

Comparison of response of F4 and F3 generations of tomato from year to year selection

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Abstract

Segregating breeding generations may fluctuate in performance from year to year. The purpose of our study was to evaluate the performance of these generations in each year and to make selection according to the existing environmental conditions. The research was conducted in two consecutive years (2016 and 2017) and the performance of F3 and F4 generations was analyzed. It was found that mean values of all the studied parameters in F4 population, in this study, were lower than the mean values of F3 generation, however maximum range in F4 exceeded F3 for some parameters. The selection differential values were also found as negative. V_a (Additive variance) values for all the parameters in F3 and F4 generations were found to be almost same PCV (Phenotypic coefficient of variation) for most of the parameters in F4, like yield/plant, fruits/plant, fruit/cluster and fruit length exceeded the PCV values in F3. Highest value of heritability was noted for yield/plant in F4 while in F3 highest value was observed for fruit weight. Heritability percentage and genetic advance for all the parameters in F3 was higher than F4. Mean difference values indicated that some of the F4 lines were higher than the grand mean of F4 population (in all the studied parameters). Additionally, means of few F4 lines were also found to be greater than the means of F3 population for most of the parameters. These results may indicate that these lines could be selected for better performance if advanced to next generation.

Keywords: Tomato Lines, Performance, Quantitative Traits, Heritability, Genetic Advance

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Introduction

Tomato belongs to large and diverse Solanaceae family also called as nightshade (Bauchet and Causse, 2012). It is a self-pollinated crop with $2n=24$. Deeming its importance on world level it is indispensable to develop new varieties and hybrids which could encounter the environmental changes at global level. Like other self-pollinated crops, hybridization, mass and pedigree selection methods are used to bring novelty in the existing genetic resources of this crop. Selection is the most decisive stage after hybridization

where breeders have to select or reject the lines in the segregating generations. Due to environmental effects the superior lines may fail to perform well in any generation, consequently there is risk of screening out of precious genetic material. Therefore, the major problem faced by plant breeders in trying to improve self-pollinated crop is the identification of genotypes having high yield potential in the segregating generations (Singh and Sharma, 2015). In breeding generations, F2 through F6 are the critical stages for selection and evaluation of the segregants. The breeders have to evaluate the segregating lines during



these stages and selection is made at each successive stage. As the selection for each generation is done in next year, one should also take into consideration the change in environment from one year to next year. Sometime the selected lines or all the population which has performed well in previous year may show low performance in the next year. The accurate selection from F2 to F6 stages can be made sure by calculating the means, variance (additive, environmental and phenotypic), heritability and genetic advance. However during year to year selection and evaluation some time unexpected results may be obtained due to change in environmental conditions. Brown and Caligari (2008) noticed that year to year environmental variation is always unpredictable and the highest yielding progeny lines derived from F2 and F3 generation may fail some time to produce the highest yielding segregants. Bejiga (1987) found that there is no significant association among F2 to F6 lines for some quantitative traits like yield and yield components which reveals that these characters are not stable from generation to generation. Virupakshappa 1984 also did not find any significant inter generation correlations between F3 and F4 lines of two cowpea crosses. O'Brien *et al*, (1978) concluded that genotypic x environmental interaction is the cause of reduction in correlation among the generations. Therefore, the breeders should determine their criteria of selection according to changing environment from generation to generation, as there is risk of losing superior genotypes of particular generation performing low in the particular year.

Our research aims to study the change in response of breeding lines of succeeding generations in different years and to identify best performing lines in adverse environmental conditions. Therefore we collected data at each generation from each segregating line and analyzed the data by finding the parameters like means, heritability, genetic advance etc.

Material and Methods

The research was conducted at Hazara agricultural research station Abbottabad. F3 lines were sown as nursery in the year 2016. After 45 days, plantlets were transplanted in the field. Row to row distance was kept to be 100 cm and distance between plants was maintained to be 50 cm. On maturity data were collected on No of flowers/cluster, No of fruits/cluster,

fruit diameter, fruit length, No of fruits/plant, fruit weight and yield/plant. Superior plants were selected from F3 population and seeds were extracted through fermentation. In the year 2017, the F4 seeds collected from F3 were sown as nursery and 45 days old plantlets were transplanted in the field. Data were recorded for the parameters as discussed above.

Statistical and genetic analysis

Additive Variance (V_a) for the means of F3 and F4 lines was calculated by using the approach of Wrike and Weber (1986) as following:

Genotypic variance (V_g) between means of lines in F3 $= (V_a + 1)/4V_d$

The value of $1/4V_d$ is so small that its negligence does not make any difference.

Therefore $V_g = V_a$

V_g between means of lines in F4 $= V_a$, as variance in F4 generation is contributed by only additive gene action and there is no role of dominant gene action. Therefore V_d (Variance of dominant genes) is negligible.

Heritability for F3 and F4 lines was calculated by using the formula $H_b = V_g/V_p$, Since $V_g = V_a$ in F4 and F3, therefore $H_b = V_a/V_p$.

Heritability% and genetic advance were calculated by using the following formula as used by Ahmad *et al*, (2017), in their study.

$H_b\% = V_a/V_p \times 100$ and $GA\% = GA/x \times 100$, respectively. Where H_b = broad sense heritability, V_a = additive variance, V_p = phenotypic variance, GA = genetic advance and x is mean of population.

Selection difference (SD) between F3 and F4 was calculated by using the formula as $SD = F_4 - F_3$

Degree of resemblance between lines and population was calculated by using the formula of Falconer (1960), as following:

$t = O^2B / (O^2B + O^2W)$ where t = degree of resemblance, O^2B = Standard deviation between the lines, O^2W = Standard deviation within the lines.

Mean difference between the means of individual F4 lines and means of F3 and F4 populations were calculated by the following method:

$MD_4 = PF_4 - LF_4$ and $MD_3 = PF_3 - LF_4$, where MD_4 and MD_3 = mean differences, PF_4 = Population mean of F4, PF_3 = Population mean of F3 and LF_4 = means of F4 lines.

Genotypic and phenotypic coefficient of variation were computed by using the method of Butron and Devane (1953) as following:



Genotypic coefficient of variation (GCV%)= $\sqrt{Vg/X} \times 100$
and

Phenotypic coefficient of variation (PCV%)= $\sqrt{Vp/X} \times 100$.

Results and Discussion

A decline in population mean value was observed for all the parameters from F3 to F4 generation as shown in Table.1. On the other hand maximum value of range was observed to be higher in F4 generation for all the parameters except fruit weight and fruit diameter (Table.1). Negative values of Selection differential were observed in F4 generation for all the parameters, which indicates that the F4 population is lower in performance than F3. Chang et al. (1973) also found in his study that segregants lost their superiority in F4 generation. Superiority of F2 and F3 segregants are due to additive x additive and dominant x dominant interactions while no such types of interactions are present in later generations in case of self-pollinated crops (Mather and Jinks, 1971). The other reason for low performance of advance generations was described by Brown and Calligari, (2008). According to their findings GxE interactions affect the segregating plant's performance throughout the breeding stages due to uncontrollable environmental conditions (rainfall, wind and temperature) from one year to next year, consequently decline in performance of the segregating generation may be observed at any breeding stage.

No significant difference was observed between V_a in F4 and F3 for most of the traits except yield/plant, No of fruits and fruit weight. Values of V_a were higher in F4 for Yield/plant and No of fruits whereas value of V_a for fruit weight in F3 was higher than in F4 (Table.1). There is decrease in genetics variation from previous generation to next generation however in practical, performance from one year to next year may be highly variable and unpredictable which indicates that yearly change in environment has greater effect on the performance of breeding lines (Brown et al, 2014). Highest value of Phenotypic Coefficient of variation (PCV) was noted in yield/plant in F4 generation followed by No of fruits/plant. The values were higher than the values of the parameters in F3 generation. The value of PCV for flowers/clusters, fruits/cluster and fruit length in F4 also exceeded the value of the said parameters in F3 generation (Table 2). Since the PCV is the combination of additive and environmental variance, the increase in PCV value in next generation may be due to environmental factors, not due to

additive or dominant gene action only, because in practical there is tendency in decrease in variability in advance generations due to increase in homozygosity. Among all the parameters, highest values of heritability% and genetic advance% in F4 generation were noted for yield/plant, followed by No of fruits and fruit length and the lowest values of heritability% and genetic advance% were calculated for fruit diameter. In F3 generation, highest value of heritability% and genetic advance% were observed in fruit weight followed by fruit diameter (Table.2). Heritability values may vary from generation to generation for the same population and also affected by varying magnitude of genotypic x environmental interaction. There is no consistent tendency of increase or decrease in heritability from F3 to F4 generation (Raval et al., 2017). However, it has also been noted that heritability% and genetic advance of all the parameters in F3 is higher than F4 except for number of fruits and yield/plant (Table.2). Decrease in heritability from previous breeding generation to next breeding generation is often observed. This may be due to increase in homozygosity and decrease in heterozygosity in next generation (Wallace, 1972).

Range for degree of resemblance within lines and population was observed to be 0.40-0.65 for flowers/cluster, 0.44-0.73 for fruits/cluster, 0.35-0.74 for fruit weight, 0.35-0.83 for fruit diameter, 0.40-0.71 for fruit length, 0.43-0.76 for number of fruits/plant and 0.47-0.72 for yield/plant (Table -3). Since the lines are progeny of the same cross and as a result of selection from F2 to F4 generation some lines may be sharing the same parents in F2 or F3 generation, consequently, the range of degree of resemblance is higher. While the lower value of range indicates that some lines may not be closely related to one another.

Difference between the mean values of F4 population and means of the F4 lines (BK1-BK26) for flowers/clusters, Fruits/cluster, fruit diameter and yield/plant indicated that 12, 11, 11 and 9 of 26 lines showed negative values, respectively (Table.4), which shows that the means of these lines exceeded the means of F4 population. About 50% of the lines showed negative value for the mean difference between F4 population and F4 individual lines for the parameters fruit weight and number of fruits/plant. 15 out of 26 lines exhibited negative value for the difference between means of F4 population and means of individual F4 lines for fruit length, which shows that the most of the individual lines have better



performance than the whole population for the parameters. Up to F4 stages the means values of parameters of interest for individual plants and individual lines matter rather than the performance of whole population. Rios, (2015) stated that the selection till F4 generation is on individual plant basis in pedigree method. The statement strengthens our approach of concerning the performance of individual

plants rather than performance of whole population which can decline at any level.

Very few lines showed negative value of difference between means of F3 population and means of individual F4 lines for all the parameters except fruit weight (Table-4).The result depicts that there are still some lines which exceeded the whole F3 and F4 population means in performance.

Table-1:Means, selection difference (SD), Range, Additive variance(Va) and Phenotypic variance(Vp) in F4 and F3 population for flowers/cluster (FPC), fruit/cluster(FrPC), fruit weight(FrWt),fruit diameter (Frdia), fruit length(Frlen),Number of fruits/plant (NoF) and yield/plant(YPP).

parameter s	Means		SD	Range		Va		Vp	
	F4	F3	F3-F4	F4	F3	F4	F3	F4	F3
FPC	4.71	5.35	-0.63	2-9	4-6	0.01	0.01	0.3196	0.12
FrPC	2.89	3.81	-0.91	1-8	3- 4	0.02	0.01	0.5292	0.11
FrWt	77.48	93.03	-15.5	30-125	67-140	0.301	111.20	74.413	301.39
Frdia	4.60	5.57	-0.96	2.1-6.9	4.7-6.9	0.01	0.07	0.1551	0.30
Frlen	4.94	5.45	-0.50	2.8-6.9	4.9- 6.1	0.01	0.03	0.1987	0.13
NoF	14.48	21.7	-7.21	1-55	14.4-30.5	4.5	1.38	35.105	19.38
YPP	1226.5	1890.2	-663.7	60-4576	1153.7-2443.7	43938	1039	230203	129469

Table 2. Phenotypic coefficient of variance (PCV),Heritability% (H%) and Genetic advance % (GA%) in F4 and F3 population for Flowers/cluster (FPC), fruit/cluster(FrPC), Fruit weight(FrWt),Fruit diameter (Frdia), fruit length(Fr Len),Number of fruits/plant (NoF) and yield/plant(YPP).

Parameters	PCV		H%		GA%	
	F4	F3	F4	F3	F4	F3
FPC	11.98	6.7149	5.06	14.92	1.06	1.76
FrPC	25.16	8.7843	4.25	11.03	1.88	5.80
FrDia	8.54	9.9027	0.40	26.02	0.07	7.07
Fr Len	9.01	6.8432	11.02	28.31	1.65	5.87
FrWt	11.13	23.535	7.61	30.64	1.20	18.2
NoF	40.91	20.286	12.95	7.12	9.32	6.16
YPP	39.12	19.036	19.08	0.80	13.14	0.79

Table 3.Means(M) of F4 lines and Degree of resemblance(DR) between the F4 lines and F4 population for Flowers/cluster (FPC), fruit/cluster(FrPC), Fruit weight(FrWt),Fruit diameter (Frdia), fruit length(FrLen),Number of fruits/plant (NoF) and yield/plant(YPP).

Line	FPC		FrPC		FrWt		Frdia		Fr Len		NoF		YPP	
	DR	M	DR	M	DR	M	DR	M	DR	M	DR	M	DR	M
BK1	0.54	4.22	0.54	2.29	0.46	73	0.47	4.6	0.56	5	0.63	10	0.53	973
BK2	0.56	4.76	0.59	3.17	0.62	82	0.60	5	0.49	5.4	0.43	18	0.47	1397
BK3	0.62	4.77	0.45	2.55	0.67	82	0.57	5.3	0.55	5.7	0.64	29	0.57	2499
BK4	0.64	4.93	0.58	3.21	0.55	84	0.64	4.8	0.70	3.8	0.61	9	0.58	837
BK5	0.59	5	0.73	1.8	0.46	85	0.51	4.4	0.40	5.4	0.66	9	0.68	1627
BK6	0.61	4.46	0.68	2.78	0.35	73	0.34	4.5	0.44	5.7	0.58	18	0.55	1639
BK7	0.52	4.22	0.54	3.62	0.55	85	0.49	5.2	0.49	4.5	0.58	17	0.63	630



BK8	0.52	3.33	0.50	2	0.49	88	0.51	4.2	0.47	4.9	0.61	8	0.62	1874
BK9	0.41	5.61	0.73	1.8	0.38	65	0.35	5.1	0.59	5	0.76	21	0.64	1185
BK10	0.57	4.83	0.52	3.46	0.44	85	0.44	4.6	0.53	4.7	0.66	15	0.67	1808
BK11	0.58	6.23	0.62	3.35	0.43	77	0.53	4.5	0.65	5.1	0.55	25	0.48	768
BK12	0.53	4.13	0.46	5	0.48	71	0.54	4.8	0.57	4.8	0.50	9	0.47	1175
BK13	0.51	4.5	0.51	2.66	0.50	74	0.47	4.8	0.53	5.3	0.56	11	0.49	945
BK14	0.47	4.2	0.44	4.33	0.59	100	0.55	4.2	0.63	4.7	0.48	12	0.48	1042
BK15	0.47	4.5	0.58	2.13	0.51	77	0.54	5	0.50	4.4	0.55	15	0.52	707
BK16	0.61	5	0.58	2.8	0.47	71	0.51	4.4	0.49	5.1	0.56	11	0.53	1756
BK17	0.54	4.5	0.56	2.69	0.64	61	0.63	4.1	0.55	5.4	0.60	22	0.50	582
BK18	0.42	4.26	0.45	2.5	0.59	83	0.60	4.4	0.46	4.5	0.69	8	0.71	758
BK19	0.46	4.61	0.58	2.57	0.55	83	0.58	5	0.61	5.2	0.56	8	0.54	1333
BK20	0.58	4.94	0.51	3.44	0.62	77	0.64	4.4	0.57	4.8	0.47	15	0.48	884
BK21	0.58	5	0.60	3.14	0.74	67	0.83	4.7	0.71	4.9	0.60	13	0.64	1357
BK22	0.40	4.5	0.61	3.12	0.68	80	0.63	4.8	0.56	4.9	0.63	8	0.52	1775
BK23	0.47	4.83	0.55	3	0.62	84	0.58	4.2	0.63	5	0.71	16	0.68	839
BK24	0.65	4.52	0.61	2.58	0.64	79	0.53	3.5	0.46	5.1	0.67	24	0.72	1349
BK25	0.57	5.61	0.53	2.85	0.57	67	0.46	4.7	0.51	4	0.63	12	0.65	923
BK26	0.55	5.45	0.52	2.81	0.51	62	0.45	4.3	0.50	4	0.57	10	0.55	911

Table-4: Mean difference between F4 lines and F4 population (MD4) and mean difference between F4 lines and F3 population for Flowers/cluster (FPC), fruit/cluster (FrP), Fruit weight(FrW),Fruit diameter (FrDi), fruit length(FrL),Number of fruits/plant (NoF) and yield/plant(YPP)

Line	FPC		FrP		FrW		NoF		Fr L		FrDi		YPP	
	MD4	MD3	MD4	MD3	MD4	MD3	MD4	MD3	MD4	MD3	MD4	MD3	MD4	MD3
BK1	0.49	1.13	0.6	1.52	4.48	20.0	4.48	11.7	-0.06	0.45	0	0.97	253.5	917.2
BK2	-0.05	0.59	-0.2	0.64	-4.52	11.03	-3.52	3.7	-0.46	0.05	-0.4	0.57	-170	493.2
BK3	-0.06	0.58	0.34	1.26	-4.52	11.03	-14.5	-7.3	-0.76	-0.25	-0.7	0.27	-1272	-608.8
BK4	-0.22	0.42	-0.3	0.6	-6.52	9.03	5.48	12.7	1.14	1.65	-0.2	0.77	389.5	1053.2
BK5	-0.29	0.35	1.09	2.01	-7.52	8.03	5.48	12.7	-0.46	0.05	0.2	1.17	-400	263.2
BK6	0.25	0.89	0.11	1.03	4.48	20.03	-3.52	3.7	-0.76	-0.25	0.1	1.07	-412	251.2
BK7	0.49	1.13	-0.7	0.19	-7.52	8.03	-2.52	4.7	0.44	0.95	-0.6	0.37	596.5	1260.2
BK8	1.38	2.02	0.89	1.81	-10.5	5.03	6.48	13.7	0.04	0.55	0.4	1.37	-647	16.2
BK9	-0.9	-0.26	1.09	2.01	12.4	28.03	-6.52	0.7	-0.06	0.45	-0.5	0.47	41.5	705.2
BK10	-0.12	0.52	-0.5	0.35	-7.52	8.03	-0.52	6.7	0.24	0.75	0	0.97	-581	82.2
BK11	-1.52	-0.88	-0.4	0.46	0.48	16.03	-10.5	-3.3	-0.16	0.35	0.1	1.07	458.5	1122.2
BK12	0.58	1.22	-2.1	-1.19	6.48	22.03	5.48	12.7	0.14	0.65	-0.2	0.77	51.5	715.2
BK13	0.21	0.85	0.23	1.15	3.48	19.03	3.48	10.7	-0.36	0.15	-0.2	0.77	281.5	945.2
BK14	0.51	1.15	-1.4	-0.52	-22.5	-6.97	2.48	9.7	0.24	0.75	0.4	1.37	184.5	848.2
BK15	0.21	0.85	0.76	1.68	0.48	16.03	-0.52	6.7	0.54	1.05	-0.4	0.57	519.5	1183.2
BK16	-0.29	0.35	0.09	1.01	6.48	22.03	3.48	10.7	-0.16	0.35	0.2	1.17	-529	134.2
BK17	0.21	0.85	0.2	1.12	16.4	32.03	-7.52	-0.3	-0.46	0.05	0.5	1.47	644.5	1308.2
BK18	0.45	1.09	0.39	1.31	-5.52	10.03	6.48	13.7	0.44	0.95	0.2	1.17	468.5	1132.2
BK19	0.1	0.74	0.32	1.24	-5.52	10.03	6.48	13.7	-0.26	0.25	-0.4	0.57	-106	557.2
BK20	-0.23	0.41	-0.5	0.37	0.48	16.03	-0.52	6.7	0.14	0.65	0.2	1.17	342.5	1006.2
BK21	-0.29	0.35	-0.2	0.67	10.4	26.03	1.48	8.7	0.04	0.55	-0.1	0.87	-130	533.2
BK22	0.21	0.85	-0.2	0.69	-2.52	13.03	6.48	13.7	0.04	0.55	-0.2	0.77	-548	115.2
BK23	-0.12	0.52	-0.1	0.81	-6.52	9.03	-1.52	5.7	-0.06	0.45	0.4	1.37	387.5	1051.2
BK24	0.19	0.83	0.31	1.23	-1.52	14.03	-9.52	-2.3	-0.16	0.35	1.1	2.07	-122	541.2
BK25	-0.9	-0.26	0.04	0.96	10.4	26.03	2.48	9.7	0.94	1.45	-0.1	0.87	303.5	967.2
BK26	-0.45	0.19	0.58	1.5	3.48	19.03	-4.52	2.7	-0.26	0.25	0	0.97	614.3	542



References

- Ahmad M, Iqbal M, Khan BA, Khan ZU, Ullah I, Akbar K, Shahid M and Rehman A, 2017. Response to Selection and Decline in Variability, Heritability and Genetic Advance from F2 to F3 Generation of Tomato (*Solanum lycopersicum*). Int. J. Plant Res. 7(1):1-4.
- Bauchet G and Causse M, 2012. Genetic diversity in tomato and its wild relatives, pp: 134. In: M. Caliskan, Genetic diversity in plants. Intech publishers. DOI:10.5772/33073
- Bejiga G, 1987. Relationships among the f2 to f6 generations, and effect of spacing and selection in f4 on performance in f5 generation in chickpea. PhD thesis. Department of Genetics and Plant Breeding, College of Agriculture Andhra Pradesh, Agricultural University Raiendranagar, Hyderabad, India.
- Brown J and Caligari P, 2008. An introduction to plant breeding. Blackwell publishing. Oxford.UK.
- Brown J, Caligari P and Campos H, 2014. Plant breeding 2nd edition, John Willey and sons, West Sussex.
- Burton GW and Devane EH, 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from Replicated Colonel Material. Agron. J. 45: 478-481.
- Chang T, Li CC and Tagumpay O, 1973. Genotypic correlation, heterosis, inbreeding depression and transgressive segregation of agronomic traits in diallel cross of rice (*Oriza sativa* L) cultivars. Bot. Bull. Academicsinica.14:83-93.
- Falconer DS.1960. Introduction to quantitative genetics, Oliver and boyd Ltd, Edinberg.
- Mather k and Jinks JL, 1971. Biometrical genetics, Cornell University Press, Ithaca. O'Brien L, Baker RJ and Evans LE, 1978. Response to selection for yield in F3 of four wheat crosses. Crop. Sci. 18:1029-1033.
- Raval LJ, Pithia MS, Mehta DR and Ribadiya AH, 2017. Estimation of Inter-Generation Parameters in Various Selection Procedures in Desi Chickpea (*Cicer arietinum* L.) Crosses. Int. J. Pure App. Biosci. 5(2): 536-540. doi: <http://dx.doi.org/10.18782/2320-7051.2680>
- Rios RO, 2015. Plant breeding in omic era, Springer international publisher, Switserzland.
- Singh T and Sharma A, 2016. Early generation selection for yield and its related traits in soybean [*Glycine max* (L.) Merrill.]. Legume. Res. 39 (3): 343-348: 2016.
- Virupakshappa K, 1984. Evaluation of single seed descent, bulk and pedigree methods in cowpea (*Vigna unguiculata*). Mysore J. Agric. Sci. 18: (1):76-79.
- Wallace DH, Ozbun JL and Munger HM, 1972. Advances in agronomy, American society of agronomy, Academic press, New York, USA.
- Wrike G and Weber WE, 1986. Quantitative genetics and selection in plant breeding, Walter de Gruyter, New York, USA.

