ASEXUAL GENOME EVOLUTION IN THE APOMICTIC *RANUNCULUS AURICOMUS* COMPLEX: EXAMINING THE EFFECTS OF HYBRIDIZATION AND MUTATION ACCUMULATION

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Apomixis, the natural production of clonal progeny via unfertilized seed, has increasingly raised the attention of the scientific community because of the potential impact for agriculture. Apomictic species are thought to have an evolutionary advantage against their sexual relative (i.e two-fold-cost of sex) but also prone to extinction because of mutation accumulation (Muller's ratchet). Common characteristics for many natural apomictic species are hybridity and polyploidy, both phenomena could produced the necessary regulatory consequence that lead to the shit to apomixis. Moreover polyploidy could have a major role in masking deleterious mutation.

Here use flower-specific RNAseq and polymorphisms mining to analyze genomic effects of hybridity, polyploidy and allelic divergence in sexual and apomictic biotypes from the *Ranunculus auricomus* complex. Comparison between all genotypes supports the hypothesis of Pleistocene hybrid origin of both apomictic genotypes from *R. carpaticola* and *R. cassubicifolius,* with subsequent allelic divergence of apomictic lineages (Meselson effect). Pairwise comparisons of non-synonymous to synonymous substitution rate between apomictic and sexual genotypes for 1231 genes demonstrated similar distributions, although 324 genes demonstrated outlier (i.e. elevated) ratios. Gene ontology analyses of these outliers revealed significant enrichment of genes associated with reproduction, following predictions of divergent selection between sexual and apomictic reproduction.