

BIOMETRY OF CHROMOSOMAL VARIABILITY OF THE DIPLOID CYTOTYPES IN THE GENUS TRITICUM L. IN IRAN

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This study is based on the examination of root tip mitosis and measuring the 10 chromosomal features among 16 diploid accessions from *Triticum boeoticum* subspecies *boeoticum*, *T. boeoticum* subspecies *thaoudar*, *T. monococcum* and *T. urartu* collected from Iran. The results of this study showed that there are a total number of 14 cytotypes among the materials studied as: four cytotypes of *T. boeoticum* subsp. *boeoticum*, three cytotypes of *T. boeoticum* subsp. *thaoudar*, two cytotypes of *T. monococcum* and five cytotype of *T. urartu* accessions. The most variable features in this study found to be: the ratio of long and short chromosome arm ($\text{Coefficient Variation} = \text{Standard Deviation} / \text{Mean} \times 100 = 60\%$) in cytotypes of *T. boeoticum* subsp. *boeoticum*, the percentage of short chromosome arm to the sum of long and short chromosome arms ($\text{C.V.} = 44.4\%$) in cytotypes of *T. urartu* and the ratio of mean length of long and short chromosome arm ($\text{C.V.} = 7.6\%$) in cytotypes of *T. monococcum*. Data analysis was performed using Biometrical Methods: Cluster Analysis (Between-groups linkage Method), Discriminate Analysis (Linear Function) and Factor Analysis (Principle Components Method). Data analyzing observations are summarized as bellow: the Discriminate Analysis revealed that the cytotypes of *Triticum* were differentiated from each other. The percentage of discrimination that is *T. urartu* 85-90%, *T. monococcum* 75%, *T. boeoticum* subsp. *boeoticum* 75% and *thaoudar* 66%. The Cluster Analysis shows two groups. Two subspecies of *T. boeoticum* were grouped together, the cytotypes of *T. monococcum* are more related to the cytotypes of *T. boeoticum* subsp. *boeoticum* and *thaoudar*. Although the cytotypes of *T. urartu* showed to be classified with the groups of *T. monococcum*, *T. boeoticum* subsp. *boeoticum* and *thaoudar*, but the cytotypes of *T. urartu* were differentiated from the other diploid species. The Factor Analysis confirmed the results of Cluster and Discriminate Analysis. The cytotypes of western and central parts of Iran found to be more variable than the other parts of the country. Regarding the high genomic variability detected between diploid *Triticum* taxa in Iran, it can be concluded that there would be a high gene flow among the cytotypes of these species. The results of this study imply that the gene pools of *Triticum* species are of marked importance as potential sources of valuable traits in Wheat breeding.