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Genetic Variability, Heritability and Genetic Advance for Yield and Quality Parameters among Sweet Potato [*Ipomoea batatas* (L.) Lam.] Genotypes

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ABSTRACT: Sweet potato [*Ipomoea batatas* (L.) Lam.] is one of the world's highest-yielding crops and is widely grown as a stable food in many tropical and subtropical regions. It is a dicotyledonous plant belonging to the family Convolvulaceae (also called morning glory family). It originated from South America. Sweet potatoes are thought to be naturally hexaploidy, with a chromosome number of 2n(6x) =90, making them a highly heterozygous crop. Research was conducted in a randomized block design with three replications during *rabi* 2023-24 at Main Vegetable Research Station of Anand Agricultural University in Anand. Analysis of variance revealed that highly significant differences among the genotypes were observed for all the characters under study. The PCV was higher than GCV for all the characters. High (> 20 %) genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were observed for all the characters studied except tuber moisture content, which indicates the existence of broad genetic base and it would be useful for further selection. High heritability (> 60 %) coupled with high genetic advance as per cent over mean (> 20 %) were recorded for all the characters studied indicated the prevalence of additive gene action for these traits. Thus, there is ample scope for improving these characters through direct selection in crop improvement programme.

Keywords: Sweet Potato, Genotypes, Variability, Heritability, Genotypic coefficient of variation, Phenotypic coefficient of variation.

INTRODUCTION

Sweet potato [*Ipomoea batatas* (L.) Lam.] is one of the world's highest-yielding crops and is widely grown as a stable food in many tropical and subtropical regions. It is a dicotyledonous plant belonging to the family Convolvulaceae (also called morning glory family). It originated from South America. Sweet potatoes are thought to be naturally hexaploidy, with a chromosome number of 2n(6x) =90, making them a highly heterozygous crop.

Globally, sweet potato is the sixth most important food crop after rice, wheat, potatoes and cassava. But in developing countries, it is the fifth most important food crop. China's dominance in sweet potato production is due to efficient farming practices, high-yield varieties and large-scale cultivation. At Global level sweet potato production was approximately 84.4 million metric tons. After China, the top sweet potato producing countries includes Malawi, Nigeria, Tanzania and Indonesia. In Indian, sweet potato production was reported at 1.2 million metric tons, it is mainly cultivated in Orissa, Bihar, Uttar Pradesh Madhya Pradesh, Maharashtra and Karnataka and approximately 80% of sweet potato is grown in Asia (Anonymous, 2022). In Gujarat, sweet potato cultivation is primarily concentrated in the southern regions, particularly around Navsari.

Genetic variation for any character is a basic requirement for its improvement by use of systematic breeding activities Genetic analysis reveals the genetic nature of the inheritance of tuber yield and yield components which is required to design efficient sweet potato improvement breeding strategy. Therefore, this research was conducted with the objective to assess the extent and nature of genetic variability and heritability among the sweet potato genotypes (Jones *et al.*, 1986).

Studies on high heritability and genetic advance in per cent mean for growth, yield and quality traits among sweet potato [*Ipomoea batatas* (L.) Lam.] genotypes indicated that yield per plot followed by β-carotene content, non-reducing sugars, yield per plant, leaf area, length of vine, length of petiole, number of tuberous roots per plant, number of branches per plant, ash content, tuber width, internodal length, total sugars, reducing sugars, and tuber girth exhibited high value of PCV and GCV (Narasimhamurthy *et al*., 2018).

Sharavati *et al*. (2018) noted on analysis of variance shows the presence of genetic variation among yield and growth parameters. High heritability along with higher genetic advance was observed for several growth parameters such as vine length, number of leaves per vine, inter nodal length, vine girth, chlorophyll content, leaf area, tuber length, tuber girth, weight of tuber, dry weight of vine, tuber yield per vine, total tuber yield per plot and marketable yield per hectare.

Tripathi *et al*. (2016) conducted research on twenty-nine genotypes of sweet potato [*Ipomoea batatas* (L.) Lam.] and observed that the higher phenotypic and genotypic coefficients of variation were recorded for a trait such as leaf area followed by yield per plant and leaves per vine. They also said that high heritability along with high genetic advance were estimates for leaf area (98 % and 68 %) followed by dry matter (97 % and 22.64 %) and yield per plant (78 % and 35 %).

An experiment was conducted on genetic variability in twenty four potato genotypes in order to find out the genetic variability. The phenotypic (PCV) and genotypic (GCV) coefficient of variation computed ranged from 0.90 to 46.43 per cent and 0.75 to 40.0 per cent respectively. Shoot dry mass weight, average number of tubers, average tuber weight, unmarketable tuber yield, small size tuber and large size tubers exhibited high value of phenotypic and genotypic coefficients of variation along with high heritability (Seid *et al*., 2020).

Mekonnen *et al.* (2021) conducted an experiment to determine the variability for yield and yield related traits in twenty four orange fleshed sweet potato [*Ipomoea batatas* (L.) Lam.] genotypes. High heritability along with high genetic advances as a percent of mean were observed for marketable root yield, skin color of root, beta carotene content of tuber, harvest index, vine length, vine inter-node length and above ground fresh weight. And these several characters are governed by additive gene action and for such traits selection would be feasible.

MATERIALS AND METHODS

The experiment was conducted from September, 2023 to March, 2024 at Main Vegetable Research Station, Anand Agricultural University, Anand.

The soil was a medium sandy loam. Well matured healthy and disease-free cuttings and vines of 30 genotypes of sweet potatoes were collected from Main Vegetable Research Station, Anand have been taken for investigation. The research experiment was laid out in a randomized complete block design (RCBD) with three replications. The treatments in each replication were allotted randomly by using random number table. Sweet potato cuttings which have 2-3 buds were planted in each replication at 60 cm × 20 cm spacing within the 3 m × 3 m plot size. All other recommended cultural practices and irrigation were applies as per needed. Plots were kept free from weeds by regular hand weeding. Five plants of each genotype from each replication were used for observations.

Statistical analysis. Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1957). Phenotypic and genotypic coefficients of variation were computed according to Burton and Devane (1953). Heritability in broad sense was estimated as per Weber and Moorthy (1952). Genetic advance was estimated as per the formula proposed by Johnson *et al.* (1955). The range of genetic advance as per cent of mean was classified as low (< 10 %), moderate (10–20 %) and high (> 20%) as recommended by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Analysis of Variance. The analysis of variance for different quantitative and qualitative characters among 30 genotypes of sweet potato genotypes was represented in Table 1. The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters studied *viz*., vine length, internode length, petiole length, tuber girth, tuber length, total number of tubers per plot, tuber yield per plot, harvest index, total soluble sugar, starch content, tuber moisture content, β-carotene, reducing sugar and non-reducing sugar indicates the presence of sufficient amount of variability in all the characters under study. These findings are in line with earlier reports of Sharavati *et al*. (2018); Narasimhamurthy *et al*. (2018) in orange fleshed sweet potato, Iranna *et al.* (2022); Pallavi *et al.* (2023).

Phenotypic and genotypic coefficient of variation (PCV and GCV). As per Table 2, higher magnitude of PCV and GCV (> 20 %) were observed in the present investigation. High (> 20 %) magnitude of GCV and PCV were observed for vine length, internode length, petiole length, tuber girth, tuber length, total number of tubers per plot, tuber yield per plot, harvest index, total soluble sugar, starch content, β-carotene, reducing sugar and non-reducing sugar. Indicating wider range of variability exhibited in these traits.

Similar results were also obtained by Singh *et al.* (2015); Prarthana *et al*. (2015); Tripura *et al.* (2016), Panigrahi *et al.* (2017); Sharavati *et al.* (2018). It indicates the presence of high variability in the genotypes for selection. The differences between PCV and GCV values were minimum for most of the traits studied and indicating that, traits under study were less influenced by environment.

Hence, these characters can be relied upon and selection can be practiced for further improvement.

Heritability: High heritability (> 60 %) coupled with high genetic advance as per cent of mean (> 20 %) were recorded for vine length, internode length, petiole length, tuber girth, tuber length, total number of tubers per plot, tuber yield per plot, harvest index, total soluble sugar, starch content, tuber moisture content, β-carotene, reducing sugar and non-reducing sugar.

These results suggested that the inheritance of such traits governed mainly by additive gene effects hence selection based on phenotypic performance may performed useful. As high heritability accompanied with high genetic advance as per cent mean indicates the prevalence of additive gene action, selection would be most effective. Similar results were noticed in earlier studies by Prarthana *et al.* (2015) for vine length, inter-nodal length, number of leaves and leaf area index in sweet potato. Ramachandra and Srinivasa (2017) for leaf area in sweet potato. For vine length, number of leaves, inter-nodal length results were similar to Sharavati *et al.* (2018) in sweet potato. Thus, there is an ample scope for improving these characters by direct selection. Similar results were also reported by Madawal *et al.* (2015); Ramachandra and Srinivasa (2017); Sharavati *et al.* (2018) for traits such as number of tubers per vine, length of tuber, girth of tuber, mean weight of tuber, yield of tuber per vine, yield of tuber per plot, yield of tuber per hectare in sweet potato. For tuber yield per vine, tuber yield per plot, results were similar to Tripathi *et al.* (2016); Narasimhamurthy *et al.* (2018). The research findings of Prajapati *et al.* (2020); Seid *et al.* (2020) were similar for number of tubers per plant.

Table 1: Analysis of variance (mean sum of squares) for different characters in sweet potato.

Sr. No.	Source of variation/characters	Replication	Genotypes	Error	S.Em±	CD @ 5%
	Degrees of freedom	**2**	**29**	**58**		
1.	Vine length (cm)	3.63	4076.56**	153.87	7.16	20.27
2.	Internode length (cm)	0.64	5.66**	0.316	0.32	0.92
3.	Petiole length (cm)	1.412	98.54**	1.756	0.77	2.17
4.	Tuber girth (cm)	8.60	84.96**	4.66	1.25	3.53
5.	Tuber length (cm)	3.01	69.56**	3.93	1.14	3.24
6.	Total number of tubers per plot	12.57	1632.99**	33.54	3.34	9.47
7.	Tuber yield per plot (kg/plot)	0.50	65.32**	1.34	0.67	1.89
8.	Harvest index (%)	105.30	436.18**	76.83	5.06	14.33
9.	Total soluble sugar (%)	0.01	3.99**	0.16	0.07	0.21
10.	Starch content (%)	0.257	48.63**	0.68	0.48	1.35
11.	Tuber moisture content (%)	27.63	144.11**	10.91	1.91	5.40
12.	β-carotene (mg/100g)	0.20	15.25**	0.10	0.19	0.53
13.	Reducing sugar (%)	0.01	0.66**	0.01	0.06	0.16
14.	Non reducing sugar (%)	0.004	3.80**	0.01	0.06	0.17

*, ** Significant at 5 and 1 % level, respectively

Table 2: Estimates of range, mean, components of variance, heritability and genetic advance for sweet potato genotypes.

Sr. No.	Character	Range	Mean	GV	PV	GCV (%)	PCV (%)	h^2 (%)	GAM %
1.	Vine length (cm)	67.53-217.20	154.25	36.16	38.22	23.44	24.78	89.47	45.67
2.	Internode length (cm)	5.78-7.70	4.71	1.33	1.45	28.36	30.77	84.94	53.84
3.	Petiole length (cm)	7.30-31.23	17.58	5.68	5.83	32.31	33.18	94.84	64.81
4.	Tuber girth (cm)	9.99-29.50	18.06	5.17	5.61	28.64	31.04	85.17	54.45
5.	Tuber length (cm)	10.18-31.00	20.61	4.67	5.07	22.07	24.05	84.78	43.05
6.	Total number of tubers per plot	9.67-104.67	38.91	23.08	23.80	59.34	61.18	94.08	72.3
7.	Tuber yield per plot (kg/plot)	5.80-20.96	7.78	4.61	4.76	59.34	61.18	94.08	55.4
8.	Harvest index (%)	14.72-55.91	36.53	10.94	14.02	29.96	38.38	60.93	48.17
9.	Total soluble sugar (%)	1.24-6.07	2.28	1.15	1.15	50.51	50.81	98.81	76.8
10.	Starch content (%)	17.07-11.50	8.87	3.99	4.08	45.05	46.00	95.90	90.88
11.	Tuber moisture content (%)	57.13-89.95	66.66	6.66	7.43	10.00	11.16	80.27	18.45
12.	β-carotene (mg/100g)	0.30-8.70	2.96	2.24	2.27	83.58	84.43	98.00	78.4
13.	Reducing sugar (%)	1.03-3.17	1.45	0.46	0.47	32.25	32.99	95.59	64.95
14.	Non reducing sugar (%)	0.24-4.73	1.19	1.12	1.12	94.24	94.62	99.81	79.5

GV- Genotypic variance**;** **PV**- Phenotypic variance; **GCV**- Genotypic co- efficient of variation; **PCV**- Phenotypic co-efficient of variation; **h^2** -Heritability

GAM- Genetic advance as percent over mean


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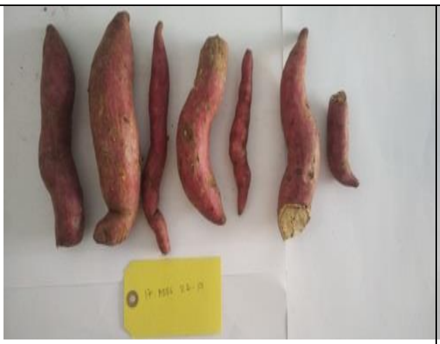
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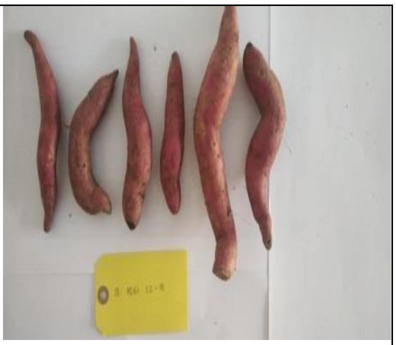
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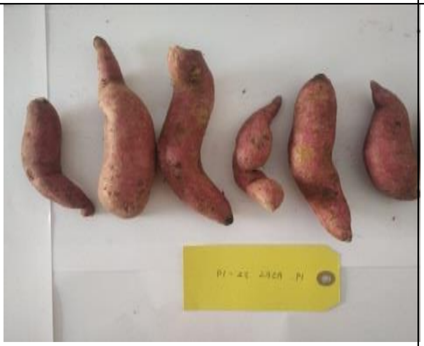
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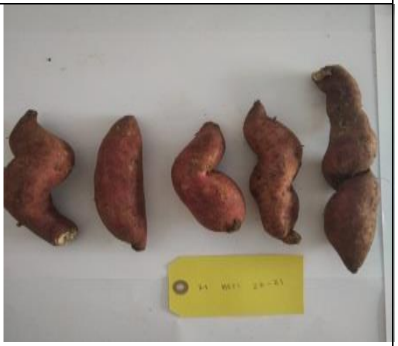
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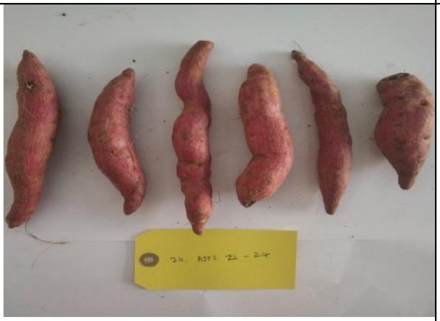
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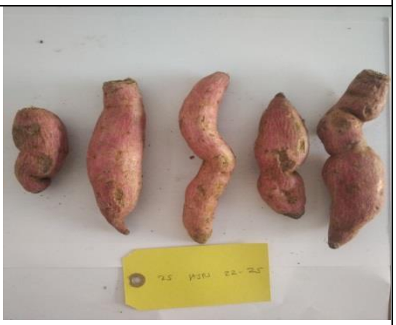
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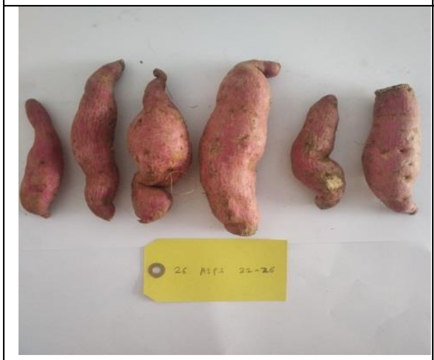
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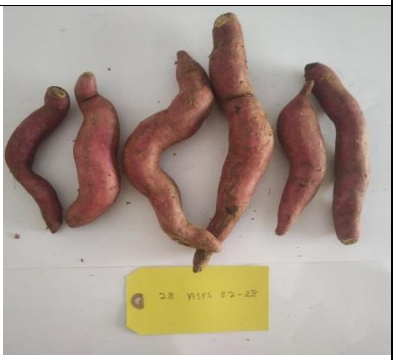
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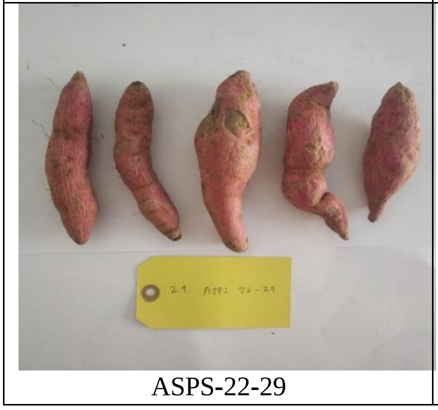
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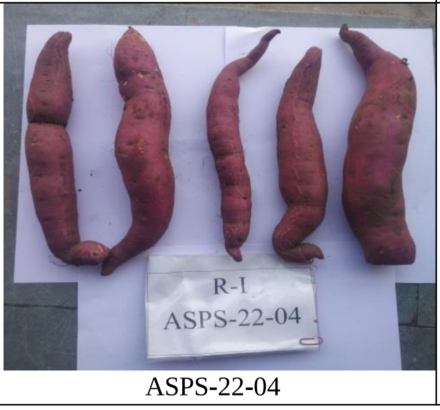

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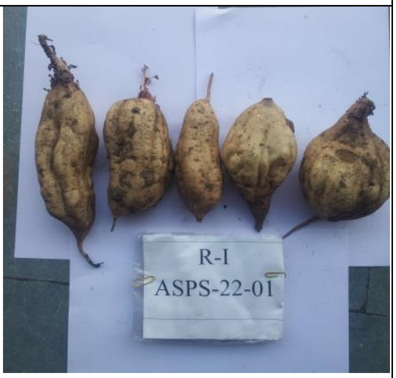

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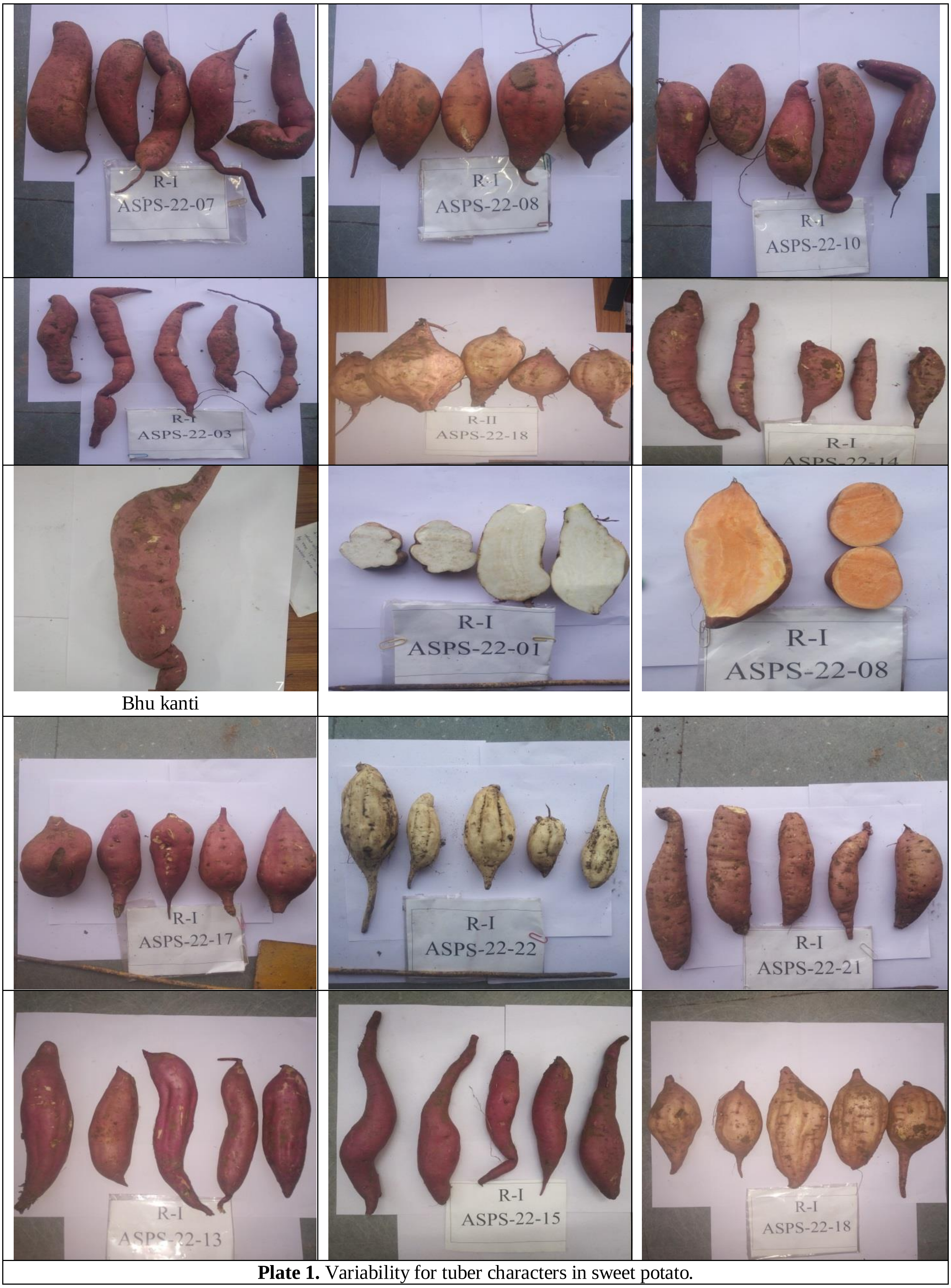

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Plate 1. Variability for tuber characters in sweet potato.

CONCLUSIONS

In conclusion, analysis of variance showed the presence of highly significant differences among the tested genotypes for the characters considered which indicates the existence of notable genetic variability among the genotypes for all the characters studied *viz.*, vine length, internode length, petiole length, tuber girth, tuber length, total number of tubers per plot, tuber yield per plot, harvest index, total soluble sugar, starch content, tuber moisture content, β-carotene, reducing sugar and non-reducing sugar indicates the presence of sufficient amount of variability in all the characters under study.

FUTURE SCOPE

Wide range of variability was present for all the characters studied. Hence, attention needs to be given for these traits during selection for improvement of tuber yield.

The genotypes included under the investigations may be evaluated at different agro-climatic zones of Gujarat to identify the most suitable genotype showing stability in performance for desirable characters.

REFERENCES

Anonymous (2022). Area and production retrieved from https://www.statista.com/statistics/68/asia-pacific-sweet-potato-production-by-country/#statisticContainer.

Burton, G. W. and Devane, D. E. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, *45*(10), 478-481.

Iranna, H., Hiremath, S., Ramachandra, N., Patil, V., Kachapur, R. and Shekharappa (2022). Morphological characterization of sweet potato (*Ipomoea batatas* (L.) Lam.) genotypes. *Biological Forum– An International Journal, 14*(1), 1204- 1209.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimation of genetic and environmental variability in soybean. *Agronomy Journal*, *47*(7), 477-483.

Jones, A., Dukes, P. D. and Schalk, J. M. (1986). Sweet potato breeding, In: M.J. Basset (Ed.). Breeding of vegetable crops, AVI Publishing Company, Westport, Conn., *1*(9), 35.

Madawal, S. L., Alloli., Madarkhandi, T. B. S. and Narasannavar, A. (2015). Genetic variability study in sweet potato (*Ipomoea batatas* L.) genotypes. *International Journal of Tropical Agriculture, 33*(2), 274-282.

Mekonnen, B., Gedebo, A. and Gurmu, F. (2021). Genetic variability for Yield and Yield Related Traits in Orange-fleshed Sweet potato genotypes evaluated at Hawassa, Ethiopia. *Agric*ulture *Forestry and Fisheries*, *10*(1), 1-6.

Narasimhamurthy, P. N., Patel, N. B., Patel, A. I. and Koteswara Rao, G. (2018). Genetic variability, heritability and genetic advance for growth, yield and quality parameters among sweet potato [*Ipomoea batatas* (L.) Lam.] genotypes. I*nternational Journal of Chemical Studies*, *6*(4), 2410-2413.

Pallavi, W., Ambresh, B. and Shantappa, T**.** (2023). Genetic Variability, heritability and genetic advance for growth, yield and quality parameters among orange-fleshed sweet potato [*Ipomoea batatas* (L.) Lam.] Genotypes. *Biological Forum – An International Journal*, *15*(1), 405-411.

Panigrahi, K. K., Pradha, J., Panigrahi, P. and Sarkar, K. K. (2017). Genetic variability, character association and path coefficient analysis of yield attributes for medium and late maturing potato cultivars. *International Journal of Current Microbiology and Applied Science, 6*(7), 2558-2566.

Panse, V. G. and Sukhatme, P. V. (1957). The application of genetics to plant breeding. IV. The inheritance of quantitative characters and plant breeding. *Journal of genetics*, *40*(3), 283-302.

Prajapati, D. R., Patel, R. N. and Gami, R. A. (2020). Study of genetic variability of tuber yield and storage related traits in potato (*Solanum tuberosum* L.). *International Journal of Current Microbiology and Applied Science, 8*(3), 188-192.

Prarthana, M., Ashok, P., Rout, M. K. and Dash, R. K. (2015). Genetic variability for yield and yield attributing characters in sweet potato (*Ipomoea batatas* (L.) Lam.). *Trends in Biosciences*, *8*(9), 2426-2429.

Ramachandra, M. K. and Srinivasa, V. (2017). Variability, heritability and genetic advance for quantitative and qualitative traits in potato genotypes under hill zone of Karnataka. *Green Farming, 8*(6), 1250-1253.

Seid, E., Mohammed, W. and Abebe, T. (2020). Genetic variability, heritability and genetic advance in totato (*Solanum tuberosum* L.) for Processing quality, yield and yield related traits. *International journal of Plant Breeding Crop Sci*ence, *7*(3), 928- 936.

Sharavati, M.B., V. Srinivasa, R.B. Anusha and Shubha, A.S. (2018). Genetic Variability Studies in Sweet Potato (*Ipomoea batatas* (L.) Lam.) Genotypes under Hill Zone of Karnataka, India. *International Journal of Current Microbiology and Applied Science, 7*(9), 850- 858.

Singh, D., Deo, C., Ram, C. N., Singh, A. and Gautam, D. K. (2015). Variability analysis for yield and yield attributes of sweet potato (*Ipomoea batatas* (L.) Lam.). *Environmental Life Science, 8*(2), 375-376.

Tripathi, V., Deo, C., Tyagi, N. and Singh, D. (2016). Genetic variability and association studies In sweet potato [*Ipomoea batatas* (L.) Lam.]. *International journal of Life Sci*ence, *11*(4), 3203-3206.

Tripura, A., Das, A., Das, B., Priya, B. and Sarkar, K. K. (2016). Genetic studies of variability, character association and path analysis of yield and its component traits in potato (*Solanum tuberosum* L.). *Journal of Crop and Weed* science, *12*(1), 56-63.

Weber, C. R. and Moorthy, H. R. (1952). Heritable and non-heritable relationship and variability of oil content and agronomic characters in the F_2 generation of soybean crosses. *Agronomy Journal*, *44*(7), 202-209.

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