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**PROGRAM,
BOOK OF ABSTRACTS,
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EDITED BY LINO OMETTO AND OMAR ROTA-STABELLI



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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

Johannes De Groeve^{1,2}, Omar Rota-Stabelli², Lino Ometto², Nico Van de Weghe¹, Tijs Neutens¹, Francesca Cagnacci²

¹Ghent University, Krijgslaan 281, S8 9000 Ghent, Belgium

²Research and Innovation Centre, Fondazione Edmund Mach, Via Mach 1, 38010 San Michele all'Adige (TN), Italy.

Contact: johannes.degroeve@ugent.be

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?

Roberto Papa¹

¹Dipartimento di Scienze Agrarie, Alimentari ed Ambientali, Università Politecnica delle Marche, 60131 Ancona, Italy.

²Cereal Research Centre, Agricultural Research Council (CRA-CER), S.S. 16, Km 675, 71122 Foggia, Italy.

Contact: rpapa@univpm.it

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

Giovanni G. Vendramin¹, Delphine Grivet², Santiago C. Gonzalez-Martinez²

¹Plant Genetics Institute, CNR, Via Madonna del Piano 10, 50019 Sesto Fiorentino (FI), Italy.

²Department of Forest Ecology & Genetics, Center of Forest Research, CIFOR-INIA, Carretera de la Coruña km 7.5, E28040 Madrid, Spain

Contact: giovanni.vendramin@igv.cnr.it

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,