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Yield stability of *Physalis peruviana* L. genotypes through multi-environment trial analysis

Estabilidad del rendimiento en genotipos de *Physalis peruviana* L. a través de análisis multiambientales

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ABSTRACT

Cape gooseberry (*Physalis peruviana* L.) is a high-value Andean fruit crop with increasing economic importance due to its nutritional properties and export potential, whose productivity is strongly influenced by environmental heterogeneity and pronounced genotype by environment interaction (GEI). These challenges hinder the identification of genotypes that combine high yield with stability, a key requirement for advancing breeding programs and ensuring consistent production in diverse climatic conditions. Therefore, this study aimed to evaluate the yield performance, stability, and adaptability of 40 genotypes grown across four contrasting high-Andean environments in Nariño, Colombia, using a randomized complete block design with three replications during a single production cycle conducted between 2019 and 2020. Multi-environment trial data were analyzed using AMMI, GGE biplot, and the Multi-Trait Stability Index (MTSI), focusing on fruit weight without calyx (FWWC), fruit number per plant, and total yield. Environmental effects contributed most to GEI, with AMMI1 efficiently capturing major interaction patterns. Gualmatán was identified as the most favorable site. Genotypes UN45, 09U089, and Puracé showed broad adaptability to both Gualmatán and Ipiales, with UN45 also expressing the highest overall yield performance. Genotypes 12U347 and UN34 displayed specific adaptation to Gualmatán, while UN52 and 13U407 exhibited high stability across environments. The MTSI index identified six top-performing genotypes (09U099, 12U352, UN49, 12U360, 12U350, and 12U374), all achieving positive selection differentials (<1.20) and classified as stable and high-performing genotypes. These findings provide robust evidence to support targeted selection of superior *Physalis peruviana* genotypes and strengthen breeding strategies aimed at achieving stable and high-yielding cultivars across diverse Andean environments.

Palabras clave:
Adaptabilidad
AMMI
Uchuva
Interacción genotipo-ambiente
MTSI

RESUMEN

La uchuva (*Physalis peruviana* L.) es un cultivo andino de alto valor, con creciente importancia económica debido a sus propiedades nutricionales y su potencial de exportación, cuyo rendimiento se ve fuertemente influenciado por la heterogeneidad ambiental y por una marcada interacción genotipo × ambiente (IGA). Estas condiciones dificultan la identificación de genotipos que combinen alto rendimiento con estabilidad, un requisito esencial para fortalecer los programas de mejoramiento y garantizar una producción consistente en diversas condiciones climáticas. Por ello, este estudio tuvo como objetivo evaluar el rendimiento, la estabilidad y la adaptabilidad de 40 genotipos cultivados en tres ambientes contrastantes del departamento de Nariño, Colombia, usando el diseño de bloques completos al azar con tres repeticiones durante un ciclo productivo del cultivo entre 2019 y 2020. Los datos de ensayos multiambiente se analizaron mediante los modelos AMMI, GGE biplot y el Índice de Estabilidad Multicaracterística (IEM), considerando variables clave como peso de fruto sin cáliz (PFSC), número de frutos por planta y rendimiento total. Los efectos ambientales fueron los principales contribuyentes a la IGA, y el modelo AMMI1 capturó de manera eficiente los patrones de interacción más relevantes. Gualmatán se identificó como el sitio más favorable. Los genotipos UN45, 09U089 y Puracé mostraron amplia adaptabilidad a Gualmatán e Ipiales, y UN45 presentó el mayor rendimiento promedio. Los genotipos 12U347 y UN34 evidenciaron adaptación específica a Gualmatán, mientras que UN52 y 13U407 destacaron por su alta estabilidad. El índice IEM seleccionó seis genotipos sobresalientes (09U099, 12U352, UN49, 12U360, 12U350 y 12U374), los cuales alcanzaron diferenciales de selección positivos (<1,20) y clasificados como genotipos estables y de alto rendimiento. Estos resultados aportan evidencia robusta para orientar la selección dirigida de genotipos superiores de uchuva y fortalecen las estrategias de mejoramiento orientadas a obtener cultivares estables y de alto rendimiento en diversos ambientes altoandinos.

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The cape gooseberry (*Physalis peruviana* L.), a member of the Solanaceae family, is an exotic fruit native to the Andean region of South America, particularly Colombia, Peru, and Ecuador, which are considered its center of origin and diversification, and is recognized for its high nutritional value, richness in bioactive compounds, and growing economic importance as a functional food in international markets (Rodríguez et al. 2021). In Colombia, commercial cultivation began in 1985, positioning the country as one of the main global producers along with India, Vietnam, and South Africa. The species grows naturally in high-altitude zones between 1,500 and 3,000 meters above sea level (masl) in the Neotropics and parts of the subtropics (Ruiz et al. 2018). Optimal cultivation conditions in Colombia occur between 2,300 and 2,800 masl, with average temperatures of 13–18 °C, annual rainfall of 1,000–2,000 mm, and relative humidity levels of 70–80%. In recent years, *P. peruviana* has gained importance as a promising commercial crop, and its adoption in the department of Nariño reflects its growing potential in production systems located in cold and moderately cold climates (Rodríguez et al. 2021).

In agricultural production systems, selecting cultivars that perform efficiently under specific environmental conditions is essential for achieving high and stable yields. This selection requires reliable information on the average performance of each hybrid or variety in contrasting environments; however, relying exclusively on arithmetic means does not fully capture the complexity of genotype–environment interactions (Halimatus and Alfian 2016). The performance of genetic material is influenced by the genotype (G), the environment (E), and the genotype-by-environment interaction (GEI), which frequently results in inconsistent yield responses among locations. This interaction complicates the identification of stable, high-yielding genotypes. Materials with broad stability tend to be better suited to traditional farming systems with limited inputs, while genotypes that are highly responsive under favorable conditions may be more suitable for producers who invest in improved management practices (Azevedo et al. 2015).

In crops such as *P. peruviana*, information on GEI remains limited, reducing the ability to identify genotypes with either broad or specific adaptability. Strengthening the understanding of GEI is essential for developing improved genetic materials, guiding resource allocation in multi-environment yield trials, and determining which traits and environments should be prioritized in breeding programs (Rathod et al. 2025).

Several biometric and quantitative models have been used to interpret GEI. The additive main effects and multiplicative interaction (AMMI) model assumes that genotype and environment effects are additive, while the interaction is multiplicative, and combines analysis of variance with principal component analysis to partition these effects. The GGE biplot model focuses on genotype effects and GEI, graphically displaying relationships among test environments and facilitating the identification of ideal environments and adapted genotypes (Olivoto et al. 2019). In addition, the Multi-Trait Stability Index (MTSI) has become an important tool for selecting genotypes that combine high performance and stability across multiple traits within multi-environment trials.

Using the AMMI, GGE biplot and MTSI models, this study aims to evaluate the interaction patterns and stability of 40 cape gooseberry genotypes across four environments in southern Colombia. The purpose is to identify genotypes with high yield and stable performance that may contribute to the genetic improvement of *P. peruviana* and strengthen regional production systems.

MATERIALS AND METHODS

Study locations

The experimental evaluation was conducted across four representative environments within the *Physalis peruviana* L. production zone in Nariño, Colombia. The selected locations included the municipalities of Gualmatán, Puerres, Ipiales, and Pasto, situated at elevations ranging from 2,760 to 2,995 masl (Table 1).

The environment were characterized by a cold climate, with temperatures ranging from 9 to 12 °C and relative humidity levels between 87 and 94%. Except for Pasto, which had a balanced silty loam soil, the other locations featured heavy soils with a sandy clay texture. Organic matter content varied across environments and remained within ranges compatible with *P. peruviana* production. In Andean environments, soils with organic matter

Table 1. Characteristics of the evaluation environments for 40 genotypes of *Physalis peruviana* L. in the production zone of Nariño.

Environment	Climate			Characteristics of the soil						
	Altitude (m)	T (°C)	RH (%)	Texture	OM (%)	pH	P (mg kg $^{-1}$)	K (cmol kg^{-1})	Ca (cmol kg^{-1})	Mg (cmol kg^{-1})
Gualmatán	2795	11	93	Ar-A	4.92	6.2	165	1.48	4.7	2.59
Ipiales	2835	12	94	Ar-A	4.04	5.7	324	1.19	8.79	1.25
Puerres	2995	9	92	Ar-A	3.5	5.3	54.9	1.12	3.21	0.96
Pasto	2760	12	87	Fr-L	3.9	5.7	69.71	1.31	8.95	1.36

RH = relative humidity, and OM = organic matter.

contents above 3%, along with adequate structure and texture, are considered suitable for this crop (Ramírez et al. 2023). Soil pH varied from strongly acidic (pH<5.5) in Puerres to moderately acidic (pH=5.5–6.0) in Ipiales and Pasto, with slightly acidic conditions (pH=6.1–6.5) in Gualmatán. Phosphorus and potassium levels were high (>30 mg kg^{-1} and >0.5 cmolc kg^{-1}, respectively), while calcium levels ranged from sufficient (2–5 cmolc kg^{-1}) in Puerres and Gualmatán to high (>5 cmolc kg^{-1}) in Ipiales and Pasto. Magnesium content was generally low (<1 cmolc kg^{-1}), except in Gualmatán, where it reached higher levels (>1 cmolc kg^{-1}).

Plant material

A total of 40 *P. peruviana* genotypes were evaluated, sourced from working collections maintained by Universidad de Nariño and the Corporación Colombiana de Investigación Agropecuaria (Agrosavia). These genotypes were planted and tested across the four-contrasting high-Andean environments in Nariño, Colombia (Table 2).

Table 2. Denomination and origin of *Physalis peruviana* L. evaluated in four producing environments in Nariño.

No.	Genotype	Source	Origin	No.	Genotype	Source	Origin
1	09U086	AT	Ecuador	21	Kenia	Unal-P	Cundinamarca
2	09U089	AT	Antioquia	22	Neira	Unal-P	Cundinamarca
3	09U099	AT	Caldas	23	Perú	Unal-P	Peru
4	09U116	AT	Antioquia	24	Puracé	Unal-P	Puracé
5	09U128	AL	Cundinamarca	25	Silvania	Unal-P	Silvania (Cauca)
6	09U136	AL	Cundinamarca	26	Regional	FS	Pupiales (Nariño)
7	09U138	AL	Francia	27	UN01	Udenar	Nariño (Nariño)
8	09U140	AL	South Africa	28	UN03	Udenar	Nariño (Nariño)
9	12U347	AT	DHL	29	UN13	Udenar	San Juan (Nariño)
10	12U350	AT	DHL	30	UN14	Udenar	Obonuco (Nariño)
11	12U352	AT	DHL	31	UN19	Udenar	Catambuco (Nariño)
12	12U357	AT	DHL	32	UN26	Udenar	La Laguna (Nariño)
13	12U360	AT	DHL	33	UN30	Udenar	La Laguna (Nariño)
14	12U368	AT	DHL	34	UN34	Udenar	El Encano (Nariño)
15	12U374	AT	DHL	35	UN35	Udenar	El Encano (Nariño)
16	12U377	AT	DHL	36	UN36	Udenar	Morasurco (Nariño)
17	12U399	AT	DHL	37	UN43	Udenar	Aldana (Nariño)
18	13U407	AT	Kenya-1(09U210)*	38	UN45	Udenar	Túquerres (Nariño)
19	13U408	AT	Kenya-1(09U210-4)	39	UN49	Udenar	Imués (Nariño)
20	Colombia	Udenar	TC	40	UN52	Udenar	Nariño (Nariño)

AT = Agrosavia Tibaitatá; AL = Agrosavia La Selva; DHL = double haploid line; Udenar = Universidad de Nariño; FS = farmer selection; TC = tissue culture; Unal-P = Universidad Nacional de Colombia; Palmira, * = self-pollination.

Experimental design

The experimental design followed a randomized complete block design (RCBD) with four replications per location. The experiment was conducted during a single production cycle spanning two years (2019–2020). The 40 genotypes served as experimental treatments. Blocking was based on plot slope and spatial variability in soil moisture or natural shading. Each experimental plot consisted of a 10-meter-long trench with five plants spaced 2 meters apart. Rows were spaced 2.5 meters apart, resulting in an experimental plot area of 25 m², with the central 20 m² considered as the effective area. The planting density was 2,000 plants per hectare.

Measured variables

Three agronomic traits were evaluated: (1) Fruit weight without calyx (FWWC), calculated as the average weight of 20 randomly selected fruits per plant; (2) Number of fruits per plant (NFP), recorded through weekly harvests; and (3) Yield, expressed in tons per hectare (t/ha), measured over a 12-month harvest period.

Data analysis

A mixed-model analysis of variance (ANOVA) was conducted to analyze data across locations, treating genotypes as fixed effects and locations as random effects. The genotype-by-environment interaction (GEI) was evaluated using the additive main effects and multiplicative interaction (AMMI) model (Olivoto et al. 2019). The model applied follows Equation 1:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger} \quad (1)$$

Where Y_{ger} is the response variable of the g-th genotype in the e-th environment in the r-repeat, μ is the overall mean, α_g is the deviation of the g-th genotype from the overall mean, β_e is the deviation of the e-th environment from the overall mean, N is the number of axes or principal components retained in the model, λ_n is the eigen or singular value of the n-th axis (scalar) of the Interaction Principal Component Analysis (IPCA), γ_{gn} is the eigen or singular vector of the g-th genotype related to the n-th axis (γ_{gn}), δ_{en} is the eigenvector or singular of the e-th environment related to the n-th axis (δ_{en}), ρ_{ge} is the residual of the genotype-by-environment interaction and ε_{ger} is the residual where ~NNN(0, $\frac{\sigma^2}{r}$) (Olivoto et al. 2019). In addition to the AMMI model and its stability measures, the GGE biplot method was used to analyze and evaluate the interaction and stability of the variables in this investigation. The GGE biplot was constructed with the first two principal components (PC1 and PC2) derived from the environment-centered variable data based on the singular value decomposition (SVD) of the interaction matrix [(GE)ge] to fit the GGE biplot model. Yan (2014) indicates that the GGE biplot model containing the effect of G and GE, is based on the environment regression model-SREG. This model is derived from the linear model $Y_{ge} = \mu + \alpha_g + \beta_e + \theta_{ge}$ by removing the α_g term and subjecting the θ_{ge} (environment-centered variable) to the SVD. Then, the GGE biplot model is given follow in Equation 2:

$$\theta_{ge} = Y_{ger} - \mu - \beta_e = \lambda_1 \gamma_{g1} \delta_{e1} + \lambda_2 \gamma_{g2} \delta_{e2} + \varepsilon_{ger} \quad (2)$$

Where Y_{ger} is the response variable of the g-th genotype in the e-th environment, r-repeat, μ is the overall mean, βe is the effect of the e-th environment, λ_1, λ_2 are the singular values (SV) for the first and second principal components (IPC1 and IPC2) in their order, γ_{g1},γ_{g2} are the eigenvectors of the g-th genotype for IPC1 and IPC2, δ_{e1}, δ_{e2} are the eigenvectors of the e-th environment for IPC1 and IPC2, ε_{ger} is the residual, θ_{ge} is the genotype g-th by the e-th environment [(GE)ge].

Statistical analyses were performed based on SAS version 9.4, the Metan version 1.18.0 library for R Studio and Excel 2016.

RESULTS AND DISCUSSION

The combined analysis of variance (ANOVA) for fruit weight without calyx (FWWC), number of fruits per plant (NFP), and yield revealed highly significant differences (P<0.01) for environments, genotypes, and genotype-by-environment interactions (GEI) (Table 3). The significant GEI indicates variable genotype performance across environments, warranting further AMMI analysis to examine genotype behavior and stability across the tested environments by partitioning the interaction into its principal components and identifying underlying response patterns (Maharana et al. 2017).

The environment contributed the most to the total sum of squares (SS) for all three variables evaluated, particularly for yield, with a contribution of 82.30% of the total sum of squares. This underscores the substantial impact of environmental factors on the expression of FWWC, NFP, and yield in *P. peruviana*, a phenomenon corroborated by

other studies (Yoseph et al. 2022). Additionally, yield is driven by chains of chemical reactions arising from the interaction of multiple genes with the environment (Burgess et al. 2022). Overall, the contribution of genotypes to total SS is smaller than the effect of environment and GEI, as seen across the three variables in this investigation (Table 3). However, a study conducted across four locations in central Colombia, examining equatorial and polar diameter, weight, and firmness of *P. peruviana* varieties Corpoica Dorada, Corpoica Andina, and the ecotype Colombia, found that GEI explained the greatest variability (74.61%), followed by genotypes (20.15%), and environments (5.24%). Indeed, the significant influence of environment and GEI can impede selection progress and complicate cultivar recommendations, as it makes interpreting main effects statistically challenging (Kang 2020).

Table 3. Mean squares of the AMMI analysis of variance for fruit weight without calyx, number of fruits per plant and fruit yield without calix of 40 genotypes of *Physalis peruviana*, evaluated in four productive environments of Nariño.

Fruit weight without calyx (g)								
Source	**DF**	**MS**	**F_{Gollob}**	**$GL_{r.AMMI}$**	**$CM_{r.AMMI}$**	**F_{R-C}**	**$P_{SS/GA}$**	**P_{GEIa}**
Rep/Env	12	2.5	3.02*	-	-	-	2	-
Env	3	243.76	293.96*	-	-	48.4	-	
Gen	39	4.45	5.37*	-	-	-	11.5	-
Gen*Env	117	1.64	1.98*	117	1.64	1.98*	12.7	-
IPC1	41	2.56	2.98*	76	1.15	1.38^{ns}	54.6	54.6
IPC2	39	1.74	2.02*	37	0.53	0.63^{ns}	35.2	89.8
Error	463	0.83	-	-	-	-	-	-
R^2 =0.75		CV=15.56%	Average = 5.85g					
Number of fruits per plant								
Source	**DF**	**MS**	**F_{Gollob}**	**$GL_{r.AMMI}$**	**$CM_{r.AMMI}$**	**F_{R-C}**	**$P_{SS/GA}$**	**P_{GEIa}**
Rep/Env	12	2921902.4	2.88*	-	-	-	1.5	-
Env	3	539755514	531.38*	-	-	-	67.7	-
Gen	39	2248997.1	2.21*	-	-	-	3.7	-
Gen*Env	117	1524142.2	1.50*	41	1524142.2	1.50*	7.5	-
IPC1	41	3399441.9	3.19*	76	512467.3	0.50^{ns}	76.4	76.4
IPC2	39	692469.2	0.65	37	322735.6	0.32^{ns}	14.8	91.2
Error	463	1015767.5	-	-	-	-	-	-
R^2 =0.81		CV=37.67%	Average = 2675.3					
Yield (t ha^{-1})								
Source	**DF**	**MS**	**F_{Gollob}**	**$GL_{r.AMMI}$**	**$CM_{r.AMMI}$**	**F_{R-C}**	**$P_{SS/GA}$**	**P_{GEIa}**
Re/Env	12	237.09	15.08*	-	-	-	3.4	-
Env	3	22888.51	1455.46*	-	-	-	82.3	-
Gen	39	45.66	2.90*	-	-	-	2.1	-
Gen*Env	117	24.23	1.54*	117	24.23	1.54*	3.4	-
IPC1	41	44.16	2.07*	76	13.48	0.86^{ns}	62.7	62.7
IPC2	39	19.25	0.9	37	7.39	0.47^{ns}	26	88.7
Error	463	15.73	-	-	-	-	-	-
R^2 =0.91		CV=22.89%	Average = 17.33		-	-	-	-

R^2 = coefficient of determination; CV = coefficient of variation; Rep = replication; Env = environment, ICP = Interaction Principal Component; FR-C = FR test of Cornelius; $P_{SS/GA}$ = contribution to total Sum of Squares (SS) for the case of main and interaction effects of ANOVA and PCs to GEI; P_{GEIa} = cumulative contribution to GEI of PC1 and PC2; * = highly significant effect (P<0.01); ns = non-significant effect.

Regarding the eigenvectors from the AMMI analysis (Table 3), the first interaction principal component (IPC1) captured 54.6% of the GEI sum of squares (SS) for FWWC, 76.4% for NFP, and 62.7% for yield. In these cases, the AMMI2 model was appropriate for explaining the GEI. For FWWC, this model accounted for 89.8% of the GEI SS, for NFP it explained 91.2%, and for yield, it accounted for 88.7%.

Although different criteria can be used to select the most apropiate AMMI model, less restrictive approaches allow the retention of additional interaction principal components (IPCs). In this study the AMMI2 model is appropriate for FWWC as IPCA1 and IPCA2 explained 54.60 and 35.20% of the GEI, respectively, indicating that both components contributed substantially to the interaction (89.80%). In contrast, the AMMI1 model would be sufficient to explain the GEI for NFP (76.40%) and yield (62.70%) in *P. peruviana* (Table 3). However, the FR criterion described in more recent AMMI methodological updates is not significant for the IPCs in the analyses presented in Table 3. The FR test, under the null hypothesis that no more than n-terms determine the interaction, was considered as a complementary criterion, where a significant result indicates that the n-term model is inadequate and that at least n + 1 multiplicative terms are required. Nevertheless, this test has limited power to detect the need for an additional multiplicative component (Neisse et al. 2018).

Spearman correlation analysis for the stability measure ranges (Table 4) indicates no association between FWWC and NFP in *P. peruviana* with their respective stability measures. However, there is a high and significant correlation among the stability parameters EV, SIPC, D, ASV, and YSI. Pour-Aboughadareh et al. (2022) observed low correlations of EV with SIPC and ASV, suggesting that while EV does not provide an advantage in favorable environments, it can be useful for recommending genotypes in less favorable environments or in situations where farmers lack advanced technology.

Table 4. Spearman correlation analysis for the variables evaluated and the ranges of AMMI and MTSI stability parameters of 40 genotypes of *Physalis peruviana* evaluated in four locations in the Nariño department.

Variable	**EV**	**SIPC**	**D**	**ASV**	
FWWC	ns	ns	Ns	ns	
EV	1	0.78	0.82	0.65	
SIPC	-	1	0.98	0.92	
DI	-	-	1	0.93	
Variable	**EV**	**SIPC**	**D**	**ASV**	
NFP	ns	ns	Ns	ns	
EV	1	0.96	0.83	0.74	
SIPC	-	1	0.82	0.85	
DI	-	-	1	0.67	
Variable	**EV**	**SIPC**	**D**	**ASV**	**YSI**
Yield	ns	ns	ns	ns	-0.75
EV	1	0.96	0.85	0.75	0.48
SIPC	-	1	0.84	0.87	0.59
DI	-	-	1	0.73	0.57
ASV	-	-	-	1	0.77

FWWC = fruit weight without calyx (g), NFP = number of fruits per plant, EV = average of the squared eigenvectors of the N^{th} CPs, SIPC = sum of the absolute values of the scores of the Interaction Principal Component with subscript, Di= distance from the i-th genotype to the point of origin in the space of the interaction principal component, ASV = AMMI stability value, YSI = yield stability index, MTSI= multitrait stability index. Subscripts 1 and 2 are measures for NFP and Yield. ns = non-significant correlation.

Based on Ward's hierarchical classification analysis, Table 5 shows the distribution of the 40 *P. peruviana* genotypes into five groups, according to the evaluated variables across four locations in the Nariño department,

along with the AMMI and MTSI analyses. Given the high correlation among stability parameters (Table 4) within the *P. peruviana* population, only the SIPC and ASV measures are displayed for each variable in Table 5, along with the YSI index for yield.

The second and fourth groups contained 25 and 40% of the 40 genotypes evaluated, respectively. These groups were characterized by a higher frequency of genotypes with stability measure values close to zero, and thus, were considered the most stable. For FWWC, the stable genotypes were as follows: Colombia from the first group, UN35 from the second, UN26 and UN34 from the third, 09U086, 09U136, Test, UN01, UN30, and UN43 from the fourth, and UN36 from the fifth group. These genotypes represented 27.5% of the evaluated genotypes and exhibited SIPC values between 0.02 and 0.19, ASV values between 0.02 and 0.22, and FWWC= 5.60±0.33 g (Table 5).

Table 5. Distribution of five groups of 40 genotypes of *Physalis peruviana* based on the variables evaluated in four localities of the department of Nariño and the stability parameters AMMI and MTSI.

Genotype	CLUSTER= 1 (6/40)											
	FWWC	SIPC	ASV	NFP	$SIPC_1$	ASV_1	Yield	$SIPC_2$	ASV_2	YSI	Class	MTSI
09U116	6.16	0.21	0.21	2023.0	0.59	2.98	12.8	0.86	4.03	76	5	2.83
09U138	6.25	0.35	0.35	2050.2	0.55	2.00	17.3	1.00	2.34	50	3	2.62
13U408	6.74	0.31	0.46	1750.4	1.12	4.57	14.96	0.6	1.86	55	4	2.92
13U407	7.24	0.34	0.41	2014.2	1.31	3.91	18.78	0.93	1.30	22	1	3.12
Colombia	5.53	0.19	0.16	2136	0.71	3.37	15.23	0.36	1.51	52	3	2.39
Peru	7.15	0.44	0.37	1953.8	0.84	3.87	14.37	0.61	1.91	58	4	3.34
Mean	**6.51**	**0.31**	**0.33**	**1987.9**	**0.85**	**3.45**	**15.57**	**0.73**	**2.16**	**52.2**	**3.33**	**2.87**
Genotype	**CLUSTER= 2 (10/40)**											
	FWWC	SIPC	ASV	NFP	$SIPC_1$	ASV_1	Yield	$SIPC_2$	ASV_2	YSI	Class	MTSI
09U089	5.99	0.47	0.41	2947.4	0.59	0.73	17.38	1.12	4.76	63	4	2.91
09U099	5.88	0.23	0.34	2891.8	0.17	0.59	18.59	0.33	1.50	26	2	**1.12**
12U352	5.9	0.3	0.38	2878.4	0.73	0.73	17.43	0.34	0.61	29	2	**1.17**
12U368	5.11	0.91	1.04	3015.1	0.19	0.82	17.99	0.87	1.92	38	3	3.39
Puracé	6.02	0.45	0.48	2909.8	0.91	3.51	19.6	0.96	3.97	38	3	3.42
UN13	5.38	0.25	0.31	3051.4	0.5	1.53	18.78	0.34	1.23	21	1	1.63
UN14	5.01	0.27	0.26	3143	1.14	2.81	16.66	0.7	3.34	61	4	2.56
UN19	5.65	0.3	0.43	2988.6	0.91	4.51	18.77	1.14	2.62	37	3	3.47
UN35	5.65	0.02	0.03	2893.2	0.98	2.84	18.37	0.33	0.67	20	1	1.77
UN49	5.87	0.28	0.28	2848.8	0.04	0.15	17.77	0.17	0.32	25	2	**0.47**
Mean	**5.65**	**0.35**	**0.40**	**2956.8**	**0.62**	**1.82**	**18.13**	**0.63**	**2.10**	**35.8**	**2.5**	**2.19**
Genotype	**CLUSTER= 3 (5/40)**											
	FWWC	SIPC	ASV	NFP	$SIPC_1$	ASV_1	Yield	$SIPC_2$	ASV_2	YSI	Class	MTSI
09U128	5.67	0.46	0.38	2421.3	0.2	0.41	14.78	0.64	1.29	51	4	2.03
09U140	5.65	0.34	0.31	2429.4	0.17	0.20	14.05	0.88	3.21	70	5	2.53
12U357	6.02	0.61	0.54	2307.8	0.63	1.06	15.87	0.45	0.45	36	2	1.77
UN26	5.66	0.11	0.09	2536.7	0.99	3.12	18.16	0.09	0.14	14	1	1.25
UN34	5.45	0.18	0.17	2487	0.95	4.37	15.75	1.11	4.42	69	5	3.66
Mean	**5.69**	**0.34**	**0.30**	**2436.4**	**0.59**	**1.83**	**15.72**	**0.63**	**1.90**	**48.0**	**3.4**	**2.25**

Table 5

Genotype	CLUSTER= 4 (16/40)											
	FWWC	SIPC	ASV	NFP	$SIPC_1$	ASV_1	Yield	$SIPC_2$	ASV_2	YSI	Class	MTSI
09U086	5.56	0.19	0.17	2790.6	1.39	4.14	16.22	1.2	4.52	68	5	3.69
09U136	5.62	0.07	0.06	2673.5	0.66	0.82	15.27	0.69	2.01	56	4	1.53
12U360	6.04	0.24	0.23	2765.1	0.14	0.20	17.81	0.22	0.26	22	1	**0.62**
12U377	5.96	0.48	0.6	2655.8	0.3	0.52	16.95	0.24	0.30	31	2	1.48
12U347	6.2	0.25	0.23	2565.7	0.13	0.41	18.12	1.41	2.88	44	3	2.34
12U350	6.53	0.29	0.28	2726.1	0.36	1.53	18.83	0.23	0.47	12	1	**1.02**
12U374	5.71	0.42	0.37	2787.3	0.5	0.58	17.13	0.25	0.63	35	2	**1.2**
12U399	5.63	0.36	0.31	2600.6	0.47	2.25	17.33	0.16	0.80	34	2	1.21
Kenia	5.55	0.36	0.31	2767	1.12	2.48	18	0.81	2.17	40	3	2.22
Neira	7.19	1.88	1.69	2746.2	0.84	2.41	19.35	0.6	1.96	26	2	5.87
Silvania	5.63	1.05	1.07	2563.8	0.32	1.26	18.04	0.72	2.55	42	3	3.68
Test	6.22	0.12	0.11	2726.5	0.59	2.66	17.22	0.73	2.49	52	4	1.94
UN01	5.58	0.18	0.15	2660.3	0.62	2.74	18.3	0.96	3.77	46	3	2.59
UN03	5.52	0.24	0.21	2713.8	0.8	3.50	17.97	0.87	3.37	51	4	2.64
UN30	5.94	0.12	0.11	2622.8	0.82	2.31	17.95	0.54	1.62	37	3	1.65
UN43	5.00	0.18	0.22	2659.8	0.5	1.96	15.25	1.56	4.59	73	5	3.41
Mean	**5.87**	**0.40**	**0.38**	**2689.06**	**0.60**	**1.86**	**17.48**	**0.70**	**2.15**	**42**	**3**	**2.32**
Genotype	**CLUSTER= 5 (3/40)**											
	FWWC	SIPC	ASV	NFP	$SIPC_1$	ASV_1	Yield	$SIPC_2$	ASV_2	YSI	Class	MTSI
UN36	5.16	0.17	0.17	3559.1	1.57	5.19	18.99	0.32	0.87	16	1	3.09
UN45	5.29	0.34	0.46	3339.9	0.94	2.62	20.21	1.49	2.72	30	2	3.83
UN52	5.79	0.45	0.4	3288.9	1.10	3.56	19.85	0.83	1.23	14	1	3.05
Mean	**5.41**	**0.32**	**0.34**	**3395.97**	**1.20**	**3.79**	**19.68**	**0.88**	**1.61**	**20**	**2**	**3.32**

FWWC = fruit weight without calyx (g); NFP = number of fruits per plant; SIPC = sum of the absolute values of the interaction scores with subindex; ASV = stability value; YSI = RASV + RY with the following classes: 1 = (9-22), 2= (23-36), 3 = (37-50), 4 = (51-64), 5 = (65-78); RY= range of average yield; MTSI = stability index. Subscripts 1 and 2 are measures of NFP and yield. Shaded and italicised genotypes are genotypes selected by MTSI.

The genotypes that contributed to the FWWC GEI included the following: 09U089, 12U368, and Puracé from the second group; 09U128 and 12U357 from the third group; 12U377, Neira, and Silvania from the fourth group; and UN52 from the fifth group. The FWWC of these genotypes ranged from 5.11 to 7.19 g, with a mean of 5.93±0.55 g and a higher frequency of weights above 5.60 g. The SIPC values ranged between 0.45 and 1.88, and ASV values between 0.41 and 1.69. In Table 5, the average of some non-stable genotypes, such as Neira with an FWWC of 7.19 g, showed high values in the AMMI stability parameters (SIPC = 1.88; ASV = 1.69). This genotype was closer to the Puerres location, where it achieved a fruit weight of 9.20 g, making it a suitable recommendation for this location if high FWWC genetic material is desired.

The overall mean FWWC was 5.85±0.54 g, with values ranging from 5.00 to 7.24 g. These weights fell within the FWWC range, and the natural ranges reported for the species. Previous studies on Colombian hybrids have reported mean fruit weights close to 6.6 g, confirming the variability of this trait and its dependence on genotype and environmental factors (Lagos-Burbano et al. 2020). In this study, except for UN43 (FWWC = 5 g), the research population exceeded the upper limit of Colombian *P. peruviana* weights, demonstrating

population variation and a tendency among producers to favor larger fruits. The stable genotypes exhibited FWWC values ranging from 5 to 6.53 g, with a mean of 5.76 g. For *P. peruviana*, high average and stability values can be used as criteria to select and enhance FWWC (Kang 2020).

Among the locations, the most stable was Gualmatán (SIPC = 0.65; ASV = 0.55) with a mean FWWC of 5.32 g, and Ipiales (SIPC = 0.68; ASV= 0.64) with an FWWC of 6.10 g. Obonuco (FWWC = 7.44 g) and Puerres (FWWC = 7.44 g) were further from the origin in both CP1 and CP2, making them the most discriminative and unstable locations, with SIPC= 1.74 and ASV = 1.62 for the first location, and SIPC = 1.51 and ASV = 1.45 for the second.

The stability parameters are derived from calculations based on the eigenvector scores of the principal interaction components. Thus, genotypes with higher contributions to CPI, whether positive or negative, are more specifically adapted to particular environments, while those with the lowest scores are classified as the most stable across all tested environments (Olivoto et al. 2019).

For NFP at the start of the harvest, the ranking analysis (Table 5) indicated that the lowest averages of stability parameters (SIPC1 and ASV1) were found in the second, third, and fourth groups. The stable genotypes for NFP were as follows: 09U099, 12U368, and UN49 in the second group; 09U128 and 09U140 in the third group; and 12U360, 12U377, and 12U347 in the fourth group. These genotypes represented 20% of the population studied and showed NFP values ranging from 2,421.30 to 3,015.10, with a mean of 2,699.13±218.22, SIPC1 values between 0.04 and 0.30, and ASV1 values between 0.15 and 0.82.

The genotypes that contributed most to NFP GEI, with a mean of 2805.26±513.81, SIPC1 values between 0.91 and 1.57, and ASV1 values between 2.48 and 5.19 (Table 5), were as follows: 13U408 and 13U407 from the first group; Puracé, UN14, UN19, and UN35 from the second; UN26 and UN34 from the third; 09U086 and Kenia from the fourth; and UN36, UN45, and UN52 from the fifth group. The most stable environment was Obonuco, with SIPC1 = 0.46 and ASV1= 1.86, though it had the lowest average yield, with 1131.81 fruits per plant. In general, the environments were positioned on opposite axes of the biplot plane for CP1 and CP2, indicating differential discriminative power across the four locations. Gualmatán (NFP = 5117.24), with SIPC1= 1.05 and ASV1 = 5.16, was the farthest from the origin and the most unstable location. Genotypes Puracé, UN19, UN35, UN36, and UN52, with NFP values between 6215 and 7603, were well adapted to this location. In Ipiales (SIPC1 = 0.76; ASV1= 1.38), genotypes 12U352, 13U407, Kenia, and UN14 were adapted, with NFP values between 2967 and 4510, while in Puerres (SIPC1 = 0.95; ASV1 = 2.10), genotypes 09U086 and Kenia showed adaptation with NFP values of 2,626 and 2,351 fruits per plant, respectively. Both Gualmatán and Puerres exhibited the highest SIPC1 and ASV1 values, indicating a strong impact on the GEI of *P. peruviana* NFP (Esan et al. 2023).

Quevedo et al. (2015) report that NFP depends not only on the location's plant density but also on the planting and trellising system, obtained yields of 6,000 to 7,200 fruits with a density of 5,000 plants per ha, 4,974 to 6,076 fruits with 2,500 plants per ha, and 5,975 to 6,636 fruits with 1,666 plants per ha. These values exceed the averages observed in the evaluated locations; however, within these genotypes, production ranged from 6,200 to 7,600 fruits per plant, aligning with the data from Quevedo et al. (2015) and significantly surpassing the 600 fruits per plant reported under greenhouse conditions in southern Colombia (Criollo et al. 2014).

Regarding yield, Figures 1, 2, and 3A display the various biplots generated from the GGE biplot analysis. Figure 3B presents the genotypes selected in the MTSI analysis based on FWWC, NFP, and yield variables recorded across the 40 *P. peruviana* genotypes evaluated in the four locations of Nariño. The average yield across these locations was 17.33 t ha^{-1}, surpassing both the departmental average of 10.47 t ha^{-1} and the national average of 12.47 t ha^{-1} (MADR 2019). The discrimination versus representativeness established with environmentally centered data from the GGE biplot analysis is illustrated in Figure 1A, which shows how the ideal environment can be both informative and representative. This environment is indicated by the

arrow with the longest vector (Figure 1A) and is further highlighted by an arrow and circle in Figure 2B, projecting positively on the axis of the environmental mean (Khan et al. 2021). The concepts of informativeness and representativeness focus on environments in terms of their ability to identify the top-performing genotypes (discriminativeness) and to adequately represent the test environments (representativeness) (Esan et al. 2023).

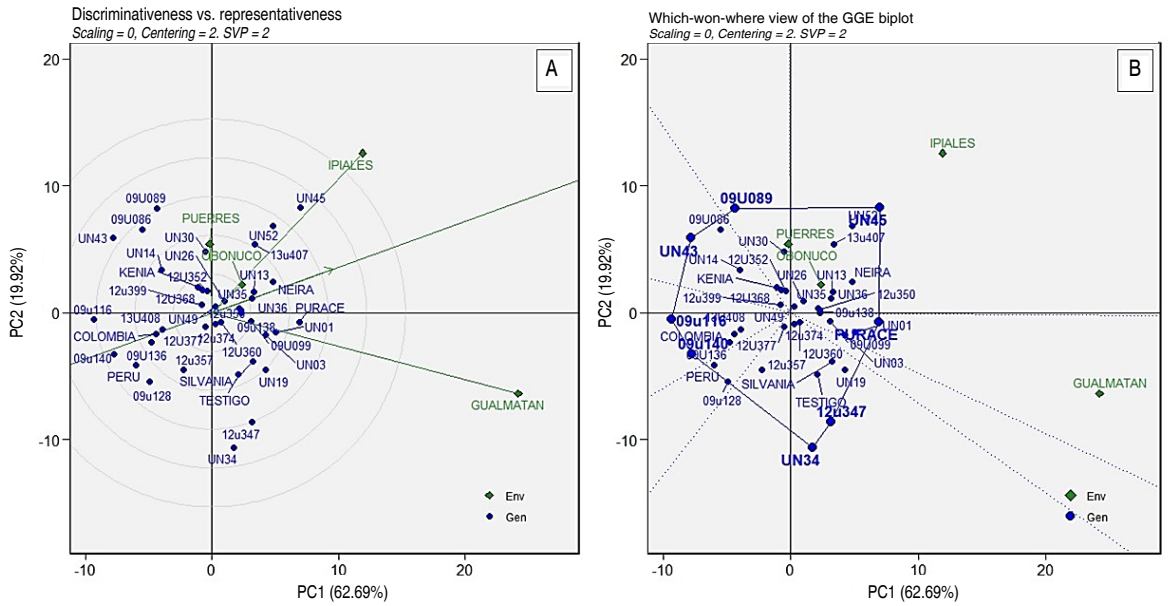


Figure 1. GGE biplot. **A**. discriminatory power versus representativeness based on data centered around the environment; and **B**. polygon of the GGE biplot analysis for who won where under the effects of the GEI.

An environment is considered more desirable when it is closer to the ideal environment (Yan 2014). In this study, Gualmatán, with a yield of 31.67 t ha^{-1}, was the locality closest to the ideal environment, making it the most discriminative and representative. Ipiales, with a yield of 22.28 t ha^{-1}, was also relatively close to the ideal environment. Thus, Gualmatán emerged as the most desirable environment for identifying superior-performing *P. peruviana* genotypes.

Puerres (yield = 10.95 t ha^{-1}) and Obonuco (yield = 4.43 t ha^{-1}) were considered undesirable environments for identifying high-yielding genotypes. As shown in Figures 1A and 2B, the longer the environmental vector, the greater its capacity to discriminate among genotypes, while a smaller angle with the abscissa indicates a more representative environment (Yan 2014).

In the "who-won-where" biplot, a product of the GGE biplot analysis (Figure 1B), the biplot polygon enabled the identification of winning genotypes under genotype-environment interaction patterns (Wardofa et al. 2019). The genotype plus GEI variation (G + G x E) for yield was 82.61%, with PC1 explaining 62.69% and PC2 explaining 19.92%, providing a valid approximation of the G x E variation in the data.

According to the yield evaluation of the 40 *P. peruviana* genotypes across four environments, the GGE biplot was divided into six sections, each containing one, two, or three vertex genotypes. The environments were situated in a single, largest section of the biplot, featuring different winning genotypes. The vertex genotypes included 09U089, UN45, Puracé, 12U347, 09U140, 09U116, UN34, and 09U089 (Figure 1B). These genotypes were the top responders and could be the best or worst performers in some or all environments. The apex genotype in each quadrant represents the highest yield for the environment within that quadrant (Olivoto et al. 2019). In this context, genotypes 09U089, UN45, and Puracé exhibited the highest yields. UN45 yielded 35.65 t ha^{-1} in Gualmatán and 30.40 t ha^{-1} in Ipiales.

Puracé produced 37.93 t ha^{-1} in Gualmatán and 25.35 t ha^{-1} in Ipiales. Genotype 09U089 yielded 25.97 t ha^{-1} in Gualmatán and 23.59 t ha^{-1} in Ipiales, while 12U347 with 36.92 t ha^{-1} and UN34 with 35.28 t ha^{-1} showed specific adaptability to Gualmatán. Genotypes 09U140, 09U116, and 09U089, located at opposite vertices, did not achieve top performance in any of the four environments, and are thus considered among the lowest-performing genotypes in certain or all environments (Yan 2014).

Figure 2A shows the biplot known as the "ranking of genotypes," which visualizes genotype performance in the average environment (AE). The thick line extending from the origin of the biplot toward a small circle represents the center of concentric circles and is referred to as the average environment axis (AEA). Another line, perpendicular to the AE and passing through the biplot origin, separates genotypes with below-average yields from those with above-average yields (Oliveira et al. 2019). Genotypes are ranked according to their performance relative to the AEA along the AE, with higher averages in the direction of the arrow. The best averages were reported for UN45 (20.21 t ha^{-1}) > UN52 (19.85 t ha^{-1}) > Puracé (19.60 t ha^{-1}) > and Neira (19.35 t ha^{-1}).

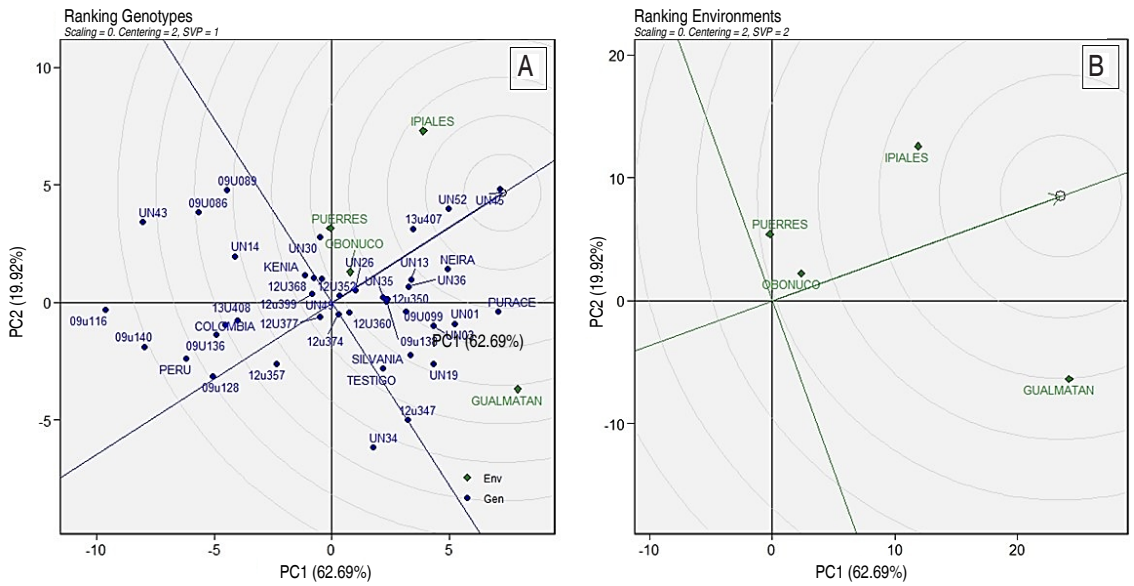


Figure 2. A. Classification of genotypes; and **B**. Ranking of environments resulting from the GGE biplot analysis based on the GEI evaluation.

Considering the stability parameter YSI (Table 5), genotypes UN45 (YSI = 30), UN36 (YSI = 16), and UN52 (YSI = 14) from the fifth group fall into class two based on the YSI frequency distribution classification. Similarly, Neira (YSI = 26) from the fourth group and 13U407 (YSI = 22) from the first group also belong to class two, while UN13 (YSI = 21) from the second group is in class one. These genotypes were considered stable for yield due to their low YSI values. YSI integrates both yield and yield stability into a single index, addressing the limitation of using yield stability alone as a selection criterion, given that the most stable genotypes do not necessarily have the highest yields. The YSI parameter associated with genotype classification is based on the ASV parameter, which involves IPC1 and IPC2 (Pour-Aboughadareh et al. 2022).

Figure 3A shows the classification of genotypes based on the criterion of average yield versus stability. This figure represents the "Average Environmental Coordination" (AEC), which facilitates comparisons between genotypes by average yield and stability across all environments within a mega-environment. The longest vector, with an arrow pointing to a small circle representing the average environment, extends from the biplot origin and is surrounded by concentric circles. This average environment is defined by the mean scores of IPC1 and IPC2 across all environments (Figure 2). The average environment (AE) can be viewed as a virtual tester (Oliveira et al. 2019). Figure 3A also shows a line with an arrow originating from the biplot's origin and pointing toward the average environment. This line is known as the average

environmental axis (AEA) or the average environmental coordination abscissa (AECA). Additionally, another line passes through the biplot origin perpendicular to the AEA, with a set of lines parallel to this perpendicular line that starts from each genotype marker and project toward the AEA.

The projections of the genotype markers onto the AEA represent the main effects of the genotypes (G). The arrow on the AEA axis points in the direction of higher average genotype yields, thereby ranking genotypes according to their average yield. In this case, the highest average yield corresponds to genotype UN45. According to the ANOVA (Table 3), significant differences were found between genotypes, indicating that the ranking of genotypes along the AEA abscissa is strongly correlated with G (Shirzad et al. 2025). Based on G (Figure 3A), the genotypes are ranked as follows: UN45 > UN52 > Puracé > Neira > 13U407 > UN01 > UN13 > UN13 > UN36 = UN03 > Test > Mean (17.33 t ha^{-1}) > 09U89 > ... > Colombia > ... > 09U116. The GGE analysis represents the contribution of G+GE, and since the AEA abscissa approximates the contributions of genotypes to G, the AEA ordinate should approximate the contributions of genotypes to GE. Thus, this serves as a measure of genotype stability or instability (Achenef 2022). In this context, the most stable genotype was UN45, positioned almost directly on the AEA abscissa with a projection close to zero on the AEA ordinate. Genotypes UN52, 13U407, UN36, UN13, UN49, UN26, 12U360, and Neira, with YSI values ranging from 14 to 26, can also be considered stable. These genotypes were primarily in class one in the YSI frequency distribution classification, except for UN49 and Neira, which were in class two. Conversely, Puracé, UN01, UN03, UN19, Silvania, UN30, and Test were among the least stable, with yields between 17.22 and 19.60 t ha^{-1}, higher than the overall mean. These genotypes fell into the third and fourth YSI classes, with values ranging from 37 to 52 (Table 5).

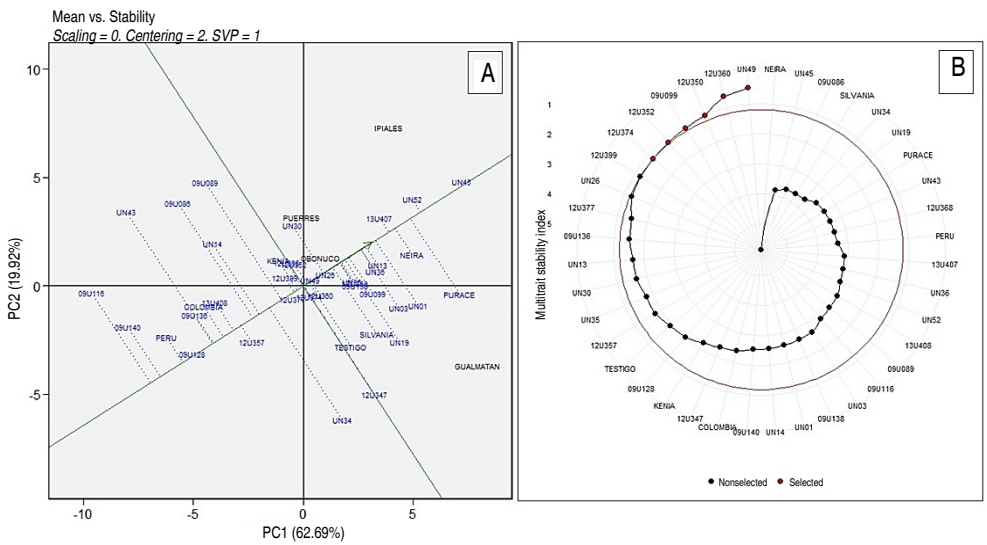


Figure 3. A. Mean and stability performance of genotypes derived from GGE biplot analysis; and **B**. Selected genotypes of *Physalis peruviana* L. based on multiple trait stability index (MTSI).

An "ideal" genotype is defined as a hypothetical genotype that combines the highest mean performance and absolute stability across environments. In the GGE biplot, genotypes are ranked according to their distance from this "ideotype", with those closest considered the most desirable. In this study, the concept of the ideal genotype was used to graphically support the identification of superior and stable genotypes, while the final selection was strengthened by the MTSI index, integrating both visual stability patterns and multi-trait performance (Yan 2014). An ideal genotype should consistently achieve high yields across all environments and is graphically represented by the longest vector in IPC1 and IPC2 with no projections. This is indicated by the arrow pointing to a small circle surrounded by concentric circles (Figures 2A and 3A). Although this genotype is theoretical, it serves as a benchmark for

evaluating genotypes, aiming to place the most promising ones as close as possible to it (Abreu et al. 2019). This aligns with the results above, where UN45 would be the ideal genotype, followed by other stable genotypes such as UN52 and 13U407.

The yields observed in the evaluated population exceed the averages reported by Mayorga-Cubillos et al. (2019), who evaluated a collection of 14 *P. peruviana* genotypes under the conditions of the Agrosavia-Tibaitatá Research Center in the department of Cundinamarca. These findings are significant because the evaluation included genotypes 09U086, 09U089, 09U099, 09U116, 09U128, 09U136, 09U138, and 09U140, which were also part of the present study and showed remarkable yields in Gualmatán and Ipiales. Similarly, the yields in this study surpass those obtained by Herrera et al. (2012), who evaluated 54 accessions from the central and northern Andean regions of Colombia under greenhouse conditions, yielding 8.4 t ha^{-1} with a planting density of 1333 plants ha^{-1}. In other regions of Colombia, there is a broad climatic diversity that aligns with the physiological requirements of the crop, leading to differences in yield and fruit composition—even at the same phenological stages for different genotypes (Monroy 2020). These findings underscore the genotype-by-environment interaction demonstrated in this research.

The MTSI index, based on FWWC, NFP, and yield (Figure 3B), enabled the selection of six genotypes as the most stable and well-balanced across these variables. MTSI is more effective than direct, univariate selection based solely on yield, highlighting its value as a robust tool for developing improved selection strategies that optimize resource and time use, thereby contributing to the sustainability of breeding programs (Olivoto et al. 2021).

Cluster factor one (FA1) linked NFP and yield, with a significant correlation coefficient of 0.62, indicating that these two variables are associated. FA2 corresponded to FWWC, which did not correlate with yield and showed a negative association with NFP (r = -0.36). The MTSI index facilitated the selection of genotypes 09U099, 12U352, UN49, 12U360, 12U350, and 12U374 (Figure 3B and Table 5), representing a selection pressure of 15%. Based on the means of the original population and the selected genotypes, the direction of selection for the analyzed variables was determined (Huanuqueño et al. 2022). In this case, for all three variables evaluated, the six selected genotypes increased the trait values, indicating a positive selection direction. The selection differential for these variables was positive, with an increase of 146.10 fruits for NFP, 0.60 t ha^{-1} for yield, and 0.14 g for FWWC. Broad-sense heritability was acceptable and moderate for NFP (h^2 = 0.32) and yield (h^2 = 0.47), and high for FWWC (h^2 = 0.63), although heritability values for economically significant traits in *P. peruviana* have not been previously reported. This heritability indicates that a considerable portion of the phenotypic variance was due to genetic factors.

The MTSI index is an efficient and rapid method for identifying high-yielding and productive genotypes (Olivoto et al. 2019). An MTSI value of 1.20 was set as the cutoff to identify stable genotypes (Figure 3B, red circle). Genotypes with values equal to or below 1.20 were considered the most stable, showing an average MTSI of 0.93. According to the classification analysis, the selected genotypes 09U099 (MTSI = 1.12), 12U352 (MTSI = 1.17), and UN49 (MTSI = 0.47) belong to the second group, while 12U360 (MTSI = 0.62), 12U350 (MTSI = 1.02), and 12U374 (MTSI = 1.20) are from the fourth group (Table 5).

CONCLUSION

Environmental effects were the primary contributors to yield expression and fruit quality traits in *Physalis peruviana* L., while genotype × environment interaction played a key role in determining genotype stability and adaptation across environments. The combined use of AMMI, GGE biplot, and MTSI models enabled the identification of genotypes with high stability and specific adaptation, such as UN45 and Puracé, which exceeded national and regional yield averages. The best performance was observed in environments such as Puerres, characterized by favorable climatic conditions, including moderate temperatures and adequate rainfall, which promoted optimal crop development. These findings confirm the importance of integrating multivariate tools to optimize genetic selection and guide breeding programs toward resilient and productive materials under climate variability scenarios.

The stability observed in key variables such as fruit weight without calyx and fruit number per plant, together with the identification of superior genotypes through the multi-trait stability index (MTSI), validates the use of these criteria as reliable references for agronomic management decisions and cultivar selection. These results not only expand knowledge of *P. peruviana* productive physiology but also strengthen the scientific basis for its positioning as a strategic Andean crop in high-value international markets.

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CONFLICT OF INTERESTS

The authors declare that there is no conflict of interest that could compromise the validity of the results presented in this manuscript, either during its preparation, evaluation, or the process of joint authorship.

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