

Hybridization in *Elytrigia* at Two Ploidy Levels: Parents, Progeny, Chromosome Numbers and Genome Size

V. MAHELKA and F. KRAHULEC

Institute of Botany, Academy of Sciences of the Czech Republic, 252 43 Průhonice,
Czech Republic, e-mail: mahelka@bot.cas.cz

Abstract: Complexity and reticulate structure within the *Triticeae* inevitably reflects close phylogenetic relationships among members of this tribe. Allopolyploid origin of many taxa enables individuals of different taxa to hybridize, which makes the complexity of the situation even more difficult, at least for botanists working in the field. Flow cytometric and karyological investigations were performed on closely related taxa *Elytrigia repens* and *E. intermedia* (*Poaceae: Triticeae*) from the Czech Republic. DNA-hexaploids ($2n = 6x = 42$) clearly prevailed among plants examined and amounted to 96.2% of all samples. Because of 16% difference in $2C$ -values between the two species, genome size allowed reliable separation of the two species as well as the identification of hybrid individuals. Natural hybridization in *E. repens*–*E. intermedia* group seems to be quite a common phenomenon as indicated from a large proportion of hexaploid samples with intermediate $2C$ -values. In addition, nonaploid cytotypes ($2n = 9x = 63$) were revealed for both species as well as for the hybrids (determined on the basis of morphological characters available), representing the first records from the field. Fusion of unreduced and reduced gametes of the hexaploids is the most plausible mode of nonaploid origin. One nonaploid individual produced several offspring, with chromosome numbers ranging between 49 and 54, indicating backcrossing to the putative hexaploid parents; and one offspring with 63 chromosomes, indicating some degree of self-pollination. Additionally, two individuals of *E. intermedia* with $2n = 47$ and 49 were recently found in a steppe grassland, demonstrating that abnormal chromosome numbers must be expected. Origin of the nonaploid plants on the basis of genome size and cpDNA data and potential to hybridize with hexaploid cytotypes is discussed here.