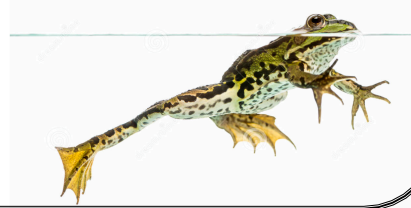


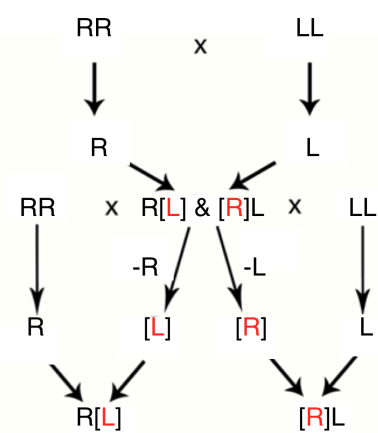
Distinct fate of the asexual genomes in two convergently evolved *Pelophylax* hybridogenetic systems.

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Hybridogenesis (HG) is a non-orthodox reproduction mode that results from incomplete postzygotic isolation, European water frogs genus *Pelophylax* represent one of the model systems. The initial cross between two parental species *P. lessonae* (genotype LL) and *P. ridibundus* (RR) leads to viable and fertile hybrids *P. esculentus* (RL) that can further reproduce hemiclonally via backcrossing to a complementary parental species.

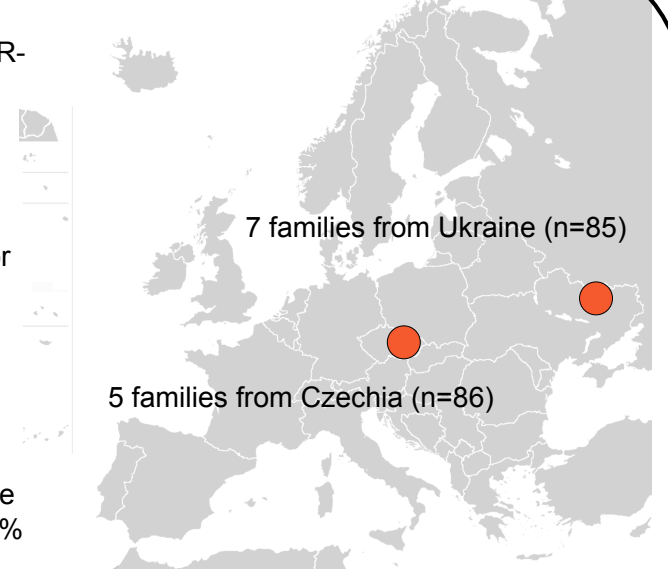


The common type of the population systems widely known from all across Europe consists of the hybrids [R]L that pass R-genome via their germline, hence their reproduction solely depends on the backcrossing to the syntopic LLs. Although, in a few allopatric cases, hybrids coexist with RR, and thus supposed to be dependent on ability to pass the [L]-genomes. Two such instances are known from the Oder river basin in Czechia¹ and the Siverskyi Donets river in Eastern Ukraine².

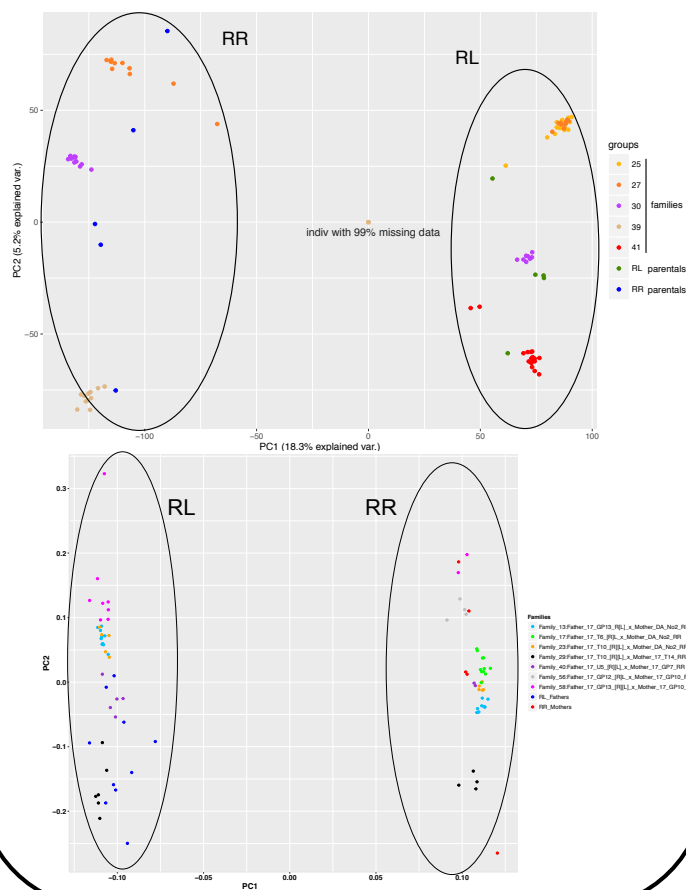
We crossed RL-males with RR-females that originated from these two natural source populations, the resulting families were genotyped with ddRADseq. Single-end data were processed separately for the Ukrainian and Czech families: mapped on the *P. lessonae* draft genome and filtered by minimum Mapping Quality >20. SNP calling was performed using ref_map.pl module of STACKS v 1.42, the final datasets had less than 5% of missing data and >6 reads per locus.

This approach yielded 1782 polyallelic loci for the Ukrainian families and 3902 loci for the Czech ones. The diploid genotypes were phased into haplogenomes with SHAPEIT2 and Bayesian clustering was done with FineSTRUCTURE.

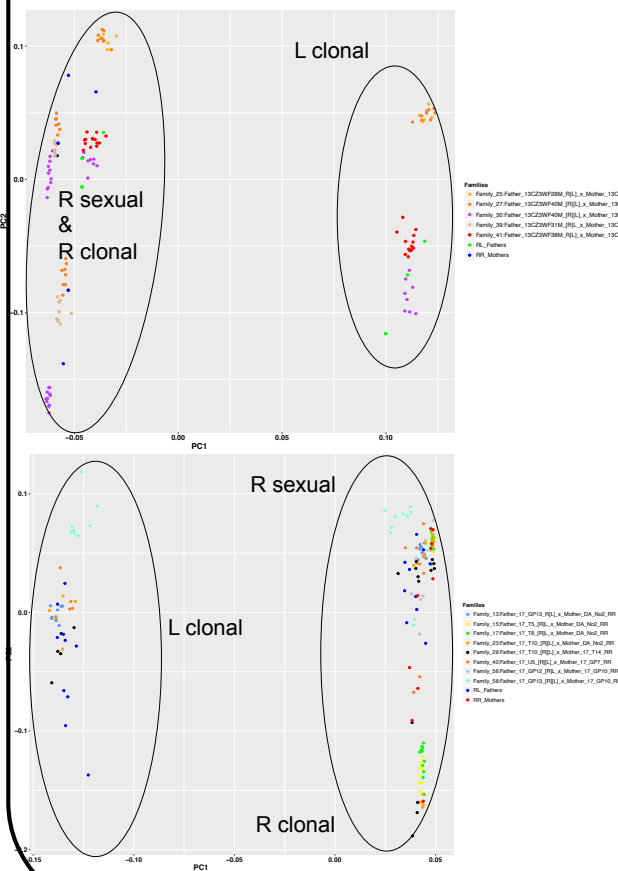
Laboratory crosses ♀RR x ♂RL:



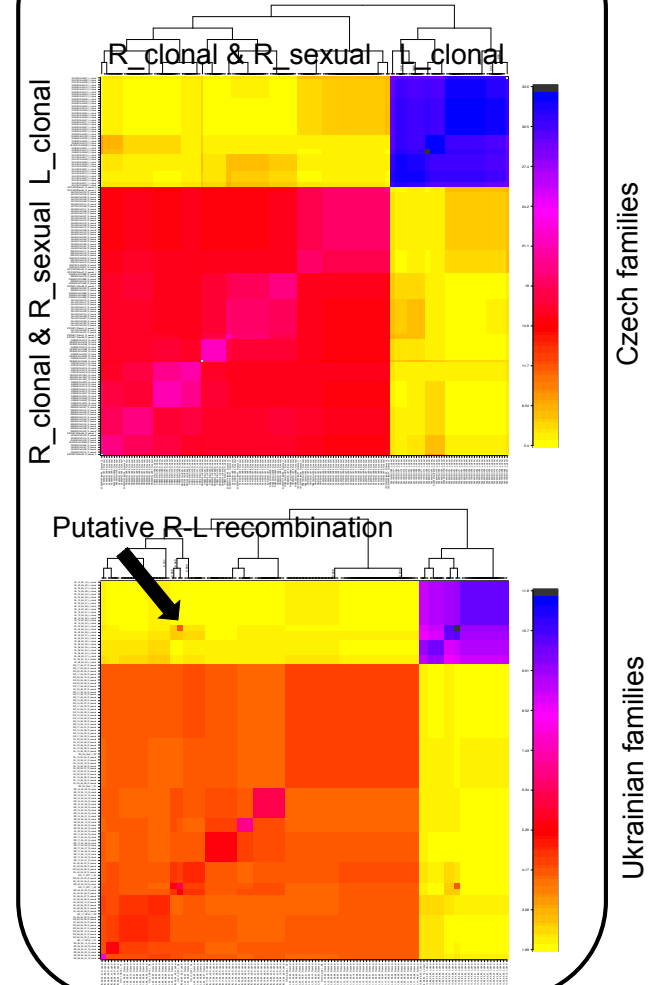
Diploid genotypes:
 ♀RR x ♂R[L] = R[L]
 ♀RR x ♂[R]L = R[R]
 ♀RR x ♂[R][L] = R[R] & R[L]



Phased genotypes:
 ♀RR -> R sexual
 ♂[R]L & ♂[R][L] -> R clonal & L clonal
 ♂R[L] -> L clonal



FineSTRUCTURE



In both Ukrainian and Czech families we revealed three types of RL males that are producing i) L-clonal, ii) R-clonal, and iii) a mixture of L- and R-clonal sperm. Bayesian clustering of the phased genomes showed higher levels of variation within L-clonal lineages possessed by the Ukrainian hybrids as well as higher levels of divergence between clonal and sexual R-genomes (i.e. high clonal diversity). In addition, in the phased progeny of a single father that produced R and L-gametes simultaneously, we observed several instances where L-clonal genomes had decreased divergence levels to the R-genomes, a sign that we consider as indicative for a rare recombination event. On the contrary, the Czech populations show lower levels of divergence between R-clonal and R-sexual genomes and we thus suggest that – in contrast to the more common L-hemiclones - the R-germ line does not persist clonally for longer than a single generation.

References:

1. Doležalková-Kaštánková et al. *Biology of Sex Differences* (2018) 9:13
2. Biriuk et al. *J. Zool. Syst. Evol. Res.* (2016); 54(3)

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