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**PROGRAM,
BOOK OF ABSTRACTS,
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interact, creating a large variety of intricate social networks. The study of social behaviour is now starting to benefit from the use of a sociology-derived approach, the social network analysis, which allows meaningfully describing and analyzing such complex social landscapes. While social behaviour is a core topic of evolutionary studies since decades, it represents, on the contrary, a rather neglected subject in the field of applied entomology. In this talk I will suggest that a greater interest toward social behaviour in pest and invasive species should be developed in order to increase our ability to protect agroecosystems. First, I will use a social wasp, *Polistes dominula*, as a model organism to show how animal social relationships can be profitably studied with Social Network Analysis (SNA). I will examine a recently discovered case of altruism that occurs inside overwintering groups of social wasps and show how SNA allowed uncovering the possible evolutionary origin of this unexpected phenomenon. Then, I will suggest how the same tools can be used to tackle applied questions for agroecosystems protection using two model species: the eusocial honeybee *Apis mellifera* and the invasive weevil *Rhynchophorus ferrugineus*.

Uncovering the tracks of a recent and rapid invasion: the case of the tiger mosquito, *Aedes albopictus* in Europe

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The dynamic aspects of the invasion process of *Aedes albopictus* has been inferred using different but complementary molecular markers (ITS2, SSRs and SNPs). The analyses of 79 ITS2 sequences from Asian, American and European populations indicates the absence of great differentiative processes and the presence of high degree of heterogeneity among individuals from these populations. This supports the expansion of this species. Using SSRs to analyze the dispersion of this species, China has been suggested as home range of the species by gene diversity estimates, cluster analyses, Bayesian analyses of ancestry and migration rates. It is clear that Chinese mosquitoes share their genomes both with American and European populations. It is evident that the dispersion pattern from this area was/is not due to natural step-by-step migration but the overall picture seems to be masked by a strong propagule pressure driven by human activities, by continued migration events and commercial traffic. We are also assessing whether this mosquito underwent adaptive processes during its invasion process. Because *Ae. albopictus* relies on olfactory cues for host-seeking, mating, blood feeding and oviposition, the antennal transcriptomes have been chosen for the identification and characterisation of chemosensory genes. The analysis of these genes in populations throughout the species range will allow us to detect single-nucleotide polymorphisms (SNPs) that may represent markers of adaptation. An outcome of this integrated analysis will be the development of a database of ITS2, SSRs and SNP fingerprints in ancestral and derived invasive populations as a tool for mosquito traceability in order to infer the origins of new outbreaks, and thus to develop risk maps for this mosquito.

Comparative morphology and evolutionary genomics provide useful clues for management of an emerging *Drosophila pest*

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Drosophila suzukii is one of the few fruit flies to lay eggs and feed on fresh fruit. Its recent outbreak in western countries, and its peculiar ecological behaviour makes it an emerging model for pest management and biology. A recent genomic survey suggested that *D. suzukii* unusual behaviour is intimately linked with an ecological pre-adaptations to temperate climates and the ability of overwinter in sexual diapause state. Here we provide comparative morphological and behavioural evidences supporting that diapause occurs preferentially in females, is temperature dependent, and is likely mediated by an enlargeable highly pigmented spermatecha. Comparative genomics reveals that a cytochrome associated with spermatecha is differentially expressed and the gene under stronger positive selection in *D. suzukii* compared to sister species. Based on these results, we advocate that an early spring trapping is key for *D. suzukii* population control as it may target the few overwintering females exiting diapause. Evolutionary genomics further identifies two genes under

positive or abnormal evolution involved in insecticide resistance and immune response to parasitoids, warning us on the feasibility of some types of control strategies. Our results show that evolutionary genomics and comparative morphology are useful tools to guide application in the field of pest management.

From evolutionary trees to behavioural ecology: exploiting SAM to visualize spatio-temporal movement patterns

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Sequence alignment methods have a long history in similarity analysis of DNA and protein sequences. However, starting from the mid-1990's sequence alignment has also been applied to a variety of other disciplines, including behavioural patterns. Although digital tracking technologies have greatly increased the availability of regular, high frequency spatio-temporal sequences of animal behavior information, sequence alignment has never been used to analyse this type of sequential data. Nevertheless, this method holds promising potential for the study of habitat selection, since contrary to standard approaches, which only consider spatial patterns, it takes also into account the temporal correlated nature of data. In this paper the applicability of sequence alignment is assessed for spatio-temporal sequences of roe deer (*Capreolus capreolus*) GPS locations and their related habitat features collected in an alpine population from Trentino (Italy.). The results can be robustly interpreted in an ecological context and are validated by previously acquired biological information. In addition, we will present a framework of a codon-based sequence alignment model which may allow to import temporal autocorrelation directly into the sequences. Prospects and current limitations of this model will be shortly discussed.

TBA The cost of domestication (if any): can we get a refund?

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Adaptation of Mediterranean forest species to climatic gradients: a forest genetic perspective

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Combining coalescence modelling, neutrality tests and environmental correlations, demographic history and non-neutral patterns of evolution in candidate genes related to drought stress and secondary compounds were investigated in two closely-related Mediterranean conifers, *Pinus pinaster* Ait. and *Pinus halepensis* Mill. Amplicons covering candidate genes were sequenced in a sample from the full range of these two species. Higher levels of nucleotide diversity in candidate genes for drought response were present in *P. pinaster* than in *P. halepensis*, despite its narrower range in the Mediterranean. Differences across species were also reflected in the haplotype distribution for each tree species, with *P. pinaster* showing many different haplotypes at similar frequencies and *P. halepensis* showing fewer haplotypes with only one that is common or even fixed. The low levels of nucleotide diversity in Aleppo pine are more noticeable in its western distribution where most genes were fixed or almost fixed for particular haplotypes, a probable consequence of long-range colonization of the Western Mediterranean from ancient Aleppo pine populations in the easternmost edge of its current distribution and a more acute impact of the Ice Ages in this range of the species. Molecular analyses also revealed intense and relatively recent bottlenecks in Aleppo pine as well as a time of split between North-African and Iberian populations of the species well predating the Last Glacial Maximum albeit not as old as the one estimated for maritime pine. In contrast,