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Evaluation of Drought Tolerance in Brassica Genotypes: Identification of Superior Lines for Water-Limited Environments

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ABSTRACT

Drought is a major constraint on *Brassica* oilseed production, reducing growth, yield, and oil quality. This study evaluated ten *Brassica* genotypes under controlled conditions to identify genotypes suited to water-limited environments. A factorial completely randomized design (CRD) with two replications was used, with three water regimes imposed for 14 days at flowering: 100% field capacity (FC; To, control), 50% FC (T1), and 25% FC (T2). Ten morphological and yield-related traits and eight quality traits (moisture, starch, protein, ash, crude fat, crude fiber, acid detergent fiber, and neutral detergent fiber) were recorded. Genotype, water regime, and their interaction were highly significant ($P < 0.01$) for all traits. On average, drought reduced plant height by 20% (T1) and 36% (T2), root length by 37% and 55%, leaf area by 25% and 37%, and number of leaves by 26% and 44%. Across the seven morphological traits with complete data, A-105, A-89, 25012, and A-79 retained the highest performance relative to the control (67.8–70.3%), whereas 18001, A-69, and 12006RJB retained the least (63.7–64.3%). A-89 combined high absolute values with comparatively small reductions, A-79 maintained the longest roots under severe stress (9.15 cm), and UAF-12 showed the poorest absolute performance. Correlations among traits became stronger as drought intensified. A-89, A-105, and A-79 are promising candidates for breeding programs targeting water-limited environments, subject to confirmation of their seed-yield advantage in replicated trials.

Introduction

With the warming global climate, drought is considered the most important abiotic factor limiting plant growth and crop yield worldwide, with serious consequences for crop production (Chen et al., 2022). Among the major oilseed crops, *Brassica* species, including canola (*Brassica napus*), mustard (*Brassica juncea*), and turnip rape (*Brassica rapa*), are globally valued for their

oilseeds, which contribute to food security, biofuel production, and industrial applications. However, they are highly sensitive to water deficit, which impairs growth, reduces seed yield, and compromises oil quality (Eyni Nargeseh et al., 2019; Zandberg et al., 2022).

Water deficit inhibits cell expansion and division, reducing leaf area and biomass, and impairs the plant's ability to maintain cell turgor, which decreases biomass accumulation and seed production (Sharma & Sardana, 2022; Yoo et al., 2024). Moreover, water stress during sensitive growth stages, particularly flowering and seed filling, can reduce yield by 30–70%, depending on the duration and severity of the stress (Batool et al., 2023; Khatun et al., 2021; Liu et al., 2024). Drought also affects germination and seedling establishment: it lowers the water-potential gradient between the seed and its environment, which restricts water uptake through the seed coat and delays or reduces germination (Bai et al., 2020; Channaoui et al., 2017). In addition, it causes the accumulation of reactive oxygen species (ROS), which damage cellular components and disturb metabolism in *B. napus* seedlings (Farooq et al., 2015).

In Pakistan, the challenge is particularly acute because of a long-standing shortage of edible oil. Domestic production meets only about 20% of the country's edible oil needs, and the remaining 80% is imported, mainly from Malaysia and Indonesia (Khan et al., 2019). Pakistan met most of its edible oil needs at the time of independence, but demand has since risen steadily with population growth, widening the shortage (Asad et al., 2020). In 1969–1970, Pakistan produced about 75% of its edible oil requirement and imported the remaining 25%, but after 1970 demand increased at an unsustainable rate (Alam, 2002). Given the growing demand and the high cost of imports, it is essential to develop high-yielding, oil-rich domestic oilseed varieties. Because of their high oil content and adaptability, oilseed *Brassica* crops could help bridge the gap between domestic production and demand, reduce dependence on imports, and strengthen the agricultural sector (Asad et al., 2020; Raza et al., 2023).

Under water deficit, *Brassica* species undergo several physiological and biochemical changes to cope with limited water availability, including reduced leaf area, altered root architecture, and adjusted osmotic potential (Sharma & Sardana, 2022; Zhu et al., 2016). Tolerant species such as *B. carinata* (Ethiopian mustard) show slower biomass reduction under stress because of deeper root systems that enhance water uptake, whereas sensitive species such as *B. oleracea* (cabbage) wilt rapidly and show stunted growth under mild drought (Ambaw et al., 2024). Drought-tolerant *Brassica* genotypes also maintain higher relative water content (RWC) through osmotic adjustment with proline, glycine betaine, and soluble sugars; for example, *B. juncea* has been reported to accumulate 40% more proline than *B. rapa* under drought, which correlates with improved membrane stability (Naveen et al., 2021). These traits are crucial for the resilience of *Brassica* crops in water-limited environments, because deep roots allow plants to access water from deeper soil layers, while efficient water use minimizes water loss and sustains physiological function (Champolivier & Merrien, 1996).

To address these challenges, breeding programs have increasingly focused on identifying and selecting *Brassica* genotypes with enhanced drought tolerance (Qamar et al., 2020). Recent advances in genetics and molecular biology have identified key traits associated with drought resistance, such as deep root systems, efficient water use, and enhanced osmotic adjustment. Understanding the physiological responses of different *Brassica* genotypes to water deficit can also inform management practices that mitigate drought impacts; some varieties, for example, regulate stomatal conductance and adjust photosynthetic rate to optimize water-use efficiency (Batool et al., 2023).

The aim of this study was to assess the performance of ten *Brassica* genotypes under controlled water-deficit conditions. The objectives were to (i) evaluate the growth, yield-related, and quality traits of the genotypes under water deficit, (ii) identify genotypes with superior drought tolerance, and (iii) recommend the best-performing genotypes for further breeding and evaluation in water-limited areas. The results provide insight into genotypic variation in drought response and contribute to the development of varieties better suited to water-scarce environments (Sheoran et al., 2024), thereby helping to reduce agricultural vulnerability and sustain crop production under growing water constraints.

Materials and Methods

The experiment was conducted under controlled conditions at the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan (31.4504° N, 73.1350° E; 184 m above sea level), during 2024–2025.

Ten *Brassica* genotypes (A-79, 25012, 9001, A-105, UAF-12, A-89, A-69, 18001, 12006RJB, and 96) were obtained from the Oilseeds Section of the same department. Seeds were surface-sterilized with a 1% NaCl solution and sown at 1 cm depth in pots containing a uniform mixture of soil, sand, and compost (2:1:1, v/v/v). After germination, seedlings were thinned to three plants per pot.

The experiment followed a completely randomized design (CRD) with a factorial arrangement (10 genotypes × 3 water regimes) and two replications (60 pots in total). Pots were spaced 30 cm apart. Standard fertilizer doses and cultural practices were applied. All plants were grown at 100% field capacity until flowering.

At the flowering stage, drought stress was imposed for 14 days by maintaining three soil moisture levels: To (control) at 100% field capacity (FC), T1 (moderate stress) at 50% FC, and T2 (severe stress) at 25% FC. Soil moisture was maintained by weighing each pot daily and adding the amount of water required to restore the assigned level. After the 14-day stress period, normal irrigation was resumed and continued until crop maturity.

At maturity, data were recorded from three plants per pot, and the mean of the three plants was used as the value for each pot. Plant height, root length, and silique length (cm) were measured with a meter rod, and leaf area (cm^2) was calculated as length × width × 0.75. The numbers of leaves and branches per plant were counted manually. Stem diameter (cm) was measured with a digital vernier caliper. For biomass estimation, shoot dry weight was determined after oven-drying samples at 70 °C for 48 h, and root dry weight was recorded after sun-drying for 5–6 days. Seed yield per plant (g) was weighed on an electronic balance after threshing.

Seed quality parameters (moisture, starch, ash, protein, crude fat, crude fiber, acid detergent fiber [ADF], and neutral detergent fiber [NDF]; %) were determined non-destructively with a portable near-infrared (NIR) analyzer (AgriNIR, Model W 999-0565). Cleaned samples from each experimental unit were scanned, and the mean value of three plants was recorded directly from the NIR printout.

Data were analyzed by two-way analysis of variance (ANOVA) for a factorial CRD (Steel et al., 1997), and means were separated with the least significant difference (LSD) test at $P \leq 0.05$. Pearson correlation coefficients among traits were calculated separately for each water regime (Kwon & Torrie, 1964). To summarize genotype performance across traits, relative performance (RP) was calculated for each trait as (mean under stress ÷ mean under control) × 100 and averaged over the seven morphological traits for which complete data were available (plant height, root length, leaf area, number of leaves, stem diameter, number of branches, and root dry weight). Genotypes were also ranked on their absolute values under stress for each of these traits.

Results

Analysis of variance. The combined analysis of variance showed highly significant effects ($P < 0.01$) of genotype (G), water regime (W), and the G × W interaction for all morphological, yield-related, and quality traits studied (Table 1). The significant G × W interaction indicates that genotypes differed in the magnitude of their response to drought, so genotypes were compared within each water regime.

Growth traits. Water deficit caused progressive and highly significant reductions in all growth traits (Figs. 1–6 and 10; Table 2). Averaged over genotypes, T1 and T2 reduced plant height by 20% and 36%, root length by 37% and 55%, leaf area by 25% and 37%, number of leaves per plant by 26% and 44%, stem diameter by 18% and 35%, number of branches per plant by 34% and 51%, and root dry weight by 17% and 34%, respectively. Under control conditions, A-89 was the tallest genotype (79.57 cm), followed by 9001 (77.58 cm), and 12006RJB was the shortest (53.28 cm; Fig. 1). At T1, A-89 (61.05 cm) and A-105 (59.72 cm) were the tallest, and at T2 the tallest were A-89 (48.75 cm), 96 (47.08 cm), and A-105 (46.73 cm). The reduction in height at T2 ranged from 29% (12006RJB and 96) to 43% (UAF-12); A-89, although the tallest, lost 39%.

Genotype 25012 had the longest roots under control conditions (19.98 cm) but lost 72% of its root length at T2 (5.57 cm; Fig. 2). A-79 had the longest roots at both T1 (13.90 cm) and T2 (9.15 cm), with reductions of 20% and 48%, whereas UAF-12 had the shortest roots at T2 (3.42 cm) but also the smallest reduction (41%), because its roots were already short under control conditions (5.82 cm). For leaf traits (Figs. 3 and 4), UAF-12 and A-79 retained the largest leaf area at T2 (51.28 and 51.08 cm^2), whereas A-89 showed the smallest reductions in leaf area (28%) and leaf number (28%) and had the most leaves at T2 (11.65 per plant). The largest reductions were recorded for leaf area in A-69 (44%) and for leaf number in 12006RJB (64%).

Stem diameter (Fig. 5) was greatest under stress in 12006RJB, 9001, and A-89 (4.57, 4.12, and 4.02 cm at T2), and the largest reduction occurred in A-69 (48%). The number of branches per plant (Fig. 6) was highest at T2 in 12006RJB (5.50) and UAF-12 (5.22), which also showed the smallest reductions (40% and 34%). Root dry weight (Fig. 10) was highest at T2 in 18001 (2.42 g) and A-79 (2.07 g); reductions were smallest in 25012 (19%), A-105 (22%), and A-89 (24%) and largest in UAF-12 (52%) and A-79 (44%).

Silique length, seed yield, and shoot dry weight. Silique length, seed yield per plant, and shoot dry weight were also significantly affected by genotype, water regime, and their interaction (Table 1; Figs. 7–9).

Quality traits. All eight quality traits declined progressively with increasing water deficit in all ten genotypes (Figs. 11–18; Table 2). Averaged over genotypes, T2 reduced moisture content by 24%, protein by 31%, NDF by 29%, ADF by 39%, crude fat by 41%, crude fiber by 41%, starch by 42%, and ash by 42%. Moisture content fell from 94.2–98.8% under control conditions to 56.9–83.6% at T2, and only genotype 9001 (56.93%) was below 70% at T2. Genotype rankings for quality traits differed from those for morphological traits: 12006RJB retained the highest moisture (83.62%), protein (34.13%), and crude fiber (10.73%) at T2, A-79 and A-89 the highest crude fat (9.50% and 8.59%), and genotype 96 the highest starch (11.28%), ADF (18.67%), and ash (12.27%). The decline in quality traits was thus a general response of all genotypes rather than a feature separating tolerant from sensitive lines.

Correlations among morphological traits. Under control conditions (Fig. 19.1), most correlations were weak to moderate (28 of 36 coefficients had $|r| < 0.40$). The strongest were negative: stem diameter with shoot dry weight ($r = -0.72$), number of branches with leaf area ($r = -0.69$) and silique length ($r = -0.57$), silique length with seed yield ($r = -0.51$), and number of branches with root dry weight ($r = -0.50$).

Under moderate drought (T1; Fig. 19.2), correlations were stronger: 15 of 45 coefficients had $|r| \geq 0.40$, compared with 8 of 36 at To. Stem diameter was strongly and negatively correlated with shoot dry weight ($r = -0.85$) and moderately with leaf area ($r = -0.55$) and root dry weight ($r = -0.48$), and silique length with seed yield ($r = -0.70$). Plant height was negatively correlated with leaf area ($r = -0.59$) and positively with seed yield ($r = 0.56$), and leaf area was positively correlated with root length ($r = 0.56$) and shoot dry weight ($r = 0.47$).

Under severe drought (T2; Fig. 19.3), 22 of 45 coefficients had $|r| \geq 0.40$. Leaf area was negatively correlated with number of leaves ($r = -0.64$), root dry weight ($r = -0.54$), and plant height ($r = -0.52$), and positively with shoot dry weight ($r = 0.58$) and root length ($r = 0.42$). Number of leaves was strongly and negatively correlated with shoot dry weight ($r = -0.71$) but positively with root dry weight ($r = 0.56$), whereas number of branches was negatively correlated with root dry weight ($r = -0.68$) and root length ($r = -0.51$). Stem diameter remained strongly and negatively correlated with shoot dry weight ($r = -0.81$), and silique length with seed yield ($r = -0.63$). Seed yield was positively correlated with plant height ($r = 0.51$) and number of leaves ($r = 0.48$). These patterns indicate a trade-off between leaf number and leaf size, and between branching and root biomass, under severe stress.

Correlations among quality traits. All pairwise correlations among the seven quality traits shown in Figs. 20.1–20.3 were positive and strong at every water regime, consistent with the parallel decline of these traits under drought. Under control conditions (Fig. 20.1), r ranged from 0.71 to 0.97; protein was almost perfectly correlated with NDF ($r = 0.96$), crude fiber ($r = 0.96$), and ADF ($r = 0.95$), and starch with crude fat ($r = 0.97$) and ash ($r = 0.96$).

Under moderate drought (Fig. 20.2), r ranged from 0.60 to 0.96, and correlations involving ash, starch, and NDF weakened (ash–starch $r = 0.60$, ash–protein $r = 0.63$, starch–NDF $r = 0.65$), whereas ash and crude fat remained closely correlated ($r = 0.96$).

Under severe drought (Fig. 20.3), r ranged from 0.57 to 0.98. Starch and ADF became almost perfectly correlated ($r = 0.98$, compared with 0.81 at To), whereas ash was less closely correlated with crude fiber ($r = 0.57$) and NDF ($r = 0.65$).

Genotype performance across traits. The ranking of genotypes differed among traits (Figs. 1–6 and 10), so no genotype was superior for every trait. Averaged over the seven morphological traits with complete data, A-105 (70.3%), A-89 (69.5%), 25012 (68.6%), and A-79 (67.8%) retained the highest performance relative to the control, whereas 18001 (63.7%), A-69 (64.3%), and 12006RJB (64.3%) retained the lowest (Table 3). Based on absolute values under stress, 25012 and A-89 had the best mean ranks (4.4 and 4.5) and UAF-12 the poorest (6.9). A-89 was therefore the most consistent genotype: it ranked second on both measures, was the tallest at all three water regimes, and showed the smallest reductions in leaf area and leaf number. A-105 retained a high proportion of its control performance but had low absolute values for several traits (for example, 5.83 leaves per plant at T2), and A-79 stood out for root length. Because the differences in relative performance among genotypes were modest (63.7–70.3%), these groupings should be regarded as provisional.

Discussion

The highly significant genotype (G), water regime (W), and G × W effects for all 18 traits indicate considerable genetic variability in drought response among the ten *Brassica* genotypes. Strong G × W interactions have been reported for *B. napus*, *B. juncea*, and related species under water deficit and underline the scope for selecting superior lines for water-limited environments. The interaction also means that genotype rankings changed with water regime and trait, as observed here, so selection should rely on performance under stress rather than on performance under control conditions alone.

Progressive water deficit from 100% to 25% FC reduced plant height (20–36% on average), root length (37–55%), leaf area (25–37%), number of leaves (26–44%), stem diameter (18–35%), number of branches (34–51%), and root dry weight (17–34%). Such responses are well documented in *Brassica* and other crops and are generally attributed to inhibited cell division and elongation, hormonal changes including elevated abscisic acid, and restricted carbon assimilation as leaf water potential declines (Fang & Xiong, 2015; Li et al., 2017). Genotype A-89 had the greatest plant height at all three water regimes, whereas A-79 had the longest roots under both stress levels (9.15 cm at T2). Because A-79 still lost 48% of its root length, this is better described as superior root length under stress than as root stability; longer and deeper roots improve access to soil water and are widely regarded as key to drought avoidance and tolerance (Kalra et al., 2024).

The decline in leaf area and leaf number is a classical drought-avoidance response that limits the transpiring surface. The reductions differed among genotypes: A-89 showed the smallest reductions in both leaf area (28%) and leaf number (28%) at T2, whereas A-69 lost the most leaf area (44%) and 12006RJB the most leaves (64%). A-79 and UAF-12 retained the largest absolute leaf area under stress (about 51 cm^2) despite relatively large reductions (both 40%), because they started with large leaves. Whether these differences reflect better stomatal regulation, osmotic adjustment, or antioxidant capacity, which have been implicated in sustaining photosynthesis under water deficit in other crops (Sehgal et al., 2017), cannot be determined from the present data because these processes were not measured.

Silique length, seed yield per plant, and shoot dry weight were significantly affected by water regime and by the G × W interaction (Table 1). Water deficit at flowering and pod filling is known to reduce seed yield in *Brassica* through its effects on flower and pod set and on seed filling (Champolivier & Merrien, 1996). [Authors: discuss genotype-specific yield responses after Figs. 7–9 are corrected.]

All eight quality traits declined with increasing water deficit in every genotype, and genotype rankings for these traits differed from those for morphological traits. The reduction in moisture content (24% on average at T2) confirms that the stress treatments altered tissue water status, and the decline in crude fat is consistent with the reduction in oil content commonly reported under water stress (Champolivier & Merrien, 1996). In contrast, protein, fiber fractions, and ash are often reported to increase under drought when expressed on a dry-matter basis, reflecting stress-protein synthesis, cell-wall thickening, and ion accumulation. The uniform decrease observed here may therefore reflect how the traits were expressed (for example, as a percentage of fresh weight), the NIR calibration, or the type of sample scanned, rather than metabolic reprogramming. These data do not allow conclusions about cell-wall reinforcement or osmolyte accumulation, which would require dry-matter-based or wet-chemistry measurements. Genotypes that were sensitive in morphological traits, such as 12006RJB, retained the highest moisture, protein, and crude fiber, indicating that these NIR-derived traits were not reliable indicators of drought tolerance in this study.

Drought intensity changed the relationships among traits. Under well-watered conditions most correlations were weak to moderate (22% of coefficients with $|r| \geq 0.40$), whereas under moderate and severe drought this proportion rose to 33% and 49%, consistent with more constrained resource allocation as plasticity declines. Under severe stress, the negative correlations between leaf number and leaf area ($r = -0.64$) and between number of branches and root dry weight ($r = -0.68$), together with the positive association of leaf area with root length and shoot dry weight, point to a trade-off between leaf number and leaf size and to reallocation of resources among organs. The negative correlation between silique length and seed yield ($r = -0.70$ at T1 and -0.63 at T2) and the positive correlation of seed yield with plant height ($r = 0.56$ and 0.51) should be re-examined once the silique length and seed yield data are verified. Likewise, the increasing starch–ADF correlation under severe drought should not be read as evidence of starch conversion into structural carbohydrates, because all quality traits declined in parallel. Correlations were calculated among genotype means within each water regime from a small number of observations and describe association, not causation.

Limitations. The study used two replications of potted plants, a single 14-day stress period at flowering, and no direct physiological measurements of plant water status, stomatal conductance, or osmolytes; genotype rankings are therefore provisional. Confirmation in replicated, multi-location field trials with direct seed-yield data is required before recommending genotypes for cultivation.

Conclusion

In this study, drought stress imposed at flowering significantly reduced growth traits in all ten *Brassica* genotypes, and genotype × water regime interactions were significant for all traits. A-89 was the most consistent performer: it combined the greatest plant height at all three water regimes with the smallest reductions in leaf area and leaf number and ranked second overall in both relative and absolute performance under stress. A-105 retained the highest proportion of its control performance (70.3%), A-79 maintained the longest roots under stress (9.15 cm at T2), and 25012 also performed well, whereas UAF-12 showed the poorest absolute performance and 12006RJB, A-69, and 18001 the lowest relative performance. A-89, A-105, and A-79 are

therefore promising parental material for breeding programs targeting water-limited environments, provided that their seed-yield advantage is confirmed in replicated field trials. The quality traits declined in all genotypes and did not discriminate between tolerant and sensitive lines.

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Table 1. Mean squares from the analysis of variance for morphological, yield-related, and quality traits of ten *Brassica* genotypes under three water regimes.

Traits	Mean squares			
	Genotype (G)	Water regime (W)	G × W	Error
Plant height	165.05**	2950.49**	20.23**	4.11
Root length	43.476**	230.086**	5.964**	0.107
Leaf area	369.93**	3574.07**	27.38**	3.63
Number of leaves per plant	22.171**	287.517**	6.473**	0.256
Stem diameter	6.7819**	17.5439**	0.5497**	0.0334
Number of branches per plant	1.528**	120.713**	0.743**	0.066
Silique length	4.365**	22.5523**	0.7411**	0.0236
Seed yield per plant	40.377**	366.075**	1.444**	0.192
Shoot dry weight	20.9145**	42.1082**	1.6824**	0.0481
Root dry weight	0.80368**	5.08674**	0.1446**	0.00675
Moisture content	54.693**	4.552**	330.719**	0.307
Starch content	3.4903**	2.368**	25.104**	0.1387
Protein content	13.523**	35.132**	116.78**	0.153

Acid detergent fiber	10.2434**	2.3107**	49.5007**	0.1445
Neutral detergent fiber	7.0587**	10.6671**	55.5045**	0.1903
Ash content	13.1636**	47.7498**	28.0295**	0.1906
Crude fat content	1.577**	1.9183**	17.1771**	0.112
Crude fiber content (%)	2.659**	8.5553**	20.3023**	0.1125

Degrees of freedom: G = 9, W = 2, G × W = 18, error = 30. ** Significant at P ≤ 0.01. Water regimes: To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

Table 2. Means of ten *Brassica* genotypes at each water regime and mean reduction (with range among genotypes) relative to the control.

Trait	To	T1	T2	Reduction at T1 (%)	Reduction at T2 (%)
Plant height (cm)	67.5	53.8	43.3	20 (10–31)	36 (29–43)
Root length (cm)	11.7	7.3	5.0	37 (15–56)	55 (41–72)
Leaf area (cm^2)	70.5	52.6	44.4	25 (13–33)	37 (28–44)
Number of leaves per plant	16.8	12.0	9.3	26 (12–49)	44 (28–64)
Stem diameter (cm)	5.19	4.17	3.32	18 (9–45)	35 (25–48)
Number of branches per plant	9.4	6.2	4.6	34 (26–42)	51 (34–57)
Root dry weight (g)	2.92	2.40	1.90	17 (2–34)	34 (19–52)
Moisture content (%)	96.7	86.0	73.7	11 (7–20)	24 (15–42)
Starch content (%)	13.8	10.9	8.1	21 (17–26)	42 (30–57)
Protein content (%)	45.3	38.1	31.2	16 (11–20)	31 (26–36)
Acid detergent fiber (%)	23.1	18.9	14.0	18 (14–28)	39 (29–56)
Neutral detergent fiber (%)	32.8	28.0	23.1	14 (10–19)	29 (22–40)
Ash content (%)	15.1	12.2	8.9	19 (8–31)	42 (30–58)
Crude fat content (%)	12.8	10.2	7.6	21 (15–32)	41 (30–54)
Crude fiber content (%)	14.5	11.5	8.6	21 (16–28)	41 (33–49)

To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC. Reductions are means of genotype-level reductions relative to To. Silique length, seed yield, and shoot dry weight are not shown because the charts in Figs. 7–9 contain plant-height data. [Authors: add these traits when the data are corrected.]

Table 3. Relative performance (RP, % of control) of ten *Brassica* genotypes averaged over seven morphological traits.

Genotype	RP at T1 (%)	RP at T2 (%)	Mean RP (%)	Mean rank under stress	Rank by mean RP
A-105	79.3	61.4	70.3	6.1	1
A-89	76.8	62.1	69.5	4.5	2
25012	77.5	59.7	68.6	4.4	3
A-79	78.0	57.6	67.8	5.7	4

9001	75.4	56.6	66.0	4.9	5
96	73.4	57.7	65.6	5.6	6
UAF-12	73.6	57.2	65.4	6.9	7
A-69	71.9	56.8	64.3	5.7	8
12006RJB	70.7	57.8	64.3	6.0	9
18001	70.2	57.2	63.7	5.2	10

RP = (mean under stress ÷ mean under control) × 100, averaged over plant height, root length, leaf area, number of leaves, stem diameter, number of branches, and root dry weight. Mean rank under stress is the average rank of the genotype's absolute values at T1 and T2 across the same seven traits (1 = best).

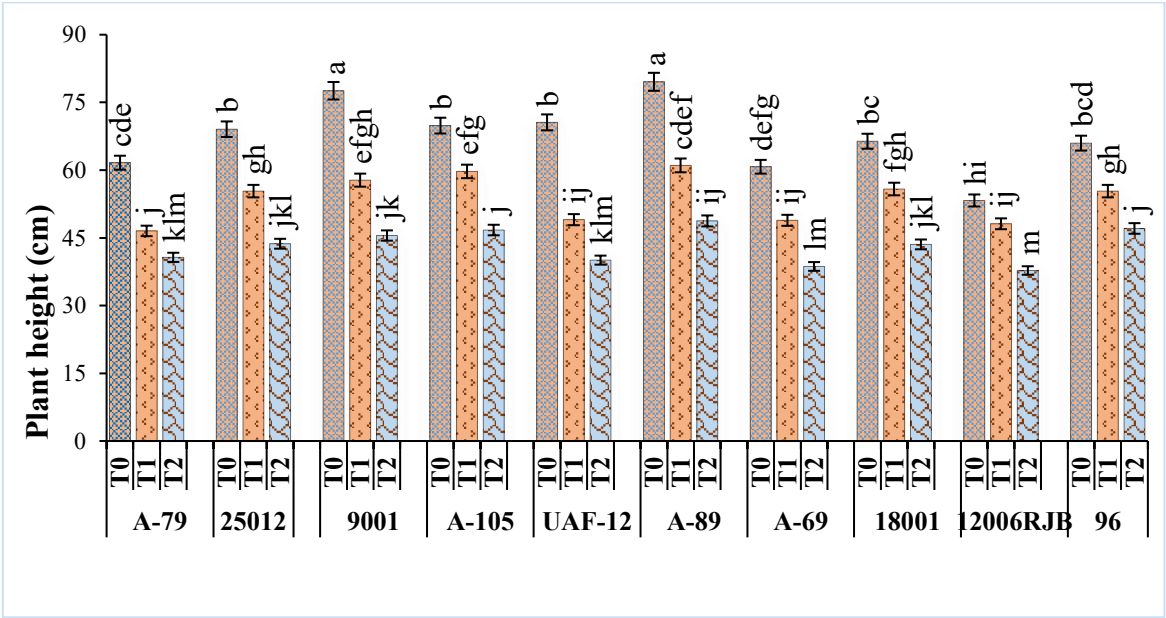


Figure 1. Effect of water regime on plant height (cm) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

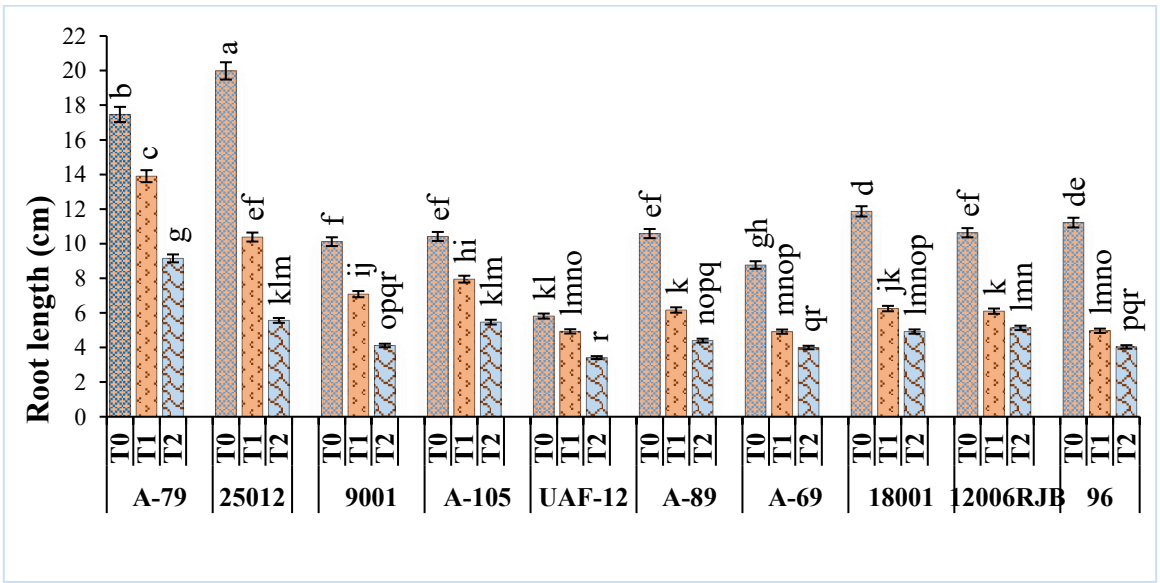


Figure 2. Effect of water regime on root length (cm) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

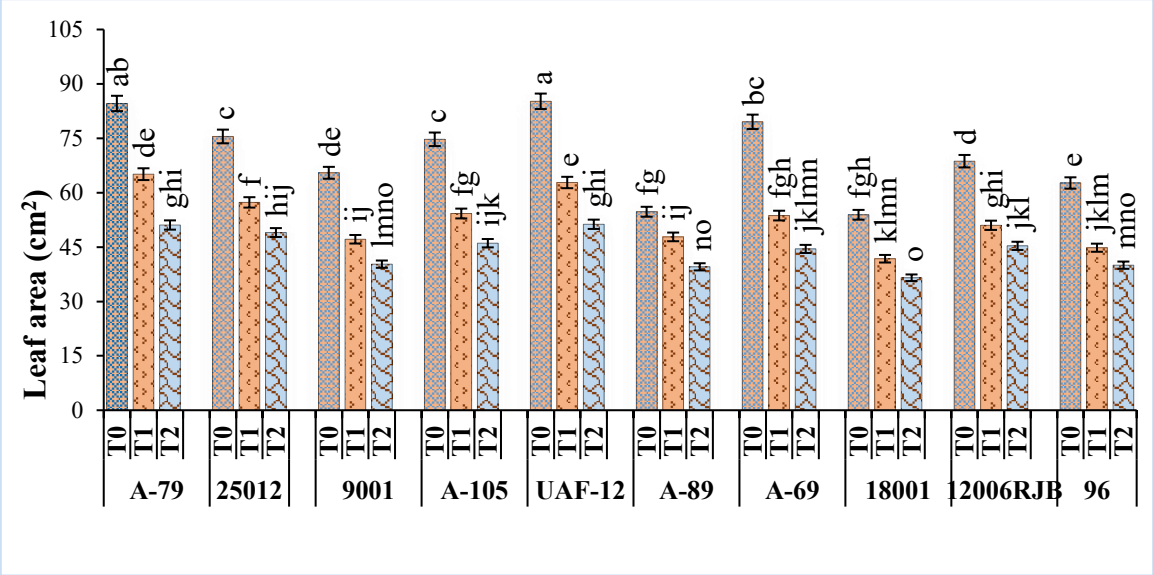


Figure 3. Effect of water regime on leaf area (cm^2) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

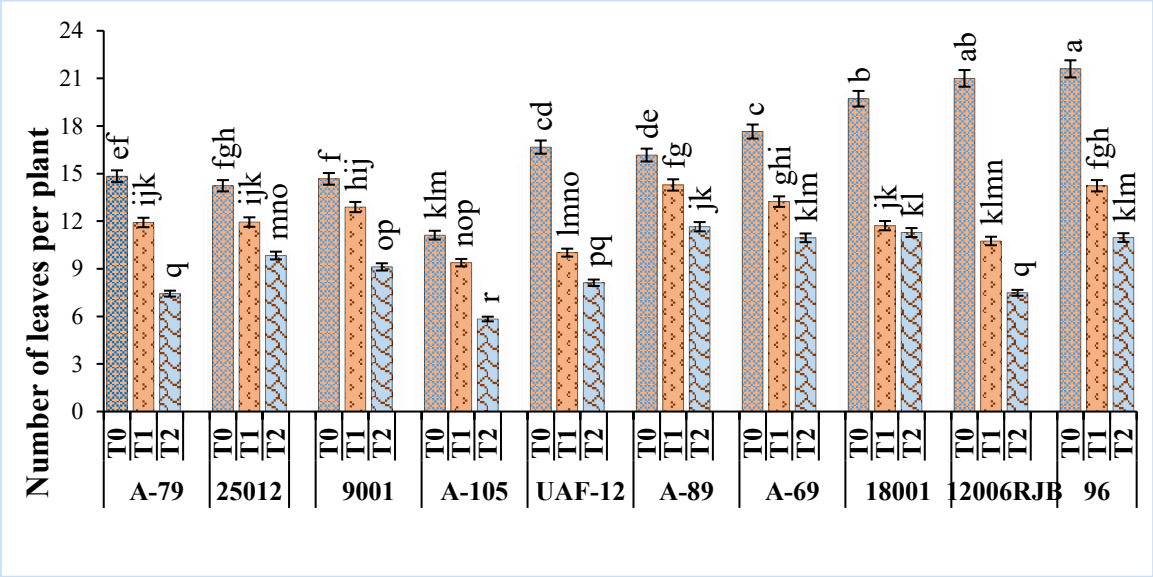


Figure 4. Effect of water regime on number of leaves per plant of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

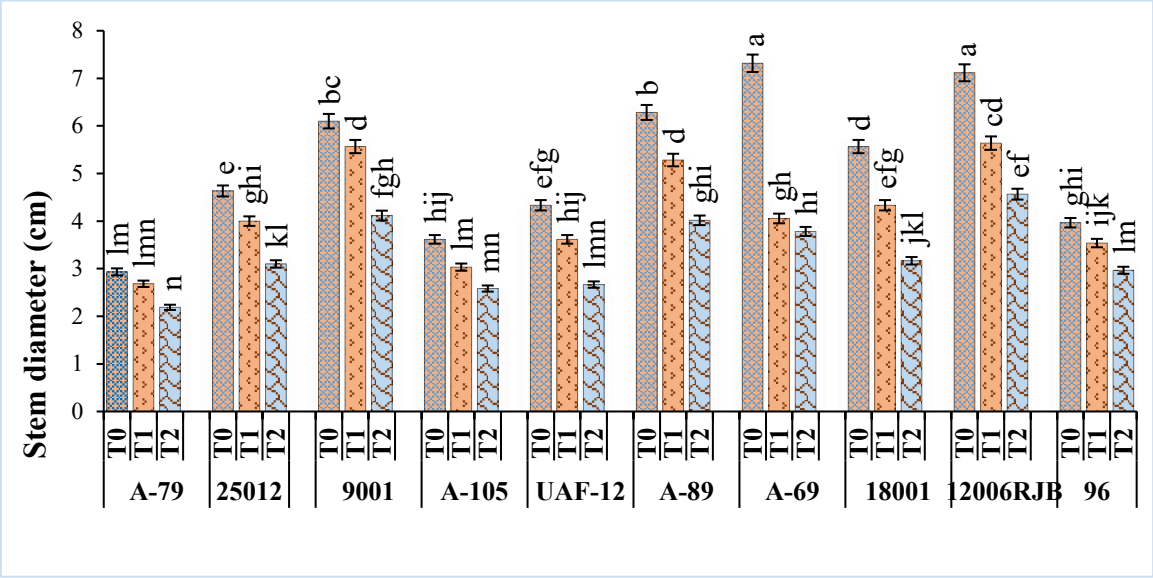


Figure 5. Effect of water regime on stem diameter (cm) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

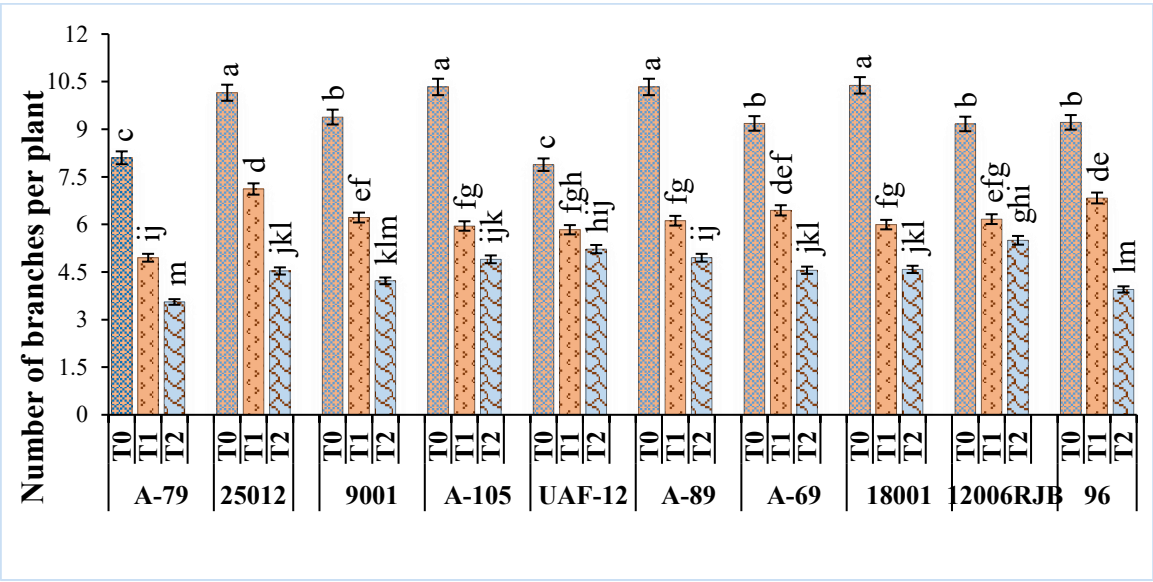


Figure 6. Effect of water regime on number of branches per plant of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

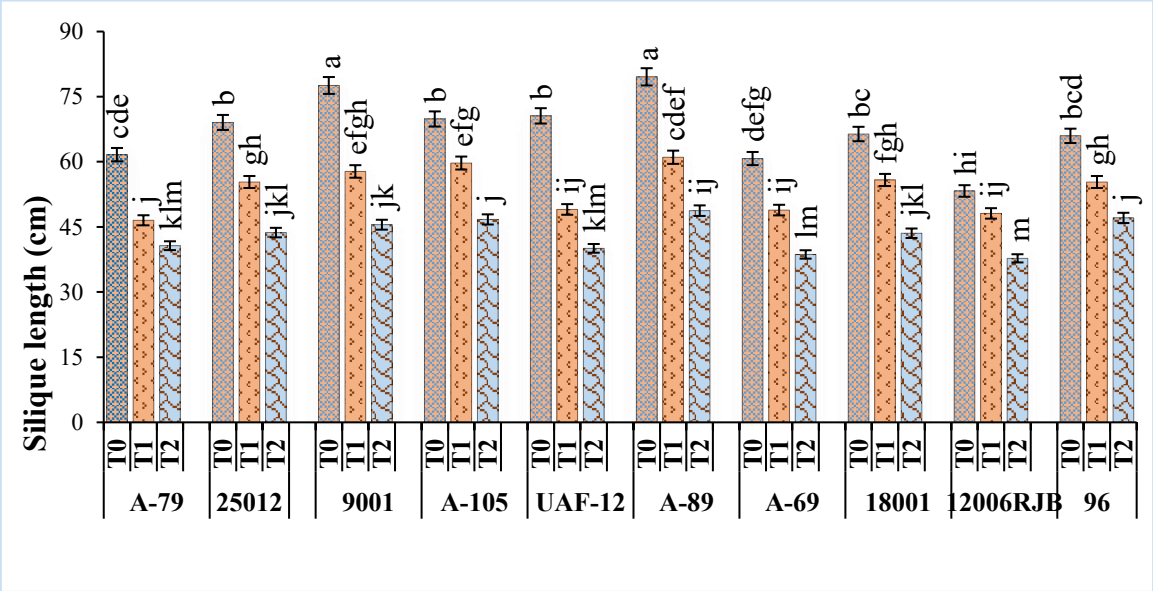


Figure 7. Effect of water regime on silique length (cm) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

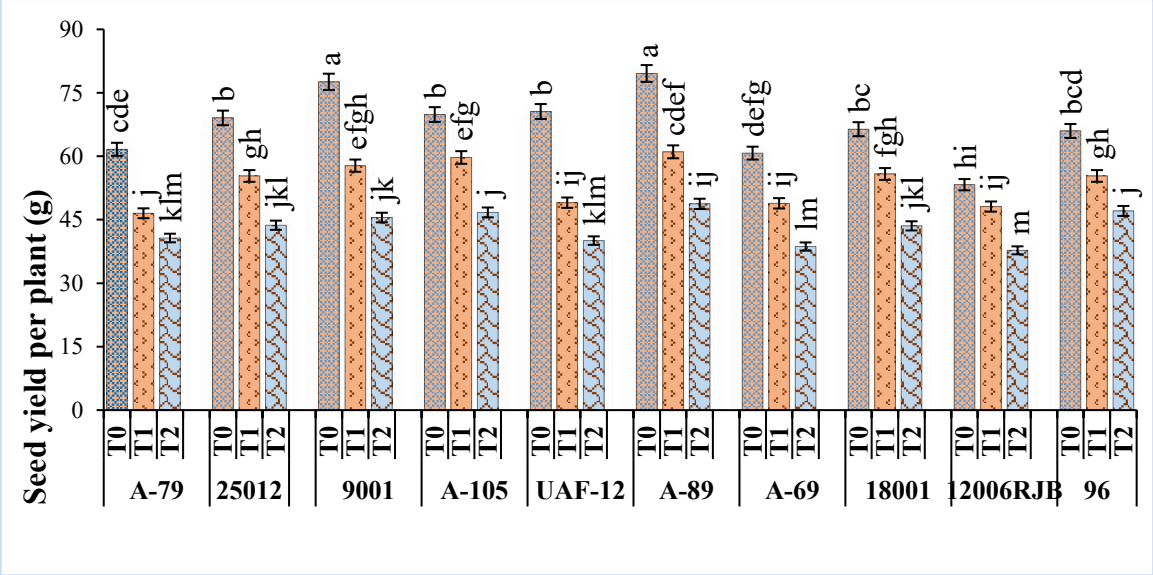


Figure 8. Effect of water regime on seed yield per plant (g) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

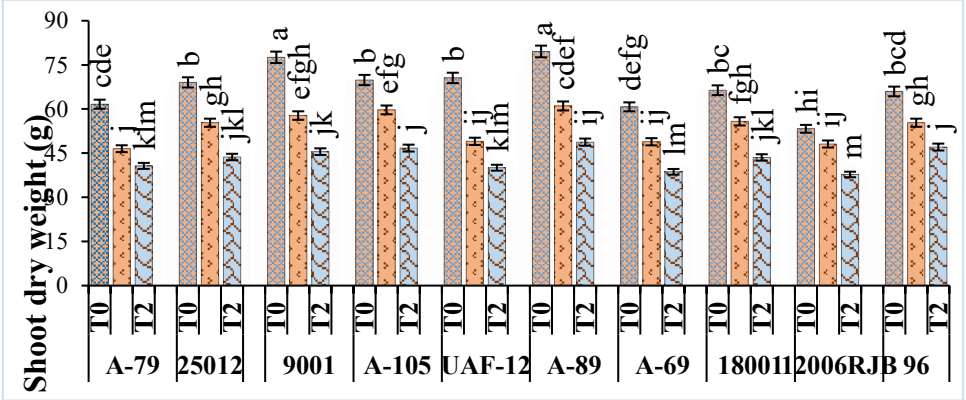


Figure 9. Effect of water regime on shoot dry weight (g) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

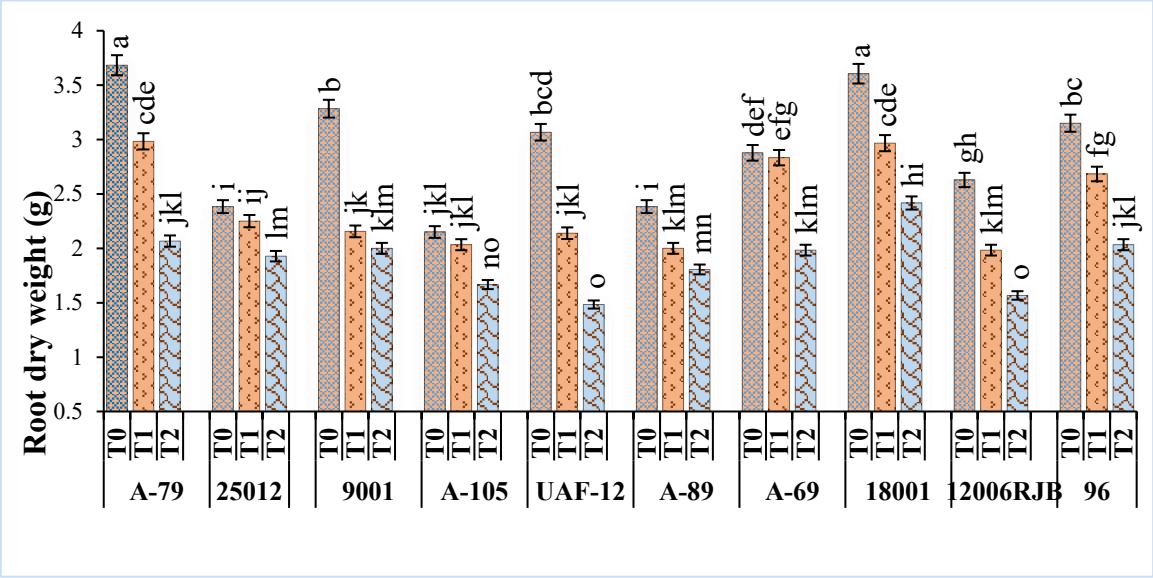


Figure 10. Effect of water regime on root dry weight (g) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

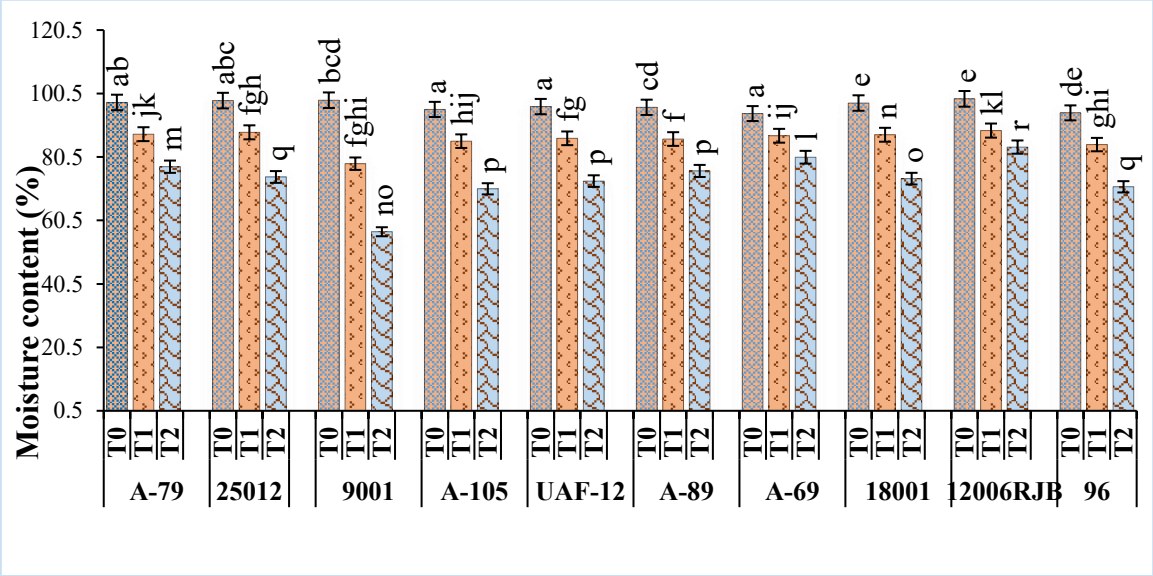


Figure 11. Effect of water regime on moisture content (%) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

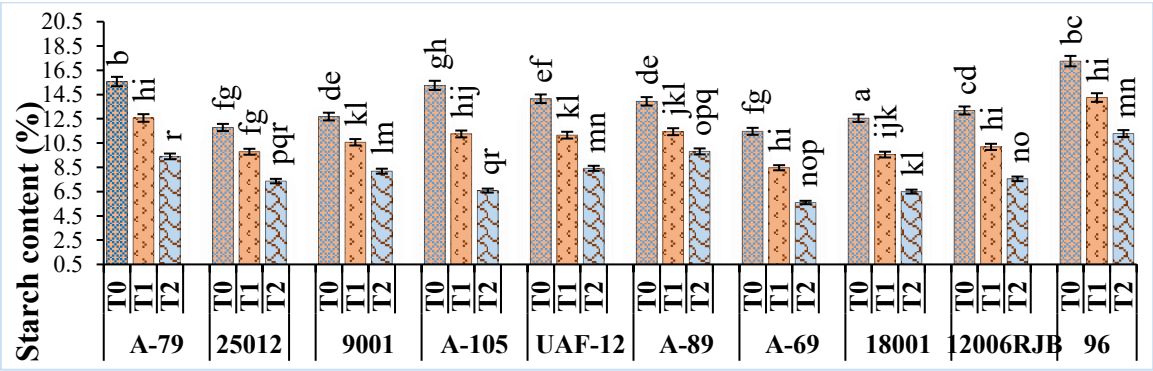


Figure 12. Effect of water regime on starch content (%) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

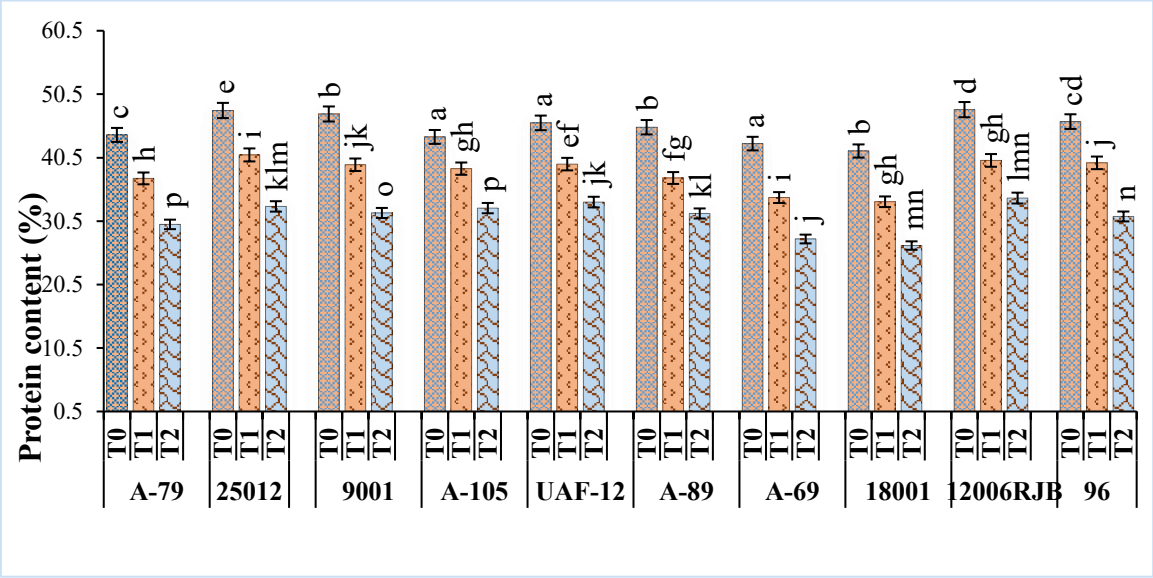


Figure 13. Effect of water regime on protein content (%) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

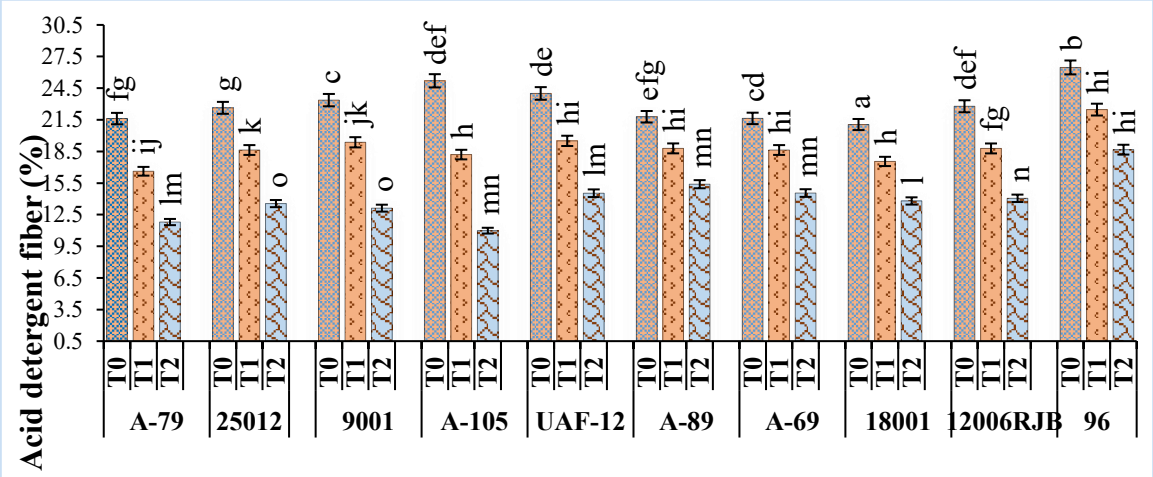


Figure 14. Effect of water regime on acid detergent fiber (ADF, %) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

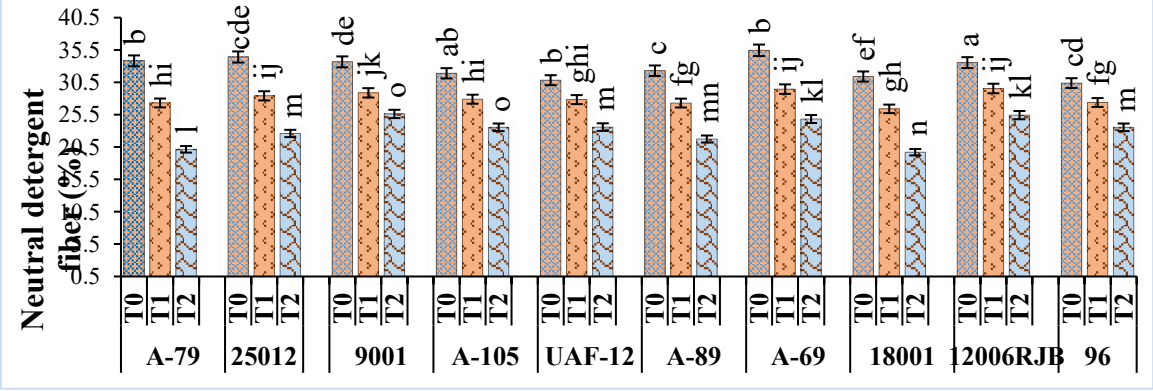


Figure 15. Effect of water regime on neutral detergent fiber (NDF, %) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

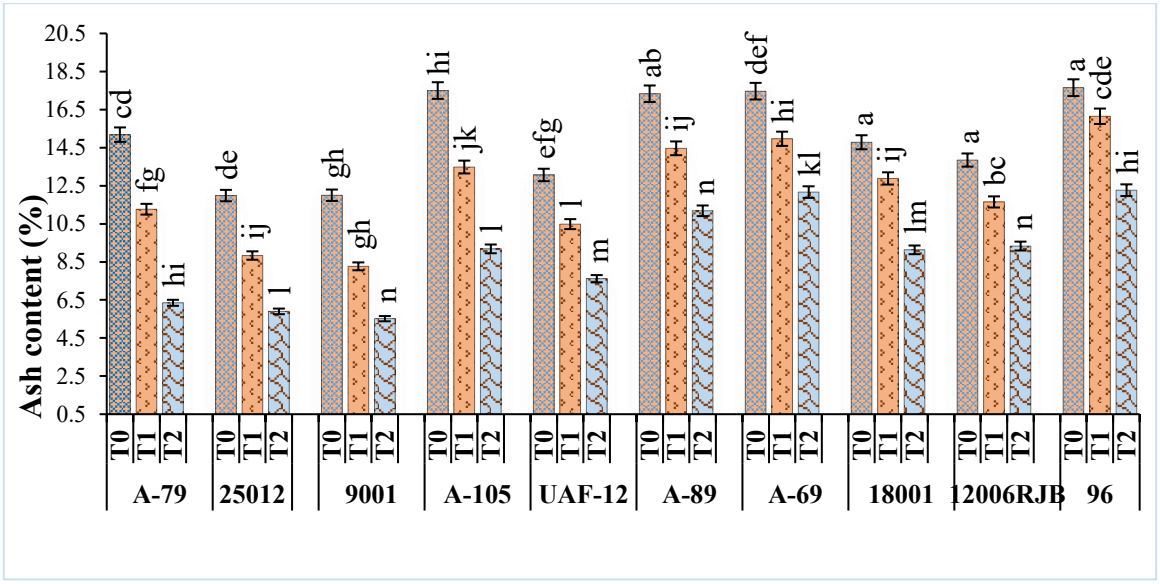


Figure 16. Effect of water regime on ash content (%) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

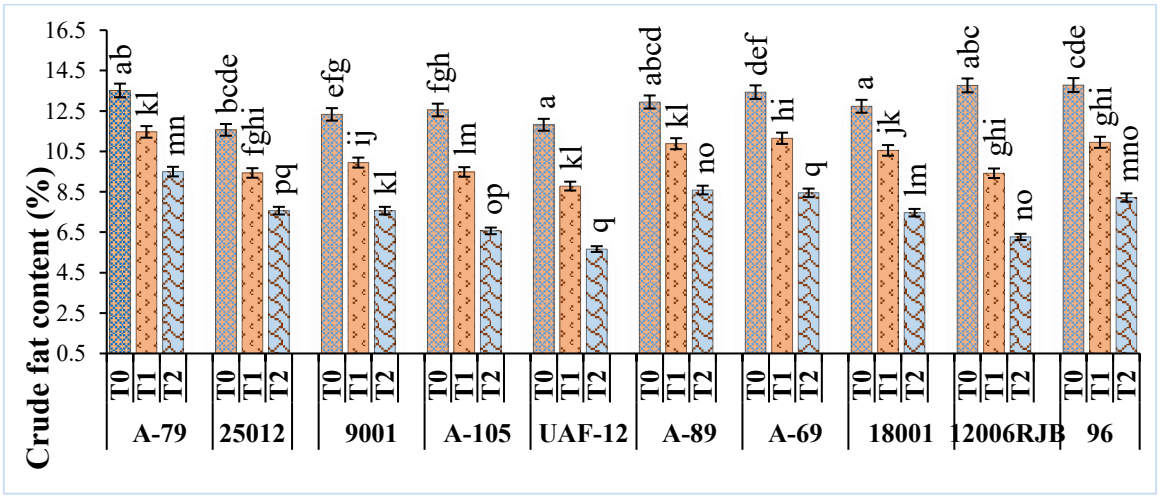


Figure 17. Effect of water regime on crude fat content (%) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

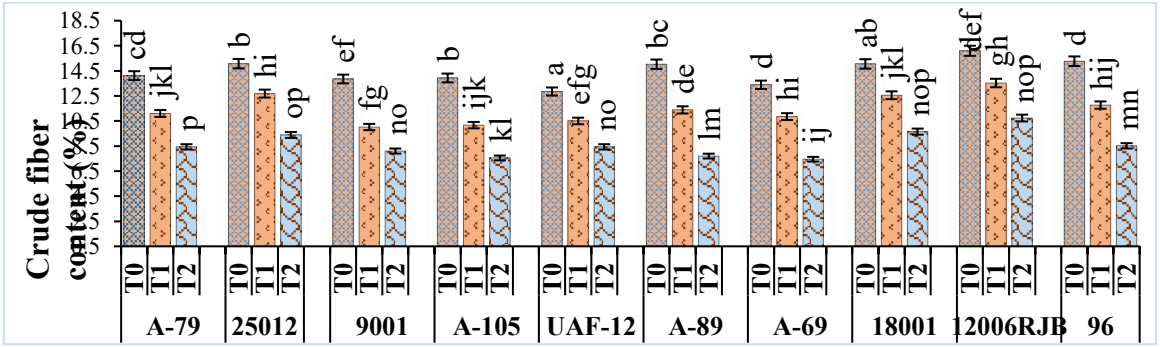


Figure 18. Effect of water regime on crude fiber content (%) of ten *Brassica* genotypes. To = 100% field capacity (FC), T1 = 50% FC, T2 = 25% FC.

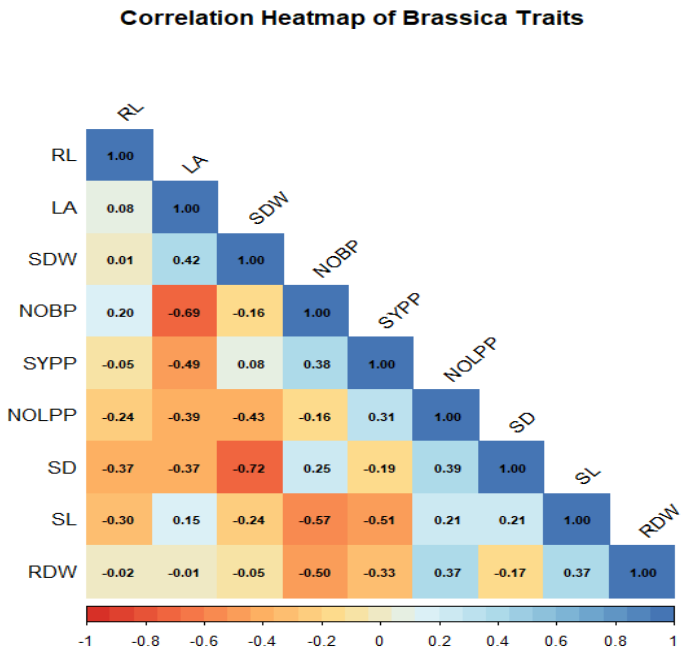


Figure 19.1. Heatmap of Pearson correlation coefficients among morphological traits of ten *Brassica* genotypes under control conditions (To, 100% FC).

Abbreviations: RL, root length; LA, leaf area; SDW, shoot dry weight; NOBP, number of branches per plant; SYPP, seed yield per plant; NOLPP, number of leaves per plant; SD, stem diameter; SL, silique length; RDW, root dry weight.

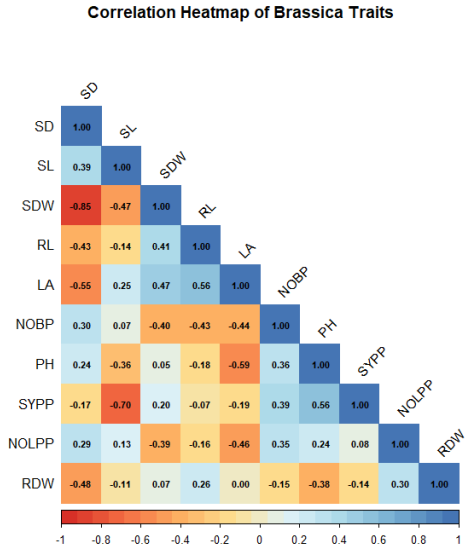


Figure 19.2. Heatmap of Pearson correlation coefficients among morphological traits of ten *Brassica* genotypes under T1 (50% FC).

Abbreviations: RL, root length; LA, leaf area; SDW, shoot dry weight; NOBP, number of branches per plant; SYPP, seed yield per plant; NOLPP, number of leaves per plant; SD, stem diameter; SL, silique length; RDW, root dry weight; PH, plant height.

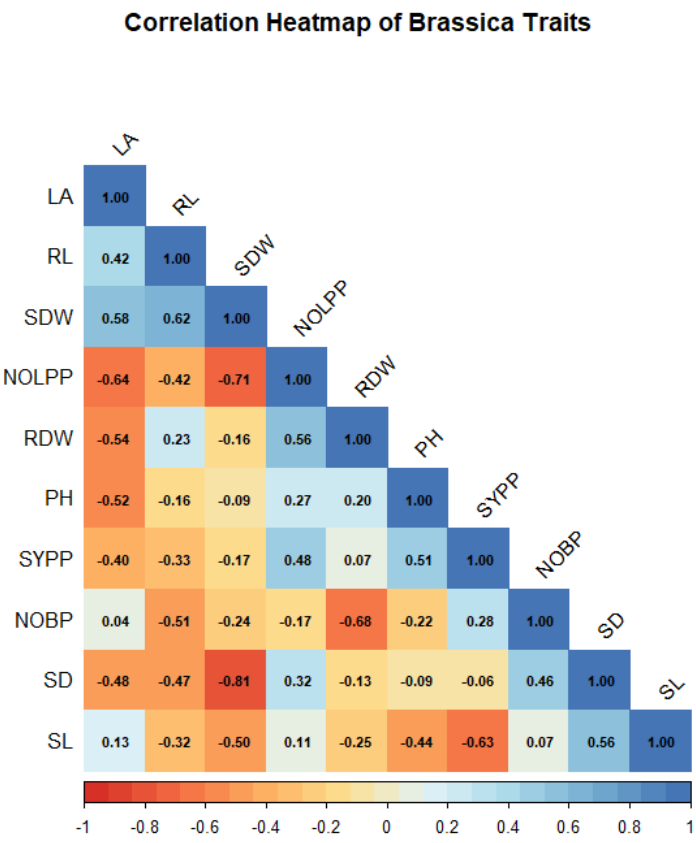


Figure 19.3. Heatmap of Pearson correlation coefficients among morphological traits of ten *Brassica* genotypes under T2 (25% FC).

Abbreviations: RL, root length; LA, leaf area; SDW, shoot dry weight; NOBP, number of branches per plant; SYPP, seed yield per plant; NOLPP, number of leaves per plant; SD, stem diameter; SL, silique length; RDW, root dry weight; PH, plant height.

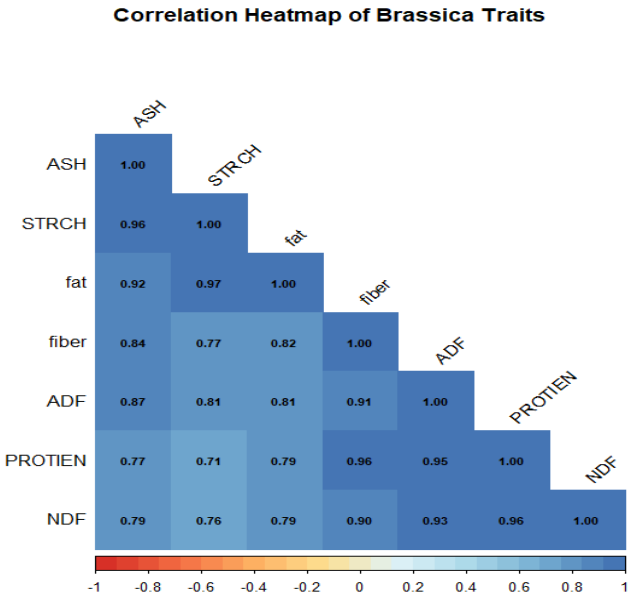


Figure 20.1. Heatmap of Pearson correlation coefficients among quality traits of ten *Brassica* genotypes under control conditions (To, 100% FC). Abbreviations: ASH, ash; STRCH, starch; fat, crude fat; fiber, crude fiber; ADF, acid detergent fiber; NDF, neutral detergent fiber; PROTIEN, protein.

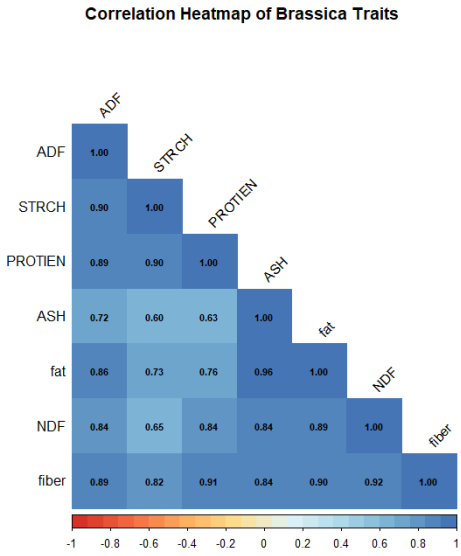


Figure 20.2. Heatmap of Pearson correlation coefficients among quality traits of ten *Brassica* genotypes under T1 (50% FC). Abbreviations as in Fig. 20.1.

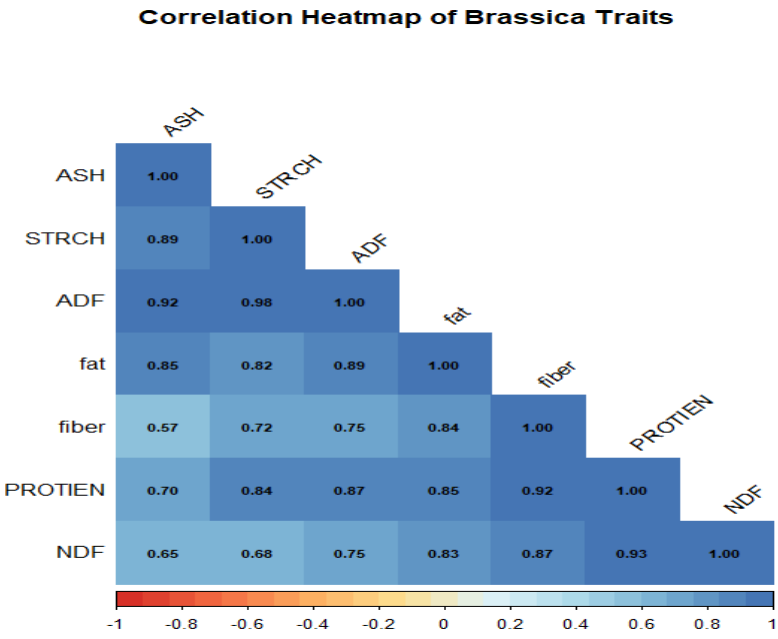


Figure 20.3. Heatmap of Pearson correlation coefficients among quality traits of ten *Brassica* genotypes under T2 (25% FC). Abbreviations as in Fig. 20.1.

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