GENETIC ANALYSIS OF QUANTITATIVE CHARACTERS OF IN HEAT TOLERANT TOMATO (Solanum lycopersicum L.)

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ABSTRACT

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Genetic analysis for days to 50% flowering, flowers per cluster, percent fruit set, fruit clusters per plant, fruits per plant, individual fruit weight, fruit yield per plant, fruit length, fruit diameter, branches per plant, plant height, seeds per fruit, percent brix and percent viable pollen grain in tomato (*Solanum lycopersicum* L.) were studied. In Wr/Vr graph the slope of the regression line was significantly below from 1.0, suggesting significant non-allelic interaction for all the characters. A simple additive genetic system with incomplete dominance or partial dominance was observed for flowers per cluster, percent fruit set, individual fruit weight, fruit length, branches per plant and percent viable pollen grain. An additive genetic system with complete dominance for days to 50% flowering, fruit clusters per plant, fruits per plant, fruit yield per plant, fruit diameter, plant height, seeds per fruit and percent brix.

Key words: gene action, Wr/Vr graph, Wr+Vr/parental mean graph, yield and yield contributing character and heat tolerant tomato

INTRODUCTION

The development of a meaningful breeding programme needs information on the nature of gene actions controlling the economic characters and other characters of importance. Knowledge of genetic architecture of the characters under improvement is essential for adopting appropriate breeding procedure. Such knowledge leads the plant breeder to develop new commercial varieties of the crop. Gardner (1963) stressed that information on variation attributable to genetic differences and also on the relationship among various quantitative traits is fundamentally significant in a crop improvement programme.

Villareal and Lai (1979) reported that heat tolerance is controlled by largely recessive genes and inherited in a complex fashion with low heritability, which are typical of polygenetic traits. They also suggested that the heat tolerant genes are easily influenced by environment. In another observations (AVRDC 1988) pointed out that heat tolerance in tomato may not be as complex as had been reported previously by Villareal and Lai in (1979). Genetic information of tomatoes in this respect under the hot humid conditions of Bangladesh is not available, as almost no work has been done in this regard. Therefore, the present study was undertaken with the objective to determine the mode of gene action in governing characters under high temperature stress.

MATERIALS AND METHODS

The experiment was conducted at the experimental farm of Olericulture Division, HRC, Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur during the month of July to November 2006. The average minimum and maximum temperature during the crop period was 25.47°C and 32.16°C respectively. The mean minimum and maximum relative humidity was 80.26% and 93.31% respectively. A diallel cross of 8 x 8 excluding reciprocals were constructed from the eight parental lines viz., P1 (TM051), P2 (TM053), P3 (TM017), P4 (TM026), P5 (TM025), P6 (TM041), P7 (TM044), P8 (TM002). Seeds of the eight selfed parents and their twenty-eight F1 hybrids were sown in seed bed on 16th July May 2006. Then at the age of 35 days, seedlings were transplanted in the main experimental plots. The experiment was set up in a randomized complete block design (RCBD) with four replications. Thirty-six genotypes (28 F1's + 8 parents) of tomato were considered as the 36 treatments of the experiment. The unit plot size was 5.0 x 1.0m and the plants were spaced 50cm on row. Each unit plot contained single row accommodating 10 plants where data were collected from randomly selected 5 plants leaving 2 border plants. The experimental plots were covered by transparent polytuunel with minimum interruption of photosynthesis. The polytuunels were 2.3 meter wide having two 1.0 meter wide bed with 30 cm drain in between, which serves as irrigation channel. The tunnels were used to protect the plants from high rainfall. All the sides of tunnel were open for good aeration. The recommended dosage and method of application of manure and fertilizers were used. Weeding and mulching was done followed by top-dressing and irrigation was applied at 15 days interval. Five plants were selected randomly from each unit plot. Data on days to 50% flowering, flowers per cluster, fruit set (%), fruit clusters per plant, fruits per plant, individual fruit weight (g), yield per plant (g), fruit length (cm), fruit diameter (cm), branches per plant, plant height (cm), seeds per fruit, brix (%) and viable pollen grain (%) were recorded. All the quantitative data taken were subjected to ANOVA. The total variances of each character were partitioned into block, genotype and error differences. The differences within the classes of effects were tested by F-test. Combining ability analysis of the traits with significant genotypic differences was done according to the Model 1 and Method 2 of Griffing (1956 a, b). The fixed effect model was more appropriate in the present case since the parents selected were self-pollinated lines and the parents and F1s were the populations considered. This analysis partitioned the variation due to genotypic differences into general combining ability (GCA) and specific combining ability (SCA) effects.

RESULTS AND DISCUSSION

The interpretation of Wr/Vr graph and Wr + Vr/parental mean graph

In Wr–Vr graphs, the two directional depictions made based on the parental variance (Vr) and parent offspring co-variance (Wr) are presented in the Figures 1 through 14 for the 14 characters studied. Further graphical tests with Wr + Vr versus parental means are also presented in the figures 1 to 14. In this approach Hayman's graphical analysis was done and the findings are presented individually for the fourteen characters.

Days to 50% flowering

The regression line of the Wr/Vr graph (Fig.1) had a slope significantly different from 1.0 (0.170 ± 0.146) indicated non-allelic interaction and intersected the Wr axis through the origin which indicated nearly complete dominance. Furthermore, all the Wr, Vr points were captured within the boundary of the limiting parabola. The parents P8 and P7 had lower Wr, Vr values fall nearest to origin, hence, had the most dominant alleles whilst P2 and P3 with larger values of Wr, Vr fall farthest from origin and, hence, had mostly recessive alleles. Rest parents are clearly hold intermediate positions containing equal frequencies of dominant and recessive alleles (Fig. 1.a1). The array points representing their respective parental numbers were clustered into 3 distinct groups along the regression line of the graph indicating diversity existed among the parents. The graph Wr + Vr against the parental mean further confirms the diversity among the parents (Fig. 1.b1). Here in this figure P3 fell farthest from the intersecting point of the regression line with the parental axis and were also the latest to flower whilst in contrast parent P8 were closest to the origin of parental axis having mostly dominant. Thus it is quite clear that earliness is associated with parents having dominant alleles in the direction of lower values and lateness with recessive alleles in the direction of higher values. The other parents in-between are intermediate in earliness. Similar findings were reported by Rashid *et al.* (1995) in eggplant.



Fig. 1. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) for days to 50% flowering

Flowers per cluster

For flower number per cluster, the regression line of the Wr/Vr graph (Fig. 2) had a slope significantly different from 1.0 (0.645 \pm 0.039) and indicated presence of non-allelic interaction and intersected the Wr axis above the origin indicating partial dominance. Lewis (1954) reported such behaviour of genes for this trait. All the Wr, Vr points fall within the boundary of the limiting parabola. It was evident from Wr/Vr graph the parent P3 and P8 had mostly dominant and P1 had mostly recessive alleles while the parents P2, P4, P5, P6 and P7 had equal proportion of dominant and recessive alleles (Fig. 2.a1). The graph Wr + Vr versus parental means further tests the consistency of dominance against the parental score (Fig. 2.b1). Parental mean suggested that the parents which contained the most dominant alleles were low scoring whereas parents with recessive alleles were high scoring. A high number of flowers per cluster were therefore consistently associated with parents having recessive alleles in the direction of high values. El-Ahmadi and Stevens (1979) also reported that recessive genes are associated with higher flower numbers both at normal and high temperature conditions.



Fig. 2. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) for flower number per cluster

Percent fruit set

It was observed from the Wr/Vr graph (Fig. 3) that the regression line had a slope of 0.797 ± 0.077 significantly different from 1.0 indicating presence of non-allelic interaction. The regression line intersected the Wr axis above the origin indicating partial dominance. This might be due to the fluctuating behaviour of the genes controlling the trait under varying time of crop growing specially temperature condition. The relative values of the Vr and Wr showed the parents P5 and P7 had the lowest values and, hence, had the most dominant alleles, while the parent P3, P6 and P8 had the highest Vr, Wr values and hence, had the most recessive alleles. The other three parents P1, P2 and P4 fell in between these and occupied intermediate positions. Parents clustered into 3 distinct groups on the regression line showing diversity in the parents. In Wr + Vr/parental mean graph (Fig. 3.b1), parental mean suggested that the parents which contained the most dominant alleles were high scoring whereas parents with recessive alleles were low scoring. El-Ahmadi and Stevens (1979) also reported that, at high temperature dominant genes have positive effects on fruit setting i.e. increased percent fruit set.



Fig. 3. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) for % fruit set

Fruit clusters per plant

The regression line of Wr/Vr graph (Fig. 4) had a slope significantly different from 1.0 (0.654 ± 0.162) indicated non-allelic interaction and intersected the Wr axis below the origin indicating over dominance. It was evident from Wr/Vr graph (Fig. 4. a1) that parent P2 and P7 had mostly dominant and P3 had mostly recessive alleles while the other parents fell intermediate with equal proportion of dominant and recessive alleles. In Wr + Vr/parental mean graph (Fig. 4.b1), parental mean suggested that the parents having most dominant alleles were high scoring and parents having most recessive alleles were low scoring in general. Therefore, more number of fruit clusters was associated with parents having dominant alleles.



Fig. 4. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) for fruit cluster/plant

Fruits per plant

The regression line of the Wr/Vr graph (Fig. 5) had a slope significantly different from 1.0 (0.791 ± 0.080) indicated non-allelic interaction and intersected the Wr axis almost nearly to the point of origin indicated the existence of nearly complete dominance. It was evident from array position in Wr/Vr graph that the parent P1, P2, P4 and P7 had mostly dominant alleles and P3 had mostly recessive alleles. The other parents have middle groups with equal frequency of dominant and recessive alleles. In Wr + Vr/parental mean graph (Fig. 5.b1), the parental means suggested that the parents having most dominant alleles were high scoring and parents having most recessive alleles in the direction of higher values. Sahrigy *et al.* (1970) reported the importance of dominance effects in the inheritance of both yield and number of fruits per plant.

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Fig. 5. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) for fruits per plant

Individual (average) fruit weight (g)

It was observed from the Wr/Vr graph (Fig. 6) that the regression line had a slope of 0.544 ± 0.121 which was significantly different from 1.0 indicating presence of non-allelic interaction. The regression line intersected the Wr axis a little above the point of origin indicated partial dominance. The relative values of the Wr and Vr showed that the parent P4 and P8 had the lowest values and, hence had the most dominant alleles; while the parent P5 had the highest Vr, Wr values and, hence, had the most recessive alleles. The other 5 parents fell in between these and occupied intermediate positions (Fig. 6.a1). The Wr + Vr/parental mean graph (Fig. 6.b1) confirms that the parents which contained the most dominant alleles were low scoring in general whereas parent P5 with most recessive alleles were high scoring. Therefore, parents having high fruit weight was consistent by associated with recessive alleles in the direction of higher values.



Fig. 6. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean in (b1) for individual fruit weight (g)

Fruit yield per plant

The slope of the regression line for fruit yield (Fig. 7) was significantly below $1.0 (0.460 \pm 0.082)$, suggesting significant non-allelic interaction for this character. The regression line intersected the Wr axis nearly through the origin, suggested complete dominance to the interaction. The relative values of Vr and Wr showed that the parent P2 and P4 had the lowest values and hence contained the most dominant alleles while the parent P3 had the highest Vr, Wr values and have the most recessive alleles (Fig. 7.a1). The other 5 parents fell in between. The Wr + Vr/parental mean graph (Fig. 7.b1) confirms that the parents which contained the most dominant alleles were high scoring in general whereas parents with most recessive alleles were low scoring. Therefore, parents having high yield was consistently associated with dominant alleles in the direction of higher values. Sahrigy *et al.* (1970) have reported the importance of dominance effects in the inheritance of yield and number of fruits per plant.



Fig. 7. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) for yield per plant (g)

Fruit length (cm)

The regression line of Wr/Vr graph (Fig. 8) had a slope not significantly different from 1.0 (0.820 ± 0.199) indicated no gene interaction and intersected the Wr axis well above the origin suggesting incomplete or partial dominance. It was also revealed from the graph that the parent P3 being closer to origin had most dominant alleles and P5 being the farthest from origin had most recessive alleles and other parents fell in the middle group in sowing 1 (Fig. 8.a1). Wr + Vr/parental mean graph (Fig. 8.b1) showed that the fruit length was conditioned by recessive alleles with high scoring parents as P7.



Fig. 8. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) for fruit length (cm)

Fruit diameter (cm)

The regression line of Wr/Vr graph (Fig. 9) had a slope significantly different from 1.0 (0.403 ± 0.125) indicated non-allelic interaction and intersected the Wr axis almost to the point of origin suggesting complete dominance in addition to interaction. It was evident from the graph that parent P4 being the closest to origin had the most dominant alleles and P5 being the farthest from origin had most recessive alleles. Other parents lie in intermediate position having equal frequency of recessive and dominant alleles. The Wr + Vr versus parental mean graph (Fig. 9.b1) confirm that the fruit diameter was conditioned by recessive alleles with high scoring parents as P5.



Fig. 9. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) for fruit diameter (cm)

Branches per plant

It was observed from the Wr/Vr graph (Fig. 10) that the slope of the regression line had significantly different value than unity (0.169 ± 0.078) indicating presence of non-allelic interaction. The regression line intersected the Wr axis above the point of origin suggesting incomplete or partial dominance in addition to the interaction. The relative position of arrays showed that the parent P7 fell nearest to the origin having most dominant alleles and parent P4 fell farthest from the point of origin with most recessive alleles. The remaining 6 other parents fell in intermediate position with equal frequency of dominant and recessive alleles. The Wr + Vr versus parental mean graph (Fig. 10.b1) confirms that the number of branches per plant was conditioned by dominant alleles with low scoring parents in general with a little inconsistency about the control of dominance in high scoring parents.



Fig. 10. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) for branch per plant

Plant height (cm)

The regression line of Wr/Vr graph (Fig. 11) had a slope significantly different from unity (0.606 ± 0.076) suggesting that there was presence of non-allelic interaction. The regression line passes through the Wr axis just below the point of origin indicating slight over dominance in addition to the interaction. It was evident from the graph that the parent P3 and P8 were closer to point of origin indicated with most dominant alleles and P4 fell farthest from origin and, hence contained the most recessive alleles. The remaining parents are in-between with equal proportion of dominant and recessive alleles. The Wr + Vr versus parental mean graph (Fig. 11.b1) farther test the consistency of dominance against the parental score. Here in this figure it was evident that the parent P3 and P8 contained the most dominant alleles and tall plant height was conditioned by dominant alleles with high scoring parents while dwarfness by recessive alleles with low scoring parents.



Fig. 11. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) for plant height (cm) *Seeds per fruit*

The regression line of Wr/Vr graph (Fig. 12) for the trait had a slope significantly different from 1.0 (0.375 \pm 0.108) indicating presence of non-allelic gene interaction. The regression line also intersected Wr axis in different position and it passes almost through the origin suggesting complete dominance. El-Ahmadi and Stevens (1979) reported about the position of regression line for this trait that the line is close to the origin at normal temperature and below the origin at high temperature, indicating over dominance. As for the trait, although the positions of the parents on the Wr/Vr and Wr + Vr Vs parental mean graph (Fig. 12.b1) were inconsistent which may be due to significant block differences. However, the trend was that the dominance was conditioned by dominant alleles with high scoring parents.



Fig. 12. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) for seeds per fruit *Percent brix*

The regression line of Wr/Vr (Fig. 13) graph for percent brix had a slope significantly different from 1.0 (0.581 \pm 0.187) indicated non-allelic gene interaction, intersecting the Wr axis well below the point of origin indicated over dominance. Wr + Vr Vs parental mean graph (Fig. 13.b1) indicated recessive alleles are associated with high scoring parents but the trend was not so consistent.



Fig. 13. Wr, Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) for brix (%)

Percent of viable pollen grain

In the Wr/Vr graph (Fig. 14) that the slope of the regression line had significantly different value than unity (0.467 ± 0.068) indicating the presence of non-allelic interaction for the character. The regression line passes through the Wr axis a little above the origin suggested partial dominance. It was evident from the graph that parent P8 fell nearest to the point of origin and P1 to the farthest, indicated most dominant and most recessive alleles respectively. The Wr + Vr Vs parental mean graph (Fig. 14.b1) confirm further the consistency of dominance against parental score. Here in this graph it was evident that parent P8 with the most dominant alleles had represented the low scoring parent and parent P1 with most recessive alleles had represented the high scoring parent and was revealed that the dominance was conditioned by recessive alleles.



Fig. 14. Wr. Vr regression and limiting parabola (a1) and Wr + Vr Vs parental mean (b1) (b2) for % of viable pollen grain

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