Website : www.asthafoundation.in
Frontiers in Crop Improvement
Vol 12 (2) : 84-88 (July-2024) Print ISSN : 2393-8234 Online ISSN : 2454-6011
Astha Foundation, Meerut (U.P.) India

Genetic Association and Variability Studies of Maize Inbred Lines under Saline, Water Deficient Soils of Chidambaram

James M.[1,2*], Priyadarsini V.[1], Sathyaraj D.[1], Angelin Gladina P.[1] and Senthil Kumar P.[1]
[1]*Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University-608002*
[2]*School of Crop Improvement, College of Post Graduate Studies in Agricultural Sciences, Meghalaya-793103*
**Corresponding Author Email : mailmejames.2009@gmail.com*

Abstract

In the present investigation fifty-two maize genotypes were collected from various locations ofsouth India and were evaluated in Plant Breeding Farm, Department of Genetics and Plant Breeding, Annamalai University during rabi, September, 2018 – January 2019 to estimate variability and correlation to identify potential inbreds to use them as parents for hybridization. Ten quantitative characters *viz.,* Days to 50% tasseling (DT), Days to 50% silking (DS), Plant height (PH), Cob height (CH), Cob length (CL), Cob girth (CG), Number of kernels per cob (NK), Test weight (TW), Single plant yield (SPY) and Leaf area (LA) was recorded. Analysis of variance showed significant differences for the eleven quantitative traits. The study of mean performance for the 10 traits showed that genotypes, G34 followed by G11, G32, G38 and G48 showed highest single plant yield. While the genotypes G20 and G50 showed early days to tasseling and silking. Variability studies showed the highest PCV, GCV, heritability and genetic advance as per cent of mean for three characters *viz.,* leaf area, number of kernels and single plant yield showing that these characters are under additive gene action. Association studies showed that the single plant yield had significantly positive association with number of kernels, cob length, test weight, plant height and cob girth. Also, single plant yield had significant negative association with days to 50% silking and days to 50% tasseling.

***Key words** : Inbred, variability studies, association study, single plant yield.*

Introduction

Maize (*Zea mays L.*) (2n = 2x = 20) also known as corn is one of the most essential and fundamental food crops next to rice and wheat, all together feeding around 60 per cent of the world population. It is the most adapted cereal across varied agro-climatic conditions and is known as “Queen of cereals” because of the huge genetic potential to produce high yielding heterotic hybrids. It is used for multi-purposes as human food, livestock feed, biofuel, and as raw material in many industries (1). Maize is available in different forms as popcorn, sweet corn, dent corn, flint corn, flour corn etc. (2). This wide diversity coupled with high outcrossing and utilization of C_4 carbon fixation makes it as the world’s most dominant and productive crop (3). The worldwide production of maize was 1235.73 mmt, the highest among cereals, and in India the maize production was 38 mmt (4). Projected demand for maize production by 2050 in India is around 121 mt and this demand is due to rising number of poultry farms. To meet these demands expanding the cultivated area, adopting proper management practises, and increasing the productivity is crucial.

As known, variability is the primary interest to the plant breeder as it plays a significant role in framing successful breeding programme. Variability is the primary interest to the plant breeder as it plays a significant role in framing successful breeding programme (5, 6). Study of variability, heritability and genetic advance in the germplasm will help to ascertain the real potential value of the genotypes (7, 8). Correlation enables to identify the characters which might be useful as indicator of high yield by way of evaluating relative influence of various characters on yield and among themselves as well (6, 9). Study of variability, heritability and genetic advance in the germplasm will help to ascertain the real potential value of the genotypes. Correlation enables to identify the characters or combination of characters which might be useful as indicator of high yield by way of evaluating relative influence of various characters on yield and among themselves as well. Therefore, thorough knowledge on genetic parameters like mean, variability, heritability, genetic advance as per cent of mean and correlationwill provide basis for selecting inbred lines based on important traits to plan a systematic breeding strategy for crop improvement and to increase yield potential of the genotypes.

Materials and Methods

Study site, experiment layout and observations recorded : The present investigation was conducted at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Chidambaram, Tamil Nadu, in rabi 2018. The field is situated 15 kms away from the sea shore (Bay of

Received : June-2024; Revised : June-2024; Accepted : July-2024

Table-1 : List of fifty-two maize genotypes used in the study.

Code	Name	Type	Source	Code	Name	Type	Source
G1	16K1816	Inbreds	AP	G27	17PRC1018	Inbreds	TG
G2	16K1818	Inbreds	AP	G28	17PRC1019	Inbreds	TG
G3	16K1887	Inbreds	AP	G29	17PRC1020	Inbreds	TG
G4	16K1899	Inbreds	AP	G30	17PRC1021	Inbreds	TG
G5	16K1900	Inbreds	AP	G31	17PRC1022	Inbreds	TG
G6	16K1901	Inbreds	AP	G32	17PRC1023	Inbreds	TG
G7	16K1904	Inbreds	AP	G33	17PRC1024	Inbreds	TG
G8	16K1914	Inbreds	AP	G34	17PRC1025	Inbreds	TG
G9	16K1915	Inbreds	AP	G35	AU18M01	Inbreds	TN
G10	17PRC1001	Inbreds	TG	G36	AU18M02	Inbreds	TN
G11	17PRC1002	Inbreds	TG	G37	AU18M03	Inbreds	TN
G12	17PRC1003	Inbreds	TG	G38	AU18M04	Inbreds	TN
G13	17PRC1004	Inbreds	TG	G39	AU18M05	Inbreds	TN
G14	17PRC1005	Inbreds	TG	G40	AU18M06	Inbreds	TN
G15	17PRC1006	Inbreds	TG	G41	AU18M07	Inbreds	TN
G16	17PRC1007	Inbreds	TG	G42	AU18M08	Inbreds	TN
G17	17PRC1008	Inbreds	TG	G43	AU18M09	Inbreds	TN
G18	17PRC1009	Inbreds	TG	G44	AU18M10	Inbreds	TN
G19	17PRC1010	Inbreds	TG	G45	AU18M11	Inbreds	TN
G20	17PRC1011	Inbreds	TG	G46	AU18M12	Inbreds	TN
G21	17PRC1012	Inbreds	TG	G47	AU18M13	Inbreds	TN
G22	17PRC1013	Inbreds	TG	G48	AU18M14	Inbreds	TN
G23	17PRC1014	Inbreds	TG	G49	Vilupuram L.	Selfed OPV	TN
G24	17PRC1015	Inbreds	TG	G50	PeruRani	Selfed OPV	TN
G25	17PRC1016	Inbreds	TG	G51	Karnataka L.	OPV	KN
G26	17PRC1017	Inbreds	TG	G52	Sivagangai L.	OPV	TN

TN- Tamil Nadu; AP- Andhra Pradesh; TG- Telangana; KN- Karnataka; OPV- Open pollinated variety; L.- Local variety (OPV).

Bengal), 5.2 m above mean sea level, situated at 17º 19' N latitude and 78 º 41' E longitude. The soil was clay loamy with a pH of 7 and electrical conductivity was more than 1 (slightly saline), also the soil had poor nitrogen content, whereas phosphorous and potassium were in optimum levels.Water was unavailable during the critical flowering stage and after a stress of around 15-20 days (December, 2018) irrigation was done using water tankers. Sixty-four genotypes were collected from various states of south India *viz*., Tamilnadu, Andhra Pradesh, Telangana, and Karnataka. They were grown in completely randomized block design (RBD) with three replications and the borders were planted with Salem popcorn hybrid. Each genotype was grown in rows of 3 m length, spacing of 60 x 25 was maintained and thinning was done 15 days after sowing. Out of these, fifty-two genotypes had sufficient plant population in all three replications (Table-1). Observations were recorded on randomly selected five plants of a genotype in each replication. Ten phenotypical observations *viz*., Days to 50% tasseling (DT, in days), Days to 50% silking (DS, in days), Plant height at maturity (PH, in cm), Cob height at maturity (CH, in cm), Cob length (CL, in cm), Cob girth (CG, in cm), Number of kernels per cob (NK, in numbers), Test weight (TW, in g), Single plant weight (SPY, in g) and Leaf area at maturity (LA) were recorded; LA as per (11).

Statistical analysis : Genotypic (GCV) and phenotypic (PCV) co-efficient of variation were calculated as, PCV = $\frac{\sqrt{Vp}}{Mean}\quad 100$; CV = $\frac{\sqrt{Vg}}{Mean}\quad 100$ (12). Where, 'Vp' and 'Vg' are the phenotypic and genotypic variance obtained from analysis of variance (ANOVA). Heritability in broad sense was calculated as $h^2 = \frac{Vp}{Vg}\quad 100$, genetic advance (GA = $h^2 \quad \sqrt{V_{ph}} \quad K$), where, 'K' is the 2.06 at 5 % per cent selection intensity (2.06) and genetic advance as per cent of mean (GA(%)) = $\frac{\text{Genetic advance}}{\text{Grand mean}}\quad 100$, (PCV and GCV was categorized as low (< 10 %), moderate (10 – 20 %), high (>20%), whereas h^2 was categorized as low(<30 %), moderate (30 – 60%), high (>60%) (13). GA as per cent of mean was classified aslow (<10%), moderate (10 – 20%) and high (>20%) (Robinson *et al.* 1949). The genotypic correlation co-efficient were worked out as $(rg_{xy}) = \frac{(Cov\ (g_x \quad g_y))}{\sqrt{\quad g_x} \quad {}^2g_y}$; where, 'Cov (gx. gy)' is the genotypic covariance between character x and y, ' ^{2} gx' and ' ^{2} gy' are the genotypic variance of character x and y, respectively.

Results and Discussion

Performance of the studied maize genotypes : The mean performance and analysis of variance (ANOVA) for the 52 lines of maize genotypes for 10 quantitative characters *viz*., DT, DS, PH, CH, CL, CG, NK, TW, SPY

Table-2 : Mean performance of fifty two maize genotypes for the ten characters.

Genotypes	Days to 50% tasseling	Days to 50% silking	Plant height	Cob height	Leaf area	Cob length	Cob grith	Number of kernels	Test weight	Single plant yield
G1	60.7	67.3	88.3	23.2*	203.8	10.6	3.2	132.3	16.9	42.6
G2	57.7	62.3	151.2*	57.3	350.3*	11.08	3.9	160.3	22.1*	65.0*
G3	57.3	61.3	140.3*	47.5	221.3	11.2	3.9	200.7*	19.5	76.6*
G4	63.3	66	111.7	44.7	316.7*	9.8	3.4	136	19.8	78.9*
G5	67	76.3	101.4	30.2*	257.6	8.6	3.3	109.7	17.1	36.1
G6	63.7	66.7	145.6*	60.1	278.5	8.8	3.2	102	20.5	39.7
G7	55.0*	60.0*	151.6*	45.4	282.0	9.9	3.7	146.7	18.7	67.9
G8	63.3	65.3	106.4	27.7*	206.1	8.9	3.4	115.6	20.8	46.3
G9	63.3	65	137.9	39.5	312.2*	8.5	3.3	98	24.2*	44.9
G10	57	68.7	104	43.6	286.2	9.4	3.4	128.7	16.9	46.9
G11	55.0*	59.7*	144.9*	26.3*	236.0	14.1*	3.8	336.0*	20	120.7*
G12	54.3*	67.3	134.5	43.4	166.7	15.8*	3.6	217.1*	15.9	79.3*
G13	51.3*	60.7*	144.8*	35.5*	203.4	14.8*	4.1*	193.7*	16.9	70
G14	57.3	69	135.3	40	240.4	7.8	3	111	20.6	42.6
G15	50.3*	56.0*	150.3*	31.4*	179.6	12	3.4	166.3	24.5*	77.2*
G16	53.3*	55.3*	112.3	46.8	422.2*	12.4*	3.4	164.7	18.2	71.3
G17	60.7	70.7	121.1	39.4	230.3	8.6	3.5	109	18.8	38.4
G18	54.7*	59.3*	139.8*	31.4*	180.0	12	3.5	178	16	71.4*
G19	61	68.7	150.5*	44	296.7	9.5	3.9	170.3	26.1*	91.4*
G20	56.3	53.7*	120.9	44.3	573.9*	10.4	3.1	104	19.6	60.8*
G21	50.3*	54.7*	168.2*	39.1	358.4*	14.6*	4.0*	277.3*	23.3*	98.3*
G22	57.3	63	153.3*	39.3	374.2*	13.7*	4.1*	235.7*	22.9*	99.8*
G23	53.3*	59.7*	108.7	41.4	197.9	10.1	3.6	172.7	20.5	37.6
G24	55.3*	62.3	108.8	29.5*	204.0	9.5	3.7	132.7	19.5	37.4
G25	58	65.7	97.2	23.6*	206.0	9	3.4	142.7	23.1*	62.7
G26	50.0*	57.0*	128.4	37	275.1	12.5*	3.4	154.3	23.7*	48.2
G27	61.3	66.7	128.4	38.1	340.5*	9.3	4.1*	142.3	17.3	33
G28	61	64.3	134.6	39.9	386.6*	10	3.6	170	18.9	39.8
G29	56.7	64.3	120.5	41.2	347.4*	9.1	3.5	125.7	19	47.4
G30	55.0*	63	130.7	21.0*	191.2	15.3*	3.8	242.3*	22.2*	68.3
G31	58.3	65	129.3	55.7	340.8*	10.5	3.7	176.3	23.2*	75.3*
G32	54.2*	57.7*	170.3*	42.4	349.3*	17.9*	3.4	234.3*	22.5*	112.2*
G33	61.3	70.3	80.8	23.2*	285.4	10	3.5	172.7	18.2	44.7
G34	53.3*	55.0*	141.8*	28.2*	491.3*	19.3*	4.2*	339.1*	24.6*	135.6*
G35	56	62.3	131.6	52.4	347.5*	14.2*	3.4	244.3*	21.8	69.4*
G36	57.3	62	135.7	45.5	408.5*	9.8	4.0*	135.3	19.6	38.9
G37	56	60.7*	154.1*	47.7	405.2*	14.7*	3.6	188	24.0*	83.5*
G38	55.3*	57.3*	149.0*	43.9	423.9*	15.3*	4.2*	225.3*	24.9*	106.6*
G39	60	67.3	102.6	25.0*	274.1	8.5	3.5	113.7	17.2	40.3
G40	55.0*	58.0*	167.0*	50	256.6	8.9	3	108	18.7	50.5
G41	56.7	60.3*	106.1	26.0*	242.7	7.6	3.2	101.3	18.6	56.6
G42	55.0*	65.3	108.1	33.1*	272.8	7.6	3.5	132.3	20.3	40.5
G43	57	59.7*	125.2	45.5	292.3	12.1	3.6	177.3	23.5*	84.1*
G44	58.3	62.7	104.7	21.8*	266.5	9.1	3.6	110.7	21	64.9
G45	71.3	81	103.2	29.9*	164.2	8.5	3.4	116	17.4	32.9
G46	56	62.3	131.2	33.2*	335.1*	8.9	3.3	142.3	19.5	53.5
G47	56.3	64.7	119.5	20.8*	234.4	8.5	3.4	125.3	23.1*	56.4
G48	52.0*	56.3*	170.7*	35.2	181.6	14.3*	3.4	215.7*	22.0*	100.7*
G49	58	63	122.8	45.4	319.0*	13.8*	4.1*	228.7*	28.0*	72
G50	50.3*	53.7*	154.3*	55.1	371.6*	11.2	4.1*	153.7	24.0*	82.5*
G51	59.3	64	154.7*	34.8	294.9	11.8	3.4	147	18.2	52
G52	58.7	64.7	153.8*	40.8	447.2*	13.6*	3.4	198.0*	15.9	90.7*
Grand Mean	57.3	63	130.5	38.2	294.8	11.2	3.6	166.6	20.6	65.1
CD	1.72	2.06	7.56	4.71	11.92	1.06	0.41	25.29	1.33	10.12

CD-Critical difference, *Significanct deviation from the mean based on CD values (p >0.05 level of significance)

Table-3 : Analysis of variance for various traits in maize genotypes.

Characters	Mean Sum of Squares		
	Replication (df = 2)	Genotype (df=51)	Error (df=102)
Days to 50% tasseling	6.78	53.95**	1.12
Days to 50 % silking	5.55	88.44**	1.62
Plant height	1.32	1454.96**	21.8
Cob height	15.71	298.96**	8.44
Leaf area	19.69	23681.28**	55.5065
Cob length	3.27	23.14**	0.42
Cob girth	0.77	0.29**	0.06
Number of kernels	2493.96	9543.12**	243.76
Test weight	0.28	21.46**	0.67
Single plant yield	400.62	2076.33**	39.03

**Significance at 1% level

Table-4 : Variability parameters for the ten quantitative traits among the 52 maize genotypes.

Characters	GCV	PCV	h^2	GAM
Days to 50 % tasseling	7.33	7.56	0.94	14.64
Days to 50 % silking	8.54	8.78	0.94	17.13
Plant height	16.74	17.12	0.95	33.7
Cob height	25.74	26.84	0.91	50.86
Leaf area	30.02	30.35	0.97	61.18
Cob length	24.54	25.22	0.94	49.17
Cob girth	7.72	10.44	0.54	11.75
Number of kernels	33.42	34.71	0.92	66.30
Test weight	13.88	14.44	0.92	27.50
Single plant yield	41.21	42.38	0.94	82.56

GCV-Genotypic coefficient of variance, PCV-Phenotypic coefficient of variance, h^2-Heritability in broad sense, GAM-Genetic advance as percentage of mean.

Table-5 : Association study among the ten characters of maize at genotypic level.

Characters	DT	DS	PH	CH	LA	CL	CG	NK	TW	SPY
DT	1	0.84*	-0.45*	-0.12	-0.09	-0.52*	-0.29	-0.46*	-0.27	-0.45*
DS		1	-0.53*	-0.22	-0.38*	-0.51*	-0.27	-0.42*	-0.38*	-0.55*
PH			1	0.47*	0.24	0.53*	0.31	0.45*	0.32*	0.60*
CH				1	0.42*	0.12	0.14	0.11	0.19	0.13
LA					1	0.26	0.25	0.19	0.22	0.36*
CL						1	0.48*	0.87*	0.32	0.76*
CG							1	0.59*	0.40*	0.46*
NK								1	0.34*	0.77*
TW									1	0.44*
SPY										1

*Significance at 5% level (p> 0.05)

and LA revealed highly significant variations among the genotypes (Table-1 and 2).

Similar results of significant variations for the studied characters were observed by (14). DT exhibited a range of 50.00 to 71.30 days and the overall mean was 57.33 days. Out of 52 genotypes, 19 genotypes had DT significantly lower than the mean value (Table-2). DS ranged from 53.7 to 81.00 days in with a population mean of 63.00 days. Among the genotypes, 19 genotypes had significantly lower value than the general mean. PH ranged from 80.8cm in G33 to 170.7cm in G48 with an average mean of 130.5cm. Among the 52 genotypes, 20 genotypes had significantly higher value than the general mean. CH ranged from 18cm in G47 to 60.1cm in G6 with a population mean value of 38.2cm. Among the genotypes, 19 genotypes had significantly lower value than the general mean. LA ranged from 164.2cm^2 in G45 to 573.9cm^2 in G20 with a general mean value of 294.8 cm^2. CL exhibited a range from 7.6cm in G41 to 19.3cm in G34 with an average value of 11.2cm. Among the genotypes16 genotypes had significantly higher value than the general mean. For CG the genotypes exhibited a range of 3.0cm in G40 to 4.2cm in G34 and G38 and the mean was 3.6cm. NK ranged from 98 kernels in G9 to 339.1 kernels in G34. The average TW was 20.6g and it ranged from 15.9g in G12 to 28g in G49. SPY ranged from 32.9g in G45 to 135.6g in G34 with an average of 65.1g. Among the 52 maize genotypes, 21 of them had significantly higher plant yield than the concerned general mean. Based on the mean performance the accessions identified to be superior for the ten quantitative characters are given in table-3.

Variability among the studies traits : It is apparent from the table-4, that there is almost perfect relation between PCV and GCV of each character. The higher magnitudes of both PCV and GCV show that these characters were under the influence of genetic control. So, the characters can be relied upon and simple selection is effective for further improvement. PCV had a wide range from 7.56% in DT to 43.92% in SPY. High PCV and GCV were observed for SPY, NK, LA, CH and CL. Low PCV and GCV were observed for DS and DT. This was similar to the findings of (15). The difference between the estimates of PCV and GCV were low for all traits showing low environmental effects in the expression of these characters (14). High heritability was observed for all the characters, except cob girth indicating that they were least influenced by the environmental effects. Cob girth showed moderate heritability, it shows there was a little environmental influence on the character. High heritability with moderate genetic advance was recorded for DT and DS. Moderate heritability with moderate genetic advance was observed for CG. These traits appear to be under the control of both additive and non-additive gene actions. In the present investigation, high heritability coupled with high genetic advance was observed for SPY, NK, LA, CH, CL and PH.

Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by pedigree method of breeding. Similar results of higher PCV, GCV, heritability and genetic advance as per cent of mean for LA, NK and SPY were observed by Al-Naggar et al., 2021.

Correlation among the studied traits : SPY had significantly positive association with NK, CL, TW, PH and CG, whereas SPY had significant negative association with DS and DT (Table-5) (5). Thesewere slightly in contrast to the findings of (9), where he did not observe any significant correlation of NK to SPY but he reported similar positive direct effects of DT for SPY. Single plant yield had non-significant positive association with CH and LA. LA had significant positive association with CH, whereas NK had significantly positive association with CL, TW, CG and PH. DT and DS had significant and nonsignificant associations with all the other studied traits. The other associations can be seen in Table 5. The results thus emphasized the need for selection based on plant type with higher NK, larger CL, optimum PH, high TW, larger LA, less DT, very low DS, low CH and optimum CG.

References

1. Kaushal M., Sharma R., Vaidya D., Gupta A., Saini H.K., Anand A. and K.C.D. (2023). Maize: an underexploited golden cereal crop. *Cereal Research Communications,* 51(1): 3-14.
2. Kaur M., Kaur G., Birwal P. and Kaur R. (2022). Storage of maize and its products. In Maize. CRC Press pp. 325-356.
3. Djalovic I., Kundu S., Bahuguna R.N., Pareek A., Raza A., Singla-Pareek S.L., Varshney R.K. (2024). Maize and heat stress: Physiological, genetic, and molecular insights. *The Plant Genome,* 17(1): e20378.
4. Anonymous (2024). Statista-The Statistics Portal for Market Data, Market Research and Market Studies. Available from: https://www.statista.com/. Accessed on: 20th January, 2024.
5. Bharathi P., Ravikesavan R., Yuvaraja A., Boopathi N.M., and Iyanar K. (2021). Genetic variability and correlation in maize inbred lines under irrigated and moisture stress condition. *Electronic Journal of Plant Breeding,* 12(3): 928-933.
6. Patil Y.G., Mevada K.D., Vaghela G.M., Bedis M.R. and Singh S.P. (2023). Effect of intercropping rabi maize (*Zea mays* L.) with chick pea (*Cicer arietinum* L.) on growth and yield under middle Gujarat condition. *Progressive Research: An International Journal,* 18(1): 23-29.
7. Neelima C., Sarankumar C., Sudha M., Ganesan K.N., Ravikesavan R. and Senthil N. (2020).Estimation of variability, heritability, genetic advance and assessment of frequency distribution for morphological traits in intercross population of maize.*Electronic Journal of Plant Breeding,* 11(2): 574-580.
8. Kulkarni S., Sharanappa P., Rathod A. and Biradar R. (2023). Performance of cotton (*Gossypium spp.*) under integrated crop management practices in Northern Dry Zone of Karnataka. *Progressive Research: An International Journal,* 18 (2): 139-141.
9. Aman J., Bantte K., Alamerew S., and Sbhatu D.B. (2020). Correlation and path coefficient analysis of yield and yield components of quality protein maize (*Zea mays* L.) hybrids at Jimma, western Ethiopia. *International Journal of Agronomy,* 1: 965-970.
10. Patel A.A., Patel J.M., Patel R.M., Gajjar K.D., Chaudhary D.R. and Soni N.V. (2023). Combining ability and gene action analysis for yield and yield attributing traits in kharif maize (*Zea mays* L.). *Frontiers in Crop Improvement*, 11(1): 31-36.
11. Musa T., Tanko U., Hassan U.T. (2016). Leaf area determination for maize (*Zea mays*), okra (*Abelmoschus esculentus*) and cowpea (*Vigna unguiculata*) crops using linear measurements. *Journal of Biology, Agriculture and Healthcare*, 6(4): 103–111.
12. Burton G.W. (1952). Quantitative inheritance in grasses. International Grassland Congress Proceedings 1: 277–283.
13. Sivasubramanian J. and Madhavamenon P. (1973). Genotypic and phenotypic variability in rice. *Madras Agric. J.*, 12: 15-16.
14. Magar B.T., Acharya S., Gyawali B., Timilsena K., Upadhayaya J. and Shrestha J. (2021). Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. *Heliyon*, 7(9): 726-731.