

Abstract

Family *Poaceae* is one of the most derived groups of monocots. Major mechanisms of grasses evolution and particularly of tribe *Triticeae* and genus *Elymus* are polyploidisation and hybridisation.

Presented diploma thesis assessed frequency and direction of hybridisation between *Elymus hispidus* and *E. repens* in Central Europe. Thesis also evaluated evolutionary importance (significantly higher ratio of hybridisation and polyploidisation) of hybrid swarm in Nature Reserve Čertoryje (Bílé Karpaty Mountains/the White Carpathians, the Czech Republic).

Putative hybridizing populations were 14,4 % of sampled localities, i.e. direct presence hybrids (7,9 %) or both parental species (8,4 %). Aneuploids and higher polyploids were found exclusively in Čertoryje hybrid swarm, except one putative DNA nonaploid plant.

The genome *in situ* hybridisation confirmed and improved knowledge of particular species/cytotypes chromosome counts and further specified their genome composition. GISH newly characterized genome composition of interspecific hybrids and higher allopolyploids and revealed their heterogeneous origin.

Flow cytometry revealed continuum of absolute genome sizes among parental species and their hybrid. The continuum was rather asymmetric in direction towards *E. hispidus*.

Model hybrid swarm Čertoryje produce significantly higher amount of hybrids (29,6 %) and allopolyploids (8,9 %) than in other populations. An enormous variation was found at the level of genome constitution followed by morphology.

Thus interspecific hybridisation of studied species is widely spread phenomenon and its character is asymmetric which implies introgressive hybridisation towards *E. hispidus*. Repeated origin of new polyploid cytotypes (mainly within hybrid swarms) was also confirmed to play an essential evolutionary role.

Key words: *Elymus*, hybridisation, allopolyploidy, absolute genome size, GISH, karyology