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ARTICLE

Effects of salt stress on yield and quality traits of Quinoa (*Chenopodium quinoa* Willd.) genotypes

Adrita Abdullah, Sadia Akter, and Mohammad Anwar Hossain*

Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh-2202, Bangladesh

ABSTRACT Over 30% of the coastal cultivable land in Bangladesh is affected by salinity, necessitating the introduction of salt-tolerant crops to enhance food security and climate resilience. Quinoa (*Chenopodium quinoa* Willd.), a facultative halophyte, can thrive under saline conditions. This study evaluated yield and quality traits of six quinoa genotypes, including two released varieties, under long-term salt stress to identify promising materials for cultivation in Bangladesh. A pot-culture experiment was conducted in a completely randomized design with three treatments: control (EC 0 dS m^{-1}), moderate (EC 15 dS m^{-1}), and strong salinity (EC 20 dS m^{-1}). ANOVA revealed significant genotypic differences in key agronomic traits, including days to maturity (DM), plant height (PH), panicle weight (PW), aboveground biomass (AGB), thousand-seed weight (TSW), yield per plant (YP), and harvest index (HI). Salinity stress reduced all yield-related traits. However, GPBQ-3, GPBQ-1, and SAU Quinoa-1 maintained comparatively higher yield stability under severe salinity, as supported by stress-tolerance indices. Yield per plant showed a strong positive association with PW under both control and saline conditions. A PCA biplot indicated that GPBQ-1, GPBQ-3, and SAU Quinoa-1 were the most divergent genotypes. Considering all traits under salinity, SAU Quinoa-1, GPBQ-1, and GPBQ-3 emerge as the most promising salt-tolerant genotypes for further testing and deployment.
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***Corresponding author**
E-mail: anwargpb@bau.edu.bd

INTRODUCTION

Quinoa (*Chenopodium quinoa* Willd.) is a dicotyledonous species in the Amaranthaceae that has been cultivated and consumed in the Andean region for millennia (Alandia et al. 2020). Its global popularity as a food crop has increased markedly (Jacobsen et al. 2003). Although often termed a pseudocereal due to its culinary and functional similarity to cereal grains, quinoa is taxonomically distinct as a dicot (Kadereit et al. 2003). Quinoa seeds are used in breakfast cereals, flour, and a wide array of baked and processed foods. Owing to their high nutrient density, quinoa grains provide essential minerals, vitamins, dietary fiber, unsaturated fatty acids, and a complete set of amino acids that enhance protein quality (Vega-Gálvez et al. 2010; Ain et al. 2023). Advances in food processing have broadened its potential contributions to human health, including roles in weight management and dietary management of celiac disease and metabolic disorders such as hyperlipidemia, obesity, hypertension, and diabetes (Adetunji et al. 2021).

Bangladesh relies heavily on rice, wheat, and maize, yet these staples are increasingly constrained by shifting weather patterns, soil degradation, and coastal salinity. The country covers 147,570 km², with coastal zones accounting for ~20% and extending up to 150 km inland. Of 2.85 million ha of coastal and offshore land, ~1.056 million ha are arable—over 30% of the nation's cultivable land (SRDI 2010). A substantial share is affected by salinity (Petersen and Shireen 2001), and ~53% of coastal regions experience salinity-related constraints that hinder year-round crop production (Haque 2006). In southern Bangladesh, significant tracts remain fallow during the Rabi season; recurrent drought contributes to seasonal production losses and food insecurity (Bhuiyan et al. 2002). Screening and deploying genotypes with improved tolerance to abiotic stress is therefore essential.

Most conventional crops are highly sensitive to salinity and fail to produce economic yields when exposed to electrical conductivity (EC) >12 dS m^{-1}. Integrating halophytes can help restore salinity-degraded land and reduce pressure on freshwater resources (Nanduri et al. 2019; Koyro and Eisa 2008). Quinoa, a facultative halophyte (Jacobsen et al. 2005; Adolf et al. 2013; Koyro et al. 2008), has been cultivated successfully across a wide salinity range, including 15–20 dS m^{-1} (Wilson et al. 2002; Bosque Sanchez 2003; Adolf et al. 2012), at which many crops show severely reduced growth and yield (Munns and Tester 2008; Shabala et al. 2013). Thus, quinoa offers potential to convert fallow coastal lands into productive systems, increase cropping intensity, and bolster GDP.

Beyond undernourishment, "hidden hunger"—widespread micronutrient deficiencies—remains a major public health issue (Burchi et al. 2011). Diet quality is central to preventing non-communicable diseases (Coulston et al. 2017). In Bangladesh, rice-dominant diets with suboptimal nutrient profiles contribute to malnutrition, particularly among women and children (White HN 2005). Quinoa can help diversify diets, offering higher protein content with a balanced amino-acid profile relative to common cereals (Angeli et al. 2020). While ~80% of global quinoa is produced in Bolivia and Peru (Bazile et al. 2016), yield stability outside the Andean region remains variable due to soil, water, and climate differences (Scanlin and Lewis 2017), underscoring the need for locally adapted cultivars.

In Bangladesh, quinoa is still under-researched, especially regarding long-term salinity responses and potential effects on grain quality. We recently introduced six diverse genotypes; however, their salinity tolerance over the full crop cycle has not been established. Therefore, this study aimed to evaluate the effects of long-term salt stress on yield and quality traits of six quinoa genotypes under contrasting salinity levels and to identify promising lines for breeding and cultivation in Bangladesh. We hypothesized that increasing salinity would depress growth and yield overall, but that genotypes would differ in tolerance, with some maintaining relatively higher performance under salt stress. The findings are expected to support sustainable agriculture and contribute to SDG 2 (Zero Hunger), SDG 3 (Good Health and Well-being), and SDG 13 (Climate Action).

MATERIALS AND METHODS

Experimental site and period

The experiment was conducted in the net house of the Farm Research Laboratory, Department of Genetics and Plant Breeding, Bangladesh Agricultural University (Mymensingh-2202), from November 2023 to January 2024.

Soil and climatic conditions

The site belongs to the Sonatola soil series of the Grey Floodplain within the Old Brahmaputra Floodplain (Agro-Ecological Zone 9) (FAO-UNDP, 1988). The landscape comprises ~35% of medium-high land, and the soil is silty in texture with low organic matter and low fertility. Soil pH ranged from 6.5 to 6.7. The regional climate is characterized by hot temperatures and heavy rainfall during the kharif (April–October), followed by cooler, drier conditions in the rabi season (November–March). During the experimental period (November–January), mean monthly temperatures were 18–25 °C and relative humidity remained high (80–85%).

Plant materials and seed sources

Six quinoa genotypes, including two released varieties—GPBQ-1, GPBQ-2, GPBQ-3, GPBQ-4, Regalona, and SAU Quinoa-1—were evaluated. SAU Quinoa-1 was obtained from Sher-e-Bangla Agricultural University (SAU), Dhaka, Bangladesh. The other seed lots were available at the Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU), sourced originally from Australia and Uzbekistan.

Experimental design, pot preparation, and sowing

A completely randomized design (CRD) with three replicates and three salinity treatments was used: control (EC 0 dS m^{-1}), moderate salinity (EC 15 dS m^{-1}), and strong salinity (EC 20 dS m^{-1}). Earthen pots were filled with 7 kg of field soil. Basal fertilization was applied at the following equivalent field rates: urea 70 kg $acre^{-1}$, triple superphosphate (TSP) 100 kg $acre^{-1}$, muriate of potash (MoP) 40 kg $acre^{-1}$, gypsum 40 kg $acre^{-1}$, zinc 2 kg $acre^{-1}$, and boron 2 kg $acre^{-1}$. Seeds were sown in moist soil in November 2023, and seedlings were managed under non-saline conditions until stress imposition.

Salinity stress imposition

Two weeks after emergence, seedlings were irrigated with NaCl solutions to achieve EC 15 dS m^{-1} and 20 dS m^{-1}, applied every two days to maintain ~80% field capacity, and continued until physiological maturity. Control plants were irrigated with non-saline water.

Crop management

Weeding and other intercultural operations were performed as needed. An insecticide (Tido Plus 70 WDG) was applied at 2 g 10 L^{-1} on 14 December and 27 December 2023.

Harvest and post-harvest handling

Harvesting began on 21 January 2024 when ≥90% of grains had turned yellow to deep brown. Five randomly selected, mature plants were sampled from each pot. Plants were sun-dried, threshed, and grains stored in net bags for further drying. Seeds were cleaned and sun-dried for 3–5 days to reach a safe storage moisture level. Aboveground biomass was separated, cut into pieces, and sun-dried similarly for 3-5 days.

Data collection

Seven quantitative traits were recorded from five randomly selected plants per replicate: days to maturity (DM),

Table 1. Two-way ANOVA for seven yield-related traits of six quinoa genotypes under control and salinity-stress conditions (factors: genotype, treatment, and G×T interaction).

Sources of variation	**DM**	**PH**	**PW**	**AGB**	**HI (%)**	**TSW**	**YP**
Genotype (G)	168.77***	83.92***	3.39***	3.41***	483.80***	0.635***	2.51***
Treatment (T)	378.91***	42.16***	11.78***	12.99***	416.58***	0.509***	9.48***
GxT	2.77***	4.46NS	0.689***	0.851***	79.81***	0.041***	0.500***
Error	0.407	3.607	0.520	0.089	7.580	0.003	0.764

Values are mean squares (MS). Significance: $p < 0.001$ (***); NS = non-significant. DM: days to maturity; PH: plant height (cm); PW: panicle weight (g); AGB: aboveground biomass (g); HI (%): harvest index; TSW: thousand-seed weight (g); YP: yield per plant (g).

plant height (PH), panicle weight (PW), thousand-seed weight (TSW), yield per plant (YP), aboveground biomass (AGB), and harvest index (HI).

Statistical analysis

Data were compiled and analyzed in R (RStudio 2023.12.0). A two-way ANOVA with fixed effects for genotype (G), treatment (T), and the G×T interaction was fitted. Pairwise mean comparisons were performed using Tukey's HSD ($\alpha = 0.05$). Pearson's genotypic correlation coefficients were estimated with the *metan* package, and path analysis was conducted on the resulting genotypic correlation matrix. Principal component analysis (PCA) was carried out in FactoMineR on the correlation matrix of the seven traits, with *factoextra* used for loadings/scores visualization and biplots; components were retained by the Kaiser criterion (eigenvalue > 1) and scree-plot inspection.

Stress tolerance indices

Stress-tolerance indices (STIs) were computed on grain yield per plant following standard definitions:

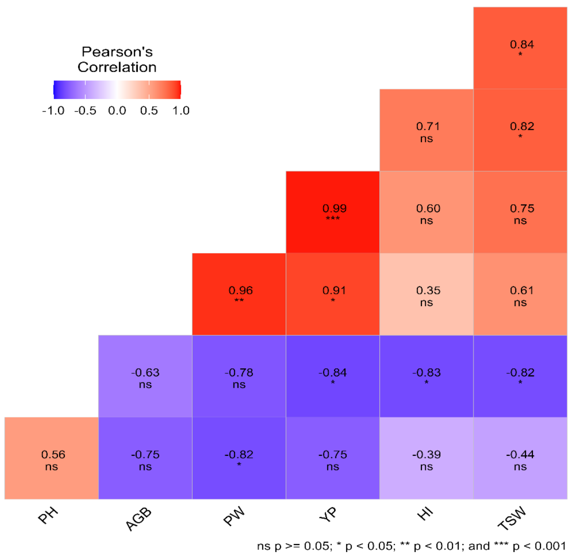
$$\text{Mean productivity (MP)} = (Y_p + Y_s)/2$$
(Rosielle and Hamblin 1981)

$$\text{Geometric mean productivity (GMP)} = \sqrt{(Y_p \times Y_s)}$$
(Fernandez 1992)

$$\text{Stress susceptibility index (SSI)} = [1 - (Y_s/Y_p)] / [1 - (\bar{Y}_s/\bar{Y}_p)]$$
(Fischer and Maurer 1978)

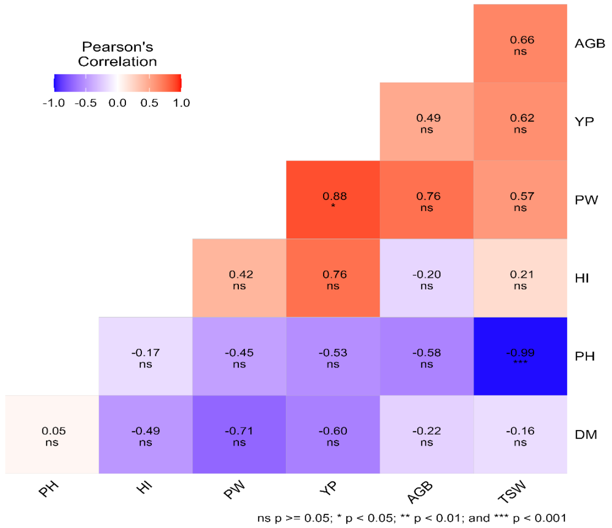
$$\text{Tolerance index (TOL)} = Y_p - Y_s$$
(Rosielle and Hamblin 1981)

$$\text{Stress tolerance index (STI)} = (Y_p \times Y_s) / (\bar{Y}_p)^2$$
(Fernandez 1992)



ns p >= 0.05; * p < 0.05; ** p < 0.01; and *** p < 0.001

Figure 1. Genotypic correlation coefficients among seven traits (DM, PH, PW, AGB, TSW, YP, HI) in six quinoa genotypes under control conditions.



ns p >= 0.05; * p < 0.05; ** p < 0.01; and *** p < 0.001

Figure 2. Genotypic correlation coefficients among seven traits (DM, PH, PW, AGB, TSW, YP, HI) in six quinoa genotypes under salinity-stress conditions.

Table 2. Mean performance of six quinoa genotypes for seven traits under control and salinity-stress conditions (EC 0, 15, 20 dS m^{-1}; CRD, three replicates).

Genotypes	Treatment	DM	PH	PW	AGB	HI (%)	TSW	YP
GPBQ-1	Control	93.00A	38.41A	3.30FG	5.12C	55.88GH	2.34I	2.86EF
	15 dS m^{-1}	84.33DE	36.23AB	3.02G-I	4.41D	50.60I-K	2.19J	2.23GH
	20 dS m^{-1}	82.66F	31.63CD	2.79I-K	4.36D	49.45JK	2.19J	2.15H
GPBQ-2	Control	83.33EF	30.89C-F	5.71A	7.38A	61.89C-E	2.91B	4.56A
	15 dS m^{-1}	75.33H	31.13C-E	4.34D	5.92B	56.92F-H	2.59FG	3.36D
	20 dS m^{-1}	74.66H	28.64EF	3.03G-I	4.33D	53.96H-J	2.56F-H	2.30GH
GPBQ-3	Control	88.66B	35.84AB	3.15G-I	4.52D	59.31E-G	2.49H	2.68F
	15 dS m^{-1}	82.66F	35.49AB	2.89I-J	4.17D-F	58.32E-H	2.37I	2.44G
	20 dS m^{-1}	79.33G	33.77BC	2.29L	3.46G	55.11G-I	1.89K	1.91I
GPBQ-4	Control	88.66B	31.14C-E	4.84C	5.92B	72.39B	3.19A	4.27B
	15 dS m^{-1}	84.66CD	27.87FG	2.92H-J	3.73FG	61.32D-F	2.81C	2.28GH
	20 dS m^{-1}	82.33F	27.55G	2.64J-L	4.32D	48.83K	2.68DE	2.11HI
Regalona	Control	93.00A	30.77C-F	3.81E	5.21C	65.39CD	2.75CD	3.41D
	15 dS m^{-1}	85.66C	30.15D-G	3.06G-I	4.45D	66.36C	2.71DE	2.95E
	20 dS m^{-1}	84.33DE	28.29E-G	2.45KL	3.82E-G	58.69E-G	2.52GH	2.24GH
SAU Quinoa-1	Control	83.33EF	29.80D-G	5.22B	6.24B	70.97B	2.79C	4.42AB
	15 dS m^{-1}	75.66H	28.02E-G	3.53EF	5.26C	71.02B	2.69DE	3.75C
	20 dS m^{-1}	74.67H	28.65D-G	3.29F-H	4.27DE	66.05C	2.62EF	2.81EF
Mean		83.13	31.35	3.46	4.78	60.84	2.57	2.93
Range		93.00-74.67	38.41-27.55	5.71-2.29	7.38-3.46	72.39-48.83	3.19-1.89	4.56-1.91
SD		5.57	3.58	0.96	1.02	9.03	0.29	0.84
LSD Value		1.06	3.14	0.38	0.49	4.56	0.09	0.24

Different letters within a column indicate significant differences by Tukey's HSD (α = 0.05). DM: days to maturity; PH: plant height (cm); PW: panicle weight (g); AGB: aboveground biomass (g); HI (%): harvest index; TSW: thousand-seed weight (g); YP: yield per plant(g).

Yield stability index (YSI) = Ys / Yp
(Bouslama and Schapaugh 1984)

Here, Yp and Ys are yield per plant of a given genotype under non-stress and stress conditions, respectively; $\bar{Y}$p and $\bar{Y}$s are the corresponding across-genotype means.

Saponin phenotyping (foam test)

Saponin content was assessed in the field using a rapid foaming test (Stanschewski et al. 2021). Five de-hulled seeds were placed in a 1.5 mL microcentrifuge tube containing 500 µL double-distilled water and shaken vigorously by hand for 30 s. The stable foam height was used as a qualitative indicator of saponin presence.

RESULTS

Analysis of variance (ANOVA)

Analysis of variance for seed yield per plant and its component traits is summarized in Table 1. Genotype (G) and treatment (T) effects were highly significant ($p \leq 0.001$) for all seven traits. The G×T interaction was also highly significant ($p \leq 0.001$) for days to maturity (DM), panicle weight (PW), aboveground biomass (AGB), harvest index (HI), thousand-seed weight (TSW), and yield per plant (YP), but not significant for plant height (PH).

Mean performance of genotypes

Mean performance under the control and two salinity levels (15 and 20 dS m^{-1}) is shown in Table 2. Under control, DM ranged from 83.33 to 93.00 days across genotypes. Moderate to severe salinity led to shorter DM in most genotypes; the greatest reduction occurred in GPBQ-1 (11.12% at 20 dS m^{-1}), while the smallest was in GPBQ-4 (4.52% at 15 dS m^{-1}).

Significant variability in PH was observed. Under control, GPBQ-1 had the tallest plants (38.41 cm) and SAU Quinoa-1 the shortest (29.80 cm). Salinity reduced PH relative to control; the largest reduction was in GPBQ-1 (17.65% at 20 dS m^{-1}), and the smallest in GPBQ-3 (0.98% at 15 dS m^{-1}).

For PW, the highest control mean was in GPBQ-2 (5.71 g) and the lowest in GPBQ-3 (3.15 g). Both salinity levels markedly reduced PW, with the largest decrease in GPBQ-2 (47.03%) and the smallest in GPBQ-3 (7.97%).

Table 3. Path-coefficient analysis (genotypic level) showing direct and indirect effects among seven traits under control conditions; diagonal bold values indicate direct effects.

Characters	DM	PH	PW	TSW	AGB	HI (%)	Genotypic correlation with YP
DM	**-0.084**	0.031	0.344	0.026	-0.823	-0.244	-0.750
PH	-0.049	**0.053**	0.341	0.047	-0.699	-0.564	-0.840*
PW	0.068	-0.043	**-0.420**	-0.044	1.039	0.383	0.985***
TSW	0.038	-0.044	-0.320	**-0.058**	0.662	0.554	0.820*
AGB	0.065	-0.034	-0.408	-0.036	**1.072**	0.260	0.913*
HI (%)	0.033	-0.048	-0.260	-0.052	0.450	**0.619**	0.710

Rightmost column reports genotypic correlations with YP. Significance: $p < 0.05$ (*), $p < 0.001$ (***). DM: days to maturity; PH: plant height (cm); PW: panicle weight (g); AGB: aboveground biomass (g); HI (%): harvest index; TSW: thousand-seed weight (g); YP: yield per plant (g).

Under control, AGB ranged from 4.52 to 7.38 g. Moderate salinity (15 dS m^{-1}) decreased AGB by 13.82% (GPBQ-1), 19.84% (GPBQ-2), 7.83% (GPBQ-3), 37.05% (GPBQ-4), 14.70% (Regalona), and 28.20% (SAU Quinoa-1). Severe salinity (20 dS m^{-1}) caused reductions of 14.87%, 41.39%, 23.41%, 26.94%, 26.80%, and 31.59% in the same order.

Salinity caused a considerable decline in HI relative to control. At 15 dS m^{-1}, the largest drop was in GPBQ-4 (15.29%), followed by GPBQ-1 (9.45%), GPBQ-2 (8.04%), and GPBQ-3 (1.67%). At 20 dS m^{-1}, reductions were greatest in GPBQ-4 (32.54%), followed by GPBQ-2 (12.83%), GPBQ-1 (11.51%), Regalona (10.24%), GPBQ-3 (7.08%), and SAU Quinoa-1 (6.93%).

Under control, TSW was highest in GPBQ-4 (3.19 g) and lowest in GPBQ-1 (2.34 g). The maximum reduction at 15 dS m^{-1} occurred in GPBQ-4 (11.82%), whereas at 20 dS m^{-1} it was greatest in GPBQ-3 (24.20%).

For YP, control values ranged widely, with GPBQ-2 highest (4.56 g) and GPBQ-3 lowest (2.68 g). Under 15 dS m^{-1}, GPBQ-3 had the highest yield; under 20 dS m^{-1}, GPBQ-1 was the highest-yielding. Yield reductions at 15 dS m^{-1} were greatest in GPBQ-4 (46.56%), followed by GPBQ-2 (26.32%), GPBQ-1 (21.95%), SAU Quinoa-1 (15.35%), and Regalona (13.59%). At 20 dS m^{-1}, the largest reductions were in GPBQ-4 (50.56%), GPBQ-2 (48.87%), SAU Quinoa-1 (36.49%), Regalona (34.33%), and GPBQ-3 (28.88%).

Genotypic correlation coefficients

Pearson's genotypic correlations among traits are presented in Figures 1 and 2. Under control, 9 of 21 associations were significant: five positive and four negatives. Under salt stress, 2 of 21 associations were significant (one positive, one negative). In control, DM correlated negatively with PW ($r = -0.82$*). PH correlated negatively with YP (−0.84*), HI (−0.83*), and TSW (−0.82*). Under stress, TSW correlated negatively with PH (−0.99***). PW showed strong positive correlations with AGB (0.96**) and YP (0.99***) in control and remained positively associated with YP (0.88*) under stress. AGB was positively correlated with YP (0.91*). HI correlated positively with TSW (0.84*) and negatively with PH (−0.83*) in control; no HI correlations were significant under stress. TSW correlated positively with YP (0.82*) and negatively with PH (−0.82*) in control.

Path coefficient analysis

Path analysis at the genotypic level (Tables 3-4) used YP as the dependent variable. Under control, AGB had the largest positive direct effect on YP (1.072), followed by

Table 4. Path-coefficient analysis (genotypic level) showing direct and indirect effects among seven traits under salinity-stress conditions (EC 20 dS m^{-1}); diagonal bold values indicate direct effects.

Characters	DM	PH	PW	TSW	AGB	HI (%)	Genotypic correlation with YP
DM	**-0.083**	-0.005	0.092	0.015	-0.149	-0.474	-0.605
PH	-0.005	**-0.095**	0.057	0.093	-0.477	-0.125	-0.532
PW	0.063	0.045	**-0.122**	-0.055	0.505	0.447	0.882 *
TSW	0.013	0.098	-0.074	**-0.090**	0.482	0.210	0.624
AGB	0.019	0.069	-0.094	-0.066	**0.657**	-0.131	0.485
HI (%)	0.042	0.013	-0.058	-0.020	-0.092	**0.937**	0.761

Rightmost column reports genotypic correlations with YP. Significance: $p < 0.05$ (*). DM: days to maturity; PH: plant height (cm); PW: panicle weight (g); AGB: aboveground biomass (g); HI (%): harvest index; TSW: thousand-seed weight (g); YP: yield per plant (g).

Table 5. Principal component analysis (PCA) of seven yield-related traits in six quinoa genotypes under control and salinity-stress conditions: loadings, eigenvalues, and variance explained.

Variable	PC1	PC2	PC3
DM	0.110	0.746	0.624
PH (cm)	-0.288	0.872	-0.127
PW (g)	0.937	0.194	-0.266
AGB (g)	0.858	0.342	-0.336
HI (%)	0.690	-0.313	0.339
TSW (g)	0.839	-0.229	0.322
YP (g)	0.978	0.104	-0.073
Eigenvalue	3.846	1.631	0.813
% of Variance	54.95	23.31	11.61
Cumulative % of Variance	54.95	78.25	89.86

DM: days to maturity; PH: plant height (cm); PW: panicle weight (g); AGB: aboveground biomass (g); HI (%): harvest index; TSW: thousand-seed weight (g); YP: yield per plant (g).

HI (0.619) and PH (0.053). Negative direct effects were observed for PW (−0.420), TSW (−0.058), and DM (−0.084). Under stress, HI (0.937) and AGB (0.657) had the largest positive direct effects, whereas PH (−0.095), PW (−0.122), TSW (−0.090), and DM (−0.083) had negative direct effects.

Principal components analysis

PCA considered DM, PH, PW, TSW, AGB, YP, and HI (Table 5; Fig. 3). Two principal components had eigenvalues > 1. The first three PCs together explained 89.86% of the total variance (PC1 = 54.95%, PC2 = 23.31%, PC3 = 11.61%). PC1 loadings were positive for YP (0.978), PW (0.937), AGB (0.858), TSW (0.839), HI (0.690), and DM (0.110), and negative for PH (−0.288). PC2 accounted for 23.31% of variation, with highest positive loadings for PH (0.872) and DM (0.746), and negative loadings for HI (−0.313) and TSW (−0.229). PC3 contributed 11.61%, with positive coefficients for DM (0.624), HI (0.339), and TSW (0.322).

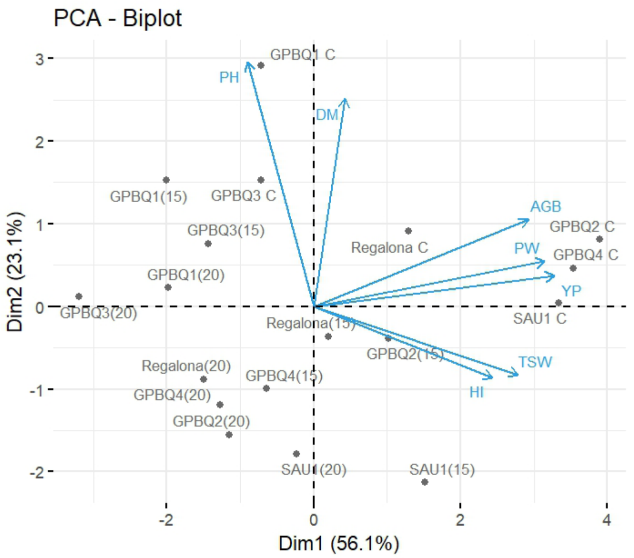


Figure 3. Principal component analysis (PCA) biplot of the seven yield-related traits (DM, PH, PW, AGB, TSW, YP, HI) for six quinoa genotypes under control and salinity-stress conditions.

The biplot (Fig. 3) indicated that Regalona, GPBQ-2, and SAU Quinoa-1 tended to align on the positive side of PC1. GPBQ-4, GPBQ-3, GPBQ-1 (for both 15 and 20 dS m^{-1}), and Regalona and SAU Quinoa-1 (at 20 dS m^{-1}) clustered on the negative side of PC2. From the biplot, Regalona, GPBQ-2, and SAU Quinoa-1 appeared to have higher TSW and HI; GPBQ-4, GPBQ-2, and Regalona showed higher AGB, PW, and YP under control. PH was higher in GPBQ-1 and GPBQ-3 under both control and stress.

Stress tolerance indices

Stress-tolerance indices calculated from YP are provided in Table 6. SAU Quinoa-1 had the highest MP (3.62), GMP (3.53), and STI (0.91). GPBQ-3 had the lowest MP (2.29) and STI (0.37). SSI was highest in GPBQ-4 (1.30) followed

Table 6. Stress-tolerance indices (MP, GMP, SSI, TOL, STI, YSI) calculated from yield per plant under control and salinity-stress conditions.

Genotypes	MP	GMP	SSI	TOL	STI	YSI
GPBQ-1	2.50	2.48	0.63	0.70	0.45	0.75
GPBQ-2	3.45	3.26	1.25	2.23	0.78	0.51
GPBQ-3	2.29	2.26	0.74	0.77	0.37	0.71
GPBQ-4	3.19	3.00	1.30	2.16	0.66	0.49
Regalona	2.82	2.76	0.88	1.17	0.56	0.66
SAU Quinoa-1	3.62	3.53	0.94	1.62	0.91	0.64

MP: mean productivity; GMP: geometric mean productivity; SSI: stress susceptibility index; TOL: tolerance index; STI: stress tolerance index; YSI: yield stability index; Yp: yield under non-stress; Ys: yield under stress.

by GPBQ-2 (1.25). TOL was highest in GPBQ-2 (2.23) followed by GPBQ-4 (2.16). YSI was highest in GPBQ-1 (0.75) followed by GPBQ-3 (0.71).

Anti-nutritional (saponin) test (qualitative)

Saponin content, assessed by the foam test, varied among genotypes: GPBQ-2 showed the lowest foaming (lowest saponin), followed by GPBQ-3, GPBQ-4, Regalona, and SAU Quinoa-1; GPBQ-1 showed the highest foaming, indicating the highest saponin content.

DISCUSSION

Quinoa is a promising crop for saline-affected regions, offering diversification and food-security benefits on marginal lands. In this study, salinity significantly reduced all yield-related traits, in line with reports linking salinity to impaired photosynthesis, nutrient uptake, and osmotic stress (Jacobsen et al. 2003; Munns and Tester 2008; Araus et al. 2013; Hussain et al. 2016; Taleisnik et al. 2009). The highly significant main effects of genotype (G) and treatment (T), together with significant G×T interactions for most traits, indicate differential genotypic responses and scope for selection (Ruiz-Carrasco et al. 2011; Long 2016; Cai and Gao 2020; Qureshi and Daba 2020; Shahid and Thushar 2021).

Mean performance showed clear reductions in seed yield, biomass, and harvest index with salinity, consistent with multi-location findings (Long 2016; Algosaibi et al. 2015; Hussain et al. 2018; Iqbal et al. 2019; Shahid and Thushar 2021). Jacobsen et al. (2003) reported maximum quinoa yield around 15 dS m^{-1}, with ~10% reduction at 20 dS m^{-1} relative to 5 dS m^{-1}, and ~44% reduction at seawater-like salinity (~40 dS m^{-1}).

Earlier maturity can be advantageous under water scarcity but often coincides with lower biomass and yield. Here, salinity shortened days to maturity across genotypes, echoing previous observations (Shahid and Thushar 2021; Algosaibi et al. 2015). Plant height (PH) declined under salinity—strongly in GPBQ-1 at severe stress, while GPBQ-3 was comparatively stable at moderate stress—aligned with prior reports (Koyro et al. 2008; Adolf et al. 2012; Long 2016; Algosaibi et al. 2015; Hussain et al. 2018; Shahid and Thushar 2021). Mechanistically, sodium exclusion and compartmentation (e.g., tonoplast Na^+/H^+ exchange and vacuolar sequestration) and the SOS pathway help maintain cellular function (Blumwald et al. 2000; Apse et al.1999; Apse and Blumwald 2007; Shabala and Mackay 2011; Hasegawa et al. 2000; Qiu et al. 2002; Mullan et al. 2007), with quinoa homologs (cqSOS1A, cqSOS1B) identified (Maughan et al. 2009; Adolf et al. 2013). Additional tolerance mechanisms include ROS tolerance, stomatal patterning and maintenance of water-use efficiency, salt bladders for excretion, and leaf K^+ retention (Shabala et al. 2012; Waqas et al. 2017; Percey et al., 2016; Hinojosa et al., 2018; Waqas et al. 2021).

Thousand-seed weight (TSW) decreased under salinity in our study, indicating sensitivity of grain filling to environment despite genetic control of seed size (Long 2016; Algosaibi et al. 2015; Shahid and Thushar 2021). Correlation analysis is useful to set selection priorities (Ghafoor et al. 2013). We found panicle weight (PW) strongly and positively associated with aboveground biomass (AGB) and yield per plant (YP) in control, and with YP under stress; by contrast, PH correlated negatively with YP, suggesting excessive height can be maladaptive—a pattern consistent with reports that elongated main inflorescences are more failure-prone, reducing yield (Shah et al. 2020; De Santis et al. 2016; Fuentes and Bhargava 2010; Kaya and Aydemir 2020; Tiwari and Ameen 2022; Tang et al. 2024). Positive, YP-aligned traits (e.g., PW, AGB) can also serve as indirect selection targets (Henry and Krishna 1990; Akinyele and Osekita 2006).

Path analysis—partitioning correlations into direct and indirect effects (Singh and Kakar 1977; Rashid et al. 2010)—showed that under control AGB had the largest positive direct effect on YP, whereas PW had a negative direct effect despite positive correlation, implying that PW contributes mainly indirectly (e.g., via biomass). Under stress, HI and AGB remained the strongest positive direct contributors, while PH and TSW had negative direct effects. This supports selection for biomass accumulation and efficient assimilate partitioning (higher HI) under salinity, and for more compact plant architecture.

PCA captured the multivariate structure: two components had eigenvalues >1; the first three PCs explained 89.86% of variance overall. PC1 loaded positively on YP, PW, AGB, TSW, and HI, and negatively on PH, consistent with the correlation/path patterns. The biplot interpretation follows standard practice (Yan and Rajcan 2002) and resembles variance structures reported under salinity (Cueva-Flores et al. 2024; Waqas et al. 2021). In our biplot, Regalona, GPBQ-2, and SAU Quinoa-1 aligned with positive PC1 under optimal conditions, whereas several genotype–treatment combinations shifted toward lower performance under salinity; a similar tolerant–sensitive separation was noted by Prajapat et al. (2024).

Stress indices (MP, GMP, SSI, TOL, STI, YSI) discriminated against tolerant vs. sensitive entries as expected: larger TOL and SSI denote greater sensitivity (Khan and Kabir 2014; Krishnamurthy et al. 2016), whereas larger STI and YSI indicate tolerance/stability (Rosielle and Hamblin 1981; Bouslama and Schapaugh 1984; Anshori et al. 2018; Girma et al. 2017). Here, SAU Quinoa-1 excelled for MP, GMP, and STI, while GPBQ-1 and GPBQ-3 showed higher YSI; the utility of these indices has been supported elsewhere (Majidi et al. 2011; Badran and Moustafa 2014; Badran 2015; Al-Ghamdi and El-Zohri 2021).

Regarding grain quality, saponins—triterpenes in the seed coat—affect palatability; "sweet" types have low levels (Ruiz et al. 2015; Mastebroek et al. 2000). The Peruvian standard NTP 205.062–2021 classifies quinoa as sweet below 0.12% saponin (Alania-Choque et al. 2024). Our qualitative test indicated meaningful genotypic differences; irrigation and salinity can raise seed saponins (Gómez-Caravaca et al. 2012; Pulvento et al. 2012), and field rankings may differ (Naim et al. 2024).

Overall, salinity (15–20 dS m^{-1}) markedly depressed yield components, but GPBQ-3, GPBQ-1, and SAU Quinoa-1 retained comparatively higher performance under stress. Correlations, path analysis, and PCA converged on AGB and HI as primary selection targets, while stress indices consistently highlighted SAU Quinoa-1, GPBQ-1, and GPBQ-3 as promising for saline environments.

CONCLUSION

Long-term salinity (15–20 dS m^{-1}) significantly depressed quinoa yield components. Nevertheless, GPBQ-3, GPBQ-1, and SAU Quinoa-1 maintained comparatively higher yield under stress. PW and AGB were the most informative correlates of YP; path analysis emphasized AGB and HI as primary direct contributors to yield, and PCA reinforced their roles in discriminating high performers. Stress-tolerance indices and the PCA biplot consistently flagged SAU Quinoa-1, GPBQ-1, and GPBQ-3 as the most promising genotypes for saline environments. Field-level validation under farmers' conditions remains essential before recommendation for large-scale cultivation.

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