oils and plant extracts will be carried out on populations of *D. suzukii* to evaluate the negative effects on vitality, oviposition, behavior and physiology of the pathogen.

References

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CURRICULUM GENETICA ED EVOLUZIONE – Sede: Università degli Studi di Ferrara

Position with scholarship

Research Title: *Model-based population genomic inference through the analysis of whole-genome data*

Scientific Tutor: Prof. Silvia Ghirotto

A faithful reconstruction of a species demographic dynamics is important both to improve our knowledge about the past and to disentangle the effects of demography from those of natural selection. In recent years, thousands of modern and ancient complete genome sequences have become available, potentially containing vast amounts of information about the evolutionary history of populations. However, these genomes do not speak by themselves. To best extract the evolutionary information, computational methodologies for population genetic inference are rapidly being developed (Beaumont 2010, Li and Durbin, 2011, Excoffier et al 2013). Methods based on Machine Learning (ML) techniques recently emerged within population genetics (e.g. Pudlo et al 2016), and while being still in their infancy, these approaches could have the potential to revolutionize the practice of population genetic data analysis (Schrider and Kern 2018). Recently we developed an Approximate Bayesian Computation (ABC) inferential framework based on ML methods, for the analysis of whole genome data (Ghirotto et al 2020), providing a robust approach to perform a more accurate and reliable inference of past population dynamics.

Within this PhD program we are planning to extend this work, developing new ML algorithms able to maximize the information that can be retrieved from Low-Coverage genomes, as those coming from ancient specimens or elusive species, with the aim of integrating sub-optimal covered genomes within an ABC-based inferential framework. The successful candidate will also apply the new developed methodology to the study of past demographic dynamics of the Italian peninsula, analysing whole genome sequences generated within the PRIN project “1000 Ancient Italian Genomes: Evidence from ancient biomolecules for unravelling past human population Dynamics”.

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CURRICULUM GENETICA ED EVOLUZIONE - Sede: Università degli Studi di Ferrara

Position with scholarship

Research Title: *Biology of spatial and migratory behaviour in teleost fishes*

Scientific Tutor: Dr. Tyrone Lucon-Xiccato

Spatial movements, including migrations, are critical to find resources such as food, shelter, social companions and reproductive partners. However, how individuals move in their environment remains poorly understood [1]. By combining experimental studies in the laboratory and observations in nature, we will investigate key aspects of fish' movement biology with a comprehensive approach.

The PhD candidate will develop novel, computer-based procedures to study spatial navigation in the laboratory [2] in response to different sensory modalities [3]. The laboratory species exploited will be the zebrafish (*Danio rerio*), the guppy (*Poecilia reticulata*), and the medaka (*Oryzias latipes*). Individual-level behavioural measures obtained with the spatial tasks will be correlated to brain activation [4] and to genetic polymorphisms that have been associated with spatial movements in other vertebrates [5].

The wild species of reference will be the European eel (*Anguilla anguilla*), which perform an astonishing migration—from the Sargasso Sea to Europe and back. Immature specimens collected in the wild be assayed with spatial tasks to assess adaptive ontogenetic variation in spatial behaviour and related brain circuits' activation. Adult specimens caught in the wild in light of the Life project LIFEEL ('Urgent measures in the Eastern Mediterranean for the long-term conservation of endangered European eel') will be assayed in behavioural tasks [6,7] and tissues samples will be collected for genotyping. The specimens will be then released with radio tag implants to track their migration in the river Po basin [8]. Individuals' migratory behaviour will be correlated with results of the laboratory tasks and with genetic polymorphisms.

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CURRICULUM ECOLOGIA ED ETOLOGIA – Sede: Università degli Studi di Firenze

Position with scholarship

Research Title: *The impact of climatic changes on Italian freshwater communities: an eco-physiological approach*

Scientific Tutor: Stefano Cannicci

It is well known that the impact of climate change is pervasive across the planet and all ecosystems are affected (Burrows et al., 2011). Researchers are increasingly aware, however, that temperatures are increasing, and are projected to increase, at faster pace at medium to high latitudes than in the tropics and this increment showed to affect more heavily aquatic communities with respect to terrestrial ones (Pinsky et al., 2019). This latter difference is due to the lower thermal tolerance showed by water-breathing ectotherms (Pörtner & Farrell, 2008). For what concerns freshwater species, the above interactions among critical environmental factors act in parallel with the reduction of water in freshwater bodies, also linked to global warming, putting the mid and high latitude freshwater species at the brink of extinction (Woodward et al., 2010; Xenopoulos et al., 2005).

The candidate will study 1) the thermal tolerance (Verberk et al., 2015) and of 2) the physiological and behavioural adaptations to temperature alterations (Deutsch et al., 2008) of keystone invertebrate and vertebrate ectotherms of the Italian inland water bodies. The candidate will also assess the role of such species in the freshwater systems' food web and, ultimately model the impact of climate changes on communities, ecosystems and interactions among keystone species (Timoner et al., 2021).

The main techniques involved in this study will be in field behavioural ecology study techniques (temperature and spatial preferences, rhythmic behaviour), eco-physiological tests in the laboratory (intermittent-chambers' respirometric techniques, hearth rates measurements and oxygen concentration in the blood across temperature ramps) and stable isotopes analyses across the food web. The results of the present project will lay the foundations of advanced and scientific based management and conservation strategies needed to protect our fragile freshwater communities in a changing world.

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CURRICULUM ECOLOGIA ED ETOLOGIA – Sede: Università degli Studi di Firenze

Position with scholarship

Research Title: *Improving and applying biomonitoring scheme to Mediterranean insect communities*

Scientific Tutor: Leonardo Dapporto

Diversity is declining with an impressive pace in the last decades due to the effects of several human activities (Warren et al., 2021). Due to their short lifespan, strong specialization and high dispersal capabilities, insects are among the organisms reacting faster to environmental changes (Devictor et al., 2012). A famous study has identified a 75% loss in biomass in 27 years in Germany even inside protected areas (Hallmann et al., 2017) and over Europe butterflies have lost 40% of their density in the last two decades (Warren et al., 2021). Given the fundamental ecosystem services providing by insects, especially pollinators, there is growing interest in establishing relatively simple and effective monitoring schemes (Montgomery et al., 2021). In the Mediterranean, a major problem hampering an effective insect monitoring is represented by the high diversity of these organisms resulting in the necessity of deep taxonomic knowledge.

In recent years an eclectic approach to biomonitoring is emerging. This approach is based on i) introducing and testing simplified monitoring schemes (e.g. identification of individuals above species level), ii) the construction and the use of DNA-barcode libraries to facilitate identification (Hebert et al., 2003), and iii) integrating the data collected by academic researchers with those available in citizen science repositories.

Taking advantage of the recent pollinator directives 2019-2021 of the Italian Ministry, the project is intended on developing biomonitoring techniques for pollinators in the National Parks of Central Italy. The activity will be mainly focused in applying standardised data collection (transects, light traps, pan traps) and the use of DNA-barcoding to the main groups of pollinator (Lepidoptera, Hymenoptera, Diptera). Other than setting a snapshot of current diversity for these parks, to be compared with future data, the project will provide fundamental insights to identify the best strategies for biomonitoring in the complex Mediterranean region.

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Position with scholarship

Research title: HERBIOME: exploiting the *microbiome* of medicinal plants to find new natural green medicines against Cystic Fibrosis pathogens

Scientific tutor: Prof. Renato Fani

Continued administration of antimicrobial compounds to cystic fibrosis (CF) patients may lead to increasing antibiotics resistance and favor the emergence of multidrug-resistant (MDR) pathogens. Therefore, it is mandatory to prioritize research to discover new antimicrobials. Medicinal plants (MPs) produce a plethora of bioactive antimicrobial compounds of pharmacological interest. Plants, including MPs, host a wide range of microorganisms that contribute to plant growth and metabolism. These microorganisms and their genetic functions are collectively referred to as the plant microbiome. Components of the MPs-associated microbiome can synthesize antibacterial natural compounds directly, influence production of plant secondary metabolites, or chemically modify plant-derived compounds. The MPs-associated microbiome is a very promising source of new antibacterial compounds to be used against MDR pathogens, as those frequently colonizing the airways of CF patients. This project aims at establishing a translational research group dedicated to the exploitation of the MPs microbial bioreservoir for the discovery of new antibiotics especially active against MDR pathogens for the control of infections in CF patients. Specific aims of the project are:

- i) To characterize the microbiome associated with the medicinal plant *Origanum vulgare* L. through culture-dependent and culture-independent methods.
- ii) To identify, in the *O. vulgare*-associated microbiome that produce bioactive antimicrobial molecules capable of inhibiting bacterial CF pathogens. To this purpose, isolated microorganisms will be tested against MDR reference strains.
- iii) To identify, in the *O. vulgare*-associated microbiome, microbes able to promote MP growth (PGP) and production of plant bioactive molecules. For this purpose, in vitro models of *O. vulgare* plants will be set up and axenic plants will be compared with plants inoculated with isolated PGP microbes, including arbuscular mycorrhizal fungi.
- iv) To carry out the chemical characterization of the secondary metabolites produced by bacteria and fungi isolated from *O. vulgare* and active against MDR strains.
- v) To determine the nucleotide sequence of the entire genome of the most promising bacteria in order to identify genes involved in the biosynthesis of antimicrobial compounds.

References

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CURRICULUM GENETICA ED EVOLUZIONE - Sede: Università degli Studi di Firenze

Position with scholarship

Research title: *Computational modelling of bacterial metabolism*

Scientific tutor: Dr. Marco Fondi

Bacterial metabolism plays a central role in many different contexts, from microbial infections to biological associations, from ecosystem maintenance to biotechnological applications. Metabolism, for example, can be a primary and relatively untapped target to fight bacterial infections. At the same time, its manipulation can boost the industrial production of valuable compounds such as biofuels or antibiotics. For these reasons, a detailed understanding of the intimate functioning of microbial metabolism is desirable and, in recent years, new technologies (e.g. NGS) and theoretical modeling have been widely adopted to this aim. In the computational and systems biology lab (ComBo, dbefcb.unifi.it) of the Dep. of Biology, Florence University, we make use of theoretical and experimental resources to investigate basic and applied aspects of microbial metabolism. In particular, we are currently focusing on the systems biology of Antarctic bacteria. The advent of next-generation sequencing techniques resulted in the accumulation of bacterial genome sequences, also from Antarctica and its Oceans. Comparative genomics analyses combined with theoretical modelling contributed to unravelling some molecular mechanisms involved in the adaptation to cold lifestyles, but our comprehension on how the genome expression is modulated over the growth and by the changes of environmental parameters is still fragmentary and requires new working models.

Besides enhancing our comprehension of bacterial functioning, these exhaustive models will help us in highlighting the limits, if any, of bacterial adaptation to a changing environment, such as the global warming of seawater, contributing precious information to the prediction of future scenarios of the entire marine ecosystem functions. Also, it will permit to investigate basic and long-debated scientific topics such as the microbial strategy to cope with multiple nutrient sources. The main objective of this PhD project is to merge the study of global transcriptional regulatory and metabolic networks of Antarctic marine bacteria, especially in terms of the potential impact of global warming of Antarctic sea water and biotechnological application of these microorganisms (e.g. microplastic degradation). The PhD candidate will use mainly genomic and expression (RNAseq) data and bacterial strains collected in previously-funded projects. Coding and NGS-analysis skills represent primary requirements for the applicants.

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CURRICULUM ECOLOGIA ED ETOLOGIA – Sede: Università degli Studi di Parma

Position with scholarship funded by the project Dipartimenti Universitari di eccellenza 2018_2022, SCVSA_2018-2022_DIP_ECCELLENZA, cod CUP - D91G18000140001

Research title: *Carrying capacity of coastal lagoons with molluscs farming: evaluation of biogeochemical services, thresholds and risks*

Scientific tutor: prof. Marco Bartoli

Long-term pressures on coastal ecosystems such as nutrient loading, heat waves, variable freshwater discharge, reduced light availability and molluscs farming can lead to major shifts in biodiversity, productivity, and energy flow (Ryther & Dunstan 1971, Scheffer et al. 2001). Long-term nutrient enrichment in coastal ecosystems can drive a transparent system formerly characterized by submerged, rooted plants to one dominated by phytoplankton or floating macroalgae (Valiela et al. 1992), although as the pressure is released following reductions in nutrient load, the system can return to its previous condition (Lefcheck et al. 2018). In a shift like this, where the system responds uniformly over time under pressure, the community characteristics change, but variance along the trajectory of change can remain homogeneous, indicating rapid restructuring of processes within the system. Pressures may also lead to the development of non-linear, or even oscillatory, patterns in community characteristics and structure as feedback loops and interactions between guilds and trophic groups in the system develop and change (Benincà et al. 2008). Non-linear patterns may be indicated by greater variance within the system over time, and potential changes in mean community characteristics or function for brief time periods. In other cases, the system may be resistant to the pressure, and no change in mean or variance will occur. Molluscs farming applies pressure to the benthos by moving significant quantities of material suspended in the water column to sediments below, and the molluscs themselves excrete dissolved nutrients. There is much interest in how molluscs may change sediment biogeochemical processes, yet recent studies yield conflicting results, possibly due to only collecting measurements in a relatively short period of time, and not considering how sediment biogeochemistry may respond over time. If we consider molluscs as a pressure on sediment processes, and investigate how this pressure regulates sediment biogeochemical processes and biogeochemical services over time, we may improve our understanding of the impact of molluscs on benthic and pelagic processes, of the lagoons carrying capacities and of the risks associated to such activities (Bartoli et al., 2001; Nizzoli et al., 2006; Welsh et al., 2015; Naldi et al., 2020). This research will be based on a coupled biogeochemical and ecological modeling approach analyzing how farmed molluscs (clams, mussels and oysters) affect dissolved gas, metals and nutrient dynamics and benthic functioning in coastal lagoons. Investigations will be carried out in collaboration with the IMC (Centro Marino Internazionale) of Oristano and with the University of Ferrara in a lagoon of the Po Delta, the Sacca di Goro, which is intensively cultivated with *Tapes philippinarum* since the late '80 of the last century and in a Sardinian lagoon, S'Ena Arrubia, where molluscs farming (clams and oyster) is an expanding commercial activity.

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Position with scholarship

Titolo: *Predicting the effect of the Common Agricultural Policy (CAP) measures on the supply of ecosystem services through positive agent-based modeling*

Scientific tutor: prof. Michele Donati

Since its first implementation in the early 1960s, the Common Agricultural Policy (CAP) exerts a relevant influence on the European Union agriculture driving the farm behavior through subsidies (direct and indirect), production constraints, and trade regulations. Across the different reforms, the CAP objectives have undergone a progressive transformation: from the agricultural production strengthening to the provision of public goods. Despite the environmental principles embedded in the CAP regulations, the agricultural practice intensification is undermining important ecosystem services, such as climate change mitigation, water quality, pollination, biodiversity conservation, physical and psychological experience, and heritage. The “greening” measures introduced in the last CAP reform demonstrated their inadequacy to meet the demand from society for an EU agriculture more aware of its role in enhancing regulatory and cultural services. During the last decade, several economic models have been developed and applied to support policy makers and stakeholders to evaluate CAP greening mechanisms from an ex-ante perspective. For instance, the main results provided by CAPRI, PASMA, IFM-CAP models suggested that the CAP measures addressed to generate environmental benefits are not so effective as expected whilst increasing the administrative costs. A recent ex-post analysis confirmed the consistency of the results achieved. This empirical evidence supports the idea that economic modeling is a useful decision tool for designing more effective agricultural policies. This project aims to develop an economic model for the ex-ante evaluation of the impact of CAP measures on the provision of ecosystem services from agriculture. This tool will be based on Positive Mathematical Programming (PMP), a methodology widely used in agricultural policy assessment. A distinctive feature of the PMP is its ability to recover important entrepreneurial decision variables, such as past farming experience, risk attitude, and productive expectations. Its farm-based structure enables the assessment of the impact of policy mechanisms according to the characteristics of farms in their territory. The PMP model will assume the characteristics of an agent-based model capable to capture the interactions among farms in the use of scarce resources. The project consists of three main activities: 1) building the PMP agent-based model and formulating the mathematical optimization structure to represent the agricultural policy mechanisms characterizing the post-2020 CAP reform; 2) collection, organization, and harmonization of agricultural and environmental data, mainly based on the Farm Accountancy Data Network (FADN); 3) assessing the impact of CAP scenarios on ecosystem services, land use, and farm income.

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CURRICULUM ECOLOGIA ED ETOLOGIA – Sede: Università degli Studi di Parma

Position with scholarship funded by the project Dipartimenti Universitari di eccellenza 2018_2022, SCVSA_2018-2022_DIP_ECCELLENZA, cod CUP - D91G18000140001

Research title: *The impact of catastrophic event Vaia on soil features and soil living community in Italian Alps*

Scientific tutor: prof Cristina Menta

In Europe, disturbances caused by windthrow are the prime cause of alteration in forest ecosystems (Schelhaas et al., 2003). Wind disturbances have profound and long-term effects on soil properties, involving structural changes to the physical environment and introducing microclimatic complexity. Moreover, the microsites, which are found in pit-and-mound topography characteristic of windthrows, differ pedogenically (Ulanova, 2000). The removal of canopy material (and the deposition on the forest floor) increases dead wood supply, while uprooted trees can redistribute the mineral and organic soil horizons, exposing the forest floor to light penetration, and changing the density of the pore network in the rooting zone (Mitchell S.J., 2013; Kramer et al. 2004). Changes in litter input, and conditions of heat and water near the soil surface can result in altered dynamics in humus formation, and influence multi-trophic food webs, species-specific interactions, and therefore ecosystem stability (Lüscher P., 2002; Coyle et al. 2017). Many researchers have highlighted the importance of contribute to a clearer understanding of the mechanisms and pathways underlying catastrophic events, to devise effective strategies of ecosystem management and restoration (Johnstone and Chapin III, 2006; Cuchta et al 2012).

The candidate will collect data from forest areas affected by Vaia storm, a catastrophic event that hit the eastern sector of Italian Alps in October 2018, with consistent damages to a forest area of about 42,500 ha (Zanella et al., 2020). The candidate will investigate the overtime effects of the windthrow on soil structure and processes, focusing on the examination of the humus forms and on changings in edaphic fauna community composition. Since humus forms the basic framework for the diversity and community structure of soil biota and this last plays a key role in soil litter breaking and soil organic translocation, regulating nutrient cycling, soil structure formation, and water regulation, interaction between these components may play an important role in successional changes of the ecosystem (Ponge, 2003; Menta & Remelli, 2020, Lakshmi et al., 2021). This line of research aims to explore the interactions between soil biota (namely soil micro- and mesofauna) and the development of topsoil layers (namely humus layers and features) and to investigate their potential functional relationships, in order to contribute to the interpretation and prediction of ecosystem dynamics and responses to future changes in disturbance regime.

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CURRICULUM ECOLOGIA ED ETOLOGIA – Sede: Università degli Studi di Parma

Position with scholarship

Research title: *From molecular genetics to genomics for management and conservation of native salmonids*

Scientific Tutor: prof. Francesco Nonnis Marzano, Marco Bartoli

Recent regulations issued by the Italian government request a strict management of natural populations of salmonids, mainly the Mediterranean brown trout *Salmo ghigii* or *S. cettii* and the marble trout *S. marmoratus*, and represent a turning point for the conservation of native strains. The consistent manipulation of populations which has been ongoing for over a century has put the entire Italian taxon under major threats. Therefore, the above mentioned species are nowadays listed as Critically Endangered according to the IUCN guidelines.

At the same time a wide debate is still open about the choice for the best molecular marker available to taxonomically identify the so called “Mediterranean trout” in Apennine areas and the “pure marble trout” in alpine water basins.

Starting from different approaches based on mitochondrial DNA and nuclear loci, the project will selectively search for brown and marble trout populations distributed all over Italy with the intent to identify source genetic strains to be addressed to conservation programs. After a preliminary assessment based on classic molecular markers, a further improvement will consider a new genomic approach based on RAD Sequencing with the aim of applying an innovative methodology to obtain high throughput data. Results should fill the still existing gap referred to the taxonomic uncertainty and phylogenetic origin of the different populations and allow the planning of reliable conservation strategies also based on new candidate genes playing an adaptive role.

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Position with scholarship

Research title: *Study of the metabolic and physiological variations of plants in response to mycotoxins treatment*

Scientific Tutor: Dott. Enrico Rolli **Co-tutor:** Prof. Alessandro Petraglia.

Being sessile organisms, plants may be continuously exposed to biotic agents, including attacks by other organisms. However, their biochemical machinery allows them to implement defensive strategies against predators and pathogens. These defenses can be active, aimed at limiting the attack by the activation of the secondary metabolism with consequent release of toxic substances for the host. On the other hands, passive defense is devoted to minimizing the spread of the pathogen and the damage eventually induced in the plant tissue. Many pathogenic fungi (*Fusarium*, *Aspergillus*) can infect plants and produce toxic metabolites, known as mycotoxins. These secondary metabolites can be toxic for both for the plants and for the animals that feed on them. The plant defense activated against pathogenic fungi are non-specific defenses, which can also potentially be induced by any other biotic or abiotic stress. The use of *in vitro* plant cultures will indeed offer the possibility excluding any biotic interference on the plants under investigation and at the same time minimizing environmental variables. Therefore, by using *in vitro* plant cultures, the present project aims at: 1) evaluating the metabolic response following mycotoxins treatment using metabolomics and establishing response-differences at the organ level; 2) get new insight into the cellular and physiological mechanisms of plant stress; 3) understanding the role of mycotoxins for the fungi themselves.

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