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### DIVERSITY IN THE GENOME SIZE IN *Drosophila* HYBRID

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**Abstract:** Hybridization is a factor that can affect the genome size, which can induce large and rapid genomic changes, including chromosomal rearrangements, changes in DNA satellite content, and mobilization of transposable elements, consequently accompanied with increase in genome size. The aim of this study was to estimate the genome size of the two species - *Drosophila mojavensis* and *D. arizonae* - and to know to what extent the estimated genome size is affected in hybrids between these sister species. We estimated the relative genome size of (C-value) in F1 hybrids derived from strains of populations of *D. mojavensis* and *D. arizonae* originally found in nature in allopatry, as well as in sympatry. The genome size was estimated by flow cytometry of somatic cells from the heads of male and female tissue. Our estimates for samples of *D. mojavensis* produced a mean value of 0.190pg for females and to 0.188pg for males. The mean genome size of *D. arizonae* was 0.203pg and 0.195pg, respectively in females and males. We showed thus that the estimated genome size is variable and depends on the populations and species studied. In addition, we identified a parental effect in the genome size, suggesting the occurrence of changes in the chromatin structure that may be associated with sterility observed in hybrids derived from certain directions of the crosses between *D. mojavensis* and *D. arizonae*.

**Key-words:** *Drosophila mojavensis*, c-value, cytometry