



**ARTICLE**

# Characterization and Genetic Diversity of Tea (*Camellia sinensis* (L.) O. Kuntze) Genotypes for Waterlogging Tolerance

Md. Riyadh Arefin<sup>1,2</sup>, Md. Sabibul Haque<sup>1</sup> and A. K. M. Golam Sarwar<sup>1,\*</sup>

<sup>1</sup>Department of Crop Botany, Bangladesh Agricultural University, Mymensingh, 2202, Bangladesh

<sup>2</sup>Botany Division, Bangladesh Tea Research Institute, Moulvibazar, 3210, Bangladesh

\*Corresponding Author: A. K. M. Golam Sarwar. Email: drsarwar@bau.edu.bd

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## ABSTRACT

Tea estates in Bangladesh are currently experiencing frequent waterlogging stress due to heavy rainfall or flooding under changing climate scenarios. The development of waterlogging-tolerant tea cultivars is, therefore, crucial for sustainable tea production with increased yield in waterlogging-affected areas. In this study, a total of two hundred tea genotypes were screened for waterlogging tolerance based on yield and quality potentials. Tea genotypes were raised at the nursery and evaluated with 13 traits at the seedling and mature stages. Descriptive and multivariate analysis of the recorded data of measured traits were performed for clustering the studied genotypes in relation to their yield and quality potential. The 200 tea genotypes were categorized into six clusters and the measured traits were classified into two groups. Cluster-5 comprised 46 closely related tea genotypes whereas other clusters-Cluster-1, 2, 3, 4, and 6 contained 39, 20, 24, 29, and 42 genotypes, respectively. PCA-biplot showed that the first two principal components (PC 1 and PC 2) cumulatively described 56.9% of total variations. From the genetic diversity analysis, the characteristics like green leaf yield (GLY), plucking points (PP), spreading of bush frame (SBF), plucking interval (PI), dormancy period (DR), black tea quality score (QSB), fermentation rate (SF) and number of pubescence (NP) exhibited high to moderate heritability, indicating to consider these traits as selection criteria for tea breeding program. The trait GLY showed a strong positive correlation with PP, and SBF and a negative association with PI and DR. The key quality trait, QSB had a positive correlation with SF and NP. Based on these studied descriptors, a total of 11 tea genotypes were selected, found potential for waterlogging tolerance, and can be considered for varietal improvement programs.

## KEYWORDS

Tea; genotypic diversity; waterlogging tolerance; qualitative traits; multivariate analysis

## Abbreviation

BTRI	Bangladesh Tea Research Institute
C	Cluster
DR	Number of Dormancy Periods
G	Group
GA	Genetic Advance
GAM	Genetic Advance as Percent of Mean



GCV	Genotypic Coefficient of Variation
GDP	Gross Domestic Product
GLY	Green Leaf Yield
$h^2b$	Heritability in Broad Sense
LB	Length of Bud
NF	Number of Flower
NP	Number of Pubescence of Leaf Bud
PC	Principal Component
PCA	Principal Component Analysis
PCV	Phenotypic Coefficient of Variation
PI	Number of Days of Plucking Interval
PP	Number of Plucking Points
Q1	First Quartile
Q3	Third Quartile
QSB	Quality Score of Black Tea
QSW	Quality Score of White Tea
r	Correlation Coefficient
RCBD	Randomized Complete Block Design
RP	Recovery Days after Pruning
SBF	Spreading of Bush Frame
SF	Score of Fermentation Rate of Leaf
SP	Survivability Percentage
TE	Tea Estate
VP	Vegetative Propagated

## 1 Introduction

Tea (*Camellia sinensis* (L.) O. Kuntze) is one of the most popular drinks for health benefits worldwide [1]. China was the first place where tea was cultivated, and because of its restorative and rejuvenating properties, people have been drinking it for medical purposes since ancient times [2,3]. Tea contains more than 700 compounds including caffeine, catechin, different flavonoids, vitamins (C, E, K) with amino acids, etc., and these components are mainly responsible for the therapeutic value of tea [4].

The tea industry in Bangladesh has immense contributions to the national economy by contributing 1% to the Gross Domestic Product [5]. Commercial tea cultivation in Bangladesh was started in 1854 [6], tea industry in Bangladesh has touched the milestone of record production of 102.92 million kg in 2023 [7]. The increase in Bangladesh's average daily intake of tea, one of the main cash crops for export, has converted tea into an import. To restore our lost glory of exports, tea production in our limited land must be increased to such an extent, so that, there is a surplus after meeting domestic demand. But our yield has not increased significantly compared to other tea-producing countries due to various reasons such as climate extremes related to climate change, low soil organic carbon, less use of high-yielding and tolerant varieties, improper agronomic management, different kinds of biotic and abiotic stresses and so on [8,9].

Different kinds of abiotic stresses are responsible for lower yields in many crops. Among the various abiotic stresses, waterlogged stress is one of the major factors for yield reduction. The waterlogging situation stunts growth by creating abiotic conditions in the root zone [10]. It can reduce 7.48%–57.42% of rice production [11], 7.75%–16.30% in wheat [12], and 7%–80% in maize [13] throughout different growth stages of the crop. Waterlogging has become a serious issue for tea cultivation reducing yield by 15%–20% annually in North-East India [14]. In Bangladesh, almost all tea estates of the greater Sylhet

division have suffered from waterlogging to various extents. However, in this country, till now, there has been a lack of waterlogging-tolerant varieties or sufficient research for the development of waterlogging-tolerant varieties of tea. So, the collection of germplasm from waterlogged areas, screening them by genetic diversity analysis with consideration of yield and quality as well as further screening them based on waterlogging tolerant ability could be a possible solution to face waterlogging problems by selection breeding strategy.

A successful breeding technique comprises several steps, such as collecting germplasms, evaluating the performance of germplasms by different analyses, and conserving them for future research. So, the evaluation of genetic variation through multivariate analysis is the base of any crop improvement program [15]. Genetic multivariate diversity analyses measure the extent and pattern of variations that exist among the genotypes [16]. Conservation of germplasms also requires analysis of genetic variability to avoid duplication within existing genotypes. Estimation of genetic and phenotypic variability is also important to realize the effect of the environment on phenotypic expression which is related to productivity [17]. Characters associated with economic yield with less environmental interaction and higher heritability from parent to offspring with high genetic gain (genetic advance) of a particular crop are the basic interest of any breeder [18]. The objective of the research was to identify important characters as well as genotypes with high yield and quality potential for waterlogging tolerance through characterization and analysis of genetic variability.

## 2 Materials and Methods

### 2.1 Genotypes and Collection Site

A total of 200 tea genotypes were collected from waterlogged areas of twenty-one Tea Estates (TEs) spread over different agroecological zones of Sylhet division from 2021–2023 by selection breeding process. Plantations of tea estates comprise both seedling and clonal planting materials; therefore, the current germplasm selection process was carried out in old seedling population areas to exploit more natural variations. The collection of sources (name of the TE) of germplasms with genotype names and code names were provided in [Table A1](#). Some important agrometeorological data like monthly total precipitation (mm), monthly maximum and minimum temperature (°C), monthly total evaporation (mm), monthly average sunshine hour, and monthly average relative humidity (%) of germplasm collection sites (greater Sylhet) from 2021 to 2023 [19,20] are given in [Table A2](#).

Currently, in Bangladesh, 168 tea estates are having a production of 102.92 million kg in 2023 [7]. Almost 73% of the total output came from three districts of the Sylhet division (Moulvibazar district: 50%, Habiganj district: 18% and Sylhet district: 5%). On the other hand, 16% of production came from the Northern region of the country, which is generally flat lands planting clonal varieties with limited waterlogging problems. The remaining 11% of tea production came from the Chattogram district [21]. Till now, few records have been found for waterlogging problems in the tea estates of the Chattogram region. So, current research was conducted mainly focusing on the Sylhet division, in which some areas are now severely affected by waterlogging problems and collected the tea genotypes from these affected areas.

### 2.2 Experimental Design and Data Collection Parameters

Collected genotypes from naturally waterlogged areas (standing plantations) of tea estates were raised at the Vegetative Propagated (VP) nursery of Bangladesh Tea Research Institute (BTRI), Sreemangal, Moulvibazar. Plants were raised by following standard procedure [22]. The experiment was conducted by Randomized Complete Block Design with four replications. Data were collected under 13 parameters (characters) from plants of one-year saplings at BTRI VP nursery as well as mature tea bushes from estates and BTRI New Germplasm Center. Measured characters with brief descriptions and calculation methods are given below.

### 2.2.1 Green Leaf Yield-GLY ( $\text{g Plant}^{-1}$ )

GLY was the average weight of green leaf (g) per plant [23] of eight plucking rounds. Based on the average GLY of a minimum of eight plucking rounds, the genotypes were categorized as high (over  $200 \text{ g plant}^{-1}$ ), average ( $150 \text{ to } 200 \text{ g plant}^{-1}$ ), and low yielder (less than  $150 \text{ g plant}^{-1}$ ) [24].

### 2.2.2 Number of Plucking Points-PP ( $\text{m}^{-2}$ )

PP was the number of plucking points per square meter area of bush [25].

### 2.2.3 Number of Days of Plucking Interval-PI (Days)

PI referred to as the plucking interval is the number of days between two successive plucking rounds [26].

### 2.2.4 Spreading of Bush Frame-SBF ( $\text{cm}^2$ )

The size or spreading of the tea bush area [27] was calculated by the area ( $C$ ) =  $2\pi r$  formula (where  $C$  is the circumference,  $r$  is the radius of the bush, and  $\pi \approx 3.14$ ).

### 2.2.5 Number of Dormancy Period-DR

The dormancy period or dormancy cycle or banjhi period is the alternate period of flushing which ranges from 2 to 4 in a cropping year [28].

### 2.2.6 Number of Pubescence of Leaf Bud-NP

Number of pubescence of a single leaf bud which is an indicator of made tea quality [29] was recorded by compound microscope.

### 2.2.7 Score of Fermentation Rate of Leaf-SF

The rate of fermentation (oxidation) by chloroform (Sigma-Aldrich, USA, supplied by Supelco) test [30] was done out of 10 marks.

### 2.2.8 Length of Bud-LB (cm)

LB refers to the length of a single bud (cm) which has a relation with quality and economic use [31].

### 2.2.9 Quality Score of Black Tea-QSB

Quality Scoring of CTC black tea of each genotype was recorded out of 50 marks by organoleptic tasting method [32]. Genotypes are classified based on quality scores, such as excellent quality (score more than 34), average (32–34), and below average (less than 32).

### 2.2.10 Quality Score of White Tea-QSW

White tea of each genotype was manufactured and scored out of 50 marks by organoleptic tasting method [33].

### 2.2.11 Recovery Days after Pruning-RP (Days)

RP was the days to reach bush height to tipping height after the pruning operation.

### 2.2.12 Number of Flower-NF ( $\text{Plant}^{-1}$ )

NF refers to the number of flowers of every plant during the flowering season.

### 2.2.13 Survivability Percentage-SP (Percent)

Cuttings from selected bushes were planted in the nursery and then the survival percentage of cuttings of each genotype was calculated by  $\text{SP} = (\text{Cuttings survived} \div \text{Cuttings planted}) \times 100$  formula.

## 2.3 Statistical Analysis of Experimental Data

The range, first quartile (Q1), median, third quartile (Q3), mean and outliers were graphically presented by boxplot through descriptive statistical analysis [34,35] by R software (version 4.3.2). The data were standardized and a hierarchical clustering heatmap was constructed using R software (version 4.3.2). The

principal component analysis (PCA) [36] and Pearson's correlation matrix [37–39] were made using *fviz\_pca* and the *corrplot* package of the R program.

The genotypic coefficient of variation (GCV) is expressed as percent and calculated by [(square root of genotypic variance ÷ mean value of the character) × 100] formula, while the phenotypic coefficient of variation (PCV) is determined by [square root of phenotypic variance ÷ mean value of the character) × 100] formula also expressed as percent [40]. GCV and PCV were classified as low, moderate, and high when the values were less than 10%, 10%–20%, and more than 20% respectively [41]. Heritability in a Broad sense ( $h^2b$ ) is a percent ratio of genotypic variance and phenotypic variance [42] which is classified as high (>75%), moderate or medium (50%–75%), and low (<50%) [43]. Genetic advance (GA) is classified as low (less than 10%), moderate (10%–20%), and high (greater than 20%) which is obtained by multiplication of three factors: selection differential which is standardized at a 5% level of intensity, phenotypic standard deviation and  $h^2b$  [44]. Genetic advance as percent of mean (GAM) is the ratio of GA and mean value which is also expressed as percent [45]. In this study, genetic diversity analysis and analysis of variance with multiple comparisons (Tukey's HSD test) was performed by R statistical software (version 4.3.2).

### 3 Results

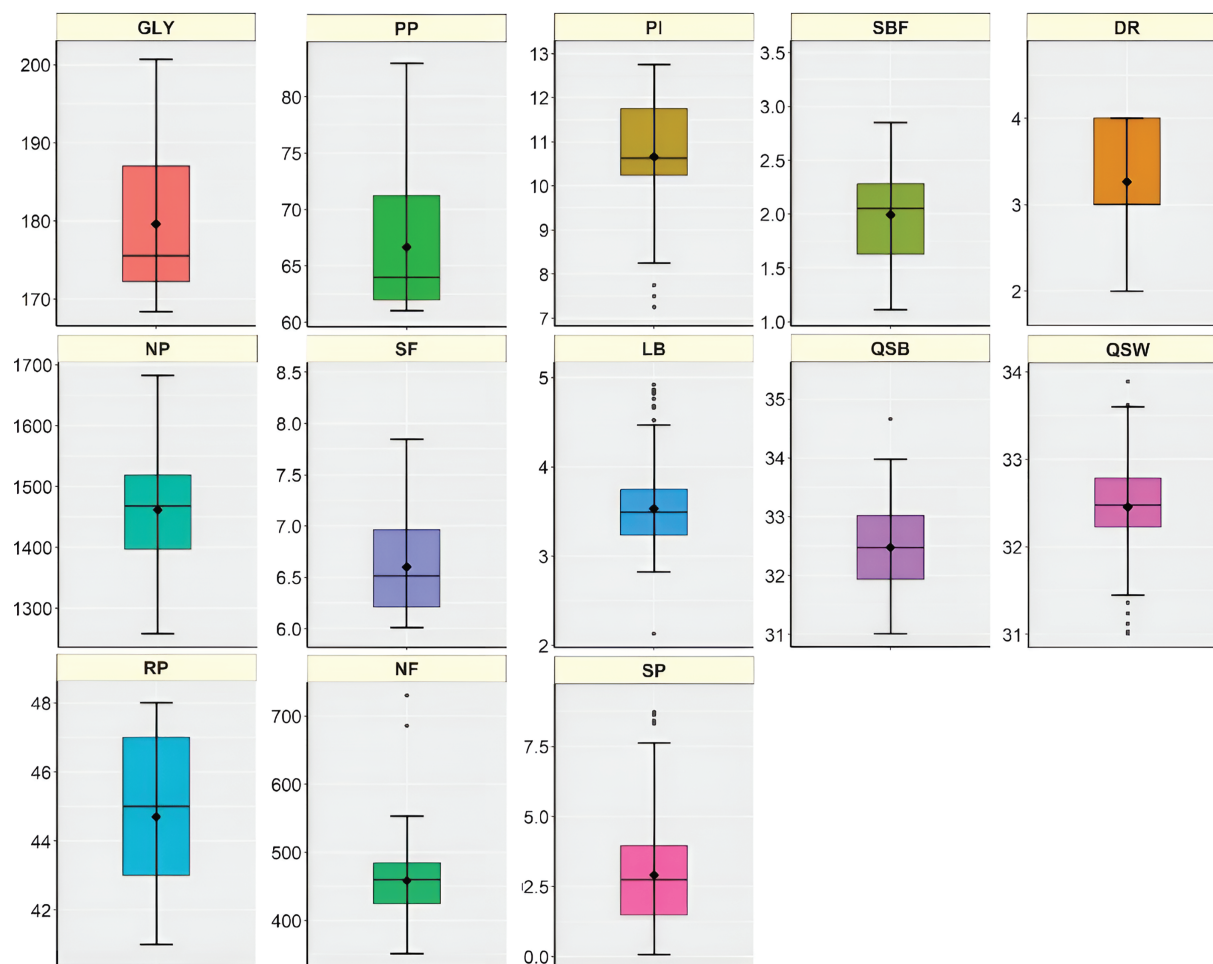
#### 3.1 Descriptive Analysis of 200 Genotypes under 13 Measured Characters

The boxplots indicating lower and upper values, first quartile (Q1), median, third quartile (Q3), mean and outliers of 13 measured characters of 200 genotypes are presented in Fig. 1. The GLY per plant ranged from 168.34 to 200.72 g with mean value of 179.6 g of which 25% values were placed under 172.22 g (Q1) and 75% values were found under 187.37 g (Q3). PP and PI ranged from 61 to 83 in  $m^{-2}$  and 7.25 days to 12.75 days which had a mean value of 66.67 in  $m^{-2}$  and 10.66 days respectively. The character SBF had a mean value of 1.99  $cm^2$  while DR values were found ranging from 2 to 4 with an average value of 3.27. The mean values of NP, SF, LB, QSB, QSW, NF, and SP were 1461.45, 6.60, 3.53 cm, 32.48%, 32.46%, 458.37% and 92.91%, respectively. The data were uniformly distributed in RP having mean values of 44.7 days while PI, LB, QSB, QSW, NF, and SP had some outliers (Fig. 1).

#### 3.2 Cluster Analysis of Genotypes and Variables

Two hundred tea genotypes and their performance are illustrated in a two-way hierarchical clustering heatmap (Fig. 2). The genotypes and characters were divided into clusters and groups, respectively based on the variations that existed among them, but closely interlinked variables were placed within a single cluster or group. The left side of the heatmap represented the column of the dendrogram with six clusters while the genotypes within the corresponding clusters were presented on the right side of the heatmap. The maximum number (46) of closely associated genotypes were found in Cluster-5 (C-5) while the other clusters such as Cluster-1 (C-1), Cluster-2 (C-2), Cluster-3 (C-3), Cluster-4 (C-4) and Cluster-6 (C-6) comprised of 39, 20, 24, 29 and 42 genotypes, respectively. On the contrary, two groups (G-1 and G-2) of dendrogram were found at the upper side of the heatmap while the characters were placed group-wise at the bottom. The characters like GLY, PP, and SBF possessed genotypes closely associated in Cluster-1 and Cluster-2 with higher normalized values (deep green color). On the other hand, PI and DR comprised of genotypes with lower normalized values (deep red color) were also grouped into Cluster-1 and Cluster-2. However, the genotypes having better quality full black tea potential were found in Cluster-3, Cluster-4, and Cluster-1.

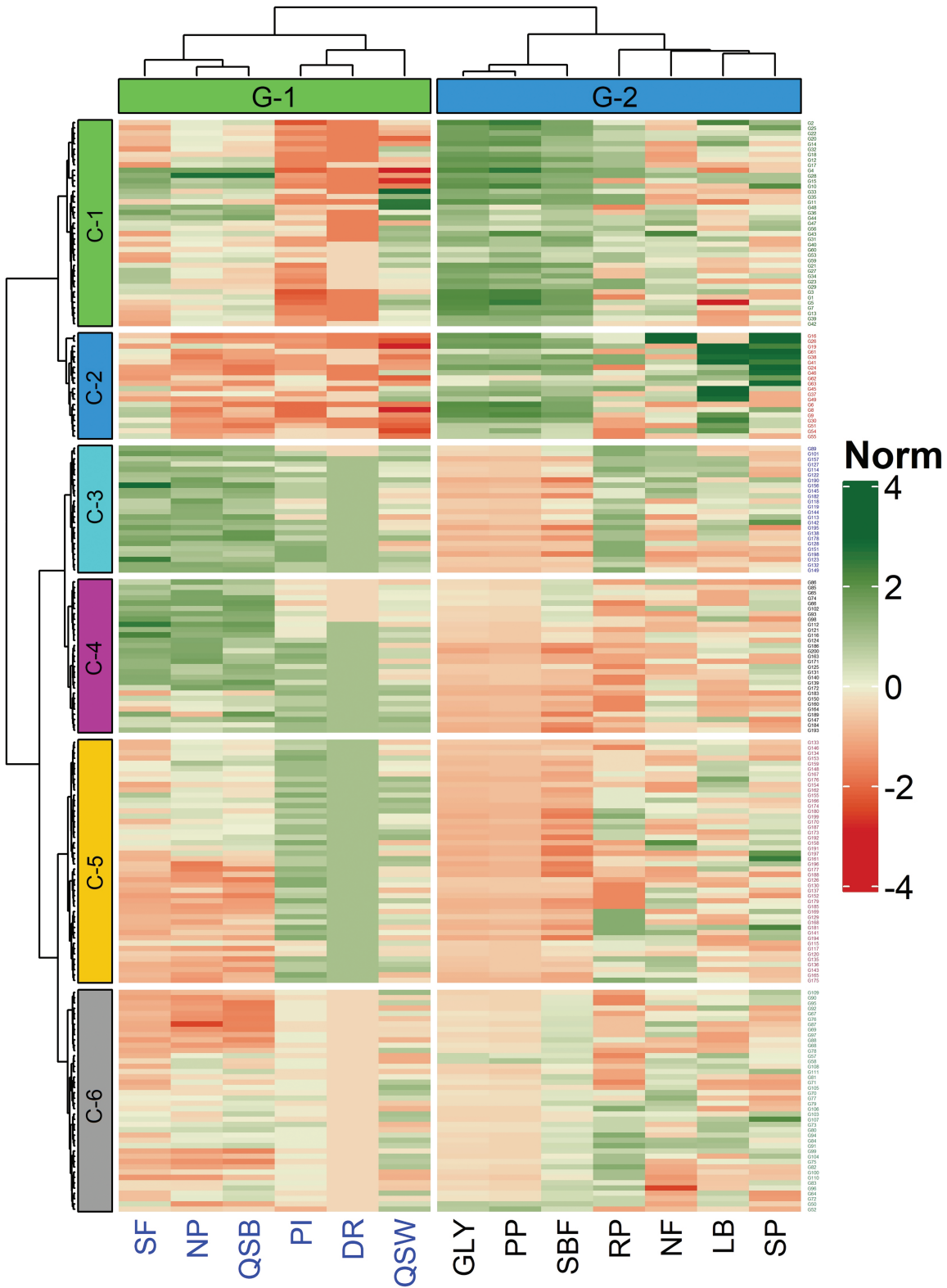
Mean values of 200 genotypes against 13 characters according to six clusters are presented in Table 1. GLY, PP, and SBF were found significantly higher while PI and DR were observed lower in Cluster-1 and Cluster-2. On the other hand, NP, SF, and QSB were noticed significantly higher in Cluster-3, Cluster-4, and Cluster-1.



**Figure 1:** Descriptive summary of 200 Genotypes against 13 characters as presented by boxplots. The horizontal line, upper boundary, and lower boundary of each box indicated the median, 1st percentile (Q1), and 3rd percentile (Q3). The upper and lower whiskers and black circles denote the  $Q3 + 1.5$  interquartile range,  $Q1 - 1.5$  interquartile range, and mean value respectively. Interquartile range (IQR) =  $Q3 - Q1$ . Descriptions of the characters: GLY: Green leaf yield plant<sup>-1</sup> (g), PP: Number of plucking points in m<sup>-2</sup>, PI: Number of days of plucking interval, SBF: Spreading of bush frame (cm<sup>2</sup>), DR: Number of dormancy period, NP: Number of pubescence of single leaf bud, SF: Score of fermentation rate of green leaf, LB: Length of single bud (cm), QSB: Quality score of black tea, QSW: Quality score of white tea, RP: Recovery days after pruning, NF: Number of flowers plant<sup>-1</sup>, SP: Survivability percentage of cuttings of each genotype

### 3.3 Principal Component Analysis (PCA)

The first four principal components (PCs) having eigenvalue of more than one, were responsible for cumulatively 75.6% of total variations (Table 2). The first two components (PC 1 and PC 2) cumulatively described 56.9% of total variations (Table 2). The characters GLY, PP, PI, SBF, and DR mostly contributed to PC 1 which explained 38% of the total variation (Table 2 and Fig. 3a,c). These characteristics were mainly referred to as yield-contributing traits in the case of tea. On the other hand, the characters QSB, NP, and SF were indicated as quality contributing characters which were strongly associated with PC 2 (Fig. 3b,c). PC 2 accounted for 18.9% of total variation (Table 2 and Fig. 3c).



**Figure 2:** The two-way hierarchical clustering heatmap with dendrogram illustrates the grouping and association of genotypes and characters. 200 tea genotypes were grouped into six clusters (Cluster-1,

**Figure 2** (continued)

Cluster-2, Cluster-3, Cluster-4, Cluster-5 and Cluster-6) with 2 groups of characters (Group-1 and Group-2). The mean values are normalized with a scale of 4 to (-) 4 of deep green to deep red color respectively to describe the intensity of the effect against each character. Descriptions of the characters: SF: Score of fermentation rate of green leaf, NP: Number of pubescence of single leaf bud, QSB: Quality score of black tea, PI: Number of days of plucking interval, DR: Number of dormancy period, QSW: Quality score of white tea, GLY: Green leaf yield plant<sup>-1</sup> (g), PP: Number of plucking points in m<sup>-2</sup>, SBF: Spreading of bush frame (cm<sup>2</sup>), RP: Recovery days after pruning, NF: Number of flower plant<sup>-1</sup>, LB: Length of single bud (cm), SP: Survivability percentage of cuttings of each genotype

**Table 1:** Mean values of six clusters from 200 genotypes considering 13 characters

Characters	Cluster-1	Cluster-2	Cluster-3	Cluster-4	Cluster-5	Cluster-6
GLY	194.55 a	191.31 b	172.795 d	173.192 d	171.605 d	177.22 c
PP	75.64 a	74.55 a	62.46 c	62.69 c	61.91 c	64.98 b
PI	8.75 c	9.16 c	11.65 a	11.51 a	12.02 a	10.51 b
SBF	2.59 a	2.51 a	1.67 cd	1.71 c	1.50 d	2.12 b
DR	2.33 d	2.47 d	3.92 ab	3.74 b	4 a	3 c
NP	1482.44 b	1367.75 d	1559.42 a	1542.86 a	1425.00 c	1414.29 c
SF	6.58 b	6.48 bc	7.18 a	7.05 a	6.34 c	6.32 c
LB	3.44 b	4.18 a	3.57 b	3.35 b	3.46 b	3.49 b
QSB	32.66 b	31.56 d	33.396 a	33.32 a	32.07 c	32.10 c
QSW	32.51 a	31.83 b	32.56 a	32.59 a	32.53 a	32.46 a
RP	45.58 ab	44.35 b	47.04 a	42.41 c	44.54 b	44.45 b
NF	463.05 ab	484.15 a	458.50 ab	447.35 b	455.63 ab	452.26 ab
SP	92.86 b	95.39 a	92.45 b	92.19 b	92.91 b	92.52 b

Note: Mean values in a row that possess different letters are significantly different at 5% levels of probability. Multiple comparisons between the clusters in a row were done by Tukey's HSD test. Descriptions of the characters: GLY: Green leaf yield plant<sup>-1</sup> (g), PP: Number of plucking points in m<sup>-2</sup>, PI: Number of days of plucking interval, SBF: Spreading of bush frame (cm<sup>2</sup>), DR: Number of dormancy period, NP: Number of pubescence of single leaf bud, SF: Score of fermentation rate of green leaf, LB: Length of single bud (cm), QSB: Quality score of black tea, QSW: Quality score of white tea, RP: Recovery days after pruning, NF: Number of flowers plant<sup>-1</sup>, SP: Survivability percentage of cuttings of each genotype.

**Table 2:** Eigenvalue, % variance, and cumulative % variance of principal components (PCs) of morphological traits of 200 tea genotypes

Principal components (PCs)	Eigenvalue	% variance	Cumulative % variance
PC 1	4.94	38	38
PC 2	2.45	18.9	56.9
PC 3	1.38	10.6	67.5
PC 4	1.05	8.1	75.6
PC 5	0.96	7.4	83
PC 6	0.71	5.5	88.5

(Continued)



<b>Table 2 (continued)</b>			
Principal components (PCs)	Eigenvalue	% variance	Cumulative % variance
PC 7	0.59	4.6	93.1
PC 8	0.34	2.6	95.7
PC 9	0.21	1.6	97.3
PC 10	0.13	1	98.3
PC 11	0.12	0.9	99.2
PC 12	0.09	0.7	99.9
PC 13	0.02	0.1	100

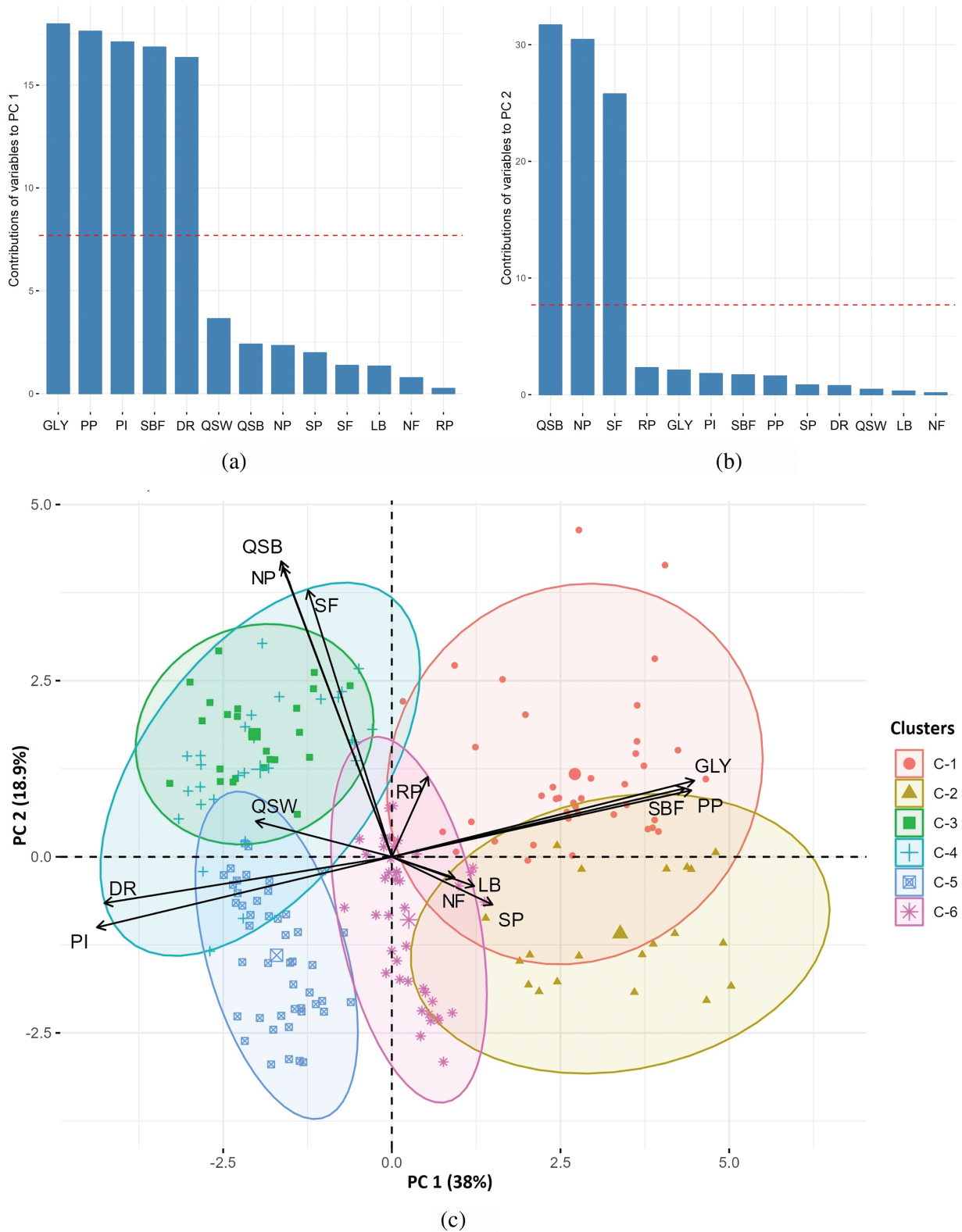
A PCA-biplot was constructed where 200 genotypes are presented with six clusters along with 13 contributing characters of respective PCs (Fig. 3c). PC 1 was strongly positively associated with GLY, PP, and SBF while negatively with PI and DR. However, the variables QSB, NP, and SF were highly contributed to PC 2. The genotypes under Cluster-1 and Cluster-2 possessed more yield potentials, on the contrary, genotypes under Cluster-3 and Cluster-4 had more quality potentials (Fig. 3c).

### 3.4 Correlation of Characters

The correlation matrix with the value of correlation coefficient ( $r$ ) is demonstrated in Fig. 4 to understand the pattern and degree of relationship among the 13 characters. GLY were found to be related significantly, positively, and strongly with both PP (0.97) and SBF (0.90) while negatively with PI (-0.91) and DR (-0.86). It was also observed that PP had a positive strong correlation with SBF (0.85) but negative with DR (-0.82). PI possessed a positive association with DR (0.83) but negatively related with both PP (-0.89) and SBF (-0.89). No significant relationship was observed between the characters like GLY, NP, SF, and RP. So, it can be concluded that the yield potential of tea genotypes is mostly associated with GLY, PP, SBF, PI, and DR. On the other hand, QSB was significantly and positively related to both NP (0.88) and SF (0.72), while SF was strongly related to NP (0.68). QSB had no relationship of significance with NF, LB, and RP. So, it can be assumed that black tea quality was closely associated with QSB, SF, and NP.

### 3.5 Genetic Diversity Analysis

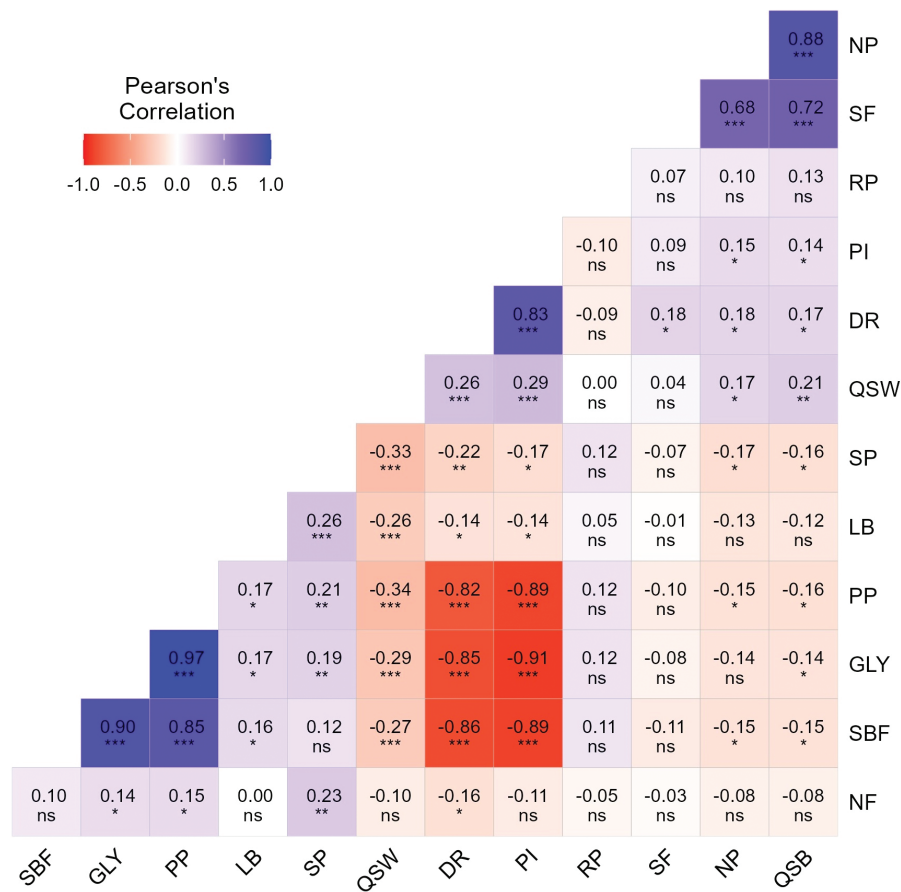
The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), the difference between PCV and GCV, heritability in a broad sense ( $h^2_b$ ), genetic advance (GA) and genetic advance as percent of mean (GAM) are presented in Table 3. The range of GCV (%) and PCV (%) was found from 1.34% to 23.87% and 1.42% to 24.65%, respectively. Higher GCV values (more than 20%) were observed in SBF (23.87%) and DR (22.7%) as well as moderate (10% to 20%) in PI and LB. In the case of PCV%, a higher value was observed also in SBF (24.65%) and DR (23.04%) as well as moderate in PI (15.05%), LB (12.25%), NF (10.54%), and PP (10.33%). The difference between PCV (%) and GCV (%) revealed that PCV was consistently higher than GCV, indicating that all the characters were influenced by environmental factors. However, the lower differences illustrated that the influence of environment was found to a small extent, therefore the performances of all characters can be further improved by selection breeding.



**Figure 3:** Principal component analysis (PCA) considering 13 traits of 200 tea genotypes. (a) Contributions of variables to PC 1, (b) Contributions of variables to PC 2. Red dashes are referred to as reference lines and

**Figure 3** (continued)

the variables that lie above the reference lines affect the particular component most, (c) PCA-biplot showing the degree of association between the variables and clusters of genotypes. Descriptions of the variables: GLY: Green leaf yield plant<sup>-1</sup> (g), PP: Number of plucking points in m<sup>-2</sup>, PI: Number of days of plucking interval, SBF: Spreading of bush frame (cm<sup>2</sup>), DR: Number of dormancy period, NP: Number of pubescence of single leaf bud, SF: Score of fermentation rate of green leaf, LB: Length of single bud (cm), QSB: Quality score of black tea, QSW: Quality score of white tea, RP: Recovery days after pruning, NF: Number of flowers plant<sup>-1</sup>, SP: Survivability percentage of cuttings of each genotype



**Figure 4:** Correlation matrix with correlation coefficient (r) values of 13 measured characters of 200 genotypes. Pearson’s correlation is displayed on a scale of –1 to 1 and the color gradient represents the extent of positive (blue) and negative (red) correlations among the characters. Non-significant, significant at 0.1%, significant at 1%, and significant at 5% level of probability are referred to as ns, \*, \*\*, and \*\*\*, respectively. Descriptions of the traits: GLY: Green leaf yield plant<sup>-1</sup> (g), PP: Number of plucking points in m<sup>-2</sup>, PI: Number of days of plucking interval, SBF: Spreading of bush frame (cm<sup>2</sup>), DR: Number of dormancy period, NP: Number of pubescence of single leaf bud, SF: Score of fermentation rate of green leaf, LB: Length of single bud (cm), QSB: Quality score of black tea, QSW: Quality score of white tea, RP: Recovery days after pruning, NF: Number of flowers plant<sup>-1</sup>, SP: Survivability percentage of cuttings of each genotype

**Table 3:** Genetic diversity analysis of 13 characters of 200 tea genotypes

Characters	GCV (%)	PCV (%)	PCV (%) - GCV (%)	$h^2b$ (%)	GA	GAM (%)
GLY	5.46	5.6	0.14	95	19.71	10.97
DR	22.7	23.04	0.34	97	1.5	46.06
PI	13.28	15.05	1.77	78	2.58	24.16
SBF	23.87	24.65	0.78	94	0.95	47.59
PP	8.99	10.33	1.34	76	10.75	16.13
NF	8.77	10.54	1.77	69	68.86	15.02
NP	5.33	5.8	0.47	84	147.5	10.09
RP	4.37	7.04	2.67	39	2.5	5.6
LB	11.6	12.25	0.65	90	0.8	22.65
SF	6.51	6.94	0.43	88	0.83	12.58
QSB	2.42	2.56	0.14	89	1.53	4.71
QSW	1.34	1.42	0.08	89	0.85	2.61
SP	2.08	2.1	0.02	99	3.96	4.26

Note: Description of the parameters: GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation,  $h^2b$ : Heritability in a Broad sense, GA: Genetic Advance, GAM: Genetic Advance as Percent of Mean as well as GLY: Green leaf yield plant<sup>-1</sup> (g), PP: Number of plucking points in m<sup>-2</sup>, PI: Number of days of plucking interval, SBF: Spreading of bush frame (cm<sup>2</sup>), DR: Number of dormancy period, NP: Number of pubescence of single leaf bud, SF: Score of fermentation rate of green leaf, LB: Length of single bud (cm), QSB: Quality score of black tea, QSW: Quality score of white tea, RP: Recovery days after pruning, NF: Number of flowers plant<sup>-1</sup>, SP: Survivability percentage of cuttings of each genotype.

Heritability is an important tool for a crop improvement program that calculates the influence of parents on the next generation and measures the rate of successful transfer of the characters to offspring. Heritability in broad sense ( $h^2b$ ) ranged from 39% to 99%. A lower value of  $h^2b$  (less than 50%) was observed in RP, a medium value (50% to 75%) in NF, and the rest of the characters were found to have high heritability (Table 3). The high heritability of characters indicated that the genotypic expressions of the characters were less influenced by various environmental factors and can be important tools for crop improvement programs due to their higher domination to the next generations.

GA is the measurement of the genetic gain of offspring over parents through a selection process. Higher GA values (more than 20%) were observed in NP (147.5%) and NF (68.86%) while moderate values (10% to 20%) in GLY (19.71%) and PP (10.75%). On the other hand, high heritability with high GAM was found in SBF (47.59%), DR (46.06%), PI (24.16%), LB (22.65%), PP (16.13%), NF (15.02%), SF (12.58%), GLY (10.97%) and NP (10.09%) which implies that selection of genotypes by those characters could be beneficial because of successful transfer to next generation and higher performance over parents (Table 3).

### 3.6 Yield and Quality Contributing Characters with Best-Performed Genotypes

The most important yield contributing characters were identified as GLY, PP, PI, SBF, and DR from PCA (Fig. 3a,c) and correlation matrix (Fig. 4). Mean values of best performed (top ten) genotypes against important yield contributing characters (GLY, PP, PI, SBF, and DR) were presented in Tables 4 and A3. The genotypes G1 to G10 were high green leaf-yielding genotypes ranging from 200.72 g to 199.02 g plant<sup>-1</sup> (Tables 4 and A3) where the lower value of GLY was 168.34 g plant<sup>-1</sup> (Fig. 1 and Table A3). PP and SBF values of the top ten genotypes differed from 83 in m<sup>-2</sup> (G4 and G2) to 79 in m<sup>-2</sup> (G12) and 2.85 cm<sup>2</sup> (G9) to 2.76 cm<sup>2</sup> (G31) (Table 4). PI and DR both had a negative effect on GLY (Fig. 4), therefore lower value of PI and DR was responsible for higher GLY. Less number of days of PI was observed in G2 (7.25) while the top ten genotypes shared a similar number (2) of DR (Table 4).

**Table 4:** Best-performed genotypes (top ten) with mean values of five important yield contributing characters

Sl. No.	GLY (g plant <sup>-1</sup> )	PP (m <sup>-2</sup> )	PI* (days)	SBF (cm <sup>2</sup> )	DR*
1	G1 (200.72 a)	G4 (83 a)	G2 (7.25 j)	G9 (2.85 a)	G1 (2 c)
2	G2 (200.62 a)	G2 (82 a)	G3 (7.25 j)	G1 (2.84 ab)	G2 (2 c)
3	G3 (200.43 a)	G5 (82 ab)	G1 (7.50 ij)	G5 (2.83 a-c)	G3 (2 c)
4	G4 (200.40 ab)	G1 (81 a-c)	G4 (7.50 ij)	G13 (2.82 a-c)	G4 (2 c)
5	G5 (200.21 a-c)	G10 (81 a-c)	G5 (7.75 ij)	G3 (2.82 a-c)	G5 (2 c)
6	G6 (200.07 a-c)	G3 (81 a-c)	G6 (7.75 ij)	G38 (2.81 a-c)	G6 (2 c)
7	G7 (199.65 a-d)	G6 (81 a-c)	G8 (7.75 ij)	G4 (2.81 a-c)	G7 (2 c)
8	G8 (199.53 a-e)	G43 (80 a-d)	G9 (7.75 ij)	G12 (2.78 a-d)	G10 (2 c)
9	G9 (199.06 a-f)	G9 (80 a-d)	G7 (8.25 h-j)	G21 (2.78 a-d)	G11 (2 c)
10	G10 (199.02 a-f)	G12 (79 a-e)	G10 (8.25 h-j)	G31 (2.76 a-d)	G12 (2 c)

Note: \* A lower value indicates a higher contribution to yield. Mean values in a column that possesses different letters are significantly different at 5% levels of probability. Multiple comparisons between the genotypes in a column were done by Tukey's HSD test. Description of the characters: GLY: Green leaf yield plant<sup>-1</sup> (g), PP: Number of plucking points m<sup>-2</sup>, PI: Number of days of plucking interval, SBF: Spreading of the bush frame (cm<sup>2</sup>), DR: Number of dormancy period.

The quality of black tea mostly depends on QSB, NP, and SF characters (Fig. 3b,c and Fig. 4). The quality contributing characters (QSB, NP, and SF) with mean value of best performed (top ten) genotypes are demonstrated in Table 5. A higher score of QSB was noticed in G28 (34.66) to G102 (33.81) (Table 5) while a lower score was observed in G24 (31.01) (Fig. 1 and Table A3). The pubescence number (NP) varied from G28 (1682) to G172 (1591) in better performed ten genotypes (Table 5). A remarkable score during fermentation (SF) was observed in G156 (7.85) to G4 (7.32) (Table 5) while lower score was found in G17, G32, G62, and G110 (6.01) (Fig. 1 and Table A3).

**Table 5:** Best-performed genotypes (top ten) based on important quality-determined characters

Sl. No.	QSB	NP	SF
1	G28 (34.66 a)	G28 (1682 a)	G156 (7.85 a)
2	G189 (33.98 b)	G118 (1599 b)	G112 (7.69 ab)
3	G178 (33.98 b)	G178 (1598 b)	G123 (7.65 ab)
4	G138 (33.97 b)	G112 (1597 b)	G116 (7.59 bc)
5	G112 (33.93 b)	G171 (1597 b)	G101 (7.38 cd)
6	G156 (33.93 b)	G101 (1596 bc)	G98 (7.36 d)
7	G139 (33.91 bc)	G190 (1596 bc)	G195 (7.35 de)
8	G66 (33.89 bc)	G4 (1596 bc)	G128 (7.34 de)
9	G4 (33.82 b-d)	G66 (1592 b-d)	G36 (7.32 d-f)
10	G102 (33.81 b-d)	G172 (1591 b-d)	G4 (7.32 d-f)

Note: Mean values in a column that possesses different letters are significantly different at 5% levels of probability. Multiple comparisons between the genotypes in a column were done by Tukey's HSD test. Description of the characters: QSB: Quality score of black tea, NP: Number of pubescence of single leaf bud, SF: Score of fermentation rate of green leaf.

#### 4 Discussion

Hybridization and mass selection are the most commonly practiced breeding techniques to introduce new cultivars of tea. Naturally huge number of variations are found because tea is a highly cross-pollinated crop [46]. Any breeding operation with fewer parents can generate a result of the population having a narrow genetic base [47]. So, seeking and identifying the parents having longer distinct genetic relationships is very essential for a substantial breeding technique.

The yield of tea can be hampered by many abiotic factors, such as drought conditions, waterlogging stress, cold stress, etc. In recent times, waterlog due to excessive rainfall has been one of the major stresses responsible for the reduction of yield in many countries, such as India [48,49], Sri Lanka [50], and China [51]. In the current study, 200 genotypes were collected from naturally waterlogged areas of different tea estates to analyze the inherent variations present in them which could be useful in further breeding programs under waterlogged conditions.

Descriptive Statistical Analysis is very helpful in interpreting the pattern, behavior, and distribution of data sets by summarizing them graphically or numerically [52–54]. This analysis is very helpful in interpreting the pattern, behavior, and distribution of data sets by summarizing them graphically or numerically [55]. In the current study, GLY per plant ranged from 168.34 to 200.72 g where only six genotypes were above 200 g (Fig. 1 and Table A3) which can be a good indicator of being a high-yielding variety [24]. The green leaf yield of each plant is very important to determine the productivity of tea [56–58]. The number of plucking points (PP) per square meter area of tea bush ranged from 61 to 83 with a mean value of 66.67 (Fig. 1). Higher number of plucking points always leads to higher yield, therefore, the number of plucking points is always closely associated with yield in tea plants [59,60]. The number of days of plucking interval (PI) has a great impact on both yield and quality of tea which ranges from 7 days to 21 days (or even more) in different countries [61,62]. In this experiment, the average plucking interval of eight plucking rounds ranged from 7.25 days to 12.75 days with a mean value of 10.66 days. Spreading of the bush frame (SBF) is an essential criterion for tea yield, effective use of land as well as maintaining enough foliage for the physiological processes of plants [63]. On the other hand, the number of dormancy periods (DR) or ‘banjhi period’ is an endogenous rhythm of tea bushes that causes a continuous flushing cycle followed by several dormancy periods. In this study, SBF and DR ranged from 1.11 to 2.85 cm<sup>2</sup> and 2 to 4, respectively. A number of pubescence of leaf bud (NP), a score of fermentation rate of the leaf (SF), and length of bud (LB) are generally associated with made tea quality. Generally longer bud contains numerous pubescence which leads to higher fermentation scores as well as better-made tea quality [29–31]. Here, the NP, SF, and LB ranged from 1258 to 1682, 6.01 to 7.85, and 2.13 to 4.92 cm with a mean value of 1461.45, 6.60, and 3.53 cm respectively. The quality score of black tea (QSB) and white tea (QSW) is the scoring of teas by organoleptic tasting or sensory method ranging from 31.01 to 34.66 and 31.01 to 33.89 which mainly varies with the different genotypes in many studies [64,65]. The lower and higher values of recovery days after pruning (RP) were 41 days and 48 days, which were uniformly distributed (Fig. 1) with an average value of 44.7 days. The flowering habit or number of flowers (NF) can be changed in many crops under different stress conditions [66,67]. The survivability percentage of cuttings (SP) is also an inherited character that can differ along with different varieties of tea [68]. In the present study, NF and SP ranged from 351 to 730 and 90.06% to 98.72% with a mean value of 458.37% and 92.91%, respectively. The survival percentage of cuttings in nursery beds is a prime criterion for selection as well as extension programs because vegetative propagation is the most commonly used technique for rapid multiplication and regeneration in tea [69].

Principal component analysis (PCA) is a sort of analysis where a huge number of interrelated data sets are transformed into different components or dimesons to explain the total variations [70]. In most of the cases, the first few principal components (PCs) reflect most of the variations having higher eigenvalue [71]. It was found

that the first two components (PC 1 and PC 2) are responsible for 56.9% of total variations (Table 2). Out of thirteen characters, the characters like GLY, PP, PI, SBF, and DR were found above the reference line in PC 1 (Fig. 3a). So, it can be concluded that GLY, PP, PI, SBF, and DR were the main contributing characters for PC 1. The characters GLY, PP, PI, SBF, and DR were mainly associated with yield and, therefore, identified as yield-contributing characters. The shoot weight of different leaves is also mentioned as yield contributing characters in many studies [72–74]. On the other hand, characters like QSB, NP, and SF were noticed above the line in PC 2 (Fig. 3b). These characters played vital roles in PC 2 and were recognized as quality contributing characters. The quality scoring of black tea by sensory tasting (QSB), the number of pubescence (NP), and the scoring of fermentation time (SF) are also recognized as quality-related characteristics in many studies [75–77]. In a Principal Component Analysis-biplot (PCA-biplot), the distance of arrows from the center illustrates the intensity of association; a longer distance reflects higher contribution and *vice versa* [78]. From the PCA-biplot graph (Fig. 3c), it was observed that GLY, PP, PI, SBF, and DR pointed away from the center, thus largely affecting PC 1. Characters like GLY, PP, and SBF were found to affect positively, while DR and PI were negatively associated with PC 1. Both dormancy period (DR) and plucking interval (PI) adversely affect tea yield, which is in line with many findings [79–81]. On the other hand, QSB, NP, and SF possessed longer distances and were isolated as the most associated characters for PC 2. PCA-biplot (Fig. 3c) also indicates the possibility of having yield potential genotypes which resided under Cluster-1 and Cluster-2. Again, Cluster-1, Cluster-3, and Cluster-4 possessed the genotypes which could be more quality potential (Fig. 3c).

A correlation matrix was developed to measure the pattern, type, and intensity of the variables to each other. The yield potential of the genotypes (GLY) is positively related to PP and SBF while negatively associated with PI and DR. On the other hand, the quality of black tea (QSB) relied on NP and SF (Fig. 3a–c and Fig. 4). From both PCA-biplot and correlation matrix it can be decided that, yield and quality potentials of tea germplasms strongly associated with GLY, PP, PI, SBF, DR and QSB, NP, SF characters, respectively, which is a sort of agreement with various studies [72,82–84].

Before conducting any crop improvement program through a plant breeding strategy, it is a prime need to exploit genetic variations of characters over the existing population. Genetic diversity analysis is a proper guideline to point out the variations and effectiveness of selected traits [85]. Any trait is a cumulative expression of genetic and environmental effects. Diversity analysis is also used to calculate the extent of environmental effects and genetic effects on the characters. So, genetic variability and diversity analysis of characters are preconditions of a successful breeding program. In this corresponding experiment, the PCV of all the characters was higher than GCV and the differentiations were very low, implying that traits were less influenced by the environment (Table 3). Higher PCV values were also observed in many crops, like rice [86], wheat [87], maize [88], etc., with different characters. All the characters were except RP were highly to moderate heritable which found in line with Fig. 1 (uniformly distributed). High heritability with high GAM was found in SBF, DR, PI, LB, PP, NF, SF, GLY, and NP which indicates that selection breeding with these characters will be fruitful for further research. So, it can be concluded that for conducting a crop improvement program, selection based on GLY, PP, PI, SBF, DR, QSB, NP, and SF could have an immense effect on better yield and quality. A similar sort of interpretation was also made from PCA analysis (Fig. 3a–c). Medium GCV and PCV were observed in the number of shoots per bush while high heritability was found in several shoots (99%), bush diameter (97%), recovery days from pruning (88%), and green leaf yield (84%) in some tea genotypes of Southwestern Ethiopia [89].

Cluster analysis with a dendrogram is generally used to classify the variables within numerous clusters based on their relationship and normalized value [90]. Here, 13 measured traits were categorized into two groups while 200 genotypes were divided into six clusters. Six clusters of genotypes indicated that a large number of variations were presented among the genotypes. Cluster-1 and Cluster-2 possessed the genotypes related to high yield potentials characters (GLY, PP, PI, SBF, and DR) while Cluster-3, Cluster-4, and Cluster-1 carried the genotypes with high black tea quality traits like QSB, NP and SF (Table 1

and Fig. 2). This result was found to be similar with the interpretation of PCA-biplot graph (Fig. 3c). Several numbers of clustering also found in different studies [91–94].

Waterlogging has become one of the major abiotic stressors limiting yield and quality in many shrub and tree species, such as peach, coconut, cotton, coffee, tea, etc. [95–99]. When plants are subjected to waterlogging conditions, the oxygen supply in their roots is reduced and the aerial influx of CO<sub>2</sub> is prevented, generating the reactive oxygen species (ROS) and also directly causing stomatal closure hindering respiration and photosynthesis which ultimately affects growth and yield [100,101]. To minimize yield losses, it is crucial to develop waterlogging-tolerant crop varieties with sustainable and feasible breeding strategies to combat waterlogging conditions [102]. To conduct any long-term breeding program, the selection and collection of germplasms of desired traits among a wide range of populations is a prerequisite step. In the present experiment, 200 genotypes were collected from naturally waterlogged areas of different tea estates under 13 parameters. Out of 200 genotypes, the best-performed (top ten) yield and quality potential genotypes were identified through variance analysis with multiple comparisons (Tables 4 and 5). P/LAL/08/23 (G1), P/AFN/11/35 (G2), P/OTI/31 (G3), P/AFN/11/46 (G4), P/LAL/08/62 (G5), P/LAL/09/116 (G6), P/AFN/13/90 (G7), P/CHM/18/74 (G8), P/MPR/12/58 (G9) and P/AFN/13/97 (G10) were the genotypes with higher GLY values. These ten genotypes were performed with satisfaction in other yield contributing characters like PP, PI, SBF, and DR. All these genotypes were from Cluster-1 and Cluster-2 which was a match to the results of cluster heatmap with dendrogram and PCA-biplot (Figs. 2 and 3c) and these ten genotypes were identified for future breeding interest. In the case of black tea quality, the top ten genotypes were also sorted out by the performance of quality contributing characters like QSB, NP, and SF. But amongst 200 genotypes, only one genotype P/AFN/11/31 (G28) was given excellent quality liquor (quality score of 34.66 out of 50) (Tables 5 and A3). QSB, NP, and SF were high heritable characters (Table 3) that denote the consistency of tea quality generation after generation. So, P/AFN/11/31 (G28) is the only genotype with higher quality potential from Cluster-1 (Figs. 2 and 3c) that can be selected for further research programs. So, finally it can be concluded that total eleven (11) genotypes like P/LAL/08/23, P/AFN/11/35, P/OTI/31, P/AFN/11/46, P/LAL/08/62, P/LAL/09/116, P/AFN/13/90, P/CHM/18/74, P/MPR/12/58, P/AFN/13/97 and P/AFN/11/31 were found promising with higher yield and quality potential which can be used for further research and breeding program for quantify their waterlogging tolerance ability.

## 5 Conclusion

Phenotypic selection breeding of tea is a conventional technique used to improve desired traits like yield, quality, or inducing tolerance. Among the 13 measured attributes of the current experiment, traits like GLY, DR, PI, SBF, PP, NF, NP, LB, SF, and QSB were highly heritable characters suggesting that these traits should be taken into consideration as selection criteria for breeding programs of tea. The yield of tea (GLY) was positively related to PP, and SBF but negatively to PI and DR, whereas quality of tea (QSB) highly relied on NP and SF. Finally, eleven genotypes (P/LAL/08/23, P/AFN/11/35, P/OTI/31, P/AFN/11/46, P/LAL/08/62, P/LAL/09/116, P/AFN/13/90, P/CHM/18/74, P/MPR/12/58, P/AFN/13/97 and P/AFN/11/31) were identified considering yield and quality potentials which might be taken for further investigation facilitating future crop improvement program for waterlogging tolerance.

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**Availability of Data and Materials:** The authors confirm that the data supporting the findings of this study are available within the article.

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## Appendix A

**Table A1:** List of collected 200 tea genotypes with codes and sources (TE: Tea estate)

Codes.	Genotype names	Sources (TE)	Codes	Genotype names	Sources (TE)
G1	P/LAL/08/23	Lallakhal TE	G46	P/KRM/14/103	Kurmah TE
G2	P/AFN/11/35	Afifanagar TE	G47	P/HSB/32	Hossenabad TE
G3	P/OTI/31	Ootterbagh TE	G48	P/LAL/08/48	Lallakhal TE
G4	P/AFN/11/46	Afifanagar TE	G49	P/BRN/11/29	Brindabon TE
G5	P/LAL/08/62	Lallakhal TE	G50	P/LAL/08/66	Lallakhal TE
G6	P/LAL/09/116	Lallakhal TE	G51	P/TLP/5/56	Telipapara TE
G7	P/AFN/13/90	Afifanagar TE	G52	P/LAL/09/103	Lallakhal TE
G8	P/CHM/18/74	Champarai TE	G53	P/LAL/08/51	Lallakhal TE
G9	P/MPR/12/58	Monipore TE	G54	P/RJG/11/114	Rajghat TE
G10	P/AFN/13/97	Afifanagar TE	G55	P/SBR/29	Sribarie TE
G11	P/LAL/09/71	Lallakhal TE	G56	P/AFN/11/4	Afifanagar TE
G12	P/LAL/08/69	Lallakhal TE	G57	P/CHM/18/98	Champarai TE
G13	P/AFN/11/68	Afifanagar TE	G58	P/LAL/08/11	Lallakhal TE
G14	P/MPR/12/66	Monipore TE	G59	P/LAL/09/86	Lallakhal TE
G15	P/AFN/11/41	Afifanagar TE	G60	P/AFN/11/15	Afifanagar TE
G16	P/AFN/11/52	Afifanagar TE	G61	P/AFN/13/78	Afifanagar TE
G17	P/AML/12/54	Amrail TE	G62	P/RJG/11/112	Rajghat TE
G18	P/AFN/13/80	Afifanagar TE	G63	P/AML/12/43	Amrail TE
G19	P/LAL/08/43	Lallakhal TE	G64	P/AFN/11/29	Afifanagar TE
G20	P/MDP/13/112	Madhabpur TE	G65	P/AFN/11/17	Afifanagar TE
G21	P/RJG/8/69	Rajghat TE	G66	P/LAL/09/73	Lallakhal TE
G22	P/AFN/11/19	Afifanagar TE	G67	P/LAL/08/58	Lallakhal TE
G23	P/SMR/27	Shumshernugger TE	G68	P/LAL/09/84	Lallakhal TE
G24	P/LAL/09/110	Lallakhal TE	G69	P/LAL/08/21	Lallakhal TE
G25	P/NHR/48	Nahar TE	G70	P/LAL/09/112	Lallakhal TE
G26	P/LAL/09/81	Lallakhal TE	G71	P/LAL/09/101	Lallakhal TE
G27	P/SGL/34	Sagurnal TE	G72	P/LAL/09/79	Lallakhal TE
G28	P/AFN/11/31	Afifanagar TE	G73	P/LAL/09/88	Lallakhal TE
G29	P/NHR/66	Nahar TE	G74	P/LAL/08/41	Lallakhal TE
G30	P/MPR/16a/106	Monipore TE	G75	P/AFN/11/50	Afifanagar TE
G31	P/LAL/08/16	Lallakhal TE	G76	P/AFN/11/21	Afifanagar TE
G32	P/LAL/09/119	Lallakhal TE	G77	P/LAL/09/118	Lallakhal TE
G33	P/LAL/08/9	Lallakhal TE	G78	P/LAL/08/60	Lallakhal TE
G34	P/OTI/30	Ootterbagh TE	G79	P/LAL/09/92	Lallakhal TE

(Continued)

<b>Table A1 (continued)</b>					
Codes.	Genotype names	Sources (TE)	Codes	Genotype names	Sources (TE)
G35	P/PAT/7/61	Patrokhola TE	G80	P/AFN/11/38	Afifanagar TE
G36	P/LAL/08/28	Lallakhal TE	G81	P/LAL/08/19	Lallakhal TE
G37	P/ODL/62	Oodalia TE	G82	P/AFN/13/77	Afifanagar TE
G38	P/NJN/62	Nurjahan TE	G83	P/LAL/09/91	Lallakhal TE
G39	P/CKL/62	Chaklapunji TE	G84	P/AFN/13/75	Afifanagar TE
G40	P/LAL/08/55	Lallakhal TE	G85	P/AFN/11/14	Afifanagar TE
G41	P/AFN/11/26	Afifanagar TE	G86	P/LAL/09/114	Lallakhal TE
G42	P/MDP/12/52	Madhabpur TE	G87	P/AFN/11/72	Afifanagar TE
G43	P/LAL/08/63	Lallakhal TE	G88	P/AFN/11/55	Afifanagar TE
G44	P/AFN/11/53	Afifanagar TE	G89	P/AFN/11/69	Afifanagar TE
G45	P/RHN/87	Rehana TE	G90	P/LAL/08/12	Lallakhal TE
G91	P/AFN/11/2	Afifanagar TE	G140	P/AFN/11/9	Afifanagar TE
G92	P/LAL/08/57	Lallakhal TE	G141	P/AFN/11/1	Afifanagar TE
G93	P/AFN/11/3	Afifanagar TE	G142	P/LAL/09/72	Lallakhal TE
G94	P/AFN/13/83	Afifanagar TE	G143	P/AFN/11/18	Afifanagar TE
G95	P/LAL/08/42	Lallakhal TE	G144	P/LAL/08/26	Lallakhal TE
G96	P/AFN/13/92	Afifanagar TE	G145	P/AFN/11/44	Afifanagar TE
G97	P/LAL/08/27	Lallakhal TE	G146	P/AFN/11/42	Afifanagar TE
G98	P/AFN/11/48	Afifanagar TE	G147	P/LAL/09/107	Lallakhal TE
G99	P/AFN/11/36	Afifanagar TE	G148	P/AFN/11/5	Afifanagar TE
G100	P/LAL/09/78	Lallakhal TE	G149	P/AFN/11/27	Afifanagar TE
G101	P/AFN/11/33	Afifanagar TE	G150	P/AFN/13/82	Afifanagar TE
G102	P/LAL/08/4	Lallakhal TE	G151	P/LAL/09/106	Lallakhal TE
G103	P/AFN/11/7	Afifanagar TE	G152	P/AFN/11/32	Afifanagar TE
G104	P/AFN/11/10	Afifanagar TE	G153	P/LAL/09/77	Lallakhal TE
G105	P/LAL/09/75	Lallakhal TE	G154	P/AFN/11/63	Afifanagar TE
G106	P/LAL/08/34	Lallakhal TE	G155	P/LAL/09/87	Lallakhal TE
G107	P/LAL/08/37	Lallakhal TE	G156	P/LAL/09/74	Lallakhal TE
G108	P/LAL/09/108	Lallakhal TE	G157	P/LAL/08/61	Lallakhal TE
G109	P/AFN/11/70	Afifanagar TE	G158	P/AFN/13/93	Afifanagar TE
G110	P/LAL/09/94	Lallakhal TE	G159	P/AFN/13/76	Afifanagar TE
G111	P/LAL/08/13	Lallakhal TE	G160	P/LAL/08/7	Lallakhal TE
G112	P/LAL/09/100	Lallakhal TE	G161	P/LAL/08/32	Lallakhal TE
G113	P/AFN/11/65	Afifanagar TE	G162	P/AFN/11/60	Afifanagar TE
G114	P/AFN/11/56	Afifanagar TE	G163	P/LAL/08/6	Lallakhal TE

(Continued)



**Table A1 (continued)**

Codes.	Genotype names	Sources (TE)	Codes	Genotype names	Sources (TE)
G115	P/LAL/08/26	Lallakhal TE	G164	P/AFN/13/91	Afifanagar TE
G116	P/LAL/08/36	Lallakhal TE	G165	P/LAL/09/109	Lallakhal TE
G117	P/LAL/09/105	Lallakhal TE	G166	P/LAL/09/102	Lallakhal TE
G118	P/LAL/08/22	Lallakhal TE	G167	P/LAL/08/20	Lallakhal TE
G119	P/AFN/11/59	Afifanagar TE	G168	P/AFN/11/67	Afifanagar TE
G120	P/LAL/09/82	Lallakhal TE	G169	P/LAL/09/83	Lallakhal TE
G121	P/LAL/09/80	Lallakhal TE	G170	P/LAL/09/115	Lallakhal TE
G122	P/LAL/08/1	Lallakhal TE	G171	P/AFN/11/71	Afifanagar TE
G123	P/AFN/11/24	Afifanagar TE	G172	P/LAL/08/24	Lallakhal TE
G124	P/LAL/09/95	Lallakhal TE	G173	P/LAL/08/25	Lallakhal TE
G125	P/AFN/11/62	Afifanagar TE	G174	P/AFN/11/51	Afifanagar TE
G126	P/LAL/08/14	Lallakhal TE	G175	P/LAL/09/113	Lallakhal TE
G127	P/LAL/08/3	Lallakhal TE	G176	P/LAL/08/15	Lallakhal TE
G128	P/AFN/11/66	Afifanagar TE	G177	P/AFN/11/6	Afifanagar TE
G129	P/LAL/08/27	Lallakhal TE	G178	P/AFN/11/28	Afifanagar TE
G130	P/AFN/11/13	Afifanagar TE	G179	P/LAL/08/59	Lallakhal TE
G131	P/LAL/08/31	Lallakhal TE	G180	P/AFN/11/58	Afifanagar TE
G132	P/AFN/11/34	Afifanagar TE	G181	P/LAL/08/30	Lallakhal TE
G133	P/LAL/09/117	Lallakhal TE	G182	P/LAL/08/35	Lallakhal TE
G134	P/AFN/11/43	Afifanagar TE	G183	P/AFN/13/81	Afifanagar TE
G135	P/AFN/11/25	Afifanagar TE	G184	P/LAL/09/93	Lallakhal TE
G136	P/LAL/09/98	Lallakhal TE	G185	P/LAL/08/5	Lallakhal TE
G137	P/AFN/11/16	Afifanagar TE	G186	P/LAL/08/40	Lallakhal TE
G138	P/LAL/08/8	Lallakhal TE	G187	P/AFN/11/37	Afifanagar TE
G139	P/AFN/11/54	Afifanagar TE	G188	P/AFN/11/23	Afifanagar TE
G189	P/AFN/13/74	Afifanagar TE	G195	P/LAL/09/99	Lallakhal TE
G190	P/LAL/08/18	Lallakhal TE	G196	P/AFN/11/12	Afifanagar TE
G191	P/LAL/09/104	Lallakhal TE	G197	P/AFN/11/49	Afifanagar TE
G192	P/AFN/11/20	Afifanagar TE	G198	P/AFN/11/64	Afifanagar TE
G193	P/LAL/08/2	Lallakhal TE	G199	P/LAL/09/89	Lallakhal TE
G194	P/AFN/11/57	Afifanagar TE	G200	P/RHN/87	Rehana TE

**Table A2:** Some important meteorological data of experimental period (2021–2023)

Month	a: Average monthly precipitation (mm)			b: Maximum temperature (°C)			c: Minimum temperature (°C)		
	2021	2022	2023	2021	2022	2023	2021	2022	2023
January	3	21	0	24.23	24.61	26.67	10.05	11.53	10.50
February	0	27	1	29.38	26.90	29.43	11.19	11.30	13.10
March	109	30	90	33.47	32.24	31.27	18.08	16.28	17.45
April	39	120	100	35.14	33.97	34.87	21.44	22.73	21.02
May	236	608	224	34.40	31.30	34.40	23.93	22.67	23.11
June	171	553	622	32.99	31.82	33.37	25.43	25.00	25.06
July	295	257	306	32.47	34.07	34.42	26.25	25.90	26.22
August	408	406	379	32.90	33.99	32.59	25.42	25.54	26.27
September	176	301	193	34.33	33.54	34.64	25.29	25.29	26.56
October	166	378	104	33.46	31.14	32.39	23.95	21.98	23.20
November	2	0	114	30.22	31.67	29.92	16.04	17.30	19.09
December	66	1	39	26	27.50	27.12	12.83	13.80	15.15
Month	d: Total monthly evaporation (mm)			e: Average monthly sunshine hour			f: Average monthly relative humidity %		
	2021	2022	2023	2021	2022	2023	2021	2022	2023
January	77.90	67.30	64.40	5.63	5.58	6.53	68.24	72.38	69.25
February	94.10	90.60	87.90	7.33	7.60	6.96	60.10	75.40	61.79
March	146.40	144.70	112.80	7.94	7.88	6.33	57.86	56.01	63.50
April	174.50	142.10	148.80	8.68	6.96	8.46	60.93	68.93	62.69
May	168.20	113.20	143.90	6.56	4.73	6.79	70.80	77.97	66.55
June	129.10	87.80	67.50	4.27	2.01	3.65	78.68	85.66	80.23
July	130.10	141.40	126.10	3.60	6.09	5.20	80.81	78.36	75.56
August	111.80	138.60	90.60	3.64	5.99	3.33	82.50	77.04	82.79
September	131.10	127.70	119.10	6.41	4.93	6.24	78.08	81.08	78.31
October	118.20	119.90	93.50	7.17	6.57	5.85	78.88	81.25	79.97
November	87.90	121.30	75.10	7.75	8.22	7.68	72.93	72.45	75.34
December	87.70	54.30	51	6.13	6.70	5.94	72.69	74.60	76.85

**Table A3:** Mean value and least significance difference (LSD) value of 200 genotypes under 13 selection criteria

Genotypes	GLY	PP	PI	SBF	DR	NP	SF	LB	QSB	QSW	RP	NF	SP
G1	200.73	81	7.50	2.84	2	1448	6.55	3.25	32.81	32.72	41	455	90.93
G2	200.62	82	7.25	2.75	2	1469	6.36	4.47	32.82	32.34	45	437	94.98
G3	200.43	81	7.25	2.82	2	1498	6.8	3.96	32.31	32.22	43	487	90.98
G4	200.40	83	7.50	2.81	2	1596	7.32	2.83	33.82	31.03	48	484	91.94
G5	200.21	82	7.75	2.83	2	1475	6.35	2.13	32.56	32.99	46	477	92.78
G6	200.07	81	7.75	2.76	2	1379	6.75	3.20	31.07	31.69	44	402	90.93
G7	199.65	76	8.25	2.72	2	1436	6.26	3.36	32.91	32.78	44	488	93.97
G8	199.53	79	7.75	2.76	3	1322	6.94	3.55	31.90	31.01	46	444	95.58
G9	199.06	80	7.75	2.85	3	1341	6.96	4.33	31.80	31.79	43	468	93.05
G10	199.02	81	8.25	2.74	2	1534	7.18	3.28	33.28	31.70	47	423	96.98
G11	198.94	78	8.25	2.72	2	1464	6.39	2.82	32.03	33.60	48	418	91.93
G12	198.58	79	8.25	2.78	2	1497	6.39	3.48	32.97	32.13	47	408	92.54
G13	198.34	77	8.25	2.82	2	1468	6.17	2.99	32.75	32.45	46	495	91.01
G14	197.91	79	8.25	2.52	2	1468	6.24	4.19	32.19	31.87	47	407	91.94
G15	197.91	77	8.50	2.63	2	1514	7.28	3.94	33.18	31.24	42	465	94.65
G16	197.71	79	8.50	2.25	2	1321	6.36	3.36	31.21	31.62	45	730	98.63
G17	197.34	77	8.25	2.51	3	1477	6.01	3.16	32.81	32.25	47	423	91.96
G18	197.25	77	8.25	2.54	2	1426	6.45	3.60	32.15	32.61	47	405	91.95
G19	197.23	78	8.50	2.71	2	1489	6.07	4.84	32.28	31.12	47	415	97.34
G20	196.60	78	8.75	2.54	2	1469	6.23	3.93	32.43	31.55	46	474	93.02
G21	196.51	78	8.25	2.78	3	1439	6.70	3.26	32.31	32.84	44	466	92.97
G22	196.44	75	8.25	2.74	2	1463	6.31	3.67	32.19	32.03	46	473	94.01
G23	196.31	76	8.25	2.34	3	1421	6.98	3.07	32.04	32.40	48	470	90.97
G24	196.30	78	8.75	2.74	2	1354	6.08	3.89	31.01	31.92	41	460	98.64
G25	196.15	79	8.75	2.76	2	1469	6.12	3.51	32.29	32.14	47	428	96.29
G26	196.01	77	8.75	2.64	2	1354	6.53	3.35	31.42	31.45	45	686	98.62
G27	195.41	76	8.75	2.43	3	1466	6.99	3.15	32.03	32.40	43	487	91.97
G28	195.36	76	8.75	2.68	2	1682	7.18	3.90	34.66	31.88	48	506	94.64
G29	194.79	74	8.75	2.56	3	1428	6.76	3.63	32.17	32.39	48	486	92.98
G30	194.23	76	8.50	2.64	2	1365	6.57	4.52	31.32	31.63	42	462	93.96
G31	193.87	72	8.75	2.76	2	1468	6.48	3.94	32.25	32.96	45	478	90.96
G32	193.87	73	8.75	2.42	2	1464	6.01	3.66	32.12	32.84	46	417	92.97
G33	193.76	72	10.25	2.55	2	1424	7.05	3.19	32.81	33.89	45	437	91.03
G34	193.58	73	8.50	2.71	3	1468	6.99	3.55	32.12	32.52	43	488	93.97
G35	193.35	75	8.50	2.75	3	1498	6.96	3.35	32.65	33	48	411	92.02

(Continued)

**Table A3 (continued)**

Genotypes	GLY	PP	PI	SBF	DR	NP	SF	LB	QSB	QSW	RP	NF	SP
G36	192.37	71	9.50	2.36	2	1524	7.32	3.31	33.51	32.48	43	499	93.03
G37	192.37	76	8.75	2.44	3	1457	6.31	4.92	32.48	32.78	43	479	91.01
G38	192.22	73	8.75	2.81	3	1322	6.55	4.66	31.52	31.65	48	416	98.37
G39	192.09	75	8.75	2.42	2	1479	6.15	3.06	32.57	32.53	45	461	92.94
G40	191.89	72	8.75	2.67	3	1461	6.2	3.49	32.11	32.78	46	470	91.03
G41	191.56	74	8.75	2.54	3	1348	6.47	4.76	31.28	31.88	48	484	97.53
G42	191.23	74	8.75	2.45	3	1469	6.07	3.07	32.18	32.45	44	440	91.98
G43	191.10	80	10.25	2.54	2	1482	6.06	3.60	32.87	32.88	46	553	92.95
G44	190.32	68	10.25	2.36	2	1564	7.05	3.38	33.71	33.18	46	493	93.97
G45	190.30	74	10.25	2.45	2	1348	6.87	4.82	31.98	32.58	48	443	93.95
G46	189.49	72	9.25	2.67	2	1364	6.05	4.14	31.05	32.67	45	481	98.32
G47	189.10	71	9.50	2.49	2	1498	6.71	3.40	32.38	32.05	46	513	94.68
G48	188.97	66	9.75	2.51	3	1568	7.06	3.54	33.38	33.62	41	480	92.98
G49	187.65	69	9.75	2.68	3	1348	6.09	4.68	31.70	32.95	46	485	90.94
G50	187.53	71	10.25	2.34	3	1348	6.77	3.74	31.64	32.62	46	411	91.98
G51	186.87	71	9.50	2.24	2	1347	6.87	4.24	31.02	31.51	42	402	93.96
G52	186.81	74	9.25	2.18	3	1423	6.46	3.41	32.17	32.86	42	425	90.98
G53	186.54	75	9.50	2.20	3	1464	6.12	3.66	32.63	32.92	47	473	92.94
G54	186.47	75	10.25	2.21	3	1354	6.52	4.35	31.38	31.36	41	504	92.68
G55	186.29	71	10.25	2.19	3	1367	6.76	3.67	31.86	31.63	41	431	91.02
G56	185.02	68	10.50	2.26	2	1455	6.76	3.21	32.24	32.97	47	454	94.98
G57	184.91	68	10.25	2.12	3	1464	6.19	3.97	32.79	32	41	463	92.98
G58	184.65	72	10.75	2.22	3	1498	6.44	3.66	32.12	32	42	486	92.97
G59	182.92	72	10.50	2.24	3	1486	6.06	3.24	32.88	32.60	47	455	91.94
G60	182.65	71	10.25	2.27	3	1436	6.53	3.82	32.49	32.64	45	475	91.87
G61	182.42	71	10.25	2.12	3	1347	6.64	4.86	31.54	31.98	42	488	98.72
G62	180.42	65	10.75	2.15	2	1431	6.01	3.97	32.09	31.50	44	512	96.28
G63	180.11	72	10.50	2.27	3	1397	6.20	3.50	31.29	31.86	46	491	98.41
G64	177.93	65	10.25	2.19	3	1468	6.28	3.79	32.75	32.85	45	411	90.29
G65	177.89	65	10.25	2.19	3	1589	6.96	3.09	33.03	32.48	45	454	93.64
G66	177.85	65	9.75	2.27	3	1592	7.31	3.08	33.89	32.56	41	434	94.01
G67	177.76	65	10.50	2.12	3	1348	6.24	3.51	31.19	32.56	42	456	91.38
G68	177.65	65	10.25	2.14	3	1355	6.21	3.11	31.48	32.42	43	431	92.49
G69	177.59	65	10.25	2.14	3	1344	6.13	3.21	31.15	32.29	43	468	91.93
G70	177.57	65	10.50	2.10	3	1436	6.54	3.49	32.23	32.83	45	501	92.02
G71	177.53	65	10.75	2.20	3	1469	6.13	3.04	32.02	32.81	41	467	90.49

(Continued)

<b>Table A3 (continued)</b>													
Genotypes	GLY	PP	PI	SBF	DR	NP	SF	LB	QSB	QSW	RP	NF	SP
G72	177.52	65	10.50	2.19	3	1469	6.28	3.68	32.81	32.33	46	423	90.39
G73	177.37	65	11.50	2.17	3	1478	6.58	3.93	32.86	32.09	46	431	94.28
G74	177.17	65	10.75	2.09	3	1587	7.11	3.09	33.77	32.44	44	453	93.57
G75	177.12	65	10.25	2.08	3	1347	6.11	3.56	31.19	32.77	47	421	93.48
G76	177.01	65	10.50	2.16	3	1344	6.19	3.64	31.15	32.16	43	454	90.98
G77	176.98	65	11.25	2.08	3	1461	6.58	3.23	32.86	32.65	44	511	90.68
G78	176.97	65	10.50	2.18	3	1385	6.13	3.15	31.91	32.81	42	410	92.74
G79	176.96	65	10.25	2.25	3	1438	6.55	3.52	32.62	32.19	46	492	91.19
G80	176.94	65	10.75	2.07	3	1499	6.74	3.94	32.97	32.19	46	450	93.25
G81	176.82	64	10.25	2.28	3	1436	6.28	3.38	32.29	32.43	42	478	91.02
G82	176.65	64	10.50	2.28	3	1364	6.21	3.24	31.66	32.84	48	413	91.64
G83	176.64	64	10.75	2.23	3	1434	6.47	3.27	32.63	32.21	45	408	93.79
G84	176.53	64	10.75	2.11	3	1468	6.41	3.96	32.57	32.84	47	497	92.53
G85	176.46	64	10.50	2.21	3	1510	7.08	3.34	33.02	32.58	44	429	91.84
G86	176.38	64	10.25	2.16	3	1587	6.85	3.05	33.22	32.19	42	496	90.38
G87	176.36	64	10.25	2.17	3	1258	6.14	3.12	31.18	32.33	43	505	91.61
G88	176.34	64	10.75	2.26	3	1394	6.05	3.01	31.25	32.05	45	424	92.74
G89	176.27	64	10.25	2.12	3	1567	7.21	3.27	33.45	32.79	48	504	92.16
G90	175.87	64	10.25	2.07	3	1344	6.08	3.55	31.68	32.27	41	450	94.02
G91	175.83	64	10.75	2.19	3	1485	6.68	3.92	32.92	32.72	48	501	93.12
G92	175.74	64	10.50	2.11	3	1364	6.14	3.96	31.12	32.07	44	418	90.78
G93	175.74	64	11.25	2.15	3	1586	7.25	3.69	33.62	32.35	42	405	91.59
G94	175.71	64	10.75	2.17	3	1469	6.23	3.73	32.49	32.61	48	438	93.57
G95	175.67	64	10.50	2.09	3	1354	6.17	3.52	31.08	32.73	41	474	93.98
G96	175.65	64	10.50	2.28	3	1436	6.47	3.29	32.97	32.18	47	351	93.14
G97	175.63	64	10.75	2.17	3	1369	6.23	3.01	31.63	32.31	43	490	91.98
G98	175.63	64	10.50	2.11	3	1547	7.36	3.99	33.56	32.48	44	431	90.28
G99	175.61	64	10.25	2.18	3	1354	6.14	3.79	31.19	32.37	46	477	93.84
G100	175.56	64	10.75	2.04	3	1438	6.34	3.38	32.51	32.04	47	411	91.49
G101	175.54	64	11.50	2.06	3	1596	7.38	3.32	33.32	32.68	48	493	91.39
G102	175.43	64	10.50	2.01	3	1526	7.11	3.63	33.81	32.54	42	495	94.02
G103	175.38	64	10.50	1.89	3	1425	6.61	3.43	32.97	32.88	45	461	94.44
G104	175.32	64	10.75	1.96	3	1380	6.25	3.11	31.86	32.82	47	457	94.68
G105	175.29	64	10.75	1.89	3	1436	6.21	3.10	32.46	32.96	42	476	90.68
G106	175.28	64	10.50	2.04	3	1469	6.49	3.03	32.67	32.06	48	483	91.48
G107	175.11	64	10.25	1.88	3	1431	6.68	3.84	32.43	32.82	46	470	97.05

(Continued)

**Table A3 (continued)**

Genotypes	GLY	PP	PI	SBF	DR	NP	SF	LB	QSB	QSW	RP	NF	SP
G108	174.95	64	10.75	1.98	3	1498	6.16	3.85	32.06	32.38	43	479	92.48
G109	174.88	64	10.50	1.91	3	1397	6.14	3.43	31.92	32.94	42	457	94.58
G110	174.85	63	10.50	1.93	3	1354	6.01	3.26	31.88	32.02	47	401	91.67
G111	174.85	63	10.25	1.92	3	1469	6.48	3.70	32.92	32.17	42	465	95.01
G112	174.81	63	10.75	1.93	4	1597	7.69	3.37	33.93	32.26	44	421	91.58
G113	174.79	63	10.25	1.96	4	1571	7.25	3.49	33.81	32.07	48	403	94.78
G114	174.67	63	10.75	1.94	4	1567	7.21	3.86	33.45	32.53	48	492	91.21
G115	174.67	63	10.25	1.96	4	1469	6.51	3.04	32.29	32.61	45	474	90.97
G116	174.63	63	10.50	1.90	4	1564	7.59	3.43	33.52	32.63	43	473	92.98
G117	174.38	63	10.50	1.86	4	1364	6.22	3.29	31.31	32.33	45	450	90.68
G118	174.37	63	10.25	1.92	4	1599	6.88	3.57	33.16	32.39	47	413	91.91
G119	174.37	63	10.50	1.98	4	1574	6.88	3.66	33.15	32.65	46	458	93.75
G120	174.33	63	10.25	1.87	4	1417	6.39	3.53	32.08	32.31	44	434	92.02
G121	174.31	63	10.50	1.77	4	1572	7.11	3.24	33.78	32.77	42	422	91.49
G122	174.19	63	12.25	1.86	4	1546	7.03	3.99	33.26	32.48	47	478	91.01
G123	174.06	63	12.75	1.78	4	1534	7.65	3.31	33.26	32.88	47	411	90.67
G124	174.01	63	11.50	1.89	4	1581	7.21	3.48	33.14	32.77	43	466	91.08
G125	173.88	63	11.25	1.88	4	1521	7.14	3.49	33.56	32.74	41	417	94.33
G126	173.87	63	12.75	1.78	4	1348	6.10	3.15	31.11	32.56	42	416	92.64
G127	173.84	63	11.50	1.77	4	1487	7.14	3.97	32.57	32.58	47	498	92.02
G128	173.69	63	12.50	1.68	4	1539	7.34	3.23	33.36	32.09	48	472	92.33
G129	173.68	63	12.50	1.66	4	1396	6.22	3.13	31.96	32.57	48	455	92.95
G130	173.67	63	12.75	1.68	4	1384	6.21	3.07	31.47	32.43	41	444	93.09
G131	173.58	63	12.25	1.63	4	1517	7.21	3.33	33.47	32.36	43	419	94.01
G132	173.56	63	11.75	1.69	4	1578	7.19	3.37	33.51	32.73	46	429	92.48
G133	173.52	63	11.75	1.62	4	1467	6.21	3.51	32.36	32.18	43	475	91.74
G134	173.21	63	12.50	1.81	4	1469	6.31	3.68	32.41	32.25	44	432	91.48
G135	173.17	63	12.25	1.76	4	1384	6.34	3.28	31.29	32.66	47	501	91.85
G136	172.97	63	11.75	1.66	4	1368	6.16	3.49	31.78	32.79	45	498	93.35
G137	172.97	63	11.50	1.70	4	1434	6.15	3.56	31.56	32.11	41	491	91.37
G138	172.95	63	12.25	1.62	4	1547	7.15	3.86	33.97	32.69	47	412	91.95
G139	172.84	63	11.25	1.66	4	1569	7.22	3.14	33.91	32.54	41	473	93.79
G140	172.69	63	12.25	1.64	4	1543	7.23	3.31	33.32	32.29	41	434	93.35
G141	172.67	63	12.25	1.62	4	1423	6.11	3.33	32.06	32.45	48	510	94.58
G142	172.57	63	12.25	1.70	4	1548	7.14	3.81	33.48	32.36	47	446	96.74
G143	172.54	63	11.75	1.73	4	1385	6.18	3.19	31.36	32.88	44	489	91.46

(Continued)

**Table A3 (continued)**

Genotypes	GLY	PP	PI	SBF	DR	NP	SF	LB	QSB	QSW	RP	NF	SP
G144	172.43	62	11.50	1.71	4	1569	6.95	3.41	33.03	32.45	47	457	92.96
G145	172.43	63	11.75	1.70	4	1536	7.21	3.72	33.56	32.37	45	511	92.47
G146	172.36	62	11.50	1.68	4	1477	6.21	3.67	32.31	32.42	41	453	91.36
G147	172.31	62	12.75	1.65	4	1534	6.79	3.94	33.47	32.99	42	478	90.16
G148	172.29	62	12.25	1.63	4	1498	6.59	3.81	32.52	32.46	44	457	92.82
G149	172.27	62	11.75	1.76	4	1568	7.19	3.15	33.62	32.68	48	452	92.72
G150	172.27	62	11.75	1.66	4	1497	6.84	3.19	32.88	32.59	41	459	91.47
G151	172.21	62	12.75	1.68	4	1528	6.89	3.19	33.17	32.25	48	432	91.13
G152	172.13	62	11.75	1.63	4	1354	6.06	3.39	31.17	32.39	41	467	90.28
G153	172.13	62	12.75	1.64	4	1468	6.19	3.33	32.76	32.69	44	416	90.68
G154	172.08	62	12.50	1.71	4	1431	6.12	3.92	32.21	32.78	43	405	91.67
G155	171.75	62	12.75	1.49	4	1468	6.98	3.62	32.31	32.65	45	459	93.64
G156	171.72	62	11.75	1.45	4	1588	7.85	3.73	33.93	32.62	47	486	93.38
G157	171.65	62	12.75	1.55	4	1539	6.93	3.92	33.51	32.95	47	498	91.49
G158	171.62	62	12.75	1.53	4	1497	6.64	3.46	32.78	32.13	42	546	94.34
G159	171.52	62	12.25	1.48	4	1536	6.58	3.79	32.95	32.41	44	422	93.67
G160	171.44	62	11.75	1.49	4	1469	6.51	3.07	32.88	32.78	41	486	90.96
G161	171.42	62	11.75	1.49	4	1413	6.18	3.46	32.09	32.91	44	434	97.64
G162	171.35	62	11.75	1.41	4	1479	6.25	3.78	32.29	32.91	45	404	91.83
G163	171.33	62	12.75	1.48	4	1589	7.19	3.52	33.19	32.69	42	417	91.03
G164	171.29	62	12.25	1.55	4	1466	6.29	3.15	32.68	32.64	41	469	91.64
G165	171.28	62	12.75	1.46	4	1358	6.23	3.48	31.77	32.11	45	462	91.47
G166	171.24	62	11.75	1.58	4	1478	6.77	3.3	32.82	32.97	45	494	91.67
G167	171.24	62	12.25	1.44	4	1469	6.48	3.76	32.32	32.32	45	438	93.47
G168	171.14	62	11.25	1.49	4	1364	6.21	3.07	32.21	32.68	48	428	93.47
G169	171.11	62	11.50	1.55	4	1364	6.15	3.46	31.59	32.19	48	411	94.82
G170	171.08	62	11.50	1.49	4	1447	6.23	3.29	32.56	32.42	46	425	93.46
G171	171.07	62	12.50	1.48	4	1597	7.14	3.03	33.24	32.23	42	461	90.95
G172	171.05	61	12.25	1.51	4	1591	6.78	3.15	33.63	32.86	43	470	92.95
G173	171.02	61	12.25	1.51	4	1467	6.64	3.07	32.48	32.87	46	423	94.18
G174	170.97	61	12.50	1.52	4	1467	6.68	3.44	32.43	32.85	45	459	92.04
G175	170.81	61	12.25	1.48	4	1348	6.18	3.56	31.82	32.32	48	504	91.75
G176	170.59	61	11.75	1.48	4	1469	6.56	4.16	32.47	32.95	44	439	93.18
G177	170.55	61	12.50	1.25	4	1328	6.31	3.91	31.25	32.35	43	407	92.35
G178	170.49	61	11.50	1.33	4	1598	7.26	3.76	33.98	32.96	47	415	91.81
G179	170.46	61	12.75	1.31	4	1398	6.11	3.07	31.46	32.78	41	497	92.75

(Continued)

Table A3 (continued)

Genotypes	GLY	PP	PI	SBF	DR	NP	SF	LB	QSB	QSW	RP	NF	SP
G180	170.42	61	11.75	1.23	4	1489	6.39	3.68	32.18	32.92	47	458	92.53
G181	170.38	61	12.75	1.31	4	1398	6.19	3.94	31.84	32.23	48	485	97.28
G182	170.31	61	11.75	1.26	4	1531	7.19	3.68	33.46	32.28	45	497	94.01
G183	170.26	61	12.50	1.37	4	1469	6.14	3.08	32.08	32.94	42	432	90.24
G184	170.26	61	12.25	1.27	4	1478	6.78	3.36	32.56	32.84	43	443	90.67
G185	170.22	61	11.75	1.36	4	1354	6.14	3.54	31.49	32.44	41	485	92.96
G186	170.09	61	12.75	1.31	4	1584	7.13	3.58	33.15	32.26	42	419	94.02
G187	170.06	61	12.25	1.31	4	1478	6.48	3.61	32.48	32.62	47	410	93.49
G188	169.96	61	12.25	1.12	4	1348	6.23	3.39	31.95	32.34	43	409	90.38
G189	169.96	61	11.75	1.16	4	1396	7.24	3.17	33.98	32.83	44	453	93.22
G190	169.93	61	11.25	1.11	4	1596	6.98	3.37	33.01	32.88	45	513	94.97
G191	169.92	61	11.75	1.15	4	1439	6.52	3.69	32.66	32.57	43	507	93.33
G192	169.64	61	11.50	1.15	4	1465	6.53	3.19	32.85	32.98	46	462	93.28
G193	169.61	61	12.25	1.13	4	1501	7.05	3.50	33.14	32.88	42	442	90.96
G194	169.46	61	12.75	1.14	4	1397	6.24	3.01	31.57	32.18	46	477	94.85
G195	169.43	61	11.50	1.15	4	1578	7.35	3.95	33.32	32.37	48	431	90.06
G196	169.42	61	11.75	1.17	4	1319	6.32	3.73	31.98	32.83	44	467	94.75
G197	169.40	61	12.25	1.13	4	1488	6.21	3.13	32.19	32.26	42	410	96.57
G198	169.35	61	12.75	1.18	4	1542	6.96	3.06	33.01	32.76	48	403	91.33
G199	169.16	61	12.25	1.14	4	1489	6.79	3.39	32.44	32.44	48	470	93.68
G200	168.34	61	12.25	1.16	4	1584	7.24	3.67	32.71	32.68	43	422	93.41
Mean	179.6	66.68	10.66	1.99	3.27	1461.44	6.6	3.53	32.48	32.46	44.7	458.37	92.91
LSD	2.5	4.60	1.02	0.13	4.2e <sup>-14</sup>	41.79	0.22	0.17	0.37	0.21	3.38	37.16	0.27

Note: Description of the parameters: GLY: Green leaf yield plant<sup>-1</sup> (g), PP: Number of plucking points in m<sup>-2</sup>, PI: Number of days of plucking interval, SBF: Spreading of bush frame (cm<sup>2</sup>), DR: Number of dormancy period, NP: Number of pubescence of single leaf bud, SF: Score of fermentation rate of green leaf, LB: Length of single bud (cm), QSB: Quality score of black tea, QSW: Quality score of white tea, RP: Recovery days after pruning, NF: Number of flowers plant<sup>-1</sup>, SP: Survivability percentage of cuttings of each genotype.