Estimation of Genome Size and Ploidy Level in Salicornia Species for Understanding the Extent of Genetic Variation

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Due to population growth, food consumption has risen, thus increasing the need for greater food productivity by 70 percent by the year of 2050. At the same time, fresh water for crop irrigation has become scarcer and conventional solutions consume financial and energy resources. On the other hand, seawater for crop irrigation has the potential to solve both problems. Salicornia bigelovii is a valuable halophytic plant adapted for growth in coastal deserts. Salicornia's ploidy level was hypothesized to be inconstant from one cell to another due to phenotype variations within the same species. This novel research aims to determine the approximate genome size and ploidy level of second-generation Salicornia inbred progenies to understand the extent of genetic variation and to improve its species. Ploidy level and genome size estimation of 53 Salicornia bigelovii samples was done using flow cytometry to measure DNA content of plant cell nuclei. A sample for Flow-Cytometry must be a liquid suspension of intact plant tissue. Sample nuclei was isolated and then a DNA-binding fluorescent dye was added. The samples were taken to flow cytometer for analysis. Results have shown that 51 of the samples tested contained two ploidy variations within the same sample, Diploid and Tetraploid cells, while two samples displayed distinctive results having contained 100% Diploid cells. Having steady ploidy Salicornia plants simplifies understanding and improving plant production by producing pure lines that can be turned into a supplemental or alternative food crop for top food sources that are irrigated with fresh water.