

A COMPARISON OF CHROMOSOME STRUCTURE IN *SECALE SEGETALE* ZHUK. AND *S. VAVILOVII* GROSSH, BASED ON AN ANALYSIS OF CONJUGATION MODE

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Chromosome aberrations are believed to be the reason for species differentiation within the *Secale* genus. This investigation was an attempt to locate duplications in the genomes of *Secale segetale* and *S. vavilovii*, on the basis of an analysis of conjugation mode.

Material for the study, in form of grain, was received from IHAiR in Radzików. The plants were cultivated on experimental plots in Kraków. The corn ears for study were collected in 1999 and 2000. The material was stained using the Feulgen method and C-banding. The band patterns were established based on the analysis of mitotic chromosomes from the C-banded root apical meristem. They served as the basis for the identification of chromosome types in meiocytes. The conjugation process, like all of meiosis, was regular in the majority of cells – in 82.2% in *Secale segetale* and in 66.6% *S. vavilovii*. Most of the aberrations were observed in prophase I – 19% in *Secale segetale* and 41% in *S. vavilovii*. Extraordinary chromosome conjugation can be a result of duplication. The located sites of unexpected chromosome conjugation and the results of investigations of four species of rye *Secale segetale*, *S. vavilovii*, *S. dlamaticum* and *S. cereale* are presented.

The comparison of the duplication locations in particular genomes can be used for establishing the routes of species differentiation within the *Secale* genus.