

MATING PATTERNS IN PERENNIAL RYEGRASS: CONSEQUENCES FOR SEED REGENERATION

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Genebank accessions stored *ex situ* as seed populations require periodic rejuvenation in order to maintain sufficient numbers of viable seeds. During regeneration the genetic integrity of an accession may be compromised by various factors, including variation in pollination rates between plants. For a rejuvenated accession of *Lolium perenne* (L.), consisting of 49 parental plants, a paternity exclusion analysis was performed by means of molecular analysis. Investigation of a total of 551 offspring showed that mating within the study population was clearly non-random, as 61.9% of the identified pollen donors

were located within 1m distance from the mother plant. Observed pollination rates were very well described by an inverse quadratic function of inter-plant distance between potential mating pairs. However, contamination was considered more threatening to the genetic integrity of the accession than variation in pollination rates between plants. Within the total sample 5 cases of pollen contamination and 4 cases of seed contamination were observed. This indicated the need for improved measures during the rejuvenation of perennial ryegrass germplasm in order to avoid gene flow between accessions.

DIVERSITY OF SEED STORAGE PROTEIN PATTERNS IN JOINTED GOATGRASS (*AEGILOPS CYLINDRICA* HOST) POPULATIONS FROM SLOVAKIA

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Variations in seed storage protein patterns for twelve *Aegilops cylindrica* populations collected in Slovakia within the framework of Hungarian-Slovakian Intergovernmental S and T Cooperation Programme in 2006 was investigated. The present study covered the populations of jointed goatgrass collected from the southwestern (Sereď, Dunajská Streda), southern (Chľaba, Kamenica nad Hronom) and southeastern (Čierna nad Tisou, Dobrá) parts of Slovakia. Seed storage protein patterns were analyzed using acid polyacrylamide gel electrophoresis (A-PAGE) method. Electrophoreogram peaks for each population were scored. Electrophoretic analysis has revealed appreciable polymorphism in the number of gliadin

bands. The most variation in gliadin bands among the populations were observed from Dunajská Streda. Small differences were detected among the populations from Čierna nad Tisou, Dobra, Kamenica nad Hronom and Sereď. The lowest variations were detected in populations from Chľaba. The result from comparison with protein types of Hungarian populations reveal that protein type from Kamenica nad Hronom population contain similarity bands with Bokros 4 populations from Hungary. The present investigation showed that the jointed goatgrass populations collected from Slovakia exhibit valuable genetic resources for wheat crop improvement programs.

USING OF MOLECULAR MARKERS IN TRITICALE

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Genetic variability was detected in 15 varieties of triticale (*XTriticosecale* Wittmack., $2n = 6x = 42$, BBAARR) registered in the Czech Republic from 1994 to 2004 by means of

polymorphism of DNA using the RAPD method and the SSR method. For detection we used 80 RAPD primers. The lower reproducibility of the RAPD markers was resolved by means of repeated