



## Conservation genetics and genomics of the fire salamander, *Salamandra atra*

Leon Blaustein, Institute of Evolution-University of Haifa, Israel

E-mail: [leon@research.haifa.ac.il](mailto:leon@research.haifa.ac.il)

*Salamandra atra* is considered as a threatened species in Israel. However, since when we started studying *Salamandra*, we have found many more breeding sites in the past 10 years than were known previously. In addition, O. Rybak (unpublished results) has found that *Salamandra* does well in urban habitats on Mount Carmel. *Salamandra atra* has strong pond site fidelity that likely results in differential genetic structure among breeding sites. Strong pond site fidelity has been found by multiple researchers. An exception is that on Mount Carmel, S Bar David found dispersal as far as 1280 m, which is likely to result in overlapping genetic structuring. During our first genetics study, in which nine breeding sites in Mount Carmel and 11 sites in the Galilee were surveyed and tissue samples were taken from 475 adults. Microsatellites were used for observing differences in genetic structure in the study which was performed in Prof Juha Merilä's Lab (University of Helsinki, Finland). In this study, we found that there were substantial genetic differences between Mount Carmel and the Galilee. Allelic richness was much higher in the Galilee than in Mount Carmel; 40 unique alleles were found in the Galilee and 0 in Mount Carmel. Unrooted neighbour joining tree diagrams resulted in pure separations between Mount Carmel and the Galilee. Structure analysis showed strong differences between the Galilee and Mount Carmel. A second microsatellite study was conducted in Finland in Juha Merilä's Lab. The goal was to consider genetic diversity in peripheral populations compared to populations closer to the core. We collected 692 tissue samples from adult and juvenile fire salamanders from 33 breeding sites (13 from upper Galilee, ten from lower Galilee, nine from Mount Carmel and one from Tel Dan). This study also considered vegetation types and meteorological aspects such as elevation, average temperature and precipitation. Maximum entropy analysis was also used to score major regions. The lower Galilee had the lowest stability values of the three regions. Allelic richness increased with maximum entropy scores in the Upper Galilee. Allelic richness also increased with latitude. A Bayesian analysis of population structure (BAPS) also demonstrated that Mt Carmel and the upper Galilee were homogeneous genetically while the lower Galilee contained genetically differentiated populations. Lastly, we performed transcriptomics/gene expression studies on fire salamander larvae. We insisted that *Salamandra* tailfins (which do not cause damage to the *Salamandra* larvae) can demonstrate gene expression as opposed to using the whole body. We found that *Salamandra* larvae turn darker when exposed to ultra violet radiation and they turn darker with increased density. We are currently conducting gene expression studies on *Salamandra* larval development, oxygen ranges, colour change and temperature change. The utilization of similar habitats by different species provides an ideal opportunity to identify genes underlying adaptation and acclimatization. Here, we analysed the gene expression of two closely related salamander species: *Salamandra atra* in Central Europe and *Salamandra atra* in the Near East. These species inhabit similar habitat types: 'temporary ponds' and 'permanent streams' during larval development. We developed two species-specific gene expression microarrays, each targeting over 12 000 transcripts, including an overlapping subset of 8331 orthologues. Gene expression was examined for systematic differences between temporary ponds and permanent streams in larvae from both salamander species to establish gene sets and functions associated with these two habitat types. Only 20 orthologues were associated with a habitat in both species, but these orthologues did not show parallel expression patterns across species more than expected by chance. Functional annotation of a set of 106 genes with the highest effect size for a habitat suggested four putative gene function categories associated with a habitat in both species: cell proliferation, neural development, oxygen responses and muscle capacity. Among these high effect size genes was a single orthologue (14-3-3 protein zeta/YWHAZ) that was downregulated in temporary ponds in both species. The emergence of four gene function categories combined with a lack of parallel expression of orthologues (except 14-3-3 protein zeta) suggests that parallel habitat adaptation or acclimatization by larvae from *S. atra* and *S. atra* to temporary ponds and permanent streams is mainly realized by different genes with a converging functionality. Parallel evolution of phenotypic traits has been described for a broad range of organisms and is seen as an evidence for natural selection. Case studies of parallel phenotypic evolution can reveal genes and functions underlying the repeated evolution of adaptive traits. Evolutionary adaptation only takes place in phenotypically expressed traits that are exposed to natural selection. Hence, acclimatization, a plastic response in which gene expression and its phenotype change to accommodate variable environmental conditions within an organism's lifespan, can be intimately linked with adaptation. The idea that phenotypic plasticity may play an important role in adaptive evolution has a long history, but the underlying genetic mechanisms are still being explored. Although phenotypically plastic traits and a fixed adaptive divergence are difficult to distinguish, studies of parallel phenotypic divergence in relation to environmental factors provide the basis to identify how plasticity and adaptation may interact.

**Bottom Note:** This work is partly presented at *EuroScicon congress on Biochemistry, Molecular Biology & Allergy* October 11 - 12, 2018 Amsterdam, Netherlands

*EuroScicon congress on Biochemistry, Molecular Biology & Allergy*

October 11 -12, 2018 Amsterdam, Netherlands