



RESEARCH ARTICLE

Performance of ginger (*Zingiber officinale* Rosc.) varieties on yield, quality, incidence of shoot borer and rhizome rot in Alfisol of Nagaland

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Received: 07 December 2025; Accepted: 16 March 2026; Available online: Version 1.0: 14 May 2025

Cite this article: Ravi S, Graceli IY, Maiti CS, Ajeet K, Rishabh KS, Tsarili SI, Mili RM, Raj K. Performance of ginger (*Zingiber officinale* Rosc.) varieties on yield, quality, incidence of shoot borer and rhizome rot in Alfisol of Nagaland. Plant Science Today (Early Access). <https://doi.org/10.14719/pst.13113>

Abstract

A field trial entitled performance of ginger (*Zingiber officinale* Rosc.) varieties on yield, quality, incidence of shoot borer and rhizome rot in Alfisol of Nagaland with nine genotypes. Among all genotypes, Bhaise emerged as the top performer across various growth parameters, including plant height (PH) (61.8 cm), number of tillers (NT) (7.6) and number of leaves (NL) (21), with the highest values recorded in John ginger. In terms of yield, Bhaise consistently produced the highest yields/clump (135.99 g), yield per plot (YPP) (2.04 kg), projected yield/ha (10.19 t ha⁻¹) and weight of mother rhizome (WMR) (19.67 g). Quality assessments revealed that Nadia recorded the highest oleoresin (OLR) content (9.06 %), PGS 102 the highest crude fiber (CF) content (7.29 %) and John ginger the highest essential oil content (OC) (2.39 %). Mahima was found to have the highest dry recovery (RCV) percentage (25.7 %). Mahima showed the least susceptibility to rhizome rot and shoot borer among these genotypes. Genotypic correlation analysis revealed strong positive associations among PH, NT and yield traits. Yield per clump (YPC) showed a high positive correlation with YPP and projected yield per hectare (PYH). Principal component analysis (PCA) extracted five components, which cumulatively explained 93.73 % of the total variability. The first two components, principal component 1 (PC1) and PC2, accounted for 61.6 % of the variance. PC1 (42.12 %) was associated with PH, NT and yield attributes forming a yield vigour axis, while PC2 (19.54 %) represented quality traits such as oil content (OC). The PCA biplot grouped Bhaise, Gorubathani and Nadia on the positive side of PC1, whereas Mahima, John Ginger and Karbi Ginger clustered along PC2. These findings highlight the potential of high-yielding, high-quality lines for developing improved ginger cultivars under the Alfisol conditions of Nagaland.

Keywords: correlation; ginger genotypes; pest resistance; PCA; quality traits; yield

Introduction

Ginger (*Zingiber officinale* Rosc.) is an herbaceous perennial in the Zingiberaceae family and has been an important cash crop in India and China since ancient times. Ginger holds significant cultural and medicinal importance, known as Mahaoushadhi or great medicine in Ayurveda. It is utilized in various forms, including fresh, dried, preserved and processed products such as ginger powder, oil and oleoresin (OLR). India is a prominent producer of ginger, with the North Eastern Region (NER) contributing significantly to the national production (1). In 2023–24, ginger cultivation in India covered a total of 194,243 hectares, producing 2333000 metric tonnes. Among all states, Madhya Pradesh recorded the highest contribution with 36880 ha and 608318 MT of production, followed by Karnataka with 21344 ha and 232839 MT and Odisha with 19870 ha and 255660 MT. Other key producing regions include Assam (18346 ha; 174920 MT), West Bengal (12438 ha; 139537 MT), Maharashtra (9999 ha; 141727 MT) and Sikkim (15278 ha; 81818 MT). Northeastern states such as Meghalaya (10290 ha; 68628 MT), Mizoram (8713 ha; 60291 MT) and

Arunachal Pradesh (3433 ha; 59463 MT) also contributed significantly (2). The spice's economic importance stems from its diverse applications in the food, beverage and pharmaceutical industries. Two widely recognised Indian varieties, Cochin and Calicut ginger, are exported globally due to their superior quality. The spice is valued for its rich composition of carbohydrates, proteins, essential oils, resins and pungent compounds with zingiberene and phellandrene primarily contributing to its characteristic aroma and flavour (3). Despite its significance, ginger cultivation faces several challenges, particularly in India. A major constraint is the low productivity attributed to pest infestations and diseases, including rhizome rot, bacterial wilt and shoot borer infestations (4). The shoot borer (*Conogethes punctiferalis* Guenee) and rhizome fly (*Calobata indica*) are particularly detrimental, causing significant yield losses. Insect pests damage the pseudo stems and rhizomes, leading to reduced crop health and productivity. Reports indicate yield losses of up to 40 % due to shoot borer infestation in key ginger-growing regions such as Kerala (5). The limited genetic diversity of ginger, due to its vegetative propagation, further hinders the development of

resistant varieties. Although the NER of India, particularly states like Assam and Nagaland have emerged as a hub for organic ginger production (6). This research article aims to explore yield and quality, pest dynamics and disease challenges associated with ginger cultivation, while emphasizing suitable varieties for cultivation in Nagaland.

Materials and Methods

The research trial entitled performance of ginger (*Zingiber officinale* Rosc.) varieties on yield, quality, incidence of shoot borer and rhizome rot in Alfisol of Nagaland was conducted at the experimental farm of the Horticulture Department, School of Agricultural Sciences, Nagaland University, Medziphema Campus. The site is situated at an altitude of 360 m above mean sea level (MSL) with geographical coordinates of 25°45' N latitude and 93°53' E longitude. The experimental site experiences a humid subtropical climate with moderate temperatures ranging from 28 °C to 32 °C during summer and 10 °C to 15 °C during winter. The area receives an annual rainfall of 2000–2500 mm, primarily between June and July. The soil in the experimental field is sandy loam with moderate fertility.

The initial physicochemical properties of the soil were analyzed, with a soil reaction pH of 5.2 measured using a glass-electrode pH meter (7). Available nitrogen was recorded at 168.1 kg Nitrogen (N) ha⁻¹ using the alkaline permanganate method (8), available phosphorus was 26.8 kg phosphate (P₂O₅) ha⁻¹ as determined by Olsen's method (9) and available potassium was 145.6 kg potash (K₂O) ha⁻¹ measured using the neutral ammonium acetate method (7). The experiment was laid out in a randomized block design (RBD) with 3 replications, yielding a total of 27 plots (9 varieties × 3 replications). Nine ginger varieties were tested T₁ Gorubathani (Spices Research Centre, Sikkim), T₂ John ginger (IISR, Kozhikode), T₃ Nadia (AICRP, Spices, Medziphema, Nagaland), T₄ Mahima (IISR, Kozhikode), T₅ PGS 95 (High Altitude Spices Research Station, OUAT, Pottangi), T₆ PGS 102 (HASRS, OUAT, Pottangi), T₇ PGS 125 (HASRS, OUAT, Pottangi), T₈ Karbi Ginger (AICRP, Spices, Medziphema, Nagaland) and T₉ Bhaise (UBKV, Cooch Behar, W.B.). Each plot measured 2.0 m x 1.0 m, with a row-to-row distance of 30 cm and a plant-to-plant distance of 25 cm. The land was applied with FYM (20 t ha⁻¹) and mixed into the soil during land preparation. Recommended dose of NPK (100:50:50 kg NPK ha⁻¹) was applied and cultivation practices were followed as per the recommended package of practices. Earthing up was done to cover exposed rhizomes as and when necessary. The crop was irrigated once a month during the dry period. The crop was kept weed-free and timely plant protection measures were taken to manage pests and diseases. Plant morphology and yield attributing characters were recorded from the pre-tagged five plants selected from each plot and the mean data were recorded for further analysis. The observations for the growth characters of the plants, viz., plant height (PH), number of tillers (NT) and number of leaves (NL), were recorded at critical growth stages, i.e., 90 and 120 days after sowing (DAS) and leaf area (LA) was recorded at 120 and 150 DAS. Plant heights were measured using a scale from ground level to the terminal apex and the NT per tagged plant was counted. The mean number of tagged plants per plot was calculated. Leaf area was calculated using the laser Leaf Area Meter and the values were expressed in cm². The weight of the mother rhizome (WMR) and the yield per clump (YPC) were measured by using a weighing balance.

The yield of rhizomes per plot was recorded as the weight of fresh rhizomes harvested from each plot (kg). Per-hectare yield of the different genotypes was estimated in (t ha⁻¹) on the basis of the plot yield recorded for each genotype by using the following formula:

Yield per hectare (t ha⁻¹) =

$$\frac{\text{Yield per plot (kg)}}{\text{Area of plot (m}^2\text{)}} \times 10000 \quad (\text{Eqn. 1})$$

Estimation of quality parameters of ginger

Extraction of ginger oil

Fresh ginger oil was extracted using the modified Clevenger's method, as described in the Official Methods of Analysis (10). Two hundred grams of fresh ginger were ground using a mortar and pestle. Then it was transferred to the apparatus and 500 mL of distilled water was added. It took 6 hr to extract the fresh ginger oil for each sample. The percentage of extracted oil was measured as the volatile oil (mL) per sample weight (g) using the following formula

Fresh ginger oil (%) =

$$\frac{\text{Volume of oil extracted (mL)}}{\text{Volume of sample taken for extraction (g)}} \times 100 \quad (\text{Eqn. 2})$$

Estimation of oleoresin content

For the estimation of OLR content (%), dry ginger OLR was extracted using the "Soxhlet extraction" method. 10 g of finely ground powdered ginger was put into the titration pipette. 50 mL of acetone was added and kept overnight. The extract was drained into the beaker, which had already been weighed. Afterward, 30 mL of acetone was added and the mixture was kept for 1 hr, then placed in the oven for 2 hr to evaporate the acetone. The weight was immediately taken after it was taken out of the oven (11). The percentage of non-volatile ether extract was taken as the OLR content and calculated using the following formula:

% Oleoresin =

$$\frac{\text{Mass of non-volatile - Mass of empty beaker}}{\text{Mass of ginger sample taken}} \times 100 \quad (\text{Eqn 3})$$

Determination of fiber content

To determine the fiber content (%) in rhizomes, Liebig's digestion apparatus was used. 2 g of fine powdered ginger was put into a beaker and 200 mL of 1.25 % sulfuric acid (H₂SO₄) was added. Then it was boiled for 30 min in the digestion bench. The contents of the beaker were then filtered through a muslin cloth and the residue was washed thoroughly with distilled water until the pH was neutralized. pH paper was used to check the pH while washing the residue. After washing, the residue was transferred to the beaker and 200 mL of 1.25 % sodium hydroxide (NaOH) was added. Again, it was boiled for 30 min in the digestion bench and the contents were again filtered and washed. The residue was then transferred to the Gooch crucible, which had already been weighed and it was oven-dried for 1 hr. After it had been oven-dried, the weight was taken. Then the sample is kept in a muffle furnace for 20 min to obtain the ash content. The crucible is cooled and the weight was taken (12). The fiber content was calculated using the following formula:

$$\% \text{ Fiber} = \frac{(W_1 - W_b) - (W_2 - W_b)}{W_s} \times 100 = \frac{W_1 - W_2}{W_s} \times 100$$

(Eqn. 4)

Where W_1 = weight of dried residue (crucible + residue after drying) (g)

W_2 = weight of crucible + ash (after muffle-furnace ignition) (g)

W_b = weight of the empty crucible (g)

W_s = weight of the original sample taken (g)

To estimate dry matter content in ginger, 100 g of freshly harvested, cleaned ginger was weighed, cut into small slices, dried in an oven at 60 °C for 24 hr, then removed and weighed on a weighing machine. The value was converted to percent dry recovery.

Shoot borer infestation

The tillers infested by shoot borer (withered and dried shoots or dead heart) were identified and the NT infested was counted in each plot and expressed as a percentage of infestation per plot at 120 and 150 days after planting. For rhizome rot incidence, the disease incidence (DI) was calculated using the standardized formula (13).

Disease Incidence (DI) =

$$\frac{\text{Number of infected plants}}{\text{Total number of plants}} \times 100$$

(Eqn. 5)

Disease severity was assessed by calculating the percent disease index (PDI) using the standard score chart for rhizome rot of ginger. The disease scoring was performed using the method proposed by (14).

Data analysis

The data recorded for various parameters were analyzed according to the RBD design suggested by (15). The results have been interpreted based on the 'F' test value and the critical difference (CD) was calculated at the 5 % level of significance. The standard error of mean (SE ± m) and critical difference (C.D. at the rate 5 %) for comparing the mean of any two treatments were computed as follows. The statistical analysis was done using R software (version 4.5.0). The 'ggplot2' and 'factoextra' packages were used for Correlation and PCA analysis (16).

Results and Discussion

Growth attributes

The data of growth parameters are mentioned in Table 1, showing significant variation in among genotypes. At 90 and 120 DAS, maximum PH was recorded in Bhaise (42.19 cm and 61.80 cm at 90 and 120 DAS, respectively), followed by Gorubathani (41.59 cm, 61.40 cm) and Nadia (41.49 cm, 57.27 cm). The lowest PH was consistently recorded in Karbi Ginger (32.39 cm and 30.80 cm). Variation in PH among genotypes can be attributed to their differential genotypic responses to environmental conditions and soil fertility under Alfisol soils. Similar trends were earlier reported by (17). The superior performance of Bhaise, Gorubathani and Nadia aligns with findings of earlier studies (18, 19), confirming their adaptability and growth potential across varied agro-climatic conditions. The NT per plant differed significantly among genotypes at both 90 and 120 DAS. At 90 DAS, Bhaise produced the highest NT (5.83), followed by Gorubathani (4.83) and Nadia (4.25). The lowest tiller count was observed in Karbi Ginger (2.46). At 120 DAS, both Bhaise and Gorubathani recorded the highest NT (7.60), while PGS 102 (4.40) and Karbi Ginger (4.33) recorded the lowest. These results corroborate earlier reports (20, 21). At 120 DAS, John Ginger exhibited the highest NL (21), followed by Mahima (20) and Nadia (18), while Gorubathani had the lowest (13). The variation in leaf number may be attributed to genotypic potential and adaptation to Alfisol soil conditions (22, 23). At 150 DAS, Gorubathani exhibited the maximum LA (28.80 cm²), followed by John Ginger (26.06 cm²) and Karbi Ginger (25.45 cm²), while PGS 95 recorded the lowest (17.69 cm²). Larger LA contributes to greater photosynthetic capacity and, consequently, higher biomass accumulation. Similar results were obtained in earlier studies, indicating genetic and environmental influences on leaf development among ginger genotypes (24–27).

Yield attribute

The yield attribute data are presented in Table 2 showing significant variation among genotypes. The highest YPC was recorded in Bhaise (135.99 g), followed by Gorubathani (127.57 g) and Nadia (122.19 g), while the lowest was found in Karbi Ginger (72.49 g) and Mahima (87.07 g). The superior performance of Bhaise may be attributed to its vigorous growth, higher tiller number and better LA contributing to photosynthetic efficiency. Yield per plot (YPP) followed a similar pattern, with Bhaise (2.04 kg), Gorubathani (1.91 kg) and Nadia (1.83 kg) outperforming others, while Karbi Ginger (1.09 kg) and Mahima (1.31 kg) yielded the least. The projected yield per hectare (PYH) also recorded significant differences with Bhaise (10.19 t ha⁻¹),

Table 1. Growth parameters of different genotypes of ginger at different growth stages

Treatment	Plant height (cm)		Number of tillers		Number of leaves		Leaf area (cm ²)	
	90 DAS	120 DAS	90 DAS	120 DAS	90 DAS	120DAS	120 DAS	150 DAS
T1 (Gorubathan)	41.59	61.4	4.83	7.6	8	13	25.02	28.8
T2 (John ginger)	34.69	50	3.46	5.2	13	21	22.28	26.06
T3 (Nadia)	41.49	57.27	4.25	6.33	11	18	21.02	24.8
T4 (Mahima)	35.09	56.37	4.04	5.8	12	20	20.47	24.25
T5 (PGS 95)	34.49	48.97	3.83	4.83	9	14	13.91	17.69
T6 (PGS102)	32.79	38.2	4.04	4.4	12	18	16.58	20.36
T7 (PGS 125)	40.59	51.53	3.83	5.27	8	16	18.43	22.21
T8 (Karbi ginger)	32.39	30.8	2.46	4.33	11	16	21.67	25.45
T9 (Bhaise)	42.19	61.8	5.83	7.6	10	19	18.11	21.89
C.D. at 5 %	1.752	2.131	0.196	0.261	0.449	0.854	0.912	1.3
SE±(m)	0.579	0.705	0.065	0.086	0.149	0.282	0.302	0.43
SE(d)	0.819	0.997	0.091	0.122	0.21	0.399	0.426	0.608
C.V.	2.694	2.408	2.756	2.619	2.465	2.839	2.649	3.169

C.D. at 5 %: Critical difference at 5 % level of significance; C.V.: Coefficient of variation; SE(d): Standard error of the difference; SE(m): Standard error of the mean

Table 2. Yield and biochemical parameters of different genotypes of ginger

Treatment	Yield/clump (g)	Yield/plot (kg)	Projected yield ha ⁻¹ (t)	Weight of mother rhizome (g)	Oil content (%)	Crud Fiber (%)	Oleoresin (%)	Dry recovery (%)
T1 (Gorubathan)	127.57	1.91	9.56	12.03	2.26	6.00	2.6	20.3
T2 (John ginger)	89.89	1.35	6.74	8.59	2.39	6.58	4.99	17.4
T3 (Nadia)	122.19	1.83	9.16	18.78	1.93	4.52	9.06	24
T4 (Mahima)	87.07	1.31	6.53	11.58	2.29	5.55	4.08	25.7
T5 (PGS 95)	89.33	1.34	6.70	14.2	2.01	6.84	3.46	16.8
T6 (PGS102)	117.25	1.76	8.79	16.92	2.19	7.29	4.03	23.7
T7 (PGS 125)	121.64	1.83	9.12	12.45	2.04	6.25	3.27	19.2
T8 (Karbi ginger)	72.49	1.09	5.43	9.02	2.04	5.24	5.6	18.5
T9 (Bhaise)	135.99	2.04	10.19	19.67	1.937	5.79	6.81	17.4
C.D at 5 %	3.76	0.086	2.631	0.689	0.084	0.222	0.255	0.819
SE±(m)	1.244	0.029	0.87	0.228	0.028	0.073	0.084	0.271
SE(d)	1.759	0.04	1.231	0.322	0.039	0.104	0.119	0.383
C.V.	2.012	3.083	1.877	2.882	2.284	2.464	2.658	2.066

C.D. at 5 %: Critical difference at 5 % level of significance; C.V.: Coefficient of variation; SE(d): Standard error of the difference; SE(m): Standard error of the mean

Gorubathani (9.56 t ha⁻¹) and Nadia (9.16 t ha⁻¹). These findings agree with reports of previously conducted studies, which found that yield variation among genotypes can be attributed to genetic factors, soil characteristics and agro-climatic conditions (17, 28, 29). The enhanced performance of local genotypes under standardised management practices highlights favorable genotype-by-environment interactions (29–31). Variation in the WMR among genotypes was statistically significant. Bhaise (19.67 g) recorded the highest value, followed by Nadia (18.78 g), PGS 102 (16.92 g) and PGS 95 (14.20 g), while John Ginger recorded the lowest (8.59 g). This parameter reflects the genotype's ability to store reserves and is closely associated with total yield performance.

Quality parameters

Significant differences in biochemical quality traits, dry recovery, OLR, crude fibre and essential OC were observed among genotypes (Table 2). The highest dry recovery (RCV) was recorded in Mahima (25.7 %), followed by Nadia (24.0 %) and PGS 102 (23.8 %), while PGS 95 had the lowest (16.8 %). These results align with findings of earlier investigations (29, 32). Oleoresin content varied significantly, with Nadia (9.06 %) showing the highest concentration, followed by Bhaise (6.81 %) and Karbi Ginger (5.60 %), while Gorubathani (2.60 %) and PGS 125 (3.27 %) had the lowest. Crude fibre was maximum in PGS 102 (7.29 %), followed by PGS 95 (6.85 %) and John Ginger (6.59 %). Oil content was highest in John Ginger (2.39 %), followed by Mahima (2.30 %) and Gorubathani (2.26 %), while Nadia (1.93 %) and Bhaise (1.94 %) recorded the lowest values. The variability in quality traits can be attributed to genotypic diversity and environmental

influences such as soil moisture, temperature and nutrient availability, as reported by (33, 34). Genotypes with higher dry matter content often exhibit superior dry recovery, while those rich in volatile oils and OLRs are preferred for processing and medicinal applications.

Pest and disease incidence

At 150 DAS, Nadia exhibited the highest rhizome rot incidence (55.69 %), followed by PGS 95 (50.36 %) and Bhaise (49.03 %), whereas Mahima recorded the lowest (37.69 %) (Table 3). Regional variation in rhizome rot severity has been previously reported (35), with tolerant genotypes such as Suprabha and Himachal Pradesh identified in Karnataka (36) and Maran reported from Kerala (37, 38). Mahima showed relative tolerance among these genotypes, indicating potential for use in resistance breeding programs. Shoot borer incidence varied significantly among genotypes, PGS 125 (35.50 %) and PGS 102 (34.50 %) showing the highest infestation, while Mahima recorded the lowest (18.89 %). The low infestation in Mahima suggests potential resistance mechanisms that can be exploited in integrated pest management and breeding programs. These results corroborate the findings of (39, 40). None of the evaluated genotypes exhibited complete resistance to rhizome rot or shoot borer infestation. However, Mahima consistently exhibited lower disease severity and reduced shoot borer incidence, indicating greater tolerance among the genotypes. So, certain genotypes with relatively lower susceptibility may serve as potential candidates for cultivation in disease-prone areas when integrated disease and pest management strategies are adopted

Table 3. Severity and incidence of diseases and pests in ginger

Treatment	Severity of rhizome rot (PDI)		Shoot borer incidence (%)	
	120 DAS	150 DAS	120 DAS	150 DAS
T1 (Gorubathan)	29.69	42.36	24.23	28.3
T2 (John ginger)	31.69	48.36	23.65	27.5
T3 (Nadia)	43.02	55.69	22.5	25.6
T4 (Mahima)	25.02	37.69	16.35	18.89
T5 (PGS 95)	40.35	49.03	28.5	31.32
T6 (PGS102)	35.36	50.36	30.2	34.5
T7 (PGS 125)	23.02	45.69	32.5	35.5
T8 (Karbi ginger)	24.11	40.78	25.3	27
T9 (Bhaise)	36.36	49.03	20.25	23.25
C.D at 5 %.	1.451	1.564	1.217	1.504
SE±(m)	0.48	0.517	0.403	0.497
SE(d)	0.678	0.732	0.569	0.703
C.V.	2.591	1.925	2.808	3.079

C.D. at 5 %: Critical difference at 5 % level of significance; C.V.: Coefficient of variation; SE(d): Standard error of the difference; SE(m): Standard error of the mean

Correlation analysis

To assess the degree of interrelationship among various traits, the study of correlation coefficients is an important tool for establishing an effective selection criterion. Such information is valuable for predicting correlated responses to direct selection and for implementing indirect selection strategies. In the present investigation, correlation coefficients were computed among 16 traits at the genotypic level (Table 4). Genotypic correlation analysis revealed that PH at 90 DAS was positively associated with PH at 120 DAS (0.814), NT at 90 DAS (0.735) and 120 DAS (0.852), LA at 120 DAS (0.262) and 150 DAS (0.262), YPC (0.821), YPP (0.821), PYH (0.821), WMR (0.488) and OLR content (0.265). In parallel, PH at 120 DAS showed positive associations with NT at 90 DAS (0.804) and 120 DAS (0.879), NL at 120 DAS (0.054), LA at 120 DAS (0.214) and 150 DAS (0.214), YPC (0.612), YPP (0.610), PYH (0.612), WMR (0.371), OLR (0.102) and RCV (0.084).

Moreover, NT at 90 DAS exhibited positive correlations with NT at 120 DAS (0.847**), NL at 120 DAS (0.035), YPC (0.827**), YPP (0.826**), PYH (0.827**), WMR (0.708*), OLR (0.132) and RCV(0.043). Consistently, NT at 120 DAS correlated positively with LA at 90 DAS (0.412) and 120 DAS (0.412), YPC (0.688*), YPP (0.686*), PYH (0.688*), WMR (0.401), OLR (0.192) and RCV(0.011).

Further, the NL at 90 DAS showed positive associations with the NL at 120 DAS (0.826**), LA at 120 DAS (0.081) and 150 DAS (0.081), OC (0.419), OLR (0.379) and RCV(0.340). Likewise, the NL at 120 DAS was positively correlated with LA at 120 DAS (0.042) and 150 DAS (0.042), WMR (0.053), OC (0.289), OLR (0.448) and RCV (0.270).

Leaf area at 120 DAS was strongly and positively associated with LA at 150 DAS (0.971**) and also showed positive correlations with YPC (0.013), YPP (0.011), PYH (0.018), OC (0.444), OLR (0.080) and RCV (0.155).

Regarding yield attributes, YPC correlated positively with YPP (0.926**), PYH (0.987**), WMR (0.714*), OLR (0.150) and RCV (0.096). In turn, YPP was positively associated with PYH (0.913**), WMR (0.711*), OLR (0.152) and RCV (0.096). Projected yield per hectare also showed positive correlations with WMR (0.720*), OLR (0.150) and RCV(0.096). Finally, . At the same time, OC exhibited positive associations. The WMR was positively associated with OLR (0.505) and RCV (0.224). In contrast, OC was positively associated with crude fibre (0.390) and RCV (0.183). The consistently positive

genotypic correlations among early and mid-season vegetative traits (PH, NT and LA) and yield components indicate a largely reinforcing genetic architecture in which vigor-related traits co-vary with sink capacity (rhizome biomass) and scale predictably from clump to plot to projected hectare yield. In particular, the strong associations of tiller number (at 120 DAS) and PH with all three yield measures, together with the positive correlations between mother-rhizome weight and yield/quality attributes, suggest that indirect selection on these traits would be effective for simultaneous improvement of yield and processing-related quality (OLR, RCV). Such patterns are consistent with genetic correlation arising from pleiotropy or linkage disequilibrium among loci controlling vegetative growth, assimilate acquisition and partitioning to rhizomes. The positive association between fresh rhizome yield was positively and significantly correlated with rhizome thickness, NT, rhizome spread, PH, LA, OLR and leaf length. This was consistent with the earlier reports (41-43).

At the genotypic level, several vegetative, yield and quality traits exhibited negative correlations, suggesting potential trade-offs among canopy development, biomass allocation and phytochemical attributes. Specifically, PH at 90 DAS showed inverse associations with NL at 90 DAS (-0.575) and 120 DAS (-0.166), OC (-0.379), CF (-0.408) and RCV (-0.031). Likewise, PH at 120 DAS was negatively correlated with the NL at 90 DAS (-0.334), OC (-0.014) and crude fibre (-0.244). In a similar vein, the NT at 90 DAS showed negative relationships with the NL at 90 DAS (-0.312), LA at 90 DAS (-0.061) and at 120 DAS (-0.061), OC (-0.202) and crude fibre (-0.010). Consistently, the NT at 120 DAS was negatively associated with the NL at 90 DAS (-0.374) and 120 DAS (-0.067), OC (-0.103) and crude fibre (-0.372).

Turning to leaf traits, the NL at 90 DAS exhibited negative correlations with YPC (-0.441), YPP (-0.440), PYH (-0.442), WMR (-0.127) and crude fibre (-0.015). Similarly, the NL at 120 DAS was inversely correlated with YPC (-0.113), YPP (-0.111), PYH (-0.114) and crude fibre (-0.090). Moreover, LA at 120 DAS showed negative associations with the WMR (-0.440) and crude fibre (-0.495).

With respect to yield and quality attributes, YPC was negatively correlated with OC (-0.307) and crude fibre (-0.009); YPP showed the same pattern with OC (-0.309) and crude fibre (-0.009) and PYH likewise correlated negatively with OC (-0.307) and crude fibre (-0.008). In addition, the WMR was inversely associated with OC (-0.635) and crude fibre (-0.108). Among quality traits, OC was

Table 4. Correlation between yield and its attributing traits at the genotypic level in ginger

	PH 90	PH 120	NT 90	NT120	NL90	NL120	LA90	LA120	YPC	YPP	PYH	WMR	OC	CF	OLR	RCV
PH90	1.000	0.814**	0.735*	0.852**	-0.575	-0.166	0.262	0.262	0.821**	0.821**	0.821**	0.488	-0.379	-0.408	0.265	-0.031
PH120		1.000	0.804**	0.879**	-0.334	0.054	0.214	0.214	0.612	0.61	0.612	0.371	-0.014	-0.244	0.102	0.084
NT90			1.000	0.847**	-0.312	0.035	-0.061	-0.061	0.827**	0.826**	0.827**	0.708*	-0.202	-0.01	0.132	0.043
NT120				1.000	-0.374	-0.067	0.412	0.412	0.688*	0.686*	0.688*	0.401	-0.103	-0.372	0.192	0.011
NLV90					1.000	0.826**	0.081	0.081	-0.441	-0.44	-0.442	-0.127	0.419	-0.015	0.379	0.34
NLV120						1.000	0.042	0.042	-0.113	-0.111	-0.114	0.053	0.289	-0.09	0.448	0.27
LA90							1.000	0.971**	0.013	0.011	0.018	-0.44	0.444	-0.495	0.08	0.155
LA120								1.000	0.015	0.012	0.012	-0.44	0.445	-0.494	0.08	0.155
YPC									1.000	0.926**	0.987**	0.714*	-0.307	-0.009	0.15	0.096
YPPLT										1.000	0.913**	0.711*	-0.309	-0.009	0.152	0.096
PJY											1.000	0.720*	-0.307	-0.008	0.15	0.096
WMR												1.000	-0.635	-0.108	0.505	0.224
OC													1.000	0.39	-0.523	0.183
CF														1.000	-0.682*	-0.286
OLR															1.000	0.145
RCV																1.000

PH 90: Plant height at 90 DAS; PH 120: Plant height at 120 DAS; NT 90: Number of tillers at 90 DAS; NT 120: Number of tillers at 120 DAS; NL 90: Number of leaves at 90 DAS; NL 120: Number of leaves at 120 DAS; LA 90: Leaf area at 90 DAS; LA 120: Leaf area at 120 DAS; YPC: Yield clump⁻¹ (g); YPP: Yield plot⁻¹ (kg); PYH: Projected yield ha⁻¹ (t); WMR: Weight of mother rhizome (g); OC: Oil content (%); CF: Crude fiber (%); OLR: Oleo-resin (%); RCV: Dry recovery (%)

negatively correlated with OLR (-0.523), whereas crude fibre (%) was negatively associated with OLR (%) (-0.682*) and RCV (%) (-0.286). Taken together, these inverse genotypic correlations indicate that increases in certain vegetative or yield components may coincide with modest reductions in specific quality parameters (e.g., OC, crude fibre, or OLR), underscoring the importance of balanced selection indices that mitigate undesirable trade-offs while targeting overall genetic gain.

Principal component analysis of ginger genotypes

Principal Component Analysis (PCA) was done on different traits in 9 genotypes of ginger in this study. Table 5 shows the proportion of variance, cumulative proportion and eigenvalues. Principal Component Analysis (PCA) was performed to determine the relative contributions of different traits to the total genetic variability among the ginger genotypes. As shown in Table 5, five Principal Components (PCs) had eigenvalues greater than 1.00, accounting for a cumulative variance of 93.73 % across all variables studied. A similar result was reported by (42).

The PC1 had the highest eigenvalue (6.74) and explained 42.12 % of the total variation, indicating that it captured the largest proportion of genetic diversity among the genotypes. The PC2 accounted for 19.54 % of the total variation (eigenvalue: 3.13), followed by PC3 (15.30 %), PC4 (11.05 %) and PC5 (5.72 %). Principal Component Analysis effectively reduces data dimensionality by transforming interrelated variables into a smaller set of uncorrelated components while retaining most of the original information. This technique is widely used in multivariate genetic studies to identify the fewest PCs that explain most of the variability and to rank genotypes by their PC scores. In this study, the first few components, particularly PC1 and PC2, accounted for more than 60 % of the total

variance, indicating that these components are key to explaining the major differences among genotypes. The high variance in the first few PCs suggests that a small number of key traits predominantly govern genetic variability in ginger. Therefore, genotypes with contrasting loadings on the first two PCs can be considered divergent parents for hybridization, thereby increasing the probability of developing transgressive segregants in subsequent generations.

A scree plot Fig. 1 was constructed by plotting the eigenvalues against the corresponding PC numbers to illustrate the percentage of variance explained by each component. In the present study, the PC1 accounted for the greatest variability (42.1 %), with an eigenvalue of 6.74, followed by PC2 (19.5 %), PC3 (15.3 %) and PC4 (11.1 %). After the fourth component, the line on the scree plot formed a gentle curve that gradually flattened, indicating minimal contribution from subsequent components. This graphical trend shows that the first few PCs capture most of the genetic variation, whereas later components contribute little to the total variance. Such a pattern indicates that PC1 and PC2 are the most influential in explaining overall genotype diversity. The sharp decline after PC4 and the near-linear trend thereafter further confirm that the inclusion of additional components adds little explanatory power.

Table 6 presents 5 PCs and their factor loadings. In PC1, the highest positive loadings were for YPC (0.935), PYH (0.935), YPP (0.934) and key vigor traits PH at 90 DAS (PH90, 0.932), tillers at 90 DAS (NT90, 0.894) and tillers at 120 DAS (NT120, 0.854) with a notable contribution from mother-rhizome weight (WMR, 0.723). These results indicate that PC1 primarily represents a yield vigor axis. Traits with negative loadings on PC1 included NL at 90 DAS (NL90, -0.500) and OC (-0.409). In PC2, LA at 90 and 120 DAS (LA90, LA120, both

Table 5. Eigenvalues, percentage of variance and cumulative percentage of variance of ginger genotypes

	Eigenvalue	Percentage of variance (%)	Cumulative percentage of variance (%)
PC 1	6.74	42.12	42.12
PC 2	3.13	19.54	61.67
PC 3	2.45	15.30	76.96
PC 4	1.77	11.05	88.02
PC 5	0.92	5.72	93.73

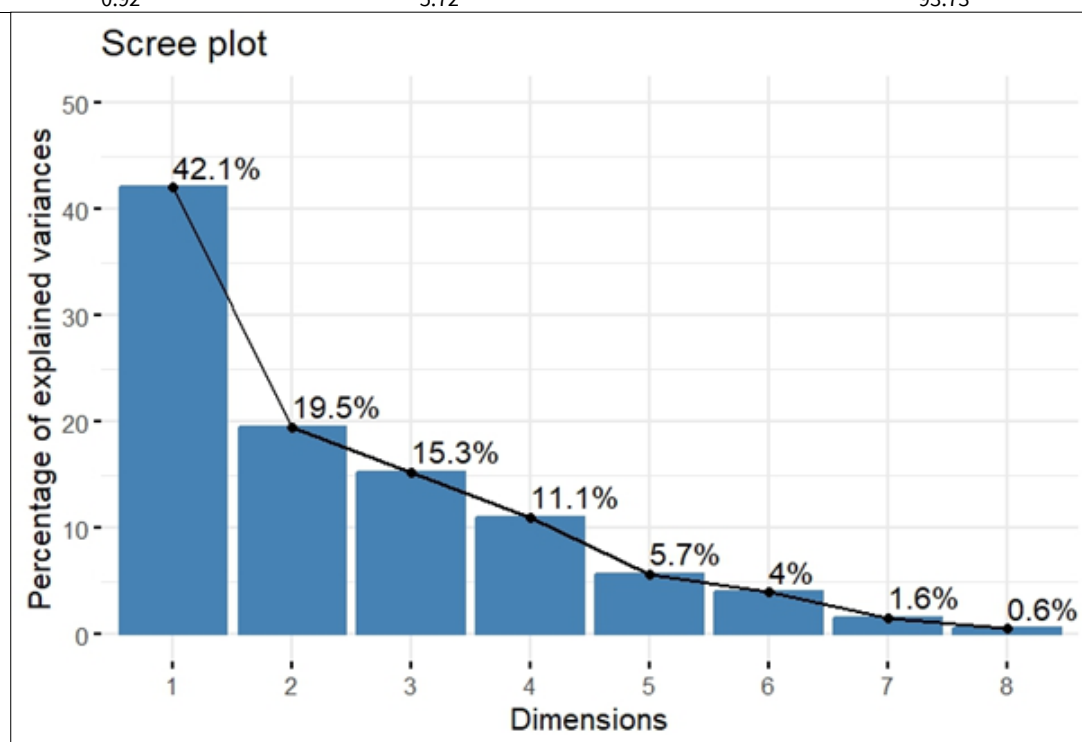


Fig. 1. Scree plot illustrates eigenvalue distribution across principal components.

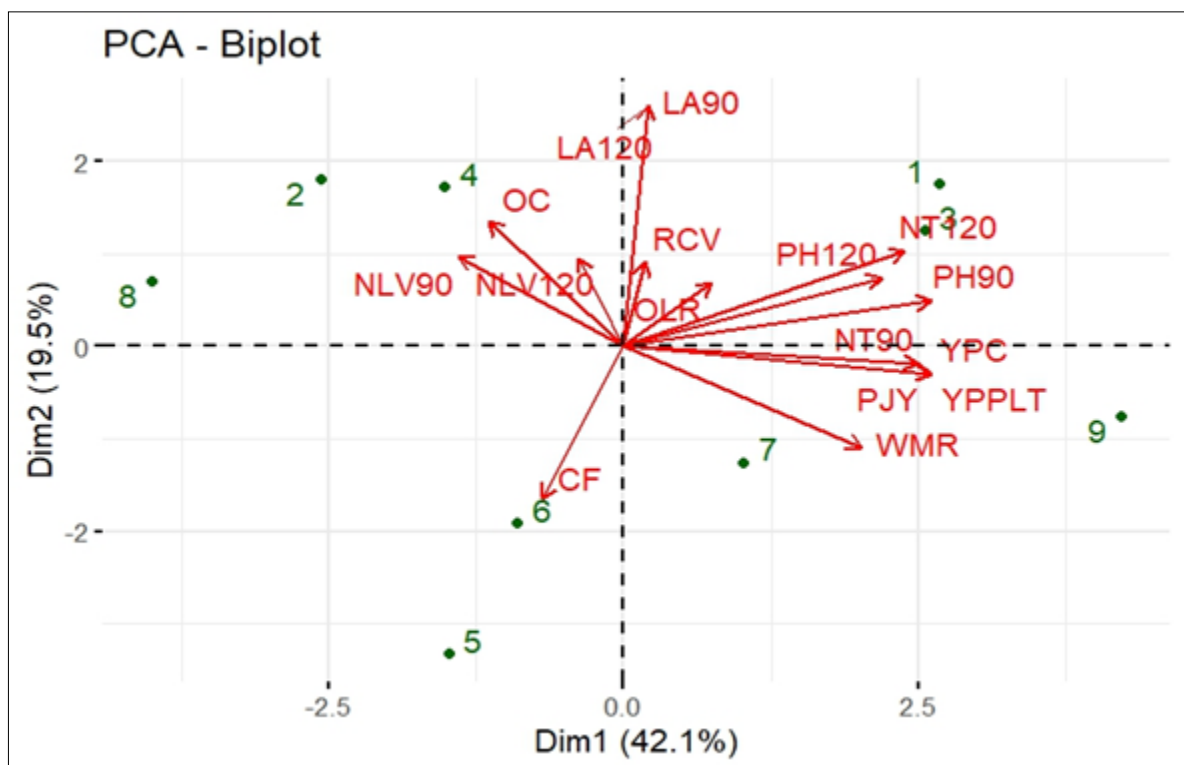
Table 6. Five principal components along with their factor loadings

	PC 1	PC 2	PC 3	PC 4	PC 5
PH90	0.932	0.177	-0.122	-0.179	-0.078
PH120	0.784	0.266	-0.116	0.174	-0.243
NT90	0.894	-0.065	0.025	0.301	-0.172
NT120	0.854	0.369	-0.155	0.015	-0.200
NL90	-0.500	0.343	0.654	0.406	-0.105
NL120	-0.136	0.341	0.678	0.480	-0.318
LA90	0.073	0.927	-0.280	-0.099	0.065
LA120	0.073	0.927	-0.280	-0.099	0.065
YPC	0.935	-0.106	-0.030	0.184	0.130
YPP	0.934	-0.108	-0.029	0.186	0.130
PJY	0.935	-0.106	-0.029	0.185	0.130
WMR	0.723	-0.390	0.522	0.040	0.121
OC	-0.409	0.482	-0.357	0.681	-0.007
CF	-0.245	-0.589	-0.361	0.642	-0.089
OLR	0.269	0.245	0.813	-0.367	-0.157
RCV	0.064	0.324	0.398	0.291	0.750

0.927) showed the largest positive loadings, followed by OC (0.482) and leaf numbers (NL90, 0.343; NL120, 0.341). Crude fiber (-0.589) and mother-rhizome weight (WMR, -0.390) loaded negatively, indicating a canopy development/LA axis inversely related to fiber and, to some extent, rhizome mass. PC3 was dominated by OLR (0.813) alongside leaf numbers (NL120, 0.678; NL90, 0.654), indicating a leafiness-OLR axis; several composition traits loaded negatively (e.g., OC, -0.357; CF, -0.361). PC4 captured rhizome composition, with strong positive loadings for OC (0.681) and CF (0.642) and moderate positive loadings for NL120 (0.480) and NL90 (0.406), while OLR had a negative loading (-0.367). Finally, PC5 was driven by RCV (0.750), with only minor contributions from other traits, indicating a post-harvest recovery axis largely independent of the preceding components. Taken together, the mixture of positive and negative loadings across PCs reveals contrasting correlation patterns between trait groups. Consequently, the traits loading most strongly and positively within each PC contributed most to the observed diversity and most clearly separated clusters of genotypes along those component axes (e.g., high-yield/vigorous types on PC1; broad-leaf, oil-rich types on PC2; OLR-rich, leafy types on PC3).

PCA biplot of 11 traits and 9 ginger genotypes

Principal Component 1 (42.1 %) and PC2 (19.5 %) were plotted against each other in a biplot to determine the relationships among ginger genotypes based on yield and associated traits (Fig. 2). Together, these components explained 61.6 % of the total variation among the studied genotypes. Genotypes and traits lying in the same quadrant and direction of the arrows are positively correlated, while those in opposite directions indicate negative associations. In the present study, PC1 was mainly influenced by PH (PH90, PH120), NT (NT90, NT120), YPC, YPP, PYH, and WMR traits that contribute significantly to yield and plant vigor. A similar result has been reported in another study (44). PC2 was primarily associated with LA at 90 and 120 DAS (LA90, LA120), OC and RCV, which represent canopy development and quality-related parameters. The biplot revealed that T₁, T₃ and T₉ were positioned on the right side, showing strong positive associations with yield-contributing traits such as PH, NT, YPC and WMR. Among these, T₃ appeared most prominently in the upper-right quadrant, near PH120 and NT120, indicating that it possessed superior PH and tiller number traits, which are directly linked to higher productivity. These genotypes, therefore, represent

**Fig. 2.** Biplot among 11 traits and 9 genotypes in ginger.

vigorous and high-yielding types. In contrast, T₂, T₄ and T₈ were placed on the left side, associated with LA (LA90, LA120) and OC, suggesting that they possess better canopy development and oil richness but relatively moderate yield potential. T₅ and T₆ were positioned in the lower-left quadrant, closer to CF, indicating higher fibre content and lesser association with yield traits. T₇, though near the yield vectors, was slightly displaced downward, indicating a moderate yield potential with good rhizome weight. Overall, the distribution pattern suggests that improvements in traits aligned with PC1 (PH, NT, YPC, WMR) would yield greater gains. Meanwhile, PC2 reflects variability in canopy and biochemical quality traits. Hence, crosses between high-yielding genotypes (T₁, T₃ and T₉) and oil-rich or canopy types (T₂, T₄ and T₈) could be strategically utilized to combine yield potential and quality traits in future ginger breeding programs.

Contribution of various yield and quality traits to the significant PCs was presented in the corplot Fig. 3. PC 1, explaining 42.12 % of the total variance, was mainly associated with PH (PH90, PH120), NT (NT90, NT120), YPC, YPP, PYH and WMR. PC 2, contributing 19.54 %, was influenced by LA (LA90, LA120) and OC. PC 3 explained 15.30 % of the variation and was governed by OLR and the NL (NL90, NL120). PC 4 and PC 5 were related to CF and RCV, respectively, indicating their roles in rhizome composition and processing efficiency.

Conclusion

The present study demonstrated substantial variability among ginger (*Zingiber officinale* Rosc.) genotypes grown under Alfisol conditions of Nagaland. Among the evaluated genotypes, Bhaise showed superior performance in growth and yield attributes, whereas Mahima exhibited comparatively lower susceptibility to rhizome rot and shoot borer infestation. Significant positive correlations between vegetative traits (PH and tiller number and

yield components highlight their potential as reliable indirect selection criteria for improving productivity. Principal Component Analysis further revealed that yield-vigor and canopy quality traits were the primary contributors to genetic variability among genotypes. The PCA biplot distinctly grouped Bhaise, Gorubathani and Nadia as high-yielding genotypes and Mahima, John Ginger and Karbi Ginger as quality-oriented lines. However, the study was conducted in a single location and during a single growing season, limiting the ability to draw broader inferences. Future research should focus on multi-environment validation, genotype × environment interaction studies and integration of molecular tools to identify markers associated with yield and pest resistance. Such approaches will accelerate the development of high-yielding, resilient and quality-rich ginger cultivars suitable for sustainable production in the Nagaland conditions.

Acknowledgements

The authors express their sincere gratitude to ICAR-All India Coordinated Research Project (AICRP) Nagaland Centre for facilitating the research work and financial assistance for publication and the Department of Horticulture School of Agricultural Sciences, Nagaland University for their invaluable assistance and providing the necessary facilities for carrying out this research.

Authors' contributions

RS carried out the field experiment. GY conducted the literature review and contributed to manuscript writing. CSM was involved in conceptualization, experimental design and data interpretation. AK handled the statistical analysis and data visualization. RKS performed the laboratory analyses and validated the results. ITS assisted with formatting and references, ensuring compliance with journal guidelines. MRM and RK reviewed and edited the manuscript. All authors read and approved the final manuscript.

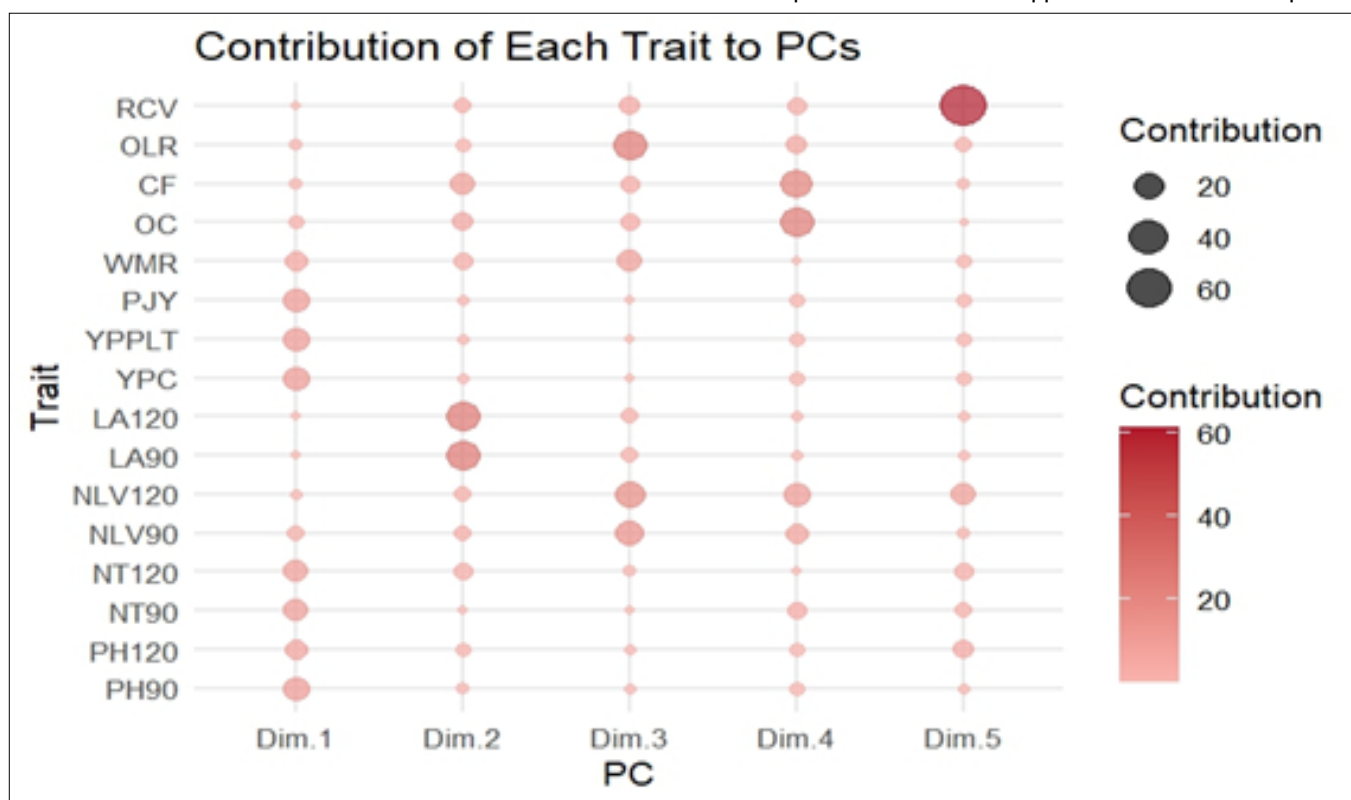


Fig. 3. Contribution of different traits to significant PC.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work, the authors used Grammarly to avoid grammatical mistakes. After using this tool/service, the authors reviewed and edited the content as needed and takes full responsibility for the content of the publication.

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Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

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