



Genetic Component Analysis in Bread wheat (*Triticum aestivum* L. em. Thell) under Heat Stress Condition

Asaye Demelash Limenie^{1*}, D. K. Gothwal², M. L. Jakhar², Manohar Ram² and G. L. Kumawat²

¹

selected plants from each plot in each replication of parents and F_1 's in two environments separately for all the characters except days to anthesis, days to maturity and 1000-grain weight, where these were observed on plot basis. The data were subjected to analysis of variance using the standard procedures. The observations were recorded on ten randomly selected competitive plants from each plot in each replication in case of parents and F_1 s in two environments separately on five distinct quantitative characters viz; days to anthesis, flag leaf area, grains/spike, grain yield/plant and chlorophyll content [2].

↓

The diallel analysis with Hayman's approach is the graphic representation of the variance (V_r) of all components of the r^{th} array and the covariance (W_r) of all the offspring in each parental array with the non-recurring parents. The information of gene action was inferred by plotting the covariance (W_r) of each array against its variance (V_r).

The slope and the position of regression line fitted to the array points within the limiting parabola ($W_r^2 = V_p \times V_r$) and from zero origin showed the degree of dominance and the presence or absence of gene interaction. The corresponding values of W_r for all observed V_r values were calculated as $(V_p \times V_r)^{0.5}$, where V_p = variance of the parents. The different arrays were plotted within the limits for the parabola using the individual variance and covariance as their limiting points. Parent array points nearest to the origin possessed most recessive genes, and intermediate position signified the presence of both dominant and recessive genes in the array and farthest most points indicated presence of dominant genes. For the additive-dominance model to be adequate and hence the fulfillment of the assumptions is provided by regression analysis of W_r and V_r . According to Mather & Jinks (1982) the regression coefficient is expected to be significantly different from zero but not significantly different from unity if all the assumptions are fulfilled. Failure of this test means either genes show non-allelic interaction i.e., is not independent in their action or show non-random association among the parents i.e., is non-independent in their distribution. Secondly, adequacy of this additive-dominance model is that of $W_r + V_r$ and $W_r - V_r$. If dominance is present $W_r + V_r$ must change from array to array and at the same time if there is non-allelic interaction between the alleles, $W_r - V_r$ will vary between arrays. However, if dominance is present, $W_r - V_r$ will not vary more than expected from error variation. If data fulfill both tests, the additive dominance model is completely adequate for further analysis. However, if one of them fails to fulfill assumptions, the additive-dominance model is partially adequate [3].

↓

Diallel analysis developed by Hayman (1954), Jinks (1954) and applied by Mather was used for genetic analysis. Parameters used in this experiment were: D, variation attributed to additive effects; H_1 , variation due to dominance effects; H_2 , variation due to dominance

not affected the expression of this trait. The ratio of average degree of dominance as measured by $(H_1/D)^{0.5}$ was more than unity indicating over dominance. The value of proportion of genes with positive and negative effects i.e. $[H_2/4H_1]$ for this trait was 0.16; which was less than 0.25. This indicated unequal distribution of positive and negative alleles in the parents. The ratio of dominant and recessive alleles in parents i.e. $[(4DH_1)^{0.5} + F] / [(4DH_1)^{0.5} - F]$ in E_1 environment was greater than unity suggesting accumulation of dominant alleles. The number of gene groups i.e. h^2/H_2 ratio was 0.38 for this trait suggesting that at least one group of genes might be operating in the inheritance of this trait and expressing dominance. The value of heritability in narrow sense i.e. $h^2_{(ns)}$ was observed as medium (0.45) for this trait [8].

Significant deviation of 'b' from zero and non-significant departure from unity was observed for this character under normal environment which indicated the adequacy of additive-dominance model in E_1 environment only. Genetic component of variance revealed that the variance due to additive effects (D) of genes was found significant under normal environment, which indicated the importance of additive variation in the inheritance of grains per spike. Variance of H_1 and H_2 were also positively significant in E_1 indicating that both additive and non-additive components were operating in the expression of this trait.

The value of F was non-significant in E_1 suggesting that the dominant and recessive alleles were present in equal proportion in the parents. Environmental component of variance i.e. E was non-significant which indicated that impact of the environment did not have expression on this trait. The ratio of average degree of dominance as measured by $(H_1/D)^{0.5}$ was more than unity indicating over dominance. The value of proportion of genes with positive and negative effects i.e. $[H_2/4H_1]$ for this trait was 0.21; this value was less than 0.25, which indicated unequal distribution of positive and negative alleles in the parents. The ratio of dominant and recessive alleles in parents i.e. $[(4DH_1)^{0.5} + F] / [(4DH_1)^{0.5} - F]$ in E_1 environment was greater than unity suggesting accumulation of dominant alleles. The number of gene groups i.e. h^2/H_2 ratio was 0.38 for this trait suggesting that at least one group of genes might be operating in the inheritance of this trait and expressing dominance. The value of heritability in narrow sense i.e. $h^2_{(ns)}$ was observed as medium (0.45) for this trait [8].