### Genomic (un)stability in hybridogenetic clonal forms of European loaches (genus Cobitis)

Oldřich Bartoš1,2, Jan Röslein1,3, Jan Kočí1,3, Martin Mokrejš4 and Karel Janko1,3

1. Institute of Animal Physiology and Genetics, Laboratory of Fish Genetics, The Czech Academy of Sciences, Liběchov, Czech Republic
2. Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic
3. Department of Biology and Ecology, Faculty of Science, University of Ostrava, Ostrava, Czech Republic
4. IT4Innovations, VŠB – Technical University of Ostrava, Ostrava, Czech Republic

Although molecular and cytological mechanisms underlying meiosis are highly conserved they have been disrupted in numerous ways during the evolution leading to emergence of so called asexual lineages (Bengtsson, 2009). The origin and mainly persistence of asexual organisms represents major challenge for evolutionary biology (Bell, 1982). Interestingly, quite recently it has been reported that asexual *Daphnia* strains lose their genes (DNA) in a pace of cca. two genes per generation, which has been interpreted as possible/suitable solution to so called “paradox of sex” (Tucker, 2013).

Previous cytogenetic study of Majtánová *et al.* (2016) reported no detectable chromosomal rearrangements concerning the European loaches asexual hybrid lineages. So, it seems that species-specific chromosomes are passed from generation to generation exactly in the same form as inherited from the parental species in the time of clonal lineage establishment (clonality). However, will this overall impression of genomic stability persist on “fine” genomics scale?

In this study we have evaluated 46 fish samples - parental species as well as their hybrids. We applied exome capture pair-end sequencing to discover species specific SNPs and determined their coverage (GATK 3.8, samtools 0.1.19, R 3.3.2 and custom python scripts). Which allowed us to identify all presumably Loss Of Heterozygosity loci. Suggesting that gene conversion or gene loss are the processes that stand behind LOH, we ask what is their relative contribution to the overall pattern. To distinguish between those two processes, we utilize the basics of logic used in rna-seq (DifferentialExpression) experiments.

We found out that the hypothesis of “clonality” roughly holds. Nevertheless, we have identified significant amount of interplay between the parental genomes which is manifested/detected as Loss Of Heterozygosity. Further we demonstrate that amount of such interplay is (evolutionary) time-dependent.

This work was also partially supported by The Ministry of Education, Youth and Sports from the Large Infrastructures for Research, Experimental Development and Innovations project "IT4Innovations National Supercomputing Center - LM2015070".

References:  
Bell, G. (1982). The Masterpiece of Nature:: The Evolution and Genetics of Sexuality. CUP Archive.

Bengtsson, B. O. (2009). Asex and evolution: a very large-scale overview. In Lost sex (pp. 1-19). Springer, Dordrecht.

Majtánová, Z., Choleva, L., Symonová, R., Ráb, P., Kotusz, J., Pekárik, L., & Janko, K. (2016). Asexual reproduction does not apparently increase the rate of chromosomal evolution: karyotype stability in diploid and triploid clonal hybrid fish (Cobitis, Cypriniformes, Teleostei). PloS one, 11(1).

Tucker, A. E., Ackerman, M. S., Eads, B. D., Xu, S., & Lynch, M. (2013). Population-genomic insights into the evolutionary origin and fate of obligately asexual Daphnia pulex. Proceedings of the National Academy of Sciences, 110(39), 15740-15745.