

## Abstract

Meiosis is functionally conserved across eukaryotes, thus not expected to vary considerably among different species, and even less so among lineages within a species. However, recent studies showed that this is not necessarily the case in *Arabidopsis arenosa*. Genome scanning identified an excess differentiation in meiosis genes between *A. arenosa* diploids and tetraploids, interpreted as meiosis adaptation to the whole genome duplication in tetraploids and differentiation was also found between two diploid lineages. Thus, I present a population-based analysis of positive selection acting on meiosis proteins across multiple lineages of *A. arenosa*. I showed that meiosis proteins were under positive selection in all diploid lineages, mainly in the Pannonian and South-eastern Carpathian lineage. The evidence for positive selection in diploid lineages suggested differential pathways of meiosis adaptations in the species, probably reflecting the necessity to adapt to local environments, among all to temperature. The highest enrichment of amino acid substitutions (AASs) under positive selection was identified in tetraploids, in consistence with previous genome-scan results. As several interacting meiosis proteins were under positive selection in the same *A. arenosa* lineage, I hypothesize that the close physical and/or functional proximity might have driven their co-evolution. The selected AASs tended to occur in proteins being overall under positive selection (identified as excess of non-synonymous over synonymous substitutions). Moreover, the selected AASs were enriched at protein positions having low pairwise alignment identity of the respective orthologous sites across embryophytes, supporting the assumption that selection acted preferably on AASs in sites less conserved throughout plant evolution. No stop and start codon gains and losses were identified to be fixed in any of the lineages, suggesting strong purifying selection against them. Finally, the observed difference in pollen viability in different *A. arenosa* lineages under varying temperature suggested local adaptation of meiosis to temperature. In summary, my study brings uniquely deep population-level view on molecular evolution of one of the key biological processes, meiosis. It shows a dynamic evolution of protein sequence within a single species, a surprising fact, given that meiosis is an evolutionally conserved process.

**Key words:** protein evolution, meiosis, *Arabidopsis arenosa*, amino acid substitution, synonymous substitution, pairwise alignment identity, pollen viability