

Abstract

This bachelor's thesis addresses polyploidy induced by whole genome duplication and its consequences to the evolution of *Medicago sativa* species complex, i.e. wild relatives of an important forage crop alfalfa. This complex encompasses several interfertile taxa naturally occurring as diploid ($2n = 16$) or tetraploid ($2n = 32$) cytotype. Several recently conducted studies attempted to explain origin and evolution of this complex and relationships among its members using modern molecular methods, however, the results are still fragmentary and inconclusive. Two most widespread members of the complex: purple flowering *Medicago sativa* and yellow flowering *Medicago falcata* are genetically differentiated both at diploid and tetraploid level, what is supporting their recognition as distinct taxa. Furthermore, it has been shown that tetraploid *M. sativa* subsp. *sativa* is an autopolyploid that originated from diploid *M. sativa* subsp. *caerulea* by intraspecific whole genome duplication. On the other hand, the origin of tetraploid *M. falcata* seems to be more complex, presumably involving autopolyploidization followed by past introgression from *Medicago prostrata*. Most of the studies concerning this topic were performed on accessions, which are sometimes of uncertain ploidy and origin, obtained from germplasm databases. This fact leaves our knowledge on the origin and mechanisms of diversification of the *Medicago sativa* complex only fragmentary.

Keywords

polyploidy, evolution, *Medicago sativa* complex, reproductive barriers, hybridization