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NGS approach for investigating evolutionary transition from oviparity to viviparity in squamate reptiles

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Some squamate reptile species provide a unique model system for gaining crucial information about the evolutionary transition from oviparity to viviparity in vertebrates. The lizard *Zootoca vivipara* is one of the few species with distinct reproductive modalities in different subspecies; in particular, *Z. v. carniolica* is an egg-laying lizard while *Z. v. vivipara* is a live-bearing one; they both live in the Eastern Italian Alps, sometimes in syntopy. This provides an interesting natural setting for studying the evolutionary shift in reproductive mode. Some populations were analysed using classical genetic markers (mitochondrial, nuclear DNA sequences and autosomal microsatellites). The mtDNA results indicated a marked divergence between the two subspecies (around 5% at the *cytochrome B*), as well as nuclear microsatellites. Possible existence of hybrid individuals in Carnic Alps, as recently reported by morphological evidences, has boosted the interest on this topic. RAD-tag sequencing, a next-generation sequencing technique that allows simultaneously discovering and analyzing hundreds of thousands of SNPs, was then applied to *Zootoca vivipara* subspecies in order to identify mutations correlated with the reproductive modality and with related adaptive traits.

The touch of death: Killer Mediated Contact Inhibition and Hsp12p Secretion determines Differential Fitness in a Community of Grape Yeast Isolates.

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The budding yeast *Saccharomyces cerevisiae* represents the best-understood and most powerful genetic model systems as its genome was the first, out of all the eukaryotic organisms, to be completely sequenced. Recently it has been possible to establish an interaction between genotype and environment to describe fitness in terms of better adaptation to stress. Lately, several disciplines have converged to turn *S. cerevisiae* into a model for the genetic study of ecology and evolution. During wine production, the yeast strains with the best fitness establish strategies to compete for spaces and resources, dominating the natural microbial ecosystems, although it is also possible that they establish behaviours that contribute to intraspecies coexistence. Little is known about the genes and their transcripts responsible for ecological interactions (cooperation and competition) among yeasts. To fill this gap, we performed a genome-wide analysis of two natural yeast strains. Our findings demonstrate that both Heat Shock Protein 12 (*Hsp12p*) and *PAU* genes are not only important for the fitness of the yeast during fermentation, but are also fundamental for cooperation and competition behaviours, respectively. The results highlight the existence of previously unknown cooperative compartment dependent on the secreted *Hsp12p*, counter-balanced by contact-dependent killer inhibition. This work represents a good approach to the use of the yeast *S. cerevisiae* as a model to improve our understanding in the study of the genetics of the ecology.

Stochastic gene expression and fitness

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With the development on gene expression studies on single cells, it appears that stochastic gene expression (SGE) is not only a background 'noise', but a documented constitutive parameter of all living beings, that deserves scrutiny at the evolutionary level. This widespread phenomenon, from prokaryotes to eukaryotes, may challenge the classic view of adaptive evolution at the molecular level as a fine-tuned process of precise regulations, in particular in multicellular organisms. It has conversely also been described as a source of flexibility and even a counter intuitive source of