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Research Article

Genetic architecture of some yield and biochemical traits of tomato *Solanum lycopersicum* L

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Abstract
The present study was carried out to determine fruit yield related traits by crossing 8 diverse tomato lines/varieties in partial diallel manner. Eight parents, 28 F_1 and 28 F_2 were evaluated in RBD with three replications. Analysis of variance showed that genotypes and both generations differed significantly among each other for all the traits studied.The estimate of component of genetic variation revealed that additive components (D) of variance, dominant genetic variance (H_1 and H_2) and dominance effect were found significant for plant height and fruits plant^{-1} in both generations. The estimates and dominance component (H)were greater than additive component(D) of variance indicating preponderance of dominant gene action for the expression of all the characters under the study. The ratio of dominant and recessive gene(KD/KR) in the parents showed their asymmetric distribution among the arrays. The $H_2/4H_1$ ratio showed an excess of dominant alleles among the patents and dominance was unidirectional in both F_1 and F_2 generations. Environment factor E significantly influenced harvest span. The estimates of mean degree of dominance revealed over dominance for all the characters in both generations. All the characters except fruit yield in F_1 were appeared to be controlled by at least one gene group. High heritability estimates were noticed for fruit acidity content in F_1 generation suggesting preponderance of additive gene effects. Low to high heritability estimates in narrow sense were observed for all the traits, controlled predominantly by dominant genes.Fruit yield showed low heritability (7.52 in F_1 and 8.19 in F_2 generation)indicated non additive gene action suggesting exploitation of heterosis breeding in F_1 and selection of desirable segregants infurthergenerations.

Keywords : Tomato, first and second generation, yield parameters, gene action, heritability

Introduction

Tomato (*Solanumlycopersicum* L.) is the second most consumed vegetable of the world after potato with a production of 161.70 million tons from 4.80 million ha area and productivity of 33.68 tons ha^{-1}(FAO, 2014). In India during 2012-13, tomatowas cultivated in an area of 8.88 lakh hectares with a production of 182.28 lakh tonnes (Anon, 2014) and productivity of 20.11 tonnesha^{-1}.Although productivity of tomato is 25.2 tonnes ha^{-1}, In India Gujarat ranks sixth (5.81 %) in production of tomatoes (9.78 lakh tons)from an area of 38800 ha (Anon, 2011).

Although many commercial cultivars of tomato have high agronomic performances, they perform poorly because of some genetic hindrances in diverse cross combinations. Crossing in a diallel fashion is the only specific and flourishing approach of measurement for the identification and selection of superior genetically recombined material. The diallel analysis advocated by Hayman (1954) and Mather and Jinks (1982) provides reliable method particularly in autogamous crops to review the genetic system and gene action involved in the expression of plant attributes, right in the first generation (F_1) and second generation (F_2). The nature of gene action involved in the inheritance of various characters are very important to decide any breeding methodology for crop improvement. This can be determined by numerical approach based on genetic components of variation. In this context, present study was executed to estimate the genetic components of variance and heritability of some yield related traits in tomato Indian and exotic genotypes which can be recommended for subsequent plant breeding programmes for achieving fruitful results.

Materials and Methods

The present investigation was conductedat Instructional farm, Junagadh Agricultural University, Junagadh. Geographically Junagadh is located at 21.5^0 N latitude and 70.5^0 E longitudes with an altitude of 60 m above the mean sea level. Eight tomato diverse inbred lines *viz.*, Gujarat Tomato 1(GT 1), Pusa Ruby, H 24, EC 490190, ArkaVikas, EC 163599, EC 177371and EC 398704were crossed in half diallel fashion to get F_1 seeds. All the F_1 seed was sown, and at the time of pollination about 10 plants were selfed to get F_2 seeds. All the 64 genotypes (8 parents, 28 F_1 hybrids and 28 F_2) were evaluatedin a randomized block design with three replications. The seedlings were transplanted at the spacing of 75 cm between rows and 60 cm between plants and were grown by

following recommended cultural practices and plant protection measures of J.A.U.to raise crop successfully.

The data obtained from half diallel for yield and biochemical traitswere tested for significance by the method suggested by Panse and Sukhatme (1987). The Total soluble solids (^{0}Brix) of fruits were recorded with a hand refractometer calibrated in ^{0}brix values were corrected at 20^{0}C. Fruit acidity content was estimated as per the method of Ranganna(1977) and genetic parameters by Hayman (1954).

Results and Discussion

The analysis of variance for the experiment showed significant differences among the treatments (parents, F_1 and F_2) for all the traits studied indicating the presence of substantial genetic variability (Table 1).

Analysis of genetic parameters revealed that all parameters were significantly different from zero (Table 2). Estimates of additive component of variance, dominant genetic variance (H_1 and H_2) and dominance effect were found significant for plant height, fruits plant^{-1},TSS and fruit yield in both generations except dominance (D) for fruit yield and TSS in F_2generation. Estimates of component of genetic variation and genetic ratios exhibited higher values of H_1 and H_2 compared to D indicating that non additive gene effects had a greater role than additive gene effects in the genetic control. The positive and significant estimates of H_2 for all traits under both generations suggested that the dominant gene were in the favorable direction and the significant positive H_1 value confirmed the positive direction of dominance which also confirmed in earlier findings (Bhatt *et. al.* 2001 and Biswas*et.al* 2011). Expected environmental components of variance significantly influenced harvest span in both generations. Earlier Khalil *et al.* (1986),Kanthaswamy*et al.* (1995)andChadha*et al.* (2001) reported similar results for additive gene effects in tomato.Asymmetrical distribution of genes among parents, over dominance and preponderance of dominant genes in both sets is confirmed from the studies of Sekar (2001).

The component ratio (Table 3) indicated that the average degree of dominance (H_1/D) over all loci was more than unity for all traits suggested the prevalence of over dominance.Non significant but positive F values for most of the characters signified symmetrical distribution of dominant and recessive genes among parents (Bhutani 1981and Bhutani and Kallo 1983).

The $H_2/4H_1$ index estimate the frequency of positive and negative alleles showed dominance in parents. The index value was less than unit (0.25) for all traits indicated unequal combinations of genes with positive and negative effect at loci exhibiting dominance among the parents. The ambidirectional dominance effect and the uncorrelated distribution of genes among the parents may be one of cause for low estimate of this ratio for the traits (Mather and Jinks, 1971). The proportion and the KD/KR ratio that represents dominant and recessive genes in parents for all traits except fruits plant^{-1} in F_2 generation and fruit yield plant^{-1}in both generations indicated an excess of dominant than recessive genes among the parents.

Fruit yield plant^{-1}appeared to be controlled by both additive and non additive components in F_1 (Bhutani and Kalloo, 1981 and Rai*et al.* 1997) and bynon additive gene action in F_2 generation. Two to three genes having more of dominanceeffects than recessive effects governedthis trait. The estimates of mean degree of dominance revealed over dominance over the generations. But the KD/KR as well as F value indicated more of recessive genes among the parents.

Low heritability (narrow sense) was recorded for fruit yield plant^{-1}(12.50, 12.93), fruits plant^{-1}(17.42, 10.15), harvest span (4.28, 2.81) and TSS (20.86, 12.60) in F_1 and F_2 generations, respectively. Earlier, Patil and Bojappa (1986), Omara*et al.* (1988), Kanthaswamy*et al.* (1995), Srivastava*et al.* (1998) and Sekar (2001)also reported lower heritability estimates (narrow sense) indicating non additive gene action suggesting exploitation of heterosis breeding in F_1 and selection of desirable segregates in F_2 generation(Kumar *et al.*1997, Rai*et al.* 1997,Roopa*et al.*2001, Joshi *et al.* 2005 and Biswas*et al.* 2011).Moderate or high heritability was recorded for days to 50% flowering (29.58 in F_2), plant height (29.46 in F_1 and 37.98 in F_2) and fruit acidity (53 in F_1). Characters having high heritability can be improved by simple selection (Singh *et al.* 2002) for selecting transgressivesegregants in later generations for developing genotypes having good quality traits with higher yield.

Conclusions

The analysis of variance revealed significant differences among genotypes (8 parents, 28 F_1 and 28 F_2) for all the studied traits, except primary branches plant^{-1}and fruits plant^{-1}where block effects were non significant. The genetic system that controls in the inheritance of most traits in both generations is mainly dominance, hence hybridization can play a great role in breeding method of these traits. On contrary, additive genetic effects was evident in some cases. Over dominance was predominant and partial dominance

was also, observed in some cases.The genetic component (H_2) was recorded with low magnitude than (H_1) for all traits, indicating that beneficial positive alleles are not proportional to that of deleterious negative alleles at all loci among parents.The F value was positive for all traits except fruits plant $^{-1}$in F_2 and yield plant^{-1} in F_1 and F_2 generations, respectively. The positive significant F value indicated that dominance alleles were more than recessive alleles. The proportions of positive and negative alleles ($H_2/4H_1$) were less than 0.25 in all cases. This suggests inequality of distribution of increasing and decreasing alleles. The estimates of the consistency of expression of the degree of dominance across all segregating loci(KD/KR) was more than unity for all traits except fruits plant^{-1} in F_2 and yield plant^{-1} in F_1 and F_2 generations, respectively. The absolute value of the statistic ranged from 0.01 to 1.51, where 1 indicates a constant dominance level over all loci. The narrow sense heritability was low to high and the lowest values were also observed in some cases. Additive gene effects and highheritability estimates for plant height and fruit acidity suggested that these traits could be improved effectively by simple selection for selecting transgressivesegregants in later generations.

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References

Anonymous 2011. Indian Horticulture Database (Tomato). National Horticulture Board, Ministry of Agriculture, Govt. of India, Gurgaon, Haryana.p. 15.

Anonymous 2014. Hand Book on Horticulture Statistics 2014. Department of Agriculture and Cooperation, Ministry of Agriculture, Government of India, New Delhi p 48.

Bhatt, R.P., Biswas, V.R. and Kumar, N. 2001. Heterosis, combining ability and genetics for vitamin C, total soluble solids andyield in tomato *(Lycopersicon esculentum L.)* at 1700 m altitude. *J. Agri. Sci, Cambridge*,**137**: 71-75.

Bhutani, R.D. 1981. Screening and diallel study for yield and quality characters in tomato (*Lycopersicon esculentum* Mill.). *Thesis Abstrts*.,**7**(2): 170-171.

Bhutani, R.D. and KalIoo, G. 1991. Inheritance studies of locule number in tomato *(Lycopersicon esculentum* Mill.). *Haryana J. Hort. Sci.,* **20**(1-2): 119-124.

Biswas, V.R. Bhatt, R.P. & Kumar,N. 2011.Gene action in Tomato *(Lycopersicon esculentum* Mill*)* under open and protected environments.*Veg. Sci*., **38**(2): 206-208

Chadha, S. Kumar, J. and Vidyasagar.2001. Combining ability over environments in tomato. *Indian. J. Agri. Res.*, **35**(3): 171-175.

FAO, 2014.Area and production statistics of tomato**.http://faostat.fao.org.**

Hayman, B.I. 1954. The theory and analysis of diallel cross. *Genetics*, **39**: 789-809

Joshi, A., Thakur, M.C. and Kohli, U.K. (2005).Heterosis and correlation studies for polygalactouronase activity and other shelf life governing traits in tomato.*Harayana J. Hort. Sci*., **34**(1/2): 99-103.

Kanthaswamy, V.,Mohideen, M.K. and Thamburaj, S.1995. A study of generation mean analysis in tomato (*Lycopersicon esculentum* Mill). *South Indian Hort.,* **43**(1/2): 25-29.

Khalil, R.M.; El Sayed, M.M. and El Gazar, T.M. 1986.Genetics and heritability of earliness in tomato, *Lycopersicon esculentum* Mill.*Minufiya J. Agric. Res.*, **7**: 319-335.

Kumar, T.P.,Tewari, R.N.,Pachauri, D.C. 1997. Line x tester analysis for processing characters in tomato. *Veg. Sci.*,**24**(1): 34-38.

Mather, K, Jinks, J.L. 1982. Introduction to biometrical genetics. Chapman and Hall Ltd., London. p.19.

Omara, M.K.,Younis, S.E.A.,Sherif, T.H.I., Hussein, M.Y. and El Aref, H.M.A. 1988. A genetic analysis of yield and yield components in the tomato (*Lycopersicon esculentum* Mill.).*AssiutJ. Agric. Sci.,* **19**(1): 227-238.

Panse, V.G. and Sukhatme, P.V. (1985).Statistical Methods for Agricultural Workers.ICAR New Delhi.p. 576.

Patil, A. A. andBojappa, K.M. (1986). Combining ability for certain quality traits in tomato (*Lycopersicon esculentum* Mill.).*Prog. Hort.*,**18**(1/2): 73-76.

Rai, N.,Syamal, M.M., Joshi, A.K. and Rajput, C.B.S. 1997. Genetics of yield and yield components in tomato (*Lycopersicon esculentum* Miller).*Indian J.Agric. Res.*, **31**(1): 46-50.

Ranganna, S. 1977.Manual for Analysis of Fruit and Vegetable Products. Tata McGraw Hill Publ. Co Ltd., New Delhi. p. 634.

Roopa, L.S., Sadashiva, A.T., Reddy, K.M., Rao, K.P.G. and Prasad, B.C. 2001.Combining ability studies for long shelf life in tomato.*Veg. Sci.,***28**: 24-26.

Sekar, S. 2001. Genetic analysis in tomato *(Lycopersicon esculentum* Mill).*Madras J. Agric. Sci.,* **88**(1-3): 43-45.

Singh, Parvinder Singh Surjan, Cheema, D.S. and Dhaliwal, M.S. 2002. Genetic variability and correlation study of someheat tolerant tomato genotypes. *Veg. Sci.***29**: 68-70.

Srivastava, J.P., Singh, H.,Srivastava, B.P. and Verma, H.P.S. 1998. Heterosis in relation to combining ability in tomato.*Veg. Sci.*,**25** (1): 43-47.

Table 1. Analysis of variances for someyield and biochemical traits in F_1 and F_2 diallel crosses of the eight parents in tomato

Source	d. f.	Days to 50 % flowering	Plant height (cm)	Primary branches plant^{-1}	Fruits Plant^{-1}	Harvest span (days)	Total soluble solids (^{0}Brix)	Fruit acidity (%)	Fruit yield (kgplant^{-1})
Blocks	2	241.31**	31059.2**	140.95	2.04	7714.39**	3.00**	0.079**	3.92**
Genotypes	64	41.23**	580.95**	5.35**	258.14**	106.12**	1.16**	0.080**	0.38**
Parents	7	32.39**	609.24**	3.13**	127.27**	30.53**	0.70**	0.067**	0.12**
F_1	27	47.76**	591.42**	5.06**	200.24**	84.71**	0.98**	0.036**	0.34**
F_2	27	27.19**	493.86**	4.89**	366.61**	133.86**	1.52**	0.085**	0.41**
P Vs F_1	1	109.69**	2152.16**	43.09**	58.08**	524.72**	0.10**	0.004**	2.74**
P Vs F_2	1	15.93**	304.08**	38.84**	61.94**	172.02**	0.39*	0.005**	1.01**
Error	128	2.00	19.67	0.28	4.58	9.47	0.007	0.001	0.023

*'** Significant at 5 % and 1 % level, respectively

Table 2 Estimates of genetic components for some yield and biochemical traits in F_1 and F_2 diallel crosses of the eight parents in tomato

Source	Days to50 %flowering		Plant height(cm)		Number of primary branches plant-1		Fruits plant $^{-1}$		Harvest span (days)		Total soluble solids(^{0}Brix)		Fruit acidity (%)		Fruit yield (kg plant^{-1})	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
D	9.66 ±5.84	10.43** ±2.69	194.69** ±81.47	195.51** ±39.97	0.99 ±0.82	0.92 ±1.07	39.69** ±18.79	41.59* ±32.52	5.43 ±4.82	4.99 ±5.60	0.23** ±0.10	0.23 ±0.17	0.02 ±0.01	0.02 ±0.01	0.33** ±0.03	0.04 ±0.03
H_1	57.84** ±13.42	128.31** ±24.73	489.07** ±87.39	1573.98** ±367.52	9.29** ±1.88	33.05** ±9.87	177.95** ±43.20	1362.4** ±299.05	123.26** 11.08±	623.49** ±51.54	0.97** ±0.22	6.95** ±1.53	0.02 ±0.01	0.46** ±0.09	0.33** ±0.07	1.52** ±0.29
H_2	51.43** ±11.68	110.99** ±21.51	355.68** ±162.94	971.96** ±319.74	7.33** ±1.63	22.38** ±8.59	160.36** ±37.59	1281.36** ±260.17	99.57** ±9.64	577.46** ±44.84	0.81** ±0.12	6.27** ±1.33	0.02 ±0.01	0.43** ±0.08	0.29** ±0.06	1.28** ±0.25
h^2	17.50* ±7.83	2.45 ±3.61	349.41** ±109.28	46.56 ±53.61	7.04** ±1.10	6.32** ±1.44	8.33 ±25.21	9.80 ±43.52	24.01** ±6.46	25.95** ±7.52	0.01 ±0.13	0.06 ±0.22	0.01 ±0.01	0.07 ±0.01	0.45** ±0.04	0.17** ±0.04
F	11.55 ±13.80	17.40 ±12.71	56.61 ±192.51	209.30 ±188.88	2.59 ±1.93	5.23 ±5.07	0.76 ±44.41	-48.07 ±153.69	21.16 ±11.39	8.61 ±26.49	0.11 ±0.23	0.29 ±0.79	0.01 ±0.01	0.03 ±0.04	-0.04 ±0.07	-0.04 ±0.15
E	1.44 ±1.95	0.36 ±0.90	8.40 ±27.16	7.58 ±13.22	0.06 ±0.27	0.13 ±0.36	2.73 ±6.26	0.84 ±10.84	4.75** ±1.61	5.19** ±1.87	0.01 ±0.03	0.01 ±0.06	0.01 ±0.01	0.01 ±0.01	0.01 ±0.01	0.01 ±0.01

*'** Significant at 5 % and 1 % level, respectively

D: additive genetic variance, H_1: dominance genetic variance, H_2: corrected dominance genetic variance, h^2: total genetic dominance relative to the heterozygous loci, F: product of additive by dominance and E: expected environmental variance.

Table 3 Estimates of genetic ratios for some yield and biochemical traits in F_1 and F_2 diallel crosses of the eight parents in tomato

Source	Days to50 %flowering		Plant height(cm)		Number of primary branches plant-1		Fruits plant $^{-1}$		Harvest span (days)		Total soluble solids(^{0}Brix)		Fruit acidity (%)		Fruit yield (kg plant^{-1})	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
$(H_1/D)^{1/2}$	2.45	3.51	1.58	2.84	3.06	6.01	2.12	5.72	4.77	11.18	2.05	5.48	1.01	4.56	3.16	6.37
$H_2/4H_1$	0.22	0.22	0.18	0.15	0.20	0.17	0.23	0.24	0.20	0.23	0.21	0.23	0.21	0.24	0.22	0.21
KD/KR	1.65	1.62	1.20	1.47	2.49	2.81	1.01	0.82	2.38	1.17	1.26	1.26	1.33	1.37	0.70	0.84
h^2/H_2	0.34	0.02	0.98	0.05	0.96	0.28	0.05	0.01	0.84	0.04	0.02	0.02	0.01	0.17	1.51	0.13
Heri. (ns)	15.95	29.58	29.46	37.98	12.50	12.93	17.42	10.15	4.28	2.81	20.86	12.60	53.00	17.95	7.52	8.19

*'** Significant at 5 % and 1 % level, respectively

$(H_1/D)^{1/2}$:average of degree dominance, $H_2/4H_1$: frequency of positive or negative alleles in loci which showed dominance, with a maximum value of 0.25, KD/KR: proportion of dominance genes, h^2/H_2: number of gene groups which control the traits and show some degree of dominance, (ns): heritability for diallel in a narrow sense