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Genetic analysis of F1 generation of tomato for quantitative traits

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Abstract

The research was conducted at Hazara Agricultural Research Station Abbottabad and Agricultural Research Center Haripur during the year 2013 and 2014 in two sowing seasons. The purpose of present study was to find the Vg,Vp,Ve,PCV,GCV,heritability(Hb) and Genetic Advance(GA) for the traits :Number of flowers per cluster(fpc),number of fruits per cluster(frpc),fruit length(frl),fruit diameter(frd) ,fruit size(frs), plant height(pl.ht) ,Number of fruits per plant(nof),fruit weight(fwt) and yield per plant(yield/pl). Yield per plant showed highest value of Vg(92698) and Vp (221588) and Fruits/cluster, fruit length, fruit diameter and flowers per cluster showed lowest value of Vg and Vp. For all the traits PCV value was higher than GCV. Little difference was found among GCVand PCV for the traits like plant height, fruit diameter, fruit size and fruit weight. There is high difference between GCV and PCV for the parameters like Number fruit per clusters, Number of flowers per cluster and yield per plant. High value of heritability percentage was noted in parameters like plant height (91.34%), fruit diameter (90.22%), fruit size (93.53%), Number of fruits per plant (83.69%) and fruit weight (83.69531). Low value of heritability was noted for fruits per cluster, flowers per clusters and yield per plant. Highest genetic advance (91.94%) was noted for the trait, No of fruits per plant which is coupled with high heritability.

Key words: Tomato,Genetic Variability,Phenotypic Variability, V,PCV,Heritabilty,Genetic Advance

Introduction

Tomato (Lycopercicum esculentum) belonging to Solanacea family is one of the most important vegetable crops of Pakistan and is cultivated on area of 52.30 thousand hectares with average production of 10.10 tons/hectare (Ramzan et al. 2014) . It is the world's second most important crops after potato. It contains important components which are essential for human in their diet like potassium, phosphorous, magnesium and iron as well as antioxidants such as carotenoids, lycopene and phenolics. It is also contributes vitamins like small amounts of ascorbic acid, vitamins B1, B6, PP vitamin and vitamin E. (Hasan *et al.*2014)

Like other self-pollinated crops, tomato also needs our attention to make improvement in its current cultivars. When we initiate our breeding programme we should also be aware of the fact that our selection for the desired traits may be under the influence of environment i.e. the variability in the population may be environmental instead of genetic ,consequently ,the selection may not gain positive results in next generation therefore we should have knowledge of existing genetic variability in order to develop high yielding varieties (Reddy et al. 2015).Assessment of genenotypic and phenotypic variability regarding yield and its components become absolutely indispensable before planning for an appropriate breeding strategy for genetic improvement.(Sunday et al 2014). Therefore, it is important to partition the observed variability into its heritable and non heritable components by suitable genetic analysis (G.E. Nwofia and Q.U.Okwu 2012). Hence, there is need to evaluate genetic resources properly to understand and estimate the genetic advance and heritability. The individual characteristics are measured quantitatively, so that by doing variance analysis we may partition variability into heritable and non-heritable with the help of genetic parameters such as Genetic co-efficient of variation (GCV), heritability and Geneti Advance (Osekita and Ajai. 2013).

Heritability estimate along with genetic advance was more useful than heritability estimate alone in predicting resultant effect for the selection of the best individual.
(Chaurasia *et al.*2012). Genetic advance which estimates the degree of gain in a trait obtained under a given selection pressure is an important parameter that guides the breeder in choosing a selection programme (Hamdi *et al*. 2003). High heritability and high genetic advance for a given trait indicates that it is governed by additive gene action and, therefore, provides the most effective condition for selection (Tazeen *et al*. 2009)

In our study we have estimated the genetic components like Vg,Vp,GCV,PCV ,heritability and GA which has enabled us to find about the variability in the trait whether that is genetic or environmental.

Material and methods

During the sowing season April 2013, seed of tomato varieties (Newyaorker, Zhezha, Sashaaltai ,Nepoli, Continental, Bushbeef-steak,Riogrande and Nagina) was sown as nursery at Hazara Agricultural Research station Abbottabad and the plantlets were transplanted in the field in June 2013. The varieties started flowering after a month of transplantation and breeding work was initiated, consequently. Crosses were made among the varieties in the following combinations: Zhezha x Riograde, Nepoli x Newyorker, Sashaaltai x Nepoli, VCT1 x continental, Bushbeefsteak xNangina Zhezha x Nagina and Continental x Nagina . The seed was collected from the successful crosses.Then the collected F1 seed along with their parental varieties was sown as nursery at Agricultural Research Center Haripur(Sub Station of Hazara Agricultural Research Station) during the year January 2014 and plantlets were transplanted in march 2014.Plant to plant distance was kept as 30 cm and Row –Row distance was 1m and the row length was kept as 2.5 . The data was collected on the following parameters: number of flowers per cluster, number of fruits per cluster, Fruit weight(grams), Fruit diameter(cm) ,Fruit-length(cm) ,Fruit size (cm)'number of fruits per plant and yield per plant(grams).Data was analyzed by using the soft-ware Statistix.8 .

The values of Vg, Vp and Ve were calculated by using the following formulae as suggested by Wricke *et al.* 1986.

Vg= MSG-MSE/r

Vp=MSG/r

Ve=MSE/r

Then by finding these values, Broad sense heritability (Hb) was calculated by using the following formaula as suggested by Allard 1999.

Hb=Vg/Vp

Expected Genetic Advance and Genetic Advance % was calculated by using the formaula of Shukla et al. 2006.

Expected genetic advance $(GA) = i\sigma ph$

Genetic Advance percentage (GA%)=GA/x * 100

Where, *i:* standardized selection differential, a constant (2.06), σp: phenotypic standard deviation and h: broad-sense heritability.

Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated by using the following formula suggested by Singh and Chaudhary (1985) .
PCV =($^{\delta}$p/x)* 100
GCV=($^{\delta}$g/x) * 100
Where, $^{\delta}$p, $^{\delta}$g, and X are the phenotypic, genotypic standard deviation and grand mean of the traits respectively.

Results and discussion

Data regarding the Vg(Genotypic Variance),Vp(Phenotypic Variance) ,Ve (Environmental variance),PCV(Phenotypic Coefficient of Variation),GCV(Genotypic Coefficient of Variation), heritability broad-sense(Hb) and Genetic advance percentage(GA %) is presented in Table .It is clear from the data that Variance of genotype (Vg) and Variance of phenotype (Vp) is highest for the yield per plant ,while moderate value was observed for number of fruits per plant ,fruit weight and plant height. Lowest values of genotypic variance (Vg) were observed for the traits like number of fruits per cluster, fruit length, fruit diameter and number of flowers per cluster. Meena and Bahadur .2014 also found the highest value of Vg and Vp for yield per plant than other parameters. This indicates the scope for effective selection for further generations. High genotypic variance indicates more contribution of genetic component for the total variation. Therefore, these characters could be considered and exploited for selection purpose whereas high phenotypic variance indicates the strong influence of environmental factors for their expression.

PCV (Phenotypic coefficient of variation) value was higher than GCV (genotypic coefficient of variation) value for all the traits in our study. Same were the findings of Panday and Mall .2014 who also found the value of PCV higher than values of GCV for all the traits under study. The higher value of PCV than GCV reveals that the traits are under the influence of environment more than the influence of genetic effects.

Little difference was found among GCV and PCV for the traits like plant height, fruit diameter, fruit size and fruit weight, suggesting that these traits are under the less influence of environmental effects and also heritability value in these traits was above 90% or close to the value of 90% with moderate genetic advance. Therefore selection for these traits is useful for further breeding programme. On the other hand there is high difference between GCV and PCV for the parameters like number of fruit per clusters, number of flowers per cluster and yield per plant. Same were the findings of Tasisa *et al.*2011 who found smallest difference between GCV and PCV for the traits like plant height and higher PCV and GCV difference for traits like number of fruits per cluster, number of flowers per cluster and yield per plant.Khanom *et al.* 2008 also found relatively higher difference between PCV and GCV in their research for yield/plant than other parameters.

The table also shows the values of heritability and genetics advance. High value of heritability was noted in parameters like plant height, fruit diameter, fruit size, number of fruits/ per plant and fruit weigh which reveals that environmental influence is less on these traits. Our findings matched with the study of Shankar et al. 2013, who also found high value of heritability for the traits like plant height and fruit diameter. Pradeepkumar *et al.* 2001 also found high value of heritability for fruit weight in his study. High heritability values also indicate that the traits are under the influence of additive gene action. The selection for such traits is effective for further breeding programme. While, low value of heritability was noted for number of fruits per cluster, number of flowers per clusters and yield per plant which reveals high effect of environment on these traits. Mohamed et al .2012 also found low value of heritability (43%) coupled with low value of Genetic advance (33%) for yield per plant, which is much closer to the values in our study for the said parameter.

Highest genetic advance (91.94%) was noted for number of fruits per plant which is coupled with high heritability. Saleem *et al.* 2013 also found high genetic advance value for number of fruits per plant as well as other traits. High heritability along with high genetic advance is helpful in effective selection in F1 generation for the desired traits to proceed to F2 generation. The traits under our study which showed high value of heritability were accompanied by moderate value of genetic advance which ranged from 33-48%.

Conclusion: it is concluded from the present study that heritability for yield per plan is low so the selection on mere phenotypic observation may not be effective for further breeding programme. On the other hand some yield components like fruit size, fruit diameter, Number of fruits per plant and fruit weight have high heritability so the selection on phenotypic basis may bear good results in the future.

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Table :Genetic components and heritability for No of flowers/cluster(fpc),No of fruits/cluster(frpc),fruit length(frl),fruit diameter(frd ,fruit size(frs),)plant height(pl.ht) ,no of fruits/plant(nof),fruit weight(fwt) and yield/plant(yield/pl)

S.No	Parameter	Vg	Vp	Ve	GCV(%)	PCV(%)	Heritabilty%	GA(%)
1	FrPC	0.344855	1.02446	0.6796	13.09	22.56	33.66	15.64
2	PL.ht	144.9275	158.663	13.7355	24.72	25.86	91.34	48.67
3	Fr.length	0.171515	0.22497	0.05345	8.15	9.33	76.24	14.66
4	fr.dia	0.769045	0.8524	0.08335	17.31	18.22	90.22	33.87
5	Yield/plant	92698	221588	128890	22.77	35.21	41.83	30.34
6	fpc	0.757065	2.31779	1.56073	14.16	24.78	32.66	16.67
7	frsize	41.10535	43.9484	2.843	24.41	25.24	93.53	48.64
8	Nof	195.5905	233.694	38.103	48.78	53.32	83.69	91.94
9	frwt	195.5905	233.694	38.103	18.61	20.34	83.69	35.08