



Article

Sweet Potato Varietal Selection Using Combined Methods of Multi-Trait Index, Genetic Gain and Stability from Multi-Environmental Evaluations

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Abstract: Adaptation to several environmental conditions is a challenge for breeders for producing new varieties. Breeders select genotypes which show higher performance according to desired traits compared to the average of a large segregant population. In several crops, the selection index is mainly based on traits such as yield, quality, adequate plant architecture, etc. Therefore, multi-trait selection allows for the identification of genotypes that integrally exhibit a better profile and stability, in addition to the dissection of promising varieties based on their superiority in an evaluated population. In this paper, a multi-trait index included in an R tool named *CropInd* was used to estimate the agronomic performance of 19 sweet potato genotypes in multi-environmental evaluations (three cycles and eight locations). Here, the multi-trait index incorporated variables such as total and commercial fresh root yield, along with survival percentage, which were used in this study. Simultaneously, stability and genetic gain analysis were included to select superior sweet potato genotypes. Results showed that the *CropInd* script is a suitable and convenient tool for genotype selection based on multi-trait and multi-environmental data. Indexes for specific environment and general behavior (combining multi-environments) were the main output used for genotype selection. Multi-trait selection index, stability, and genetic gain analysis assisted the phenotypic selection performed by breeders. This study resulted in the selection of 0113-672COR as new variety for the Colombian Caribbean region due to its multi-trait performance and stability.

Keywords: genotype by environment interaction; selection index; phenotype; plant breeding



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1. Introduction

Climate change impacts agriculture through the reduction in crop productivity, becoming a threat to global food security [1]. This is true particularly in the tropical regions of the world, which are suffering from drought, heat, and floodings. Climate models suggest that global warming will increase the frequency of the Niño Southern Oscillation (ENSO) phenomenon [2,3] and tropical precipitation will decrease in certain areas along the margins of the convection zones, which already suffer from water scarcity [4]. Other expected changes are the increase in carbon dioxide (CO₂) in the air and also the temperature of the environment. Recent evidence shows that temperature has been raised by an average of 0.6 ± 0.2 °C since 1900 [5]. All these challenges require a novel agricultural model that integrates breeding strategies and different agronomic practices to deal with the main plant stressors which include drought, salinity, elevated CO₂, and temperature (low and high), among others [1,5]. Therefore, to develop and select high yielding varieties, adaptation to

challenging and specific climate conditions has to be recognized. Generally, plant breeding primarily depends on the presence of substantial genetic variation to address maximum genetic yield potential among crops and exploitation of this variation through effective selection for improvement [6]. However, adaptation to climate fluctuation and stress conditions is very a critical issue for current breeding programs [1] and evaluations under a wide range of environmental conditions confirm phenotypic plasticity of promising genotypes, through which agronomic relevance is expressed in the increase in yield productivity. Therefore, it can be considered one of several strategies to tackle climate change [7].

Agrobiodiversity is key for making production systems more resilient [8], and its use in evaluations under multi-environmental conditions is an important step in the selection process for ideotypes identification [1]. Sweet potato (*Ipomoea batatas* (L.) Lam) is an herbaceous species from Convolvulaceae family, and *I. batatas* is the only species with economic importance as crop [9]. Sweet potato is a staple crop and is cultivated worldwide using more than 7 million hectares and producing 88 million tons [10]. It is a versatile species that can adapt to a wide range of environmental conditions [11]. However, in Colombia, this crop remains neglected and underutilized. Despite its nutritional root quality and broad adaptability, it is still considered an alternative crop [9,12], although one which is being introduced into commercial agricultural production systems.

Agronomic evaluation of sweet potato cultivars in multiple locations evidence that the main source of variation is caused by environment effect [13]. This high plasticity of the sweet potato plant is evidenced also in its adaptation to several conditions, including adaptation at different altitudes, from 0 to 3000 m above sea level (masl) [14,15]. Sweet potato is sensitive to environmental variation, as shown by Genotype \times Environment ($G \times E$) interaction studies in agronomic traits such as total root yield, commercial root yield, dry matter content, vine length, storage root length, storage root girth, marketable storage root number per plant, weight of above ground biomass, and harvestable index [16–19]. Generally, the environmental contribution to total variation in sweet potato yield is greater than that of the genotype [17] and only some quality traits are relatively more stable [12,19]. Only a few cases have identified genotypes with stable performance in different locations (wide adaptability) [20–22], while mostly specific adaptability is shown [23,24].

Currently, several bioinformatic tools have been established with the primary aim of aiding breeding decisions in early planning and implementation phases through combination of breeding strategies such as phenotypic selection, genomic selection, and speed breeding with genomic information with a high degree of flexibility [25,26]. However, plant ideotype is produced in the mind of experienced breeders. Plant ideotype generally integrates a group of desirable traits which can be measured independently in the field. Therefore, selection procedure under current challenging environmental conditions should be systematic and dynamic to better understand the genotype-by-environment interaction in multi-environment trials [27,28]. Multi-trait selection was proposed for plant breeding many years ago [29]. The assignment of subjective economic weight to each trait is performed by the breeder and has been a simple method to analyze. Similar indexes have been proposed for the selection of multiple traits, and an example of its use in defining a plant ideotype was presented. The use of eigenvalues in the analysis helps reduce multicollinearity, and this approach eliminates the need for assigning weights [30,31]. However, a selection index (SI) has been a way to simplify the selection process by integrating the information from various desired traits found within a plant ideotype into a single estimated value. Traits such as root yield, dry matter content, plant type, etc., are computed in an SI equation to produce estimated values for specific environmental conditions or a multi-environmental response. In cassava, a SI with weight based on the breeder's judgement is used; however, the variables should be standardized before in order to avoid a problem due to the range of magnitude among selected variables. The standardization is performed through classical statistical formulas that use total average and standard deviation [32]. Furthermore, the SI is calculated for selected variables, assigning them optimal weightings based on informed judgment [33].

Selection analysis complemented by $G \times A$ interaction studies allows for the identification of cultivars with high yields for a given region and identification of ideal cultivation conditions. Among the multivariate statistical techniques, AMMI (Additive Main Effects and Multiplicative Interactions) determine the stability of genotypes to adjust their productive capacity to the widest environmental variation [34]. The $G \times A$ interaction is the factor that most interferes in the identification of specific clones for specific environments, which limits the precision in yield estimation [23,35].

The aim of this study was to combine multi-trait selection index, stability, and genetic gain analysis to assist phenotypic sweet potato selection from multi-environmental conditions determining their specific or wide adaptability, developing and validating the R software-based script *CropInd* to facilitate this multi-trait and multi-environmental data analysis.

2. Materials and Methods

This study included the evaluation of several sweet potato genotypes according to two last steps of the breeding cycle to produce new varieties. Therefore, field data collection to evaluate agronomic performance under multi-environmental conditions was conducted and further analysis included development and validation of R software script to support genotype selection.

2.1. Plant Material

Nineteen sweet potato genotypes which are part of a working collection of Agrosavia were evaluated in this study. Although there is evidence of some genotypes being introductions from other countries, all the genotypes were collected in farms of sweet potato producers. The genotypes evaluated in this study were the following: 0113-672COR, 0113-668VAL, 0113-657VAL, 0113-664VAL, 0113-671VAL, 0113-634VAL, 0113-670VAL, 0113-660VAL, 0113-663VAL, 0113-674VAL, 0113-665VAL, 0113-659VAL, 0113-673VAL, 0113-669VAL, 0113-656COR, 0113-662VAL, 0113-658COR, 0113-666VAL and CRIOLLA, a traditional clone, was used as a check.

2.2. Growth Conditions

Sweet potato genotypes were established in eight localities in sub-humid region in the Colombian Caribbean coast in crop cycles evaluated during years 2014, 2015, and 2016 (Table 1). Agroclimatic conditions in this region provide an excellent environment to develop the commercial sweet potato crop [9]; however, for this, improved varieties were needed. According to breeding process in this population, during 2014 and 2015, a uniform yield test (UYT) was established using the mentioned nineteen genotypes under conditions of Codazzi, Corozal, Cerete, Carmen-B, and Riohacha. Furthermore, genotype selection based in their agronomic performance resulted in nine genotypes, which were evaluated during 2016. This step named the agronomic evaluation test (AET) was established at Jagua, Codazzi, Corozal, Cerete, Carmen-B, Tolu, and Dibulla.

Table 1. Characteristics of localities in this study.

Features *	Units	Corozal	Codazzi	Jagua	Cerete	Carmen B	Dibulla	Tolu	Riohacha
Coordinates		9°17'34.38" N, 75°20'9.00" W	10°00'01.2" N, 73°15'22.4" W	10°31'59.0" N, 73°06'09.6" W	8°50'27.47" N, 75°48'27.56" W	9°42'50.8" N, 75°06'26.9" W	11°12'45.2" N, 73°24'20.2" W	9°29'21.6" N, 075°34'12.9" W	11°07'15.05" N, 72°59'22.87" W
Landscape		Plain	Piedmont	Hills	Plain	Mountains and Piedmont	Hills	Hills and valley	Hills
Mean temperature	(°C)	26.9	28.1	27.6	27.7	26.9	28.3	27.6	28.3
Annual rainfall	(mm)	1127	1560	1122	1264	1179	1426	1129	588
Soil characteristics									
Soil texture		Sandy-loam	Sandy-loam	Silty-loam	Clayed	Clay-loam	Sandy-loam	Sandy	Sandy
pH		7.21	7.84	8.18	6.99	7.18	5.72	6.03	6.71
OM	%	1.31	1.66	1.46	2.87	2.55	1.08	3.07	1.22
P	mg/kg	15.78	150.30	119.9	10.09	28.83	21.90	20.38	29.83
S	mg/kg	3.32	4.17	14.35	8.77	2.32	3.91	6.2	17.57
Ca	cmol(+)/kg	17.29	13.04	29.80	14.79	21.74	6.69	18.68	9.68
Mg	cmol(+)/kg	5.77	1.14	2.32	6.11	6.69	1.45	8.81	2.40
K	cmol(+)/kg	0.30	0.31	1.15	0.50	0.20	0.23	0.92	0.24
Na	cmol(+)/kg	0.40	0.32	0.39	0.20	0.29	0.20	2.18	0.80
CEC	cmol(+)/kg	23.76	14.80	33.66	21.59	28.92	8.56	30.59	13.14
EC	dS/m	0.19	0.61	0.42	0.92	0.20	0.56	0.3	0.92
Fe _{av}	mg/kg	13.20	27.19	38.41	44.16	46.15	54.45	77.05	31.77
Cu _{av}	mg/kg	1.28	2.87	1.85	5.90	1.29	2.06	3.15	1.29
Mn _{av}	mg/kg	<1.00	3.20	11.71	<1.00	13.22	1.74	16.82	2.96
Zn _{av}	mg/kg	<1.00	1.28	1.32	1.04	1.20	1.55	3.08	1.32
B _{av}	mg/kg	0.23	0.21	1.89	0.27	0.51	0.22	0.26	0.49
Harvest dates		20152016	20152016	2016	2015A2015B2016	20152016	2016	2016	2015

* pH water: soil 2.5:1.0, organic matter (MO), phosphorus (P) Bray II, sulfur (S) phosphate monocalcic, Calcio (Ca), Magnesium (Mg), Potassium (K) and Sodium (Na), cation exchange capacity (CEC), electric conductivity (CE) relation 2.5:1.0, available Iron (Fe), Copper (Cu), Manganese (Mn), Zinc (Zn), and Boron (B).

2.3. Experimental Design

Genotypes were established under experimental conditions of two steps in a conventional breeding scheme [35]: a uniform yield test (UYT, also named multi-local trials) and an agronomic evaluation test (AET, following regulations in Colombia for new varieties development). Experimental units using the UYT were established under randomized complete block design (RCBD) with three replications. Each plot consisted of four rows, each measuring five meters in length, with a planting density of 25,000 plants per hectare (spaced at 1 m between rows and 0.4 m within rows). This resulted in a total of 48 plants per plot. Using the AET, experimental units followed same experimental design (RCBD) with four replications, with each plot with five rows, each measuring five meters in length and with the same previous density, which resulted in a total number of 60 plants per plot. At 120 days after planting, survival percentage was estimated from established versus initially planted plants. Forage yield was estimated from a sample taken in a 1 m² square. Furthermore, yield components (number and weight) were determined for plant from five plants per experimental unit. Total and commercial roots (first category) from experimental unit were weighted to further estimate total and commercial yield, respectively.

2.4. Phenotypic Selection Index and CropInd Implementation

Breeders select genotypes according to their superiority in desired traits regarding average population performance. To consider multiple traits in the selection process, a selection index (SI) is routinely used in some crops. The selection index in this study applied to sweet potato was based in traits such as total fresh root yield (TFRY), high commercial fresh root yield (CFRY), and good establishment represented by survival percentage (SP).

In order to simplify the multi-traits analysis across selection process, an R software-based script *CropInd* was developed. *CropInd* required a data frame, where the first three columns of excel file should be ordered as environment (it could combine location and year in a single column), genotype, and repetition. The following columns included any traits collected in the field, and in this case, were TFRY, CFRY, and SP (in the file more traits can be added). Selected desired traits that were used for SI together with their respective assigned judgment weight were added in the first two rows of the excel file.

The breeder's selection index was established based on the breeder's expertise. Specific traits were chosen and assigned optimal weights based on informed judgment [33], demonstrated as follows:

$$SI: (TFRY \times 10) + (CFRY \times 25) + (SP \times 5)$$

The values in the selection index formula depend on their contribution to improve the characteristics of a breed genotype; thus, in traits in which meaning is related to detriment of genotype, the assign value should be subtracted, then the negative weight should be added, such root cracking in sweet potato, which is a desired target. Desired targets are represented by a lower number (1 desired and 5 undesired character). In general, a SI is defined as a linear function of two or more phenotypes weighted according to their relevance, economic importance, or selection objectives. The SI can be written as:

$$SI = b_1P_1 + b_2P_2 + \dots + b_nP_n$$

$$SI = \sum b_k P_k$$

where, P_k is the phenotypic value of the k^{th} trait to select and b_k corresponds to their assigned weight.

Initially, *CropInd* calculates standardized values for each trait as follows:

$$P_k = \frac{(p_k - \overline{p_k})}{sd(p_k)}$$

where, P_k is the standardized phenotypic value, p_k corresponds to the individual phenotypic value, \bar{p}_k is the phenotypic mean in the sample, and $sd(P_k)$ is the standard deviation from entire sample (*General Selection Index*). SI for specific environment is calculated through standardization as follows:

$$P_{ke} = \frac{(p_k - \bar{p}_{ke})}{sd(p_{ke})}$$

where, P_{ke} is the phenotypic value, p_k corresponds to the individual phenotypic value, \bar{p}_{ke} is the phenotypic mean in specific environment, and $sd(P_{ke})$ is the standard deviation from specific environment. Further, averaged SI for each genotype is estimated from single values in replicates.

Subsequently, the phenotypic values for each individual are transformed into individual selection indices for the entire evaluated population, as well as for each environment specified by the user.

To improve the user-friendliness during analysis performance, a start file named *Start CropInd* was designed. To perform the *CropInd* analysis in an R session, the following instructions can be followed:

```
source("CropInd.R") # Load CropInd functions
data = read.table("File.txt", header=T, na.string=".", skip=2) # Read data
IS = read.table("File.txt", na.string=".", nrow=2) # Read Selection Index Weights
IdxRun(data, IS) # Perform Selection Index estimation.
```

The first row of *File.txt* must provide information about desired traits and the second row must provide the weights based on trait importance or selection criteria. The third row contains the column names of data, and subsequently rows provide the sample information and traits values to evaluate (Supplementary File S1). There is no limit in the number of traits to evaluate, as well no limits in environments or genotypes. The user can include experimental replicates (column Replicates in *File.txt*) with a number to differentiate each. In case of absence of replicates, user must include this column using a number one for each sample in this column.

2.5. AMMI and Data Analysis

A combined analysis of variance was used to test genotype and environment effects and magnitude of $G \times E$ interaction. AMMI analysis was used to determine main or additive genotype and environmental effects, and multiplicative effects for $G \times E$ interaction. Tukey's multiple comparison test was used for mean comparison between genotypes and locations ($\alpha = 0.01$). Statistical Analysis System (SAS, version 9.4) y R (version 3.3.0) were used to perform the analysis.

3. Results

3.1. Agronomic Behavior of Evaluated Genotypes

The genotypes evaluated in uniform yield trials (UYT) showed a differential behavior through different environments for their yield components (Table 2). In general, all the genotypes evaluated were superior to the Criolla cultivar, local variety. This was true in all the variables, with the exception of root weight per plant. The 0113-672Cor, 0113-668Val, and 0113-634Val genotypes had the highest number and weight of roots per plant, with a survival rate greater than 66%. However, these genotypes have significantly lower forage production than that evidenced in other materials with lower root yield.

The 0113-672Cor, 0113-657Val, 0113.668Val, and 0113-634Val genotypes had higher tuberization percentages ($\geq 90\%$), commercial root yield (≥ 8 Tn/ha), and total roots (>10 Tn/ha) compared to the rest of the evaluated genotypes (Table 3).

The influence of environmental conditions on root number, weight per plant, commercial root yield, and total root yield was evidenced, and dry environments such as Riohacha negatively affected all parameters. Environmental conditions found in other locations affected differentially the performance of genotypes during evaluated crop cycles (Tables 2 and 3). The results showed that sweet potato genotypes respond depending on

the soil and environmental conditions in which they are cultivated. The soil textures found in locations where this study was conducted show different physio-chemical conditions, especially related to nutrient availability and water holding capacity (WHC) [36]. Fine textures such as clayed and clay-loam soils show higher water holding capacity than sandy soils. The Cerete and Carmen de Bolivar locations showed clayed tendency and a high level of organic matter. Corozal, Codazzi, and Riohacha had sandy soils. Similar nutrient composition was found and only values of phosphorous content and sulfur were significantly higher at Codazzi and Riohacha, respectively; meanwhile, Riohacha showed the lower values of calcium, magnesium, potassium, and cation capacity exchange. Conditions of high content of organic matter produce a significant reduction in storage roots, and this phenomenon was observed in locations such as Cerete and Carmen Bolivar. The obtained results in Corozal and Codazzi, locations with sandy soils, demonstrated that temporal water deficiency promotes root starch accumulation which was related to survival and tuberization capacity but not to foliar biomass production.

Pearson correlation confirmed that genotypes with high yield of commercial roots also have a high survival rate ($\hat{r} = 0.39$), tuberization ($\hat{r} = 0.57$), number ($\hat{r} = 0.55$), and weight of roots per plant ($\hat{r} = 0.81$). The positive correlation, as previously reported, confirmed that these traits are important root yield components (Ebem et al. 2021). This was contrary to genotypes with a high forage yield which showed reduced root formation, with a lower root number ($\hat{r} = -0.21$) and weight ($\hat{r} = -0.21$) per plant (Table 4).

Table 2. Mean values of survival, forage yield, and yield components in 19 sweet potato genotypes evaluated by UYT across eight environments.

Genotype/Location	Survival (%)	Forage Yield (Tn/ha)	Roots Number/P	Roots Weight/P (gr)
Genotypes				
0113-672COR	70.05 ± 24.49	23.11 ± 14.48	4.03 ± 1.71	0.88 ± 0.58
0113-657VAL	61.7 ± 27.06	22.09 ± 13.78	3.3 ± 1.14	0.85 ± 0.47
0113-668VAL	67.63 ± 23.91	27.16 ± 18.63	2.61 ± 0.75	0.9 ± 0.65
0113-634VAL	66.11 ± 25.58	27.44 ± 10.6	2.5 ± 0.95	0.68 ± 0.37
0113-664VAL	65.24 ± 21.77	23.73 ± 11.37	2.41 ± 0.98	0.65 ± 0.39
0113-671VAL	60.87 ± 17.1	20.93 ± 11.71	1.83 ± 0.62	0.67 ± 0.28
0113-670VAL	66.97 ± 23.81	25.58 ± 11.76	2.45 ± 0.78	0.58 ± 0.43
0113-663VAL	65.38 ± 24.02	31.62 ± 15.42	2.14 ± 1.23	0.39 ± 0.4
0113-660VAL	68.36 ± 24.43	21.13 ± 12.56	2.01 ± 0.85	0.5 ± 0.46
0113-673VAL	63.77 ± 21.37	30.07 ± 17.78	1.75 ± 0.95	0.33 ± 0.37
0113-674VAL	65.61 ± 18.96	25.93 ± 13.87	1.69 ± 1.29	0.3 ± 0.39
0113-659VAL	57.97 ± 27.96	28.7 ± 17.09	2.27 ± 1.33	0.32 ± 0.29
0113-665VAL	66.68 ± 24.46	28.56 ± 17.47	2.04 ± 1.25	0.38 ± 0.41
0113-669VAL	60.55 ± 18.83	19.45 ± 13.03	0.91 ± 0.8	0.24 ± 0.3
0113-656COR	49.67 ± 18.17	19.02 ± 11.02	1.06 ± 0.95	0.25 ± 0.52
0113-658COR	67.67 ± 18.46	22.08 ± 13.74	1.13 ± 0.92	0.11 ± 0.13
0113-662VAL	58.99 ± 19.4	22.17 ± 13.57	0.7 ± 1.34	0.1 ± 0.19
0113-666VAL	66.45 ± 25.61	23.65 ± 15.25	0.68 ± 1.04	0.07 ± 0.14
CRIOLLA	49.25 ± 21.63	14.5 ± 6.47	1.5 ± 0.6	0.41 ± 0.22
LSD	13.52	6.29	0.92	0.32
Locations				
Codazzi_2014	60.13 ± 10.71	53.13 ± 12.51	ND	ND
Codazzi_2015	62.05 ± 18.36	17.65 ± 7.98	2.9 ± 1.15	1.02 ± 0.53
Corozal_2015	83.88 ± 18.35	29.1 ± 7.39	1.95 ± 1.42	0.53 ± 0.5
Cerete_2015a	78.45 ± 12.57	39.69 ± 6.54	1.88 ± 2.01	0.26 ± 0.29
Cerete_2015b	79.46 ± 10.67	25.62 ± 4.94	1.79 ± 0.99	0.48 ± 0.47
Cerete_2014	23.08 ± 0	7.17 ± 2.08	2.91 ± 0.95	0.64 ± 0.33
Carmen-B_2015	62.89 ± 16.48	25.32 ± 5.8	1.57 ± 1.06	0.28 ± 0.23
Riohacha_2015	42.17 ± 16.42	12.43 ± 8.14	1.79 ± 0.6	0.2 ± 0.25
LSD	7.57	3.50	0.46	0.16

LSD: least significant difference determined by Tukey's test ($p < 0.01$).

Table 3. Mean values of tuberization, commercial, and total yield in 19 sweet potato genotypes evaluated by UYT across eight environments.

	Tuberization (%)	Commercial Root Yield (Tn/ha)	Total Root Yield (Tn/ha)
Genotypes:			
0113-672COR	91.29 ± 22.44	10.28 ± 8.44	16.49 ± 11.11
0113-657VAL	90.9 ± 20.51	8.54 ± 5.44	13.98 ± 10.22
0113-668VAL	89.56 ± 14.26	7.99 ± 6.44	13.64 ± 13.95
0113-634VAL	94.03 ± 10.04	6.32 ± 4.75	10.31 ± 8.06
0113-664VAL	86.37 ± 13.73	6.02 ± 5.47	9.71 ± 8.56
0113-671VAL	76.67 ± 22.26	6.49 ± 3.94	9.06 ± 5.3
0113-670VAL	87.03 ± 16.05	5.35 ± 3.94	8.52 ± 8.13
0113-663VAL	72.67 ± 34.85	3.37 ± 5.6	6.79 ± 8.41
0113-660VAL	65.03 ± 31.46	4.15 ± 4.5	6.45 ± 5.97
0113-673VAL	56.13 ± 31.49	2.17 ± 3.31	5.28 ± 5.68
0113-674VAL	57.95 ± 35.48	3.18 ± 5.5	4.79 ± 5.93
0113-659VAL	68.37 ± 32.42	2.65 ± 3.62	4.56 ± 5.49
0113-665VAL	66.03 ± 35.25	3.04 ± 5.57	4.55 ± 5.88
0113-669VAL	34.9 ± 33.4	1.72 ± 2.35	3.12 ± 4
0113-656COR	36.78 ± 30.67	1.71 ± 3.53	2.5 ± 4.64
0113-658COR	27.36 ± 20.97	0.49 ± 0.86	2.3 ± 3.91
0113-662VAL	14.61 ± 27.75	0.79 ± 1.87	1.46 ± 2.42
0113-666VAL	14.5 ± 20.62	0.46 ± 1.22	1.06 ± 1.9
CRIOLLA	44.69 ± 36.76	2.01 ± 2.01	2.29 ± 2.16
LSD	21.91	3.15	4.55
Locations:			
Codazzi_2014	ND	ND	13.41 ± 9.23
Codazzi_2015	76.57 ± 30.55	9.1 ± 6.9	12.7 ± 9.58
Corozal_2015	73.71 ± 35.32	5.27 ± 5.74	13.1 ± 13.06
Cerete_2015a	51.49 ± 38.41	2.74 ± 3.69	3.97 ± 5.16
Cerete_2015b	62.89 ± 30.1	5.35 ± 6.41	6 ± 6.81
Cerete_2014	98.89 ± 6.09	3.28 ± 2.02	6.18 ± 4.38
Carmen-B_2015	64.83 ± 37.44	3.33 ± 3.62	4.32 ± 3.99
Riohacha_2015	39.68 ± 32.39	0.76 ± 1.09	0.76 ± 1.09
LSD	11.17	1.60	2.53

LSD: least significant difference determined by Tukey's test ($p < 0.01$).**Table 4.** Pearson's correlation between forage yield, yield components, and total yield in 19 genotypes evaluated by UYT across eight environments.

Variable	n	Forage Yield (Tn/ha)	Roots Number/P	Root Weight per Plant (gr)	Survival (%)	Tuberization (%)	Commercial Root Yield (Tn/ha)
Roots number/P	340	−0.21 ***					
Root weight per plant (g)	339	−0.21 ***	0.64 ***				
Survival (%)	339	0.45 ***	0.04	0.10			
Tuberization (%)	339	−0.06	0.71 ***	0.60 ***	0.15 *		
Commercial root yield (Tn·ha)	336	−0.03	0.57 ***	0.82 ***	0.33 ***	0.57 ***	
Total fresh root yield (Tn·ha)	338	0.10	0.55 ***	0.81 ***	0.39 ***	0.57 ***	0.89 ***

*** ($p < 0.0001$), * ($p < 0.01$).

3.2. Stability and Selection of Promising Genotypes through UYT Using CropInd

Stability and adaptability of evaluated sweet potato genotypes by UYT was estimated following AMMI methodology, where the main effects of genotypes and environments, along with the additive effects, were determined for total fresh root yield (Table 5). The main effect in this trait resulted from environment, followed by genotype and further by $G \times E$ interaction.

Table 5. Combined analysis of variance for total yield in 19 genotypes evaluated by UYT across eight environments.

Source of Variation	Degrees of Freedom	Total Fresh Root Yield
Genotype	18	386.1 ***
Environment	7	1136.7 ***
Rep	2	192.4 *
Genotype * Environment	98	84.04 ***
Error	228	17.05
PC1		219.7 *** (54.3%)
PC2		114.5 *** (25.9%)
PC3		50.24 *** (10.3%)

The values correspond to the mean square in the evaluated traits. *** ($p < 0.0001$), * ($p < 0.01$).

The biplot graphics showed that environments were contrasting and, unlike the environments Corozal_2015 and Codazzi_2015, in most of the localities and years, the genotypes showed a relatively stable behavior; in fact, most of genotypes evaluated were located near origin (Figure 1A). However, genotypes with greater stability were also those that had a lower yield. The genotypes 0113-672Cor, 0113-657Val, 0113-668Val, 0113-634Val, and 0113-664Val exhibited higher yield (TFRY). Notably, genotypes 0113-657Val and 0113-664Val exhibited major stability and their high yield was associated to localities such as Corozal_2015 and Codazzi_2015 (Figure 1b).

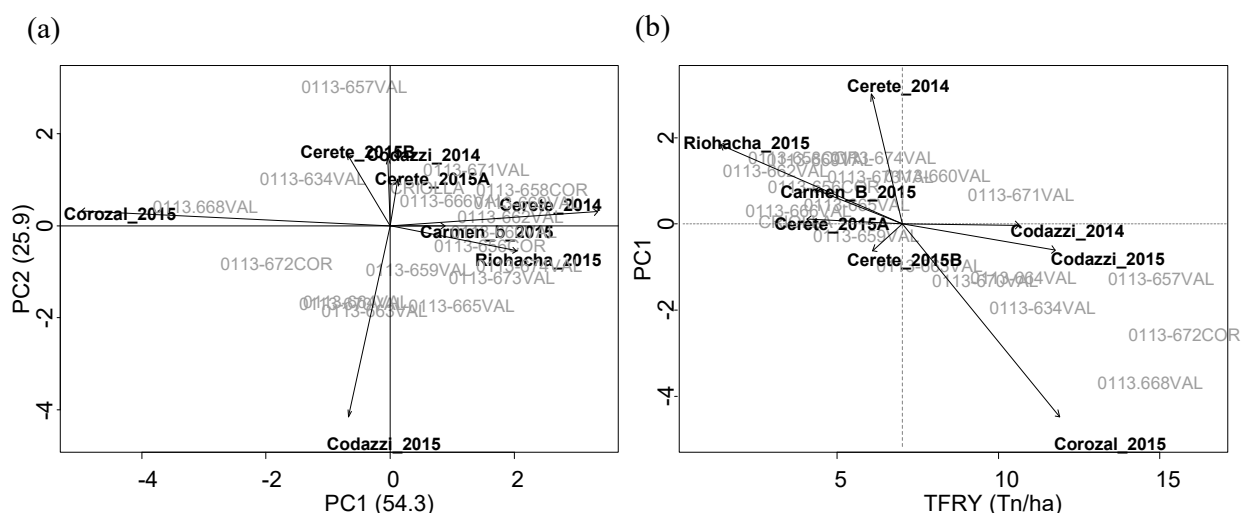


Figure 1. Additive main effects and multiplicative interaction (AMMI) and selection index in selected genotypes evaluated by UYT. (a) Biplot AMMI obtained for total fresh root yield (TFRY) of 19 genotypes evaluated at 120 DAP in seven environments. (b) Biplot AMMI for TFRY vs. PC1 in 19 genotypes evaluated at 120 DAP in seven environments.

3.3. Validation of CropInd R Software Script Using Multi-Trait Selection Index

The database utilized for estimating selection indexes in *CropInd* was constructed in the form of an Excel file. The first three columns of excel file were ordered as follows: environment, genotype, and repetition, and desired traits and respective assigned judgment weight were added to the first two rows. Furthermore, a *.txt file was read by start *CropInd* script under R software following the steps described in the Materials and Methods section. *CropInd* is a tool based in the programming language of R software, which has been developed to calculate a semiautomatically selection index in crops during the breeding process. Using several instructions, it was possible to perform a basic analysis to define standardized values per data point. This was performed using the general experimental mean and standard deviation, with each data point representing a replicate. This ensured all variations were considered during in the analysis. *General selection index* was calculated

according to assigned-judgment weight and computed with a single average per genotype using all multi-environmental data. To estimate “environment” Selection Index, standardized values per data point were calculated using each environmental mean and standard deviation. Then, “environment” Selection Index was calculated according to assigned judgment weight and an average per genotype was calculated in each environment.

The results using selection index (SI), which were built and performed using the *CropInd* tool, demonstrated consistent output after giving a value for the relative importance of characteristics that impact crop yield. These were classified as TFRY (assigned weight: 10), commercial fresh root yield CFRY (assigned weight: 25), and survival percentage SP (assigned weight: 5). The SI was calculated for each location by a UYT and integrated within each location to obtain a general SI (Table 6). All these data allowed for a ranking with genotypes to be built according to integrated agronomic performance in general (multi-environment) and specific environmental conditions. The best ranked genotypes, according to the general SI, were 0113-672COR (26.88), 0113-668VAL (20.16), 0113-657VAL (19.78), and 0113-664VAL (13.13). These results agreed with the genotypes that demonstrated better yield across the evaluated localities and demonstrated adaptability to environment with better conditions for crop production (Corozal and Codazzi).

Table 6. Selection index scale obtained per general (multi-environment) and specific environment analysis for 19 genotypes.

Genotype	General	Codazzi_2015	Corozal_2015	Carmen_B_2015	Cerete_2015a	Cerete_2015b	Riohacha_2015
0113-672COR *	26.88	55.12	29.2	14.63	16.74	56.1	4.32
0113-668VAL *	20.16	21.06	55.01	11.57	29.07	43.82	22.04
0113-657VAL *	19.78	-7.59	33.22	63.29	32.04	59.7	-1.91
0113-664VAL *	13.13	35.39	25.31	21.43	4.21	2.23	39.71
0113-671VAL *	8.1	-7.28	-1.31	30.14	22.92	19.24	9.7
0113-634VAL *	7.64	-5.45	20.46	3.75	49.62	16.91	21.07
0113-670VAL	7.21	20.38	22.23	26.98	-2.64	-15.88	28.43
0113-660VAL *	6.84	6.74	-2.03	29.89	7.73	-9.96	29.52
0113-663VAL	0.72	26.71	-1.15	-13.96	-15.86	-14.7	9.18
0113-674VAL	0.53	20.4	-20.49	-19.09	-13.22	-17.18	35.75
0113-665VAL	-0.23	28.08	-13.58	-21.05	-16.04	-21.35	1.22
0113-659VAL	-5.46	-0.41	1.9	-25.36	-9.62	-12.46	-0.04
0113-673VAL	-6.26	-0.08	-13.38	-15.37	-18.5	-10.81	-2.57
CRIOLLA(check)	-6.84	-25.28	-	-	-	-12.87	-17.32
0113-669VAL	-8.45	-18.46	-23.32	-27.81	-17.35	-0.3	-4.7
0113-656COR *	-13.7	-16.79	-23.09	-31.58	-11.89	-17.24	-13.09
0113-662VAL	-14.65	-16.16	-22.05	-25.76	-20.84	-27.05	5.91
0113-658COR	-16.86	-20.32	-22.9	-19.28	-21.14	-22.19	2.24
0113-666VAL	-17.72	-31.17	-24.63	-21.97	-19.5	-24.93	45.06
TFRY (Tn/ha)	6.07 ± 8.12	11.84 ± 10.55	7.85 ± 9.19	3.41 ± 3.97	3.62 ± 5.02	5.77 ± 6.52	0.81 ± 1.57
CFRY (Tn/ha)	3.92 ± 5.77	9.13 ± 8.28	3.09 ± 3.97	2.34 ± 3.29	2.74 ± 4.11	5.16 ± 6.26	0.83 ± 1.63
RC (%)	8.73 ± 24.42	10.03 ± 24.15	5.27 ± 19.98	1.85 ± 12.56	7.47 ± 21.74	8.78 ± 23.67	21.53 ± 37.41
SURV (%)	64.34 ± 22.73	69.47 ± 22.98	67.48 ± 15.57	62.99 ± 16.80	70.94 ± 17.79	81.71 ± 13.02	47.77 ± 22.05

Values indicate average ± standard deviation. Color scale shows lower values as red color, intermediate values as orange and higher values as yellow. * marks selected genotypes for next evaluation cycle.

The potential results obtained by the appropriate statistical procedures executed in *CropInd* have demonstrated it to be a useful and feasible tool for selecting individuals (genotypes) with good performance under different environmental conditions. During the analysis of multi-environmental trials, the experimental design is a core component because of its control of plot-plot variability [37]. Therefore, *CropInd* takes into account the standard deviation for each genotype as an indicator of variability.

3.4. Agronomic Performance of Selected Genotypes in AET

Following the sweet potato breeding scheme, using a UYT evaluation of sweet potato genotypes, eight (8) genotypes were selected that were evaluated using the AET. Yield components data obtained from the AET cycle were analyzed to determine the agronomic behavior of evaluated genotypes and this data was combined with some previous UYT data to increase the number of environments. The genotypes 0113-672COR, 0113-664VAL, and 0113-660VAL showed a higher survival percentage compared to the rest of genotypes in most of the evaluated environments (Table 7). The 0113-672COR genotype exhibited high

root number and weight per plant, as well as tuberization percentage, when compared with the rest of evaluated genotypes. Genotypes such as 0113-668VAL and 0113-634VAL showed high forage production; however, their commercial root production was significantly lower in comparison to the other genotypes.

Table 7. Mean values of survival, forage yield and yield components in nine sweet potato genotypes from combined analysis of UYT and AET.

	Survival (%)	Forage Yield (Tn/ha)	Roots Number/P	Root Weight per Plant (gr)
Genotypes:				
0113-672COR	78.87 ± 15.6	37.3 ± 22.82	3.96 ± 1.16	1.16 ± 0.69
0113-664VAL	78.88 ± 10.69	33.12 ± 11.79	2.65 ± 1.24	0.8 ± 0.39
0113-660VAL	77.21 ± 15.23	35.04 ± 13.12	2.53 ± 0.82	0.78 ± 0.4
0113-668VAL	74.27 ± 14.2	45.02 ± 26.47	2.35 ± 0.83	0.81 ± 0.39
0113-657VAL	70.54 ± 19.05	37.87 ± 24.75	3.12 ± 0.97	0.81 ± 0.38
0113-634VAL	74.18 ± 13.46	42.41 ± 19.65	2.53 ± 0.83	1.89 ± 7.8
0113-656COR	66.72 ± 18.96	29.35 ± 14.25	1.77 ± 0.95	0.59 ± 0.55
0113-671VAL	59.69 ± 23.57	33.04 ± 15.58	1.74 ± 0.7	0.56 ± 0.33
CRIOLLA	70.32 ± 16.94	32.7 ± 14.48	2.03 ± 0.54	0.66 ± 0.35
LSD	5.91	5.83	0.46	1.77
Locations:				
Jagua_2016	83.52 ± 7.76	44.78 ± 11.32	2.89 ± 1.03	1.25 ± 0.54
Codazzi_2016	89.24 ± 6.52	45.94 ± 9.94	2.65 ± 0.77	1.08 ± 0.3
Codazzi_2015	64.31 ± 16.53	21.51 ± 9.52	3.03 ± 1.07	1.13 ± 0.52
Corozal_2015	68.61 ± 6.73	20.82 ± 4.56	2.36 ± 1.28	0.71 ± 0.35
Corozal_2016	65.34 ± 19.64	28.37 ± 6.25	2.79 ± 1.09	2.24 ± 8.8
Cerete_2016	76.23 ± 19.92	58.62 ± 27.53	2.73 ± 1.07	1.02 ± 0.62
Cerete_2015b	80.7 ± 9.49	23.91 ± 4.54	2.35 ± 0.8	0.69 ± 0.34
Cerete_2015a	72.35 ± 10.73	36.32 ± 6.39	2.98 ± 1.36	0.5 ± 0.2
Carmen-B_2016	86.83 ± 9.44	61.94 ± 19.3	1.73 ± 0.9	0.46 ± 0.21
Carmen-B_2015	63.86 ± 11.84	22.75 ± 5.33	1.78 ± 0.9	0.35 ± 0.18
Tolu_2016	63 ± 19.87	34.18 ± 11.1	2.64 ± 1.24	0.79 ± 0.29
Dibulla_2016	66.51 ± 12.62	38.99 ± 9.17	2.8 ± 1.4	0.73 ± 0.36
Riohacha_2015	47.98 ± 16.18	10.72 ± 7.38	1.89 ± 0.46	0.19 ± 0.15
LSD	7.68	7.59	0.60	2.31

LSD: least significant difference determined by Tukey's test ($p < 0.01$).

Similarly, the 0113-672COR genotype exhibited a high tuberization percentage, commercial, and total fresh root yield, compared with the rest of evaluated genotypes (Table 8). In sub-humid conditions, sweet potato genotypes expressed different productive potential and better adaptation was observed in environments with sandy soils and limited water availability, such as La Jagua_2016, Codazzi_2015 and 2016, and Corozal_2015. Under these environmental conditions, good establishment and high root production were observed (Tables 7 and 8). The Cerete and Carmen de Bolivar locations showed a clayed tendency and a high level of organic matter. Corozal, Codazzi, Dibulla, Tolu, and Riohacha had sandy soils, and Jagua showed soils with a silty-loam texture. A major content of phosphorous, sulfur, calcium, magnesium, potassium, and minor elements were present generally at Tolu and Jagua, which also showed a high cation exchange capacity. This was contrary to Dibulla, a location with lower soil nutritional availability. As previously discussed, excessive nutrient and water availability in soils promoted major foliar biomass growth and negatively impacted root production.

Table 8. Mean values of tuberization, commercial and total yield in nine sweet potato genotypes from combined analysis of UYT and AET.

	Tuberization (%)	Commercial Root Yield (Tn·ha)	Total Fresh Root Yield (Tn·ha)
Genotypes:			
0113-672COR	89.58 ± 15.13	8.07 ± 7.23	18.38 ± 13.42
0113-664VAL	81.92 ± 15.8	5.87 ± 4.92	11.96 ± 7.37
0113-660VAL	76.77 ± 20.44	4.96 ± 4.45	11.92 ± 9.37
0113-668VAL	83.49 ± 16.01	5.73 ± 4.61	11.26 ± 8.23
0113-657VAL	84.59 ± 17.22	6.42 ± 5.96	9.73 ± 7.51
0113-634VAL	78.09 ± 17.81	3.91 ± 3.51	7.71 ± 4.67
0113-656COR	54.63 ± 28.06	3.1 ± 4.29	7.25 ± 8.98
0113-671VAL	64.47 ± 20.64	4.19 ± 3.44	7.11 ± 5.85
CRIOLLA	67.66 ± 19.12	3.23 ± 2.94	7.79 ± 5.79
LSD	9.04	1.96	4.01
Locations:			
Jagua_2016	81.7 ± 15.8	7.96 ± 4.92	20.23 ± 12.23
Codazzi_2016	85.41 ± 14.16	7.48 ± 5.39	16.34 ± 8.56
Codazzi_2015	76.13 ± 20.88	9.63 ± 7.67	13.14 ± 10.17
Corozal_2015	85.53 ± 23.38	5.23 ± 2.79	12.83 ± 6.75
Corozal_2016	79.53 ± 14.95	2.72 ± 3.36	8.44 ± 6.88
Cerete_2016	81.55 ± 22.65	2.68 ± 3.19	10.65 ± 12.25
Cerete_2015b	79.71 ± 13.96	8.84 ± 5.5	10.02 ± 5.94
Cerete_2015a	80.11 ± 19.29	5.15 ± 2.65	6.89 ± 3.07
Carmen-B_2016	75.44 ± 18.87	6.55 ± 5.48	9.84 ± 5.73
Carmen-B_2015	74.56 ± 30.38	4.06 ± 2.52	5.84 ± 3.17
Tolu_2016	63.64 ± 19.26	0.91 ± 1.03	8.16 ± 5.88
Dibulla_2016	75.99 ± 20.28	4.24 ± 3.43	7.71 ± 4.89
Riohacha_2015	47.04 ± 21.93	0.99 ± 0.82	0.98 ± 0.84
LSD	11.75	2.55	5.23

LSD: least significant difference determined by Tukey's test ($p < 0.01$).

3.5. Genetic Gain and Heritability Analysis of Selected Genotypes in AET

Parameters related to genetic gain showed that high environmental variance was associated with $G \times A$ interaction (Table 9), which limited an efficient estimation of heritability in the broad sense. However, mean genotype heritability ($h2mc$) recognized that the number of roots per plant, percentage of tuberization, and the total yield were variables with possible genetic gain given by clonal selection among the evaluated genotypes. Therefore, these traits should be considered in preliminary evaluations to accelerate development and selection processes in sweet potato breeding.

Table 9. Parameters and estimated genetic gain in yield components of sweet potato genotypes evaluated in different environments.

Variable	σg^2	σgxe^2	σe^2	σf^2	$h2g$	$h2mc$	Acclon	rgloc	CVg%	CVe%	Mean
Forage yield	15.22	234.66	104.63	354.51	0.043 ± 0.037	0.20	0.45	0.06	8.73	22.89	44.69
Root number/p	0.35	0.34	0.63	1.33	0.267 ± 0.092	0.63	0.79	0.51	22.84	30.51	2.60
Root weight/p	0.023	0.091	0.18	0.29	0.079 ± 0.05	0.29	0.54	0.20	17.15	47.42	0.89
Tuberization (%)	61.89	215.49	269.92	547.30	0.11 ± 0.06	0.39	0.62	0.22	10.48	21.88	75.09
Commercial yield	0.056	13.49	9.37	22.92	0.0024 ± 0.0088	0.013	0.11	0.004	5.23	67.42	4.5
Total yield	13.69	33.06	49.00	95.75	0.14 ± 0.0674	0.45	0.67	0.29	32.76	61.99	11.29

σg^2 = genotypic variance; σgxe^2 = variance of the Genotype \times Environment interaction; σe^2 = residual variance; σf^2 = individual phenotypic variance; $h2g$ = heritability of individual plots in the broad sense; $h2mc$ = mean genotype heritability, assuming complete survival; Acclon = precision of genotype selection, assuming complete survival; rgloc = genotypic correlation between performance in various environments; CVg% = genotypic coefficient of variation; CVe% = residual coefficient of variation.

According to predicted genotypic effect of evaluated traits, 0113-672COR genotype showed high values in the analyzed traits, especially in agronomic characters such as number of roots per plant, percentage of tuberization, and total yield (Table 10).

Table 10. Predicted genotypic effect and genotypic mean in yield components of sweet potato genotypes evaluated in different environments.

Genotypes	Forage Yield		Roots Number/P		Roots Weight/P		Tuberization (%)		Commercial Root Yield		Total Root Yield	
	g	NMean	G	NMean	g	NMean	g	NMean	g	NMean	g	NMean
0113-634VAL	1.87	47.59	−0.11	2.96	0.03	1.03	−1.47	77.53	−0.05	4.54	−3.09	11.29
0113-656COR	−2.48	44.69	−0.40	2.76	−0.05	0.92	−9.40	75.09	−0.02	4.56	−1.11	13.04
0113-657VAL	1.30	47.05	0.47	3.39	−0.01	0.95	5.35	82.67	0.02	4.59	−1.70	12.12
0113-660VAL	−0.56	46.15	0.14	3.07	0.02	0.99	2.13	80.42	0.02	4.58	2.34	15.85
0113-664VAL	−1.56	45.32	0.16	3.18	0.02	0.97	−1.36	79.08	0.01	4.57	0.75	14.58
0113-668VAL	3.91	48.61	−0.24	2.86	−0.03	0.94	4.03	81.49	0.00	4.56	−0.01	13.75
0113-671VAL	−1.35	45.68	−0.71	2.61	−0.17	0.89	−7.70	76.26	−0.03	4.55	−2.72	11.68
0113-672COR	0.75	46.65	1.09	3.69	0.25	1.14	9.82	84.91	0.06	4.61	6.76	18.06
CRIOLLA	−1.88	45.00	−0.40	2.69	−0.07	0.91	−1.41	78.18	−0.02	4.55	−1.24	12.54

g = predicted genotypic effect; NMean = new genotypic mean.

3.6. Selection of Potential Variety Adapted to Caribbean Region

Combined variance analysis showed the influence of several factors related to phenotypic expression on survival, tuberization percentage, TFRY, and CFRY (Table 11). Variation in tuberization was the single trait that was explained in major proportion by genotype, followed by environment (ENVIR); in contrast, the rest of analyzed traits were mostly influenced by environment, followed by genotype. $G \times E$ interaction was detected in all analyzed traits, revealing the restrictive wide adaptation of those genotypes. Conversely, specific adaptations to certain conditions could also be observed.

Table 11. Combined analysis of variance for agronomic traits and yield components in nine genotypes evaluated across 13 locations.

Source of Variation	df.	Survival	Tuberization	TFRY	CFRY
Genotype	8	1760.7 ***	5588.8 ***	585.4 ***	116.5 ***
ENVIR	12	4169.9 ***	3044.8 ***	746.5 ***	256.5 ***
Rep	3	206.9	485.9	99.8	42.63
Genotype * ENVIR	93	390.4 ***	576.3 ***	79.1 ***	35.26 ***
Error	276	80.12	185.6	36.3	8.72
PC1				219.6 *** (49.3%)	85.07 *** (42.0%)
PC2				90.8 *** (18.3%)	57.42 *** (25.4%)
PC3				66.9 *** (11.9%)	33.75 *** (13.2%)

*** $p < 0.0001$.

In fact, AMMI analysis using TFRY and CFRY data confirmed the high influence of the environment (Figure 2a–d). Sweet potato genotypes showed low stability, evident from distant positioning relative to the biplot origin. Among them, only the genotypes 0113-664VAL, 0113-671VAL, and 0113-634VAL showed close proximity (Figure 2a). The first component explained about 49.3% of the total variation and its relationship with TFRY demonstrated that genotype 0113-672COR, although not completely stable, had a yield which was significantly higher compared to the rest of genotypes (Figure 2b). Similar behavior was observed for CFRY; however, the genotypes were closer to the biplot origin (Figure 2c). Similarly, genotype 0113-672COR showed its superiority in this agronomic trait (Figure 2d).

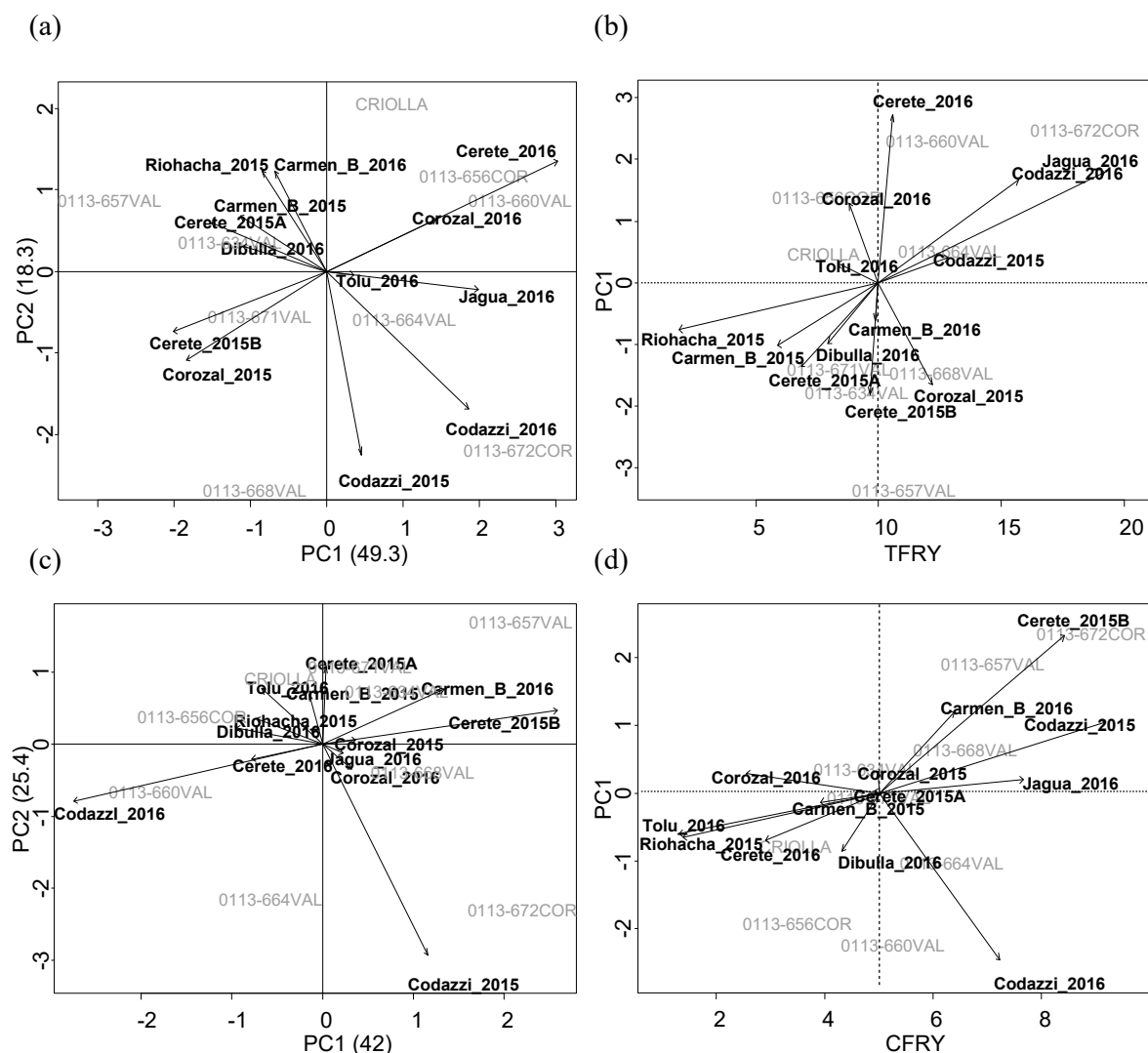


Figure 2. Additive main effects and multiplicative interaction (AMMI) and selection index in promising genotypes. (a) Biplot AMMI obtained for total fresh root yield (TFRY) of nine genotypes evaluated in 15 locations. (b) Biplot AMMI for TFRY vs. PC1 of nine genotypes evaluated in 15 locations. (c) Biplot AMMI obtained for commercial fresh root yield (CFRY) of nine genotypes evaluated in 15 locations. (d) Biplot AMMI for CFRY vs. PC1 of nine genotypes evaluated in 15 locations.

In this last step, a selection index combining TFRY, CFRY, and survival was used to identify the best genotype adapted to the Caribbean region using R software script named *CropInd* (Table 12). Multilocal selection index identified genotype 0113-672COR with the better profile with good TFRY, CFRY, and survival percentage. Genotypes 0113-664VAL, 0113-657VAL, 0113-668VAL, and 0113-660VAL followed the ranking; however, although the single environment selection index showed that all these genotypes were adequate for more than eight environments, the total and commercial yield obtained for 0113-672COR allowed to us to postulate this as a commercial variety for the Colombian Caribbean zone, which has actually been named Agrosavia Aurora.

The morphological and physiological attributes (growth) demonstrated good adaptation to Caribbean region (Figure 3a). This is variety with ovoid roots (Figure 3b), yielding higher than 20 T/ha, and β -carotene content that reaches more than 200 $\mu\text{g/g}$. This particular component is associated with the orange-flesh color of these roots [38].

Table 12. Selection index obtained per location and combined analysis for nine genotypes.

IS Locations	General	Codazzi_2015	Codazzi_2016	Corozal_2015	Corozal_2016	Jagua_2016	Carmen_b_2015	Carmen_b_2016	Cerete_2015a	Cerete_2015b	Cerete_2016	Dibulla_2016	Riohacha_2015	Tolu_2016
0113-672COR *	14.8	49.9	−0.5	19.1	75.5	26	−6.1	33.6	−3.6	33.2	36.4	−48.1	−7.6	9.4
0113-664VAL	12.6	46.7	24.7	12.7	12.1	10.6	5.7	−12.4	−23.2	−17.7	9	61.1	54	−15.9
0113-657VAL	9.9	−9.5	−30.7	22.9	−24.7	7.7	60.9	61.6	14.4	45.7	−21.2	41.9	−13.9	10.2
0113-668VAL *	8.8	20.6	4.3	56.8	−11	12	−15.3	−15	18.7	31.9	−5.9	19	19.6	NaN
0113-660VAL *	7.7	−15.1	38.4	−23.3	7.9	11	17.8	−9.7	−17	−33.2	21.6	24.9	36.6	−0.6
0113-634VAL	−10.5	−16.5	−44.1	4.2	−1.2	−13.5	−16.1	−17.5	46.9	−1	−1.4	−32.6	27.7	−33.2
0113-656COR	−11.7	−25.4	32.2	−58.1	−6.5	−38.5	−62.7	−3.6	−45.2	−38.6	−4.9	−31.2	−36.7	18.9
0113-671VAL	−12.4	−13.8	7.2	−34.3	−40.4	−12	15.7	−13.7	9.1	−2.8	−35.7	−17.1	−9.5	−0.2
CRIOLLA	−13.2	−36.8	−31.6	NA	−10.1	−3.2	NA	−23.3	NA	−34.3	2	−18.1	−42.2	−3.3

Color scale shows lower values as red color, intermediate values as orange and higher values as yellow. * marks selected genotypes for next evaluation cycle.

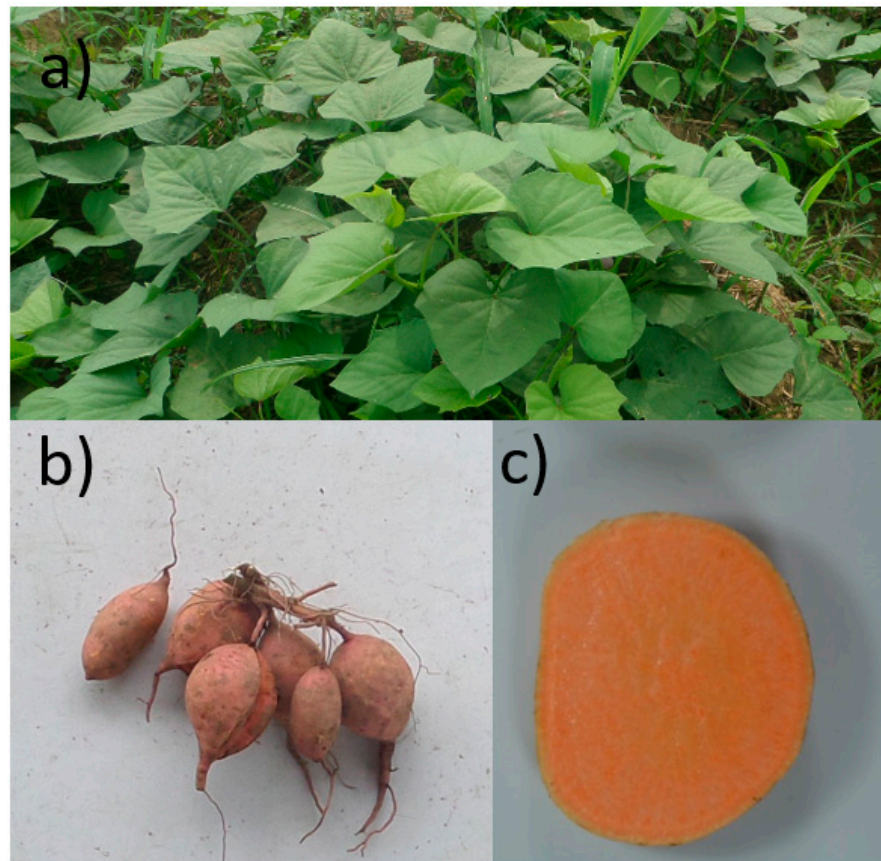


Figure 3. Morphologic features of Agrosavia Aurora (0113-672COR). (a) Plant morphology, (b) storage root shape, (c) root flesh.

4. Discussion

4.1. Agronomic Behavior of Evaluated Genotypes

The results confirmed a differential response of the evaluated genotypes to environmental conditions. While some genotypes exhibited better phenotypic plasticity to adapt to diverse environmental conditions, particularly in traits of economic importance (yield and quality), others seemed to be adapted to specific conditions. This important feature of the sweet potato crop contributes to its uses as a staple food in many countries around the world [10], as well as its cultivation in a wide range of environmental conditions [11,14,15]. In Colombia, despite it being a traditional crop, it faced low marketability and its production was limited to family use [9]. However, in recent years, the sweet potato supply chain in Colombia evidenced the need to have commercial varieties with specific profiles to respond to the demands of fresh root markets and value-added products. Thus, superior agronomic performance observed among genotypes such as 0113-672Cor, 0113-657Val, 0113.668Val, and 0113-634Val using UYT evaluation was the initial step to select potential promising genotypes, and their more stable agronomic performance was in line with previous studies that demonstrated differences among the response of genotypes cultivated under different conditions [39].

The agronomic performance of some genotypes is consistent with previous reports, showing that efficiency of cover ground is a determinant trait for sweet potato yield, but it is not completely related to above-ground biomass yield [40,41]. The differential response of evaluated genotypes could be associated to their specific morphological and physiological traits, which determine better adaptation to determined environmental conditions. Thus, traits such as leaf shape, size, and thickness have a relationship with cell number, chlorophyll content, and ribulose-1,5-biphosphate carboxylase/oxygenase

(RuBisCO) per unit area when exposed to sunlight, which influences leaf photosynthetic rates [42,43].

High-content conditions of organic matter produce a significant reduction in storage roots due to the induction of apical meristem production and growth, as well as a reduction in the sink capacity in storage roots [44]. Major above-biomass yield is not directly associated to major efficiency in photosynthetic process because overlapping leaves produce light competition [40].

4.2. Stability and Selection of Promising Genotypes in UYT Using CropInd

The most stable genotypes were not necessarily those with the best yield, suggesting that information produced by AMMI analysis supports the selection of superior genotypes with high yield and adaptability to the environmental conditions appropriated for better crop performance. Stability analysis is a useful approach to identify stable and location-specific genotypes. Here, we found that evaluated population exhibited low stability and genotypes with high yield had better performance under better environmental conditions. Similar findings were reported previously, as some genotypes can express their genetic potential only under specific growing conditions; therefore, selected and ideal genotypes must be developed based on the adaptability of each genotype [45].

Selection index enabled a ranking according to the desired selected traits. It also facilitated a comparison of the genotypes evaluated in a multilocal trial from both a specific and wide adaptation viewpoint; thus, the results helped to determine the superiority of promising genotypes under a wide range of environmental conditions. Although there are various software tools and scripts to analyze the performance of genotypes in multi-environmental trials [37], only a limited number of them give the opportunity to analyze profiles involving several desired traits and generally require a high level of expertise in data analysis [46–48]. *CropInd* is a tool developed for an integrated and user-friendly script. Its execution creates a ranking of the genotypes based on a desired ideotype. Such analysis is consistent with breeder requirements that look for stable ideotypes [49]. Thus, stability analysis, together with SI obtained by script *CropInd*, were demonstrated to be key procedures for helping the breeder to identify which genotypes have specific and/or general adaptability to a wide range of environmental conditions; moreover, the integration of desired traits became achievable through the incorporation of the selection index. It also aided an understanding of the environmental conditions in Colombia which are appropriated for sweet potato cultivation. Here, we demonstrated how the combination of several analysis are needed in the selection of superior and stable genotypes [45,50,51].

4.3. Agronomic Performance of Selected Genotypes in AET

Genotypes with high root yield showed adequate adaptation to evaluated conditions, and even under stress conditions their yield was superior to the rest of genotypes, confirming their superiority. Possibly, these genotypes combine a strategy for resource allocation and development, with initial allocation of resources to leaves that accelerate growth to increase ground-cover efficiency, whereas allocation to non-photosynthetic tissues (roots) reduced the foliar growth at the end of the cycle [41,52]. Consistently, this physiological behavior represented an important trait for selection of adapted genotypes.

The superior genotypes exhibited high values in yield and yield components. This was contrary to some sweet potato genotypes that exhibited a low sink capacity in the storage root system but greater sink capacity in foliar tissue [44]. These genotypes showed higher efficiency for starch accumulation in storage roots producing both higher root number and weight.

The obtained results consistently confirm the preference of sweet potato for soil with a loose texture, which is attributed to the presence of a sufficient percentage of sand and loam in the soils. In general, tubers and roots crops grow very well on well-drained soils, with adequate organic matter, and especially those with loose and friable fertile clay loam or loam [53]. Environmental conditions with high water and nutrient availability induced

major foliar biomass production, which was due to the induction of apical meristem production and growth, reducing the sink capacity in storage roots [44]. Contrary, under sub-humid conditions with sandy and loam soils, the temporal water deficiency promotes early tuberizing and increases the capacity for root starch accumulation. This is related to ground cover efficiency but not to foliar biomass production [41].

In this study, it was possible to confirm that variables with a higher genetic base such as the number of roots and the capacity of tuberization are key traits to be considered for genotype selection [54]. It should be considered that vegetative propagation in sweet potato maintains dominance and epistasis effects between crop cycles [55]. Therefore, selected superior genotypes must have several favorable attributes simultaneously because selection based on single traits can result in unsatisfactory performance in other traits [56,57].

5. Conclusions

This study compiles results from steps of the sweet potato breeding scheme, in which genotype selection was assisted by a combination of multi-trait index, genetic gain, and stability analysis. This demonstrated its utility for genotypes selection through (i) major adaptation to several environments, (ii) better plant ideotype across several concurrently assessed traits, and (iii) inclusion of traits with substantial heritability in the selection process. The *CropInd* script for R software was built and validated in this study as a tool that easily performs selection index for a specific environment and a general (multi-environments) agronomic profile, giving results according specific or wide adaptability of genotypes. All processes were validated during the identification of genotype 0113-672COR as the most promising sweet potato commercial variety for the Colombian Caribbean zone. This orange-fleshed variety was the first registered and released commercial variety in Colombia.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/horticulturae9090974/s1>.

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