

## **Evaluation of Gene Effects and Heritability of Quantitative Traits in Tomato through Generation Mean Analysis<sup>1</sup>**

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In order to estimate heritability and magnitude of genes action in some quantitative traits in tomato, 'Peto Early' cultivar (P<sub>1</sub>) and Guilan local variety (P<sub>2</sub>) were crossed. Parents, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations were planted in a randomized complete block design with three replications in research field, College of Agricultural Sciences, University of Guilan, Rasht, Iran. The results of analysis of variance indicated that mean squares in generations were significant for all traits. Therefore generation mean analysis was used to estimate genetic parameters of all traits with six generations. Generations mean analysis showed that additive – dominance model was the best model in genetic to control of all studied traits except average weight of fruits and yield for which in addition to additive and dominance gene effects, while in addition to additive and dominant gene effects, the epistasis effects consist of additive × additive was involving in the weight of fruits, and the six-parameter model was effective in controlling the yield and the epistasis effects consist of the dominance × dominance of the genes were more important than other epistasis in controlling this trait. Furthermore, the results revealed that the additive effects of genes had the highest effects on inheritance of almost all traits such as number of leaf node before first inflorescence, plant height at date of flower bud formation, leaf length, leaf breadth, petal and sepal length, number of fruits in truss, average weight of fruits and yield, while days to formation of first flower was often controlled by dominance effects of genes. Average broad sense and narrow sense heritability were between 0.55-0.91 and 0.47-0.76 percentage, respectively. Number of genes involving in expression of the studied traits were estimated to be 1 to 39 genes.

**Key Words:** Broad sense heritability, Generation mean analysis, Genetic parameters, Number of gene, Narrow sense heritability.

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