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Phenotyping of Quinoa (*Chenopodium quinoa* Willd.) Genotypes for Morphological, Yield and Nutritional Quality Traits

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ABSTRACT

Quinoa (*Chenopodium quinoa* Willd.) is regarded as a superfood due to its exceptionally high nutritional value and ability to withstand stress. Six quinoa genotypes (*viz.*, SAU Quinoa-1, Regalona, GPBQ-1, GPBQ-2, GPBQ-3, and GPBQ-4) were characterized for morphological, yield, and nutritional quality attributes while being grown under the agro-climatic conditions of Bangladesh. The field experiment was carried out in the winter season (November 2022–March 2023) at the Agronomy Field Laboratory of the Department of Agronomy, Bangladesh Agricultural University, Mymensingh, using a randomized complete block design with three replications. Data on various qualitative and quantitative traits related to growth and yield-attributes were recorded. A large variability was observed among the genotypes for growth habit, stem color, panicle shape, and panicle color at maturity. The whitish color of the seed was found in GPBQ-3 which indicates less saponin content as confirmed by saponin test. Yield attributing quantitative traits (*viz.*, days to first flowering, days to maturity, plant height, stem diameter, panicle weight, 1000-seed weight, yield plant^{-1}, above-ground biomass, and harvest index) also showed significant variation among the genotypes studied. Genotypes SAU Quinoa-1 and GPBQ-2 were identified as early maturing genotypes. The higher yield plant^{-1} was recorded in GPBQ-1 and GPBQ-3 genotypes. The phenotypic coefficient of variation for the majority of the traits evaluated was slightly higher than the corresponding genotypic coefficient of variation. For stem diameter, panicle weight, 1000-seed weight, yields plant^{-1}, and above-ground biomass, high heritability and high genetic advancement were seen as percentages of the mean. Yield plant^{-1} showed significant positive correlation with days to first flowering, days to maturity, plant height, stem diameter, panicle weight, and above-ground biomass (0.568*, 0.812***, 0.744***, 0.895***, 0.993***, and 0.985***, respectively). The first two components accounted for 85.5% of the overall variation among the genotypes, according to principal component analysis. Significant variability was also found for seed mineral contents (*viz.*, calcium, copper, iron, potassium, magnesium, manganese, and zinc) in the studied genotypes. The SAU Quinoa-1 genotype contained the highest amount of calcium and zinc, whereas, the highest amount of potassium was recorded in the GPBQ-1 genotype. We found a non-significant variability in carbohydrate, protein, fat, fiber, and vitamins (*viz.*, thiamine, riboflavin, niacin, and folic acid) contents in the studied genotypes. Considering all the yield and nutritional quality traits under study, the genotypes GPBQ-1, GPBQ-3, and GPBQ-4 were selected for future variety development program.

1 Introduction

Food systems are under intense pressure from climate change, which highlights the need for stable crops and varieties that can withstand abrupt soil and environmental changes. It is also important to diversify crops to address increasing yield losses that threaten food security, especially with the growing global population [1]. In addition to concerns about undernourishment, many people are not getting enough micronutrients, which is referred to as "hidden hunger" [2]. In Bangladesh, undernutrition continues to be a serious public health problem. Diversifying the food system is crucial, as climate change poses a threat to human nutrition and food security. One such strategy is the use of quinoa (*Chenopodium quinoa* Willd.) in our food system which is a highly nutritious and climate-resilient crop species.

Quinoa is known as a miracle crop for its great adaptation in diverse edaphic conditions. A dicotyledonous plant (C_3), quinoa is a member of the Amaranthaceae family. It yields achene fruits, often known as chenopod grains, which have spherical seeds measuring 1.5–4 mm [3]. With ecotypes growing well at high elevations and in poor soils where other cereal crops, like wheat, rice, and maize, do not grow well, the quinoa plant's extensive genetic diversity enables it to be highly resistant to cold, salt, and drought conditions [4]. While quinoa is becoming more and more popular as a food source globally, Andean indigenous communities have been consuming it for thousands of years [5]. Quinoa is frequently called a "superfood" because of its high nutritional content and resilience to stress. Because of its characteristics that resemble those of cereal grains like corn, wheat, and rice, quinoa is wrongly thought to be pseudo-cereal; in reality, it is categorized as a dicot [6]. The quinoa seed has been eaten in a variety of forms, including flour in baked and toasted foods (bread, noodles, biscuits, cookies, flakes, pancakes, and tortillas) and in breakfast cereals. Furthermore, quinoa is a very nutrient-dense food that includes a range of minerals (like calcium, iron, potassium, potassium, copper, magnesium, and zinc), vitamins (like A, B_1, B_2, B_3, B_5, B_6, B_9, C, and E), dietary fiber, natural antioxidants like polyphenols, and high-quality protein with a high concentration of essential amino acids (reviewed in Ain et al. [7]). Quinoa is processed using particular technologies to address specific health issues in people, like improving fitness, losing weight, celiac disease, and other metabolic issues like diabetes, obesity, hypertension, and hyperlipidemia [8]. After being rediscovered in the latter part of the 20th Century, quinoa has been studied and distributed to more than 120 nations worldwide [5]. Due to its exceptional nutritional value and balance, as well as its remarkable adaptability to a variety of unfavorable conditions like salt and drought, it is anticipated to become a key player in the global solution to food and nutrition issues.

Bangladesh is one of the countries that would be most affected by climate change. Climate change has increased the frequency of certain problems such as drought, unpredictable rainfall, high temperatures, sea level rise, and soil salinity that are both directly and indirectly related to agricultural production. Ensuring food security for all is one of the primary concerns that Bangladesh is now confronting. Salinity is a major threat to crop productivity in the southwestern part of Bangladesh affecting 30% of the arable land of the coastal areas [9]. Bangladesh's rice yield is expected to drop by 33% by 2100 according to the climate change model, but we need to raise rice production by 50% to feed the country's growing population. Importantly, rice production may fall by 10% due to salinity only by 2050 [10]. Therefore, it is high time to introduce crops like quinoa in Bangladesh to include the non-cultivated land of the southern part of the country under cultivation and increase cropping intensity, which in turn will boost the gross domestic product. Despite being the primary grain in Bangladesh, rice lacks essential nutrients,

leading to high rates of malnutrition and micronutrient deficits in women and children [11]. As a result, quinoa can be a helpful addition to rice or other cereals in addressing malnutrition. The goal of quinoa breeding is to create cultivars that can thrive in a variety of agroclimatic zones and have higher grain yields and high-quality components. Nevertheless, not much has been done in Bangladesh to alter its genetic makeup or create a new crop variety. Although a quinoa variety called SAU Quinoa-1 has recently been released, there is currently little information available in Bangladesh regarding the characterization of quinoa for productivity, nutritional quality, and adaptive potential. To develop a variety, breeders need to evaluate a range of cultivars and genotypes to understand the phenotypic and genotypic variability present in the germplasm. In addition, understanding the genetic parameters such as genotypic co-efficient of variation, heritability and genetic advance and inter-relationship among the traits is quinoa essential for its genetic improvement through a reliable selection program. Consequently, an in-depth investigation of quinoa variability in terms of morpho-agronomic and qualitative characteristics is required. Development of improved quinoa variety through appropriate breeding techniques might have a significant impact on nutritional food security and sustainable agricultural production systems as well as to achieve the SDGs. We hypothesize that significant variation is present in the studied quinoa genotypes in terms of morphological, yield, and nutritional quality traits that might be helpful in boosting genetic gain through additional selective breeding. Considering the above issues in mind, the present investigation was thus aimed to (i) characterize exotic quinoa genotypes based on morphological, yield, and nutritional quality traits; and (ii) phenotypic and genotypic dissection of the traits for effective selection to develop new variety for maximizing genetic gain.

2 Materials and Methods

2.1 Experimental Site, Soils and Season

The field experiment was conducted during the winter season (November 2022–March 2023) at the Agronomy Field Laboratory of the Department of Agronomy, Bangladesh Agricultural University, Mymensingh. A map of the study site, along with its coordinates, is presented in Fig. 1. The trial site was categorized as medium high land in Agro-Ecological Zone-9 (Old Brahmaputra Flood Plain), with a sandy loam texture and a pH range of 6.5 to 6.7 in the soil. The location's climate was typified by low temperatures and little rainfall during the winter or Rabi season (November to March), and comparatively high temperatures and considerable rainfall during the Kharif or summer season (April to October).
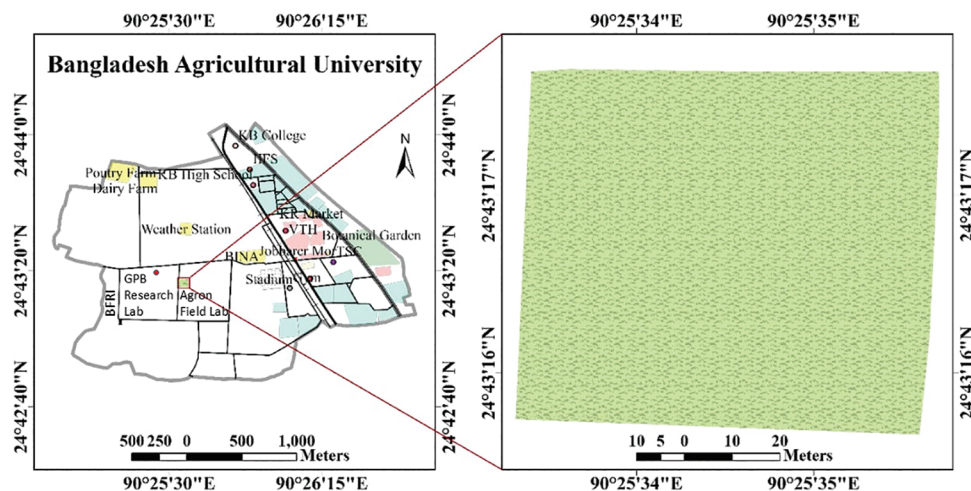
Figure 1: Bangladesh Agricultural University map along with the study site

2.2 Plant Materials

The experiment was conducted using six quinoa genotypes out of which four genotypes (*viz*., GPBQ-1, GPBQ-2, GPBQ-3, and GPBQ-4) were collected from the University of Tasmania, Australia and the variety Regalona was collected from Uzbekistan, and SAU Quinoa-1 was collected from Sher-e-Bangla Agricultural University (SAU), Dhaka, Bangladesh.

2.3 Design and Layout of the Experiment

Using three replications, the experiment was carried out using a randomized complete block design. There were six experimental units in per block. The unit plot size was four square meters (2 m × 2 m). Each plot contained six rows, with a 30 cm gap between rows and a 5 cm gap between each plant in a row. Using a table of random numbers, the genotypes were put in each experimental unit in an arbitrary order.

2.4 Land Preparation, Fertilization and Seed Sowing

Using a power tiller, the experimental field was prepared by plowing and cross-ploughing. When the land was being prepared, the weeds and debris were pulled out. To tilt and level the soil properly, the right laddering was done. Full amount of all fertilizers was applied at the time of final land preparation except Urea. Fertilizer such as Urea-TSP-MoP-Gypsum-Zinc-Boron was applied 70 kg acre^{-1}, 100 kg acre^{-1}, 40 kg acre^{-1}, 40 kg acre^{-1}, 2 kg acre^{-1}, and 2 kg acre^{-1}, respectively. In the last stage of land preparation, the soil was combined with half of the urea and all of the other fertilizers. Twenty-five to thirty days after seeding, half of the urea was applied. Seeds of the quinoa genotypes were sown on 14 November 2022 following line sowing methods.

2.5 Intercultural Operation

A light irrigation was applied for the quinoa cultivation after 30 days after seed sowing. Weeding and thinning were done one time just before the application of irrigation at 25 days after sowing to maintain a proper plant-to-plant distance of 5 cm.

2.6 Harvest and Post-Harvest Operations

Harvesting took place in February 2023 when 90% of the grain turned yellow to deep brown. Five mature plants were randomly collected from each plot, sundried, threshed, and placed in net bags for further drying. The seeds were cleaned and sun-dried for 3 to 5 days to achieve safe moisture level. The above-ground biomass was cut into pieces and also sun-dried for 3 to 5 days.

2.7 Data Collection

2.7.1 Qualitative Traits

Data on ten qualitative traits such as growth habit (GH), stem shape (SS), plant stem color (PSC), pigmented axil (PA), leaf shape (LS), leaf margin (LM), panicle shape (PS), panicle color at flowering (PCF), panicle color at maturity (PCM), and seed color (SC) were taken from randomly selected plants. These traits were measured according to descriptors for quinoa as described by Stanschewski et al. [12].

2.7.2 Quantitative Traits

Data on nine quantitative traits such as days to first flowering (DFF), days to maturity (DM), plant height (PH) (cm), stem diameter (SD) (mm), panicle weight (PW) (g), 1000-seed weight (1000-SW) (g), yield plant^{-1} (YPP) (g), above-ground biomass (AGB) (g), harvest index percentage (HI%) were taken from five plants chosen at random from each genotype's replication.

2.7.3 Nutritional Quality Traits

The seeds were analyzed using the "Official Methods of Analysis of AOAC International" [13] to gather information related to nutritional quality attributes such as fiber, protein, fat, and carbohydrates. We used a

Shimadzu ICP-OES 9820 to measure calcium (Ca), magnesium (Mg), iron (Fe), zinc (Zn), and potassium (K) in $mgKg^{-1}$ (ppm). Utilizing Ultra-Pressure Liquid Chromatography (UPLC), the amount of water-soluble B vitamins (B_1, thiamine; B_2, riboflavin; B_3, niacin; and B_9, folic acid) was measured from the quinoa samples. Vitamin contents were expressed as mg/100 g, while all other micronutrients were expressed as mg kg^{-1}.

2.7.4 Saponin Test

The following technique, as outlined by Stanschewski et al. [12], was used to measure the seed saponin content. Simply, five loosely-hulled quinoa seeds were taken in a 1.5 mL microcentrifuge tube and then 500 μL of double-distilled water was added. The tubes were then violently shaken for thirty seconds by hand until foam with a consistent height appeared. The intensity of the saponin component was shown by foam height.

2.8 Estimation of Genetic Parameters

Genetic parameters, including genetic variance, heritability in the broad sense (h^2_b), phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV), genetic advance (GA) and genetic advance as percentage of mean (GA%) for the quantitative traits under study, were calculated using equations put forth by biometricians such as Allard [14] and Johnson et al. [15]. The PCV and GCV estimates were categorized as low, <10%, moderate, 10%–20%, high, >20% according to Deshmukh et al. [16]. The heritability in the broad sense (h^2_b) was calculated and classified as low, 0%–30%, medium, 31%–60%, high, >60%, and the GA% as low <10%, moderate, 10%–20%, and high, >20% according to Johnson et al. [15].

2.9 Statistical Analysis

SPSS was utilized to do a one-way analysis of variance (ANOVA) for every trait in order to investigate the variations among the genotypes. To differentiate the means, the Tukey's test was used at a 5% probability level. In order to identify quantitative variation patterns with the eigen vectors and eigen values, Minitab 19 statistical software was used for principal component analysis (PCA). We used the formula proposed by Miller et al. [17] to estimate the phenotypic correlations.

3 Results

3.1 Qualitative Traits

For the examined growth-related qualitative features, a significant amount of variation was found between the genotypes (Table 1). Most of the genotypes (i.e., SAU Quinoa-1, Regalona, GPBQ-2, and GPBQ-4) showed simple growth habit but two genotypes (GPBQ-1 and GPBQ-3) showed branching from the base with more significant panicle type growth habit (Fig. 2). Green color stem was noted in the genotypes Regalona, GPBQ-1, GPBQ-3, and GPBQ-4, whereas yellow color stem was found in SAU Quinoa-1 and GPBQ-2. The stem shape of all the studied six genotypes was angular and also had pigmented axile. Three types of leaf shapes (*viz*., rhomboidal, triangular, and linear) were present in all the studied quinoa genotypes and rhomboidal and triangular types leaf contain dentate-type leaf margins and linear-type leaves contain entire leaf margins in all the studied genotypes (Fig. 3). Four quinoa genotypes such as SAU Quinoa-1, Regalona, GPBQ-2 and GPBQ-4 had intermediate-type panicle shapes while the genotypes GPBQ-1 and GPBQ-3 had glomerulate-type panicles. At the flowering stage, all of the genotypes showed green color panicle, however, three genotypes such as SAU Quinoa-1, GPBQ-2 and GPBQ-4 showed orange color, two genotypes (GPBQ-1 and GPBQ-3) showed pink color, and one genotype (Regalona) showed yellow color panicle at physiological maturity stage (Fig. 4). Whitish color seed was found in the genotype GPBQ-3, light brown in Regalona, light yellow in GPBQ-1 and deep brown was seen for the genotypes SAU Quinoa-1, GPBQ-2, and GPBQ-4 (Fig. 5).

Table 1: Qualitative traits of six quinoa genotypes grown in BAU farm during the winter season of 2022–2023

Genotypes	GH	SS	PSC	PA	LS	LM	PS	PCF	PCM	SC
SAU Quinoa-1	Simple	Angular	Yellow	Present	Rhomboidal, triangular & linear	Entire & dentate	Intermediate	Green	Orange	Deep brown
Regalona	Simple	Angular	Green	Present	Rhomboidal, triangular & linear	Entire & dentate	Intermediate	Green	Yellow	Light brown
GPBQ-1	Branching from the base with more significant panicles	Angular	Green	Present	Rhomboidal, triangular & linear	Entire & dentate	Glomerulate	Green	Pink	Light yellow
GPBQ-2	Simple	Angular	Yellow	Present	Rhomboidal, triangular & linear	Entire & dentate	Intermediate	Green	Orange	Deep brown
GPBQ-3	Branching from the base with more significant panicles	Angular	Green	Present	Rhomboidal, triangular & linear	Entire & dentate	Glomerulate	Green	Pink	White
GPBQ-4	Simple	Angular	Green	Present	Rhomboidal, triangular & linear	Entire & dentate	Intermediate	Green	Orange	Deep brown

Here, GH = Growth habit, SS = Stem shape, PSC = Plant stem color, PA = Pigmented axil, LS = Leaf shape, LM = Leaf margin, PS = Panicle shape, PCF = Panicle color at flowering, PCM = Panicle color at maturity and SC = Seed color.

3.2 Quantitative Traits

For all of the quantitative characters examined, the analysis of variance results revealed highly significant ($p < 0.001$) genotypic variation (Table A1). The mean performance of nine quantitative traits across six quinoa genotypes is presented in Table 2. Among the studied genotypes, the genotypes GPBQ-1 and GPBQ-3 required maximum days to first flowering (27.33 days), whereas SAU Quinoa-1 and GPBQ-2 required minimum days (22.33 days) for flowering and they were significantly different from the rest of the genotypes (Table 2). GPBQ-2 and SAU Quinoa-1 were the early maturing genotypes as these genotypes required minimum days (74.67 and 75.00 days, respectively), to mature. In contrast, GPBQ-1 and GPBQ-3 required maximum days to mature (84.67 and 85.00 days, respectively). Maximum PH (101.45 cm) was recorded in the genotype GPBQ-1 followed by GPBQ-3, Regalona, GPBQ-4, and SAU Quinoa-1 (100.33, 95.20, 90.68 and 86.20 cm, respectively), whereas minimum plant height (81.07 cm) was recorded in GPBQ-2 (Table 2). GPBQ-1 showed the maximum stem diameter (10.84 mm), however, the minimum was found in Regalona (6.54 mm). Among the studied genotypes, GPBQ-1 showed the highest panicle weight (30.69 g) followed by GPBQ-3, GPBQ-4, SAU Quinoa-1, and Regalona (20.58, 15.51, 12.54, and 11.37 g, respectively) whereas the lowest panicle weight was produced by GPBQ-2 (10.87 g). Maximum of 1000-SW (4.61 g) was recorded in GPBQ-4, followed by SAU Quinoa-1, Regalona, GPBQ-2, and GPBQ-3 (3.74, 3.63, 3.47, and 3.24 g, respectively). In contrast, the minimum of 1000-SW was found in GPBQ-1 (2.29 g). Importantly, the highest yield plant^{-1} (22.40 g) was recorded in GPBQ-1 followed by GPBQ-3, GPBQ-4, SAU Quinoa-1, and Regalona (14.80, 10.48, 9.46, and 7.97 g, respectively), however, the minimum (7.80 g) YPP was recorded in GPBQ-2. In case of above ground biomass, maximum was found in GPBQ-1 (61.74 g) and the minimum amount was found in GPBQ-2 (19.66 g). SAU Quinoa-1 showed maximum harvest index (54.32%) (Table 2).

3.3 Genetic Variability Analysis

Variances in phenotype and genotype, PCV, GCV, heritability, GA, and GA% of the traits under study are displayed in (Table 3). The characters that showed high phenotypic and genotypic variance were AGB (236.62 and 234.63, respectively), PH (65.47 and 63.99, respectively), PW (59.59 and 57.68, respectively), and YPP (31.92 and 31.58, respectively), whereas, the lowest phenotypic and genotypic variances were recorded in 1000-SW (0.61 and 0.55, respectively). Co-efficient of variation studies indicated that the values of PCV were higher than those of the GCV for all the traits. In contrast, the characteristics of DM (5.86 and 5.66, respectively) and HI (4.68 and 4.08, respectively) had the lowest PCV and GCV values, while the trait of YPP had the highest values (46.49 and 46.24, respectively). Overall, all of the examined traits showed strong broad-sense heritability (>60%). While HI had the lowest heritability (75.61%),

AGB had the highest heritability (99.16%). The highest genetic advance was found in ABG (31.42). Genetic advance as a percentage of the mean (GA%) ranged from 7.29% to 94.74%. High GA% (>20%) was found in YPP (94.74) followed by AGB, PW, SD, and 1000-SW, (94.13%, 90.95%, 43.53%, and 41.63%, respectively). Medium GA% (20%–10%) was recorded in PH, DFF, and DM 17.61%, 16.64%, and 11.26%, respectively, on the other hand, low GA% (<10%) was found in HI (7.29) (Table 3).

Figure 2: Variation in growth habit of the studied quinoa genotypes grown at BAU farm during the winter season of 2022–2023
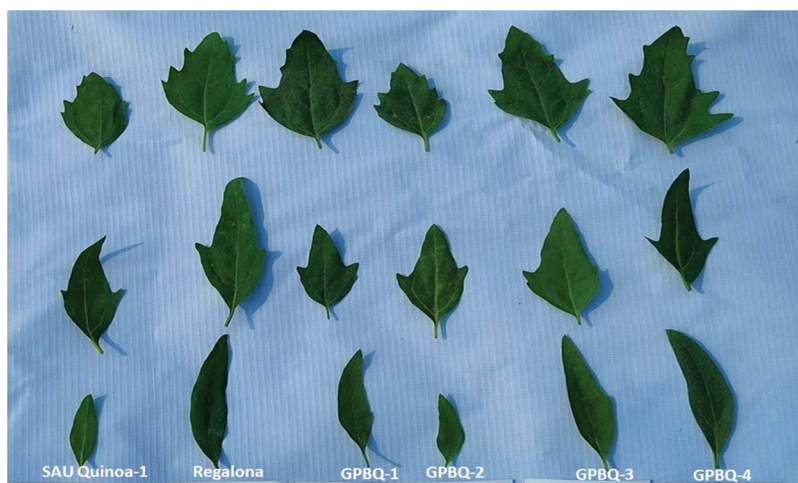
Figure 3: Variation in leaf shape and leaf margin of the studied quinoa genotypes grown at BAU farm during the winter season of 2022–2023

Figure 4: Variation in panicle color at physiological maturity of the studied quinoa genotypes grown at BAU farm during the winter season of 2022–2023

Figure 5: Variation in seed color of the studied quinoa genotypes grown at BAU farm during the winter season of 2022–2023

Table 2: Quantitative traits of six quinoa genotypes grown in BAU farm during the winter season of 2022–2023

Genotypes name	DFF	DM	PH (cm)	SD (mm)	PW (g)	1000-SW (g)	YPP (g)	AGB (g)	HI%
SAU Quinoa-1	22.33 ± 1.5 B	75.00 ± 1.0 C	86.20 ± 1.1 D	6.62 ± 0.04 B	12.54 ± 0.75 CD	3.74 ± 0.14 B	9.46 ± 0.12 CD	24.35 ± 0.19 D	54.32 ± 0.97 A
Regalona	26.00 ± 1.0 A	78.67 ± 1.1 B	95.20 ± 1.1 B	6.54 ± 0.64 B	11.37 ± 0.94 D	3.63 ± 0.25 B	7.97 ± 0.42 DE	24.44 ± 0.75 D	48.72 ± 0.45 B
GPBQ-1	27.33 ± 0.57 A	84.67 ± 1.5 A	101.45 ± 1.4 A	10.84 ± 0.41 A	30.69 ± 2.19 A	2.29 ± 0.14 C	22.40 ± 0.85 A	61.74 ± 1.02 A	50.68 ± 0.71 B
GPBQ-2	22.33 ± 1.5 B	74.67 ± 1.5 C	81.07 ± 1.4 E	7.16 ± 0.67 B	10.87 ± 1.06 D	3.47 ± 0.25 B	7.80 ± 0.64 E	19.66 ± 1.40 E	49.67 ± 0.52 B
GPBQ-3	27.33 ± 0.57 A	85.00 ± 1.0 A	100.33 ± 0.97 A	10.22 ± 0.74 A	20.58 ± 2.4 B	3.24 ± 0.19 B	14.80 ± 0.73 B	37.45 ± 0.79 B	50.83 ± 1.23 B
GPBQ-4	27.00 ± 1.0 A	78.00 ± 1.0 B-C	90.68 ± 1.5 C	7.80 ± 0.99 B	15.51 ± 0.49 C	4.61 ± 0.35 A	10.48 ± 0.19 C	30.86 ± 1.50 C	48.31 ± 2.23 B

Here, DFF = Days to first flowering, DM = Days to maturity, PH = Plant height, SD = Stem diameter, PW = Panicle weight, 1000-SW = 1000-seed weight, YPP = Yield plant^{-1}, AGB = Above ground biomass and HI = Harvest index. Values are means ± standard errors of three replications. Different letters in the same column indicates statistically significant differences between means at $p \leq 0.05$ (Tukey test).

Table 3: Genetic parameters of different traits of six quinoa genotypes

Traits	Phenotypic variance	Genotypic variance	PCV%	GCV%	(h^2_b)%	GA	GA%
DFF	6.81	5.35	10.28	9.11	78.57	4.22	16.64
DM	21.65	20.18	5.86	5.66	93.21	8.93	11.26
PH (cm)	65.47	63.99	8.74	8.65	97.74	16.29	17.61
SD (mm)	3.80	3.37	23.83	22.44	88.69	3.56	43.53
PW (g)	59.59	57.68	45.61	44.88	96.79	15.39	90.95
1000-SW (g)	0.61	0.55	22.29	21.23	90.63	1.46	41.63
YPP (g)	31.92	31.58	46.49	46.24	98.94	11.52	94.74
AGB (g)	236.62	234.63	46.08	45.89	99.16	31.42	94.13
HI (%)	5.57	4.21	4.68	4.07	75.61	3.67	7.29

Here, DFF = Days to first flowering, DM = Days to maturity, PH = Plant height, SD = Stem diameter, PW = Panicle weight, 1000-SW = 1000-seed weight, YPP = Yield plant^{-1}, AGB = Above ground biomass and HI = Harvest index, PCV = Phenotypic co-efficient of variation, GCV = Genotypic co-efficient of variation, h^2_b = Heritability in broad sense, GA = Genetic advance, GA (%) = Genetic advance in percentage of mean.

3.4 Correlation Co-efficient Analysis

The association between yield and yield-contributing features was evaluated using the simple Pearson's correlation coefficient, and the findings are shown in Table 4. Days to first flowering showed significant positive correlation with DM (0.735***), PH (0.831***), SD (0.63**), PW (0.611**), YPP (0.568*) and AGB (0.617**), whereas, it showed a non-significant negative correlation with 1000-SW and HI. Days to maturity had a positive significant correlation with PH (0.908***), SD (0.846***), PW (0.817***), YPP (0.812***), and AGB (0.792***). On the other hand, it demonstrated a noteworthy inverse relationship with 1000-SW (−0.574*). Plant height had a positive significant correlation with SD (0.738***), PW

(0.745***), YPP (0.744***) and AGB (0.768***) but it showed a significant negative correlation with 1000-SW (0.517*). In contrast to its strong negative connection with 1000-SW (−0.628*), stem diameter exhibited a significant positive correlation with PW (0.901***), YPP (0.895***), and AGB (0.851***). Panicle weight showed significant positive correlation with YPP (0.993***) and AGB (0.98***). On the contrary, it showed a significant negative correlation with 1000-SW (−0.664**). 1000-seed weight showed significant negative correlation with YPP (−0.715***), and AGB (−0.671**), however, it showed a non-significant positive correlation with HI. Importantly, yield plant^{-1} showed significant positive correlation with DFF (0.568*), DM (0.812***), PH (0.744***), SD (0.895***), PW (0.993***), and AGB (0.985***).

Table 4: Correlation co-efficient among yield and yield contributing traits

	DFF	DM	PH	SD	PW	1000-SW	YPP	AGB
DM	0.735***							
PH	0.831***	0.908***						
SD	0.63**	0.846***	0.738***					
PW	0.611**	0.817***	0.745***	0.901***				
1000-SW	−0.187	−0.574*	−0.517*	−0.628*	−0.664**			
YPP	0.568*	0.812***	0.744***	0.895***	0.993***	−0.715***		
AGB	0.617**	0.792***	0.768***	0.851***	0.98***	−0.671**	0.985***	
HI	−0.341	−0.097	−0.109	−0.044	0.04	−0.261	0.104	0.028

Note: *, ** and *** indicates significant at 5%, 1% and 0.1% level of probability, respectively. Here, DFF = Days to first flowering, DM = Days to maturity, PH = Plant height, SD = Stem diameter, PW = Panicle weight, 1000-SW = 1000-seed weight, YPP = Yield plant^{-1}, AGB = Above ground biomass and HI = Harvest index.

3.5 Principal Component Analysis (PCA)

Table 5 shows the PCA that was performed taking into account every quantitative trait. There was a cumulative 85.5% variation in the quinoa genotypes for the nine quantitative variables that were investigated, explained by two components that had Eigen values larger than one. PCA revealed that the first component accounted for 69.5% of the total variation where PW (0.383) and YPP (0.383) had the highest positive loadings followed by AGB (0.380), SD (0.370), DM (0.368), PH (0.354) and DFF (0.293), respectively, whereas, the characters 1000-SW (−0.278) and HI (−0.010) showed the negative loadings. The second component accounted for 16% of the total variation. The highest positive loadings were found for the character DFF (0.458) followed by 1000-SW (0.416), PH (0.190), and DM (0.118), respectively, whereas, the highest negative loadings were found for the trait HI (−0.724) followed by YPP (−0.159), AGB (−0.089), and SD (−0.013), respectively.

Table 5: Principal Components (PCs) for yield and yield-related traits in 6 quinoa genotypes from PCA with Eigen vectors (loadings) of the first two PCs

Variable	PC1	PC2
DFF	0.293	0.458
DM	0.368	0.118
PH	0.354	0.190
SD (mm)	0.370	−0.013
PW (g)	0.383	−0.097

(Continued)

Table 5 (continued)

Variable	PC1	PC2
1000-SW (g)	−0.278	0.416
YPP (g)	0.383	−0.159
AGB (g)	0.380	−0.089
HI %	−0.010	−0.724
Eigenvalue	6.2546	1.4407
Proportion	0.695	0.160
Cumulative	0.695	0.855
Variation explained	69.5%	16%
Cumulative variance (%)	69.5%	85.5%
ANOVA for PC scores		
Genotype	20.9794***	4.5266***
Replication	0.0907	0.1958
Error	0.1250	0.1468

Here, PC1 = First Principal Component, PC2 = Second Principal Component, DFF = Days to first flowering, DM = Days to maturity, PH = Plant height, SD = Stem diameter, PW = Panicle weight, 1000-SW = 1000-seed weight, YPP = Yield plant^{-1}, AGB= Above ground biomass and HI = Harvest index. *** indicates significant at 0.1% level of probability.

3.6 Mineral Contents

Significant differences in mineral concentrations were found between the genotypes under study (Table 6 and A2). The highest amount of Ca^{2+} was found in SAU Quinoa-1 (630.2 mg kg^{-1}) on the other hand, the lowest amount of Ca^{2+} was found in GPBQ-1 (433.5 mg kg^{-1}). The higher Cu^{2+} content was recorded in Regalona (6.36 mg kg^{-1}) whereas SAU Quinoa-1 contained low amount of Cu^{2+} (4.74 mg kg^{-1}) as compared to others. GPBQ-4 showed the highest Fe^{2+} content (44.3 mg kg^{-1}) whereas GPBQ-2 had the lowest amount of Fe^{2+} content (42.7 mg kg^{-1}). Maximum K^+ content was found in GPBQ-1 (6157.9 mg kg^{-1}) and the minimum amount was found in Regalona (5603.4 mg kg^{-1}). Regalona contained higher amount of Mg^{2+} (1196 mg kg^{-1}) on the contrary, GPBQ-1 (1098.8 mg kg^{-1}) contained lower amounts of Mg. GPBQ-2 was highly enriched with Mn^{2+} (13.69 mg kg^{-1}) but less amount was recorded in Regalona (12.30 mg kg^{-1}). SAU Quinoa-1 had the highest amount of Zn^{2+} content (29.4 mg kg^{-1}), whereas, the lowest amount was recorded in GPBQ-1 (22.1 mg kg^{-1}).

Table 6: Mean performance of seed mineral compositions in six quinoa genotypes

Genotypes name	Ca^{2+}	Cu^{2+}	Fe^{2+}	K^+	Mg^{2+}	Mn^{2+}	Zn^{2+}
SAU Quinoa-1	630.2 ± 2.8 A	4.74 ± 0.24 C	43.3 ± 0.38 BC	5988.4 ± 25.9 C	1149.5 ± 9.5 BC	12.44 ± 0.10 B	29.4 ± 0.77 A
Regalona	462 ± 3.0 BC	6.36 ± 0.04 A	43.7 ± 0.39 AB	5603.4 ± 15.86 D	1196 ± 15.4 A	12.30 ± 0.10 B	27.2 ± 0.66 B

(Continued)

Table 6 (continued)

Genotypes name	Ca^{2+}	Cu^{2+}	Fe^{2+}	K^+	Mg^{2+}	Mn^{2+}	Zn^{2+}
GPBQ-1	433.5 ± 10.5 C	5.69 ± 0.09 B	43.0 ± 0.29 BC	6157.9 ± 19.7 A	1098.8 ± 10.61 D	12.6 ± 0.89 AB	22.1 ± 0.18 D
GPBQ-2	475.5 ± 4.5 B–C	5.8 ± 0.05 B	42.7 ± 0.02 C	5980.4 ± 8.10 C	1129.7 ± 3.21 CD	13.69 ± 0.31 A	24.2 ± 0.84 C
GPBQ-3	508.5 ± 1.5 B	6.04 ± 0.14 AB	43.7 ± 0.16 A–C	5980.4 ± 8.10 C	1169.8 ± 12.25 AB	12.93 ± 0.28 AB	26.1 ± 0.73 B
GPBQ-4	521 ± 2.0 B	6.2 ± 0.09 A	44.3 ± 0.56 A	6090.2 ± 7.91 B	1185.7 ± 6.81 A	13.59 ± 0.05 A	27.1 ± 0.19 B

Note: Values are means ± standard errors of three replications. Different letters in the same column indicates statistically significant differences between means at $p \leq 0.05$ (Tukey test).

3.7 Vitamin Contents

Table 7 displays the vitamin content data for the genotypes under study. The genotypes did not differ significantly in terms of specific vitamin content, according to the results. Vitamin B_1 content ranged from 1.43 to 1.31 mg/100 g dry matter whereas B_2 ranged from 2.34–2.85 mg/100 g. Almost every genotype had nearly 1 mg of B_3 content per 100 g dry matter. Among the vitamin contents studied, B_9 content was higher in all of the quinoa genotypes, and the value ranged from 6.45–6.77 mg/100 g.

Table 7: Constitution of B-vitamin complex in the studied quinoa genotypes

| Genotypes	B_1 (mg/100 g)	B_2 (mg/100 g)	B_3 (mg/100 g)	B_9 (mg/100 g)
SAU Quinoa-1	1.37 ± 0.51	2.51 ± 0.43	1.13 ± 0.98	6.87 ± 1.43
Regalona	1.31 ± 1.2	2.46 ± 0.06	1.15 ± 0.78	6.45 ± 0.97
GPBQ-1	1.35 ± 0.91	2.85 ± 1.03	1.21 ± 0.50	6.73 ± 0.67
GPBQ-2	1.43 ± 0.49	2.76 ± 0.95	1.10 ± 0.71	6.51 ± 0.87
GPBQ-3	1.36 ± 0.57	2.34 ± 1.5	1.09 ± 0.89	6.45 ± 0.56
GPBQ-4	1.42 ± 0.73	2.53 ± 0.67	1.05 ± 0.19	6.77 ± 0.59

Note: Values are means ± standard errors of three replications.

3.8 Proximate Composition of Quinoa Seeds

The nutritional composition of different quinoa genotypes is presented in Fig. 6. The main constituents of quinoa seeds were the available carbohydrate ranged from 68.21%–68.83%, and followed by protein (14.12%–14.87%), fat (6.37%–6.61%) and fibre (3.15%–3.48%). Importantly, proximate composition of the studied quinoa genotypes showed a non-significant difference.

3.9 Saponin Content

Saponin is an anti-nutritional component that causes bitterness in quinoa. In our study, GPBQ-3 had the lowest amount of saponin followed by GPBQ-4, Regalona, GPBQ-2 and GPBQ-1, respectively. The highest amount of saponin content was found in SAU Quinoa-1 (Fig. 7).
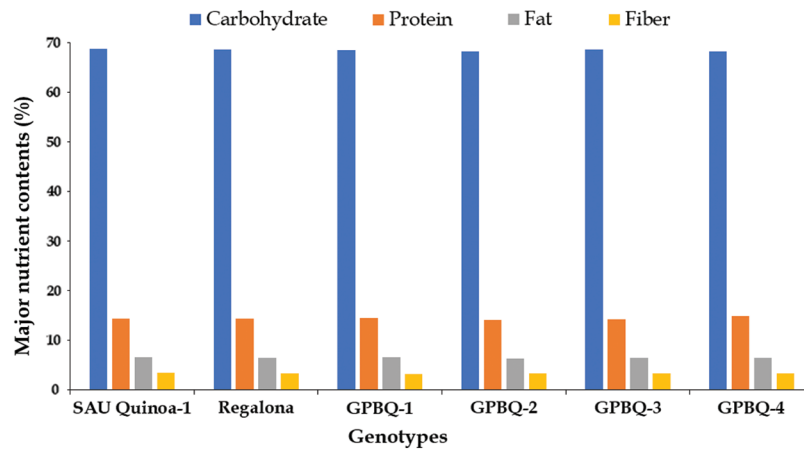
Figure 6: Proximate composition of the seeds of the studied quinoa genotypes grown at BAU farm during the winter season of 2022–2023

Figure 7: Saponin content in the seeds of the studied quinoa genotypes grown at BAU farm during the winter season of 2022–2023

4 Discussion

Continuous collection, characterization, and evaluation of unknown quinoa genotypes are urgently needed in developing nations like Bangladesh due to the need for high-quality quinoa products and its exceptional tolerance to harsh climates. Characterization and documentation of quinoa genotypes are therefore imperative for current and future quinoa breeders to ensure global food and nutritional security. In the current study, we have studied the adaptive potential of six quinoa genotypes and also characterized these genotypes based on morphological, yield, and nutritional quality traits. Although these physical characteristics are typically impacted by the environment, measurements of morphological attributes offer a straightforward method of evaluating genotype performance under certain growth conditions while also analyzing genetic variation [18]. The current research results identified a significant diversity among the quinoa genotypes concerning various qualitative traits (Table 1). The majority of genotypes exhibited a simple growth habit (Fig. 1), and two genotypes displayed branching from the base, indicating potential genetic differences in plant architecture as their panicle shape became glomerular which further provided higher yield. According to Kir and Temel [19], planting density, nutrition, and other environmental elements all affect the branching habit. Nevertheless, there was

diversity in stem color, with most showing green stems while a few displayed yellow ones, indicating potential genetic differences in pigment synthesis pathways. A similar type of phenotypic variation was also reported by Tabatabaei et al. [20] and Coronado et al. [21]. Furthermore, the presence of pigmented axils in all genotypes highlights a common genetic determinant for this trait. Leaf morphology (Fig. 3) across all genotypes in terms of shape was rhomboidal, triangular, and linear, whereas, the margin was entire and dentate. Panicle shape and color also showed diversity, with implications for seed yield and quality (Fig. 4). In a study resembling ours, Sarwar et al. [22] also reported that quinoa plants exhibited an angular yellow-green stem and simple, rhomboidal green leaves. They observed that the panicle shape was intermediate, displaying both glomerular and amaranthiform shapes. Additionally, they also noted that the panicle was green during flowering but turned pink, orange, and yellow at the physiological maturity stage. Similar to our results, variability in inflorescence color was also reported by Voronov et al. [23]. Characteristics variation was also observed in the seed color of the genotypes studied (Fig. 5). Variation in seed color in different quinoa genotypes was also reported by others [24].

Variability in that particular attribute among the available germplasm is necessary in order to use it in a quinoa breeding program. Additionally, the adaptive potentiality of a particular genotype is assayed based on yield under particular agroclimatic conditions. Significant variations were found between the genotypes and attributes under investigation in the current experiment's analysis of variance *viz.*, DFF, DM, PH, SD, PW, 1000-SW, YPP, AGB, and HI. Significant variability in yield and yield-attributing traits in quinoa was also reported by de Santis et al. [24], Pathan et al. [25], and Toderich et al. [26]. In the present study, DFF ranged from 22.33 to 27.33 days and DM ranged from 74.67–85.00 days. Similar to our results, Manjarres-Hernández et al. [27] and Pathan et al. [25] also reported that flowering and maturity in quinoa range from 68–121 days and 80–106 days, respectively. While de Santis et al. [24], Bhargava et al. [28], Shah et al. [29], and Granado-Rodríguez et al. [30] reported a longer mean DM 129 days (range: 109–163 days), 116 days (range: 95–150 days), 131 days (range: 105–148 days) and 119 days (range: 107 to 135 days) respectively. The genotypes used in our experiment were primarily short-duration genotypes. These short-duration genotypes hold significant potential for developing early-maturing quinoa varieties, which could be advantageous for regions with drought, shorter growing seasons, or for achieving multiple cropping cycles within a year. The PH of the genotypes ranged from 81.07 to 101.54 cm. This finding is similar to the observation of Granado-Rodríguez et al. [30] who also found that the PH ranged from 60 to 135 cm. Additionally, the studies by Coronado et al. [21], Bhargava et al. [28], Coronado et al. [31], and Laki et al. [32] also support this result demonstrating similar range and mean of PH. The SD of the current study ranged from 6.54 to 10.84 mm. Similar to our results, Tang et al. [33] also reported that stem thickness ranges from 9.64–10.72 mm in low-, medium-, and high-yielding genotypes. Therefore, the variability in PH and SD further highlighted distinct growth patterns among genotypes, with GPBQ-1 demonstrating the tall stature and thickest stems, and GPBQ-2 showing the short stature and smallest dimensions, indicating potential differences in resource allocation and yield potentiality. The genotypes differed significantly in PW and AGB. Panicle weight ranged from 10.87 to 30.69 g, while AGB ranged from 19.66 to 61.74 g. Bhargava et al. [28] also found that the AGB ranged from 1.11 to 52.89 g. The thousand seed weight of the genotypes varied from 2.29 to 4.61 g, which was similar with the findings of Coronado et al. [21], Sarwar et al. [22], Bhargava et al. [28], Granado-Rodríguez et al. [30] and Craine et al. [34]. The harvest index (HI) of the genotypes ranged from 48.31% to 50.68%, which was higher than the mean HI reported by Laki et al. [32] and Rojas [35], and they showed that the HI ranged from 34% to 40%, respectively. Quinoa typically exhibits low average HI values, as noted by Bertero et al. [36]. The higher HI observed in the genotypes indicates a greater proportion of biomass is allocated to seed yield, suggesting higher economic efficiency. A significant variation in YPP was found in the genotypes which ranged from 7.80 to 22.40 g which was similar to the results reported by Shah et al. [29] and Manugade et al. [37] where YPP mean were 19.86 and 15.00 g, respectively. In contrast,

de Santis et al. [24], Bhargava et al. [28] and Craine et al. [34] reported much lower mean YPP of 4.06, 5.51 and 6.33 g, respectively. These findings suggest the presence of high-yielding genotypes in our study, which could be valuable for selection programs aimed at breeding improvements and the development of high-yielding quinoa varieties.

The existence of genetic diversity and the patterns of inheritance of the desired traits are critical to crop breeding success. Analyzing genetic variation is crucial for breeders as it enables them to identify suitable breeding schemes and selection criteria for improving target traits. Therefore, generally, the phenotypic variance is larger than the genotypic variance. A similar statement was also given by Al-Naggar et al. [38] that PCV was a little higher than GCV for all studied traits. Higher heritability and less environmental effect on the expression of a particular trait were indicated by a low difference between genotypic and phenotypic variance. The PCV was marginally greater than the GCV for the majority of the characteristics examined in this study, indicating that environmental influences have little effect on trait expression. Importantly, SD, PW, 1000-SW, YPP and AGB displayed the highest values for both PCV and GCV, indicating considerable potential for genetic improvement in these traits through selection.

Heritability estimations aid in the selection of plants by breeders according to phenotypic performance. Genetic gains in succeeding generations are generally higher in cases of higher heritability. A high heritability also suggests a high degree of genetic control over the particular trait, which aids in the efficient selection of a particular trait for future development [39,40]. For the majority of the traits in the current study, the estimated heritability ranged from 90 to 100 percent (Table 3). This indicated that the environment had little effect on the traits under study, which are mostly controlled by genetics. The GA, a measure of the potential for genetic improvement, varied across traits, with AGB exhibiting the highest value and 1000-SW the lowest. When expressed as a percentage of the mean, GA ranged from 7.29% to 94.74%, with YPP showing the highest value and HI the lowest. High heritability (>60%) coupled with high genetic advance (>20%) was recorded for YPP, AGB, PW, SD and 1000-SW. In quinoa, other people have experienced similar outcomes [24,28]. Since the expression of these attributes is greatly influenced by genetic constitution, this data implies that genetic improvement of these traits is extremely likely and that selection based on phenotypic expression may be a useful tactic.

The correlation coefficient analysis reveals the intricate relationships among various yield and yield-contributing traits (Table 4). The correlation analysis underscores the significance of YPP to various crucial traits. YPP exhibited significant positive correlations with DFF, DM, PH, SD, PW, and AGB (0.568*, 0.812***, 0.744***, 0.895***, 0.993***, 0.985***, respectively), whereas, it showed significant negative correlation with 1000-SW (−0.715***). Positive associations imply that an increase in YPP corresponds to increases in these traits, suggesting a potentially synergistic relationship that contributes to overall yield enhancement. Similar to our results, de Santis et al. [24], and Bhargava et al. [28] reported a significant positive correlation between YPP, DFF and PH. de Santis et al. [24] and Bhargava et al. [28] shed light on the importance of morphological traits such as DFF, DM, PH, 1000-SW, leaf area, branches plant^{-1}, inflorescence length, inforesence plant^{-1} and harvest index in influencing grain yield in quinoa genotypes. This suggests that genotypes with taller plants are likely to produce higher grain yields in quinoa cultivation. Pathan et al. [25] reported a similar finding with ours that yield had positive correlation with DM and PH. Furthermore, there was a significant negative correlation observed between YPP and 1000-SW, suggesting that as YPP increases, there is a tendency for 1000-SW to decrease. This negative correlation suggests a trade-off scenario where increasing yield per plant may lead to a reduction in individual seed size, this is the opposite of de Santis et al. [24], studies. Thus, the genotypes with greater PH, SD, and ABG, as well as early flowering and maturity, should be chosen in order to increase yield in quinoa breeding, according to the aforementioned findings.

The PCA conducted on the quantitative traits of six quinoa genotypes yielded insightful findings. The PCA unveiled two components, collectively explaining 85.5% of the total variation among the studied traits. Notably, the first two components accounted for a significant portion of this variability, cumulatively explaining 85.5%. Manjarres-Hernández et al. [27] and Wu et al. [41] found that 59.26% to 64.6% of the observed phenotypic variation is explained by the first two components. The first component, responsible for 69.5% of the variance, underscored the substantial positive influence of traits like PW and YPP, indicating their pivotal roles in shaping overall trait variability. Traits such as 1000-SW and HI exhibited negative loadings on this component. This suggests that as YPP increases, there may be a tendency for 1000-SW and HI to decrease, implying a possible trade-off scenario between YPP and individual seed size. The second component, contributing 16% to the total variation, emphasized the significance of traits such as DFF and 1000-SW in further delineating trait variability among the studied genotypes. These findings offer valuable insights into the underlying relationships among the traits and their contributions to overall trait diversity within quinoa genotypes. By elucidating the role of these specific traits in shaping trait variability, the PCA results provide a deeper understanding of the complex dynamics governing trait expression and variability in quinoa populations.

Mineral contents (*viz.*, Ca^{2+}, Cu^{2+}, Fe^{2+}, K^+, Mg^{2+}, Mn^{2+}, and Zn^{2+}) measured in the quinoa genotypes showed significant variations which indicates a substantial diversity in mineral accumulation within the quinoa varieties under evaluation. Consistent with our findings, significant differences in the mineral contents of quinoa grains were also observed by Nowak et al. [42] and de Bock et al. [43]. Moreover, similar variability was also mentioned by others [28,43–45], where they quantified a large variation in micronutrients levels like Ca^{2+} (275 to 1487 mg kg^{-1}), Cu^{2+} (2 to 51 mg kg^{-1}), Fe^{2+} (14 to 168 mg kg^{-1}), Mg^{2+} (260 to 5020 mg kg^{-1}), K^+ (75 to 12000 mg kg^{-1}), and Zn^{2+} (28 to 48 mg kg^{-1}) in various diverse quinoa genotypes of geographical origin.

The examination of proximate composition (Fig. 6) in the studied quinoa genotypes revealed uniformity across various nutritional components, including carbohydrate (68.21%–68.83%), protein (14.12%–14.87%), fat (6.37%–6.61%), and fiber content (3.15%–3.48%). Similar to our results, Pedrali et al. [46], Agarwal et al. [47] and Oustani et al. [48] also reported that carbohydrate content in quinoa genotypes ranged from 55%–77%, protein content ranged from 13%–19%, fat content ranged from 5%–8% and soluble dietary fiber content ranged from 1.3%–4.1%. These nutritional indices did not significantly differ across the cultivars under study, despite phenotypic diversity. This consistency in grain composition aligns with previous studies that have also reported minimal variability in protein and lipid content among different quinoa genotypes by Repo-Carrasco-Valencia et al. [44] and Pedrali et al. [46] however, they have reported significant differences in carbohydrate and fiber content. The insignificant differences in proximate composition among genotypes suggest a high level of stability in the nutritional quality of quinoa grains, which is advantageous for consumers seeking consistent nutritional benefits [49]. However, further research investigating a broader range of genotypes and environmental conditions may provide deeper insights into the factors influencing quinoa grain composition.

The assessment of B-vitamin complexes showed less variability across the studied quinoa genotypes. B_1, B_2, B_3, and B_9 content showed non-significant differences among the genotypes. The amount of B_3 content ranged from 1.05–1.21 mg/100 g. Similar to our results, Kozioł [50] also reported 1.06 g 100 g^{-1} of B_3 content in quinoa. Importantly, B_9 content was higher as compared to the others which ranged from 6.45–6.87 mg 100 g^{-1}. Similar to our results, Agarwal et al. [47] also reported 6.50 mg 100 g^{-1} of B_9 content in quinoa. These findings suggest that quinoa is a rich source of essential B-vitamin complex which is vital for various physiological functions.

A class of natural substances called saponins is generated by certain plants to guard against insects, birds, and hazardous microbes [51]. Researchers reported the presence of saponin, an anti-nutritional

substance causing bitterness in quinoa, across different quinoa varieties (reviewed in Suárez-Estrella et al. [52]). In quinoa, these substances are mostly found in the husk. Our study also reported the presence of varying degrees of saponin content among the tested quinoa genotypes, GPBQ-3 contained the lowest amount content of saponin content while SAU Quinoa-1 showed the highest amount of saponin (Fig. 7). Significant variation in saponin content in quinoa genotypes was also reported by others [53]. In another study, Diaz-Valencia et al. [54] reported that quinoa grains contain about 0.00%–4.4% saponins. Although it has been considered as antinutritional fact, recent studies reported that saponin has some positive roles for human health. El Hazzam et al. [55] concluded that quinoa saponins have many important nutritional characteristics such as anticancer, antiobesity, analgesic, hypocholesterolemic, antiallergic, and antioxidants.

5 Conclusion

Significant variability was observed among the studied qualitative (*viz.*, GH, PSC, PS, PCM, and SC) as well as quantitative traits (viz., DFF, DM, PH, SD, PW, 1000-SW, YPP, AGB, and HI) which offers ample scope of improvement of quinoa for yield and quality. Few of the studied genotypes (*viz.*, GPBQ-1, GPBQ-3, and GPBQ-4) showed better yield performance as compared to the commercial varieties. For the majority of the characteristics under study, PCV was found to be marginally greater than GCV, indicating that environmental influences had little effect on trait expression. The highest values for PCV and GCV were shown by SD, PW, 1000-SW, YPP, and AGB, suggesting significant potential for selection-based genetic improvement in these variables. High h^2_b coupled with high GA% was recorded for SD, PW, 1000-SW, YPP, and AGB which indicates that improvement could be made in the aforesaid characters. YPP showed a significant positive correlation with DFF, DM, PH, SD, PW, and AGB (0.568*, 0.812***, 0.744***, 0.895***, 0.993***, 0.985***, respectively). This suggests that increased YPP could be achieved by proper selection pressure. According to PCA analysis, the first three PCs accounted for 85.5% of the genotypes' overall variation. Significant variation was also observed among the genotypes for vitamins and mineral contents, however, a non-significant variation was observed for carbohydrate, protein, fat, and fiber contents. Considering all the traits, the genotypes GPBQ-1, GPBQ-3, and GPBQ-4 can be considered as potential in terms of yield and others. According to the findings of our research, quinoa can be added to the cropping systems as a new winter crop in Bangladesh. However, further research should be conducted under variable agroclimatic conditions in Bangladesh to study their stability and suitability for release as a new variety.

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Ethics Approval: Not applicable.

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Appendix A

Table A1: Analysis of variance (mean square) for different yield and yield attributing traits of quinoa genotypes

Source of variation	DFF	DM	PH (cm)	SD (mm)	PW (g)	1000-SW(g)	YPP (g)	AGB (g)	HI
Replication	0.056	1.17	2.93	0.42	4.11	0.042	0.21	0.44	1.66
Genotype	17.52***	62.00***	193.45***	10.55***	174.95***	1.71***	95.09***	705.87***	14.01***
Error	1.46	1.57	1.48	0.43	1.91	0.057	0.34	1.99	1.36

Note: *** indicates significant at 0.1% level of probability. Legends: DFF = Days to first flowering, DM = Days to maturity, PH = Plant height, SD = Stem diameter, PW = Panicle weight, 1000-SW = 1000-seed weight, YPP = Yield/plant^{-1}, AGB = Above ground biomass and HI = Harvest index.

Table A2: Analysis of variance (mean square) for quinoa seed mineral compositions

Source of variation	Ca^{2+}	Cu^{2+}	Fe^{2+}	K^+	Mg^{2+}	Mn^{2+}	Zn^{2+}
Replication	659.7	0.03	0.19	418	305.82	0.17	0.31
Genotype	14259.8***	1.01***	0.95**	114315***	3999.40***	1.08**	19.40***
Error	566.3	0.01	0.10	382	98.35	0.17	0.43

Note: ** and *** indicates significant at 1% and 0.1% level of probability, respectively.