

The Possible Origin of the “StY”-genome *Elymus*: a New Mechanism of Allopolyploidy in Plants

B.-R. Lu and Q. Liu

Ministry of Education Key Laboratory for Biodiversity Science and Ecological Engineering, Institute of Biodiversity Science, Fudan University, Shanghai 200433, China, e-mail: brlu@fudan.edu.cn

Abstract: Understanding how polyploids originate provides insight into evolutionary processes and facilitates the genetic improvement of crop species. The exclusively polyploid genus *Elymus* contains approximately 150 perennial species, which provide ideal material for studies of polyploid speciation. Five basic genomes (haplomes), **St**, **H**, **P**, **W**, and **Y**, occur in different combinations in the genus. The **St** genome found in all *Elymus* species, was supposedly donated by *Pseudoroegneria*. The **H**, **P**, and **W** genomes are derived from *Hordeum*, *Agropyron*, and *Australopyrum*, respectively. However, the diploid donor of the **Y** genome is unknown. To study speciation and phylogenetic relationships within *Elymus*, DNA sequences of nuclear ribosomal ITS, and *Adh2*, *Adh3*, and *Waxy* genes of more than 40 accessions containing various genomes (**StY**, **StH**, **StHY**, **StPY**, **StWY**) were analyzed, together with those of the ancestral genera, *Pseudoroegneria*, *Hordeum*, *Agropyron*, and *Australopyrum*. Based on analyses of 5,210 aligned nucleotides, we obtained a well-resolved and well-supported estimate of genomic relationships of *Elymus* species which strongly supports data from prior cytological studies. The molecular data revealed a distinct phylogenetic relationship of the *Elymus* polyploids and their diploid donors, but the **St** and **Y** genomes did not show any separation. The phylogenetic trees illustrated clearly that the **St**, **H**, **P**, and **W** genomes in polyploid *Elymus* have been donated by *Pseudoroegneria*, *Hordeum*, *Agropyron*, and *Australopyrum*, respectively. Further analysis suggested that the **St** and **Y** genomes might have the same origin. In other words, the allopolyploid **StY**-genome *Elymus* may have an origin from autopolyploids (**StSt**), and the same genomes differentiated gradually within the polyploid species resulting in today's **StY**-genome allotetraploid *Elymus*. This conclusion is strongly supported by many results obtained from previous cytological studies of *Triticeae* and other plant species. This represents a new mechanism of allopolyploidy in plants.