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

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Abstract

Eight parental genotypes of bread wheat were selected on the basis of broad range of genetic diversity and heat tolerance. 28 F_1 progenies produced by 8×8 half diallel fashion along with parents were evaluated in normal and heat stress environments during 2019-20. Adequacy tests indicated that data for days to anthesis, flag leaf area, grains/spike, grain yield/plant and chlorophyll content were fitted for additive - dominance model. Additive component of variation (D) was significant (P<0.01) and prominent over H_1 and H_2 components for days to anthesis, flag leaf area, grains/spike, grain yield/plant and chlorophyll content. Partial dominant genes were mainly controlling factors for days to anthesis while flag leaf area, grains/spike, grain yield/plant and chlorophyll content were sustained over dominance by the value of $(H_1/D)^{0.5}$. Values of $H_2/4H_1$, h^2/H_2 and $[(4DH_1)0.5 + F] / [(4DH_1)^{0.5} - F]$ demonstrated asymmetrical and unequal distribution of dominant genes in parents for most of the characters. Days to anthesis exhibited high narrow sense heritability due to the existence of additive gene action with partial dominance suggesting that these traits might be useful for the development of high temperature stress tolerant varieties using modified pedigree selection method.

Keywords: Genetic component; Heat stress; Wheat; Additive dominance

Introduction

Wheat is one of the most widely consumed cereal crop in India as well as in world. Wheat is the leading grain crop in the temperate climates of the world. It is a polyploidy series of genetic origin and its species of Triticum and their close relatives can be divided into diploid (2n = 2x = 14; AA), tetraploid (2n = 4x = 28; AABB) and hexaploid (2n = 6x = 42; AABBDD), in which the basic chromosome number x = 7. Wheat grains have pleasant flavor, long shelf-life and unique gluten-forming characteristics. Its flour is used for making chapati, breads, cookies, cakes, pasta, noodles and other bakery products. Wheat is also fermented to make alcohol and biofuel. The protein content of wheat grain provides about 8 - 20 per cent of the total energy necessities in food for human body. Wheat has esteemed supplement for nutritional requirement of human body as it contains 14.70 per cent protein and 78.10 per cent carbohydrate; and additionally its straw is used for fodder and mulching material. In addition, wheat provides food to 36 per cent of the overall population contributing 20 per cent of total food calories for the world people as well as for many countries as a national primary food in many countries).

Eventually, wheat improvement is an important component of global wheat breeding programmes for thermo-tolerance types. Wheat production is significantly affected by abiotic stresses particularly at high temperature during the grain filling stage. Heat stress during crop growing period, predominantly after anthesis and grain filling stages restricts wheat production and productivity. Wheat does not tolerate prolonged exposure to temperature exceeding 350C. High temperature stress can be a single significant factor in reducing yield and quality of wheat. There is a need to establish new genotypes with a genetic structure to survive heat stress and to maintain and boost wheat productivity in warmer areas of India. Since the essence of gene action is correlated with the genetic structure of the population involved in hybridization, parents need to be tested for their ability to combine. Therefore, selecting parents on the basis of their genetic values is important. For the production of new crop varieties for heat stress conditions with stress adaptation mechanisms, breeders need better understanding and useful knowledge. Therefore, the present study was carried out to identify stress tolerance and inheritance mechanism under normal and heat stress conditions, in terms of the types of gene action [1].

Materials and Methods

The experimental materials consisting of eight genotypes selected on the basis of broad range of genetic diversity for major yield components, heat tolerance and their suitability for different yield traits, were crossed in half diallel fashion resulting in 28 F_1s during the year 2018-19. The eight genotypes namely, PBW 343, PBW 502, Raj 3777, Raj 3765, HD 3086, Raj 4238, PBW 550 and WH 1021 along with their 28 F_1s were evaluated in two environments i.e. Normal (E_1) and heat stress (E_2) in three replications in a randomized block design during *Rabi* 2019-20. The heat stress environment was created by manipulating date of sowing. In order to create heat stress at post anthesis stage, the sowing was delayed by about four weeks later than the normal sowing. Parents and F_1s were represented by a plot of two rows each. Rows were planted in 2.5 m length spaced at 30 cm with 10 cm interplant distance under both the environments. Observations were recorded on 15 distinct characters viz; days to anthesis, days to maturity, anthesis to maturity, plant height (cm), total tillers/plant, productive tillers/plant, flag leaf area (cm^2), spike length (cm), grains/spike, 1000-grain weight (g), biological yield/plant (g), grain yield/plant (g), harvest index (%), proline content (µg/100 mg fresh weight) and chlorophyll content (SPAD) . Data were taken on ten randomly

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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_1s in two environments separately on five distinct quantitative characters viz; days to anthesis, flag leaf area, grains/spike, grain yield/plantand chlorophyll content [2].

Statistical analysis

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 off springs 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 ($Wr^2=V_p$ x V_r) and from zero origin showed the degree of dominance and the presence or absence of gene interaction. The corresponding values of Wr 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 fitted 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].

Genetic analysis

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 effects corrected for gene distribution: F determine the relative frequency of dominant to recessive alleles in the parental populations and the variation level over loci, which is positive displaying the important role of the frequency of dominant genes: h^2 indicated the dominance effects due to heterozygous loci. The value of $(H_1/D)^{0.5}$ is the measure of average degree of dominance, which is equal to one when the dominance is complete (H_2) $[(4DH_1)^{0.5} + F] / [(4DH_1)^{0.5} - F]$ is the measure of ratio of dominant and recessive alleles and E, is expected environmental component of variation. Heritability in narrow-sense was estimated according to Mather and Jinks (1971) [4].

Results and Discussion

The occurrence of significant deviation of regression coefficient "b" from zero but non-significant deviation of "b" from unity suggested the adequacy of additive-dominance model (Hayman, 1954). Additive-dominance model was fitted for days to anthesis, flag leaf area, grains per spike, grain yield per plant and chlorophyll content. These results revealed that the assumptions of diallel analysis were fulfilled for these traits. The components of genetic variances were determined as per Hayman's approach. But where additive-dominance model was inadequate, only graphical analysis was performed which indicated the existence of epistatic interactions [5]. This showed the importance of testing the genetic material in more than one environment in order to obtain unbiased estimates of various components. But here only components of genetic variance are taken into consideration. Similar result of adequacy of additive-dominance model in wheat was reported by Rabbani for flag leaf area; by for grains per spike and grain yield per plant; by Yao for grain yield per plant; by Irshad for days to anthesis, grains per spike and grain yield per plant; by Farshadfar and Amiri (2015) for chlorophyll content and proline content; by Eftekhari for chlorophyll content and by Kumar (2018) for days to 50% flowering, flag leaf area and spike length [6].

Days to anthesis

Significant deviation of 'b' from zero and non-significant withdrawal from unity was observed for days to anthesis in E_1 environment only which indicated the adequacy of additive-dominance model. 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 days to anthesis. The component analysis exhibited that both additive (D) and non-additive components (H_1 and H_2) of genetic variance were significant, which indicated that both components (additive and non-additive) were operating in the expression of the trait. The magnitude of H_1 was higher than that of H_2, which demonstrated unequal allelic frequencies at relevant loci. The significant value of 'F' advocated that dominant alleles were more frequent than recessive. Environmental component of variance i.e. 'E' was found significant, suggesting impact of the environment on expression of this trait. The mean degree of dominance $(H_1/D)^{0.5}$ was less than unity evidenced partial dominance. $H_2/4H_1$ ratio was less than 0.25 evidenced unequal distributions of positive and negative alleles in the parents. The ratio of dominant and recessive alleles $[(4DH_1)^{0.5} + F] / [(4DH_1)^{0.5} - F]$ was more than unity where additive-dominance model fitted which displayed accumulation of dominant alleles. The ratio of h^2/H_2 was 0.56, suggested that at least one group of genes might be operating in the inheritance of dominance. The value of heritability in narrow sense i.e. h^2 (ns) was observed as high as 0.63 for days to anthesis [7].

Flag leaf area (cm^2)

Significant deviation of 'b' from zero and non-significant departure from unity was observed under normal environment which indicated the adequacy of additive–dominance model in E_1 environment only. Genetic components 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 flag leaf area. Variance of H_1 and H_2 were also positively significant in E_1 offsprings indicating that both additive and non-additive component was operating in the expression of this trait. Similar finding was observed and reported higher dominant component for flag leaf area by Kandil (2016). The value of F was significant in E_1 suggesting that the dominant and recessive alleles were in unequal proportion in the parents. Environmental component of variance i.e. E was non-significant, suggesting the environment did

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].

Grains /spike

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 had 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 1.03 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 low as 0.28 for this trait [9].

Grain yield /plant (g)

Significant deviation of 'b' from zero and non-significant departure from unity was observed under heat stress environment which indicated the adequacy of additive–dominance model in E_2 environment only for grain yield per plant. The value of D component was found significant under heat stress environment, which indicated the importance of additive variation in the inheritance of grain yield per plant. Genetic component of variance H_1 and H_2 were also positively significant in E_2 indicating that both additive and non-additive components were operating in the expression of this trait. This finding supported by Kutlu and Olgun (2015) and Afridi *et al*. (2017) which observed higher dominant component for grain number per spike and grain yield per plant. The value of F was significant in E_2 suggesting that the dominant and recessive alleles were present in unequal proportion in the parents. Environmental component of variance i.e. E was non-significant, suggesting that there was no impact of the environment in 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 0.20. 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_2 environment was greater than unity suggesting accumulation of dominant alleles. The number of gene groups i.e. h^2/H_2 ratio was 0.89, 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 too low as 0.05 in for this trait [10].

Chlorophyll content (SPAD)

Significant deviation of 'b' from zero and non-significant departure from unity was observed under normal environment which indicated the adequacy of additive–dominance model in E_1 environment only for chlorophyll content. Genetic components of variance D, H_1 and H_2 were 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 significant in E_1 suggesting that the dominant and recessive alleles were present in unequal proportion in the parents. Environmental component of variance i.e. E was non-significant, suggesting that there was no impact of the environment expression of this trait.

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