Research Article

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Genetic analysis of F2 population of tomato for quantitative traits in the cross bushbeef X nagina

Abstract

The purpose of conducting the study was to find the genetic components like Vg,Vp, GCV, PCV, heritability and Genetic advance in F2 generation of the cross Nagina x Bushbeef-steak for quantitative traits. Data was collected on P1, P2 F1 and F2 generation for various yield components and analyzed. Analyzed data showed relatively high difference between, GCV and Vp, PCV for the traits: Flowers/cluster, Fruits/cluster and Fruit weight and relatively low difference was noted for Vg, GCV and Vp, 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, physiological traits, phenotypic co-efficient, quantitative traits

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Introduction

Tomato is world's second most important crops 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: an antioxidant which plays important role in prevention of cancer. It is also source of vitamins like vitamin B1, B6, vitamin C and small amount of ascorbic acids.[1]

Intense need is being felt to increase the production of this crop due to increasing world population and consequently increasing consumption.[2] 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 indispensible to have information about the genetic variability and corresponding heritability as the selection of superior genotypes depends on the degree of genetic variability and extent to which the characters are inherited.[3] Genetic improvement in the breeding programme depends on the utilization of available or created genetic variability. If the variability in the population is mainly contributed by genetic cause with least environmental effect, the probability of isolating superior genotypes is high. As yield of tomato fruits is a polygenic character and is dependent on many agronomic, morphological and physiological traits, so direct selection for yield may be often misleading. The progress of breeding in such a population is primarily related to magnitude, nature and interaction of genotypic and environmental variation in the various plant characters.[4] Each of these traits, however, has its own genetic systems. Furthermore, environmental fluctuation affects the yield components. Therefore, it is essential to take apart 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.[5]

Heritability, or the degree of genetic control related to some traits of interest is one of the most important parameters within the breeding research. Heritability determines how much of the phenotypic variability has a genetic origin and how much due to influence of environment, and therefore helps us select on genetic basis.[6] Genetic advance is another parameter on which effectiveness of selection depends Johnson et al.,[7] 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.[8] The objective of our research is to find the variability related parameters like GCV, PCV Vg and Vp and heritability and genetic advance for yield and yield components. The study will help us in making judicious selection in F2 generation for the desired parameters.

Materials and methods

Fied data

The experiment was conducted at Hazara Agricultural Research station Abbottabad during the sowing seasons 2013 to 2015. Crossing was done between two varieties of diverse characteristics Nagina and Bush beefsteak in the month of July 2013.Then F1 seed was collected from the fruits formed through crossing. In the year 2014 F1 seed was sown in the month of April and nursery was transplanted in June 2014.Some F1 seed was reserved for next sowing season.F2 seed was collected from F1 generation and data was also collected. In January 2015 the seed 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 100cm. 500 plants of F2 generation were transplanted in three blocks along with P1,P2 and F1 in each block. Data was collected on F2 population and from 5 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.

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.[9]

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

Where Ve=Vp1 +Vp2+Vf1/3 Vp=VF2 and Vg=Vp-Ve So Hb=Vg/Vp

Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated according to the following formula proposed by Singh and Chaudhary.[10]

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

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

Where,σp, σg, and X are the phenotypic, genotypic standard deviation and grand mean of the traits respectively.

Expected genetic advance (GA) and percentage of GA were calculated according to following formula proposed by Shukla et al.[11]

Expected genetic Advance $(GA) = i\sigma ph^2$

Percentage of Genetic Advance $(GA\%) = GAX \times 100$

Where, i: standardized selection differential, a constant (2.06), σp: phenotypic standard deviation.

Results and discussion

The results regarding F2 population of cross combination Nagina x Bush beefsteak for Phenotypic variance (Vp) ,Genotypic variance (Vg) ,Genotypic co-efficient of variance (GCV),Phenotypic Coefficient of Variance(PCV),Heritability%(Hb) and 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 the traits under study. Same were

the findings of Mohamed et al.[12] and Gosh et al.,[13] except for fruit-length and fruit diameter in his study .In the F2 population 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 indicates that environment has more contribution in the phenotypic appearance of the traits than their genetic make-up.

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.[4] also found smaller difference between GCV and PCV value for the trait fruits/length while Kaushik et al.,[14] 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 reveals that the traits are under the influence of environmental effect and non-dominance and non-additive gene actions are involved in the determination of particular traits. Highest value of GCV (79.90%) and PCV (92.79%) were noted in the trait: yield/plant which indicates that diversity in the trait is highest than any in other trait. So there is wide range of selection for the breeder. Sivaprasad et al.,[15] also reported high value of GCV and PCV for yield/plant. There is 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 reveals that variation in the trait is lowest than in any other trait so range for selection is narrow. 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 indicate 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 1 Variance of genotype(Vg),Variance of phenotype(Vp),Variance of environment (Ve), Genotypic coefficient of variation(GCV), Phenotypic coefficient of variance(PCV) , broad-sense heritability (Hb), Expected genetic advance (GA) and Genetic advance percentage (GA %) for F2 population of cross combination Nagina x Bush beefsteak

Parameters	Mean	Range	Vg	Vp	Ve	GCV	PCV	Hb%	GA	GA%
Flowers/cluster	4.18	9-Jan	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	213.2	16.97	28.61	35.17	13.14	20.73
Fruit diameter	4.6	2.1-6.5	0.53	0.63	0.1	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	82.6	17.7	117.43
Yield/plant	930.85	0-3010	553205	746202	192997	79.9	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 result matched with the findings of Haydar et al.[16] and Sharanappa et al.,[17] who also found high value of heritability and GA% for the trait. Lower GA% for flowers/cluster (19.72%) fruits/cluster (31.44%) and fruit weight (20.73%) is coupled with lower heritability. The result shows that these traits are under the influence of non-additive gene actions. Mere phenotypic selection for such traits cannot bear any fruitful result in 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 result match with the findings of Saleem et al.,[18] 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 control of additive genes, whereas with high heritability and low genetic advance are under the control of non-additive (dominant and/or epistatic) genes which limits the scope of improvement through selection.[19] 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 most variable traits among other traits 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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Conflict of interest

The author declares no conflict of interest.

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