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CYTOLOGICAL EVALUATION OF SOME SUPERIOR PERSIAN WALNUT (JUGLANS REGIA L.) GENOTYPES IN THE BAVANAT REGION OF NORTH OF FARS PROVINCE IRAN

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Plant genetic diversity (PGD) is the fundamental of plant breeding programs to improve desirable characteristics. Evaluation of genetic diversity is the first step in fruit breeding programs. Because of high genetic diversity in Persian walnut (Juglans regia L.) population in Fars province, the southwest of Iran; this study was carried out to evaluate 16 superior walnut genotype in the aspect of cytological traits. For this purpose, 81 out of 412 walnut genotypes were morphologically evaluated based on IPGRI and UPOV descriptors during 2010-2015. Finally, 16 superior genotypes with high yield, light and extra light kernel and high kernel percentage were selected. Based on the results, nut weight and lateral bearing of selected superior genotypes ranged between 12.54-18.18 g and 54-94.47%, respectively. For cytological evaluation of select superior genotypes, Flow cytometric studies were performed using PI staining method and Solanum lycopersicum cv. Stupicke (2C DNA = 1.96 pg) as a reference standard. Based on the results, all studied superior genotypes were diploid (2n=2x=32) that average genome size was 1.33 pg. The highest and lowest amount of 2Cx DNA were observed in FaBaNs12 (1.40 pg) and FaBaAv2 (1.29 pg) genotypes, respectively. The monoploid genome size (1Cx DNA) of studied walnut genotypes ranged 0.64-0.70 pg and 629.53-684.42 Mbp.

<u>Keywords</u>: Germplasm evaluation, Genome size, Lateral bearing, Flow cytometry, Persian Walnut