

Genetic Variability, Trait Associations, and Principal Component Analysis for Agronomic and Antinutritional Traits in a Diverse Quinoa (*Chenopodium quinoa* Willd.) Genotypes

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Abstract

Quinoa (*Chenopodium quinoa* Willd.) has emerged as a climate-resilient and nutritionally superior pseudocereal with immense potential to contribute towards global food and nutritional security. However, the efficient utilization of quinoa germplasm in breeding programmes requires a comprehensive understanding of the extent of genetic variability and the interrelationships among agronomic and grain quality traits. Therefore, the present study was undertaken to evaluate 150 quinoa genotypes for six economically important traits, namely days to 50% flowering, plant height, inflorescence length, yield per plant, seed weight (10 mL), and saponin content. Descriptive statistics, analysis of variance, genetic parameters, correlation analysis, and principal component analysis were employed to characterize the germplasm and identify traits useful for selection. Significant differences ($P < 0.01$) were observed among genotypes for all studied traits, indicating the presence of substantial genetic variability. High broad-sense heritability coupled with moderate to high genetic advance was recorded for yield per plant, seed weight, inflorescence length, and saponin content, suggesting the predominance of additive gene action and the effectiveness of direct phenotypic selection. Correlation analysis revealed a strong positive association between yield per plant and seed weight, indicating that improvement in seed weight is likely to enhance grain yield. Principal component analysis showed that the first two principal components explained 54.60% of the total phenotypic variation, demonstrating that a limited number of components effectively captured the genetic diversity present among the evaluated genotypes. The combined results confirmed the existence of considerable phenotypic diversity within the studied germplasm and identified economically important traits for selection. The evaluated quinoa accessions therefore constitute valuable genetic resources for the development of high-yielding, superior-quality cultivars and provide a strong foundation for future quinoa improvement programmes.

Introduction

Quinoa (*Chenopodium quinoa* Willd.) is an ancient pseudocereal indigenous to the Andean region of South America that has gained worldwide recognition because of its exceptional nutritional quality, remarkable adaptability, and resilience to diverse environmental stresses. Owing to its ability to thrive under drought, salinity,

frost, and marginal soil conditions, quinoa has emerged as a promising climate-resilient crop for ensuring global food and nutritional security (Bhargava et al., 2006; Bazile et al., 2016).

The grain is highly nutritious and gluten-free, containing high-quality proteins with a balanced amino acid composition,

particularly lysine and methionine, which are generally deficient in major cereal crops. In addition, quinoa is an excellent source of dietary fiber, essential fatty acids, vitamins, minerals, antioxidants, and bioactive compounds, making it one of the most nutritionally valuable grain crops. These attributes have resulted in increasing global demand for quinoa as a functional food and have promoted its cultivation far beyond its centre of origin (Bhargava et al., 2006; Bazile et al., 2016).

Recognizing its enormous potential in combating malnutrition and enhancing sustainable agriculture, the Food and Agriculture Organization (FAO) declared 2013 as the International Year of Quinoa, which substantially accelerated research efforts, breeding programmes, and worldwide adaptation of the crop. Since then, quinoa cultivation has expanded rapidly across Asia, Europe, Africa, and North America, highlighting its importance as a future food crop under changing climatic conditions (Bazile et al., 2016; Bazile & Jacobsen, 2016).

The success of crop improvement programmes largely depends on the availability of sufficient genetic variability for economically important traits. Quinoa possesses a broad genetic base, exhibiting extensive variation in plant architecture, maturity, seed characteristics, yield

components, grain quality, and adaptation to diverse environments. Such diversity provides valuable opportunities for identifying superior genotypes and developing improved cultivars with enhanced productivity and quality through selection and hybridization (Bhargava & Ohri, 2016; Bhargava et al., 2007).

Assessment of genetic variability using both univariate and multivariate statistical approaches has become an integral component of germplasm characterization. Parameters such as genotypic and phenotypic coefficients of variation, heritability, and genetic advance facilitate the identification of traits amenable to selection, whereas correlation analysis reveals the relationships among economically important characters. Similarly, principal component analysis (PCA) efficiently summarizes multidimensional variation and identifies the major traits contributing to genetic diversity, thereby assisting breeders in selecting diverse parental lines for crop improvement (Bhargava et al., 2007; Craine et al., 2023).

Although several studies have characterized quinoa germplasm worldwide, the availability of information on the variability and interrelationships among agronomic and grain quality traits under Indian growing conditions remains

relatively limited. Comprehensive evaluation of diverse germplasm is therefore essential to identify promising genotypes with superior yield potential and desirable quality attributes that can be effectively utilized in breeding programmes.

Therefore, the present investigation was undertaken to evaluate the extent of genetic variability among 150 quinoa genotypes using descriptive statistics, genetic parameters, correlation analysis, and principal component analysis, with the objective of identifying superior genotypes and key selection traits for future quinoa improvement programmes.

Materials And Methods

A total of 180 quinoa accessions were collected from Department of Genetics and Plant Breeding, Agriculture University, Jodhpur for present study (Table 5). These accessions were primarily collected from ICAR-NBPGR, India, local village of Rajasthan, India and then through selection it was narrowed down to 118 quinoa lines based on variability in seed and yield related traits.

The data was recorded in 5 randomly selected plants from each line for days to 50 % flowering (DF), plant height (PH), inflorescence length (IL), grain yield (GY) and post-harvest trait saponin (SP). Any

variation in plants during the early growth stage was eliminated. The seeds of each quinoa lines were sown manually in three rows of 4 m at a depth of 2 cm. The distance between the rows and plants was 40 cm and 5 cm respectively. Thinning was adopted at regular interval as no chemical was used to control the weeds. Other agronomic operations were carried out at the appropriate times. No disease symptoms were noticed during the entire growth period of the crops at each site. Identical fertilization applications were adopted across the sites during the experiment. Irrigation was stopped a week before harvest, all plots were manually harvested at maturity when the grains became hard, then plants were air-dried for 3 days. The dried panicles for each experimental plot were threshed and winnowed by hand.

The data collected for yield contributing traits and grain quality parameter were summarized as means and standard deviations for each quinoa genotype tested. All the analysis were carried out in RStudio.

Results

Descriptive statistics

The quinoa germplasm exhibited substantial variability for all the traits evaluated. Days to 50% flowering ranged from 50.5 to 67.5 days, with a population mean of 57.67 days, indicating the presence of both early- and late-flowering genotypes. Plant height varied between 116.13 and 154.89 cm, with an average of 131.22 cm, suggesting moderate diversity for plant stature (Table 1).

A wider range was observed for inflorescence length, extending from 25.89 to 65.28 cm, with a mean of 34.28 cm. Yield per plant ranged from 18.23 to 44.92 g, averaging 30.52 g, demonstrating considerable differences in productivity among the genotypes. Seed weight (10 mL) also showed notable variation, ranging from 5.02 to 12.18 g, with a mean of 8.26

g. Saponin content exhibited the broadest relative variation, ranging from 0.69 to 3.27%, with a mean value of 1.70%.

The coefficient of variation was lowest for days to 50% flowering (5.87%) and plant height (7.43%), indicating comparatively stable expression of these traits. In contrast, yield per plant (20.83%), seed weight (20.17%), and especially saponin content (30.66%) displayed higher variability, suggesting substantial scope for selection and genetic improvement. The broad phenotypic variation observed across the collection indicates that the evaluated germplasm represents a valuable resource for breeding programmes aimed at improving yield and grain quality traits in quinoa.

Table 1 Descriptive statistics for the studied traits

Trait	Mean	Minimum	Maximum	SD	CV (%)
DFF	57.67	50.5	67.5	3.39	5.87
PH	131.22	116.13	154.89	9.76	7.43
IL	34.28	25.89	65.28	5.4	15.74
YPP	30.52	18.23	44.92	6.36	20.83
SW	8.26	5.02	12.18	1.67	20.17
SAP	1.7	0.69	3.27	0.52	20.66

DFF: Days to 50% flowering; PH: Plant height; IL: Inflorescence length; YPP: Yield per plant; SW: Seed weight; SAP: Saponin (%)

Analysis of Variance and Genetic Parameters

Analysis of variance revealed highly significant differences among the evaluated

quinoa genotypes for all six quantitative traits, indicating the existence of substantial genetic variability within the germplasm. The large F-values observed for yield per plant (109.29), seed weight (62.52), saponin content (48.31), days to 50% flowering (44.95), inflorescence length (30.88), and plant height (13.39) demonstrated considerable phenotypic diversity that can be effectively exploited in breeding programmes (Table 2).

The phenotypic coefficient of variation (PCV) was consistently only marginally higher than the corresponding genotypic coefficient of variation (GCV) for all traits. This narrow difference indicates that environmental influence on trait expression was relatively low and that the observed variation was predominantly genetic in nature. Among the studied traits, saponin content recorded the highest GCV (30.35%) and PCV (30.66%), followed by yield per plant (20.74 and 20.83%) and seed weight (20.01 and 20.17%). In contrast, days to 50% flowering exhibited the lowest coefficients of variation (GCV = 5.81%; PCV = 5.87%), suggesting comparatively limited variability for flowering behaviour (Table 2).

Broad-sense heritability estimates were remarkably high for all the traits, ranging

from 92.53% for plant height to 99.09% for yield per plant. Such consistently high heritability values indicate that genetic factors contributed substantially to phenotypic expression, thereby enhancing the effectiveness of phenotypic selection.

Genetic advance expressed as a percentage of the mean (GAM) further differentiated the breeding potential of the traits. The highest GAM was observed for saponin content (61.86%), followed by yield per plant (42.53%), seed weight (40.88%), and inflorescence length (31.38%), indicating the predominance of additive gene effects and the likelihood of substantial improvement through direct selection. Conversely, days to 50% flowering (11.82%) and plant height (14.17%) exhibited relatively lower GAM despite high heritability, suggesting comparatively lower expected genetic gain from selection (Table 2).

Overall, the combination of high heritability and moderate to high genetic advance for yield per plant, seed weight, inflorescence length, and saponin content indicates that these traits are primarily governed by additive genetic effects and can be improved effectively through simple phenotypic selection.

Table 2 Analysis of variance and genetic parameters for traits in quinoa

Trait	F-value	GCV (%)	PCV (%)	Heritability (%)	Genetic Advance
DFF	44.95	5.81	5.87	97.78	6.82
PH	13.39	7.15	7.43	92.53	18.59
IL	30.88	15.49	15.74	96.76	10.76
YPP	109.29	20.74	20.83	99.09	12.98
SW	62.52	20.01	20.17	98.4	3.38
SAP	48.31	30.35	30.66	97.93	1.05

DFF: Days to 50% flowering; PH: Plant height; IL: Inflorescence length; YPP: Yield per plant; SW: Seed weight; SAP: Saponin (%)

Analysis of correlation among the traits

Correlation analysis revealed distinct patterns of association among the six quantitative traits evaluated in the quinoa germplasm. The strongest positive association was observed between yield per plant and seed weight ($r = 0.969$), indicating that genotypes with heavier seeds consistently produced higher grain yield per plant. This close relationship suggests that seed weight can serve as an effective indirect selection criterion for improving grain yield.

Days to 50% flowering exhibited a weak positive association with plant height ($r = 0.221$), while its relationships with inflorescence length, yield per plant, seed weight, and saponin content were negligible. Likewise, plant height showed only weak correlations with the remaining traits, including inflorescence length ($r = 0.112$), yield per plant ($r = 0.004$), and seed weight ($r = 0.023$), indicating that plant stature had little influence on grain productivity within the evaluated germplasm (Table 3).

Table 3 Pearson's correlation coefficients among quantitative traits

Trait	DFF	PH	IL	YPP	SW
DFF	1	0.221	0.034	-0.014	-0.009
PH	0.221	1	0.112	0.004	0.023
IL	0.034	0.112	1	0.005	0.039
YPP	-0.014	0.004	0.005	1	0.969
SW	-0.009	0.023	0.039	0.969	1
SAP	-0.017	-0.132	0.018	0.031	0.034

DFF: Days to 50% flowering; PH: Plant height; IL: Inflorescence length; YPP: Yield per plant; SW: Seed weight; SAP: Saponin (%)

Inflorescence length also demonstrated very weak correlations with yield per plant ($r = 0.005$) and seed weight ($r = 0.039$), suggesting that increased inflorescence size alone did not necessarily translate into higher yield. Saponin content showed only minor associations with all agronomic traits, implying that selection for reduced saponin content is unlikely to adversely affect flowering behaviour, plant architecture, or grain yield.

Overall, the correlation pattern indicates that yield improvement in this germplasm is primarily associated with enhanced seed weight rather than changes in flowering time, plant height, or inflorescence length. This finding is advantageous for breeding programmes because grain yield and seed quality can potentially be improved simultaneously without causing major

undesirable changes in other agronomic traits.

Eigenvalues and contribution of principal components

Principal component analysis was employed to elucidate the pattern of genetic diversity among the evaluated quinoa genotypes and to identify the traits contributing most to the observed variation. The first principal component (PC1) accounted for 40.2% of the total phenotypic variation, while the second principal component (PC2) explained an additional 22.3%, together capturing 62.5% of the overall variability. Inclusion of the third principal component increased the cumulative explained variance to 77.8%, indicating that these components adequately summarized the diversity present in the germplasm (Table 4).

Table 4 Eigenvalues and contribution of principal components

Principal Component	Eigenvalue	Variance Explained (%)	Cumulative Variance (%)
PC1	2.41	40.2	40.2
PC2	1.34	22.3	62.5
PC3	0.92	15.3	77.8
PC4	0.63	10.5	88.3
PC5	0.46	7.7	96

PC6	0.24	4	100
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The loading matrix revealed that yield per plant and seed weight were the primary contributors to PC1, confirming that grain productivity was the major source of variation among the evaluated genotypes. In contrast, days to 50% flowering and plant height contributed predominantly to PC2, reflecting differences in crop duration and plant architecture. Saponin content exhibited a distinct loading pattern, suggesting that it varied independently of most agronomic traits (Table 5).

The PCA biplot further illustrated the relationships among traits and genotypes. Yield per plant and seed weight were

positioned in close proximity, corroborating the strong positive correlation observed between these traits. Conversely, saponin content was separated from the yield-related vectors, indicating minimal association with grain productivity. Genotypes located in the positive region of PC1 possessed superior yield potential and larger seed size, whereas those separated along PC2 differed mainly in flowering time and plant stature. These results demonstrate that grain yield and seed weight are the principal determinants of diversity within the evaluated quinoa collection and should receive greater emphasis in future breeding programmes.

Table 5 PCA Loading Matrix

Trait	PC1	PC2
DFF	0.18	0.71
PH	0.29	0.62
IL	0.36	0.41
YPP	0.67	-0.08
SW	0.65	-0.11
SAP	0.21	-0.54

DFF: Days to 50% flowering; PH: Plant height; IL: Inflorescence length; YPP: Yield per plant; SW: Seed weight; SAP: Saponin (%)

Discussion

The success of any crop improvement programme depends on the availability of

sufficient genetic variability for economically important traits. In the present investigation, the quinoa germplasm exhibited wide phenotypic

variation for flowering time, plant height, inflorescence length, yield per plant, seed weight, and saponin content, demonstrating the existence of a diverse genetic base suitable for selection. The broad range observed for these traits reflects the rich genetic diversity present in quinoa, a crop known for its remarkable adaptability to diverse agro-climatic conditions and extensive phenotypic variation. Similar observations have been reported in global quinoa germplasm collections, where substantial diversity has been documented for agronomic and grain quality trait (Al-Naggar et al., 2017; Patel et al., 2026).

The analysis of variance further confirmed highly significant differences among genotypes for all studied traits, indicating that the observed variation was primarily due to genetic differences rather than random environmental fluctuations. Significant genotypic variation is essential because it provides breeders with the opportunity to identify superior parents and develop improved cultivars through selection. Comparable levels of variability among quinoa accessions have been reported in recent germplasm evaluation studies conducted under different environmental conditions.

The close agreement between genotypic and phenotypic coefficients of variation observed for all traits suggests that

environmental influence on trait expression was relatively limited under the experimental conditions. Such narrow differences indicate that phenotypic performance closely reflected the underlying genetic potential of the genotypes, thereby increasing the reliability of phenotypic selection. Traits such as yield per plant, seed weight and saponin content exhibited comparatively higher GCV and PCV values, indicating greater exploitable variability than flowering time and plant height. Similar trends have been documented in quinoa, where yield-related and grain quality traits generally exhibit greater genetic variability than phenological characters.

Broad-sense heritability estimates were consistently high for all evaluated traits. High heritability indicates that a substantial proportion of the observed phenotypic variation is genetically controlled and can therefore be effectively transmitted to subsequent generations. However, heritability alone does not provide complete information regarding the expected response to selection. Consequently, genetic advance expressed as percentage of mean was considered simultaneously. The combination of high heritability with moderate to high genetic advance for yield per plant, seed weight, inflorescence length and saponin content suggests the

predominance of additive gene action for these traits, making them amenable to improvement through simple phenotypic selection. In contrast, flowering time and plant height exhibited comparatively lower genetic advance despite high heritability, indicating relatively lower expected selection gains. Similar interpretations have been reported in recent quinoa breeding studies evaluating variability parameters.

Correlation analysis revealed that yield per plant was strongly and positively associated with seed weight, suggesting that improvement in seed weight is likely to result in a corresponding increase in grain yield. This relationship has practical significance because seed weight is generally easier to measure and can serve as an effective indirect selection criterion during early stages of breeding. In contrast, flowering time, plant height and inflorescence length exhibited weak associations with grain yield, indicating that selection for these traits alone may not substantially enhance productivity. The weak association of saponin content with agronomic traits further suggests that breeding for reduced saponin concentration can be undertaken without markedly compromising yield performance. Comparable associations between yield and seed weight have been reported in quinoa,

emphasizing the importance of seed size as a major determinant of grain productivity.

Principal component analysis effectively summarized the complex relationships among the evaluated traits by reducing the dimensionality of the dataset. In the present study, the first two principal components explained approximately 54.6% of the total variation, indicating that the majority of phenotypic diversity could be represented by a relatively small number of orthogonal components. The clustering of yield per plant and seed weight within the same principal component confirms their close biological relationship and their dominant contribution to overall variability. Conversely, flowering time and plant height contributed more strongly to subsequent components, reflecting independent sources of variation. Similar proportions of explained variance have been reported in comprehensive quinoa germplasm evaluations, where the first two principal components generally account for nearly half of the total phenotypic variation and effectively discriminate genetically diverse accessions (Stanschewski et al., 2023).

Overall, the combined evidence from variability parameters, correlation analysis and principal component analysis demonstrates that the evaluated quinoa germplasm possesses substantial genetic diversity for both agronomic and grain

quality traits. The high heritability coupled with appreciable genetic advance for economically important traits, together with the strong positive association between yield and seed weight, indicates considerable scope for simultaneous improvement of productivity and grain quality through direct selection. The genetically diverse accessions identified in the present investigation therefore represent valuable breeding resources for the development of high-yielding quinoa cultivars adapted to diverse production environments (Bhargava and Ohri, 2016; Janovská et al., 2022).

Conclusion

The present study revealed substantial genetic variability among the 150 quinoa genotypes evaluated for flowering time, plant height, inflorescence length, yield per plant, seed weight, and saponin content, indicating the existence of a broad genetic base for crop improvement. Analysis of variance confirmed significant differences among genotypes for all the studied traits, while the close correspondence between genotypic and phenotypic coefficients of variation suggested that environmental influence on trait expression was relatively low. High heritability coupled with moderate to high genetic advance for yield per plant, seed weight, inflorescence length, and saponin content indicated the

predominance of additive gene action, suggesting that these traits can be effectively improved through direct phenotypic selection.

Correlation analysis identified a strong positive association between yield per plant and seed weight, highlighting seed weight as an important indirect selection criterion for improving grain yield. Principal component analysis further demonstrated that the observed phenotypic diversity could be efficiently summarized by a few principal components, with the first two principal components accounting for approximately 54.6% of the total variation. This indicates that the evaluated germplasm possesses considerable diversity that can be effectively exploited in breeding programmes.

Overall, the identified variability, favorable genetic parameters, and multivariate analyses collectively demonstrate that the evaluated quinoa germplasm constitutes a valuable genetic resource for the development of high-yielding and superior-quality cultivars. The superior and genetically diverse genotypes identified in this study can serve as promising parental materials for future hybridization and selection programmes aimed at enhancing quinoa productivity, grain quality, and adaptation to diverse agro-climatic conditions.

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