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Estimation of Variance Components, Heritability and Genetic Advance of Yield and Yield Related Traits in Tomatoes (*Solanum* lycopersicum L)

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Heritability, genetic advance, genotype, phenotype, seed yield, variability

Abstract

Investigation and better understanding on the variability existing in a population base of crop is pivotal to crop improvement and proper understanding by plant breeder. The objectives of the study were to estimate the magnitude of genetic variability, heritability and genetic advance for yield and yield contributing characters of the twenty four tomato genotypes cultivated. Ethyl methyl sulphonate (EMS) mutagen was used at concentrations rate of 40 mM, 60 mM and 80 mM, while 0.00 mM was used for control has pre-treatment of the seeds before planting. The experiment was arranged in a Complete Randomised Design (CRD) with ten replicates. Fourteen quantitative traits were observed during different stages of development. Furthermore, data collected for each character was subjected to analysis of variance (ANOVA) to test the variations among genotypes. From the results, Phenotypic Coefficient of Variation (PCV) was relatively greater than Genotypic Coefficient of Variation (GCV) for all traits considered. Genetic variance (δ^2g) ranged from 0.18 for FPT to 8077114.00 for yield per plant in kg/ha while phenotypic variance (δ^2P) ranged from 0.30 for FPT to 8601084.00 in kg/ha. The highest heritability was observed for number of branches per plant (BPP) (95.32%), while DMF had the lowest with 60.05 %**.** The highest GAM of kg/ha was 158.67 %, and the lowest GAM was number of flowers per truss at 75days (FPT) gave 11.59**%**. In conclusion, high heritability indicated that the characters were less influenced by the environment and therefore, selection based on phenotypic performance is recommended to be dependable and effective.

Introduction

Tomato (*Solanum lycopersicum*) belongs to a member of the *Solanaceae* family and it is cultivated in tropical and sub-tropical regions (Naheed, 2014). FAO (2010) recorded that tomato is the 11th most cultivated plant used as food. Aminu et al. (2017) affirmed that tomatoes, as a cultivated crop are of high importance in some countries, while in other parts of the world have witnessed a lot of negligence. Kaushik et al. (2011) opined that tomato has medicinal values which include its use for blood purification and cure for digestive ailments. Vitamins and antioxidants in tomatoes are essential for a healthy body. Lycopene and bioflavonoid which are in close relation with beta carotene are good antioxidants found in tomatoes and had natural cancer-fighting properties. Tomato's medicinal properties were approved in continental Europe in the 16th century. In addition, tomato consumption reduces cardiovascular disease and also helps in high blood pressure reduction, a major risk factor for coronary heart disease and stroke to relieve bloodshot eyes (Adeosun et al., 2020).

Research on availability genetic variability of the tomato genotypes was limited. Therefore, there is a need to generate information on genetic variability, genotypic coefficient of variation, heritability, and genetic advance of tomato to estimate the progress of their breeding program. Dyulgerova and Valcheva (2014) referenced by Adeosun et al. (2020) defined heritability as the measure of the correspondence between breeding and phenotypic values. Heritability estimate of a character is important for plant breeder because it provides information on the extent to which a particular character can be transmitted from the parent to the progeny (Adeosun et al., 2020). Similarly, genetic advance is also important because it shows the degree of the gain obtained in a character from one cycle of selection. Therefore, high genetic advance coupled with high heritability estimates offers the most suitable condition to decide the criteria of selection (Dyulgerova and Valcheva, 2014). In view of these, the present study was done with the objectives of assessing genetic variability, heritability and genetic advance of twenty parental tomato plants (genotypes) cultivated in Ladoke Akintola University of Technology, Ogbomoso Oyo State, Nigeria. The results of this research provide an effective program for improving the yield of tomato through the release of elite varieties or mutants with interesting agronomic characteristics.

The aims of the study were to estimate the extent of genetic variability, heritability and genetic advance for yield and some yield related characters of the twenty of tomato genotypes cultivated.

Materials and methods

Plant material and experimental site

The study was conducted at the research plots in the Botanical Garden of the Department of Pure and Applied Biology, Ladoke Akintola University of Technology, Ogbomoso. Twenty varieties used in this study were sourced from the National Centre for Genetic Resources and Biotechnology (NACGRAB), Ogbomoso and Abeokuta all in Nigeria.

Table 1: Genotypes studied and their origin

S/N	Origin	Genotypes	Types
1	NACGRAB	NGB01410; NG/MR/JAN/10/001; NG/AA/SEP/09/045; NG/AA/SEP/09/037; NGB01357; NG/MR/MAY/09/006; NG/AA/SEP/ 09/040; NHGB/09/120; NG/MR/MAY/09/005; L00170; NHGB/09/113; L00169; NG/AA/SEP/09/042; NGB01254;	Accessions
2	Ogbomoso	ALAWUSA TYPE; ROMA; KEREWA; OGBOMOSO NATIVE; ALARA (ALA)	Landraces
3	Abeokuta	ABEOKUTA NATIVE (ABE)	Landrace

Experimental design and agronomic practices

Among twenty (20) varieties of tomatoes plants evaluated only four (4) varieties were selected for mutation induction at M_1. These include: ABE, ALA, NHGB 09/120 and NGB 01410.

The Chemical mutagen of Ethyl methyl Sulphonate (EMS) was used for this study. The methods used for the mutation induction were as described by Srivastava et al. (2011) and Adamu and Aliyu (2007) as follow:

Ethyl methyl Sulphonate (EMS):

i. **Pre-treatment of seeds with ethyl methyl sulphonate:** Before the EMS treatment, the tomato seeds passed through a preconditioning period. They were placed in Petri dishes on wet filter paper for 4 days at 4°C, and dried for 16 hours at room temperature.

ii. **Treatment of seeds with ethyl methyl sulphonate:** After the precondition period, the tomato seeds were soaked in EMS of concentration of 40 mM, 60 mM and 80 mM with a phosphate buffer (PH=7). The time of treatment was 4 hours and when the time elapsed, the laboratory bottle containing the seeds was placed under water and rinsed for 15 mins. The seeds were dried on a filter paper, and thereafter sowed by hand in nursery bed to obtain the seedlings and later transplanted to permanent bed. All the consumables in connection to EMS were put into 1M NaOH as a decontamination solution (Naheed, 2014).

Simultaneously, another 120 seeds were used as a control and passed through the same procedures excluding the EMS solution treatments. Seeds of the accessions were raised in nursery before transplanting. The experimental lay out was Completely Randomized Design (CRD) replicated ten times. Inter- spacing between each row was 0.6 meter (60cm) while the intra-spacing within a row was 0.5 meter (50cm). Planting was done by hand in the nursery beds with three seeds per hole which later transplanted after twenty five days of sowing. The plants were evaluated for both morphological and agronomical traits. .

Table 2: Method of scoring and code of quantitative parameter studied

S/N	Quantitative parameter studied	Code	Method of scoring
1	Plant height at (90 days) (cm)	PTH	Measured
2	Leaf area at 75days	LEA	Calculated
3	Number of leaves per plant	NLP	Counted
4	Number of Branches per plant	BPP	Counted
5	Number of flowers per truss at 75days	FPT	Counted
6	Number of fruits per truss	NFT	Counted

S/N	Quantitative parameter studied	Code	Method of scoring
7	Number of fruits at 75 days per plant	NOF	Counted
8	Number of fruits per plant	FPP	Counted
9	Weight of fruits (g)	WGH	Measured
10	Diameter of fruits (cm)	DMF	Measured
11	Yield per plant in gram (g)	YPP	Measured
12	Yield in kilogram per hectare (kg/ha)	Ykg/ha	Measured
13	Number of seeds per fruit	NSF	Counted
14	Seeds number per plant	SNP	Counted

Table 3: Accessions /landraces and concentration of mutagen used

S/N	Varieties/ genotypes	Mutagens' concentration
		EMS
1	ABE	Control 0.00mM
2	EMS % L1	40 mM
3	L2	60 mM
4	L3	80 mM
5	ALA	Control 0.00mM
6	EMS % L1	40 mM
7	L2	60 mM
8	L3	80 mM
9	NHGB09/120	Control 0.00mM
10	EMS % L1	40 mM
11	L2	60 mM
12	L3	80 mM
13	NGB 01410	Control 0.00mM
14	EMS % L1	40 mM
15	L2	60 mM
16	L3	80 mM

***Note*: ABE and ALA** were Abeokuta and Ogbomoso landraces respectively while NHGB 90/ 120 and **NGB** 01410 were collected from National Centre for Genetic Resources and Biotechnology (NACGRAB), Moor Plantation, Ibadan, Oyo State, Nigeria.

Data collection and analysis

Fourteen quantitative traits were observed during different stages of development (Table 2). The data collected for each character was subjected to analysis of variance (ANOVA) to test the variations among genotypes. The analysis of variance was calculated using IBM SPSS Statistics 20 software version for analysis, and the significance was determined by F-test at 99% confidence ($P < 01$).

Estimates of variance components:

The variability present in the population was estimated by measuring mean (π), phenotypic variance (δ^2p), genotypic variance (δ^2g), and phenotypic coefficient of variation (PCV), genotypic coefficient of variation (PCV), heritability in broad sense (h^2b), genetic advance (GA) and genetic advance over mean (GAM). They were estimated based on formula (Syukur *et al.,* 2012) as shown in the Table 4.

Table 4: Genetic parameters estimated

Parameter	Formula	Significance of terms	References
Genotypic variance (δ^2g)	$\delta^2g = (MSG - MSE) / r$	MSG: Mean Square of Genotype	Meena et al. (2017)
Phenotypic variance (δ^2p)	$\delta^2p = \delta^2g + (MSE) / r$	MSE: Mean square of error r: Number of replications	Meena et al. (2017)
Genotypic coefficient of variation (GCV)	$GCV\ (\%) = (\sqrt{\delta^2g/\pi})*100$	π: Grand mean of the character	Meena et al. (2017); Richard, et al. (2023)
Phenotypic coefficient of variation (PCV)	$PCV\ (\%) = (\sqrt{\delta^2p/\pi})*100$		Meena et al., 2017; Richard, et al., 2023)
Heritability broad sense (h^2b)	$h^2b = (\delta^2g/\delta^2p)*100$	δ^2g: Genotypic variance δ^2p: Phenotypic variance	Rosmaina et al. (2016)
Genetic advance (GA)	$GA = h^2b * \delta p * K$	K = 2.06 (at 5% selection coefficient)	Meena et al. (2017)
Genetic advance over mean (GAM)	$GAM = (GA/\pi) * 100$		Meena et al. (2017)

The Genetic parameters estimated were ranged as follow:

PVC and GCV were classified as suggested by Meena et al. (2017) and Richard et al. (2023).

Less than 10% = Low
10 - 20% = Moderate
More than 20% = High,

The heritability (h^2 (bs)) was categorised by Rosmaina et al. (2016).

0 - 30% = Low
31 - 60% = Medium
61 % and above = High

Genetic advance over mean (GAM) was categorized as suggested by Meena et al. (2017)

Less than 10% = Low
10 - 20% = Moderate
More than 20% = High

Results

The analyses of the 14 characters considered were showed in Table 5 at first mutants' generation. Variation in characters were observed as measured by range, phenotypic variances (δ^2p), genotypic variances (δ^2g), Phenotypic Coefficients of Variation (PCV), Genotypic Coefficients of Variation (GCV), heritability, genetic advance and genetic advance over mean for M_1 mutants' varieties measured from four Parental plants of ABE, ALA, NHGB 09/120 and NGB 01410.

Genetic variance (δ^2g) values ranged from 0.18 for number of flowers per truss (FPT) to 8077114.00 for yield per plant in kilometre per hectare (Ykg/ha) while phenotypic variance (δ^2P) ranged from 0.30 of FPT to 8601084.00 yields per plant in kilometre per hectare (Ykg/ha). The PCV were ranged from 9.35 % for FPT (number of flowers per truss) to 113.50% for number of fruits per truss (NFT). Similarly, the GCV ranged from 7.25 % for number of flowers per truss (FPT) to 108.17 % for number of fruits per truss (NFT) Table 5. In this study, high heritability along with genetic advance as percent of mean are exhibited by most of traits studied. However, the highest broad sense heritability was observed for number of branches per plant (BPP) (95.32%) and lowest heritability was recorded in diameter per fruit (DMF) (60.05%). Moreover, high heritability was observed for all the traits studied. There was high genetic advance for traits such as yield in kilogram per hectare (Ykg/ha) (5673.45), seeds number per plant (SNP) (996.52), leaf area (LEA) (147.59) and yield in gram per plant (YPP) (45.80). Other traits studied were moderate and low genetic advance Table 5.

Table 5: Estimates of Grand mean (π), Genotypic variation (δ^2g), Phenotypic variation (δ^2p), Genotypic coefficient of variation (GVC), Phenotypic coefficient of variation (PCV), Heritability in broad sense (h^2b), Genetic Advance (GA) and Genetic Advance over mean (GAM), for 14 traits M1 Mutants varieties.

Traits	Range				δ^2g	δ^2e	δ^2p	GCV	PCV	h^2b	GA	GAM
	Min	**Mean**	**Max**	**Mean square**								
PTH 90	22.00	52.20	93.00	3.922**	34.27	11.73	46.00	11.21	12.99	74.51	10.41	19.94
LEA	4.00	123.79	466.00	8.495**	5818.30	776.28	6594.58	61.62	65.60	88.23	147.59	119.23
NLP	7.00	12.12	28.00	10.842**	6.24	0.63	6.87	20.61	21.64	90.78	4.90	40.46
BPP	1.00	6.30	15.00	21.385**	6.91	0.34	7.25	41.75	42.76	95.32	5.29	83.97
FPT	3.00	5.85	10.00	2.502**	0.18	0.12	0.30	7.25	9.35	60.20	0.68	11.59
NFT	1.00	2.69	8.00	10.909**	8.46	0.85	9.31	108.17	113.50	90.83	5.71	212.36
NOF 90	5.00	10.73	24.00	4.809**	1.86	0.49	2.35	12.72	14.29	79.18	2.50	23.31
FPP	1.00	6.56	70.00	8.257**	25.51	3.52	29.03	76.95	82.08	87.89	9.75	148.60
WGH	3.80	21.14	81.30	20.578**	99.49	5.08	104.57	47.17	48.36	95.14	24.04	94.79
DMF	0.01	3.83	41.00	2.502**	0.78	0.52	1.30	23.07	29.77	60.05	1.41	36.83
YPP	6.90	53.22	406.50	7.270**	573.20	91.42	664.62	44.98	48.44	86.25	45.80	86.06
Ykg/ha	337.00	3575.75	26800.00	6.873**	8,077,114.00	523,970.50	8,601,084.00	79.48	82.02	93.91	5673.45	158.68
NSF	74.00	115.38	152.00	17.255**	152.02	9.35	161.37	10.69	11.01	94.20	24.65	21.37
SNP	17.00	711.41	4704.00	10.073**	259,802.20	28,634.22	288,436.40	71.65	75.49	90.07	996.52	140.08

***Note*:** PHT- Height of plants at (90 days) cm; LEA-Leaf area; NLP- Number of leaves per plant; BPP- Number of branches per plant; FPT- Number of flowers per truss; NFT - Number of fruits per truss; NOF- number of fruits per plant at 90 days; FPP- Number of fruits per plant; WGT- Weight of fruit in (g); DMF- Diameter of fruits in (cm); YPP – fruits yield per plant in gram (g); Ykg/ha – Yield per plant in kg per hectare; NSF- Number of seeds per fruit; SNP – Number of seeds per plant

Table 6: Comparing the Broad sense heritability estimates of fourteen agronomic traits of twenty four accessions and mutants' varieties selected from evaluation of four parental tomato plants at (M_1)

	(π)		**GCV (%)**		**PCV (%)**		**h^2b (%)**		**GA**		**GAM (%)**	
Traits	E	M_1	E	M_1	E	M_1	E	M_1	E	M_1	E	M_1
PTH 90	76.78	52.20	22.64	11.21	22.68	12.99	99.64	74.51	35.87	10.41	46.71	19.94
LEA	121.02	123.79	37.64	61.62	37.71	65.60	99.62	88.23	94.02	147.59	77.69	119.23
NLP	37.24	12.12	36.99	20.61	37.07	21.64	99.57	90.78	28.43	4.90	76.36	40.46
BPP	3.55	6.30	26.87	41.75	27.43	42.76	95.99	95.32	2.01	5.29	56.50	83.97
FPT	5.36	5.85	11.95	7.25	12.21	9.35	95.79	60.20	1.35	0.68	25.14	11.59
NFT	2.07	2.69	47.58	108.17	47.78	113.50	99.18	90.83	2.04	5.71	98.42	212.36
NOF90	1.95	10.73	84.58	12.72	85.30	14.29	98.30	79.18	3.43	2.50	175.73	23.31
FPP	6.94	6.56	89.51	76.95	89.81	82.08	99.35	87.89	12.84	9.75	185.00	148.60
WGH	19.68	21.14	57.28	47.17	57.36	48.36	99.72	95.14	23.26	24.0	118.17	94.79
DMF	3.16	3.83	29.52	23.07	29.53	29.77	99.89	60.05	1.92	1.41	60.84	36.83
YPP	101.42	53.22	42.56	44.98	43.30	48.44	96.57	86.25	90.47	45.80	89.21	86.06
Ykg/ha	3377.96	3575.75	13.52	79.48	15.71	82.02	73.94	93.91	1093.77	5673.45	32.38	158.68
NSF	54.79	115.38	27.83	10.69	27.87	11.01	99.74	94.20	31.46	24.65	57.42	21.37
SNP	375.83	711.41	77.69	71.65	78.18	75.49	98.74	90.07	605.30	996.52	161.06	140.08

Note: π – Mean; E- Evaluation; M_1- First mutant generation

PHT- Height of plants at (90 days) cm; LEA-Leaf area; NLP- Number of leaves per plant; BPP- Number of branches per plant; FPT- Number of flowers per truss; NFT - Number of fruits per truss; NOF- number of fruits per plant at 90 days; FPP- Number of fruits per plant; WGT- Weight of fruit in (g); DMF- Diameter of fruits in (cm); YPP

– fruits yield per plant in gram (g); Ykg/ha – Yield per plant in Kg per hectare; NSF- Number of seeds per fruit; SNP – Number of seeds per plant

The phenotypic coefficient of variation (PCV) ranged from 12.21% for Number of flowers per truss (FPT) to 89.81% for number of fruits per plant (FPP), while that of M_1 ranges from 9.35% for number of flowers per truss (FPT) to 113.50% for number of fruits per truss (NFT).

High heritability were recorded for all traits evaluated but highest heritability in diameter of fruit (99.89%) while lowest heritability was confirmed from yield in kilogram per hectare (Ykg/ha) (73.94%). In M_1 highest heritability in broad sense was recorded in number of branches per plant (BPP) with the value of 95.32% and lowest noticed in diameter of fruit (DMF) with 60.05%.

Discussion

The results of this study agreed with the work of Meena, et al. (2017), where high PCV and GCV were recorded for DMF, WGT, LEA, BPP, NFT, FPP, Ykg/ha, SNP and YPP, while traits with moderate PCV and GCV were PTH and NSF. Lower PCV and GCV were recorded for FPT. The PCV are higher than the GCV for all the traits studied. This means that genotype was influenced by environment in the phenotype expression. Also, similar report was recorded by (Kambou et al., 2023).

According to Kambou et al. (2023), high heritability combined with high genetic advance is indicative of gene action. High heritability coupled with low genetic advance would resulted to non-dependence genetic effects (Kambou et al., 2023) while low heritability coupled with low genetic gain suggested that phenotypic selection may not be effective in improving traits. Moreover, selection based on both high values of heritability in broad sense and genetic advance would be more reliable in the expression of traits in progeny (Kambou, et al., 2023). Therefore, heritability when coupled with genetic advance could further strengthen the effectiveness of selection which has been documented by many researchers like, *Akbar* et al. *(2003).*

Comparing genetic parameters of evaluation with M_1 mutants' tomato plants in this present study indicated that all mutants performed better than control because of the effectiveness of chemical mutagen used to improve tomato quality and quantity traits. In studies on crop improvement, data on genetic parameters, such as range, mean, genotypic variance, phenotypic variance, genotypic and phenotypic coefficient of variation, heritability, and genetic advance for various traits would provide an indication of how to improve a trait through selection. As previously mentioned, the mutagenic treatments in the current study caused micro mutations, which led to diversity in the M_1 generation for many phenotypes. However, the extent and type of generated variations in several attributes differed with treatments (Meena et al., 2017).

Rosmaina et al. (2016) reported that heritability estimates show only the extent with which selection of genotypes could be based on phenotype but its utility increased when used along with estimates of genetic advance. High heritability values for most of the characters suggested the effectiveness of direct selection for such characters. That the heritability estimates for the characters differed between seasons suggested the different responses of various characters to changing environmental conditions, thus showing the influence of environments on the estimation of genetic parameters. Subsequent study (Ariyo and Ayo-Vaughan, 2000; Richard, et al., 2023) sees the need to breed for specific environments because the response of most characters to environments was nonlinear.

It is therefore very important for breeders to know the heritability of the agronomic characters to improve the yield of the crop effectively. According to Tazeen et al. (2009), there is a direct relationship between heritability and response to selection, which is referred to as genetic advance. High genetic advance with high heritability estimates offers the most effective condition for selection. The utility of heritability therefore increases when it is used to calculate genetic advance, which indicated the degree of gain in a character obtained under a particular selection pressure. Thus, genetic advance is another important selection parameter that aids breeder in a selection program (Mawha, et al., 2020).

Conclusion

In conclusion, based on the findings of this study, all characters could be used as good criteria for selection in the tomatoes improvement because these characters had high genotypic coefficient of variation, heritability estimate and genetic advance as percent of the mean. The high heritability estimates together with high genotype coefficient of variation (GCV) and relatively high genetic advance for number of fruits per truss, number of fruits per plant, number of branches per plant, weight of matured fruits and number of seeds per plant indicated that these characters are highly heritable. The findings presented in this paper may be a useful piece in the future breeding and tomato improvement program. Therefore, the author recommended that selection for these characters on the basis of phenotypic performance is likely to be dependable and effective.

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