

**ESTIMATION OF GENETIC PARAMETERS AND CLUSTERING IN
SEVERAL LINES OF MELON (*Cucumis melo* L.) BASED ON
QUALITATIVE AND QUANTITATIVE CHARACTERISTICS**

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ABSTRACT

Distinction between lines can be the basis for parental determination. Clustering analysis is technique that explores the naturally occurring groups within a data set known as clusters. Hybrid expression is expanding with increasing degree of distinction between the parental inbreds. The aims of this study were clustering analysis, determining the estimated value of genetic coefficient of variation, and determining the potential melon lines for further breeding program. The design of this study was a Randomized Complete Block Design (RCBD) which consist of a single factor with three replications. The treatments used were 9 melon lines consisting DS-1-2-10-21-11, DS-1-2-10-21-22, DS-1-2-10-21-31, DNG-1-47-13, DNG-1-47-22, DNG-1-47-31, DNG-1-47-32, APL-11, and APL-12. Observational data were analyzed by Analysis of Variance (ANOVA) and continued with Duncan Multiple Range Test (DMRT) with significancy level of 5%. Variation of Genetic estimated by calculating genetic coefficient of variation and broad-sense heritability values. Clustering estimated by Agglomerative Hierarchical Clustering Method Analysis. There are three clusters formed based on parameters of flowering and harvest age and fruit yield parameters, while four clusters were formed based on growth and development parameters. The variable plant height 2 weeks after planting was observed to have a wide range of estimated genetic coefficient of variation. A potential line for further breeding programs is DS-1-2-10-21-31

Keywords: *Melon, Genotype, Genetic Coefficient of Variation, Heritability, Cluster*