# Morpho-agronomic characterization and yield performance of quinoa (*Chenopodium quinoa* Willd.) genotypes

## Caracterización morfoagronómica y desempeño de rendimiento de genotipos de quinua (*Chenopodium quinoa* Willd.)

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### ABSTRACT

Quinoa (*Chenopodium quinoa* Willd.) stands out for its high nutritional value and agroecological adaptability, positioning it as a strategic crop in specialized markets. In Colombia, establishing crops in high Andean regions requires identifying improved genotypes with high yield potential and grain quality. The objective of this study was to agronomically characterize 14 improved sweet quinoa families, including the San Jorge family, and three commercial checks (Aurora, Blanca de Jericó, and Tunkahuan) under the agroecological conditions of Silvia (Cauca, Colombia), using a randomized complete block design with four replicates. Eleven morpho-agronomic variables were evaluated, and statistical analyses of ANOVA, Duncan's test ($P<0.05$), principal component analysis (PCA), hierarchical cluster analysis, and selection index were applied. The results revealed high variability among the genotypes. The highest yield per hectare and per plant was recorded for the genotype F56 (6623.1 kg ha$^{-1}$ and 30.33 g), followed by the genotype FSJ. F25 stood out for the highest thousand-seed weight (3.13 g), and F38 for the largest grain diameter (2.38 mm). Aurora exhibited the most significant plant height (132.4 cm) and panicle length (53.9 cm), while F56 and F37 had the highest panicle diameter (68.79 mm) and stem diameter (16.5 mm). PCA explained 65.21% of the total variability, highlighting F56, FSJ, Aurora, and Blanca de Jericó as the genotypes with the most significant contribution. The most influential variables were plant height, yield, and thousand-seed weight. Cluster analysis grouped the 17 genotypes into three clusters: Group 1 (Aurora and Blanca de Jericó) characterized by robust architecture; Group 2 (Tunkahuan), with intermediate traits; and Group 3 (the remaining improved genotypes), which exhibited high productive efficiency and grain quality. Finally, the selection index effectively identified superior genotypes, positioning F56 and FSJ as promising candidates for future breeding and agronomic validation programs in high-altitude Andean zones.

**Keywords:** Andean crop, genetic variability, genetic diversity, genetic improvement, selection index.

### RESUMEN

La quinua (*Chenopodium quinoa* Willd.) destaca por su valor nutricional y adaptabilidad agroecológica y la posiciona como un cultivo estratégico en mercados especializados. En Colombia, su consolidación en zonas altoandinas exige la identificación de genotipos mejorados con alto rendimiento y calidad de grano. El objetivo de esta investigación fue caracterizar agronómicamente 14 familias mejoradas de quinua dulce, incluida la familia San Jorge y tres testigos comerciales (Aurora, Blanca de Jericó y Tunkahuan) en condiciones del municipio de Silvia (Cauca, Colombia), mediante un diseño de bloques completamente aleatorizado con cuatro repeticiones. Se evaluaron 11 variables morfoagronómicas y se aplicaron análisis estadísticos de ANOVA, prueba de Duncan ($P<0.05$), análisis de componentes principales (ACP), análisis de conglomerados jerárquicos e índice de selección. Los resultados evidenciaron una alta variabilidad entre genotipos. El mayor rendimiento por hectárea y por planta fue registrado por el genotipo F56 (6623,1 kg ha$^{-1}$ y 30,33 g), seguido del genotipo FSJ. F25 destacó por el mayor peso de mil semillas (3,13 g) y F38 presentó el mayor diámetro de grano (2,38 mm). Aurora, testigo comercial, exhibió la mayor altura de planta (132,4 cm) y longitud de panoja (53,9 cm), mientras que F56 y F37 registraron los valores más altos en diámetro de panoja (68,79 mm) y de tallo (16,5 mm). El ACP explicó el 65,21% de la variabilidad total, resaltando a F56, FSJ, Aurora y Blanca de Jericó como los genotipos de mayor contribución. Las variables más influyentes fueron altura de planta, rendimiento y peso de mil semillas. El análisis de agrupamiento clasificó los 17 genotipos en tres grupos: el grupo uno (Aurora y Blanca de Jericó), caracterizado por arquitectura robusta; el grupo dos (Tunkahuan), con características intermedias; y el grupo tres (resto de los genotipos mejorados), con alta eficiencia productiva y atributos de calidad. Finalmente, el índice de selección permitió identificar genotipos con alto potencial productivo y calidad física del grano, proponiendo a F56 y FSJ como candidatos clave para futuros programas de mejoramiento y validación en zonas altoandinas.

**Palabras clave:** cultivo andino, variabilidad genética, diversidad genética, mejoramiento genético, índice de selección.

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## Introduction

Quinoa (*Chenopodium quinoa* Willd.) is a species native to the Andes, recognized for its high nutritional value, due to its high content of proteins, essential amino acids, vitamins, isoflavones, minerals, carbohydrates, and unsaturated fats (Sampaio *et al.*, 2020). Quinoa is one of the few species with a remarkable capacity to adapt to extreme climatic and edaphic conditions without being significantly affected. Its cultivation is fundamental, as it represents a key strategy to confront climate change (Reguera *et al.*, 2018). It exhibits efficient water use, tolerance to low soil moisture, and excellent adaptation to different climates, including deserts (Dehghanian *et al.*, 2024). Therefore, quinoa contributes to food security in various regions of the world (Castro *et al.*, 2023).

Quinoa yields have been boosted by genetic improvement, due to the nutritional properties of the seeds, especially the content of amino acids, macrocomponents (proteins, carbohydrates, and lipids), and some microcomponents such as vitamins, minerals, and polyphenols, which contribute to the manufacture of foods with health benefits (Argüello *et al.*, 2024). However, the nutrients found can be significantly different among ecotypes, which has prompted an increase in quinoa breeding programs in recent years to study genetic variability in the expression of phenological, morphological, agronomic, and grain compositional traits (Delgado *et al.*, 2024).

The central quinoa-producing departments in Colombia are Boyaca, Cundinamarca, Nariño, and Cauca, the latter of which has annual yields ranging from 2.5 to 3 t ha$^{-1}$. Meanwhile, in the Andean countries, annual yields of 1 to 1.5 t ha$^{-1}$ have been reported, although some yields of 4 t ha$^{-1}$ per year have also been reported (Montes-Rojas *et al.*, 2020). These quinoa-producing regions have focused on developing a national strategy to increase yields through agroecological management, utilizing both ancestral and modern practices. Crop nutrition is carried out with organic matter collected and manufactured with crop residues predominant in each region (García *et al.*, 2018). These productions are targeted at local markets to increase the country's per capita consumption of quinoa. In addition, exports have been boosted because quinoa has gained wide acceptance in North America, Africa, Asia, and Europe, mainly in countries seeking organic crops, to change the eating habits of consumers of products such as rice, potatoes, and other foods traditionally used (Pizo Ossa *et al.*, 2024).

In this context, the Aurora and Tunkahuan genotypes have been widely used in the Nariño and Cauca regions due to their adaptability to mid- and high-altitude environments (2,500–3,000 m a.s.l.), their stable vegetative cycle, grain quality accepted by the market, and reliable performance under variable climatic conditions (Montes *et al.*, 2018; Morillo-Coronado *et al.,* 2023). The Aurora ecotype has demonstrated exemplary performance in temperate environments, with a phenological cycle ranging from 160 to 170 d to harvest, average grain yields between 2,000 and 2,800 kg ha$^{-1}$, and a thousand-seed weight of approximately 2.7 g. Tunkahuan, on the other hand, is characterized by its short stature (average height of 95 cm), resistance to lodging, early maturity (125 to 140 d to harvest), low saponin content (below 0.05%), and an average yield of around 2,500 kg ha$^{-1}$ (Pizo Ossa *et al.,* 2024; Urdanegui *et al.,* 2021). Their use as parental lines in breeding programs enables the development of advanced lines with high agronomic potential, as in the present study, which aims to identify promising genotypes adapted to the agroecological conditions of eastern Cauca.

In the department of Cauca, Colombia, this crop represents an opportunity and a key economic line for indigenous and peasant communities, as it contributes to food sovereignty and security in the region (Anchico-Jojoa *et al.*, 2023). Quinoa has also contributed to combating malnutrition thanks to its nutritional properties and has boosted economic development. This crop has strengthened the ties between producers and their communities, fostering a solid and sustainable relationship with them, who encourage planting through entrepreneurship to develop sustainable alternatives, given the uses of this promising crop in agribusiness (Flórez-Martínez *et al.*, 2024).

Given the increasing need to identify genotypes adapted to specific agroecological conditions, this study focuses on the morpho-agronomic characterization of 17 quinoa genotypes, including 14 families derived from the Aurora × Tunkahuan cross and three commercial checks. The aim of this evaluation was to select genotypes exhibiting desirable agronomic traits such as shorter growth cycles, superior grain physical quality, yield stability, and adaptability to adverse edaphic and climatic conditions. The outcomes of this research are expected to support breeding programs, enhance the diversification of the regional genetic base, and promote more resilient cropping systems in mid- to high-altitude environments.

## Materials and methods

### Plant material and experimental design

Fourteen sweet quinoa families, derived from the cross between the Aurora and Tunkahuan ecotypes including one identified as the "San Jorge family" were evaluated alongside three commercial checks: Aurora, Blanca de Jericó, and Tunkahuan (Tab. 1). The 17 genotypes were established in the field on deep, well-drained soils with loamy sand to sandy clay loam texture, rich in organic matter, classified as Andisols according to the USDA Soil Taxonomy and as Humic Andosols under the WRB-FAO classification system, using a completely randomized block design with four replicates. The experimental unit consisted of a plot measuring 14 m in length and 3.0 m in width, where the 17 genotypes were randomly assigned within each plot. Row spacing was set at 0.70 m, with 0.10 m between plants, resulting in a total of 68 rows. For the evaluation, plants located within the central 2 m were harvested, and border rows were excluded.

The quinoa genotypes evaluated in this study were cultivated under homogeneous agronomic conditions, thereby eliminating the influence of management variability on the observed responses. Organic fertilization was carried out using compost, produced from the co-composting of sugarcane filter cake (a byproduct of the sugar industry) and high-quality poultry manure, which was incorporated into the soil 20 d before sowing to enhance its physical and chemical structure and ensure optimal decomposition. Additionally, the organic fertilizer Agrofertil (produced by Agrofertil S.A.S., Colombia), commonly known as A.L.O.F.A. (Aerobically Fermented and Mineralized Liquid Organic Fertilizer), was applied both foliarly and via the root system throughout the crop cycle. This product is water-soluble and produced in Colombia through aerobic fermentation of macerated plant material, complemented with trace elements, humic and fulvic acids, Huila phosphorite, silicon oxide, and organic additives. The formulation is stabilized at a pH of 5.7, ensuring a balanced organic-mineral nutrient supply to the crop. This standardized management approach enabled the differences observed among genotypes to be primarily attributed to genetic expression and their interaction with the climatic and edaphic conditions of the study area.

Harvesting was conducted once the plants reached physiological maturity, determined by observing seed color, texture, and the fingernail test. The central 2 m of each plot was used for sampling, excluding the borders, with the aid of a 3-m handmade ruler. Plants were cut using pruning shears and labeled according to genotype and number of panicles. The samples were transported to a greenhouse, where panicles were separated and left to dry for 15 to 20 d. Subsequently, manual threshing was performed. Seeds were cleaned using sieves and mesh screens, then stored in

**TABLE 1.** List of evaluated quinoa genotypes, their type, and origin used in the field trial.

| Code | Name / Family | Type of material | Origin |
| --- | --- | --- | --- |
| F1 | Family 1 | Aurora × Tunkahuan progeny | Experimental cross |
| F2 | Family 2 | Aurora × Tunkahuan progeny | Experimental cross |
| F3 | Family 3 | Aurora × Tunkahuan progeny | Experimental cross |
| F4 | Family 4 | Aurora × Tunkahuan progeny | Experimental cross |
| F5 | Family 5 | Aurora × Tunkahuan progeny | Experimental cross |
| F6 | Family 6 | Aurora × Tunkahuan progeny | Experimental cross |
| F7 | Family 7 | Aurora × Tunkahuan progeny | Experimental cross |
| F8 | Family 8 | Aurora × Tunkahuan progeny | Experimental cross |
| F9 | Family 9 | Aurora × Tunkahuan progeny | Experimental cross |
| F10 | Family 10 | Aurora × Tunkahuan progeny | Experimental cross |
| F11 | Family 11 | Aurora × Tunkahuan progeny | Experimental cross |
| F12 | Family 12 | Aurora × Tunkahuan progeny | Experimental cross |
| F13 | Family 13 | Aurora × Tunkahuan progeny | Experimental cross |
| F14 | Family San Jorge | Aurora × Tunkahuan progeny | Experimental cross |
| T1 | Aurora | Commercial check | National Institute of Agrarian Innovation (INIA), Peru |
| T2 | Blanca de Jericó | Commercial check | Native germplasm collected and improved by farmers and Colombian universities, Antioquia, Colombia |
| T3 | Tunkahuan | Commercial check | National Institute of Agricultural Research (INIAP), Ecuador |

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sealed bags and transported to the AGROSAVIA laboratory in Popayán for agronomic evaluation.

## Location

The genotypes were evaluated during the second semester of 2023 in the San Fernando district, located in the municipality of Silvia, at an altitude of 2,660 m a.s.l., with an average annual temperature of 12°C, a relative air humidity of 80% and rainfall of 1,800 mm. The plants were fertilized organically, using cachaza (a byproduct of sugar cane and chicken manure production), complemented by manual weed control.

Harvesting was done manually when the genotypes reached harvest maturity between 120.31 and 168.48 d. For agronomic characterization, 11 agronomic variables were evaluated (Tab. 2), using the descriptors of quinoa and its wild relatives (Bioversity International *et al.*, 2013).

**TABLE 2.** Agronomic variables for the characterization of 17 *Chenopodium quinoa* genotypes.

| Variable | Abbreviation | Unit of measurement |
|---|---|---|
| Plant height | PH | cm |
| Panicle length | PL | cm |
| Panicle diameter | PD | mm |
| Stem diameter | SD | mm |
| Yield per plant | YPP | g |
| Yield (kg ha⁻¹) | YPH | kg |
| Weight of one thousand seeds | WTS | g |
| Grain diameter | GD | mm |
| Grain thickness | GT | mm |
| Harvest index | HI | % |
| Grain moisture content | MC | % |

## Statistical analysis

The coefficient of variation and mean were calculated; an ANOVA analysis was used with a value ($P<0.05$) with its respective Duncan mean test ($P<0.05$). A Principal Component Analysis (PCA) was performed using the correlation matrix between the variables, which were plotted on a two-dimensional plane to group the quinoa genotypes evaluated. Subsequently, a hierarchical cluster analysis was performed using hierarchical grouping (UPGMA) where Euclidean distance was applied. Finally, for the selection of quinoa genotypes, the selection index (SI) was used using Equation 1:

$$SI = Y \left(\frac{kg}{ha}\right)(0.50) - WTS(0.20) - GD(0.30) \qquad (1)$$

where

Y: yield, WTS: thousand-seed weight, GD: grain diameter.

The software R version 4.4 was used to process the information.

## Results and discussion

Table 3 presents the results of the analysis of variance ($P\leq0.05$), revealing statistically significant differences for most evaluated traits, except for harvest index ($P\leq0.0054$) and moisture content ($P\leq0.6641$). Highly significant differences ($P\leq0.0001$) were found for plant height, panicle length, panicle diameter, stem diameter, and thousand-seed weight, indicating a high level of genetic variability among the genotypes evaluated. In addition, significant differences were also detected for yield per plant ($P = 0.0009$), yield per hectare ($P\leq .0009$), grain diameter ($P\leq0.0007$), grain thickness ($P\leq0.0040$), and harvest index ($P\leq0.0054$). Conversely, no significant differences were observed for moisture content ($P\leq0.6641$), indicating a relatively uniform behavior for this trait across the genotypes.

### Descriptive analysis for agronomic variables

For the statistical comparison among genotypes, Duncan's multiple range test ($P\leq0.05$) was used.

Regarding the plant height variable, the average was 99.35 cm. The maximum values were obtained by the Aurora, Blanca de Jericó, and Tunkahuan controls with 132.4, 121.2, and 114.2 cm, respectively. The minimum values were obtained by F27 with a value of 81.8 cm and F86 with a value of 82.6 cm. For the panicle length variable, the average was 43.49 cm. The commercial controls Aurora and Blanca obtained the maximum values in Jericó with 53.9 cm and 50.5 cm, respectively.

In comparison, the minimum value was obtained by FSJ with 33.6 cm. For the panicle diameter variable, the average was 61.28 mm. The maximum results were observed in F103 and F56 with 74.09 and 68.79 mm, respectively, while the minimum value was shown in F27 with 54.84 mm. For its part, the stem diameter variable presented an average of 15.62 mm, with the maximum value shown by

**TABLE 3.** Analysis of variance for morpho-agronomic variables evaluated in 17 quinoa genotypes.

| Variables | Source of variation | SS | MS | F | P-value |
|---|---|---|---|---|---|
| Plant height (cm) | Genotype | 126414.46 | 7900.9 | 96.28 | <0.0001 |
| | Replicate | 23377.39 | 7792.46 | 94.96 | <0.0001 |
| | Total | 203954.4 | | | |
| Panicle length (cm) | Genotype | 17454.21 | 1090.89 | 21.51 | <0.0001 |
| | Replicate | 1573.13 | 524.38 | 10.34 | <0.0001 |
| | Total | 52496.98 | | | |
| Panicle diameter (mm) | Genotype | 1221.21 | 76.33 | 12.37 | <0.0001 |
| | Replicate | 35.27 | 11.76 | 1.91 | 0.1273 |
| | Total | 5321.89 | | | |
| Stem diameter (mm) | Genotype | 209.79 | 13.11 | 6.67 | <0.0001 |
| | Replicate | 279.81 | 93.27 | 47.43 | <0.0001 |
| | Total | 1787.41 | | | |
| Yield per plant (g) | Genotype | 810.3 | 50.6 | 3.2 | 0.0009 |
| | Replicate | 39.6 | 13.2 | 0.8 | 0.4784 |
| | Total | 1603.9 | | | |
| Yield (kg ha$^{-1}$) | Genotype | 52688969.6 | 3293060.6 | 3.2 | 0.0009 |
| | Replicate | 2576885 | 858961.7 | 0.8 | 0.4783 |
| | Total | 104303939 | | | |
| Weight of one thousand seeds (g) | Genotype | 5.77 | 0.36 | 16.98 | <0.0001 |
| | Replicate | 0.1 | 0.03 | 1.58 | 0.2075 |
| | Total | 6.89 | | | |
| Grain diameter (mm) | Genotype | 0.75 | 0.05 | 2.72 | 0.0007 |
| | Replicate | 0.11 | 0.04 | 2.08 | 0.1045 |
| | Total | 4.05 | | | |
| Grain thickness (mm) | Genotype | 0.2 | 0.01 | 1.05 | 0.0040 |
| | Replicate | 0.02 | 0.01 | 0.61 | 0.6122 |
| | Total | 2.44 | | | |
| Harvest index (%) | Genotype | 225.7 | 14.1 | 1.1 | 0.0054 |
| | Replicate | 65.1 | 21.7 | 1.7 | 0.1863 |
| | Total | 915.7 | | | |
| Grain moisture content (%) | Genotype | 71.3 | 4.5 | 0.8 | 0.6641 |
| | Replicate | 3.3 | 1.1 | 0.2 | 0.8957 |
| | Total | 337.7 | | | |

SS: Sum of squares, MS: mean square.

F37 at 16.5 mm, and the minimum value corresponds to F25 with 14.5 mm (Tab. 4).

The results obtained for plant height are like those reported by Chino Nicolas *et al.* (2019), who report heights between 100.4 to 136.8 cm, and suggest that plants within this range are easy to manage in intensive and mechanized agriculture, in addition to the fact that this characteristic is related to tolerance to grain lodging and sometimes with plants with late cycles. On the other hand, El-Harty *et al.* (2021) in studies conducted in Riyadh (Saudi Arabia) have categorized the height in three classifications, short (50-70 cm), medium (70-130 cm) and long (130-190 cm), and report that individuals with medium category have higher production of quinoa, while, in the long category presented lower yields; therefore, the classification obtained in the study, allowed to identify the families as medium and the controls as long.

For the panicle length variable, the values found in the study coincided with those reported by Morillo *et al.* (2020), who evaluated 19 quinoa materials in the department of Boyacá, with ranges that fluctuated between 12 cm and 45 cm. This variable is related to plant height and panicle diameter, especially at the point of development of the apical meristem, which contributes to its growth, as well as the joint interaction of genotypes with other factors such as the type of panicle, climatic conditions, planting density,

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**TABLE 4.** Duncan's test of means (*P*>=0.05) for plant height, panicle length, panicle diameter, stem diameter, and harvest index in 17 genotypes of *Chenopodium quinoa*. Different letters in the row indicate significant differences according to Duncan's test (*P*≤0.05).

| Genotype | PH | PL | PD | SD | HI |
|---|---|---|---|---|---|
| F27 | 81.8 a | 36.7 ab | 54.84 a | 15.2 bcd | 40 a |
| F86 | 82.6 a | 40.4 cd | 63.83 cd | 14.6 ab | 45 a |
| F105 | 88.6 b | 38.5 bc | 58.45 abc | 15.5 cde | 44 a |
| F103 | 88.8 b | 39.5 bc | 74.09 f | 15.6 cdef | 43.2 a |
| F110 | 89.4 b | 40.7 cd | 59.35 abc | 15.1 abc | 43.2 a |
| Familia San Jorge | 89.8 b | 33.6 a | 58.63 abc | 15.6 cdef | 41.1 a |
| F63 | 90 b | 39.5 bc | 57.96 ab | 15.8 cdef | 40.4 a |
| F23 | 93.1 bc | 42 cde | 61.62 bc | 15.6 cdef | 40 a |
| F38 | 95.4 c | 46.2 fg | 60.81 abc | 15.2 bcd | 44.4 a |
| F25 | 96 c | 45.3 ef | 58.15 ab | 14.5 a | 45.1 a |
| F34 | 104.7 d | 43.7 def | 60.13 abc | 16.3 fg | 38.4 a |
| F56 | 104.8 d | 46.4 fg | 68.79 e | 16.3 fg | 47.5 a |
| F60 | 107.7 d | 47.2 fg | 59.45 abc | 16.2 fg | 39.3 a |
| F37 | 108.4 d | 49.2 gh | 60.84 abc | 16.5 g | 40.4 a |
| Tunkahuan | 114.2 e | 46.1 fg | 67.61 de | 15.6 cdef | 33.8 a |
| Blanca de Jericó | 121.2 f | 50.5 h | 56.14 ab | 16.1 efg | 36.5 a |
| Aurora | 132.4 g | 53.9 i | 61.04 bc | 15.9 defg | 34.9 a |
| Mean | 99.35 | 43.49 | 61.28 | 15.62 | 41.01 |
| C.V.(%) | 10.71 | 16.28 | 16.76 | 9.60 | 13.08 |

PH: plant height; PL: panicle length; PD: panicle diameter; SD: stem diameter; HI: harvest index; CV(%): coefficient of variation. Means followed by the same letter within each variable do not differ significantly according to Duncan's multiple range test (*P*≤0.05).

and fertility provided to the crop. Regarding the panicle diameter variable, the results align with those cited by Estrada-Zúniga *et al.* (2022) in agronomic studies, which reported values ranging from 47.5 to 72 mm, likewise. Manjarres *et al.* (2021) report a strong correlation between panicle length, diameter, and height.

Stem diameter values are similar to those reported by Hussain *et al.* (2020), where they recorded diameters ranging from 8.65 to 14.99 mm; furthermore, this variable contributes to the selection of genotypes with thick stems, which could improve yield, increase the number of inflorescence and other aspects such as the prevention of lodging caused by adverse weather conditions (prolonged winds, excessive rainfall), by conferring resistance to panicle weight, as well as tolerance to bird damage.

### Descriptive analysis for performance variables

In the yield variable, the results are similar to those reported by Montes-Rojas *et al.* (2018), with yields ranging from 20 g to 32 g per plant. According to Hussain *et al.* (2020), this variable is directly related to genetic, environmental components, and genotype-by-environment interaction. Quinoa is very sensitive to abrupt changes in temperature, precipitation, and relative air humidity, which could have influenced the behavior of the controls, presenting the

lowest values. At the same time, F56 and FSJ showed a better response to yield, with an average yield gain of 13.03 g (44.41%), which could be shown by exceeding the response obtained by the commercial genotypes. For yield (kg ha⁻¹), the results agree with those reported by Montes-Rojas *et al.* (2020), with values ranging between 2424.5 and 4193 kg ha⁻¹. Likewise, a yield gain of 2826.39 kg ha⁻¹ (44.06%) was observed for FSJ and F56 compared to the commercial genotypes (Tab. 5).

Regarding the variable thousand-seed weight, the values are similar to those found by Morillo *et al.* (2020) in agromorphological evaluation, with an average weight of 2.40 g. In addition, an average gain of 0.99 g (31.93%) corresponding to Fl25 was observed, surpassing the response obtained by the controls. According to Madrid *et al.* (2018), they present a classification scale for this variable, where > 3 g is considered higher weight, integrated by 2 of 17 genotypes, from 2.5 to 3 g as medium weight, standing out (11 of 17 genotypes) and < 2.5 g as lower weights represented by the commercial controls. They also indicate that this variable is the primary component of yield, allowing for the measurement of the weight and number of seeds studied in each genotype, and is essential for selection in genetic improvement programs (García-Parra *et al.*, 2020).

**TABLE 5.** Duncan's test of averages for yield per plant, yield (kg ha⁻¹), thousand-seed weight, grain moisture content, grain diameter, and grain thickness in 17 *Chenopodium quinoa* accessions. Different letters in the row indicate significant differences according to Duncan's test (*P*≤0.05).

| Genotype | YPP | YPH | WTS | MC | GD | GT |
|---|---|---|---|---|---|---|
| Blanca de Jericó | 14.23 a | 3150.7 a | 2.12 a | 13.3 a | 2.24 abcd | 1.09 a |
| F60 | 15.77 ab | 3459.5 ab | 2.44 bc | 14 a | 2.27 abcd | 1.18 ab |
| Tunkahuan | 16.99 abc | 3704.8 abc | 2.19 ab | 14.5 a | 2.1 abc | 1.15 ab |
| Aurora | 17.71 abc | 3909.9 abc | 2.03 a | 13.4 a | 2.09 a | 1.1 ab |
| F27 | 20.19 abcd | 4398.9 abcd | 2.83 de | 14.5 a | 2.13 abc | 1.21 b |
| F34 | 20.58 abcd | 4491.3 abcd | 2.66 cd | 14.5 a | 2.33 cd | 1.18 ab |
| F103 | 21.33 abcd | 4614.3 abcd | 2.74 de | 15.2 a | 2.3 bcd | 1.18 ab |
| F25 | 21.34 abcd | 4654.1 abcd | 3.13 f | 14.4 a | 2.12 abc | 1.15 ab |
| F105 | 22.23 abcde | 4852 abcde | 2.85 de | 14.4 a | 2.11 abc | 1.15 ab |
| F23 | 23.12 bcde | 5043.2 bcde | 2.7 cd | 14.4 a | 2.31 bcd | 1.2 b |
| F63 | 23.12 bcde | 5056 bcde | 2.75 de | 14.3 a | 2.08 a | 1.19 ab |
| F110 | 23.61 bcde | 5135.4 bcde | 2.65 cd | 14.7 a | 2.1 ab | 1.2 b |
| F86 | 23.9 bcde | 5224.9 bcde | 3.02 ef | 14.2 a | 2.18 abc | 1.16 ab |
| F38 | 24.31 bcde | 5252.7 bcde | 2.81 de | 14.9 a | 2.38 d | 1.17 ab |
| F37 | 25.63 cde | 5495.4 cde | 3 def | 16 a | 2.15 abc | 1.15 ab |
| Familia San Jorge | 28.45 de | 6206.6 de | 2.8 de | 14.5 a | 2.16 abc | 1.14 ab |
| F56 | 30.33 e | 6623.1e | 2.67 cd | 14.4 a | 2.25 abcd | 1.19 ab |
| Mean | 21.93 | 4780.75 | 2.67 | 14.45 | 2.19 | 1.16 |
| C.V (%) | 19.54 | 22.28 | 5.81 | 5.29 | 8.70 | 6.73 |

YPP: yield per plant; YPH: yield (kg ha⁻¹); WTS: thousand-seed weight; MC: moisture content; GD: grain diameter; GT: grain thickness; C.V. (%): coefficient of variation. Means followed by the same letter within each variable do not differ significantly according to Duncan's multiple range test (*P*≤0.05).

Regarding the grain diameter variable, the results are similar to those cited by Emrani *et al.* (2020), indicating an average of 2.09 mm, which suggests that quinoa is one of the crops where its ecotypes present greater variability and genetic diversity. However, this diversity has been progressively lost, due to the pressure of national and international markets, who demand large and white grains as a preference, being the markets the main demanders to propose the objectives of genetic improvement programs; therefore, this characteristic is one of the most suggested to be taken into account in breeding programs, because producers prefer larger grains desired by the agroindustry. Regarding the grain thickness variable, the results coincide with those reported by Chura Yupanqui *et al.* (2021), with an average of 1.06 mm. The F27 family shows a potential for thickness, surpassing the response obtained by the commercial genotypes.

### Principal component analysis

With 11 agronomic variables evaluated, 14 families, and three commercial controls, two principal components were obtained, explaining 44.59% of the variance. The second component explained 21.66%, totaling 66.25% of the variance (Tab. 6).

**TABLE 6.** Eigenvalue for each of the dimensions in the principal component analysis using 11 agronomic variables for 17 genotypes of *Chenopodium quinoa*.

| Components | Eigenvalue | Total variance % | Accumulated variance % |
|---|---|---|---|
| 1 | 5.211 | 44.59 | 44.59 |
| 2 | 2.5319 | 21.66 | 66.25 |
| 3 | 1.2985 | 11.11 | 77.36 |
| 4 | 1.1552 | 9.88 | 87.24 |
| 5 | 0.5703 | 4.88 | 92.12 |
| 6 | 0.4016 | 3.44 | 95.56 |
| 7 | 0.3037 | 2.6 | 98.16 |
| 8 | 0.1464 | 1.25 | 99.41 |
| 9 | 0.0579 | 0.5 | 99.91 |
| 10 | 0.0101 | 0.09 | 99.99 |
| 11 | 0.0009 | 0.01 | 100.0 |

The Biplot graphical interaction analysis projected the parallel results between the variables (vectors) and the genotypes contained in the components (Fig. 1).

In Figure 2A, the genotypes Aurora (AU) and Blanca de Jericó (BDJ) showed the highest contributions to the formation of the first two principal components, followed

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by FSJ, F60, and F23. In Figure 2B, the variables with the most significant contributions were yield per plant (YPP) and yield per hectare (YPH), followed by grain thickness (GT), plant height (PH), and thousand-seed weight (WTS).

In the first quadrant, the variables PH, PD, SD, and PL are positively associated. They are represented by the genotypes Tunkahuan, Aurora, F34, and F37, which showed high values for these agronomic traits. These results align with those reported by Morillo *et al.* (2020), who find that tall plants tend to have thicker stems and longer panicles, traits that provide mechanical resistance to the size and weight of the panicle and help avoid lodging under adverse environmental conditions such as wind and rain.
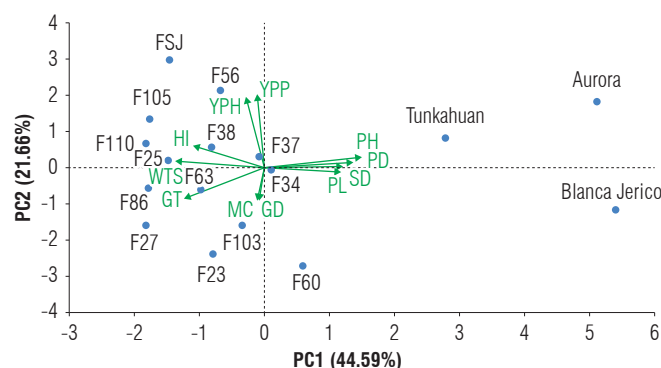


**FIGURE 1.** Representation of genotypes and variables in the first and second principal components using a composite Biplot graph for agronomic variables in 17 genotypes of *Chenopodium quinoa*. Abbreviations: PH: plant height; PL: panicle length; SD: stem diameter; PD: panicle diameter; GD: grain diameter; GT: grain thickness; MC: moisture content; WTS: thousand-seed weight; YPP: yield per plant; YPH: yield per hectare; HI: harvest index.

In the second quadrant, the variables YPP and YPH are grouped, with genotypes such as F56 and FSJ contributing most strongly in this direction. These variables, associated with productivity, showed a negative correlation with plant height and stem diameter, indicating that high-yielding genotypes tend to be shorter with thinner stems. This finding aligns with the findings of Foronda Limachi (2022), who report a positive correlation between YPP, YPH, and harvest index (HI).

The third quadrant includes genotypes such as F60, F23, and MC, along with variables GD, GT, and MC, indicating that these genotypes are associated with greater grain size, thickness, and moisture content. Although less productive, these materials could be relevant for breeding programs focused on grain quality traits.

In the fourth quadrant, the variable WTS is located along with the genotypes F27, F105, F110, F25, F86, and F63, which displayed higher values for thousand-seed weight. However, a negative correlation is observed with the yield and height-related variables (YPP, YPH, PH), suggesting that genotypes with heavier seeds may have lower overall plant productivity and shorter stature.

Finally, Blanca de Jericó, although positioned in the lower right quadrant, shows a contrasting pattern. It is far from most variables, indicating a low contribution to both principal components. However, it remains close to Aurora, suggesting possible similarities in phenotypic performance.
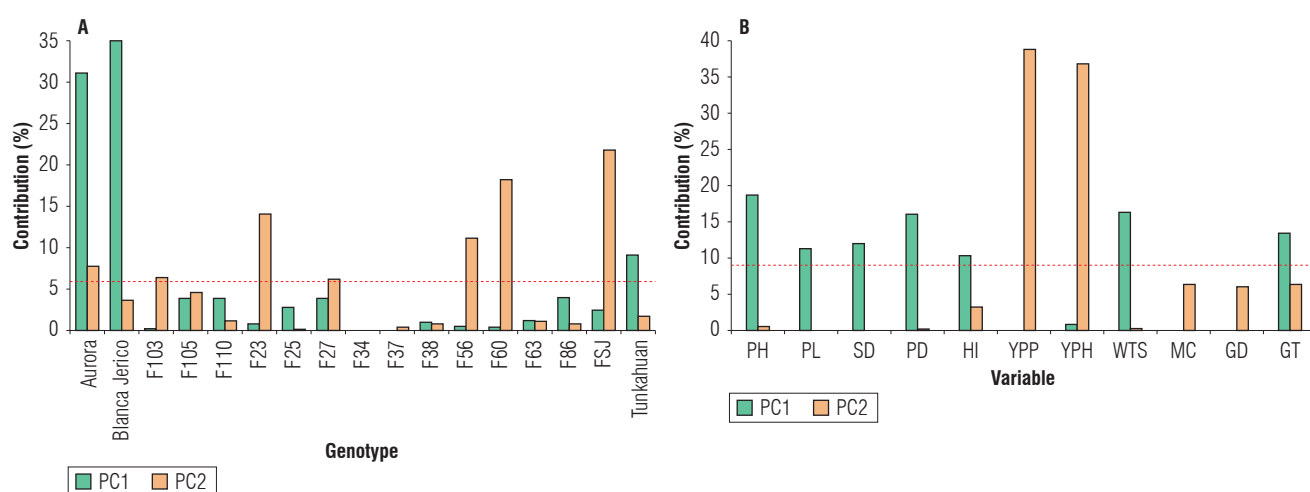


**FIGURE 2.** A) Contribution to the variance of quinoa genotypes in components 1 and 2 of the principal component analysis; B) Contribution to variance of yield variables where PL: plant height, MC: grain moisture content, PD: panicle diameter, SD: stem diameter, GT: grain thickness, HI: harvest index, PL: panicle length, WTS: thousand-seed weight, GD: grain diameter, YPH: yield per ha, YPP: yield per plant in components 1 and 2 of principal components analysis.

## Cluster analysis

The optimal number of clusters was determined using the K-means algorithm, which identified the inflection point at K = 3, indicating that three clusters group the data more efficiently (Sinaga & Yang, 2020). The cluster analysis (Fig. 3) enabled the formation of three groups. The first group (A) consisted of four genotypes, Aurora and Blanca de Jericó. The second group (B) is composed of Tunkahuan. Finally, the third group (C) consisted of 14 materials: F60, FSJ, F105, F37, F38, F86, F110, F23, F63, F27, F34, F105, F103, and F25.
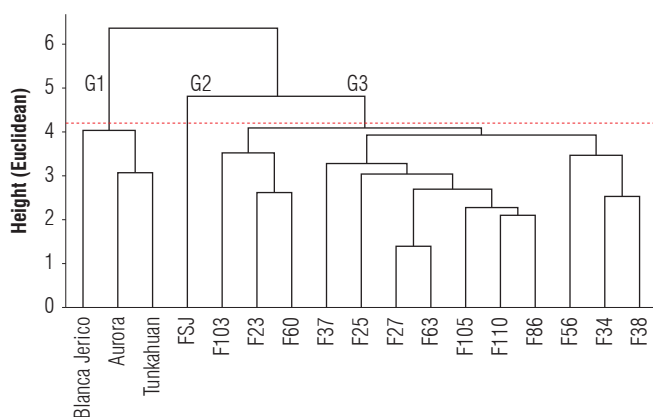


**FIGURE 3.** Dendrogram obtained by Principal Component Analysis for 17 genotypes of *Chenopodium quinoa* from 11 quantitative variables.

The grouping analysis allowed the identification of three clusters. The first group, consisting of the genotypes Aurora and Blanca de Jericó, was characterized by vigorous plant architecture, with heights ranging from 93.1 to 120.96 cm, stem diameters between 13.65 and 13.97 mm, and well-developed panicles in both diameter (50.12-53.73 mm) and length (37.74-38.15 cm). These structural features suggest a growth strategy focused on biomass accumulation and robustness, which could confer advantages in environments with heavy rainfall or strong winds. The second group, exclusively composed of Tunkahuan, displayed an intermediate profile. This ecotype exhibited relatively tall plants (114.2 cm) and long panicles (46.1 cm), characterized by a solid architecture. Its yield per plant (16.99 g) and per hectare (3704.8 kg ha$^{-1}$) were also intermediate. Although it did not outperform in any single trait, it maintained a balanced profile in terms of structure, yield, and grain quality, explaining its widespread use as a reference genotype and its value in breeding programs.

The third group, comprising most of the improved genotypes, stood out for its agronomic efficiency and grain quality. Genotypes F56 and FSJ recorded the highest yields per plant (30.33 and 28.45 g) and per ha (6623.1 and 6206.6 kg ha$^{-1}$), along with elevated harvest indices (47.5% and 41.1%, respectively). These findings suggest an efficient allocation of biomass toward reproductive structures. Regarding grain quality, genotypes such as F25, F86, and F27 exhibited the highest thousand-seed weights (3.13, 3.02, and 2.83 g, respectively), as well as greater grain thickness and diameter, which are desirable traits from an agro-industrial perspective. This group also displayed intermediate ranges in plant height (81.8 to 108.4 cm) and panicle length (33.6 to 49.2 cm), indicating that a tall stature is not necessarily required for achieving high yields, provided there is adequate physiological efficiency. This is exemplified by genotype F27, which, despite having the shortest plant height (81.8 cm), achieved outstanding performance in both yield and grain quality.
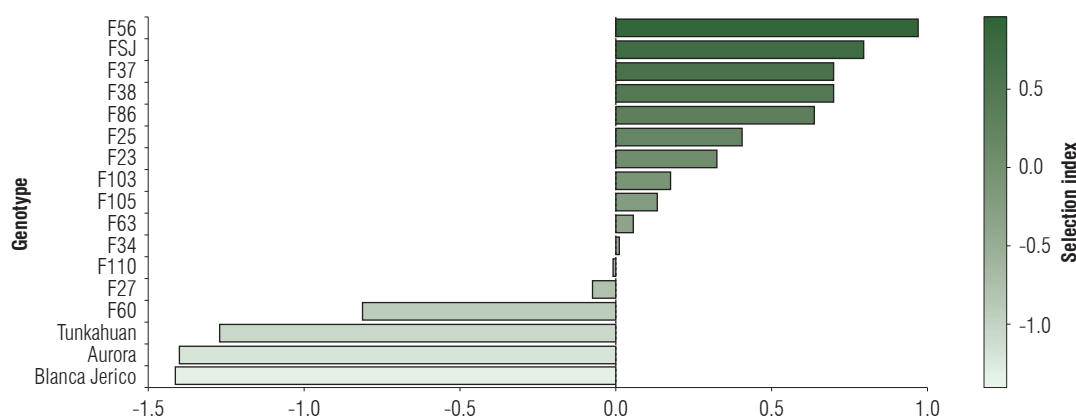


**FIGURE 4.** The selection index of promising quinoa genotypes in the locality of Silvia (Cauca), where families F56 stand out, followed by FSJ, F37, and F38.

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## Selection index

The selection index allowed for the clear differentiation among the evaluated quinoa genotypes. Genotype F56 exhibited the highest index value (0.96), with a yield of 6623.1 kg ha$^{-1}$, a thousand-seed weight of 2.7 g, and a grain diameter of 2.23 mm. It was followed by FSJ (0.79), F37 (0.69), F38 (0.69), and F86 (0.63), all of which showed yields exceeding 5,200 kg ha$^{-1}$ and outstanding values in key quality traits. Notably, F86 recorded the highest thousand-seed weight (3.02 g), while F38 exhibited the largest grain diameter (2.34 mm). In contrast, the commercial checks Blanca de Jericó, Tunkahuan, and Aurora recorded the lowest selection index values (-1.41, -1.27, and -1.40, respectively), with yields ranging from 3150.7 to 3909.9 kg ha$^{-1}$ and thousand-seed weights below the overall mean (2.68 g).

The selection index results highlighted the discriminative power of this tool in identifying quinoa genotypes with high productivity and superior grain quality. Genotype F56 stood out for combining high yield with desirable physical grain attributes, positioning it as a priority candidate for breeding programs adapted to the conditions of eastern Cauca. Likewise, genotypes FSJ, F37, F38, and F86 excelled in their overall agronomic performance, particularly in quality parameters such as thousand seed weight and grain diameter, traits highly valued by the agri-food industry. In contrast, the commercial checks exhibited lower performance, which may be associated with reduced adaptation to local conditions or limitations in biomass allocation to reproductive organs. This performance gap between improved and traditional genotypes reinforces the need to incorporate selection criteria based on multiple traits beyond yield alone.

These findings are consistent with those reported by Delgado *et al.* (2009), who demonstrate that the selection index enables the integration of multiple agronomic and quality traits to support informed decision-making in selecting outstanding materials. Although the index values observed in this study were lower than those reported by said authors (ranging from 1.78 to 0.96), the consistent performance in yield and grain quality of genotypes such as F56, FSJ, and F38 supports their inclusion in agronomic validation and technology transfer processes.

## Conclusions

This study enabled the identification of sweet quinoa genotypes with superior agronomic performance under the agroecological conditions of Silvia, Cauca (Colombia).

Genotype F56 stood out by exhibiting the highest selection index, with a yield exceeding 6600 kg ha$^{-1}$, and remarkable morpho-agronomic stability. These characteristics may be attributed to greater physiological efficiency in biomass allocation to reproductive organs, as evidenced by its high harvest index and the balance between compact plant architecture and high productivity, supported by the principal component analysis. These traits position F56 as a promising candidate for inclusion in genetic improvement programs. Similarly, FSJ proved to be an outstanding genotype, showing a high selection index, excellent yield, and favorable grain quality traits.

Both genotypes outperformed the commercial checks, which displayed more vigorous vegetative structures but lower productive efficiency. This behavior suggests that, under the agroecological conditions of the Cauca region, particularly at altitudes above 2600 m a.s.l. It is more advantageous to select genotypes with reduced plant height and enhanced resource allocation to grain production. Rather than prioritizing vigorous plant architecture, selection should focus on genotypes that optimize the production of grains with desirable physical attributes such as weight, diameter, and thickness, as observed in genotypes F25, F27, and F38.

This multi-trait selection strategy, which extends beyond yield alone, enabled the identification of agronomically efficient and highly competitive genotypes that align with the demands of the agro-industrial market, which values large, uniform, and heavy grains.

## Conflict of interest statement

The authors declare that there is no conflict of interests regarding the publication of this article.

## Author's contributions

Conceptualization: MAPZ, YMC; Research: MAPZ, GAAA, YMC; Methodology: MAPZ, YMC; Data curation:

MAPZ, JLLH; Formal analysis: MAPZ, JLLH; Writing-original draft: MAPZ, JLLH; Supervision: YMC, DCVC, ACMC; Writing-review & editing: All authors. Visualization: MAPZ. All authors reviewed the final version of the manuscript.

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