



Advanced clones of sweet potato with high yield and good suitability for processing in three environments in Peru

Clones avanzados de camote con alto rendimiento y buena aptitud para procesamiento en tres ambientes del Perú

F. J. Gamarra¹ , J. Espinoza-Trelles² , S. E. Contreras-Liza^{3*} 



<https://doi.org/10.51431/par.v4i1.754>

Abstract

Objectives: To determine the production potential, processing quality and phenotypic stability of new sweet potato clones suitable for industry. **Methodology:** The research was carried out in three tropical environments in Peru: San Ramón (Junín), Oxapampa (Cerro de Pasco) and La Molina (Lima). Evaluations of the agronomic and processing characteristics were carried out to determine the genotype by environment interaction in 20 advanced clones of the International Potato Center, using a randomized complete block design with 2 replications for each location and combined analysis of variance for each variable. **Results:** In all localities, the magnitude of the genotype x environment interaction was significant ($P < 0.05$) for most of the variables under study. The advanced clones of CIP 102022.5, 199027.1 and 199076.4 obtained a high yield of starch per hectare. The clones that stood out for their yield were: 102021.5, 102022.5, 102028.7, 102025.3 and 103094.2; also for their high starch content, clones 102022.5, 199076.4 and 199024.7 **Conclusions:** There was a significant influence of the genotype x environment interaction on the agronomic and processing characteristics of the advanced sweet potato clones under evaluation, some of which can potentially be considered as new varieties for the industry.

Keywords: Sweet potato, genotype by environment interaction, yield, processing, starch content

Resumen

Objetivos: Determinar el potencial de producción, calidad para procesamiento y la estabilidad fenotípica de nuevos clones de camote con aptitud para la industria. **Metodología:** El trabajo se llevó a cabo en tres ambientes tropicales del Perú: San Ramón (Junín), Oxapampa (Cerro de Pasco) y La Molina (Lima). Se realizaron evaluaciones de las características agronómicas y de procesamiento para determinar la interacción genotipo por ambiente en 20 clones avanzados del Centro Internacional de la Papa, utilizándose un diseño de bloques completos al azar con 2 replicaciones por cada localidad y análisis de varianza combinado para cada variable. **Resultados:** En todas las localidades la magnitud de la interacción genotipo x ambiente fue significativa ($P < 0,05$) para la mayoría de las variables en estudio. Los clones avanzados del CIP 102022.5, 199027.1 y 199076.4 obtuvieron un alto rendimiento de almidón por hectárea. Los clones que sobresalieron por su rendimiento de raíces comerciales fueron: 102021.5, 102022.5, 102028.7, 102025.3 y 103094.2; también por su alto contenido de almidón, los clones 102022.5, 199076.4 y 199024.7. **Conclusiones:** Existió una influencia significativa de la interacción genotipo x ambiente sobre las características agronómicas y para procesamiento de los clones avanzados de camote en evaluación, algunos de los cuales pueden ser considerados potencialmente como nuevas variedades para la industria.

Palabras clave: Camote, interacción genotipo por ambiente, rendimiento, procesamiento, contenido de almidón

¹ Gerencia Regional de Desarrollo Económico. Gobierno Regional de Lima.

² Independent Advisor

³ Department of Agronomy, Universidad Nacional José Faustino Sánchez Carrión, Huacho, Perú

*Author to corresponding: scontreras@unjfsc.edu.pe

Introduction

Sweet potato (*Ipomoea batatas* Lam.) is a species that produces storage roots rich in carbohydrates and β -carotene (precursor of vitamin A) and its leaves are rich in protein for fodder. The roots also contain vitamins C, complex B and E, as well as potassium, calcium and iron. In crop statistics, sweet potato ranks seventh, after cassava, with an annual production of about 9 Mt and a cultivated area of 110 Mt (FAOSTAT, 2011). In most developing countries, it is a smallholder crop that tolerates a wide range of soil and climatic conditions and is grown with limited inputs (Lebot, 2010).

Increased awareness of sweetpotato's nutritional value is driving demand from health-conscious consumers worldwide and its potential use in a wide range of value-added human and animal products is widely recognized. As the public and private sectors learn more about the benefits and opportunities of sweet potato, they have invested more in crop improvement; therefore, our understanding of the importance and potential of the crop is increasing (Mwanga et al., 2017). People who consume sweet potatoes have their preferences in terms of color, texture and taste. Preferences generally lead to low adoption rates of newly released varieties, even though they have advantages such as high yield and resistance to pests and diseases. Understanding the high variability in quality traits is necessary to target new varieties for specific market segments (Swanckaert et al., 2021).

Gruneberg et al. (2005) observed genotypes with wide adaptation and high yields (about 19 to 22 t ha⁻¹) in three environmental groups that were derived from a cluster analysis. However, one specifically adapted genotype was observed to have a considerable yield advantage over all widely adapted genotypes in low yield environments (9 to 18 t ha⁻¹). The localities differed in their selection capacity for the yield of storage roots, concluding that it is possible to improve the yield and adaptability of sweetpotato in Peru, also recommending that marginal or low-yielding environments not be neglected in breeding efforts.

The genotype \times environment interaction in

Mozambique was highly significant for storage root and foliage yields, dry matter (DM) and beta-carotene content (Andrade et al. 2017). The storage root yield and DM content for 15 clones ranged from 14.9 to 27.1 t ha⁻¹ and from 24.8 to 32.8% DM. The content of beta carotene (BC), iron (Fe) and zinc (Zn) ranged from 5.9 to 38.4 BC, 1.6 to 2.1 Fe and 1.1 to 1.5 mg/100 g dry weight of Zn. The improved clones also met the culinary tastes required by local consumers in Mozambique (Andrade et al., 2017)

According to Vishalakshi et al. (2021), DM content had a positive and highly significant correlation with starch and flour yield and a significant positive correlation with sugar content. Flour yield exhibited the highest heritability, followed by DM content, sugars, and starch content. The findings of this study suggest that varieties suitable for processing can be identified among germplasm based on evaluation of processing characteristics; nine genotypes recorded DM contents higher than 30%.

Fresh root yield varied significantly due to environment (E), genotypes (G) and their interaction (G \times E) using biplot analysis of genotypes and genotype \times environment (Mahmud et al., 2021). The authors found that the G \times E interaction effects were greater than the effect of genotypes alone. In the first year, three varieties, 'BARI Mistialu-8', 'BARI Mistialu-12' and 'BARI Mistialu-14', were identified as stable and comparatively higher-yielding at nine locations.

The main effect of the genotypes and the G \times E interaction of the sweet potato storage root yield explained 82 % of the variation in the first principal component and visualized the genetic variations and the discrimination power of each environment and the genetic correlation between environments (Swanckaert et al., 2020). Using Finlay-Wilkinson stability analysis, the authors found stable yields within the target mega-environment from which the genotypes were selected, but with no adaptation to another region, providing justification for running separate programs that allow faster genetic progress in two large West African mega-environments.

Chipungu et al. (2018) showed, through ANOVA, significant differences in the yield of

storage roots of the genotypes between seasons and locations in Malawi. The effects of genotype, environment and genotype × environment significantly influenced the variation in storage root yield of cultivars. Yield variation was attributed primarily to environmental variability (62.86%), rather than genotype variation (14.25%) and G × E interactions (15.06%).

Eberhart & Russell (1966) proposed a mathematical model to measure the magnitude of the genotype x environment interaction of a variety in different environments, which allows combining the components of environmental variation and genotype x environment interaction in the analysis of variance. The aforementioned analysis allows defining the phenotypic stability parameters B_i (regression coefficient) and S^2_{di} (regression deviations) which can be used to predict the performance of a variety in different environments. Genotypes showing a regression coefficient $B_i = 1.0$ and a regression deviation $S^2_{di} = 0$ are considered stable. Francis and Kannenberg (1978) proposed a method to evaluate yield stability, which consists of group genotypes by their coefficient of variability across environments and by mean yield.

The objective of this study was to determine the production potential, processing quality and phenotypic stability of new sweet potato clones suitable for the industry in three tropical environments in Peru.

Methodology

Locations

The experiments were developed under field conditions in three tropical locations in Peru (Table 1).

Table 1
Locations where the experiments were carried out

Location	San Ramon (SR)	La Molina (LM)	Oxapampa (OX)
Department	Junin	Lima	Cerro de Pasco
Altitude, masl	800	240	1806
Latitude	11° 06' S	12° 05' S	10° 35' S
Length	75° 18' W	75° 57' W	75° 24' W

Characteristics of the experimental area

The characteristics of the experimental fields and the agronomic management in the three environments were similar. The total area per locality was 252 m², with a distance between rows of 0.90 meters and 0.25 between plants. The size of the experimental unit was 20 cuttings per treatment, with two replications for each location. The fertilization dose (kg/ha) was 80 N - 40 P₂O₅ - 120 K₂O. Irrigation in LM was applied by sprinkler, while in SR and OX it was by rain. The soil in LM had a neutral reaction (7.33), while in SR and OX, the reaction of the soil was acid (4.77).

Genetic material

Sweet potato genetic material was provided by CIP's Breeding and Genetic Resources Department, as indicated in Table 2.

Table 2
CIP advanced sweet potato clones under evaluation

Number	CIP code	Number	CIP code
1	102007.19	11	103079.53
2	102022.5	12	103094.23
3	102025.3	13	199024.7
4	102021.5	14	199027.1
5	102028.7	15	199035.7
6	102033.1	16	199062.3
7	102033.3	17	199069.1
8	102035.7	18	199071.8
9	102043.7	19	199076.4
10	102060.11	20	440031(Jewel)

Agronomic characteristics evaluated

Commercial weight of roots: storage roots between 5 cm and 8 cm in diameter were selected to be considered commercial roots. The roots chosen from the entire plot were weighed and subsequently, their value was projected in tons per hectare.

Total root yield: all storage roots, including

commercial roots, were weighed per plot and subsequently converted to tons per hectare.

Foliage weight: all the foliage of the plot was weighed and subsequently converted to tons per hectare.

Characteristics for processing

Dry matter: the roots were cut and weighed on a digital scale; a sample of 200 g of fresh weight was placed in an oven at 105 °C for 72 hours. Finally, the samples were weighed and their dry matter content was determined.

Starch content: a sample of about one kilo of roots obtained from the plots understudy was considered. These were washed, blended and poured into one-liter containers. After 5 to 6 hours, the water was drained with the help of a fine mesh and water was added proportionally to the excess, leaving it for approximately 2 to 3 additional hours, draining the water again. The starch that remained in the mesh was taken to an oven and allowed to dry for 24 hours at 105 °C; subsequently, it was weighed and the percentage of starch was determined.

Projection of starch yield per hectare: To estimate the projected yield per hectare of starch (t ha⁻¹), the average commercial production data for each advanced clone was multiplied by the specific starch content in each locality, using the following formula:

Starch yield= Commercial production (t ha⁻¹) x starch content (%)= t ha⁻¹

Characteristics for processing

The experimental design of randomized complete blocks was used in each location, where each of the 20 clones understudy was randomly distributed, with two replications per location. An analysis of variance was developed for each locality and then a combined analysis of variance, considering both the genotypes (advanced clones) and the environments as random factors. To carry out this analysis, the homogeneity of variances between localities was previously verified, for which the Bartlett test was used (Steel & Torrie, 1980). Differences between treatment mean for commercial root yield and starch content were evaluated by LSD-Fisher comparison tests. The variables under study were tabulated in the Excel program and then a verification of the assumptions of normality and independence was made; the data was processed using the statistical program SAS version 9.1.

Results and Discussion

Analysis of agronomic and processing traits

Significant differences in foliage weight, commercial yield and total yield were obtained between advanced clones in the three environments Oxapampa, San Ramón and La Molina (Table 3).

Table 3

Mean squares in ANOVA for agronomic characteristics by location

Source	GL	Oxapampa			San Ramon			La Molina		
		Foliage Weight	Commercial Performance	Total Yield	Foliage Weight	Commercial Performance	Total Yield	Foliage Weight	Commercial Performance	Total Yield
Yield	19	36.27**	71.28**	121.66**	33.54**	83.79**	96.3**	52.90**	125.61**	68.49**
Error	19	10.10	11.58	15.06	11.17	9.90	14.07	10.44	32.48	16.71
CV %		17.09	12.75	11.24	20.60	12.18	12.59	11.58	14.94	7.96

**Mean squares (MS) with high statistical significance ($P < 0.01$). GL, degrees of freedom, CV % coefficient of variation.

Advanced sweet potato clones for processing

For processing characteristics (dry matter and starch content), high statistical significance is shown among advanced clones in the three locations (Table 4).

The combined analysis of variance showed a strong interaction in all the agronomic characteristics and also for the processing attributes, with respect to the environment (Table 5).

Table 4
Mean squares in ANOVA for processing characteristics by locality

Source	GL	Oxapampa		San Ramon		La Molina	
		Dry material%	Starch Content%	Dry material%	Starch Content%	Dry material%	Starch Content%
Clones	19	16.50**	52.50**	13.96**	37.94**	19.96**	75.61**
Error	19	12.88	27.66	10.91	19.98	15.59	39.82
CV %		12.66	12.95	12.67	12.95	12.67	12.94

**Mean squares with high statistical significance ($P < 0.01$).

Table 5
Mean squares in Combined ANOVA by environments for agronomic and processing characteristics

Source	GL	Foliage Weight	Commercial Performance	Total Yield	Dry material%	Starch Content%
Environments (A)	2	1520**	1884**	5130**	261.24**	2034**
Blocks/A	3	8.54	64.13	36.37	5.46	16.14
Clones	19	35.06*	145.35**	170.86**	50.16**	162.83**
Clones/A	38	43.98**	67.67**	57.80**	0.133**	1.61**
Error	57	10.57	17.99	15.28	13.13	29.15
CV %		15.55	10.14	10.14	12.70	13.07

**Mean squares with high statistical significance ($P < 0.01$).

*Mean squares with statistical significance ($P < 0.05$).

Dry matter and starch contents are expressed as a percentage (%).

Analysis of agronomic and processing traits

Table 6 shows the advanced clones with the highest commercial yield in each environment; some advanced clones stood out for this attribute

among them, 102021.5, 199027.1 and 102060.11, statistically surpassing the control (cv. Jewel) and with a relatively stable production between localities; the commercial yield in these clones fluctuated between 35 and 40 t ha⁻¹.

Table 6

Commercial performance of advanced sweetpotato clones in three environments (t ha⁻¹)

No.	CIP code	Oxapampa	San Ramon	La Molina	Mean
1	102021.5	37.17 a	35.25 ba	49.80 a	40.74 a
2	199027.1	32.83 ba	33.00 ba	44.80 abc	36.88 bc
3	102060.11	29.67 bc	35.83 to	39.48 abcd	34.99 bc
4	102028.7	32.00 bar	24.00 edf	48.00 abc	34.67 bcd
5	102022.5	27.50 bcd	35.42 ba	40.09 ebdac	34.34 bcd
6	103094.23	37.00 a	23.67 edf	41.20 ebdac	33.96 bcd
7	Jewel	26.75 bcde	29.00 cbd	42.67 bdac	32.81 becd
8	103079.53	29.33 bc	24.50 edf	43.91 bdac	32.58 becd
9	102033.3	23.09 cdefg	26.00 edc	43.47 bdac	30.85 edf
10	199035.7	17.50 g	32.34 ba	40.13 ebdac	29.99 fed
11	102033.1	17.84 g	35.17 ba	36.40 ebdc	29.80 fed
12	199076.4	33.59 ba	20.34 egf	32.54 edf	28.82 feg
13	199062.3	26.83 becd	19.34 gf	40.08 ebdac	28.75 feg
14	199071.8	21.17 ged	16.50 g	43.20 bdac	26.96 fg
15	102025.3	20.17 ged	20.50 egf	40.00 ebdac	26.89 fg
16	102043.7	28.67 bc	18.50 gf	33.07 edcf	26.75 fg
17	102007.19	27.17 bcde	19.25 gf	28.14 f	24.85 hg
18	199024.7	21.34 ged	23.17 edf	29.54 ef	24.68 hg
19	102035.7	20.00 g	23.00 egdf	30.00 ef	24.33 hg
20	199069.1	24.50 geed	22.00 egf	16.20 g	20.90 hg

^{abcdefg}Advanced clones with the same letter in the vertical direction are statistically equal ($P < 0.05$)

Advanced sweet potato clones for processing

In relation to the starch content in sweet potato roots, it was found that clones 102022.50, 199076.40 and 199024.70 statistically

outperformed the control (cv. Jewel) with a higher starch content (between 18.33 to 19.86%), in relative to the rest of the genotypes.

Table 7

Starch production in advanced clones of sweet potato in three environments

No.	CIP code	Oxapampa	San Ramon	La Molina	Mean
1	102022.50	18.89 abcde	21.11 a	19.58 ab	19.86 bac
2	199076.40	20.84 a	20.09 abc	17.77 abc	19.57 a
3	199024.70	16.50 efg	21.39 a	17.10 bcd	18.33 bac
4	199027.10	19.46 ab	20.90 ab	14.37 def	18.24 bac
5	102033.10	21.13 a	19.68 abc	13.71 efg	18.17 bac
6	199069.10	17.49 b c d e f	19.68 abc	15.35 cdef	17.51 bac
7	199071.80	19.68 ab	17.60 cd	14.92 cdef	17.40 bac
8	199062.30	19.22 abcd	18.37 abcd	14.12 defg	17.24 g
9	103094.20	17.01 cdefg	19.20 abc	15.19 cdef	17.13 bac
10	102060.10	14.73 ghij	17.90 bcd	14.28 def	15.64 defg
11	102021.50	16.70 kl	15.09 ef	15.12 cdef	15.64 efg
12	199035.70	15.48 fghi	15.93 def	14.25 gh	15.22 def
13	102043.70	13.45 hij	12.98 efg	17.88 ab	14.77 bac
14	102035.70	16.91 defg	15.75 abc	11.16 fg	14.61 bac
15	Jewel	15.16 fghi	14.94 ef	13.34 def	14.48 gf
16	103079.50	13.68 hij	15.98 def	11.98 efg	13.88 dc
17	102007.20	12.28 jk	11.66 fg	14.79 cdef	12.91 back
18	102025.30	12.84 ij	13.62 ef	9.75 hi	12.07 edf
19	102028.70	8.83 kl	10.50 g	11.09 gh	10.14 egdf
20	102033.30	7.96 m	11.02 fg	9.95 fgh	9.64 edc

abcdefg Advanced clones with the same letter vertically are statistically equal ($P < 0.05$)

Projection of yield per hectare of starch

Regarding the projection of starch yield, the advanced clones 102022.5, 199027.1 and 199076.4 can be considered as the most promising for the industry, exceeding the

threshold of 8 t ha⁻¹ (between 8.44 and 8.93 t ha⁻¹), estimated values taking into account the commercial production of storage roots and the starch content per se (Table 8); the control variety (cv. Jewel) was below starch production per hectare (4.97 t ha⁻¹).

Table 8

Projected starch yield of advanced clones for environments (t ha⁻¹)

No.	IPC code	Oxapampa	San Ramon	La Molina	Mean
1	102033.30	2.54	2.86	4.95	3.45
2	103079.53	4.04	3.85	4.14	4.01
3	102025.30	2.32	4.58	5.03	3.98
4	102028.70	3.71	3.50	5.84	4.35
5	102007.19	3.29	2.32	8.02	4.54
6	Jewel	3.89	3.66	7.37	4.97
7	103094.23	4.50	4.61	7.33	5.48
8	102033.10	6.51	4.06	5.73	5.43
9	102060.11	3.62	6.35	6.91	5.63
10	102035.70	7.22	3.75	5.83	5.60
11	199069.10	6.31	3.92	6.84	5.69
12	102043.70	4.79	4.35	9.40	6.18
13	102021.50	6.31	4.01	8.58	6.30
14	199035.70	6.98	4.98	7.51	6.49
15	199062.30	5.98	7.02	7.36	6.79
16	199024.70	5.90	6.06	8.84	6.93
17	199071.80	7.93	6.69	9.09	7.90
18	199076.40	8.90	6.89	9.52	8.44
19	199027.10	8.72	9.22	8.14	8.69
20	102022.50	8.08	7.63	11.07	8.93

When considering the most appropriate environment, apparently the one that shows the greatest possibility of phenotypic differentiation would be chosen, but in turn the environment with the lowest general average would also be considered. Oxapampa is the locality where there has been a greater breadth of yields; the excesses of rain probably caused the roots to tend to be longer and not commercial. Additionally, Oxapampa had low night temperatures (12 °C), with an influence on root filling.

The environment of La Molina was favored with a higher yield of roots and starch. La Molina soil had a neutral reaction while the Oxapampa and San Ramón soils showed an acid reaction, which possibly had a negative response to normal root development.

In foliage weight, a greater variation was found in Oxapampa than in San Ramón and La Molina, in that order. The differences are due in good proportion to the high rainfall of Oxapampa, which can be considered as a factor of greater interaction with the genotype.

Possibly, the interaction with the environment will depend on the greater or lesser degree to which a genotype can efficiently develop physiological processes (Andrade et al., 2017). In La Molina, more favorable conditions were found for the development of the sweet potato crop, while in conditions of greater humidity the yields tend to decrease as in San Ramón or even more drastically if it is associated with low temperatures and high precipitation, which strongly influenced in root and foliage yield, as occurred in Oxapampa.

Phenotypic stability

As previously indicated, there was a significant interaction in sweet potato genotypes for the agronomic and processing characteristics, which coincides with what was found by other authors (Andrade et al., 2017; Chipungu et al., 2018). According to the results obtained, it can be indicated that there was an influence of the environment on both the agronomic and processing characteristics. The presence of interaction complicates inferences about the genetic value of any clone, as considered by Grüneberg et al. (2005).

Notwithstanding the difficulty represented by the genotype-environment interaction, it was possible to identify some clones that presented better phenotypic stability. Using a simple methodology such as the decomposition of the sources of variance that involves the genotype, it was possible to determine which of the advanced clones could be more stable. In this way, according to the variability of the interaction effects, it was established that the clones with the highest stability were: 102033.3, 102025.3, 102022.5 and 102021.5. These clones that simultaneously present favorable characteristics, such as yield, stability and good processing characteristics, may be candidates for release as new varieties. Although the GxE interaction is a challenge in the genetic improvement process, it serves to identify and eliminate those less stable clones (Swanckaert et al., 2020).

The advanced clones that were evaluated in the present investigation, have good productive capacity and high stability, allowing costs per hectare to decrease significantly, since they potentially present themselves as higher-yielding genotypes, in addition to being considered with greater added value if they are used for the industry as fried chips, flour or starch.

In this way, to characterize the sweet potato varieties from the point of view of their industrial use, study the factors of agricultural production that affect industrial processing, sowing times, cultivation and fertilization regions, among others, and use the information of other countries in the field of new varieties, can serve to give value to the new potential varieties.

Conclusions

A significant influence of genotype by environment (GxE) interaction was found on both agronomic and processing characteristics in 20 advanced sweetpotato clones. According to the commercial yield, the clones with a yield greater than 35 t ha⁻¹ stood out: 102021.5, 199027.1, and 102060.11. The clones that obtained a foliage weight greater than 22 t ha⁻¹ and can potentially be considered as forage sweetpotato varieties were: 102033.1, 199024.7 and 102060.11. The clones with a starch content greater than 18%

were: 102022.5, 199076.4, and 199024.7. The advanced clones of CIP 102022.5, 199027.1 and 199076.4 can be considered as promising for the industry and potentially as new varieties since they obtained a high yield of starch per hectare and have processing characteristics and good phenotypic stability.

Acknowledgements

To the International Potato Center (CIP) for the financing and technical support in the development of the research; Jorge Espinoza Trelles for supervising the research and designing the experiments in the three locations; to Universidad Nacional José Faustino Sánchez Carrión for promoting research as the main author's Agricultural Engineering thesis.

References

- Andrade, M. I., Ricardo, J., Naico, A., Alvaro, A., Makunde, G. S., Low, J., Ortiz, R., & Grüneberg, W. J. (2017). Release of orange-fleshed sweetpotato (*Ipomoea batatas* [L.] Lam.) cultivars in Mozambique through an accelerated breeding scheme. *The Journal of Agricultural Science*, 155 (6), 919-929. <https://doi.org/10.1017/S002185961600099X>
- Chipungu, F., Changadeya, W., Ambali, A., Saka, J., Mahungu, N., & Mkumbira, J. (2018). Adaptation of sweet potato [*Ipomoea batatas* (L.) Lam] genotypes in various agro-ecological zones of Malawi. *African Journal of Biotechnology*, 17 (16), 531-540. <https://doi.org/10.5897/AJB2017.16352>
- Eberhart, S. A & Russell, W. A. (1966). Stability parameters for comparing varieties. *Crop Science*. 6, 26–40.
- FAOSTAT (2011) FAOSTAT data. Available online: <http://faostat.fao.org/>
- Francis, TR, & Kannenberg, LW (1978). Yield stability studies in short-season maize. I. A descriptive method for grouping genotypes. *Canadian Journal of Plant Science*, 58 (4), 1029-1034. <https://doi.org/10.4141/cjps78-157>
- Grüneberg, WJ, Manrique, K., Zhang, D., & Hermann, M. (2005). Genotype × environment interactions for a diverse set of sweetpotato clones evaluated across varying ecogeographic conditions in Peru. *Crop Science*, 45 (6), 2160-2171. <https://doi.org/10.2135/cropsci2003.0533>
- Mwanga ROM, Andrade MI, Carey EE, Low JW, Yencho GC, Grüneberg WJ (2017) *Sweetpotato* (*Ipomoea batatas* L.). In: Genetic Improvement of Tropical Crops. Springer, Cham. https://doi.org/10.1007/978-3-319-59819-2_6
- Lebot, V. (2010) *Sweet Potato*. In: Bradshaw J. (eds) Root and Tuber Crops. Handbook of Plant Breeding, vol 7. Springer, New York, NY. https://doi.org/10.1007/978-0-387-92765-7_3
- Mahmud, A. A.; Hassan, M. M.; Alam, M. J.; Molla, M. S. H.; Ali, M. A.; Mohanta, H. C.; Alam, M. S.; Islam, M. A.; Talukder, M. A. H.; Ferdous, M. Z.; Amin, M. R.; Hossain, M. F.; Anwar, M. M.; Islam, M. S.; Dessoky, E. S.; Hossain, A. (2021). Farmers' Preference, Yield, and GGE-Biplot Analysis-Based Evaluation of Four Sweet potato (*Ipomoea batatas* L.) Varieties Grown in Multiple Environments. *Sustainability*, 13 (7), 3730. <https://doi.org/10.3390/su13073730>
- Steel, R. G. D., & Torrie, J. H. *Bioestadística: principios y procedimientos*. McGraw-Hill. Bogotá, Colombia.
- Swanckaert, J., Akansake, D., Adofo, K., Acheremu, K., De Boeck, B., Eyzaguirre, R., ... & Campos, H. (2020). Variance component estimates and mega-environments for sweetpotato breeding in West Africa. *Crop science*, 60 (1), 50. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7079561/>
- Swanckaert, J., Gemenet, D., Anglin, N.L., & Grüneberg, W. (2021). *Sweet Potato* (*Ipomoea batatas* (L.) Lam.) Breeding. In *Advances in Plant Breeding Strategies: Vegetable Crops* (pp. 513-546). Springer, Cham. https://doi.org/10.1007/978-3-030-66965-2_12
- Visalakshi, C., Anil, SR, Sheela, MN, Hegde, V., Jyothi, AN, & Sreekumar, J. (2021). Genetic variation for important processing traits and identification of potential parents for developing hybrid clones suitable for processing in sweet potato (*Ipomoea batatas* L Lam). *South African Journal of Botany*, 141 , 255-264. <https://doi.org/10.1016/j.sajb.2021.04.005>