

Genetic Analysis of F2 Population of Tomato for Studying Quantitative Traits in the Cross Bushbeef x Nagina

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Abstract

This study aims to determine the genetic components like V_g (Variance of genotype), V_p (Variance of phenotype), GCV (Genotypic co-efficient of variation), PCV (Phenotypic coefficient of variation), Hb (Heritability) and GA% (Genetic advance in percentage of means) in F2 generation of the cross Nagina x Bushbeef-steak for predicting quantitative traits. Data was collected on P1, P2 F1 and F2 generation for various yield components and were analyzed. Analyzed data showed relatively high difference between, GCV, V_p and PCV for the traits: Flowers/cluster, Fruits/cluster and Fruit weight and relatively low difference was noted for V_g , GCV and V_p , PCV value in the traits: Fruit diameter, Fruit length and fruits/plant. Highest value of GCV (79.90%) and PCV (92.79%) were noted in the trait: yield/plant and the lowest values of GCV (14.68%) and PCV (16.78%) were noted for fruit-length. Highest value (84.08%) of broad sense heritability % (Hb%) was noted in fruit diameter and the lowest value of heritability (27.58) was noted for the trait fruits/cluster. Moderate value of heritability (74.13%) along with low value (15.22) of GA% was noted for yield/plant.

Keywords: Tomato, F2, Genetic analysis, heritability, genetic advance

INTRODUCTION

Tomato is the world's second most important crop just after potato where it is consumed in raw form as well as processed form like tomato ketchup or cooked in meal. The fruit is valuable being a contributor of medically important components in our diet like lycopene as well as other necessary dietary elements like vitamin B1, B6, vitamin C and small amount of ascorbic acids (Hasan *et al.* 2014).

Intense need is being felt to increase the production of this crop to fulfill the dietary demands of growing world population (Ahmad *et al.* 2015). Like other crops, this crop may also be improved by breeding techniques for the traits like disease tolerance, yield, yield components and shelf life. For any breeding programme it is indispensable to have information about the genetic variability and corresponding heritability as the selection of superior genotypes depend on the degree of genetic variability and extent to which the characters are inherited (Nechifor *et al.* 2011). Genetic improvement in the breeding programme depends on the utilization of available or created genetic variability. The chances of selection of superior genotypes are directly proportional to the influence of genetic make-up and inversely proportional to the environmental influence. Phenotypic selection for yield in tomato may be ineffective, often, because of its being polygenic trait and dependence on other traits. Thus magnitude, nature and interaction of genotypic and environmental interaction influences the achievements in breeding. (Khanom *et al.* 2008). Parting the total variation into heritable and non-heritable components with the help of genetic parameters i.e genotypic and phenotypic co-efficient of variation, heritability and genetic advance is helpful in finding the effect of environmental fluctuation on the yield components (Maniee *et al.* 2009).

Heritability provides information to the breeders about the contribution of genetic and environmental factors to phenotypic variability, therefore, it is the one of important part of breeding research. Genetic advance is another parameter on which effectiveness of selection depends on (Johnson *et al.* 1955). For the selection to be effective and for making improvement in the crop, moderate or high heritability should be accompanied by sufficient amount of genetic advance (Eid. 2009).

The objective of our research is to find the variability related parameters like GCV, PCV V_g , V_p , heritability and genetic advance for quantifying yield and yield components. The study will help the researchers in making judicious selection in F2 generation for the desired parameters.

MATERIALS AND METHODS

(A). Field data

The experiment was conducted at Hazara Agricultural Research station Abbottabad during the sowing seasons of 2013 to 2015. Crossing was done between two varieties of diverse characteristics Nagina and Bushbeefsteak in the month of July 2013. Then F1 seeds were collected from the fruits formed through crossing. In the year 2014, F1 seeds were sown in the month of April and nursery was transplanted in June 2014. Some F1 seeds were reserved for the next sowing season. F2 seeds were collected from F1 generation and data were also collected. In January 2015 the seeds of P1, P2, F1 and F2 were sown in nursery. The plants in nursery were sown in March

2015. Plant to plant distance was kept as 50cm, row to row distance was kept as 100cm. 500 plants of F2 generation were transplanted in three blocks along with P1,P2 and F1 in each block. Data were collected on F2 population and five plants each from P1,P2 and F1 on the parameters : No of flowers/cluster, No of fruits/cluster, fruit length(cm), fruit diameter(cm), fruit weight(grams), No of fruits/plant and yield(grams)/plant.

(B).Statistical analysis

Vg (Variance of genotype), Vp (Variance of phenotype) and broad sense heritability (Hb) were calculated on MS-Excel by using the following formula suggested by Globerson *et al.* (1987).

$$Hb = \{VF2 - [1/3 (VP1 + VP2 + VF1)]\} / VF2$$

Where $V_e = V_{p1} + V_{p2} + V_{f1} / 3$ $V_p = V_{F2}$ and $V_g = V_p - V_e$ So $Hb = V_g / V_p$

Phenotypic coefficient of variation (PCV) , genotypic coefficients of variation (GCV) , expected genetic advance (GA) and percentage of genetic advance (GA%) were calculated according to the following formulas used by Bozokalfa *et al.* (2010) in their study.

$$PCV = (p / X) \times 100$$

$$GCV = (g / X) \times 100$$

$$(GA) = i \cdot ph^2$$

$$(GA \%) = \frac{GA}{X} \times 100$$

Where , p : phenotypic standard deviation , g : genotypic standard deviation X : grand mean of the traits and i : standardized selection differential, a constant (2.06) respectively.

RESULTS AND DISCUSSION

The results regarding F2 population of cross combination *Nagina x Bushbeefsteak* for phenotypic variance (Vp) ,genotypic variance (Vg) ,genotypic co-efficient of variance (GCV),phenotypic Coefficient of Variance(PCV),Heritability%(Hb) and percentage of genetic advance (GA%) are shown in Table-1. Analyzed data showed that variance of genotype (Vg) was lower than the variance of phenotype (Vp) in the F2 populations for all traits under study. Same were the findings of Mohamed *et al.* (2012) and Gosh *et al.* (2010) except for fruit-length and fruit diameter in their study . Higher difference was noted between Vg and Vp for the traits flowers/cluster, fruits/cluster, fruit weight, fruits/plant and yield/plant while lower difference was found between Vg and Vp for the traits like fruit diameter and fruit length as shown in Table-1. High difference between Vg and Vp indicated that environment has more contribution than their genetic make-up in the phenotypic magnitude of the traits.

Relatively higher difference was noted between GCV and PCV values in the traits: flowers/cluster fruits/cluster and fruit weight and relatively low difference was noted for GCV and PCV value in the traits: fruit diameter, fruit length and fruits/plant. Khanom *et al.* (2008) also found smaller difference between GCV and PCV value for the trait fruits/length while Kaushik *et al.* (2011) found small difference between GCV and PCV for fruit diameter. Moderate difference was noted between GCV and PCV in the parameter yield/plant. Higher difference between GCV and PCV for the traits revealed that the traits are under the influence of environmental effect and are determined by non-dominance and non-additive gene action. Highest value of GCV (79.90%) and PCV (92.79%) were noted in the trait: yield/plant which indicated that diversity is highest than any other trait. So, there available a wide range of selection for the breeder. Sivaprasad *et al.* (2009) also reported high value of GCV and PCV for yield/plant. There is a moderate difference between GCV% and PCV% for the yield/plant. Lowest values of GCV (14.68%) and PCV (16.78%) were noted for fruit-length which depicted that variation in the trait is lowest than in any other trait.

Highest value (84.08%) of broad sense heritability (Hb) was noted in fruit diameter followed by fruits/plant and fruit length i.e. 82.6% and 76.82% and, respectively. The results confirmed that additive gene action is involved in the traits and influence of environment is less. Lowest value of heritability (27.58) was noted for the trait fruits/cluster. Flowers/cluster and fruit weight also showed relatively lower value of Hb i.e. 33% and 35.17%, respectively.

Table:Variance of genotype(Vg),Variance of phenotype(Vp),Variance of environment(Ve),Genotypic coefficient of variation(GCV),Phenotypic coefficient of variance(PCV) ,broad-sense heriatbilty(Hb%),Expected genetic advance(GA) and Genetic advance percentage(GA%) for F2 population of cross combination *Nagina x Bushbeefsteak*.

Parameters	Mean	Range	Vg	Vp	Ve	GCV	PCV	Hb%	GA	GA%
Flowers/cluster	4.18	1-9	0.48	1.44	0.95	16.57	28.73	33	0.82	19.72
Fruits/cluster	1.87	0-6	0.29	1.07	0.77	29.01	55.33	27.58	0.58	31.44
Fruit weight	63.37	20-147	115.71	328.91	213.20	16.97	28.61	35.17	13.14	20.73
Fruit diameter	4.60	2.1-6.5	0.53	0.63	0.10	15.82	17.26	84.08	1.37	29.89
Fruit length	4.49	2.9-6.53	0.43	0.56	0.13	14.68	16.78	76.82	1.193	26.55
fruits/plant	15.07	0-79	89.47	108.31	18.83	62.72	69.01	82.60	17.70	117.43
Yield/plant	930.85	0-3010	553205	746202	192997	79.90	92.79	74.13	141.72	15.22

GA% is highest (117.43%) in fruits/plant among all the traits. The trait has also shown relatively higher value of Hb%. Our results matched with the findings of Haydar *et al.* (2007) and Sharanappa and Mogali (2014) who also found high value of heritability and GA% for the trait. Lower values of GA% for flowers/cluster (19.72%) ,fruits/cluster (31.44%) and fruit weight (20.73%) are coupled with lower heritability. The result showed that these traits are under the influence of non-additive gene actions. Mere phenotypic selection for such traits cannot bear any fruitful result in the next generation.

Moderate value of heritability was found for yield/plant i.e. 74.13%.However, relatively lower GA% (15.22) was noted for the trait. Our results matched with the findings of Saleem *et al.* (2015) who also found relatively lower value of GA% (21%) coupled with low value of heritability. The traits having high heritability with high genetic advance are deemed to be under the control of additive genes, whereas with high heritability and low genetic advance are under the control of non-additive (dominant or epistatic) genes which limits the scope of improvement through selection (Akbar *et al.* 2003). Therefore it is suggested that selection for the trait yield/plant in our study on phenotypic basis is not much effective.

Conclusion

Yield/plant is the most variable trait, however, heritability for the trait is moderate with low genetic advance, therefore, mere phenotypic selection is not effective. The selection for fruit size traits may be effective due to higher value of heritability.

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