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**Karyotypic and Morphologic Variations in some Hull-less Barley
(*Hordeum vulgare* L.) Genotypes**

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ABSTRACT

Barley is a grass belonging to the family Poaceae, the tribe Triticeae and the genus *Hordeum*. The present paper describes the morphologic and karyologic analysis in sixteen genotypes of hull-less barley (*Hordeum vulgare* L.) genotypes. Karyotypic studies were carried out, using squash technique and 2% (w/v) aceto-carmin staining method. Chromosomal parameters examined were long and short arms (L & S), total chromosome length (TL), arm ratio (AR), r-value (S/L), chromosome form percentage (F%), chromosome volume, total chromatin length (X) and the number of satellites. Genotypes tested were diploid ($2n=2x=14$). Satellite numbers were differed, ranging from 0 to 2 pairs. The most diploid chromatin length were detected in G9 (73.4 μm) while G15 demonstrated the least (30.8 μm). The type of chromosomes were determined as "m" in all genotypes, using Levan's chromosome nomenclature. Karyotypes were classified in 1A of Stebbin's classification. In addition to this, to test the karyotypic symmetry in more detail, other parameters, e.g. Romero-Zarco, karyotype total form percentage (%TF), symmetry index (%S), coefficient of variation (%CV), dispersion index (DI) were also considered. For instance, in Romero-Zarco method, the A1 and A2 coefficients were 0.37 (G2) and 0.46 (G9), respectively. The resultant morphological data were tested for normality and then were analyzed with the randomized complete block design (RCBD) with 3 replications. ANOVA

indicated high significant differences for most morphological characters. The resultant cytogenetic data were tested for normality and then were analyzed according to completely randomized design (CRD) with 5 replications of cells. ANOVA indicated high significant differences for chromosomal parameters. Correlation determined between genotypes for both morphological and cytogenetical parameters. Cluster analysis was carried out, showing 2 clusters for either morphological characteristics or chromosomal parameters. Moreover, principal component analysis (PCA) was carried out, demonstrating 8 components for morphological characters justified 91.0% of the total variations and 3 components for chromosomal parameters justified 94% of the total variations. In general, the results of this study proposed that selective genotypes for crossing in plant breeding with the best far morphological variations having the most homology in chromosomes variations.

Keywords: Cytogenetic variation, Karyotype, Chromosome, Hull-less Barley, *Hordeum vulgare* L.