

5th Congress
ITALIAN SOCIETY FOR
EVOLUTIONARY BIOLOGY
Trento, 28-31 August 2013

**PROGRAM,
BOOK OF ABSTRACTS,
AUTHOR INDEX.**

EDITED BY LINO OMETTO AND OMAR ROTA-STABELLI



V congress of the Italian Society for Evolutionary Biology. Trento, 28-31 August 2013

project BioVeL (<http://tavlite1.biovel.eu/>). This web service implements only the burn-in estimation and convergence test procedures, but is wrapped in a Python script that implements a Fisher procedure to combine p-values from several pairwise comparison of runs: this allows to generalize the approach to more than two runs.

The draft genome of *Cardamine resedifolia*: genomic tools to investigate plant adaptation to high altitude

Lino Ometto¹, Mingai Li¹, Claudio Varotto¹

¹Department of Biodiversity and Molecular Ecology, Research and Innovation Centre, Fondazione Edmund Mach, Via Mach 1, 38010 San Michele all'Adige (TN), Italy.

Contact: lino.ometto@fmach.it

Cardamine resedifolia is a perennial species usually growing on siliceous substrates in open spaces between 1,500 and 3,500 meters above sea level. The environmental and ecological factors associated to this habitat evidently impose distinct selective pressures to the species, as revealed by an in-depth analysis of the patterns of molecular evolution in genes involved in cold response in photosynthesis (Ometto *et al.* 2012). However, both protein sequence and gene regulation may be involved in adaptation. Thus, a comprehensive knowledge on the genome structure and evolution of the species is necessary to gather precious insights in the pattern of coding genes and regulatory sequence evolution. To this aim, we present the draft genome sequence of *C. resedifolia* and its partial annotation, which represent the first step to characterize the genetic basis of adaptation to high altitudes for this and also other plant species.

Mating-responsive genes from the testes and male accessory glands of the Mediterranean fruit fly, *Ceratitis capitata*

Francesca Scolari¹, Ludvik M. Gomulski¹, José M.C. Ribeiro², Paolo Siciliano¹, Alice Meraldi¹, Marco Falchetto¹, Angelica Bonomi¹, Mosè Manni¹, Paolo Gabrieli¹, Alberto Malovini¹, Riccardo Bellazzi¹, Serap Aksoy³, Giuliano Gasperi¹, Anna R. Malacrida¹

¹University of Pavia, Via Ferrata 9, Italy.

²National Institute of Allergy and Infectious Diseases, Rockville, Maryland, United States of America.

³Yale School of Public Health, New Haven, Connecticut, United States of America.

Contact: gasperi@unipv.it

Insect seminal fluid is a complex blend of spermatozoa, proteins, carbohydrates and lipids, which are produced in the male reproductive tract. This mixture is transferred during copulation and induces post-mating responses in the female. Molecular characterization of the protein components of seminal fluid in the Mediterranean fruit fly (medfly), *Ceratitis capitata*, is limited, even though different studies suggest that some of these proteins are biologically active. We report the functional annotation of 8448 expressed sequence tags (ESTs) derived from the testes and male accessory glands, to identify transcripts encoding putative secreted peptides that might elicit post-mating responses in females. The ESTs were assembled into 3344 contigs, of which over 33% produced no hits against the nr database, putatively representing novel medfly sequences. Extraction of the coding sequences resulted in a total of 3371 peptides. Four hundred peptides were found to have putative secretory activity, including odorant binding proteins, protease inhibitor domain-containing peptides, antigen 5 proteins, mucins, and immunity-related sequences. Quantitative RT-PCR on transcripts expressed in the accessory glands revealed that several changed in abundance after one or more copulations, compared to virgin males of the same age. Our results suggest the presence of transcriptional switch points possibly related to the need to replenish transcripts encoding secreted proteins with an active role in the seminal fluid. This represents the first large-scale dataset for novel studies on functions and processes associated with the reproductive biology of this invasive pest species. The identified genes may help the study of the evolution of the genome, in the light of its high adaptive potential. In addition, studies of male recovery dynamics in terms of accessory glands gene expression profiles and correlated remating inhibition mechanisms will permit the improvement of the current pest management approaches.