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Mechanoecology: Insect Attachment from the Plant Perspective

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Keywords: adhesion; biomechanics; plant protection

ABSTRACT

Most of the one million insect species described so far are associated with plants. Such insects should be able to attach successfully to plant surfaces. Dealing with attachment, we have to consider a contact problem, in which two bodies are involved. Both these parts may have various geometries, mechanical and chemical properties. Moreover, insects produce and deliver a secretory fluid into a contact zone, whereas many plant substrates bear specialised surface coverage. This talk summarises our previous structural and experimental studies on insect attachment and the effect of plant substrates on it. Plant surfaces have a wide range of textures and microsculptures. They may be smooth or structured, i.e. covered with various hairs (trichomes) or bear microscopic crystals of epicuticular waxes. To study the role of different structures of a plant surface in insect attachment, various plant surfaces were screened and four hypotheses of anti-adhesive effect of plants were proposed. (A) Roughness-hypothesis: wax crystals and/or little trichomes cause microroughness, which considerably decreases the real contact area. (B) Contamination-hypothesis or cohesion-failure-hypothesis: wax crystals are easily detachable structures that contaminate pads. (C) Wax-dissolving-hypothesis: Insect pad secretion may dissolve wax crystals. This would result in the appearance of a thick layer of fluid, making the substrate slippery. (D) Fluid-absorption-hypothesis: Structured wax coverage may absorb the fluid from the pad surface.

Chemical ecology of entomophagous insects

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Keywords: parasitoids; predators; tri-trophic interactions

ABSTRACT

Entomophagous insects, i.e., parasitoids and predators, provide important ecosystem services (natural control) and include numerous biological control agents that are essential for crop protection. While predators belong to very different taxa and typically prey upon many individuals during their life cycle, parasitoids are holometabolous insects that develop within a single host, which generally is killed at the end of parasitoid's larval development. Both parasitoids and predators use chemical cues (semiochemicals) and physical cues to communicate. Focusing on semiochemicals, entomophagous insects use pheromones for intraspecific communication and allelochemicals (mostly kairomones and synomones) when interacting with other organisms (e.g. herbivorous hosts and plants). Female parasitoids, being characterized by a limited foraging time, have evolved highly specialized strategies to optimize host finding and parasitization, thus allowing reproduction. For instance, parasitoids have acquired the ability to exploit kairomones from their host and synomones induced in plants by the host (herbivore-induced plant volatiles). Predators also use similar strategies to locate their preys. Additionally, both parasitoids and predators exploit volatile semiochemicals to locate alternative food sources and shelters. Understanding the chemical ecology of entomophagous insects offers great potential for field and laboratory application, aiming at the improvement of pest control efficacy.

Mechanisms of plant defense against insect herbivores

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Keywords: Insect pests; Plant defense; Salicylate- and jasmonate-dependent defense pathways

ABSTRACT

In nature, plants are constantly subjected to different types of both biotic and abiotic stresses. Interactions with other organisms have a particular impact on plant health and development, and consequently also on productivity and food security. Examples of biotic interactions are those with harmful organisms, such as insect herbivores against which plants have developed various response mechanisms divided into constitutive (present independently of the insect attack), or inducible (stimulated only at the moment of contact with the enemy) defenses. Constitutive defenses include physical (spines, waxy cuticles, cell walls, trichomes), or chemical (secondary metabolites with repellent and/or toxic action) barriers. Inducible defenses are divided into direct and indirect. Direct ones involve the induction of defense proteins expressed both locally at the site of attack and systemically in distal tissues. Indirect defenses involve the emission by plants of Herbivore-Induced Plant Volatiles (HIPVs) that act as attractants for the natural enemies of insects. The activation of inducible responses involves complex networks of transduction signals in which various chemical mediators, including hormonal and non-hormonal substances, are involved. In the plant-insect interaction, it is mainly salicylic acid (SA) and jasmonic acid (JA) that act as defense regulators with antagonistic or synergistic activity. This important hormonal crosstalk allows the plant to regulate the immune response by improving its adaptation to the environment.

Chemical and visual cues interaction in host-plant selection: the case study of the melon ladybird

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Keywords: olfaction; visual cues; *Chnootriba elaterii*

ABSTRACT

Host-plant selection is a complex phenomenon involving insect senses and plant cues. Using as a model the oligophagous melon ladybird *Chnootriba elaterii* (Coleoptera, Coccinellidae), feeding on different cucurbits, the present research aims to shed light on the various cues involved in the host location process, at long and short distances. For this purpose, we used electroantennographic recordings (EAG) and scanning electron microscopy (SEM) to characterize antennal olfactory sensilla and their sensitivity to the VOCs produced by seven cucurbits. Then, open and closed Y-tube olfactometers were used to evaluate the involvement of chemical and visual cues in the host-plant selection. SEM investigations described for the first time the antennal olfactory sensilla of the melon ladybug, and EAG recordings demonstrated that antennae respond to both standard compounds and plant VOCs from Cucurbitaceae (except *L. cylindrica*). Despite the EAG responses, olfaction alone did not guide females in the closed Y-tube olfactometer among different host-plant species, nor could allow the ladybirds to distinguish between Cucurbitaceae and non-Cucurbitaceae. Instead, when *C. elaterii* were tested in an open olfactometer (where could see plants), they were able to move toward the hosts only when olfactory cues were presented together with visual cues. This result proves that in the oligophagous melon ladybird, the visual aspects cannot be divorced from the chemical aspects to accomplish the host-plant selection process.

Intraspecific communication in spittlebugs

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Keywords: spittlebugs, chemical communication, vibrational communication

ABSTRACT

Spittlebugs are remarkable insects known for their unique life cycle. As nymphs, they produce a frothy mass, inside which they undergo development, while as adults they disperse and jump over meadows. Moreover, spittlebugs are known as vectors of various diseases (*e.g. Xylella fastidiosa*). For years, the way spittlebugs communicate puzzled researchers. Recently, significant progress was made unraveling the mechanisms, functions, and ecological significance of the signals used in their communication. Chemical communication represents a vital mode of communication especially when they are nymphs. The chemical cues serve as a message to other individuals indicating their presence or food availability. These compounds can be embedded into the froth or released into the environment. When adults they employ a multi-modal approach to communicate, incorporating chemical and vibrational signals. Vibrational signals hold a central role in spittlebugs communication. The subtle sounds produced by body movement conceal various information necessary for successful interaction. By unveiling the intricate vibrational and chemical dialogues we have enhanced our understanding of their behavior, which enabled us to develop strategies for successful control.

DNA-based methodological approaches and their applications

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Keywords: DNA-based analyses; genetic variability; phylogeny

ABSTRACT

Nowadays molecular techniques play a pivotal role in the study of genetic variability of living beings. In this context, the DNA sequence variation helps to define the selective and dispersal patterns of populations. The uniparental markers are the most valid tool to reconstruct the evolutionary history of populations from female and male perspectives. The analysis starts with a sample collection aimed to obtain a representative dataset of the population, and is followed by the extraction of DNA and the analysis of uniparental markers through a phylogeographic approach. This can be applied to a macro- and micro-geographic level, by focusing on specific areas and populations. The Italian peninsula is characterized by a high degree of genomic variability distributed along the north-south axis, thus reflecting the country geography. Multi-faced inputs have shaped the human gene pool and can be observed also in the micro-geographic contexts of Umbria or other regions. Additional contributions on the human history come from the parallel analysis of those animals that have followed the ancient populations along their paths. In this scenario, the uniparental markers represent a powerful tool for answering multiple questions and reconstructing the genetic history of populations, and they increase in value when framed within a multidisciplinary context.

Living with a back-seat driver, can neurotropic pathogens alter red fox behavior and habitat use?

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Keywords: red fox; neurotropic pathogens; behavioral alterations

ABSTRACT

The red fox (*Vulpes vulpes*) is the carnivore with the widest native distribution, spanning the whole boreal hemisphere. The generalist diet and the extraordinary adaptability allow this species to exploit several ecological niches, including urban environments. There is a large body of evidence that prove the role of parasitic and viral neurotropic pathogens in the alteration of host behavior. It has been shown that *Toxoplasma gondii*, an apicomplexan parasite, is responsible for the onset of risk-taking behaviors in several mammalian species including rodents, carnivores and even humans. The aims of the PhD project are: to assess the presence and prevalence of parasitic and viral neurotropic pathogens i.e., *T. gondii*, *Neospora caninum*, *Encephalitozoon cuniculi*, Borna-Disease Virus (*BoDV-1*), Canine Distemper Virus (*CDV*) and Fox Circovirus (*FoxCV*) in the red fox; and to map the occurrence of parasitic elements in functional areas of the brain throughout histological and histochemical techniques to speculate potential associations with behavioral alterations. Histopathological analyses will be performed on animals sampled within 24h from death whereas, a wider sample will be subjected to serological and molecular analyses to assess the positivity to the pathogens of interest. Furthermore, behavioral tests will be performed on both infected and non-infected foxes during their rehabilitation period in a Wildlife Rescue Center, to check if infection could be a driver for behavioral alterations.

Stable isotope analysis: a tool for the assessment of the ecological impact of non-indigenous species

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Keywords: bioinvasions; food webs; trophic niche

ABSTRACT

In recent decades, the analysis of carbon, nitrogen and sulfur stable isotopes (SIA) has emerged as a powerful, viable methodology for examining food web structure and dynamics, as well as for addressing the effects of a diverse set of anthropogenic pressures, including biological invasions. Here I will examine how SIA can assist with the assessment and management of the ecological impacts of invasive consumers on recipient communities. First, a synthesis of the basics of SIA will be presented, followed by a review of the most popular analytical approaches and isotopic metrics used in invasion biology. Finally, the limitations of the methodology based on bulk tissues isotopes will be considered, indicating how novel approaches based on fatty acid or amino acid compound specific isotope analysis (FA- or AA-CSIA) can overcome them. I will conclude emphasizing that SIA provides to date a useful, integrated toolbox of indicators of the ecological impact of invasive consumers and a unifying methodological-theoretical framework for large scale, inter-ecosystem comparisons.

Bioindicators and environmental pollution

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Keywords: Chemical fate; Contamination; Biotic indices

ABSTRACT

The chemical fate describes where a chemical substance or element goes when it gets into the environment and how it can be chemically transformed by physical, chemical or biological processes. Some chemicals have a tendency to bioaccumulate and their fate is to end up in animal tissue. The bioaccumulation and also the subsequent toxic effects depend strongly on the chemical speciation, i.e. the chemical structure, oxidation state, ionic charge of the pollutant. The direct characterization of the speciation state is very interesting but it is difficult therefore often the traditional approach is to monitor the total abundance of a chemical, which could lead to a misleading interpretation of the environmental pollution. An alternative approach is the use of bioindicators, which represent an effective natural system for detecting the effects caused by environmental contamination. Such sensitive organisms may be considered at species, group of species, or community level. Their biological response results from the complex of events to which they are subjected, and the environmental alteration is measurable through qualitative-quantitative indices. In addition, specific contaminants are subject to bioaccumulation in selected tissues of sentinel organisms. In this case, exceeding the threshold level is a predictive way to implement actions to safeguard human health and the environment.

Life programme the European tools for habitat and species conservation

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Keywords: Nature conservation; LIFE Programme; EU funded projects

ABSTRACT

Since its creation in 1992, the LIFE financing programme has supported over 1,800 nature and biodiversity projects in order to safeguard Europe's nature. Despite the programme's small size (accounting for less than 1% of the EU budget), the €2.2 billion invested so far in these projects has done much to implement EU biodiversity policy, especially, the EU Nature directives (the Birds Directive and the Habitats Directive), the Invasive Alien Species Regulation and other policies related to nature.

The 1979 Birds Directive and the 1992 Habitats directives are the cornerstone of the nature protection regime. Jointly, the two directives extend protection to around 1,400 animal and plant species and 233 habitat types. The directives articulate an integrated approach where habitat conservation is on an equal footing with protecting individual species. At the same time, they aimed to establish a coherent, continent-wide ecological network of protected areas, which led to the creation of the EU Natura 2000 network. Since 1992, EU Natura, which spans all 27 EU countries, has grown to become the world's largest coordinated network of protected areas.

Bioindicators for the evaluation of the ecological quality of surface waters: benthic diatoms

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Keywords: Biological index; algae; biodiversity

ABSTRACT

Diatoms are often the main element of phytobenthos biodiversity in inland waters, representing an important component in freshwater ecosystems and are one of the most important groups of algae for monitoring purposes. Diatoms have biological and ecological characteristics that make them a good indicator for the characterization of water quality. They have a cosmopolitan distribution and high sensitivity to water physico-chemical characteristics and environmental conditions. They are the algal group most widely used as indicators of river quality. In Italy the Intercalibration Common Metric Index (ICMi), was developed for the assessment of benthic algal ecological status. The ICMi is based on two sub-indices: the IPS index, which mainly assesses the sensitivity of species to organic pollution and the TI Index, which is based on the species sensitivity to trophic pollution. For the diatom based ecological status assessment, the value of the two sub-indices have to be expressed as Ecological Quality Ratio with the respective reference values for each river macrotype following the Italian Regulation (DM 260/2010, 2010). In compliance with the European and Italian regulations, the ARPA Umbria defined specific river monitoring programs and networks based on river type definition, human pressures and risk analysis. The main aim of this contribution was to characterize and to analyze diatom diversity and ecological status across the different regional river macrotypes in Umbria.

Breeding birds in Umbria: research methods, population trends and multi-species indicators

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Keywords: birds; trends; indicators

ABSTRACT

Common species of birds breeding in Umbria were monitored for 21 reproductive seasons from 2000 to 2022 (except year 2006) by means of an annual repeated survey of 1681 point-counts scattered across the whole region. 20 points were placed in each 10x10 km UTM grid unit, located 1 km apart from each other along low traffic roads, crossing the most representative environments. We found a total of 133 breeding species; 72 among them were present in at least 1% of all stations. We obtained yearly population indices for 72 common species and examined population trends; in order to avoid possible first-time effects, we performed all the analyses omitting the first year. Furthermore we calculated multi-species indicators for species associated with farmland (regional set of 33 species), woodland (regional set of 22 species) and grassland (regional set of 6 species) habitat, taking the geometric means of annual specific population indices. 48% of the common species (32% of all the species for which trends could be produced) have declined during the years 2001 to 2022, whilst only 36% have increased (23% of all the species). Multi-species indicators seem to show a better situation for woodland than for farmland and grassland birds. All the indicators show a worst situation considering only the last 10 years.



8 June



The SARS-CoV-2 pandemic: an epidemiological perspective

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Keywords: epidemiology; public health; pandemic

ABSTRACT

Epidemiology is a useful (fundamental) biomedical discipline for making public health choices: the SARSCoV2 epidemic was a clear example of this. The contribution to the definition of monitoring indicators and the constant analysis of the spread of the infection across the territory to articulate responses based on local characteristics are among the most emblematic activities involving epidemiology in the pandemic period. The most strategic actions implemented can be summarized as follows: assessment of care needs; analysis and return of rapid information on the use of healthcare by the population; analysis of population subgroups (risk groups) and infected clusters; ability to predict the trend of the epidemic and of the care needs also through mathematical models; contribution to the communication of decisions taken under conditions of uncertainty, trying to argue and explain them. Epidemiology was therefore asked for a strong commitment in the ability to measure, analyse, evaluate, predict, and critically reflect in the emergency, even in the current post-pandemic phase.

Genomic Aspects of the SARS-CoV-2 Evolution

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Keywords: SARS-CoV-2, whole genome sequencing, variant

ABSTRACT

SARS-CoV-2 caused millions of infection cases and more than 6 million deaths from December 2019 to May 2023. From its unclear origin, this virus keeps evolving over time resulting in several variants classified by public health impact and phenotypes. Whole genome sequencing (WGS) is the only technique that allows a proper identification and classification of variants. Unsurprisingly Next-generation sequencing (NGS), bioinformatics and databases as GISAID EpiCoV played a key role in COVID-19 pandemic to timely manage the identification and spread of a new virus variants. D614G, the first mutation in Spike glycoprotein, has been an evolutionary turning point that resulted in gradually accumulation of genetic changes acquired by replication errors or host-mediated editing. Advantageous changes are selected by natural selection inducing increased fitness and infectivity. Variants turnover is clear evidence of viral optimization and adaptation during the progress of immune landscape. From Alpha to Omicron variants has been observed a reduction of infection severity and pneumonia cases with an increased tropism for upper respiratory tract and increased transmissibility due by stronger Spike-ACE2 interaction and higher immunological escape. Recombination events are typical of coronaviruses as detectable by the numerous recombinants lineages evolving especially from Omicron BA.2 as XBB variants. Despite the rising data available there are many countries with poor variants surveillance, that is crucial for viral identification and prompt implementation of prevention strategies.

Wastewater-based surveillance of SARS-CoV-2

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Keywords: SARS-CoV-2; wastewaters; epidemiology

ABSTRACT

Despite decades of environmental surveillance of poliovirus prevalence through sewage samples, interest on Wastewater based-epidemiology (WBE) peaked during COVID-19 pandemic. WBE has proved to be a key tool for assessing virus circulation and variants prevalence. Since Oct-2021 Italy has set up a national sewage surveillance system (SARI network) in the framework of the EU Commission recommendation concerning the implementation of wastewater monitoring of SARS-CoV-2. Quantitative assessment (qPCR) and variant tracking (spike gene sequencing) in wastewater mirrored the data obtained from clinical surveillance. Indeed, the national trend of sewage SARS-CoV-2 concentrations from Oct-2021 to Sept-2022 showed four different waves, associated with the emergence of the Omicron sub-lineages (BA.1, BA.2, and BA.4/5). Besides confirming the circulation of variants already detected in swabs from patients, in Oct-2022 the identification of Omicron subvariants BQ.1 and BQ.1.1 in wastewater samples preceded that in infected subjects. These observations highlight the potential of WBE for monitoring human health threats besides SARS-CoV-2, e.g. others emerging-reemerging pathogens and antimicrobial resistance (AMR), a prospective recently recognized in the EU Urban Wastewater Treatment Directive and the Italian National Action Plan on Antimicrobial Resistance, both including permanent surveillance programs based on urban sewage analyses.

Does the Sars-Cov-2 3a Protein Function as an Ion Channel?

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Keywords: SARS-CoV-2; ORF3a; ion channels;

ABSTRACT

The Sars-Cov-2 virus is the pathogen of the coronavirus disease-19 (covid-19), responsible for the recent global pandemic. Despite the numerous antiviral therapeutic strategies or vaccines under development, to date no effective anti-covid-19 therapies have been developed. The Sars-Cov-2 genome expresses 29 proteins fundamental in the mechanism of virus replication and maturation. Open reading frame 3a (ORF3a) is among the most expressed viral proteins both in cells infected by the virus in vivo and in transfected cell cultures in vitro. Although the ORF3a protein has been known for about twenty years, its exact function is still not fully understood. While initial studies suggested that ORF3a of Sars-Cov-2 had the general properties of an ion channel, a recent paper shows that ORF3a is in fact not an ion channel.

We employed a multidisciplinary approach that ranges from molecular dynamics (MD) to molecular biology and electrophysiology to understand the function of ORF3a protein. Our preliminary results confirmed that the ORF3a protein does not have the structural properties required for ion transport and does not generate any current when expressed in HEK293 cells. Conversely, both MD and videomicroscopy approaches suggested instead that this protein may be involved in mediating the transmembrane flux of water rather than ions, as previously reported.

Regulation of transmembrane water flux by the ORF3a protein could be used by the virus to either swollen or deacidify/alkalize intracellular organelles, notably lysosomes or autophagosomes, resulting in the impairment of their degradation power of foreign material, and thereby avoid being phagocytized by them, as well as in the facilitation of virus egress from the cell.

Antimicrobial resistance in human pathogens

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Keywords: Antimicrobial Resistance

ABSTRACT

Antimicrobial resistance (AMR), of which Antibiotic Resistance is the most relevant factor, is a phenomenon that occurs naturally in microorganisms as a form of adaptation to the environment. It is due to the ability of microorganisms to mutate and acquire the ability to resist molecules that have the capacity to kill them or stop their growth. This phenomenon is mainly caused by excessive and improper use of antibiotics, which has led to an increase in the selective pressure on the bacteria over time. It should be noted that this phenomenon often involves health-related infections, which arise and spread within hospitals and other health facilities. While the rates of infection due to Multi-Drug Resistant Organisms are continuously increasing, the antimicrobial agents active against them, in particular the Gram-negative carbapenem-resistant bacteria, remain limited. Antimicrobial resistance is currently considered one of the major public health challenges due to its epidemiological and economic impact. Without effective countermeasures, there could be up to 10 million more deaths per year by 2050. For this reason, it must be addressed through an approach identified by the "One Health" model, based on the involvement of a wide range of sectors and the integration of different disciplines and aimed at designing and implementing programs, policies, regulations and research to better levels of global health.

Antimicrobial resistance of microorganisms detected in food

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Keywords: antibiotic-resistance, biocides, food

ABSTRACT

The development of bacterial resistance to antibiotics is one of the best documented cases of contemporary biological evolution. The huge consumption of this type of compound has resulted in the emergence and spread of a vast amount of antibiotic resistance determinants among bacterial population, thus creating a critical public health problem. The danger of a return to a pre-antibiotic era is now becoming a serious threat, particularly considering that no novel chemical class of antibiotics has been introduced in the past 20 years. Food borne microorganisms display a broad spectrum of resistance responses to naturally occurring and intentionally added antimicrobial agents. Resistance may be conferred by innate structural features of the bacterial strain such as an impermeable outer membrane or a mechanism for antibiotic inactivation. Cross resistance between clinical and nonclinical antimicrobials can exist and is of concern. The development of resistant food borne pathogens has been attributed to increased antibiotic use in hospitals, outpatient facilities, and veterinary applications. This paper presents an overview of problems arising from the development of microbial resistance among food borne pathogens.

Resistance to oxazolidinones in *Enterococcus* spp: an emerging threat in a One health scenario

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Keywords: *Enterococcus* spp., antibiotic-resistance, oxazolidinones

ABSTRACT

The genus *Enterococcus* includes globally important opportunistic pathogens, causing serious infections in humans, especially in hospitalized patients. Over recent decades, the emergence and dissemination of multidrug-resistant enterococci is of a particular clinical concern. Oxazolidinones, including linezolid and tedizolid, are bacteriostatic antibiotics primarily used as a “last resort” to treat severe infections due to multidrug-resistant Gram-positive pathogens. They inhibit the bacterial protein synthesis by binding to the peptidyl transferase center of the 50S ribosomal subunit. However, the increasing clinical use of last-resort antimicrobials provides a strong selective pressure for the emergence of resistant clones, thanks to the high prevalence of enterococci in healthcare settings and their ability to readily develop resistance. Accordingly, resistance to these “last-line” agents with resultant treatment failure has been increasingly reported. Over the past two decades, the onset of ribosomal mutations but even more the acquisition of transferable resistance genes (cfr/cfr-like, oprA, poxtA and its variant poxtA2). These mechanisms of resistance have led to the spread of linezolid-resistant bacteria in healthcare, as well as in animal and environmental settings, representing a globally significant public health threat. Over the last five years, our research group has investigated the occurrence of oxazolidinones-resistant enterococci in livestock, wild animals, and the environment through a One-health approach, pointing out the role of these backgrounds as a reservoir of oxazolidinone resistance genes for human bacteria.

Novel insights and perspectives on *Toxoplasma gondii*, a re-emergent foodborne and environmental pathogen

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Keywords: *Toxoplasma gondii*; seroepidemiological survey; resistance genetic marker

ABSTRACT

Toxoplasmosis is a re-emerging zoonosis caused by *Toxoplasma gondii*, an obligate intracellular parasite with a complex biological cycle. Toxoplasmosis is considered an important public health threat, even probably related to neurodegenerative disorders and glioma, according to recent studies. The major concern of infection is for pregnant women and for immunocompromised individuals. Sources of *T. gondii* transmission are environmental and/or foodborne, mainly through the consumption of raw/undercooked meat, predominantly of swine (*Sus Scrofa*), highly susceptible to the parasite infection. In the last decades, valid approaches focusing on resistance immuno-genetic markers (i.e. SNPs) was used in alternative to traditional preventive measures, to contrast infectious disease. From the association studies between phenotypic and genotypic data, the genetic traits, proven robust, could be applied in Marker Assisted Selection strategies. This approach has not yet been adopted for *T. gondii*, so this study aimed to fill this gap. Attention was firstly paid on IL-18, that plays a key role upstream of the infection. Total RNA was extracted from diaphragms of pigs from different farms of Central Italy. A RT-PCR assay followed by Sanger sequencing of IL-18 mRNA was de novo developed, obtaining a 100% of identity with reference sequence (NM_213997.1). Contextually, animals were serologically characterized by an ELISA assay, detecting *T. gondii* specific antibodies in diaphragms meat juice. Out of 179 tested animals, 98 were seropositive (54.74%), 57 seronegative (31.84%) and 24 doubtful (13.40%). Furthermore, 14 samples were also confirmed by IFI test by National Reference Center for Toxoplasmosis. These data highlighted *T. gondii* re-emerging diffusion in the investigated areas, thus gene sequencing as well as association analyses are ongoing.

Next-Generation Sequencing in Life Sciences: Explore the Technology

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Keywords: Next Generation sequencing; DNA; genomics

ABSTRACT

Next-generation sequencing (NGS) is a massively parallel sequencing technology that offers ultra-high throughput, scalability, and speed. The technology is used to determine the order of nucleotides in entire genomes or targeted regions of DNA or RNA. NGS has revolutionized the biological sciences, allowing labs to perform a wide variety of applications and study biological systems at a level never before possible. This approach can be used to study microorganism populations both in humans, plants, animals, and our environment. Today's complex genomics questions demand a depth of information beyond the capacity of traditional DNA sequencing technologies. NGS has filled that gap and become an everyday tool to address these questions.

The burden of unhealthy lifestyles: data, challenges, and perspective

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Keywords: summary measures of population health; health determinants; epidemiological data

ABSTRACT

The measurement of the burden of disease is a relevant issue in public health as it allows understanding the overall impact of different health problems on the population. This is a cornerstone for informing health policies and supporting health care management but also to bring research on health problems forward. This speech will briefly review the ways that are currently used to measure the burden of disease, in particular the disability adjusted life years (DALYs), which is a health gap measure that combine healthy life years that are lost due to both poor health and premature mortality. Starting from the DALYs and the Global Burden of Disease Study, conducted by the World Health Organisation, an overview of the impact of different health risks will be provided. In particular, the contribution of behavioral risks will be compared to occupational/environmental and metabolic risks, overall and considering the most relevant diseases in western Europe and Italy. This will represent the basis for discussing current and future challenges in the control of the burden of disease in our country.

Genomics and metabolomics of eating disorders for diagnostic and therapeutic purposes

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Keywords: eating disorders, anorexia nervosa, bulimia nervosa, binge eating, serotonin, dopamine, NGS panel, hair

ABSTRACT

Eating disorders (EDs) are serious mental conditions characterized by a disturbance in eating-related behaviors and related to distressing thoughts and emotions without a specific pharmacologic approach. Patients with anorexia nervosa (AN), bulimia nervosa (BN), and binge eating (BE), the three most common EDs, very often present comorbidities, such as anxiety, mood disorders, and personality disorders. Family studies together with candidate gene association approaches have shown that EDs are heritable. Single nucleotide polymorphisms (SNPs) in the serotonin receptor (5-HT_{2A}R) and transporter (SLC6A4), in the dopamine receptors (DRD2, DRD4), brain derived neurotrophic factor (BDNF) and others, have been identified in our cohort as potentially playing a role in the development of EDs. Moreover, we recently found, using NGS panel, syndromic forms of AN with a Mendelian transmission in PDE11A and SLC25A13 genes. New horizons have been outlined in the biochemical field: tryptophan and kynurenines were investigated in the patients' sera and their levels change considerably during EDs. In the near future, new reliable bio-markers will be extrapolated studying the metabolomics from hair. In fact, this biological sample is like a "chemical diary" that records our nutrition on a daily basis. In conclusion, genomics and metabolomics are just some pieces of a complex puzzle when talking about EDs, but could be both useful for an early diagnosis together with new therapeutic approaches.

Endocannabinoids and their congeners in obesity and mitochondrial bioenergetics

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Keywords: endocannabinoidome; obesity; mitochondrial bioenergetics

ABSTRACT

The endocannabinoidome (ECBome) is a complex lipid signaling system composed of more than 100 fatty acid-derived mediators and their receptors. Oleoylethanolamide (OEA) belongs to this system, but its involvement in metabolic and inflammatory regulation is still partially unknown. Here, we evaluated the effect of OEA administration on metabolic and inflammatory profiles in a mouse model of diet-induced obesity, focusing on its efficacy in the modulation of hepatic mitochondrial function, ECBome mediators and microbiome composition. C57BL/6J mice were divided in two groups receiving, for 18 weeks, standard diet or high-fat diet (HFD). Afterwards both groups were subdivided to receive vehicle or OEA for further 4 weeks. Energy balance, body composition, metabolic and inflammatory parameters, hepatic mitochondrial function and oxidative stress were evaluated together with LC-MS/MS analysis of ECBome mediators and 16S sequencing for gut microbiota composition. In HFD mice, OEA decreased body weight, food intake and the inflammatory state in both serum and liver and decreased hepatic and body lipid accumulation. In the liver, OEA modulated mitochondrial oxidative capacity reducing lipid accumulation and oxidative stress. OEA also affected the levels of some ECBome lipid mediators and gut microbiota composition. Our results identify OEA as a candidate in the treatment of obesity through the modulation of mitochondrial function and both metabolic and inflammatory profiles, thereby reducing the damage induced by lipid overload.

Drinking water: Genotoxicity of disinfection by-products

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Keywords: Drinking water; Disinfection by-products; Genotoxicity

ABSTRACT

Water disinfection, primarily by chlorination, is one of the greatest achievements of public health. However, more than half a century after its introduction, studies in the 1970s reported that chlorine interacted with organic matter residues present in surface water to form disinfection by-products (DBPs). The two best known DBPs, chloroform and bromoform, both trihalomethanes (THMs), were then classified as rodent carcinogens. Furthermore, several epidemiological studies have reported an association between colon or bladder cancer mortality and THM exposure. Improved water-treatment methods and stricter regulations have likely reduced such risks over the years. Anyway, the potential residual genotoxic risk, in particular, in drinking water obtained from surface sources and disinfected with chlorine and/or its compounds, still deserves to be investigated.

Influence of mycotoxins on gut health

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Keywords: Intestinal barrier; inflammation; food contamination

ABSTRACT

Food contamination by mycotoxins represent a threat to human health. Mycotoxins are secondary metabolites produced by toxigenic fungal species that colonize food crops including wheat. Mycotoxin contamination emerges through all life and process cycle of crops. Mycotoxins can indeed be detected in several foods, absorbed thorough the gastrointestinal tract, and exert biological effects on different tissues in humans and animals. Generally, intestinal barrier in the gastrointestinal tract functions as a filter against harmful mycotoxins. However, some mycotoxins have been found to exert their detrimental effects in the gastrointestinal tract. Chronic bowel diseases, such as celiac disease and inflammatory bowel disease (IBD-ulcerative colitis and Crohn's disease) are characterized by overlapping features, i.e. dysfunction of intestinal epithelial barrier and chronic intestinal inflammation. It has been proven that, in genetic predisposed subjects, environment can contribute to the pathogenesis and progression of these diseases. Although the exposure to mycotoxins via ingestion of contaminated foods, can cause alterations in intestinal and immune functions, the contribution of mycotoxin exposure to human chronic bowel diseases needs to be fully elucidated. Deciphering the impact of mycotoxins on gastrointestinal environment homeostasis will be of major importance for future risk assessment and for the maintenance of a healthy gut.



Poster session



1. MAINTENANCE OF THE FEMALE POLYMORPHISM IN
ODONATA: CONTRIBUTION FROM THE STUDY OF A
NATURAL POPULATION OF ISCHNURA ELEGANS IN
CENTRAL ITALY

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FRESHWATER ECOSYSTEM

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Concetta Elia*

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3. OXIDATIVE STRESS BIOMARKERS-BASED
BIOMONITORING OF INVASIVE ALIEN SPECIES

PROCAMBARUS CLARKII IN LAKE TRASIMENO

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Gianandrea, Dörr Ambrosius Josef Martin, Scoparo
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Graziani, B. Camilloni, A. Mencacci, R. Spaccapelo*

5. VIRULENCE TRAITS OF ENVIRONMENTAL "*LEGIONELLA PNEUMOPHILA*" STRAINS ISOLATED IN ACADEMIC BUILDINGS.

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E.Montalbani, M.Petricciuolo, S.Fabbrizzi, C.Mazzarella, S.Barigelli, A.Carnevali, M.Alunni, A.Mugnaioni, E.Amoni, P.Meniconi, M.Burini and E.Federici
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7. INDOOR AIR QUALITY: CULTURE-DEPENDENT AND CULTURE-INDEPENDENT ASSESSMENT OF MICROBIAL BIOAEROSOL.

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8. TGPQ: A NEW *TOXOPLASMA GONDII* PROTEIN INVOLVED IN C-MANNOSYLATION

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**9. RADIATION THERAPY–DEPENDENT ORAL MUCOSITIS:
HOW THE ORAL DYSBIOSIS MAY PREDISPOSE TO
OPPORTUNISTIC FUNGAL INFECTIONS AND ORAL
MUCOSITIS**

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**10. MONITORING AIR POLLUTION EFFECTS ON CHILDREN
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GUBBIO): STUDY DESIGN**

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**11. OLIVE MILL WASTEWATER EXTRACT: IN VITRO SAFETY
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Fatigoni., Villarini M., Moretti M.*
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**12. VITAMIN D INDUCES EMBRYONIC HIPPOCAMPAL CELL
DIFFERENTIATION VIA MODIFICATION OF SPHINGOLIPID
METABOLISM IN EXOSOMES**

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