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Characterization and Agronomic Evaluation of 25 Accessions of *Chenopodium quinoa* in the Peruvian Coastal Desert

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Abstract: Quinoa is a healthy food that possesses high levels of protein that is enriched for dietary essential amino acids. The crop is highly diverse and well-adapted to changing climatic conditions. In spite of being vulnerable to pests and diseases, the development of new resistant varieties is possible. Taking advantage of this genetic variability is crucial for breeding programs, especially to adapt quinoa to the shifting needs of producers. In this study, 25 Peruvian accessions and two commercial varieties were characterized and agronomically evaluated in the Peruvian Pacific desert. Specific methodologies and descriptors of existing crops were used, analyzing a total of 24 quantitative and 23 qualitative variables with 15 repetitions per accession. The data were processed using descriptive statistics and a multivariate analysis. The results showed a high variability in morphological characteristics, with an area under the disease progress curve (AUDPC) of the presence of mildew between 529 and 1725, highlighting ACC06 with a lower severity of mildew. The percentage of saponins varied between 0.04 and 0.21 percent, with ACC06 being the one with the lowest percentage. Regarding the crop yield, it ranged between 0.35 and 8.80 t ha^{-1}, highlighting the high-yielding accessions ACC55 and ACC14. These results were promising for the improvement of quinoa yield in the production conditions of the Peruvian Pacific desert.

Keywords: agro-morphological characterization; saponin percent; seed yield; mildew severity

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1. Introduction

Quinoa (*Chenopodium quinoa* Willd.) is a dicotyledonous plant of the Amaranthaceae family [1] and is widely considered as one of the most complete foods due to its high levels of fatty acids, trace elements, and amino-acid-rich proteins [2], including arginine, lysine and leucine that support human health [3]. This species possesses a high genetic variability and the capacity to adapt to diverse agro-ecological conditions [4], especially when considered as part of the New World allotetraploid goosefoot complex that includes the cross-compatible wild species *C. berlandieri* Moq. and *C. hircinum* Schrad [5,6].

Characterization studies have been carried out on genetic diversity in quinoa. Ref. [7] evaluated 29 Peruvian accessions and found a high level of genetic variability that allowed the species to adapt to different ecological conditions [4], including tolerance to drought, salinity, and a good performance on poor soils [8]. On the other hand, ref. [9] carried out research on the adaptation of quinoa to lower-altitude regions, with the aim of understanding the phenotypic and genotypic variations at various yield levels, as well as agronomic

characteristics such as 1000 grain weight. This study helps in the selection of quinoa genotypes with the potential to adapt and thrive in lower-altitude environments, which could increase the availability and sustainability of this crop in new geographic areas.

Other studies have observed a wide variability in different quinoa genotypes in Colombia [10,11] and have identified negative correlations between the phenological phases and yield in the Palouse region of the Pacific Northwest, United States [4]. Additionally, ref. [12] carried out a study on the genotype–environment interaction under the unfavorable high-temperature conditions of Brazil and Colombia. These adverse climatic factors can affect the yield, where variables such as the plant height, panicle length, grain yield, dry matter yield, 1000 grain weight, and harvest index were essential in order to evaluate the performance of the genotypes. in different environments. This allowed us to identify those with a greater stability and agronomic potential in various conditions. A similar study [13] carried out a characterization of the phenotypic diversity of twelve quinoa genotypes in the coastal conditions of Chile, identifying genotypes with high yields. Variables such as the weight of 1000 seeds and seed size were used to distinguish differences. Furthermore, significant correlations were observed between the plant height, stem diameter, and panicle length. These discoveries offer the selection criteria for future genetic improvement programs.

Despite its high genetic variability, quinoa can be susceptible to pests and diseases, but this can be overcome with new improved varieties [14]. Research has identified genotypes with a higher yield [1] and disease resistance under different conditions [15], highlighting the importance of genetic improvement to achieve disease resistance and improve food security.

This genetic variability available in quinoa should be used in breeding programs to identify specific traits of interest [16]; these characteristics may include a shorter stature, more compact panicles, heat tolerance, a lower saponin content, and disease resistance [17]. Furthermore, it is crucial to understand the interactions between genotype and the environment in order to identify germplasm that can meet the needs of producers.

The objective of this study was to characterize morphologically and conduct agronomic performance evaluations on 25 accessions originating from the Peruvian departments of Puno, Ayacucho, Arequipa, and Cusco, along with two commercial varieties (Salcedo INIA and Blanca de Juli), under the Pacific Desert conditions of the first Majes Siguas Special Project, Caylloma Province, Arequipa Department.

2. Materials and Methods

2.1. Study Location

The research project was conducted out in the agroclimatological conditions of the experimental farm of the Centro de Investigación, Enseñanza y Producción Agrícola "CIEPA Majes" of the Universidad Nacional de San Agustín de Arequipa (Table 1). The farm is located at geographic co-ordinates UTM 18K 797335 8192900, at 1432 m elevation, within Specialized Zone B1, Majes District, Caylloma Province, Arequipa Region. The experimental investigation was initiated on 27 July 2023 under 11 h 13 min daylength, and ended before 10 January 2024, when daylength had increased to 12 h 53 min. Soil and water samples were sent to the laboratory LABSAF-AREQUIPA, Anexo Santa Rita de Siguas, in June, 2023. The soil was a sandy loam with the following conditions: somewhat alkaline pH (0:1) of 7.7, which is adequate for producing high-quality grain [14]; electrical conductivity (C.E.:1:0); being non-saline (45.9 mS m^{-1}); intermediate organic matter content (1.9%); low total nitrogen (0.095%); intermediate available phosphate (7.3 ppm); high available potassium (293.76 ppm); low cation exchange capacity (14.048 meq 100 g^{-1}); high exchangeable calcium content (10.01 meq 100 g^{-1}); average exchangeable magnesium content (1.64 meq 100 g^{-1}); high exchangeable potassium content (0.70 meq 100 g^{-1}); high base saturation percentage (100%); and non-sodic soil (0.12% PSI). The irrigation water quality was classified as C2S1, signifying a moderate risk of salinization C.E.:1:0 (702 µS cm^{-1}) and low risk of sodification (7.69 SAR), usable C.E. (0.52 mS cm^{-1}), pH (0:1) of 8.0 within

the normal range, being medium-hard (25.03 mg L^{-1}), and low risk in residual sodium carbonate (−2.80 RSC meq L^{-1}).

Table 1. Agroclimatic data for the Majes irrigation for the experimental period, 2023–2024.

	July	August	September	October	November	December	January
Average temperature (°C)	17.94	18.44	18.49	19.45	19.63	19.96	20.35
Min temperature (°C)	6.70	8.30	8.80	10.75	8.85	10.85	11.80
Max temperature (°C)	29.40	30.20	30.25	29.65	28.70	28.90	29.35
Average relative humidity (%)	38.69	37.00	43.09	52.55	45.13	53.53	65.04
Min relative humidity (%)	9.50	7.50	11.50	16.50	8.00	13.50	28.00
Max relative humidity (%)	88.50	97.00	93.00	92.50	94.00	95.50	97.00

Source: Automated meteorological station Pampa de Majes 4729E39A and the meteorological station of Autodema at plot E3-67 [18,19].

2.2. Plant Material

The 25 accessions originated in the regions of Puno, Ayacucho, Arequipa, and Cusco, and were obtained from the experimental field at Camacani of the Universidad Nacional del Altiplano de Puno and with two commercial varieties checks: Salcedo INIA and Blanca de Juli from Majes.

2.3. Agro-Morphological Characterization

The list of quinoa descriptors (*Chenopodium quinoa* Willd.) and its wild relatives proposed by Bioversity International (2013) [20] was used. For determining phenological stages of quinoa, the Biologische Bundesanstalt Bundessortenamt und Chemische Industrie (BBCH) scale was used [21]. For polynomial color variables, we used the RHS Colour Chart Guide, Sixth Edition (Royal Horticultural Society. London, UK). For evaluating hectoliter weight (PH), we used a 10 mL test tube with an interior diameter of 12.40 mm. In total, 24 quantitative and 23 qualitative variables were evaluated (Table 2) with 15 repetitions per accession.

Table 2. Description of the genetic materials used.

Accessions	GB UNSA Code [1]	Region	Country
01	UNSA-CH-1900001	Cusco	Perú
03	UNSA-CH-1900003	Puno	Perú
04	UNSA-CH-1900004	Cusco	Perú
05	UNSA-CH-1900005	Cusco	Perú
06	UNSA-CH-1900006	Puno	Perú
07	UNSA-CH-1900007	Puno	Perú
08	UNSA-CH-1900008	Puno	Perú
09	UNSA-CH-1900009	Puno	Perú
10	UNSA-CH-1900010	Puno	Perú
11	UNSA-CH-1900011	Puno	Perú
12	UNSA-CH-1900012	Cusco	Perú
13	UNSA-CH-1900013	Ayacucho	Perú
14	UNSA-CH-1900014	Cusco	Perú
15	UNSA-CH-1900015	Puno	Perú
16	UNSA-CH-1900016	Cusco	Perú
17	UNSA-CH-1900017	Puno	Perú
20	UNSA-CH-1900020	Puno	Perú
21	UNSA-CH-1900021	Arequipa	Perú
22	UNSA-CH-1900022	Puno	Perú
44	UNSA-CH-1900044	Cusco	Perú
45	UNSA-CH-1900045	Cusco	Perú
51	UNSA-CH-1900051	Puno	Perú
54	UNSA-CH-1900054	Puno	Perú
55	UNSA-CH-1900055	Cusco	Perú
56	UNSA-CH-1900056	Cusco	Perú

[1] GB UNSA CODE: Code provided by the Projet Banco de Germoplasma of the Universidad Nacional de San Agustín de Arequipa.

2.4. Mildew Severity Evaluation

Infestations were evaluated according to the method of Danielsen and Ames (2001) [22], by selecting a random leaf from each third and the average of the three was recorded as the final severity value per plant. We performed eight evaluations each 10 days up to the milky grain stage. To describe pathogen development with respect to the evaluation days, we calculated the area under the disease progress curve (AUDPC) following the formula described by Estrada-Zúniga et al. (2022) [15].

$$AUDPC = \sum_{i}^{n-1} \left(\frac{y_i + y_{i+1}}{2} \right) \times (t_{i+1} - t_i) \quad (1)$$

where n = number of evaluations, y = recorded severity (%), and t = number of days post-planting when the evaluation was done.

2.5. Saponin Percent

These tests were conducted using the method of Koziol (1991) [23] with modifications as follows. Grain samples of 0.50 ± 0.02 g were weighed and placed in sample tubes having an interior diameter of 13.95 mm to which was added 5 mL of distilled water. The height of the foam was measured after agitation for 30 sec with a subsequent 5 min resting period. For quantification of the saponin percentage via the afrosimetric method, according to the Peruvian standard NTP 205.062–2021 [24], the formula described in [25,26] was used:

$$\%\ saponin = \frac{(0.441 \times h) + 0.001}{m \times 10} \quad (2)$$

where variables h = foam height (cm) and m = sample weight (g).

2.6. Seed Yield

In this calculation were included 15 repetitions per accession, taking into account the area occupied by each plant (0.045 m^2) within the central row. Yield measurements were then extrapolated to hectare-scale, as detailed in [27].

$$Yield\ \left(t\ ha^{-1}\right) = \left(\frac{Grain\ yield\ (kg)}{Area\ (m^2)} \right) \times 10 \quad (3)$$

2.7. Experimental Procedure

Observation plot area for each accession was 18 m^2, with a sowing rate of 15 kg ha^{-1} using the blows technique, depth 1 cm, distance between blows of 0.2 m (5 linear meters) and between rows of 0.9 m (4 rows), and leaving 4 plants per blow at the thinning stage. An automated drip irrigation system was set up and controlled by the DREAM v4. 109.1203 programming software, using console software Talgil DREAM (Version 4.0.6.8832) and the SPOT (Version 4.0.2136) application for the Android system (Talgil Computing & Control LTD. Naaman Center, Haifa—Acco Road Israel). Programming of the irrigation rate was based on the crop coefficient (Kc) for the different phenological phases and evapotranspiration (ETP) determined by Autoridad Autónoma de Majes [18].

2.8. Agronomic Management

2.8.1. Irrigation Management

A total of 7780.19 m^3 ha^{-1} of water was used during the experiment. Irrigation needs were calculated considering the average flow rate of the drip irrigation system, the crop coefficient (Kc) for each phenological phase of the crop—0.40 (I), 0.60 (II), 0.65 (III), 0.80 (IV), 0.60 (V), and 0.40 (VI), and the reference evapotranspiration (ETo) in mm day^{-1} [18]. The average ETo for each phenological phase of the crop is the following: 4.68 (I), 3.95 (II), 4.34 (III), 5.12 (IV), 5.27 (V), and 5.39 (VI).

2.8.2. Phytosanitary Management and Fertilization

Levels of elemental fertilizers applied (kg ha^{-1}) were N (301), P (118), K (360), Ca (38), and Mg (20), according to recommendations of the Instituto Nacional de Innovación Agraria (INIA-PERÚ) and from prior experience. For pest and disease control, measures were based on level of insect damage and to prevent diseases. Insecticide and fungicide applications were based on recommendations of the Fungicide Resistance Action Committee (FRAC) and Insecticide Resistance Action Committee (IRAC) based on doses and other specific recommendations of manufacturers of each pesticide.

2.9. Data Analyses

For the qualitative variables (Table 3), an analysis of frequency and mode was conducted, while the quantitative variables were evaluated using an analysis of variance (ANOVA), and, subsequently, measures of central tendency were calculated, including the arithmetic mean ($\overline{x}$), standard deviation (σ), coefficient of variation (CV), and the Di Rienzo, Guzmán, and Casanoves (DGC) Test at a significance level of $\alpha = 0.05$ using the program Infostat version 2020 (UNC, Argentina). For multivariate analyses, we used the software program RStudio 2023.06.1 (Posit PBC, Boston, MA, USA). Packages used within this program included "psych" [28] and "ggcorrplot" [29] for calculating the Spearman Coefficient, and, for principal component analyses, packages "FactoMineR" [30] and "factoextra" [31]. For the dendrogram, based on quantitative variables, we utilized the Manhattan method and the elbow method to determine the optimum number of groups via the package "factoextra", resulting in four groups. For the correlation analysis of qualitative variables, we utilized the package "psych" [28] to calculate the tetrachoric correlation (between −1 and +1) between binomial variables, and the polychoric correlation (between −1 and +1) among polynomial variables, and, for calculating the correlation V of Cramer (between 0 and +1) among ordinal variables, we used "polycor" [32] and "rcompanion" [33], respectively.

Table 3. Matrix of quantitative and qualitative variables for characterization and evaluation of 25 Peruvian accessions and two commercial quinoa checks.

Quantitative			Qualitative		
N°	**Code**	**Variable**	**N°**	**Code**	**Variable**
1	DFBF	floral bud formation (dds)	1	HC	growth habit
2	DIF	beginning of anthesis (dds)	2	FT	main stem form
3	D50F	50% flowering (dds)	3	PAP	presence of axillary pigment
4	DFF	end of flowering (dds)	4	PR	branching pattern
5	DGL	milky grain (dds)	5	FH	leaf form
6	DGP	doughy grain (dds)	6	MH	leaf margin
7	D50MF	50% physiological maturity (dds)	7	CGH	leaf glandular trichome color
8	AP	plant height (cm)	8	FP	panicle form
9	DTP	main stem diameter (mm)	9	DP	panicle density
10	LPE	petiole length (cm)	10	GDH	degree of dehiscence
11	LMH	maximum leaf length (cm)	11	APG	perigonium form
12	AMH	maximum leaf width (cm)	12	APC	pericarp form
13	NDH	number of leaf margin teeth	13	AE	episperm appearance
14	LPA	panicle length (cm)	14	FG	seed form
15	DPA	panicle diameter (cm)	15	CTP	main stem color
16	IC	harvest index (%)	16	CE	color of stem striations
17	RSP	seed yield per plant (g)	17	CP	petiole color
18	DG	seed diameter (mm)	18	CLF	foliar leaf color
19	EG	seed thickness (mm)	19	CPF	panicle color at anthesis
20	P1000G	1000 seed weight (g)	20	CPMF	mature panicle color
21	PHL	hectoliter weight (g/cm^3)	21	CPG	perigonium color
22	SAP	saponin percentage (%)	22	CPC	pericarp color
23	RC	seed yield (t ha^{-1})	23	CEP	episperm color
24	MILD	mildew severity (AUDPC)			

3. Results and Discussion

According to the data of the 25 accessions of *Chenopodium quinoa* and the two commercial variety controls, Salcedo INIA (T1) and Blanca de Juli (T2), all exhibited significant differences ($p < 0.05$) for all quantitative traits, as presented in the ANOVA (Table 4).

Table 4. Results of the ANOVA (variables, degrees of freedom, F value, and *p*-values) carried out on the continuous quantitative variables to determine if there are significant differences between them. df.: degree of freedom; highly significant *** = p <0.001.

Variable	df.	F	*p*-Value
AP	26	30.15	***
DTP	26	5.46	***
LPE	26	8.24	***
LMH	26	13.79	***
AMH	26	12.11	***
NDH	26	39.25	***
LPA	26	30.02	***
DPA	26	20.65	***
IC	26	16.92	***
RSP	26	9.23	***
DG	26	44.87	***
EG	26	29.11	***
P1000G	26	38.65	***
PHL	26	24.29	***
MILD	26	24.49	***
SAP	26	9.19	***
RC	26	7.51	***

The 25 accessions compared to the two commercial varieties showed different characteristics in terms of emergence and physiological maturity (Table 5). The statistics described for the continuous quantitative variables are summarized in Tables 6 and 7, where we can observe a high variability in relation to the mean ($\bar{x}$), the standard deviation (σ), and the coefficient of variation (CV).

The AP at physiological maturity has a CV of 14.24 percent, which indicates that there is variability in the data among accessions, with an average of 202.43 cm (Table 6). On the other hand, the NDH in flowering shows a CV of 33.63 percent, which is also indicative of a high variability among accessions, with an average of 19.98 teeth per leaf. Likewise, the LPA at physiological maturity exhibited a CV of 23.86 percent, with an average of 80.72 cm. Similarly, the DPA at physiological maturity presented a CV of 39.67 percent, the average being 24.46 cm. The summary of quantitative grain trait measurements reveal a high variability for crop yield (Table 7), ranging from a minimum value of 0.35 t ha^{-1} to a maximum value of 8.80 t ha^{-1}, similar to the observations of [34] who carried out their experiments in five locations in South America and noted the highest yields in Valdivia, southern Chile, at 9.8 t ha^{-1}. Similarly, for saponin, the range of variation was between 0.04 and 0.21 percent. Of all the samples evaluated, 13 accessions were classified as sweet, with a saponin percentage equal to or less than 0.12, and 14 accessions were considered bitter, with a percentage greater than 0.12. Regarding the severity of mildew (*Peronospora variabilis*), at 70 days after sowing, accession 13 and T1 showed a high severity compared to the other accessions. However, at 80 and 100 days after sowing, accession 12 presented a high severity. The AUDPC showed a high degree of variability (Table 8), ranging from a minimum value of 529 to a maximum of 1725, which reflects a variable behavior depending on the genetic characteristics of the accession, disease, and environmental conditions.

3.1. Agromorphological Characterization of Discrete and Continuous Variables

The results reveal a CV of 22.15 percent during the emergence stage, which indicates the variability between the accessions evaluated, with an average of 7 days after planting (Table 5). For these results, the choice of sowing date is crucial, since it can have a significant impact on the emergence and development of the plants. Ref. [35], there are notable variations in the germination of *Chenopodium quinoa* plants depending on the sowing date, demonstrating that each genetic accession responds uniquely to temporal variations. On the other hand, ref. [36] highlights the importance of the harvest time to guarantee the quality of the seeds, since their emergence capacity can be affected if the right time is not chosen. This is especially relevant for late accessions, which could have a lower emergence rate in future seasons.

Table 5. Vegetative period in days for the evaluated accessions. T1: Salcedo INIA; T2: Blanca de Juli. The 25 accessions were classified by their vegetative period as semi-late (33.33%) and late (66.67%), based upon results under irrigation at Majes as analyzed by AUTODEMA of the vegetative periods of the crop: early quinoa (≤105 days), semi-late (≤133 days), and late (>133 days).

Phenological Stages (dds) [1]	Accessions																											Variability		
	01	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	20	21	22	44	45	51	54	55	56	T2	T1	$\bar{x}$	σ	CV (%)
Emergence	7	7	7	7	8	7	9	7	7	5	10	7	5	8	7	7	5	8	10	10	5	7	8	8	5	5	5	7	1.57	22.15
Two true leaves	15	14	15	16	15	14	15	14	16	16	15	14	15	15	14	15	15	15	16	15	11	12	14	15	15	15	12	15	1.22	8.38
Four true leaves	22	21	22	23	23	21	22	21	23	23	20	21	22	22	21	22	22	22	23	23	19	19	21	22	22	22	19	22	1.22	5.64
Six true leaves	29	24	28	30	29	28	29	28	25	25	25	28	29	24	28	24	29	29	29	34	27	24	27	30	29	29	24	28	2.45	8.91
Eight true leaves	34	29	33	35	35	33	34	33	30	30	30	33	34	29	33	29	34	34	34	39	34	30	32	39	34	34	30	33	2.65	8.06
Floral bud formation	50	45	49	51	45	41	45	49	45	45	45	49	50	45	49	45	50	50	45	55	50	41	45	55	50	50	50	48	3.56	7.45
Beginning of anthesis	56	56	65	67	50	56	57	57	57	62	65	65	62	62	62	56	55	58	58	63	64	56	50	69	61	55	60	59	4.81	8.10
50% flowering	64	63	69	70	55	61	65	63	63	69	70	72	68	69	68	63	58	62	65	67	73	60	58	77	68	61	68	66	5.07	7.74
End of flowering	80	85	86	92	80	79	79	77	79	86	85	86	79	86	84	77	77	78	82	79	85	85	74	90	85	80	80	82	4.35	5.31
Milky grain	103	99	93	116	89	99	99	92	99	96	108	125	95	106	100	86	92	95	99	99	110	92	94	98	90	98	97	99	8.41	8.50
Doughy grain	117	109	105	136	107	110	122	106	119	119	130	136	108	126	109	99	105	105	106	110	118	106	101	109	102	110	118	113	10.13	8.98
50% physiological maturity	125	132	112	162	120	136	142	142	142	142	142	155	115	146	142	125	115	118	125	127	134	136	125	119	117	125	128	131	12.79	9.73
End of physiological maturity	135	136	150	167	133	148	147	150	148	156	152	164	129	157	152	156	124	133	137	137	151	147	135	133	135	137	137	144	11.05	7.68

[1] Phenological stages days after sowing for the different accessions of Chenopodium quinoa from emergence to the end of physiological maturity according to the BBCH scale. These phases are distinguished according to the genetics and environmental environment of each accession.

Table 6. Morphological quantitative characters in different quinoa accessions. Arithmetic mean ± standard deviation. Values followed by the same letter were not significantly different, based on the DGC Test ($p \leq 0.05$).

ACC	AP	DTP	LPE	LMH	AMH	NDH	LPA	DPA
01	190.47 ± 14.99 d	14.27 ± 1.81 d	6.35 ± 0.42 b	7.91 ± 1.11 c	7.04 ± 0.64 c	26.27 ± 4.98 c	73.47 ± 11.89 c	21.73 ± 4.22 d
03	174.33 ± 5.77 d	16.10 ± 2.22 c	5.59 ± 0.69 c	7.67 ± 0.69 c	7.45 ± 0.74 c	16.33 ± 1.76 e	89.27 ± 9.49 b	22.80 ± 8.27 d
04	219.47 ± 20.43 c	16.44 ± 3.73 c	6.58 ± 0.69 b	8.96 ± 0.78 b	7.57 ± 0.70 c	14.53 ± 4.37 e	86.27 ± 13.27 b	20.60 ± 6.93 d
05	236.80 ± 13.34 b	19.75 ± 4.91 a	7.37 ± 0.92 a	9.59 ± 0.94 a	9.39 ± 1.09 a	25.47 ± 4.45 c	116.20 ± 14.64 a	37.60 ± 8.96 b
06	217.13 ± 22.00 c	16.24 ± 2.88 c	6.75 ± 0.58 b	9.45 ± 0.94 a	9.94 ± 1.07 a	22.33 ± 7.17 d	72.67 ± 10.50 c	18.13 ± 2.92 d
07	169.47 ± 9.43 e	13.89 ± 1.93 d	4.97 ± 0.53 c	7.83 ± 0.71 c	7.28 ± 0.61 c	12.00 ± 1.89 e	83.20 ± 11.07 c	18.07 ± 5.01 d
08	207.67 ± 9.03 c	19.47 ± 3.63 a	6.84 ± 0.69 b	9.83 ± 0.15 a	8.89 ± 0.47 a	13.33 ± 1.68 e	100.20 ± 10.91 b	24.07 ± 3.65 d

Table 6. *Cont.*

ACC	AP	DTP	LPE	LMH	AMH	NDH	LPA	DPA
09	191.67 ± 20.54 d	16.19 ± 2.57 c	6.10 ± 1.51 b	8.44 ± 0.73 b	7.98 ± 1.02 c	14.80 ± 2.91 e	82.93 ± 17.79 c	20.40 ± 5.15 d
10	181.13 ± 17.11 d	15.03 ± 2.12 d	5.88 ± 0.86 c	7.39 ± 0.33 c	7.49 ± 0.91 c	13.20 ± 1.52 e	91.40 ± 14.21 b	21.93 ± 5.54 d
11	218.40 ± 28.84 c	17.67 ± 4.34 b	7.67 ± 0.78 a	10.01 ± 0.85 a	9.81 ± 1.06 a	14.53 ± 2.03 e	92.80 ± 18.95 b	25.80 ± 6.82 c
12	275.47 ± 22.26 a	16.25 ± 2.97 c	6.37 ± 0.66 b	8.82 ± 0.71 b	9.08 ± 0.85 a	28.47 ± 5.55 c	95.93 ± 8.44 b	20.07 ± 5.96 d
13	234.67 ± 19.66 b	20.43 ± 2.89 a	7.28 ± 0.89 a	9.49 ± 1.27 a	9.32 ± 1.44 a	17.00 ± 4.39 e	113.27 ± 14.62 a	54.93 ± 12.29 a
14	217.53 ± 17.40 c	14.54 ± 3.67 d	7.19 ± 0.93 a	8.86 ± 0.68 b	9.11 ± 0.92 a	37.73 ± 4.59 a	61.33 ± 15.28 d	17.13 ± 4.55 d
15	162.07 ± 11.58 e	17.92 ± 2.76 b	6.11 ± 0.89 b	8.66 ± 0.84 b	7.55 ± 0.90 c	15.40 ± 1.55 e	96.87 ± 14.15 b	28.27 ± 7.81 c
16	243.07 ± 16.09 b	17.26 ± 2.83 b	5.89 ± 1.09 c	8.22 ± 1.14 c	8.19 ± 1.00 b	15.93 ± 2.15 e	88.40 ± 13.76 b	23.00 ± 5.04 d
17	180.20 ± 23.10 d	16.37 ± 2.68 c	6.17 ± 0.74 b	8.17 ± 0.80 c	8.27 ± 1.14 b	15.13 ± 2.97 e	78.00 ± 18.96 c	20.47 ± 6.22 d
20	212.33 ± 41.24 c	16.20 ± 4.20 c	6.30 ± 0.85 b	8.81 ± 1.03 b	8.65 ± 1.29 b	20.20 ± 4.28 d	78.07 ± 14.39 c	19.65 ± 6.39 d
21	192.13 ± 22.05 d	13.45 ± 2.58 d	5.24 ± 0.63 c	7.41 ± 0.98 c	7.50 ± 1.07 c	22.33 ± 5.77 d	62.40 ± 11.43 d	20.07 ± 7.51 d
22	197.27 ± 15.41 d	16.37 ± 2.79 c	6.28 ± 0.83 b	7.83 ± 0.70 c	7.76 ± 1.11 c	13.00 ± 3.42 e	100.93 ± 11.82 b	27.27 ± 6.43 c
44	192.53 ± 19.00 d	14.60 ± 2.38 d	5.81 ± 1.15 c	8.09 ± 0.45 c	7.37 ± 1.19 c	20.20 ± 4.14 d	63.73 ± 9.34 d	17.87 ± 5.08 d
45	197.60 ± 15.56 d	14.41 ± 2.93 d	6.57 ± 1.01 b	8.61 ± 0.78 b	7.48 ± 0.81 c	16.87 ± 4.17 e	68.67 ± 9.12 c	20.80 ± 4.57 d
51	162.00 ± 6.45 e	14.01 2.32 d	5.37 ± 0.78 c	7.17 ± 0.61 c	6.63 ± 0.57 c	12.73 ± 1.83 e	73.60 ± 10.57 c	19.13 ± 4.63 d
54	176.73 ± 22.36 d	15.48 ± 2.12 c	6.19 ± 0.76 b	7.75 ± 0.69 c	7.71 ± 0.95 c	20.20 ± 4.38 d	71.00 ± 9.59 c	19.87 ± 5.74 d
55	235.67 ± 28.50 b	19.15 ± 5.08 a	6.69 ± 1.04 b	8.57 ± 0.82 b	8.71 ± 1.03 b	31.73 ± 3.13 b	58.13 ± 13.27 d	20.93 ± 4.01 d
56	207.13 ± 34.14 c	17.38 ± 4.06 b	6.42 ± 0.98 b	8.34 ± 1.09 b	8.33 ± 1.48 b	27.80 ± 7.06 c	65.00 ± 14.64 d	23.93 ± 11.13 d
T2	151.80 ± 12.54 e	14.38 ± 2.82 d	6.39 ± 0.63 b	7.23 ± 0.67 c	7.37 ± 0.92 c	26.47 ± 5.13 c	42.93 ± 6.98 e	22.53 ± 3.94 d
T1	220.87 ± 17.22 c	17.07 ± 2.17 b	6.23 ± 2.17 b	8.07 ± 0.92 c	8.33 ± 0.65 b	25.53 ± 5.76 c	48.80 ± 8.48 e	21.20 ± 5.14 d
$\bar{x}$	202.43	16.31	6.38	8.48	8.22	19.98	80.72	24.46
σ	28.83	1.89	0.65	0.80	0.90	6.72	19.26	9.70
CV (%)	14.24	11.62	10.11	9.49	10.92	33.63	23.86	39.67

Table 7. Yield quantitative characters in different quinoa accessions. Arithmetic mean ± standard deviation. Values followed by the same letter were not significantly different, based on the DGC Test ($p \leq 0.05$).

ACC	IC	RSP	DG	EG	P1000G	PHL	SAP	RC
01	23.96 ± 7.81 c	38.32 ± 27.5 b	1.67 ± 0.09 d	0.96 ± 0.06 b	1.81 ± 0.25 d	0.56 ± 0.04 b	0.14 ± 0.07 b	4.73 ± 3.48 c
03	27.71 ± 6.01 b	36.46 ± 16.86 b	1.51 ± 0.07 e	0.90 ± 0.05 c	1.58 ± 0.16 d	0.57 ± 0.04 b	0.11 ± 0.00 c	4.49 ± 2.14 c
04	44.62 ± 12.19 a	58.24 ± 30.25 b	1.82 ± 0.11 c	1.02 ± 0.11 b	2.33 ± 0.37 b	0.55 ± 0.05 b	0.15 ± 0.02 b	7.25 ± 3.83 b
05	18.38 ± 9.85 c	22.74 ± 20.45 c	1.72 ± 0.11 c	0.92 ± 0.05 c	1.82 ± 0.37 d	0.41 ± 0.05 e	0.15 ± 0.01 b	2.75 ± 2.59 d
06	26.88 ± 8.22 b	30.33 ± 17.83 b	1.63 ± 0.07 d	0.95 ± 0.03 c	1.51 ± 0.12 d	0.58 ± 0.04 b	0.05 ± 0.02 d	3.72 ± 2.26 d
07	14.04 ± 12.16 c	8.52 ± 0.09 c	1.51 ± 0.09 e	0.88 ± 0.08 c	1.21 ± 0.31 e	0.53 ± 0.08 c	0.13 ± 0.06 c	1.08 ± 1.30 d
08	26.57 ± 6.95 b	47.11 ± 21.88 b	1.65 ± 0.07 d	1.00 ± 0.04 b	1.77 ± 0.26 d	0.55 ± 0.03 b	0.20 ± 0.08 a	5.84 ± 2.77 c
09	29.47 ± 13.5 b	35.58 ± 26.82 b	1.65 ± 0.18 d	1.02 ± 0.09 b	1.67 ± 0.43 d	0.47 ± 0.06 d	0.09 ± 0.03 c	4.38 ± 3.40 c
10	11.01 ± 12.06 c	10.22 ± 16.30 c	1.47 ± 0.06 e	0.88 ± 0.10 c	1.04 ± 0.10 e	0.50 ± 0.05 c	0.12 ± 0.03 c	1.17 ± 2.07 d
11	41.09 ± 22.34 a	54.93 ± 40.65 b	1.75 ± 0.11 c	0.99 ± 0.10 b	1.35 ± 0.41 e	0.52 ± 0.04 c	0.19 ± 0.02 a	6.83 ± 5.15 b
12	12.21 ± 7.09 c	18.98 ± 13.20 c	1.71 ± 0.13 c	0.92 ± 0.08 c	1.56 ± 0.33 d	0.56 ± 0.02 b	0.16 ± 0.01 b	2.28 ± 1.67 d
13	19.74 ± 12.78 c	28.55 ± 48.12 b	1.73 ± 0.12 c	0.87 ± 0.07 c	1.47 ± 0.56 d	0.55 ± 0.05 b	0.20 ± 0.03 a	3.49 ± 6.09 d
14	36.73 ± 8.64 b	65.17 ± 31.47 b	2.05 ± 0.07 a	1.09 ± 0.05 a	2.97 ± 0.24 a	0.59 ± 0.03 b	0.10 ± 0.00 c	8.26 ± 3.99 a
15	3.51 ± 1.42 d	2.73 ± 1.62 c	1.40 ± 0.05 f	0.84 ± 0.03 d	0.63 ± 0.18 f	0.40 ± 0.05 e	0.16 ± 0.04 b	0.35 ± 0.21 e
16	25.64 ± 7.83 b	34.02 ± 16.14 b	1.89 ± 0.15 b	1.02 ± 0.07 b	2.43 ± 0.47 b	0.56 ± 0.04 b	0.10 ± 0.02 c	4.18 ± 2.04 c
17	39.48 ± 12.64 a	48.76 ± 28.27 b	1.74 ± 0.10 c	1.04 ± 0.06 b	2.06 ± 0.30 c	0.57 ± 0.05 b	0.12 ± 0.04 c	6.05 ± 3.58 c
20	22.32 ± 9.92 c	39.83 ± 28.59 b	1.79 ± 0.15 c	1.03 ± 0.07 b	2.06 ± 0.34 c	0.67 ± 0.01 a	0.08 ± 0.02 c	5.05 ± 3.62 c
21	32.69 ± 9.44 b	40.66 ± 29.72 b	1.65 ± 0.10 d	0.99 ± 0.05 b	1.79 ± 0.24 d	0.60 ± 0.04 b	0.20 ± 0.07 a	5.02 ± 3.76 c
22	31.21 ± 15.68 b	45.10 ± 30.87 b	1.73 ± 0.06 c	1.06 ± 0.08 b	2.02 ± 0.24 c	0.52 ± 0.04 c	0.18 ± 0.04 a	5.59 ± 3.91 c
44	34.65 ± 12.47 b	46.22 ± 26.35 b	1.77 ± 0.10 c	1.03 ± 0.08 b	2.04 ± 0.20 c	0.59 ± 0.03 b	0.10 ± 0.03 c	5.73 ± 3.34 c
45	11.72 ± 4.82 c	12.65 ± 11.80 c	1.18 ± 0.05 g	0.66 ± 0.08 e	0.81 ± 0.07 f	0.58 ± 0.03 b	0.08 ± 0.08 c	1.48 ± 1.49 d
51	45.07 ± 8.57 a	55.96 ± 25.88 b	1.60 ± 0.08 d	0.81 ± 0.04 d	1.63 ± 0.23 d	0.50 ± 0.07 c	0.12 ± 0.03 c	6.96 ± 3.28 b
54	33.20 ± 10.74 b	56.36 ± 41.66 b	1.75 ± 0.08 c	1.03 ± 0.04 b	2.07 ± 0.31 c	0.56 ± 0.05 b	0.14 ± 0.05 b	7.01 ± 5.28 b
55	29.15 ± 7.00 b	74.18 ± 45.57 a	1.98 ± 0.08 a	1.06 ± 0.06 b	2.53 ± 0.43 b	0.57 ± 0.04 b	0.12 ± 0.04 c	8.80 ± 5.68 a
56	31.62 ± 14.06 b	88.64 ± 42.86 a	1.80 ± 0.13 c	0.99 ± 0.05 b	2.31 ± 0.52 b	0.58 ± 0.05 b	0.15 ± 0.09 b	7.06 ± 3.62 b
T2	16.33 ± 7.68 c	14.83 ± 10.18 c	1.81 ± 0.07 c	0.98 ± 0.03 b	2.02 ± 0.38 c	0.60 ± 0.03 b	0.04 ± 0.01 d	1.88 ± 1.29 d
T1	5.57 ± 7.95 d	6.51 ± 8.70 c	1.72 ± 0.10 c	0.95 ± 0.09 c	1.69 ± 0.24 d	0.53 ± 0.04 c	0.16 ± 0.19 b	1.06 ± 1.01 d
$\bar{x}$	25.73	38.67	1.70	0.96	1.78	0.55	0.13	4.54
σ	11.41	21.41	0.17	0.10	0.52	0.05	0.04	2.40
CV (%)	44.34	55.38	10.09	9.95	29.33	8.92	33.86	52.89

Table 8. Severity and area under the disease progress curve of mildew (*Peronospora variabilis*) in different quinoa accessions at 30, 40, 50, 60, 70, 80, 90, and 100 days after sowing. Arithmetic mean ± standard deviation.

	Mildew Severity (Days) [1]								
ACC	**30**	**40**	**50**	**60**	**70**	**80**	**90**	**100**	**AUDPC**
01	0.30 ± 0.13 a	1.50 ± 0.67 a	3.00 ± 1.34 a	15.00 ± 6.71 a	10.76 ± 4.75 d	37.69 ± 10.84 a	23.78 ± 6.65 d	16.22 ± 2.78 d	999.84 c
03	0.24 ± 0.16 a	1.18 ± 0.83 a	2.36 ± 1.65 a	11.78 ± 8.25 a	22.33 ± 11.93 c	25 ± 13.45 b	11.33 ± 5.43 e	9.67 ± 4.23 e	789.29 d
04	0.20 ± 0.12 a	0.98 ± 0.62 a	1.96 ± 1.24 a	9.78 ± 6.20 a	24.75 ± 13.16 c	24.89 ± 6.56 b	25.11 ± 15.74 d	24.89 ± 6.56 c	1000.08 c
05	0.20 ± 0.16 a	1.01 ± 0.80 a	2.02 ± 1.6 a	10.11 ± 7.98 a	30.22 ± 10.16 b	22.78 ± 10.55 b	13.56 ± 6.66 e	11.00 ± 8.06 e	853.02 d
06	0.19 ± 0.14 a	0.96 ± 0.69 a	1.92 ± 1.37 a	9.62 ± 6.86 a	15.06 ± 9.76 c	19.22 ± 10.84 b	22.82 ± 12.60 d	19.11 ± 9.55 d	792.62 d
07	0.21 ± 0.11 a	1.07 ± 0.55 a	2.13 ± 1.10 a	10.67 ± 5.48 a	5.56 ± 6.60 d	15.56 ± 9.36 c	16.56 ± 6.09 e	15.56 ± 10.57 d	594.21 e
08	0.21 ± 0.19 a	1.07 ± 0.94 a	2.13 ± 1.87 a	10.67 ± 9.36 a	28.56 ± 10.74 b	20.78 ± 7.12 b	18.89 ± 6.26 e	16.33 ± 6.49 d	903.63 d
09	0.23 ± 0.20 a	1.12 ± 0.98 a	2.25 ± 1.95 a	11.22 ± 9.77 a	22.22 ± 20.73 c	22.11 ± 13.57 b	19.33 ± 5.48 e	22.11 ± 13.57 c	894.27 d
10	0.29 ± 0.15 a	1.42 ± 0.76 a	2.85 ± 1.52 a	14.22 ± 7.61 a	21.78 ± 12.79 c	9.00 ± 7.84 c	11.22 ± 9.27 e	8.33 ± 3.67 e	648.01 e
11	0.19 ± 0.17 a	0.97 ± 0.84 a	1.93 ± 1.68 a	9.67 ± 8.39 a	31.11 ± 16.21 b	19.33 ± 10.74 b	13.41 ± 7.02 e	12.67 ± 5.90 e	828.52 d
12	0.05 ± 0.05 b	0.25 ± 0.26 b	0.50 ± 0.51 b	2.49 ± 2.56 b	18.33 ± 5.64 c	41.42 ± 9.54 a	54.24 ± 6.55 a	41.42 ± 9.54 a	1379.70 b
13	0.34 ± 0.21 a	1.68 ± 1.06 a	3.36 ± 2.13 a	16.78 ± 10.64 a	40.11 ± 14.12 a	25.00 ± 17.00 b	21.44 ± 10.12 d	19.22 ± 6.17 d	1181.45 c
14	0.12 ± 0.12 a	0.60 ± 0.58 a	1.19 ± 1.17 b	5.96 ± 5.83 a	10.36 ± 2.80 d	38.49 ± 9.90 a	22.73 ± 8.82 d	14.62 ± 5.29 d	866.89 d
15	0.13 ± 0.19 a	0.67 ± 0.96 a	1.33 ± 1.93 b	6.67 ± 9.64 a	34.67 ± 18.48 b	4.89 ± 5.25 c	11.02 ± 5.42 e	4.22 ± 1.88 f	614.24 e
16	0.26 ± 0.15 a	1.30 ± 0.74 a	2.60 ± 1.47 a	13.00 ± 7.35 a	25.22 ± 17.30 c	22.89 ± 9.99 b	19.78 ± 11.68 e	17.78 ± 8.08 d	938.08 d
17	0.29 ± 0.21 a	1.47 ± 1.04 a	2.93 ± 2.09 a	14.67 ± 10.43 a	16.44 ± 7.23 c	8.22 ± 5.25 c	16.89 ± 8.09 e	15.22 ± 8.59 d	683.79 e
20	0.06 ± 0.07 b	0.29 ± 0.35 b	0.57 ± 0.70 b	2.85 ± 3.53 b	9.64 ± 7.72 d	14.89 ± 9.90 c	19.58 ± 15.03 e	10.11 ± 1.47 e	528.92 e
21	0.13 ± 0.07 a	0.63 ± 0.38 a	1.26 ± 0.75 b	6.31 ± 3.75 a	32.71 ± 12.95 b	38.69 ± 8.84 a	34.04 ± 10.26 c	24.27 ± 7.38 c	1258.45 b
22	0.25 ± 0.18 a	1.24 ± 0.91 a	2.49 ± 1.82 a	12.44 ± 9.13 a	18.33 ± 11.30 c	15.56 ± 10.66 c	14.33 ± 4.95 e	12.45 ± 7.48 e	707.46 e
44	0.29 ± 0.20 a	1.45 ± 1.03 a	2.89 ± 2.06 a	14.45 ± 10.32 a	17.86 ± 7.18 c	39.78 ± 9.04 a	37.78 ± 9.81 c	24.89 ± 6.65 c	1267.79 b
45	0.16 ± 0.08 a	0.81 ± 0.43 a	1.62 ± 0.85 a	8.11 ± 4.25 a	12.07 ± 4.63 d	48.89 ± 8.32 a	28.00 ± 9.98 d	18.00 ± 1.69 d	1085.83 c
51	0.27 ± 0.18 a	1.37 ± 0.91 a	2.73 ± 1.83 a	13.67 ± 9.13 a	11.22 ± 4.20 d	43.11 ± 9.63 a	32.89 ± 10.46 c	19.34 ± 5.23 d	1147.94 c
54	0.20 ± 0.13 a	0.99 ± 0.63 a	1.99 ± 1.26 a	9.93 ± 6.28 a	12.62 ± 7.68 d	12.82 ± 4.55 c	15.78 ± 8.58 e	14.22 ± 7.40 d	613.46 e
55	0.21 ± 0.11 a	1.05 ± 0.54 a	2.10 ± 1.08 a	10.49 ± 5.41 a	11.22 ± 4.20 d	43.11 ± 9.63 a	32.89 ± 10.46 c	19.34 ± 5.23 d	1106.31 c
56	0.22 ± 0.15 a	1.10 ± 0.76 a	2.20 ± 1.53 a	11.00 ± 7.64 a	19.48 ± 8.47 c	41.16 ± 16.19 a	44.71 ± 14.05 b	35.11 ± 18.38 b	1373.11 b
T2	0.17 ± 0.17 a	0.86 ± 0.82 a	1.72 ± 1.65 a	8.58 ± 8.24 a	30.80 ± 8.92 b	44.47 ± 10.60 a	36.00 ± 14.49 c	17.11 ± 13.91 d	1310.59 b
T1	0.30 ± 0.18 a	1.50 ± 0.90 a	3.00 ± 1.80 a	14.98 ± 90 a	40.11 ± 10.13 a	47.78 ± 9.40 a	50.66 ± 8.56 a	28.67 ± 9.50 c	1725.08 a
$\bar{x}$	0.21	1.06	2.11	10.34	21.24	27.69	24.77	18.22	966.39
σ	0.07	0.36	0.72	4.03	9.68	13.42	11.97	8.04	294.94
CV (%)	34.14	34.00	34.09	39.00	45.59	48.47	48.31	44.13	30.52

[1] Mildew severity (days): severity observed at 30, 40, 50, 60, 70, 80, 90, and 100 days after sowing. Means followed by different lowercase letters in the columns are significantly different according to the DGC test ($p \leq 0.05$).

3.2. Agromorphological Characterization of Qualitative Variables

Frequency analyses (Table 9) revealed that most of the 25 accessions presented an unbranched or branched pattern up to the lower third of the stem, while the rest presented branches at two-thirds of the stem height; furthermore, more than half of the accessions had a cylindrical stem, rather than an angular one, the latter being a predominant characteristic of the Colombian genetic material. Regarding the presence of pigmented axils, most accessions have violet-red pigmented axils. The shape of the main leaf was rhomboidal, as was also found by Morillo Coronado et al. (2023) [37], who also observed rhomboidal leaves. Similarly, about half of the accessions had leaves with toothed margins. Regarding the color of the glandular trichomes, most accessions presented white trichomes on their leaves. The panicles were predominantly of an intermediate density and had a shape between amarantiform and glomerulate. The degree of dehiscence was regular in half of the accessions, with only 22% showing strong dehiscence. In general, this material differs from the Colombian one in variables such as the margin of the leaves, having the absence of serrated margins in our evaluated material, the presence of pigmented axils, the Colombian material being very variable, with the presence or absence of axils not predominating, and the shape of the leaf; although the Colombian material also presents rhomboidal and triangular leaves, there is not a great difference between the individuals evaluated.

According to the frequency analyses in Figure 1, for the color of the main stem, 85% (23) of the accessions had an intense yellow-green color, 11% (3) were light yellow-green, and 4% (1) were moderate yellow. For the stem striation color, 48% (13) were moderate yellow-green and 26% (7) were light yellow-green, similar to the results obtained by Manjarres-Hernández et al. (2021) [10], in which 99% of their genetic material was green. With respect to petiole color, 81% (22) of the accessions were of a strong yellow-green color. For the leaf blade color, 67% (18) of accessions were moderate yellow-green and 26% (7) were grayish olive green. The panicle color at flowering was predominantly grayish yellow-green in seven accessions, representing 26%; light yellow-green in 19% (5); light gray in 11% (3); and strong purple-red in 11% (3). At physiological maturity, panicle colors were highly variable, with six accessions (22%) having a similar moderate yellow color. For the perigonium color, we also observed considerable variability, with 15% (4) having a brilliant yellow color and 19% (5) being light yellow. The pericarp color in 10 accessions was predominantly pale yellow, representing 37%, while the rest of the accessions displayed a diversity of colors. The episperm color was pale yellow in 19% (5), white in 30% (8), and yellowish white in 30% (8) of accessions, a result different from that reported by Manjarres-Hernández et al. (2021) [10], who observed mostly translucent episperm in their accessions. In general, the genetic material evaluated is very variable in aspects such as the color of the panicle in the flowering stage (CPF), the color of the panicle at physiological maturity (CPMF), the color of the perigonium (CPG), the color of the pericarp (CPC), and the color of the episperm (CEP), aspects that, in the genetic material evaluated by Manjarres Hernández, also present a lot of variability, and may be variables that help differentiate genetic material from quinoa.

Table 9. Characteristics of qualitative morphological and grain variables in different quinoa accessions.

ACC.	HC	FT	PAP	PR	FH	MH	CGH	FP	DP	GDH	APG	APC	AE	FG
01	Branched in the lower third	Angular	Absent	Present	Rhomboidal	Toothed	White	Intermediate	Lax	Regular	Semi-open	Sugary	Opaque	Cylindrical
03	Branched in the lower two-thirds	Cylindrical	Present	Present	Rhomboidal	Smooth	Purple	Intermediate	Intermediate	Regular	Closed	Ashen	Opaque	Conical
04	Simple	Angular	Absent	Absent	Rhomboidal	Smooth	White	Amaranthiform	Intermediate	Regular	Semi-open	Ashen	Opaque	Ellipsoidal
05	Branched in the lower two-thirds	Angular	Present	Present	Rhomboidal	Smooth	Purple	Intermediate	Lax	Light	Semi-open	Ashen	Opaque	Conical
06	Branched in the lower third	Cylindrical	Present	Absent	Triangular	Toothed	Purple	Intermediate	Intermediate	Regular	Semi-open	Ashen	Vitreous	Cylindrical
07	Branched in the lower two-thirds	Angular	Present	Absent	Rhomboidal	Smooth	Purple	Intermediate	Intermediate	Light	Closed	Sugary	Opaque	Cylindrical
08	Branched in the lower two-thirds	Cylindrical	Present	Present	Rhomboidal	Smooth	Purple	Intermediate	Lax	Light	Semi-open	Ashen	Opaque	Ellipsoidal
09	Branched in the lower two-thirds	Angular	Present	Present	Rhomboidal	Smooth	White	Intermediate	Intermediate	Regular	Semi-open	Sugary	Opaque	Cylindrical
10	Simple	Angular	Absent	Absent	Rhomboidal	Smooth	White	Intermediate	Intermediate	Regular	Closed	Ashen	Opaque	Ellipsoidal
11	Branched in the lower two-thirds	Cylindrical	Present	Present	Rhomboidal	Smooth	Purple	Intermediate	Intermediate	Regular	Semi-open	Ashen	Opaque	Cylindrical
12	Branched in the lower third	Angular	Absent	Present	Triangular	Toothed	White	Intermediate	Intermediate	Light	Semi-open	Sugary	Opaque	Lenticular
13	Branched in the lower two-thirds	Angular	Present	Present	Triangular	Smooth	White	Intermediate	Lax	Strong	Closed	Ashen	Opaque	Cylindrical
14	Branched in the lower third	Cylindrical	Absent	Present	Triangular	Toothed	Purple	Amaranthiform	Intermediate	Strong	Semi-open	Sugary	Opaque	Cylindrical
15	Branched in the lower two-thirds	Angular	Present	Absent	Rhomboidal	Smooth	Purple	Intermediate	Intermediate	Regular	Closed	Sugary	Opaque	Cylindrical
16	Branched in the lower two-thirds	Cylindrical	Present	Present	Triangular	Smooth	White	Intermediate	Intermediate	Light	Semi-open	Ashen	Opaque	Ellipsoidal

Table 9. *Cont.*

ACC.	HC	FT	PAP	PR	FH	MH	CGH	FP	DP	GDH	APG	APC	AE	FG
17	Branched in the lower two-thirds	Angular	Present	Present	Rhomboidal	Smooth	Purple	Intermediate	Intermediate	Regular	Closed	Sugary	Opaque	Cylindrical
20	Branched in the lower third	Cylindrical	Present	Present	Rhomboidal	Toothed	Purple	Intermediate	Intermediate	Light	Semi-open	Ashen	Vitreous	Cylindrical
21	Simple	Cylindrical	Present	Absent	Rhomboidal	Toothed	White	Intermediate	Lax	Strong	Closed	Sugary	Opaque	Cylindrical
22	Branched in the lower third	Angular	Absent	Present	Rhomboidal	Smooth	White	Glomerulate	Intermediate	Regular	Semi-open	Ashen	Opaque	Cylindrical
44	Branched in the lower third	Cylindrical	Present	Present	Triangular	Toothed	White	Intermediate	Intermediate	Light	Semi-open	Sugary	Vitreous	Cylindrical
45	Branched in the lower third	Cylindrical	Present	Present	Rhomboidal	Toothed	White	Intermediate	Lax	Regular	Semi-open	Ashen	Vitreous	Lenticular
51	Simple	Angular	Present	Absent	Rhomboidal	Smooth	White	Intermediate	Intermediate	Regular	Semi-open	Ashen	Opaque	Ellipsoidal
54	Branched in the lower third	Cylindrical	Present	Present	Triangular	Toothed	White	Intermediate	Lax	Regular	Semi-open	Sugary	Opaque	Cylindrical
55	Branched in the lower third	Cylindrical	Present	Present	Rhomboidal	Toothed	White	Amaranthiform	Compact	Strong	Semi-open	Sugary	Vitreous	Cylindrical
56	Branched in the lower two-thirds	Cylindrical	Absent	Present	Triangular	Toothed	White	Intermediate	Intermediate	Strong	Closed	Sugary	Vitreous	Cylindrical
T2	Simple	Cylindrical	Present	Absent	Triangular	Toothed	White	Intermediate	Intermediate	Regular	Semi-open	Sugary	Opaque	Cylindrical
T1	Simple	Cylindrical	Absent	Absent	Triangular	Toothed	White	Intermediate	Intermediate	Regular	Semi-open	Sugary	Opaque	Cylindrical

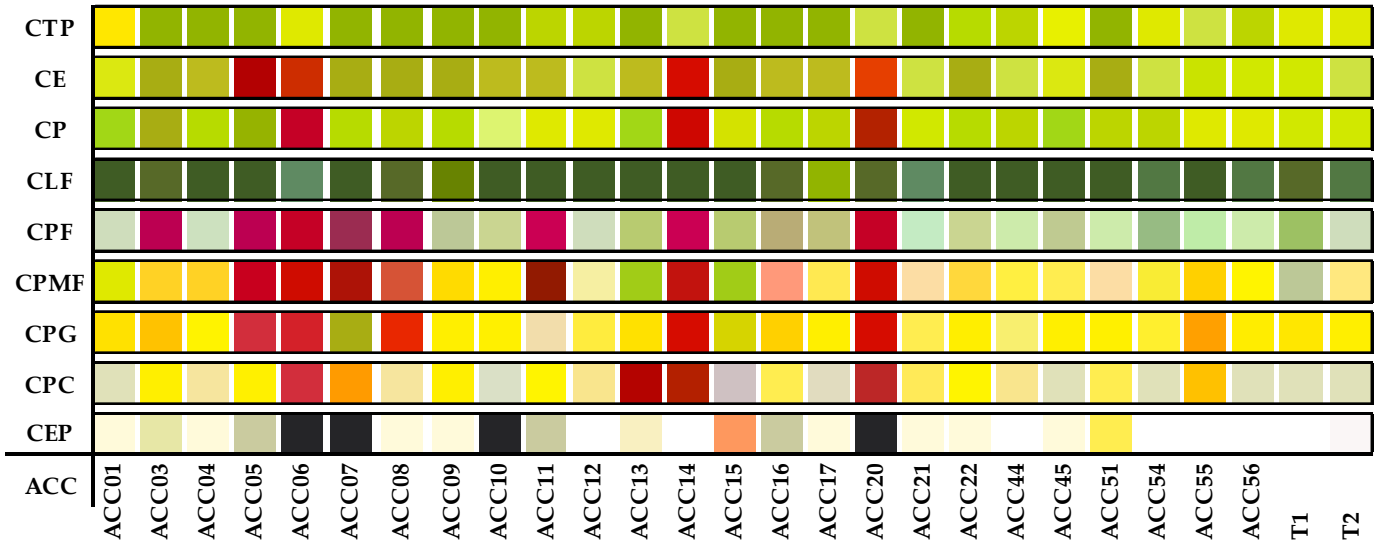

Figure 1. Polynomial color variables for the 25 accessions and the 2 commercial varieties based on the RHS Colour Chart Guide Sixth Edition (2015; 2019 reprint).

3.3. Multivariate Analysis

The tetrachoric correlation matrix of nominal binomial variables in Figure 2A showed that the highest positive correlation among two variables was between FT and AE (r = 0.65), while the highest negative correlation was between PR and APG (r = −0.32). The polychoric correlation matrix of nominal polynomial variables showed low correlations among variables (Figure 2B), with the highest positive correlation between CGH and FG and the highest negative correlation between FG and MH (r = −1). The Cramer's V correlation matrix showed a low correlation among ordinal variables (Figure 2C), with the highest being between GDH and DP (r = 0.25).

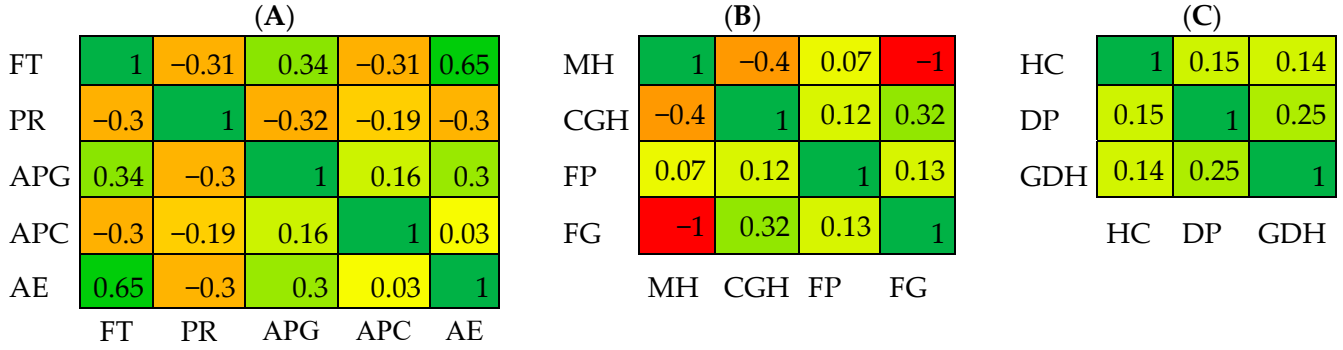

Figure 2. Correlation matrix of qualitative variables for the 25 accessions and the 2 commercial varieties: (**A**) nominal binomial variables; (**B**) nominal polynomial variables; and (**C**) ordinal variables.

The Spearman correlation coefficients presented in Figure 3 demonstrate high correlation values among variables for the discrete phenological stages including DIF and D50F (r = 0.91), DGL and DGP (r = 0.8), and DGP and D50MF (r = 0.76); between the morphological variables LPE and LMH (r = 0.58), LPE and AMH (r = 0.55), and LMH and AMH (r = 0.74); and between the grain variables RSP and RC (r = 0.99), IC and RC (r = 0.77), IC and RSP (r = 0.77), DG and P1000G (r = 0.79), and EG and P1000G (r = 0.72). There were also negative correlations, such as between EG and DGP (r = −0.46), D50MF and PHL (r = −0.46), and DGP and IC (r = −0.51), the last being the highest negative correlation. These results are concordant with those of [4], who reported a positive correlation between yield and 1000 grain weight, along with those of Thiam et al. (2021) [38], who observed positive correlations between grain yield, yield per plant, harvest index, and 1000 grain

weight. On the other hand, these results differed from those of [37] in Colombian quinoas, where they observed the highest correlations between plant height and panicle length (r = 0.94), panicle diameter and panicle length (r = 0.97), and plant height and panicle diameter (r = 0.90).

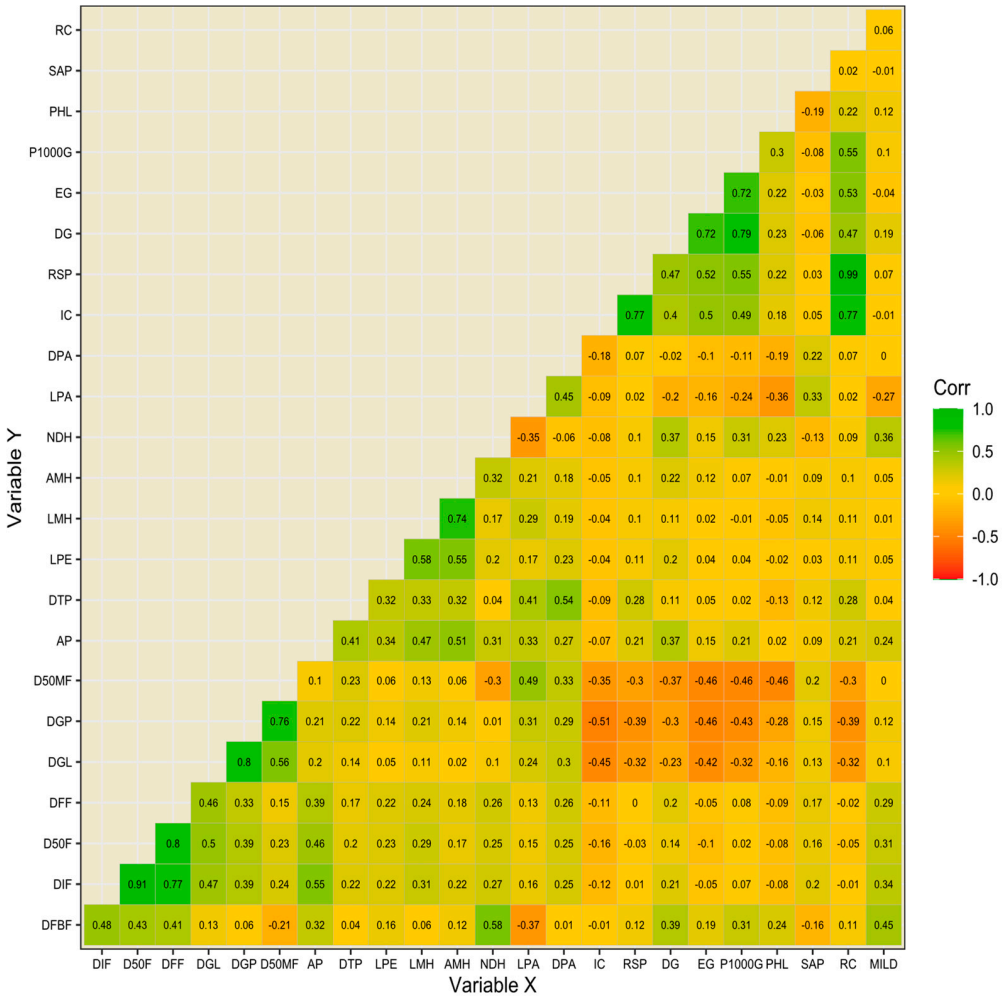

Figure 3. Spearman matrix of correlation coefficients among quantitative variables for the 25 accessions and the 2 commercial varieties.

The principal component analysis in Figure 4 among quantitative variables showed that, of the total variance, 55.3% corresponds to the two primary components, with 30.8% explained by the first component and 24.5% by the second, with the variables DGP, DGL, D50MF, and LPA being those contributing most to component one, and variables like DG, RSP, P1000G, and RC being the most important in the second component. We observed that accessions 5 and 13 were very close to the time or maturation variables, which makes sense, since these were very late-maturing accessions. Similarly, closely grouped variables included leaf, plant, and panicle length together in this quadrant, since there were positive correlations among these two groups of variables, while, on the other hand, these variables negatively correlated with yield and seed size, which were located in the second quadrant together with accessions having a higher yield.

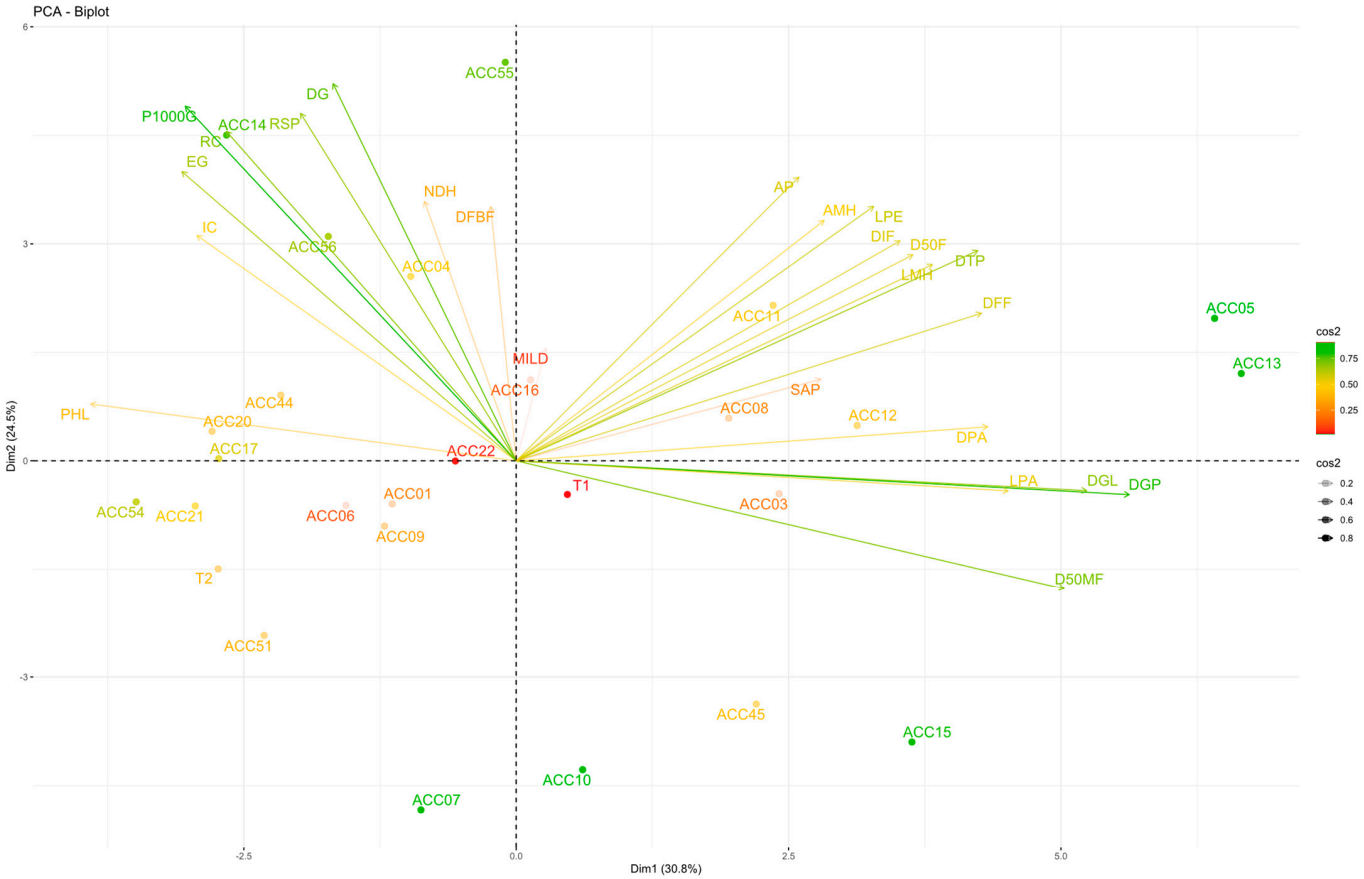

Figure 4. Analysis of principal components among quantitative variables and lines for the 25 accessions and the 2 commercial varieties.

In the conglomerate analysis, four main groups were identified and share similarities in variation for many of the variables discussed above. The first group (a) consists of four accessions: 56, 04, 55, and 14 (Figure 5). These accessions stand out as having a vegetative period of 49 to 55 days and from 112 to 119 days until 50% physiological maturity. Accessions 14 and 55 are notable for having fewer days until the end of physiological maturity (Table 5). Other characters for this group are as follows: plant height ranges from 207.13 to 235.67 cm; main stem diameter from 14.54 to 19.15 mm; petiole length from 6.42 to 7.19 cm; maximum leaf length from 8.34 to 8.96 cm; maximum leaf width from 7.57 to 9.11 cm; panicle length from 58.13 to 86.27 cm; panicle diameter from 17.13 to 23.93 cm; harvest index ranges from 31.62 to 44.62%; seed yield per plant varies from 58.24 to 88.64 g; seed diameter from 1.82 to 2.04 mm; seed thickness from 0.99 to 1.09 mm; and 1000 seed weight ranged from 2.31 to 2.97 g. Accession 14 was notable for its higher values for these last three variables and differs significantly from groups (b), (c), and (d). These results are close to those reported by Estrada-Zúniga et al. (2022) [15], who recorded higher values for seed diameter (2.41 mm) and seed thickness (1.42 mm. In their study, Urdanegui et al. (2021) [1] also recorded higher values for seed size (2.33 mm), seed thickness (1.38 mm), and 1000 seed weight (3.96 g). Downy mildew severity (AUDPC) varied between 808.44 and 1373.11; saponin percentage from 0.10 to 0.15%; hectoliter weight from 0.54 to 0.59 g/cm^3; and seed yield from 7.06 to 8.80 t ha^{-1}; notable accessions were 55 and 14 for this last variable (Table 7). Even though accession 56 had the highest yield per plant (88.64 g), this was the accession requiring the most space per plant (0.068 m^2). The results observed in this group surpassed previous trials in different regions of Peru, as was also the case for the Colombian material [10]. On the other hand, Jbawi et al. (2022) [39] and Öktem and Birden (2021) [40] mentioned that the sowing density and date are factors that significantly

affect seed yield. At the same time, Thiam et al. (2021) [38] showed the profound effects that photoperiod sensitivity and high temperatures have on quinoa seed yield.

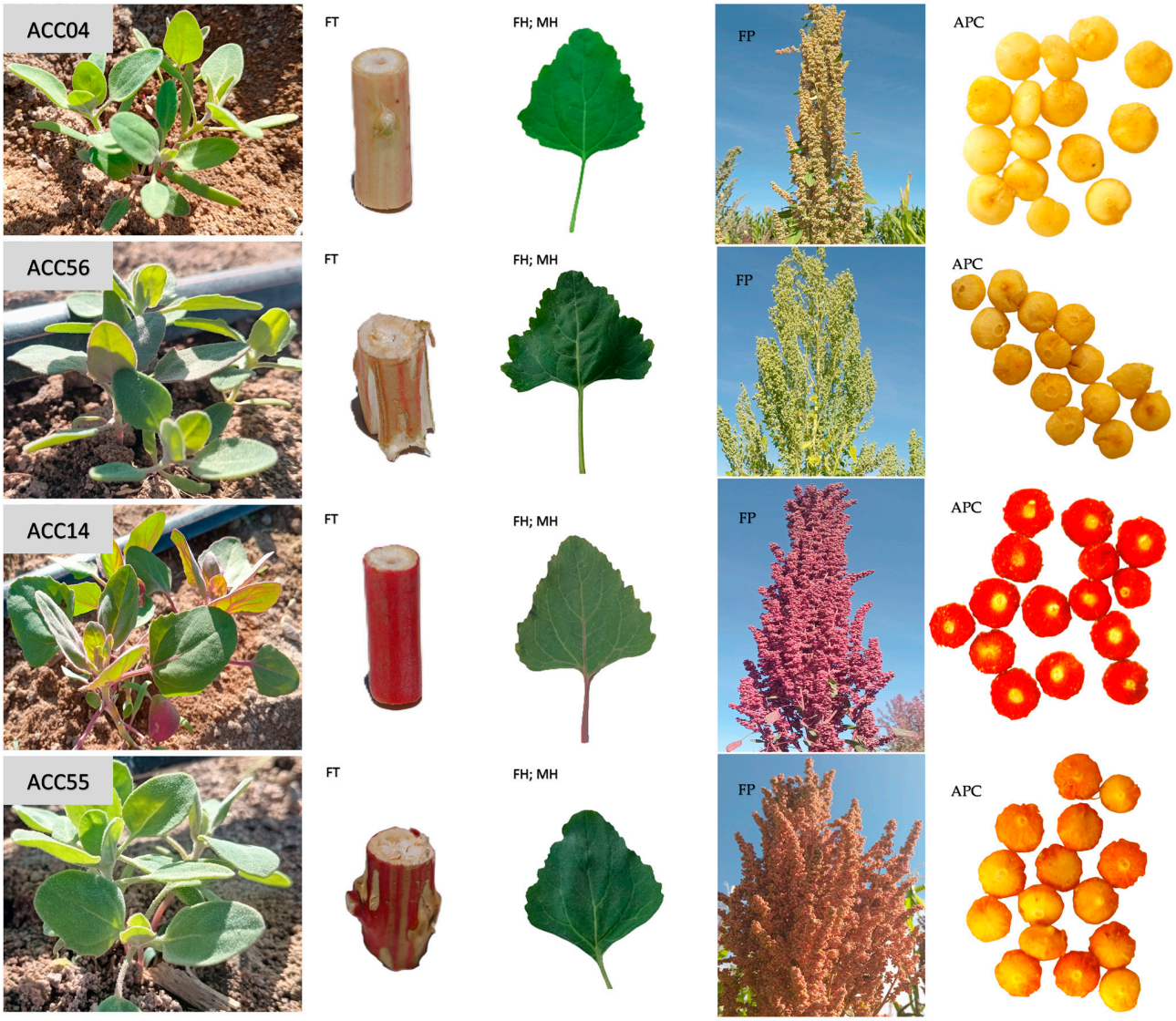

Figure 5. Qualitative characteristics of the group (a); FH: leaf shape; MH: leaf margin; FT: main stem shape; FP: panicle type; APC: pericarp appearance.

The second group (b) was composed of 11 accessions—20, 06, 09, 16, 22, 54, 17, 51, 44, 21, and 01—along with the commercial check variety Blanca de Juli (Figure 6). This group is characterized by having a vegetative period extending from 41 to 55 days and from 115 to 142 days until 50% physiological maturity (Table 5). The stem diameter varied from 13.45 to 17.26 mm; petiole length from 5.24 to 6.75 cm; maximum leaf length from 6.63 to 9.94 cm; maximum leaf width from 6.63 to 9.94 cm; seed diameter from 1.6 to 1.89 mm; seed weight from 0.81 to 1.06 mm; and hectoliter seed weight ranged from 0.52 to 0.67 g/cm^3, with accession 20 (0.67 g cm^{-3}) being the heaviest, with significant differences in comparison to groups (a), (c), and (d). With respect to saponin percentage, this group was highly variable (Table 5), with accession 06 (0.05%) having the lowest value versus groups (a), (c), and (d), similar to the check Blanca de Juli (0.04%), while accession 21 (0.21%) had the highest saponin value. These results differ from those of Estrada-Zúniga et al. (2022) [15], who reported accessions with 0.0% saponin. It was reported that the saponin is concentrated in the pericarp (from 0.01% to 5.0%) [41]. According to the Peruvian standard NTP 205.062–

2021, if the saponin percentage is lower than 0.12%, the quinoa is considered to be sweet and, if higher than this value, bitter.

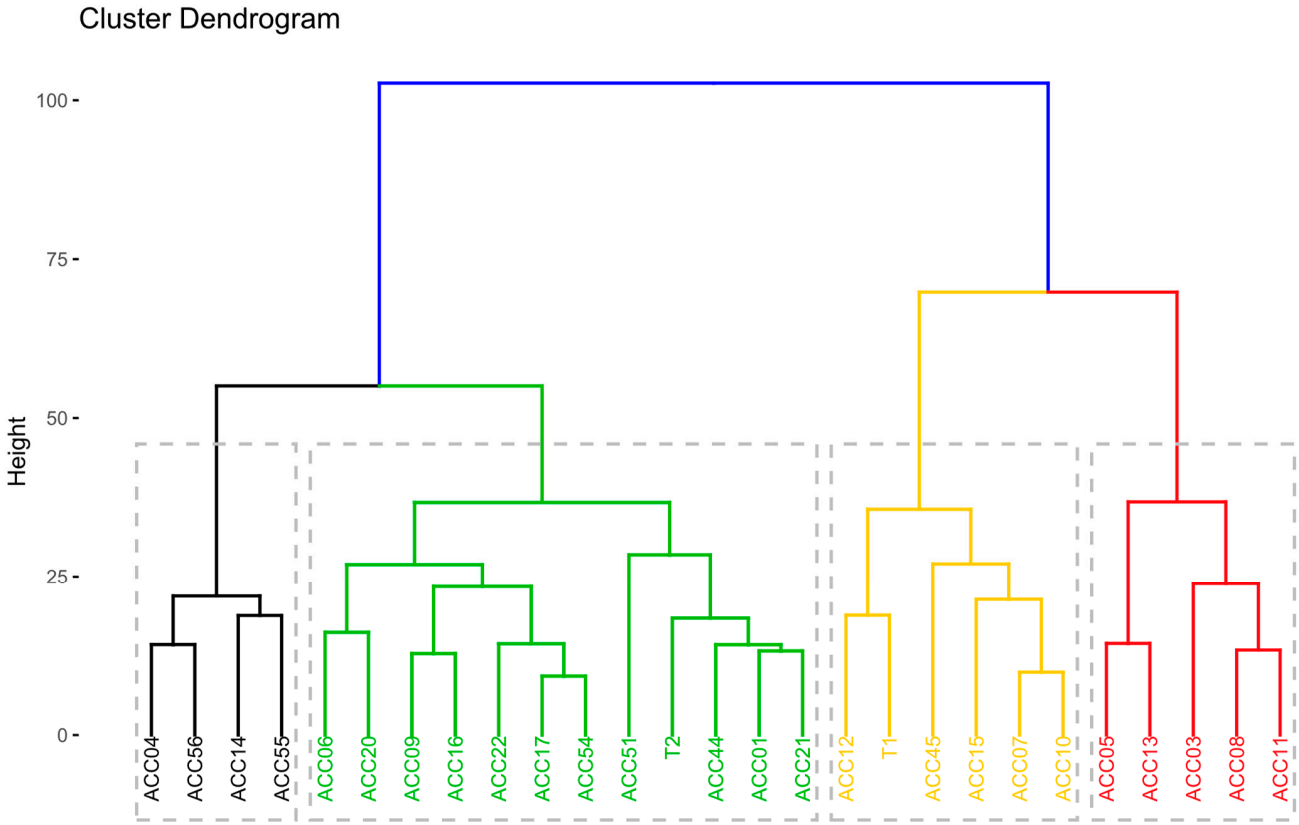

Figure 6. Dendrogram for the 25 accessions and the 2 commercial varieties. In the figure, you can clearly see the four differentiable groups that have been formed using the Manhattan method and the elbow method.

The third group (c) consisted of five accessions—15, 10, 07, 45, and 12—including the commercial variety Salcedo INIA (Figure 6). This group is characterized by having a vegetative period of 41 to 50 days until the initiation of the floral meristem and from 128 to 146 days until 50% physiological maturity (Table 5). Plant height in this group varied from 162.07 to 275.47 cm, with accession 12 (275.47 cm) being the tallest and being significantly different from groups (a), (b), and (d)—being taller than the plants in the study of Manjarres-Hernández et al. (2021) [10]. According to Jbawi et al. (2022) [39], planting density influences this trait, with a higher density resulting in taller plants due to competition for sunlight. In contrast, González et al. (2022) [42] suggested that high planting densities should reduce plant height, based on the law of yield decreases of David Ricardo. Stem diameters in this group varied from 13.89 to 17.92 mm; petiole length from 4.97 to 6.57 cm; maximum leaf length from 7.39 to 8.82 cm and leaf width from 7.28 to 9.08 cm; and the hectoliter seed weight varied from 0.5 to 0.58 g cm^{-3}. In terms of mildew severity, accessions in this group were highly variable (Table 7), with accessions 07 (594.21), 10 (648.01), and 15 (614.24) having the lowest area under the curve for disease progression (AUDPC), while being statistically similar to accessions of group (b): namely, 17 (683.79), 20 (528.92), 22 (707.46), and 54 (613.46). In comparison, the commercial variety Salcedo INIA (1725.08) registered the highest AUDPC value, similar to the report of Estrada-Zúniga et al. (2022) [15] for samples collected from the Altiplano, inter-Andean valleys, and the Pacific Coast.

The fourth group (d) is composed of five accessions: 13, 05, 03, 08, and 11 (Figure 6). These were characterized by having a vegetative period of 45 to 51 days and from 132 to

162 days until 50% physiological maturity, with the majority being late-maturing (Table 5). Plant height varied from 174.33 to 236.8 cm, with the main stem diameter ranging from 16.1 to 20.43 mm, with accession 13 (20.43 mm) having the widest stem diameter, being and significantly different from groups (a), (b), and (c). For this variable, Jbawi et al. (2022) [39] mentioned that, at higher planting densities, the stem diameter diminishes, while Öktem and Birden (2021) [40] noted that the stem diameter was affected by the sowing date. Petiole longitude varied from 6.84 to 7.67 cm; maximum leaf length from 9.49 to 10.1 cm; leaf width from 8.89 to 9.81 cm; and panicle length varied from 92.8 to 116.2 cm, with accessions 13 (113.27 cm) and 05 (116.20 cm) having significantly longer panicles in comparison with the results of Morillo-Coronado et al. (2021) [11] and Manjarres-Hernández et al. (2021) [10] and Morillo-Coronado et al. (2021). With respect to the panicle diameter, there was variation between 24.07 and 54.93 cm, with accession 13 (54.93 cm) having the widest panicles (Table 6), being significantly different from groups (a), (b), and (c), and greater than the results of Morillo-Coronado et al. (2021) [11]. Interestingly, Jbawi et al. (2022) [39] reported that the sowing density influenced this character such that, at a higher planting density, the length and diameter of the panicles were reduced. The seed diameters varied from 1.65 to 1.75 mm, seed thickness from 0.87 to 1.00 mm, and hectoliter weight from 0.43 to 0.53 g cm^{-3}.

Phenological evaluation among conglomerate groups. The statistically significant variability measured among lines is influenced by genetic and environmental influences (Table 1). Moreover, Curti et al. (2022) [43] mentioned that late-flowering quinoa populations tend to be associated with warmer environments. It is interesting that the accessions showed a high variability for physiological maturation (Table 5). Accessions like 20 (124 days) from group (b) and 14 (129 days) from group (a) were the earliest to mature. On the other hand, accessions 15 (164 days) from group (c) and 05 (167 days) from group (d) required the greatest amount of time to mature (Table 5). These results reflect the combined effects of genetics and, to a large extent, edapho-climactic factors [44]. Characteristics like the formation of the floral meristem are susceptible to changes in certain production practices, among them the alteration of the sowing date [45]. It is likely that some lines might respond differently to changes in the sowing date due to the photoperiod and ambient temperature variations, as was noted by Curti et al. (2016) [46], who indicated that plant developmental rates up to the floral meristem appearance varied considerably among 11 accessions of *Chenopodium quinoa* in experiments in the Argentine Northwest. The flowering stage was found to be the most critical in determining each genotype's yield from environment to environment [34]. The flowering process is heavily influenced by the photoperiod sensitivity of each accession, according to Patiranage et al. (2021) [47], who identified five haplotypes that cause early flowering under long days. Meanwhile, Tovar et al. (2020) [8], while studying the effect of heating on the appearance of the floral meristem, found that plants exposed to the highest temperatures kept their flowers closed, which resulted in decreased yield due to their inability to disperse pollen within the panicle. However, Eghbalishahabad et al. (2021) [48] noted that temperature has a compensatory effect for daylength during the flowering stage.

4. Conclusions

In the agro-morphological characterization of the 25 *Chenopodium quinoa* accessions, a high amount of variability was observed for the measured characters. In the agronomic evaluations, we identified accessions with relevant characters in terms of yield and grain size. Accessions 14 and 55 stood out for their significant statistical differences, along with other accessions that were less susceptible to mildew and possessed lower saponin percentages in comparison with the commercial varieties checks. These findings demonstrate that the accessions examined contain promising traits for the development of highly productive quinoa varieties in the Peruvian Pacific desert region.

Author Contributions: Conceptualization, M.E.M.-A., A.A.-A., J.A.-C., L.G.V.-E., and E.N.J.; methodology, J.A.-C., L.G.V.-E., M.E.M.-A., A.A.-A., and R.O.G.-R.; software, J.A.-C., L.G.V.-E., and R.O.G.-R.; validation, J.A.-C., L.G.V.-E., A.A.-A., and E.N.J.; formal analysis, J.A.-C., L.G.V.-E., A.A.-A., R.O.G.-R., and M.E.M.-A.; investigation, J.A.-C., L.G.V.-E., A.A.-A., and J.L.B.-M.; resources, M.E.M.-A.; data curation, J.A.-C., and L.G.V.-E.; writing—original draft, J.A.-C., L.G.V.-E., and R.O.G.-R.; writing—review and editing, J.A.-C., L.G.V.-E., and E.N.J.; visualization, A.A.-A., M.E.M.-A., and E.N.J.; supervision, M.E.M.-A.; project administration, M.E.M.-A., and J.L.B.-M.; funding acquisition M.E.M.-A., and J.L.B.-M. All authors have read and agreed to the published version of the manuscript.

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Data Availability Statement: The data presented in this study are available upon request from the corresponding author.

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