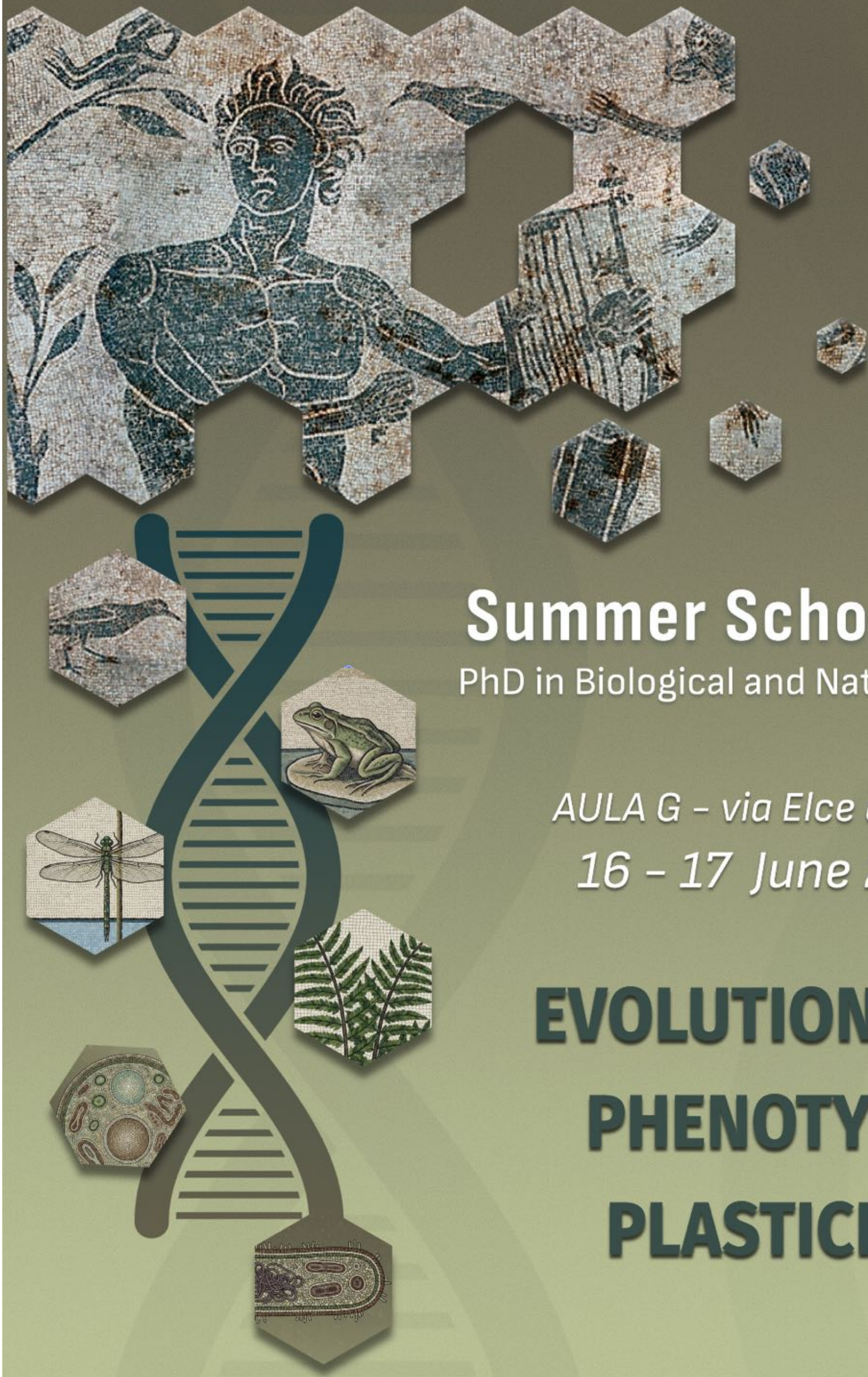
Università degli Studi di Perugia
Dipartimento di Chimica, Biologia e Biotecnologie



Summer School 2026

PhD in Biological and Natural Sciences

AULA G – via Elce di Sotto
16 – 17 June 2026

EVOLUTION AND PHENOTYPIC PLASTICITY

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PhD in Biological and Natural Sciences

Program
EVOLUTION AND PHENOTYPIC PLASTICITY

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16 June

- 9:00 Accreditation and registration

Chairs: Giulia Petroni, Lorenzo Giulivi

9:15 **Jeffrey Tomberlin** (*Department of Entomology, Texas A&M University*)
"Generalist v Specialist in Decomposition Ecology Reveal Unique Evolutionary Stable Strategies Allowing for Niche Partitioning "

9:55 **M. Olalla Lorenzo-Carballa** (CRETUS, *Department of Zoology, Genetics and Physical Anthropology*, *University of Santiago de Compostela*)
"Alternative reproductive strategies in insects: Ecological and genetical correlates of parthenogenesis in the damselfly *Ischnura hastata*"

- 10.35 coffee break

Chairs: Asmita Baral, Sara Futia

11:00 **Matthew Peirce** *(Dipartimento di Medicina e Chirurgia, Università degli Studi di Perugia)*
"Stress management in mosquitoes: Resolving the tension between survival and reproduction in the malaria vector *Anopheles gambiae*"

11:40 **Benedetto Morandi** *(Osservatorio Epidemiologico, Istituto Zooprofilattico Sperimentale dell'Umbria e delle Marche "Togo Rosati")*
"National Arbovirus Plan 2020-2025: Surveillance and Control"

- 12.30 Lunch

Chairs: Maria Vittoria Leonardi, Agnese Carnevali, Giada Sgaravizzi

14:30 **Fabrizio Carletti** (*Istituto Nazionale per le Malattie Infettive L. Spallanzani I.R.C.C.S.*)
"Molecular Evolution and adaptive Dynamics of Viruses"

15.10 **Piotr Koper** (*Maria Curie-Skłodowska University, Lublin, Poland*)
"Genome plasticity in *Legionella*: the role of plasmids and replicon diversity"

15.50 **Stefano Fiorucci** (*Dipartimento di Medicina e Chirurgia, Università degli Studi di Perugia)*
"Structure and functions of the human microbiota"

- 16:30 Closure of works

17 June

- 9.00 Accreditation and registration

Chairs: Maurizio Gildo Cavaliere, Davide Perrone

09:15 **Salvatore Tomasello** (*Department of Systematic Botany, University of Gottingen*)
"Molecular methods for species delimitation, phylogenetic and biogeographic inference. Examples from the Asteraceae"

09:55 **Emanuele De Paoli** (*Dipartimento di Scienze Agroalimentari, Ambientali e Animali, Università degli Studi di Udine*)
"From Individual Responses to Evolutionary Adaptation: Genetic and Epigenetic Control of Plant Phenology"

- 10:35 coffee break

Chairs: Alessandra Maganza, Maria Vittoria Leonardi, Camilla Mossotto

11:00 **Giulia Margaritelli** (*Dipartimento di Fisica e Geologia, Università degli Studi di Perugia*)
“Foraminifera as Ecological Indicators: Modifications and Adaptations”

11:40 **Irene Cardinali** *(Dipartimento di Chimica, Biologia e Biotecnologie, Università degli Studi di Perugia*)
"Tracing maternal histories with DNA: from macro to micro phylogeographic evolutions"

12:20 **Silvia Crotti** (*Istituto Zooprofilattico Sperimentale dell’Umbria e delle Marche “Togo Rosati”*)
“Dermatophytoses from a one health perspective: what can and should we do?”

- 13:00 Lunch

14.30 PhD students’ presentations

- 17:00 Closure of Summer School works

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Generalist v Specialist in Decomposition Ecology Reveal Unique Evolutionary Stable Strategies Allowing for Niche Partitioning

Jeffery K. Tomberlin, PHD, D-ABFE

Jeffery.tomberlin@ag.tamu.edu

Department of Entomology, Texas A&M University

Keywords: Necrobiome, Food web, Nutrition Ecology, Bioeconomy

ABSTRACT The necrobiome, the diverse community of organisms associated with decomposing remains, constitutes a complex ecological system characterized by diverse nutrient profiles, microbial interactions, and succession dynamics. As decomposition progresses, the availability and composition of nutrients such as lipids, carbohydrates, and particularly amino acids, undergo substantial shifts shaped by microbial activity and environmental factors. Amino acids, essential building blocks for life, stand out as critical resources within this dynamic milieu, influencing the metabolism of decomposers and the recycling of nutrients into ecosystems.

Among necrobiome members, flies play a pivotal role in the breakdown of organic matter, with specialist and generalist species occupying distinct ecological niches. Blow flies (Diptera: Calliphoridae), exemplifying specialists, preferentially exploit animal carcasses, adapting to the unique amino acid profiles of these protein-rich substrates. In contrast, the black soldier fly (*Hermetia illucens*), a generalist, utilizes a broad array of decomposing materials, relying on diverse enzymatic systems to extract amino acids from various sources. The fluctuating availability of specific amino acids within decaying substrates acts as a powerful selective

force: blow flies evolve specialized metabolic capacities suited to their niche, while black soldier flies are selected for flexibility in resource exploitation.

Understanding the selective pressures imposed by amino acid limitations is key for interpreting decomposition ecology. These dynamics not only determine fly community structure and nutrient recycling efficiency but also inform practical applications in forensic entomology and the bioeconomy. Insights into amino acid-driven natural selection can refine postmortem interval estimations and optimize waste-to-protein conversion systems, underscoring the need for integrating biochemical and evolutionary perspectives in necrobiome research.

“Alternative reproductive strategies in insects: Ecological and genetical correlates of parthenogenesis in the damselfly *Ischnura hastata*”

M. Olalla Lorenzo-Carballa

olalla.lorenzo.carballa@usc.es

CRETUS, Department of Zoology, Genetics and Physical Anthropology,

University of Santiago de Compostela, Spain

Keywords: asexual reproduction, islands, Odonata

ABSTRACT

The term “geographical parthenogenesis” refers to the observed pattern of non-overlapping distributions of sexual and parthenogenetic lineages of the same species. The hypotheses that explain this pattern largely rest on the idea that parthenogenetic lineages can persist in the long term if they escape interactions with biological enemies and/or sexual lineages. Hence, parthenogenetic reproduction is more likely to occur in areas that are difficult to colonize or subject to reduced biotic pressure, such as islands, where parthenogens can persist in the long term.

Ischnura hastata constitutes the only known example of parthenogenetic reproduction among the insect order Odonata. This species has a widespread distribution in the American continent, where it has colonized remote islands such as the Galápagos. *I. hastata* is also present in the Azores archipelago in the Atlantic Ocean, where female-only, parthenogenetic populations have been found.

Here I review the genetical and ecological correlates of asexual reproduction in this unique species. Population genetic analyses have revealed a metapopulation-like structure across the sexual distribution range, with no evidence of isolation by distance over more than 2,000

km. The strong protandry observed in the sexual populations – driven by shorter larval development times and shorter adult lifespans in males – may lead to reproductive asynchrony, leaving females unmated in small or marginal populations. In this scenario, mate limitation would benefit females capable of asexual reproduction, thus facilitating the establishment of an obligate parthenogenetic lineage. However, the transition from sex to parthenogenesis in *I. hastata* appears to have succeeded only in the Azores.

Stress management in mosquitoes: Resolving the tension between survival and reproduction in the malaria vector *Anopheles gambiae*

Matthew Peirce

matthew.peirce@unipg.it

Dipartimento di Medicina e Chirurgia, Università di Perugia

ABSTRACT

Finite nutritional resources must be divided between two imperatives shared by all living things: survival and reproduction. In this work we have tried to understand more about the signaling mechanisms involved in deciding how this division of resources is achieved using the malarial mosquito, *Anopheles gambiae* as a model.

What we find is that when these mosquitoes are infected by an evolutionarily unfamiliar malaria parasite, the reproductive output of the infected female (the number of eggs she devlelops after a blood meal) as well as her longevity are strongly reduced. At the same time the infection causes the activation of the ancient, stress-related signaling pathway cJun N-terminal kinase (JNK). Using RNAi we show that infected females are protected against both these fitness costs if JNK expression is reduced, supporting a causal link between JNK activation and infection-induced fitness costs.

To understand the mechanism involved, we used RNAseq to identify genes differentially expressed when JNK expression is reduced. We found that JNK regulates the expression of the p450 enzyme, Cyp315a1, which controls the production of a steroid hormone 20-hydroxyecdysone (20E), (a relative of mammalian sex hormones like estrogen), which is pivotal in driving egg development in mosquitoes. We went on to show that this transcriptional change is reflected in reduced levels of the hormone

itself in infected mosquitoes explaining the reduction in egg development in infected females.

Finally we showed that a non-infectious stress, heat shock, behaved similarly. Heat shocked females show increased JNK signalling, JNK-dependent reduction in egg production and reduced levels of 20E. Interestingly, heat-stressed JNK knock down females produced more eggs but died more frequently highlighting that in this case JNK was required for stress resistance. The findings identify a shared mechanism controlling resource allocation between reproduction and survival but also highlight how stress responses may be both protective and self damaging depending on the context.

National Arbovirus Plan 2020-2025: Surveillance and Control

Benedetto Morandi

morandi@izsum.it

Istituto Zooprofilattico Sperimentale
dell'Umbria e delle Marche "Togo Rosati"
UOS VD Osservatorio Epidemiologico

ABSTRACT

The Italian National Arbovirus Plan 2020-2025 has been officially extended through 2026 to ensure uninterrupted vector-borne disease control. The surveillance core focuses on the early detection of viral circulation through integrated human, veterinary, and entomological monitoring. Key priorities for 2026 include tracking West Nile, Usutu, and Dengue viruses, particularly in high-risk and urban areas. This extension maintains a unified network for rapid response, vector mapping, and blood donation screening to safeguard public health.

Molecular Evolution and adaptive Dynamics of Viruses

Fabrizio Carletti

fabrizio.carletti@inmi.it

Istituto Nazionale per le Malattie Infettive

Lazzaro Spallanzani I.R.C.C.S. ROMA

ABSTRACT

Viruses evolve rapidly due to high mutation rates, large population sizes, and error-prone replication, generating diverse quasispecies on which selection acts efficiently. Their genetic variation arises through mutation, recombination, and reassortment, while evolutionary forces such as natural selection, drift, and purifying constraints shape population dynamics. Concepts like fitness landscapes, host–virus coevolution, and zoonotic adaptation explain how viruses optimize replication, escape immunity, and cross species barriers. These principles illuminate real-world phenomena including immune escape, drug resistance, and the emergence of novel variants.

Genome plasticity in Legionella: the role of plasmids and replicon diversity

Piotr Koper

piotr.koper@umcs.pl>

Maria Curie-Skłodowska University, Lublin, Poland

ABSTRACT

Legionella species are ubiquitous aquatic bacteria and important opportunistic human pathogens characterized by highly dynamic and plastic genomes. While chromosomal diversity within the genus has been extensively studied, considerably less is known about the diversity and distribution of plasmids and their replication systems. This presentation focuses on a comparative analysis of the *Legionella* plasmidome based on publicly available and newly sequenced genomes. Particular attention is given to the diversity of plasmid replicons and the occurrence of related replication systems across different *Legionella* species, suggesting extensive plasmid exchange and evolutionary relationships within the genus. Examples of large and structurally diverse plasmids identified in environmental isolates are also discussed. Together, these analyses provide new insights into the contribution of plasmids to genome plasticity and diversification in *Legionella*.

Molecular methods for species delimitation, phylogenetic and biogeographic inference. Examples from the Asteraceae

Salvatore Tomasello

salvatore.tomasello@uni-goettingen.de

Department of Systematic Botany, University of Gottingen

ABSTRACT

The Asteraceae are one of the biggest families of Angiosperms. Several representatives of the family are evolutionary young and taxonomically complex, and their evolution has been often perfused by hybridization and fast radiation events. Under these circumstances, the inference of phylogenetic relationships is particularly difficult and needs the use of big amounts of genetic data and advanced phylogenetic methods.

In the last decade, the establishment of modern DNA sequencing technologies allowed us to gain massive genomic information at relatively low costs. The development of new models and methods for the analyses of DNA sequences, capable to take into account also hybridization and the stochasticity intrinsic to the speciation process (e.g., *incomplete lineage sorting*; ILS), provided us with a mathematical framework to infer phylogenies in taxonomically complex organismic groups.

Herewith, I am going to report on methods for the analysis of DNA sequences based on the coalescent-model, and used to infer species delimitation, phylogenetic and biogeographic patterns. The Asteraceae family, one of the biggest families of Angiosperms in terms of number of species, offers several examples of evolutionary young and taxonomically complex genera, which evolutionary history have been interested by reticulate evolution and fast evolutionary radiations.

From Individual Responses to Evolutionary Adaptation: Genetic and Epigenetic Control of Plant Phenology

Emanuele De Paoli

Dep. of Agricultural, Food, Environmental and Animal Sciences
University of Udine

ABSTRACT

Plant phenology, the timing of recurrent developmental events such as germination, flowering, and senescence, is highly sensitive to environmental fluctuations and represents a key determinant of plant fitness. In the context of rapid climate change, understanding how plants adjust their phenological responses across temporal and spatial scales has become a central challenge in plant biology and evolutionary ecology.

By integrating evidence from recent scientific literature with experimental insights gained at the University of Udine using forest tree species as model systems, this seminar aims to outline the current understanding of epigenetically mediated phenotypic plasticity, with particular emphasis on phenological traits. Special attention will be devoted to disentangling adaptive epigenetic responses from the confounding effects of fundamental mechanisms involved in genome stability and maintenance, which may generate molecular patterns that are difficult to interpret in an ecological and evolutionary framework. Through this perspective, the seminar will discuss both the potential and the limitations of epigenetic regulation as a driver of plant acclimation and long-term adaptation to environmental change.

Foraminifera as Ecological Indicators:
Modifications and Adaptations

Giulia Margaritelli

giulia.margaritelli@unipg.it

Dipartimento di Fisica e Geologia – Università degli Studi di Perugia

Keywords: foraminifera, paleoclimatology, paleoecology, micropaleontology, bioindicator

ABSTRACT

Foraminifera represent one of the most fascinating and scientifically significant groups of single-celled organisms on Earth. Belonging to the kingdom Protista, these amoeboid organisms first appeared over 500 million years ago and continue to inhabit every niche of the modern oceans.

The most prevalent taxa are characterized by calcareous tests, which serve as an invaluable repository of data for Earth Science studies. Indeed, through the study of their morphology and by performing chemical analyses on their shells, it is possible to understand the variations and links between these organisms and the ecological parameters of the waters in which they lived. The distribution of foraminifera is governed by environmental parameters providing palaeoceanographic studies with a significant array of proxy data such as primary production, salinity and temperature.

Furthermore, foraminifera serve as highly sensitive bioindicators for monitoring polluted marine environments, as their short life cycles allow them to record anthropogenic stress in real time. In areas contaminated by heavy metals or hydrocarbons, these organisms often exhibit significant morphological abnormalities, such as the twisting, stunting, or asymmetrical development of their calcareous tests.

The high abundance and the excellent preservation of foraminifera in marine sediment make them probably the best fossil record on Earth, providing unparalleled archives of morphological change, habitat, ecological variations and for evaluating the impact of human activities on coastal and transitional waters.

Tracing maternal histories with DNA: from macro to micro phylogeographic evolutions

Irene Cardinali

irene.cardinali@unipg.it

Department of Chemistry, Biology and Biotechnology, University of Perugia

Keywords: mitochondrial DNA; phylogeography; genetic variability; ancient DNA; maternal lineages

ABSTRACT

Human mitochondrial DNA (mtDNA) variation represents a powerful marker for reconstructing maternal ancestry, population dynamics, and human migrations across different temporal and geographic scales. Recent genomic studies have shown that the Italian population displays a remarkably high degree of genetic heterogeneity compared with other European populations, structured along a north-south cline and shaped by multiple demographic processes.

Within this framework, a micro-geographic investigation of Central Italy was performed to reconstruct the maternal genetic history of Umbria, a region historically positioned between the Tyrrhenian and Adriatic cultural spheres and inhabited since antiquity by one of the oldest Italic populations. A diachronic approach combining ancient and modern mtDNA data revealed a significant genetic differentiation between eastern and western Umbria, with evidence of long-term maternal genetic continuity from pre-Roman populations to present-day communities. In particular, eastern Umbrian groups retain mitochondrial lineages suggesting ancient connections with Central-Eastern Europe, possibly linked to Bronze Age Indo-European expansions.

To further investigate maternal mobility across Eurasia, the complete mtDNA variation was also analyzed in modern Mongolian populations. The results highlight extensive female-mediated interactions between Eastern Asia and Western Eurasia, supporting

long-lasting transcontinental exchanges intensified during historical periods such as the Silk Road and the Mongol Empire.

Overall, these findings demonstrate the role of mtDNA analyses in reconstructing human evolutionary histories from continental-scale processes to fine-scale local population structure.

Dermatophytoses From A One Health Perspective:

What Can And Should We Do

Silvia Crotti

DVM, Istituto Zooprofilattico Sperimentale dell'Umbria e delle Marche "Togo Rosati", Laboratorio Diagnostica Specialistica e Benessere Animale

ABSTRACT

Le dermatomicosi rappresentano una rilevante problematica di sanità pubblica e medicina veterinaria, in quanto infezioni fungine a potenziale zoonosico che coinvolgono l'interazione tra ospiti animali e umani, agenti patogeni ed ambiente. La loro diffusione è influenzata da molteplici fattori, tra cui la presenza di serbatoi animali, le condizioni ambientali e la suscettibilità dell'ospite. In questo contesto, l'approccio One Health si configura come uno strumento fondamentale per la prevenzione, la diagnosi e il controllo delle infezioni da dermatofiti, promuovendo una visione integrata della salute umana, animale e ambientale.

L'identificazione accurata degli agenti eziologici mediante metodiche microbiologiche e molecolari, associata alla valutazione delle possibili fonti di contagio e dei fattori di rischio, consente di adottare strategie terapeutiche e preventive efficaci, comprese le misure di igiene ambientale e la gestione dei potenziali serbatoi di infezione. In particolare, il contatto stretto con gli animali da compagnia può rappresentare un importante fattore di esposizione e deve essere considerato nell'anamnesi clinica per favorire un riconoscimento tempestivo della patologia.

La collaborazione interdisciplinare tra medici, veterinari, microbiologi e altri professionisti della salute è essenziale per garantire una gestione ottimale dei casi, limitare la trasmissione interspecifica e prevenire l'insorgenza di fenomeni di resistenza ai trattamenti antifungini. Un sistema di sorveglianza continuo basato

sui principi One Health permette inoltre di migliorare la conoscenza epidemiologica delle dermatomicosi e di sviluppare strategie di controllo più efficaci, contribuendo alla tutela della salute pubblica e del benessere animale.

Structure and functions of the human microbiota

Stefano Fiorucci

stefano.fiorucci@unipg.it

Dipartimento di Medicina e Chirurgia Università degli Studi di Perugia

Keywords: Intestinal microbiota, inflammation, dysbiosis, metabolites, intestinal permeability

ABSTRACT

The intestinal microbiota is a highly dynamic ecosystem whose composition and function continuously adapt to environmental, dietary, metabolic, and immunological stimuli. This remarkable plasticity is essential for maintaining host homeostasis, allowing rapid responses to changes in nutrient availability, pathogen exposure, and inflammatory challenges. Through the production of metabolites, including short-chain fatty acids, secondary bile acids, indoles, the microbiota regulates epithelial barrier integrity, immune cell differentiation, and systemic metabolic pathways. Loss of microbiota plasticity, often referred to as **dysbiosis**, has emerged as a central feature of several chronic inflammatory disorders. In inflammatory bowel diseases dysbiosis is characterized by reduced microbial diversity, depletion of beneficial commensals such as butyrate-producing bacteria, and expansion of pathobionts. These alterations impair mucosal barrier function, promote aberrant activation of innate and adaptive immune responses, and contribute to chronic intestinal inflammation. The importance of **microbiota plasticity extends beyond the intestine** through the gut–liver axis, a bidirectional communication network linking the gastrointestinal tract and the liver. Alterations in microbial composition and function influence bile acid metabolism, intestinal permeability, and translocation of microbial products to the portal circulation. These mechanisms have been implicated in the pathogenesis of several liver diseases, including metabolic dysfunction-associated steatotic liver disease, primary sclerosing cholangitis, primary biliary cholangitis, and cirrhosis. Restoring microbiota resilience through dietary

interventions, probiotics, postbiotics, fecal microbiota transplantation, and therapies targeting bile acid signaling pathways represents a promising strategy for treating both intestinal and liver diseases. We have established an integrated microbiome research platform that includes next-generation sequencing facilities and advanced bioinformatic capabilities for the characterization of microbial communities and their metabolic functions.