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# Genetic variability, association and path analysis of yield and its attributing traits in quinoa (*Chenopodium quinoa* Willd.)

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**Abstract**
A study named, "Genetic studies in quinoa (*Chenopodium quinoa* Willd.) agro-morphological and grain traits" was conducted at Agricultural Botany Research Farm, Mahatma Phule Krishi Vidyapeeth, Rahuri - 413 722, District- Ahilyanagar, Maharashtra (India) during *Rabi* period, 2024. The current study was conducted to assess twenty-three different quinoa genotypes in order to determine genetic variability, heritability, genetic advance, correlation coefficients, path analysis, and genetic diversity. The investigation involving twenty-three genotypes of quinoa was planted using a Randomized Block Design (RBD) with three repetitions. Data were collected for ten characters *viz.*, days to 50% flowering, days to maturity, plant height, number of spikelets/inflorescence, inflorescence length, inflorescence width, leaf length, yield per plant, seed volume weight /10 ml and saponin content. A higher level of variability was found among the genotypes for all the traits examined. The genotypic coefficient of variation was lower than the phenotypic coefficient of variation for every character. The seed yield per plant exhibited a significant and positive correlation at both the genotypic and phenotypic levels with No. of spikelets/ inflorescences, seed volume wt, leaf length, inflorescence length, plant height and inflorescence width. Seed yield per plant demonstrated a significant and negative correlation with days to 50 percent flowering both at genotypic and phenotypic level and days to maturity significant at genotypic level and non-significant at phenotypic level. Plant height, No. of spikelets/ inflorescence, inflorescence length, inflorescence width, leaf length, yield per plant, seed volume wt/10 ml showed significant positive association among one another. The path analysis indicated that inflorescence width had the highest direct positive impact on seed yield per plant, followed by the number of spikelets per inflorescence and seed volume weight per 10 ml. These traits showed strong direct effects in the favorable direction and further confirmed their significant association with seed yield/ plant, highlighting a true and consistent relationship. This suggests that direct selection based on these characteristics would be effective in identifying high-yielding quinoa genotypes.

**Keywords:** Quinoa (*Chenopodium quinoa* Willd.), genetic variability, heritability, genetic advance

## Introduction
Quinoa (*Chenopodium quinoa* Willd.)is an annual herb, which belongs to the Amaranthaceae family, though it was previously classified under the Chenopodiaceae family (Gomez-Pando, 2015) [15]. A key staple food native to South America's Andes region. Quinoa leaves are also used as a leafy green, but the harvesting and eating process is similar to that of other cereal grains. Quinoa was first cultivated by ancient Andean cultures in the highlands of present-day Bolivia and Peru. However, cultivation of quinoa has spread in a scattered pattern to the south-central region of Chile. The Food and Agriculture Organization (FAO) of the United Nations has recognized quinoa as a "future smart food" due to its nutritional value and potential to address global food security challenges. This label underscores its superior nutritional benefits, its capacity to enhance soil quality by reducing the need for chemical fertilizers, and its proven resilience under challenging climatic and agronomic conditions. (Anonymous, 2018) [3]
This plant is part of complicated group of allotetraploid taxa (2n = 4x = 36), which encompasses *C. berlandiri* subsp. *berlandiri*, *C. berlandiri* subsp. *nuttalliae*, *C. hircinum*, and *C. quinoa* originated in Southern America with Andes of Bolivia and Peru as primary centres of origin. (Ain, 2022) [1]. It is classified within the Amaranthaceae family (previously known as

Chenopodiaceae), which additionally includes other economically significant species like spinach (*Spinacia oleracea)* and sugarbeet (*Beta vulgaris*) (Giusti, 1970; Maughan *et al.*, 2004; Kadereit *et al.*, 2003) [14, 24, 18].

Quinoa breeders primarily aim to develop varieties with high grain yield and quality traits, tailored to thrive in a range of agro-climatic conditions. Despite the crop's significant nutritional value, limited efforts have been made towards its genetic improvement, resulting in a lack of information on many key aspects. Breeding a crop for specific environments requires utilizing a variety of cultivars or genotypes, as this helps assess intraspecific variability for different traits and their interactions. Genetic variability in the base population is crucial for any crop breeding program. The level of diversity in the germplasm defines the boundaries for selection and potential improvement. Traits of economic significance are typically quantitative and show a considerable interaction with the environment. Therefore, it is essential to assess the variability within the material and break it down into genotypic, phenotypic, and environmental components. Enhancing yield requires a thorough understanding of the variation present in the available germplasm, the relationships between quantitative traits and yield, the impact of environmental factors on these traits, as well as the heritability and genetic gain within the material. Correlation coefficients reveal the relationships between different traits and the strength of their linear connection. However, correlation studies alone do not provide a complete picture of the direct and indirect effects that individual traits have on yield. Therefore, simple correlations are often insufficient to clearly identify the importance of each component trait in determining yield. In such cases, path coefficient analysis becomes essential, as it considers not only the causal relationships but also the strength of the connections between the traits. Path analysis, or standardized partial-regression coefficient, breaks down correlation coefficients into direct and indirect effects. This method enables the separation of the direct influence of each trait on yield from the indirect effects resulting from the mutual relationships among the traits (Garcia del Moral *et al*., 2003) [13].

## Materials and Methods

The present investigation "Genetic studies in Quinoa (*Chenopodium quinoa* Willd.) for agro-morphological and grain traits" performed on Agricultural Botany Research Farm, Post Graduate Institute, MPKV, Rahuri - 413722 Dist. Ahilyanagar, Maharashtra in *Rabi* season, 2024. The experimental material for this experiment contains 23 genotypes of Quinoa bought from All India Co-ordinated Research Network on Potential Crops, Mahatma Phule Krishi Vidyapeeth Rahuri- 413 722 Dist-Ahilyanagar, Maharashtra. The catalogue of twenty-three genotype is presented in the Table- 1.

**Table 1:** List of 23 genotypes of quinoa

| Sr. No. | Genotypes | Sr. No. | Genotypes | Sr. No. | Genotypes |
|---|---|---|---|---|---|
| 1. | EC-896069 | 9. | EC-896115 | 17. | EC-896209 |
| 2. | EC-896073 | 10. | EC-896133 | 18. | EC-896210 |
| 3. | EC-896074 | 11. | EC-896201 | 19. | EC-896267 |
| 4. | EC-896075 | 12. | EC-896202 | 20. | EC-896268 |
| 5. | EC-896079 | 13. | EC-896203 | 21. | EC-896271 |
| 6. | EC-896082 | 14. | EC-896204 | 22. | EC-896273 |
| 7. | EC-896090 | 15. | EC-896207 | 23. | Himshakti (Check) |
| 8. | EC-896114 | 16. | EC-896208 | | |

The experiment was carried out using a Randomized Block Design (RBD) with three replications and a spacing of 30 cm x 10 cm. All necessary cultural practices, including fertilizer application, inter-culturing, and weeding, were followed to ensure optimal crop growth. The land preparation involved ploughing, followed by two rounds of cross harrowing. Plot size for quinoa was 0.60 m x 3.00 m. Fertilizer dose applied to quinoa was 25t/ha FYM, phosphobacteria 2 kg/ha, 60 kg/ha N, 40 kg/ha, P2O5 and 20 kg/he K as basal dose. The seeds were sown on 18th Nov 2024. The gap-filling operation was performed 20 days after sowing. Other cultural practices were carried out according to the recommended guidelines. Observations were made on five randomly selected plants from each treatment in every replication, and the averages were then calculated.

### Statistical Analysis

The analysis of variance was done as per suggestions of Panse and Sukhatme (1995) [26].

### Genotypic Coefficient of Variation (GCV)

It was calculated using the formula recommended by Burton (1952) [7].

$$GCV = \frac{\sqrt{\sigma^2 g}}{x} \times 100$$

### Phenotypic Coefficient of Variation (PCV)

It was calculated using the formula suggested by Burton (1952) [7].

$$PCV = \frac{\sqrt{\sigma^2 g}}{X} \times 100$$

### Heritability Percentage (Broad sense)

Heritability% in broad sense was estimated as given by Burton (1952) [7].

$h^2$ (b. s) = Vg/Vp × 100

### Genetic Advance

Calculated by the formula given by Johnson *et al*. (1955) [17].

G.A. = K x ($\sigma^2$g /$\sigma^2$p) x $\sqrt{\sigma p}$

### Correlation

To examine the relationships among the traits, genotypic and phenotypic correlation coefficients were calculated using the method outlined by Singh and Chaudhary (1977) [31].

### Path Coefficient Analysis

Path coefficient analysis was performed following the procedure recommended by Dewey and Lu (1959) [11].

## Results and Discussion

Current study on "Genetic studies in Quinoa (*Chenopodium quinoa* Willd) for agro-morphological and grain traits" was conducted with the aim of understanding genetic variability, correlation, path analysis and genetic diversity among 23 genotypes. Experiment was conducted at Agricultural Botany Research Farm, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahilyanagar, Maharashtra in *Rabi* season 2024.

**Genetic Variability**

Present study indicated a wide range of variation across all the traits studied. Among traits, inflorescence width exhibited the highest coefficient of variation (CV) at (13.47), followed by inflorescence length (11.25), seed yield/ plant (10.95), No. of spikelets\ inflorescence (8.57), seed volume weight per 10 ml (5.7), plant height (4.74), saponin content (3.27), leaf length (2.89), and days to 50% flowering (2.25). Highly notable differences were noted between the twenty-three genotypes for key agronomic characters, including plant height (ranging from 110.73 to 164.60 cm), days to maturity (99.26 to 120.20), number of spikelets per inflorescence (17.33 to 35.20), days to 50% flowering (42.33 to 55.06), inflorescence length (17.20 to 28.76), and seed yield per plant (16.56 to 25.87 g). In contrast, the remaining traits demonstrated a relatively narrow range of variability**.**

Curti *et al.* (2016) [9] noted that traits such as main stem branches, plant height and panicle length shown wide range of variability with coefficient of variation (CV) of 93.7, 44.2, 41.2 per cent, respectively. Vasconcelos *et al.* (2016) [35] noted high heritability values (80.01%) with low GCV (2.19%) for the maturity period. Al-Naggar *et al.* (2022) [2] indicated that seed yield/plant, branches/plant, leaf area, inflorescence diameter, leaves area/plant, stem diameter, leaf area index, leaves/ plant, plant height had high heritability and high genetic advance. Behra, *et al.* (2025) [4] observed significant variations in traits such as spikelet colour, leaf length, and plant height. High heritability and genetic advance were observed for traits like leaf length and seed yield. These results align with the findings reported by Szilagyi and Jornsgard. (2014) [33]. Similarly, De Santis *et al.* (2016) [10] reported considerable variability in seed yield\ plant and biological yield\ plant.

Coefficients of variation were calculated for both phenotypic and genotypic levels. For all traits studied, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV), although the differences were slight, indicating that environmental factors had a minimal impact on trait expression (Al-Naggar *et al*., 2022) [2]. Most traits exhibited either moderate or high levels of GCV and PCV. The estimates of GCV and PCV for the current study are provided in Table-2. GCV values indicate extent of genetic variability present within the germplasm. However, the extent to which this variability can be inherited from parents to offspring is reflected in heritability. The concept of broad-sense heritability, as introduced by Lush (1949) [22], is fundamental in assessing the effectiveness of utilizing genetic variability in breeding programs. As per Robinson *et al*. (1949) [29], heritability estimates are typically classified into three categories: high (above 60%), moderate (30-60%), and low (below 30%). The heritability estimates derived in the current study are also presented in Table- 2.

Heritability reflects the extent to which offspring resemble their parents (Falconer, 1960) [12], while genetic advance estimates the potential improvement in a trait following selection. Generally, traits with both high heritability and high genetic advance are considered to be governed by additive gene action. Alternatively, when high heritability is coupled with low genetic advance, or when both heritability and genetic advance are low, it could suggest the presence of non-additive gene action, such as dominance or epistasis, influencing the expression of the traits. In self-pollinated crops, traits typically exhibit both high heritability and high genetic advance. However, when phenotypic variation within the population is limited, genetic advance tends to be low, even if heritability is high. These observations emphasize the critical role of both variability and heritability in the success of any breeding program.

**1. Days to 50 percent flowering (No.)**

Low GCV and PCV was recorde for days to 50% flowering (7.23and 7.57%), it indicated that, there was limited scope for selection for this character high heritability (91.20%) In conjunction with moderate genetic advance as percent of mean (14.22%) showed for the character days to 50% flowering.

The findings from the current study align with those of Al-Naggar *et al.* (2022) [2], who observed low estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) for days to 50% flowering in quinoa, indicating limited variability for this trait. Similarly, De Santis (2016) [10] trait in quinoa demonstrated a high heritability alongside a moderate genetic gain as a percentage of the mean, indicating that, despite limited variability, the trait is mainly driven by additive genetic factors. Furthermore, Kusuma *et al.* (2007) [20] observed low GCV and PCV for days to 50% flowering in grain amaranth, indicating minimal genetic and environmental variability for this trait.

**2. Days to maturity (No.)**

For days to maturity, low genotypic and phenotypic coefficient of variation (3.61 and 3.80%, resp.) was observed, it revealed that, there was limited scope for selection for this character. High heritability (90.10%) in combination with low genetic advance as per cent of mean (7.07%) recorded for the character days to maturity.

Similar results observed in studies of Al-Naggar *et al* (2022) [2] and reported low GCV, PCV and high estimates of heritability for this trait. Benlhabib *et al.* (2016) [5] observed higher heritability for day to maturity in quinoa. Kusuma *et al.* (2007) [20] observed Low PCV and GCV were reported for days to maturity in amaranth.

**3. Plant height (cm)**

In the plant height, genotypic and phenotypic coefficient of variation was low (7.76 and 9.10%, respectively). It indicated that, there was limited scope for selection for this character. High estimates of heritability (72.80%) along with moderate genetic advance as percent mean (13.65%) showed by plant height.

Similar results observed in studies of Lokeshkumar and Murthy (2017) [21], where they reported low GCV, PCV and high heritability in relative crop grain amaranth in this case. These results contrast with the findings of Behra *et al*. (2025) [4], who reported higher genotypic and phenotypic coefficients of variation (GCV and PCV) for plant height. (33.35, 54.47)

**4. Number of spikelets per inflorescence (No.)**

High GCV (20.25) and high PCV (21.99) showed by number of spikelets per inflorescence, this revealed, there was significant potential for selection for this character. High estimates of heritability (84.80%) coupled to high genetic advance as percent of mean (38.42%) showed by number of spikelets per inflorescence. This indicates dominance of additive gene action for control of this trait and selection for spikelet per inflorescence will be more effective.

None of the author reported this character.

**5. Inflorescence length (cm)**

For inflorescence length degree of GCV and PCV was moderate (13.38 and 17.81%, respectively). Likewise, moderate

heritability (56.50%) along with higher genetic advance as percent mean (20.71%) revealed predominance of additive gene action for control of this trait and hence selection will be more effective.

Similar results were observed in the studies of Behra *et al*. (2025) [4], where high genotypic and phenotypic coefficients of variation (GCV and PCV) were recorded for the length of inflorescence.

**6. Inflorescence width (cm)**

Low GCV (8.63%) and moderate PCV (16.01%) showed in inflorescence width. Whereas low heritability (29.10%) with low genetic advance as per cent mean (9.60%). This indicated predominance of non- additive gene action for control of this character.

These results contrast with the findings of Al-Naggar *et al*. (2022) [2], who reported high GCV, PCV, and heritability values, along with a high genetic advance as a percentage of the mean for inflorescence width.

**7. Leaf length (cm)**

Higher GCV and high PCV showed by leaf length (31.05 and 31.18%, respectively), it indicated that, there great potential for selection for this character. High estimates of heritability (99.10%) coupled with high genetic advance as percent mean (63.68%) showed by leaf length. This indicated pre-dominance of additive gene action for control in this case and selection for leaf length will be more effective.

Behra *et al*. (2025) [4] reported high genotypic and phenotypic coefficients of variation (GCV and PCV) for leaf length (31.22 and 34.71, respectively), along with significant genetic advances (57.86%).

**8. Seed volume weight (g/ 10 ml)**

For seed volume wt low GCV and moderate PCV was exhibited (9.83 and 11.38%, respectively). Likewise, high heritability (74.40%) with moderate genetic advance as per-cent mean (17.52%) showed by the trait seed volume weight.

Similar results observed in studies of Tiwari *et al* (2022) [34], where moderate PCV (15.25) and low GCV (10.83) reported in case of seed volume weight. Likewise moderate genetic gain (15.86) was observed for seed volume weight (g/10ml).

**9. Seed yield per plant (g)**

Moderate Genotypic CV (11.79%) and Phenotypic CV (16.09%) founded in seed yield/ plant. Moderate heritability (53.70%) with moderate genetic advance as per-cent mean (17.80%) revealed in seed yield per plant. This indicated that there was medium scope for selection.

Al-Naggar *et al*. (2017) reported that the maximum predicted genetic advance from selection was observed for seed yield per plant (56.02%), indicating a high level of variability among the studied genotypes. This variability is believed to be governed by additive gene action, suggesting that substantial improvement for this trait could be achieved through direct selection. The results are in close harmony with studies of Behra *et al*. (2025) [4], where heritability estimates for seed yield (67.28%) was high.

**10. Saponin content (mg/g)**

High GCV and PCV values were observed for saponin content (31.47% and 33.63%, respectively), indicating significant potential for selection of this trait. The high heritability estimate (99.00%) combined with a high genetic advance as a percentage of the mean (68.63%) suggests the predominance of additive gene action in controlling this trait, making selection highly effective.

For all the traits studied, the minimal differences between the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) suggest that environmental effects on their expression are limited. This implies that phenotypic values can be reliably used for direct selection. Moreover, the genotypic and phenotypic variances were consistently higher than the environmental variance for all traits, further indicating that environmental influence was either low or negligible. As a result, selection based on these traits is likely to be effective. In the current investigation, traits such as the number of spikelets/ inflorescence, leaf length, and saponin content showed high heritability along with a high genetic advance as a percentage of the mean, suggesting that these traits are primarily controlled by additive gene action.

**Table 2:** Genetic variability parameters in 23 quinoa genotypes.

| Sr. No. | Character | Mean | Range | GCV (%) | PCV (%) | ECV (%) | $h^2$% (B.S) | Genetic Advance | Gen. Adv. as % of Mean |
|---|---|---|---|---|---|---|---|---|---|
| 1. | Days to 50% flowering (No.) | 47.66 | 42.33-55.06 | 7.23 | 7.57 | 2.25 | 91.20 | 6.78 | 14.22 |
| 2. | Days to maturity (No.) | 105.06 | 99.26- 120.20 | 3.61 | 3.80 | 1.19 | 90.10 | 7.42 | 7.07 |
| 3. | Plant height (cm) | 138.58 | 110.73- 164.60 | 7.76 | 9.10 | 4.74 | 72.80 | 18.92 | 13.65 |
| 4. | No. of spikelet/inflorescence (No.) | 24.17 | 17.33-35.20 | 20.25 | 21.99 | 8.57 | 84.80 | 9.28 | 38.42 |
| 5. | Inflorescence length (cm) | 22.13 | 17.20-28.76 | 13.38 | 17.81 | 11.75 | 56.50 | 4.58 | 20.71 |
| 6. | Inflorescence width (cm) | 17.96 | 14.17-22.26 | 8.63 | 16.01 | 13.48 | 29.10 | 1.72 | 9.60 |
| 7. | Leaf length (cm) | 4.86 | 2.73-7.91 | 31.05 | 31.18 | 2.90 | 99.10 | 3.09 | 63.68 |
| 8. | Seed volume weight /10 ml(g) | 6.48 | 5.37-7.66 | 9.83 | 11.38 | 5.72 | 74.70 | 1.13 | 17.52 |
| 9. | Seed yield per plant (g) | 21.98 | 16.56- 25.87 | 11.79 | 16.09 | 10.95 | 53.70 | 3.91 | 17.80 |
| 10. | Saponin content (mg) | 0.19 | 0.06-0.32 | 33.47 | 33.63 | 3.27 | 99.00 | 0.13 | 68.63 |

**Correlation Coefficient Analysis**

Numerous quantitative character variations serve as the foundation for selection in plant breeding programs, while knowledge of the relationships between these quantitative traits makes it easier to choose the best breeding technique and choose the parents for crop improvement. The primary goal of the majority of crop enhancement programs is to increase yield. It is thought that a number of independent yield-determining component traits work together to determine yield. Since it may aid in the simultaneous enhancement of both features, a favorable connection between yield and component characters is preferred.

The extent of the relationship between two traits under investigation is reflected by both genotypic and phenotypic correlation coefficients. The genotypic correlation coefficient provides a more accurate measure of the association between

traits and helps identify those that could be valuable for overall crop improvement. They might also be useful in determining which characters are not very important in the choosing process. In any case, they give the breeder fundamental information that is helpful (Johnson *et al.*, 1955) [17]. The selection index that is helpful for crop development through simultaneous selection is also formulated with the aid of the phenotypic correlations.

The genotypic and phenotypic correlation coefficients between yield and its related components are presented in Table- 3.

**1. Correlation of seed yield with its component**

The seed yield per plant showed significant and positive relationship at genotypic and phenotypic level with plant height (rg=0.735 and rp= 0.553), number of spikelet per inflorescences (rg =0.929 and rp =0.733), inflorescence length (rg =0.815 and rp =0.583), inflorescence width (rg =0.660 and rp =0.641), leaf length (r g =0.823 and r p =0.609) and seed volume weight (rg =0.877 and rp =0.511) respectively. The seed yield per plant showed significant and negative correlation with days to 50 per cent flowering (rg =-0.533 and (rp = -0.382) both at genotypic and phenotypic level respectively and days to maturity (rg= -0.324) and r p = -0.206) significant at genotypic and non-significant at phenotypic level.

The relationship between seed yield and its component traits observed in this study is consistent with the findings of Souri Laki *et al*. (2024) [32], they found that, the highest positive and significant phenotypic and genotypic correlations were observed between grain yield and 1000-grain weight. (0.98, 0.92), panicle length (0.86, 0.75). Mhada *et al*. (2014) [25] also reported the highest positive and significant correlation between seed yield and plant height (r: 0.40). In grain amaranthus Kusuma *et al.* (2007) [20], Yadav *et al.* (2014) [38] and Venkatesh *et al.* (2014) [36] they concluded that plant height and panicle length had a positive correlation with seed yield. According to Maliro *et al*. (2017) [23], under irrigated conditions, seed yield in quinoa exhibited a strong positive correlation with plant height (r = 0.74), days to maturity (r = 0.76), and biological yield (r = 0.87). Moreover, plant height itself showed a strong positive association with both seed yield (r = 0.74) and biological yield (r = 0.80), indicating its potential as a key contributing trait for yield improvement.

**2. Correlation between yield contributing components**

**2.1 Days to 50 per cent flowering (No.)**

Days to 50 per cent flowering had positive significant correlation with days to maturity (rg= 0.727 and rp= 0.709) both at genotypic and phenotypic level. It showed significant negative correlation with No. of spikelets per inflorescences (rg=-0.439 and r p = -0.376), inflorescence length (r g= -0.491 and rp = -0.333), leaf length (rg = - 0.615 and rp = - 0.580) both at genotypic and phenotypic level respectively. Plant height (rg = -0.229 and rp = - 0.188), inflorescence width (rg= - 0.271 and rp = -0.138) and seed volume weight/10 ml (rg = - 0.180 and rp = -0.154) showed negative significant correlation at genotypic and negative non -significant correlation phenotypic level. The results are in accordance with the findings of Bhargava *et al.* (2007) [6] for days to 50% flowering.

The present findings align with those of Tiwari *et al*. (2022) [34], who observed that days to 50% flowering exhibited a significant positive correlation with leaf length, plant height, days to maturity, and seed weight (g/10 ml), while showing a significant negative correlation with seed yield. This suggests that delayed flowering may enhance vegetative growth and seed development traits but could adversely impact overall seed yield.

**2.2 Days to maturity (No.)**

Days to maturity had significant positive correlation with days to 50% flowering (rg = 0.727 and rp = 0.709). It had significant negative correlation alongside inflorescence length (rg = -0.485 and rp = - 0.320) and leaf length (rg = -0.474 and rp = -0.464) at genotypic and phenotypic level. Number of spikelets per inflorescence showed negative significant correlation at genotypic level (rg = -0.246) and negative non-significant correlation at phenotypic level (rp = -0.191) with days to maturity. The following characters showed negative but non-significant correlation both at genotypic and phenotypic level, inflorescence width (rg = -0.187 and rp = -0.106), plant height (rg = -0.064 and rp = -0.067), and seed volume weight/10 ml (rg = -0.029 and rp = -0.041), respectively.

These results are in agreement with the outputs of Habib *et al* (2024) [16] and results are similar for correlation with the character days to maturity.

**Table 3:** Estimates of genotypic (above diagonal) and phenotype correlation coefficients (below diagonal) among seed yield and yield contributing characters in 23 Quinoa genotypes

| Sr. No. | Character | Days to 50% flowering | Days to maturity | Plant height (cm) | No. of spikelet/ Inflorescences (No.) | Inflorescence length (cm) | Inflorescence width (cm) | Leaf length (cm) | Seed volume weight (g/10 ml) | Seed yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|
| 1. | Days to 50% flowering (No.) | 1.000 | 0.727** | -0.229* | -0.439** | -0.491** | -0.271** | -0.615** | -0.180 | -0.533** |
| 2. | Days to maturity (No.) | 0.709** | 1.000 | -0.064 | -0.246* | -0.485** | -0.187 | -0.474** | -0.029 | -0.324** |
| 3. | Plant height (cm) | -0.188 | -0.067 | 1.000 | 0.810** | 0.149 | 0.169 | 0.325** | 0.690** | 0.735** |
| 4. | No. of spikelet/Inflorescences (No.) | -0.376** | -0.191 | 0.710** | 1.000 | 0.493** | 0.437** | 0.665** | 0.665** | 0.929** |
| 5. | Inflorescence length (cm) | -0.333** | -0.320** | 0.203 | 0.473** | 1.000 | 0.956** | 0.587** | 0.573** | 0.815** |
| 6. | Inflorescence Width (cm) | -0.138 | -0.106 | 0.161 | 0.250* | 0.486** | 1.000 | 0.641** | 0.680** | 0.660** |
| 7. | Leaf length (cm) | -0.580** | -0.446** | 0.270* | 0.607** | 0.437** | 0.362** | 1.000 | 0.447** | 0.823** |
| 8. | Seed volume Weight (g/10 ml) | -0.154 | -0.041 | 0.461** | 0.521** | 0.335** | 0.267* | 0.386** | 1.000 | 0.877** |
| 9. | Seed yield/ plant (g) | -0.382** | -0.206* | 0.553** | 0.733** | 0.583** | 0.641** | 0.609** | 0.511** | 1.000 |

* and ** significant at P = 5 and P = 1 level of significance, respectively.

**2.3 Plant height (cm)**

Plant height had positive highly significant correlation with No. of spikelets per inflorescence (rg=0.810 and rp=0.710), seed volume weight/10 ml (rg = 0.690 and rp = 0.461) and leaf length (rg=0.325 and rp=0.270) at both genotypic and phenotypic level. Inflorescence width (rg =0.169 and rp =0.161), inflorescence length (rg =0.149 and rp=0.203) had positive and non-significant correlation both at genotypic and phenotypic level.

Rojas (2003) [30] panicle length was positively associated with plant height showing that lines with greater plant height also developed longer panicles. Fuentes and Bhargava (2011) noticed correlation between plant height and inflorescence length

**2.4 Number of spikelets per inflorescence (No.)**
Number of spikelets/ inflorescence showed highly significant and positive correlation alongside leaf length (rg= 0.665 and rp= 0.607), seed volume weight/10 ml (rg= 0.665 and rp= 0.521), inflorescence length (rg=0.493 and rp= 0.473) and Inflorescence width (rg=0.437 and rp= 0.250) both at the genotypic and the phenotypic level respectively.
None of the author reported this character.

**2.5 Inflorescence length (cm)**
Inflorescence length indicated highly significant and positive association with inflorescence width (rg= 0.956 and rp= 0.486), leaf length (rg= 0.587 and rp= 0.437) and seed volume weight / 10 ml (rg = 0.573 and rp= 0.335) both at genotypic and phenotypic level respectively.
These results are consistent with the findings of Risi and Galwey (1989) [28], Spehar and Santos (2005), and Benlhabib *et al*. (2016) [5]. Similarly, Rojas (2003) [30] observed that panicle length was positively associated with plant height, indicating that lines with greater plant height tend to develop longer panicles

**2.6 Inflorescence width (cm)**
Inflorescence width showed significant and positive correlation with leaf length (rg= 0.641 and rp= 0.362) and seed volume weight / 10 ml (rg = 0.686 and rp= 0.267) at genotypic and phenotypic level respectively.
These findings differ from those reported by Craine *et al*. (2023) [8], noticed moderate positive correlations between inflorescence width and days to maturity.

**2.7 Leaf length (cm)**
Leaf length exhibited a positive and statistically significant correlation with seed volume weight per 10 ml at both the genotypic ($r^g$ = 0.447) and phenotypic ($r^p$ = 0.386) levels, indicating a consistent association between these traits.
These findings are in close agreement with the results of Khurana *et al*. (2013) [19], who reported a positive correlation between plant height and leaf length.

**2.8 Seed volume weight / 10 ml (g)**
The character seed volume weight/10 ml had positive and significant correlation at genotypic and phenotypic level with plant height (0.690), number of spikelets per inflorescence (0.665), inflorescence length (0.573), inflorescence width (0.680), leaf length (0.447) respectively.
Above results are closely related with the studies of Habib *et al* (2024) [16], where negative significant correlation was reported between seed volume weight and days to maturity.

**Path Analysis**
Path coefficient analysis quantifies the causal relationships between variables by decomposing correlation coefficients into direct and indirect effects mediated through other explanatory variables. Initially conceptualized by Wright (1921) [37], this statistical technique was first employed in crop improvement studies by Dewey and Lu (1959) [11] to elucidate the relative contributions of yield components. By partitioning the correlation matrix, path analysis enables precise identification of traits exerting both direct influence on seed yield per plant (the dependent variable) and indirect influence via their effects on other correlated traits, thus enhancing the efficiency of indirect selection in breeding programs.
The direct and indirect contribution of each character towards seed yield per plant is presented in Table- 4.

**1. Direct effects of component characters on seed yield**
In the present study, inflorescence width exhibited the highest direct positive effect on seed yield per plant (1.483), followed by the number of spikelets per inflorescence (1.232) and seed volume weight per 10 ml (0.368). Therefore, selecting for these traits directly could effectively enhance yield improvement programs. Conversely, inflorescence length (-1.419), leaf length (-0.547), plant height (-0.484), days to maturity (-0.477), and days to 50% flowering (-0.321) demonstrated negative direct effects on seed yield per plant.
Pawar *et al*. (2022) [27] also reported that inflorescence width (0.956) had the highest direct positive effect on seed yield per plant, followed by seed volume weight per 10 ml (0.431) and number of inflorescences per plant (0.400). Most of these findings align with those of Bhargava *et al*. (2007) [6]; however, plant height exhibited a direct negative effect on seed yield per plant in their study. In contrast, Venkatesh *et al*. (2014) [36] observed positive direct effects of seed weight, panicle length, and plant height on grain yield in grain amaranth.

**2. Indirect effect of component characters on seed yield**
**2.1 Days to 50% flowering (No.)**
Days to 50% inflorescence appearance exhibited the highest positive indirect effect on seed yield per plant through inflorescence length (0.698), followed by leaf length (0.336) and plant height (0.110). Conversely, it showed negative indirect effects via number of spikelets per inflorescence (-0.541), inflorescence width (-0.402), days to maturity (-0.347), and seed volume weight per 10 ml (-0.066)
The above results closely align with the findings of Bhargava *et al*. (2007) [6], who reported that days to flowering exerted a negative indirect effect on seed yield through days to maturity

**2.2 Days to maturity (No.)**
Maximum indirect positive effect for days to maturity was observed via inflorescence length (0.689) followed by leaf length (0.259), days to 50% flowering (0.234), plant height (0.031). Its maximum indirect negative effects were observed via number of spikelets per inflorescence (-0.303) succeeded by inflorescence width (-0.278), seed volume wt/10 ml (-0.010).

**2.3 Plant height (cm)**
For plant height maximum indirect positive effect was observed via number of spikelets per inflorescence (0.999), seed volume weight /10 ml (0.254) followed by inflorescence width (0.251), days to 50% flowering (0.073), days to maturity (0.030). Its indirect negative effects were observed via inflorescence length (-0.212) and leaf length (-0.177).
Consistent with Pawar *et al*. (2022) [27], plant height demonstrated a significant indirect positive correlation with seed volume weight per 10 ml (0.318)

**2.4 Number of spikelets per inflorescence (No.)**
Maximum indirect positive effect for number of spikelets per inflorescence was observed via inflorescence width (0.649), seeds volume weight / 10 ml (0.245), days to 50 per cent flowering (0.141) and days to maturity (0.117). Its maximum indirect negative effects were observed via inflorescence length (-0.700), suceeded by plant height (-0.392) and leaf length (-0.364).
None of the author reported this character.

### 2.5 Inflorescence length (cm)

For inflorescence length highest indirect positive effect was observed via inflorescence width (1.419) succeeded by number of spikelets per inflorescence (0.608), days to maturity (0.231), seed volume weight/ 10 ml (0.211), days to 50 per-cent flowering (0.158). Its max indirect negative effects were observed via leaf length (-0.321) followed by plant height (-0.072).

The findings align with Pawar *et al*. (2022) [27], who observed that inflorescence length positively influenced seed yield indirectly, with inflorescence width (0.713) and seed volume weight per 10 ml (0.207) acting as intermediary traits

### 2.6 Inflorescence width (cm)

the highest indirect positive effect of inflorescence width on seed yield was observed through the number of spikelets per inflorescence (0.539), followed by seed volume weight per 10 ml (0.250), days to maturity (0.089), and days to 50% flowering (0.087). Conversely, the greatest indirect negative effects were mediated via inflorescence length (-1.357), leaf length (-0.350), and plant height (-0.082).

The results closely align with those of Pawar *et al*. (2022) [27], who reported that inflorescence width exhibited an indirect positive effect through seed volume weight per 10 ml (0.116).

### 2.7 Leaf length (cm)

The maximum indirect positive effect was observed through inflorescence width (0.951), followed by the number of spikelets per inflorescence (0.820), days to maturity (0.226), days to 50% flowering (0.197), and seed volume weight per 10 ml (0.164). Conversely, the greatest indirect negative effects were mediated via inflorescence length (-0.833) and plant height (-0.157)

### 2.8 Seed volume weight g /10 ml

Its highest indirect positive effect was observed via inflorescence width (1.009) followed by number of spikelets per inflorescence (0.820), days to 50 per-cent flowering (0.058) and days to maturity (0.014). Its maximum indirect negative effects were observed through panicle length (-0.814) in succession with plant height (-0.334) and leaf length (-0.244).

Consistent with Pawar *et al*. (2022) [27], the present study found that seed volume weight per 10ml positively influenced yield indirectly through inflorescence width (0.257). The magnitude of the direct effect of a trait on yield reflects the precision and reliability of selecting that trait for yield enhancement. When the correlation coefficient between a causal trait and its direct path coefficient closely matches in magnitude, it signifies a predominantly causal relationship, indicating that direct selection on such traits is likely to be effective for yield improvement.

However, if the overall correlation coefficient between a trait and yield is positive while its direct effect is negative or negligible, then indirect causal factors must be considered simultaneously during selection. In the present study, inflorescence width exhibited the highest direct positive effect on seed yield per plant, followed by the number of spikelets per inflorescence and seed volume weight per 10 ml.Likewise, these three characters were highly correlated with each other and magnitude of indirect positive effect was high. The inflorescence width was significantly correlated with inflorescence length, leaf length and seed volume weight and magnitude of indirect positive effect was high. The second trait, number of spikelets per inflorescence, showed a significant correlation with plant height, with a substantial magnitude of indirect positive effect. Therefore, inflorescence length, leaf length, seed volume weight, and plant height should be considered as key selection criteria. Consequently, direct selection for these traits is expected to be effective in yield improvement programs.

**Table 4:** Estimates of genotypic direct (diagonal) and indirect effects (above and below diagonal) of component characters on seed yield in 23 Quinoa genotypes.

| Sr. No. | Character | Days to 50% flowering | Days to maturity | Plant height (cm) | No. of spikelet/ Inflorescences (No.) | Inflorescence length (cm) | Inflorescence width (cm) | Leaf length (cm) | Seed volume weight (g/10 ml) | Genotypic correlation with Seed yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|
| 1. | Days to 50% flowering (No.) | -0.321 | -0.347 | 0.110 | -0.541 | 0.698 | -0.402 | 0.336 | -0.066 | -0.533 |
| 2. | Days to maturity (No.) | 0.234 | -0.477 | 0.031 | -0.303 | 0.689 | -0.278 | 0.259 | -0.010 | -0.324 |
| 3. | Plant height (cm) | 0.073 | 0.030 | -0.484 | 0.999 | -0.212 | 0.251 | -0.177 | 0.254 | 0.735 |
| 4. | No. of spikelet/Inflorescences (No.) | 0.141 | 0.117 | -0.392 | 1.232 | -0.700 | 0.649 | -0.364 | 0.245 | 0.929 |
| 5. | Inflorescence length (cm) | 0.158 | 0.231 | -0.072 | 0.608 | -1.419 | 1.419 | -0.321 | 0.211 | 0.815 |
| 6. | Inflorescence width (cm) | 0.087 | 0.089 | -0.082 | 0.539 | -1.357 | 1.483 | -0.350 | 0.250 | 0.660 |
| 7. | Leaf length (cm) | 0.197 | 0.226 | -0.157 | 0.820 | -0.833 | 0.951 | -0.547 | 0.164 | 0.823 |
| 8. | Seed volume weight (g/10ml) | 0.058 | 0.014 | -0.334 | 0.820 | -0.814 | 1.009 | -0.244 | 0.368 | 0.877 |

Residual effect (R) = 0.434

## Conclusion

### Genetic Variability

High magnitudes of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for the number of spikelets per inflorescence, leaf length, and saponin content, indicating substantial genetic variability for these traits. Therefore, these characters represent valuable sources of variation and are promising targets for quinoa crop improvement programs. In contrast, moderate levels of GCV and PCV were recorded for inflorescence length and seed yield per plant.

High heritability estimates were recorded for leaf length, saponin content, days to 50% flowering, days to maturity, number of spikelets per inflorescence, seed volume weight per 10 ml, plant height, inflorescence length, seed yield per plant, and inflorescence width. These high heritability values indicate that the phenotypic expression of these traits is primarily controlled by genetic factors with minimal environmental interference. Consequently, these characters are expected to respond effectively to selection and can serve as reliable indicators for genetic improvement in quinoa breeding programs.

Saponin content indicated highest genetic advance as per cent of mean succeeded by leaf length, number of spikelets/inflorescences, inflorescence length. Moderate genetic advance as per cent mean observed for seed yield/ plant, seed

volume weight /10 ml, days to 50% flowering and plant height. High heritability estimates coupled with high genetic advance as a percentage of the mean were observed for number of spikelets per inflorescence, leaf length, and saponin content. This suggests the predominance of additive gene action governing these traits, implying that direct selection would be highly effective for their genetic improvement. In contrast, inflorescence width exhibited high broad-sense heritability but was associated with low genetic advance, indicating that the heritability is largely attributable to non-additive gene effects. Therefore, improvement of this trait may be more effectively achieved through heterosis breeding or hybrid development strategies.

**Correlation**

In the present study, seed yield per plant exhibited significant and positive correlations at both genotypic and phenotypic levels with number of spikelets per inflorescence, seed volume weight, leaf length, inflorescence length, plant height, and inflorescence width. Conversely, seed yield per plant showed a significant negative correlation with days to 50% flowering at both genotypic and phenotypic levels, and with days to maturity at the genotypic level, although the latter was non-significant at the phenotypic level. Days to 50% flowering exhibited a significant positive correlation with days to maturity. Plant height showed a highly significant positive association with the number of spikelets per inflorescence, which, in turn, was positively and significantly correlated with leaf length. Inflorescence length demonstrated a highly significant positive correlation with inflorescence width, while inflorescence width was significantly and positively associated with leaf length. Additionally, leaf length showed a significant positive correlation with seed volume weight per 10 ml at both genotypic and phenotypic levels. Furthermore, seed volume weight per 10 ml exhibited a significant positive correlation with seed yield per plant at both genotypic and phenotypic levels.

**Path Analysis**

Inflorescence width exhibited the highest direct positive effect on seed yield per plant, followed by number of spikelets per inflorescence and seed volume weight per 10 ml. These traits not only demonstrated substantial positive direct effects in the desirable direction but also showed strong and consistent associations with seed yield per plant. This indicates a true and robust relationship, suggesting that direct selection for these traits would be highly effective in identifying high-yielding genotypes in quinoa. In contrast, inflorescence length, leaf length, plant height, days to maturity, and days to 50% flowering exhibited negative direct effects on seed yield per plant, indicating limited utility for direct selection in yield improvement for these specific traits.

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