5th Congress

ITALIAN SOCIETY FOR EVOLUTIONARY BIOLOGY

Trento, 28-31 August 2013

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EDITED BY LINO OMETTO AND OMAR ROTA-STABELLI

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

NEW PhDs ON THE BLOCKS

The symposium benefits from the collaboration with FIRS>T, the PhD programme of FEM. This symposium is reserved for young scientists who would like to talk about their research, their results (no matter at which stage) and their passion towards evolutionary biology in a friendly atmosphere.

Chairs: Lino Ometto and Alessandro Gretter (Fondazione Edmund Mach)

Genetic variability in the promoter of miR397 in *Picea abies*

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Norway spruce (*Picea abies* Karst.) is a tree species that belongs to conifers, a taxon that is extremely important both from an ecological and an economical point of view. Being perennial, this species has often to face suboptimal environmental conditions and to adapt to them: microRNAs are a fundamental class of regulatory molecules, often involved in stress responses and therefore, potentially very important for plant adaptive processes. The focus of this study is on miR397: in *Arabidopsis thaliana* miR397 was shown to be involved in the regulation of copper homeostasis and of the transcription of laccases. These enzymes operate during lignin biosynthesis and therefore their regulation is really important in woody plants like Norway spruce, in order to react to mechanical stress and to resist to the attack of pathogens. In order to understand miR397 regulatory mechanisms, its promoter was isolated in this species and putative regulatory elements were identified. This region, together with the microRNA stem-loop region, was sequenced in seeds produced by individuals originating from different alpine populations in Italy, Austria and Switzerland. In the mature miR397, the most important part for microRNA regulatory function, no polymorphism was found in the analyzed samples. This result suggests that purifying selection is probably acting on this sequence in order to preserve microRNA functionality. As regards the promoter region, several single nucleotide polymorphisms (SNPs) and some insertions/deletions were identified. Some of them are located in the putative regulatory elements, therefore they are good candidates to test if they influence the microRNA expression level and if they have consequences on phenotype that can be relevant in the process of adaptation. This will provide deeper insights into the adaptive role of microRNAs in Conifers.

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Non-LTR retrotrasposon R2 molecular characterization and activity in *Bacillus rossius* (Phasmida, Bacillidae)

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The non-LTR retrotransposon R2 is one of the most analyzed transposable elements (TEs), its presence being recovered from diploblastic organisms to lower vertebrates. It inserts in the sequence 5'-TTAA↓GGTAGC-3' of the 28S ribosomal gene, thus affecting the production of functional rRNAs. The evolutionary relationship between retrotransposon activity and reproductive biology of the host species is still debated: while some studies suggest that genomes with limited effective recombination (unisexuals and asexuals) accumulate TEs with a low capacity to eliminate them, gonochoric organisms better manage their proliferation (Muller's ratchet). In order to go through this issue, we are studying R2 distribution and dynamics in the facultative parthenogenetic stick-insect *Bacillus rossius*. In Italy, *B. rossius rossius*, spreading along the Western peninsular coasts and in North-Western Sardinia, and *B. rossius redtenbacheri*, distributed along the peninsular eastern coasts, in Sicily and in South-Eastern Sardinia, occur with gonochoric and unisexual (parthenogenetic) populations. The R2 complete sequence was PCR amplified and sequenced from gonochoric populations of *B. r. rossius* from Capalbio (Tuscany) and of *B. r. redtenbacheri* from Patti (Sicily). The R2 activity was studied through the 5' end deletions analysis in selected parental individuals and in a sample (10-20 individuals) of their offspring. In particular we analyzed the progeny of two females each of the parthenogenetic *B. r. redtenbacheri* populations from