Turkish Journal of Agriculture - Food Science and Technology, 13(2): 423-438, 2025
DOI: https://doi.org/10.24925/turjaf.v13i2.423-438.7274

Turkish Journal of Agriculture - Food Science and Technology

Available online, ISSN: 2148-127X | www.agrifoodscience.com | Turkish Science and Technology Publishing (TURSTEP)

Morphological Characterization and Multivariate Analysis of Rain Fed Rice (*Oryza sativa* L) Genotypes in Northwest Ethiopia

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ARTICLE INFO

Research Article

Received : 30.10.2024
Accepted : 25.11.2024

Keywords:
Cluster
Polymorphic
Eigen value
Principal component
Shannon Weaver diversity index

ABSTRACT

Over the years, more than 3336 rice genotypes were introduced into Ethiopia from different countries and evaluated for diseases reaction and agronomic traits. However, morphological characteristics and relationships were not well investigated among genotypes. Hence, the objective of this study was to characterize 100 rice genotypes morphologically for better identification and to classify genotypes relationships. The experiment was done using triple lattice design with 10×10 in 2021/22 main cropping season. Twenty-five qualitative morphological traits were used to characterize and 13 quantitative traits were used to categorize relationships of the studied rice genotypes. The Shannon Weaver diversity index of qualitative traits were varied from 0 to 1. Moreover, based on quantitative traits the studied rain fed rice genotypes were grouped into four distinct clusters and four principal components with Eigen value >1 were contributed 78.99% of the total variation. We recommend crossing cluster I with IV genotypes to get early-maturing besides moderate grain yield variety for short rainfall season areas. And cross cluster III with IV genotypes to get medium matured, high filled spikelet per panicle, augmented harvest index, biomass and grain yield variety for long rainfall season areas.

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Introduction

Rice is the world's most essential cereal crop next to wheat by its total production and after maize by its productivity (FAOSTAT, 2020). It is also the staple food for over half of the world's population (Loitongbam et al., 2017).

In Ethiopia, rice is a recent introduced crop that the government has given emphasis to ensuring food security in the country. Rice import is consistently increasing while the volume of domestic production is increased mainly due to productivity increase, area expansion and increasing number of farmers (CSA, 2018).

Hence rice is recently introduced crop in Ethiopia, the source of genotypes until now is via introduction. Since the inception of formal rice research system many genotypes are introduced from different countries. The major source of Ethiopian genotypes are Africa Rice, International Rice Research Institute (IRRI), IRRI-ESA, China and Japan (Asmelash, 2014; Dessie et al., 2019). Between 2007 and 2018 a total of 3336 rice genotypes were introduced and pass through national evaluation procedures for variety release (Dessie et al., 2019). During evaluation stages to release variety the main concern was yield and yield related traits. However, the qualitative morphological characteristics and relationships of the introduced rice genotypes in different times were not studied and documented in detail.

Morphological characterization is essential tool for classification, evaluation of a given genotypes and for selecting lines/varieties (Sarawgi & Ojha, 2016). Qualitative characteristics are known as morphological markers for identification of a given germplasm and less influenced by environment than quantitative traits (Rebeira et al., 2014; Pachauri et al., 2020). Therefore, morphological characterization using qualitative trait is a simple accessed marker to identify and maintain distinct and uniform genotypes.

Clustering and genetic divergence is a multivariate statistical analysis system which partitioning a set of individuals into groups, so that individuals within a group are more similar and individuals in different groups are more dissimilar (Mahalanobis, 1936). Clustering is the process of organizing individuals into groups whose members are similar in some ways (Chahal & Gosal, 2002). There are two types of clustering methods which are distance and model based method clusters (Johnson & Wichern, 1992).

Principal component analysis is the oldest and most popular multivariate technique (Pearson, 1901). Principal component analysis reveals the most contributing traits that accounted for the total genetic variability at each axis of differentiation (Noirot et al., 1996; Sharma, 1998). It reduces a large data set in to correlated variables which aims to identify principal components, combinations of variables which best characterize a data set (Jolliffe, 2002; Akbar et al., 2011). The principal components have both direction and magnitude; the direction represents across which principal axis the data is mostly distributed and the magnitude signifies the amount of variance (Jolliffe, 2002). Eigen values measure the amount of the variation explained by each principal component, an Eigen value >1 is considered for a significant amount of information from the original variables (Kaiser, 1958; Akbar et al., 2011). Traits having closer to |1| within the first principal component influence the clustering more than those with a lower absolute value closer to zero (Chahal & Gosal, 2002).

Therefore, this research was conducted to characterize 100 rain fed rice genotypes morphologically using 25 qualitative traits and categorize relationships of the studied rice genotypes via 13 quantitative traits.

Materials and Methods

Description of the Study Area

The experiment was conducted at Fogera National Rice Research and Training Center (FNRRTC) experiment site in 2021/22 main cropping season. The site is located 57km away from Bahir Dar, capital city of Amhara National Regional state and 607km away from Addis Ababa, Ethiopia, in the north-western part of Ethiopia (Figure 1). The site altitude is located at an altitude 1810m above sea level with geographic coordinates of 37° 41' E longitude and 11°58' N latitude. Based on ten years' average meteorological data, the annual rainfall is 1300mm and the annual minimum is 11.5°C and maximum temperatures is 27.9°C. The soil type is Vertisol (black) with pH of 5.90 (Abebe, 2016).

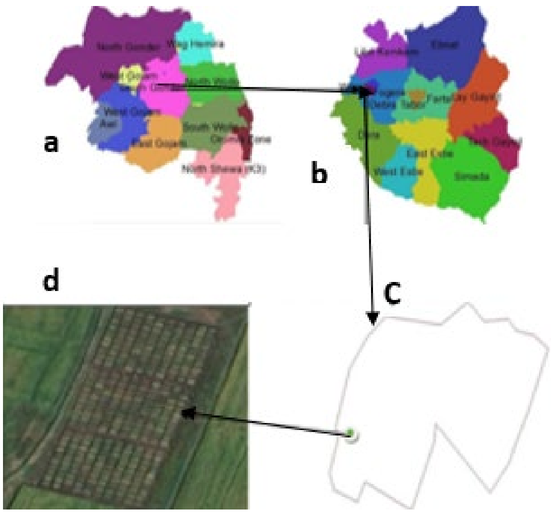

Figure 1. Map locating the study area
(a = map of Amhara region, b = map of South Gondar zone, c = map of FNRRTC experiment station and d = Location of our experiment and its satellite photo)

Experimental Materials

It was composed of 100 rain fed rice genotypes including 10 released varieties (Table 1). All genotypes were obtained from FNRRTC which was sourced from different rice research organization mainly from IRRI and Africa Rice Center. These genotypes were maintained for future breeding work.

Experimental Design

The experiment was laid out in 10 × 10 triple lattice designs. The plot size was 7.5m^2 and the net harvestable plot size was 6m^2, excluding two boarder rows. The space between rows, plots and blocks were 0.25m, 0.5m and 1m, respectively. The plot size, space between rows, plots and blocks were done based on the national rice research protocol for breeding activities of rain fed rice (Zewdu et al., 2020).

Agronomic Practices

A seed rate of 60kg ha^{-1} was applied with direct seeding methods in a row. Fertilizer application and weeding were done based on the local recommendations.

Data Collected

It was collected on plot and plant basis according to standard evaluation systems of rice (Bioversity International, IRRI and WARDA, 2007; IRRI, 2013). The total of 25 morphological traits were collected and the details are summarized in Table 2. Moreover, the details of 13 quantitative traits that were collected either on plant or plot bases and used for multivariate analysis are described as follows:

On plant basis

Plant height (cm): It was measured by taking five plants randomly (by 'X' sampling) in the harvestable plot and measured starting from the base of the main stem to the tip of the main panicle at physiological maturity.

Panicle length (cm): It was measured from 5 randomly taken rice plants of the main tiller panicle at physiological maturity.

Number of filled and unfilled spikelets /panicle: The number of filled and unfilled spikelets per panicle was counted from 5 randomly selected plants at maturity.

Tillering ability, number of fertile and non- fertile tillers per plant: Three time counting was done since the sowing method was drilling. First, number of seedlings were counted before tillering at 50cm row length from two sampled harvestable rows and tagged. Second, maximum tillers were counted at maximum tillering stage from the pre tagged samples. Third, Fertile tillers were counted at maximum tillering from the pre tagged samples too. Then, tillering ability was calculated by dividing the number of tillers at maximum tillering stage by the number of seedlings and the number of non-fertile tillers were obtained by calculating the difference between tillering ability and fertile tillers.

On plot basis

Days to 50% heading: It was recorded by visual judgment in whole plot, which was number of days counted from sowing to 50% heading.

Table 1. List of the one hundred rice genotypes tested at Fogera district, Ethiopia

Genotype #	Genotype Designations	Genotype #	Genotype Designations
G1	GSR IR1-17-Y16-Y3-Y2	G51	MET-HE-17-10
G2	GSR IR1-15-D4-D1-Y1	G52	MET-HE-17-14
G3	GSR IR1-5-D1-D1	G53	MET-HE-17-16
G4	GSR IR1-12-Y4-Y1-D1	G54	MET-HE-17-23
G5	GSR IR1-8-S9-D2-Y2	G55	MET-HE-17-25
G6	GSR IR1-12-S2-Y3-Y2	G56	Aromatic-1
G7	GSR IR1-5-D20-D2-D1	G57	Edirne
G8	GSR IR1-5-S10-D3-Y2	G58	Trakya
G9	GSR IR1-12-S8-Y1-S1	G59	Halilbey
G10	GSR IR1-8-S14-S1-SU1	G60	Osmancik-97
G11	GSR IR1-12-D10-S1-D1	G61	Tunca
G12	GSR IR1-12-Y4-D1-Y2	G62	Condai
G13	GSR IR1-12-S8-Y1-Y2	G63	Hangamchal
G14	GSR IR1-5-S10-D1-D1	G64	Hawaghaelo-2
G15	GSR IR1-8-S6-S3-S1	G65	Namcheobyeo
G16	GSR IR1-5-S12-D3-Y2	G66	Samgangbyeo
G17	GSR IR1-5-S8-D2-S1	G67	Suitou Chuukanbohon Nou 11
G18	ROJOMENA271/10	G68	PCT-11\0\0\2, Bo\2\1>487-1-6-2-3-3-M
G19	IRGA370-38-1-1F-B1-1	G69	CT11231-2-2-1-3-M-5-2-M-3-M
G20	PSBRC92	G70	PCT-11\0\0\2, Bo\2\1>1-M-3-1-2-M
G21	FKRS	G71	PCT-4\0\0\1>161-3-2-1-M
G22	IR75502-5-1-1-B	G72	PCT-4\0\0\1>204-1-3-3-M-3-M
G23	WAB95-B-B-40-HB	G73	PCT-4\0\0\1>295-2-3-1-3-3-M
G24	IR76999-52-1-3-2	G74	PCT-4\0\0\1>295-2-6-1-3-3-M
G25	WAB502-8-5-1	G75	IR 84639-7-76-3-2-1-2-4-2-2-2-B-Tsukuba
G26	WABC165(IAC165)	G76	IR 84633-9-16-5-11-2-2-4-3-2-2-B-Tsukuba
G27	Yungeng 45	G77	SCRID091-10-1-3-2-5
G28	SR35239-HB3403-27	G78	SCRID091-24-3-2-2-3
G29	MwuR4	G79	SCRID090-60-1-1-2-4
G30	Pakistan	G80	SCRID090-72-3-1-3-5
G31	SIM2 SUMADEL	G81	SCRID090-177-2-4-3-4
G32	WAS 127-12-1-2-1	G82	SCRID090-18-1-2-2-1
G33	IR-63275-B-1-1-13-2	G83	SCRID091-20-3-1-3-4
G34	IR-72593-B-B-2-3-14P1	G84	SCRID122-5-2-1-1-3
G35	HHZ 12-Y4-DT1-Y2	G85	SCRID122-13-1-1-4-3
G36	ARS755-5-B-B	G86	SCRID186-72-1-1-2
G37	CT18973-1-7-1-4SR-1P	G87	SCRID198-73-5-1-3
G38	HHZ12-SAL2-Y3-Y2	G88	Kb-2
G39	ARS 775-1-B-B	G89	Zongeng
G40	ARS 105-2-2-B	G90	Yuukeng
G41	Sahel134	G91	Selam(released variety)
G42	ARS-755-4-B-B	G92	Shaga(released variety)
G43	IR95786-9-2-1-2	G93	Wanzaye(released variety)
G44	IR98976-20-1-2-1	G94	Erib(released variety)
G45	IR92521-147-3-1-2	G95	Abay(released variety)
G46	IR98816-10-2-2-2	G96	Fogera-1(released variety)
G47	IR99648-59-1-1	G97	Ediget(released variety)
G48	IR106358-B-B-AJY6	G98	NERICA-12(released variety)
G49	IR97044-1-2-1-2	G99	X-jigina(The most cultivated cultivar)
G50	IR99637-6-1-1	G100	NERICA- 4(released variety)

Days to 85% maturity: Maturity was recorded by visual judgment of the whole plot, which was number of days from sowing to 85% physiological maturity.

Above ground biomass yield (kg/ha): It was measured in each harvestable plot after two days sundry.

Grain yield (Kg/ha): Cleaned paddy rice yield and moisture were measured. Then, the grain yield was adjusted at 14% moisture content as follows:

$$\text{Grain yield} = \frac{(Akg(100 - B))}{(\,100 - mc)}$$

Where, A=actual measured weight, B=Measured moisture content, mc= moisture content.

Harvest index (HI %): It was calculated as follows:

$$\text{HI \%} = \frac{(\text{ Economic grain yield per plot})}{(\text{ Biological yield per plot})} * 100$$

Thousand grain weights (g): It was counted by seed counter by taking whole grains randomly from clean and sun dried for each of harvestable plot and then weighed by using sensitive balance and adjusted at 14% moisture content.

Statistical Analysis

Statistical analysis for qualitative morphological traits

Shannon Weaver diversity index formula was used (Shannon and Weaver, 1949) and computed by excels as follows:

$$H' = \left[\sum \left(\frac{n}{N}\right) * \{log_2\left(\frac{n}{N}\right) * (-1)\}\right] / log_2(k)$$

Where, H' stands for standardized Shannon Weaver diversity index, k stands for number of phenotypic classes for a character, n stands for frequency of a phenotypic class of that character and N stands for total number of observations for that character.

Cluster and genetic divergence analysis

The data was standardized to have a mean of zero and variance of one before cluster analysis by using paired group algorithm. Clustering of genotypes was performed using the proc cluster procedure of SAS software version 9.4 (SAS Institute Inc., 2013). The appropriate number of clusters was determined based on Cubic clustering criterion (CCC), Pseudo F and Pseudo t^2 values (Figure 19). The points where local peaks of the CCC and pseudo F value join with small value of the pseudo-t^2 statistic followed by a larger pseudo-t^2 value for the next cluster fusion (Mohammadi & Prasanna, 2003).

Principal Component Analysis

It is used to complement cluster analysis (Lombard et. al., 2000) and to explore patterns of genetic diversity (Mohammadi & Prasanna 2003). Eigen values greater than or equal to 1 were considered important to explain the observed variability (Jeffers, 1967). The principal component analysis was computed by SAS software version 9.4 (SAS Institute Inc., 2013) and the bi-plot illustration was computed by Genstat (2015).

Results and Discussion

Morphological Characteristics

Leaf senescence

As indicated in Figure 2 and Table 2, among the tested genotypes, 35% was very early in leaf senescence at harvesting and all leaves were lost their green color before grain maturity. The other 57% of the genotypes were early (all leaves were lost their green color at harvest), 7% of the rice genotypes intermediate (one leaf were still green at harvest) and 1% of the studied genotypes were late. The result of leaf senescence showed polymorphic with Shannon Weaver diversity index of 0.57 (Table 2). In harmony with the present result, Mondal et al. (2014) reported leaf senescence as polymorphic. This wide variability in the current report is an opportunity for future breeding works. Accordingly, G33 (IR-63275-B-1-1-13-2) can be used to improve early leaf senescence for future breeding works (Table S1). Hence, late leaf senescence has significant impact on photosynthesis, nutrient remobilization, stress responses and productivity (Guo et al., 2021). In addition, the study area beneficiaries prefer stay green rice to use the straw for animal feed.

Panicle exertion

As showed in Table 2, the rice genotypes scored 18% of enclosed, 12% of partly exerted, 16% of just exerted, 42% of moderately well exerted and 12% of well exerted. The result of panicle exertion indicated polymorphic with Shannon Weaver diversity index of 0.92 (Figure 3; Table 2). In agreement, Ghimire et al. (2018) reported polymorphic with the index of 0.75. Differently, Mondal et al. (2014) and Pathak (2020) reported dimorphic panicle exertion. Therefore, the present study had better genetic variability on panicle exertion. The more exerted is better, because decreased panicle exertion as a causal factor of spikelets sterility in moisture stressed rice (O' Toole & Namuc, 1983).

Panicle threshability

As indicated in Table 2, panicle threshability of the rice materials were polymorphic with Shannon Weaver diversity index of 0.80. Similarly, Pathak (2020) reported polymorphic of panicle threshability.

Leaf blade color and pubescence

As showed in Table 2, leaf blade color of the studied rice genotypes were polymorphic with Shannon Weaver diversity index of 0.45. While the leaf blade pubescence showed dimorphic with the index of 0.56. Similarly, Rawte & Saxena (2018) reported polymorphic for leaf blade color. Differently, Sinha & Mishra (2013) showed polymorphic of leaf blade pubescence and also Pathak (2020) reported non polymorphic of leaf blade pubescence (all glabrous).

Basal leaf sheath anthocyanin coloration

Ninety eight percent of the rice genotypes had no basal leaf sheath anthocyanin coloration, only 1% (G31 = SIM2 SUMADEL) showed medium and 1% (G18 = ROJOMENA271/10) showed strong basal leaf sheath anthocyanin coloration (Figure 4; Table 2, 3). Its result indicated very small evenness of polymorphic with Shannon Weaver diversity index of 0.08.

Leaf angle

As indicated in Figure 5 & Table 2, 66% the genotypes were erect and 34% were intermediate. Leaf angle was dimorphic with Shannon Weaver diversity index of 0.58. In different result to this study, Ghimire et al. (2018) reported polymorphic with the index of 0.69. This implies that the present study genotypes are more advanced than Ghimire et al. (2018) cold tolerant rice accessions because the more erect leaf angle are better for effective light interception.

Flag leaf angle

As indicated in Table 2, flag leaf angle was polymorphic with Shannon Weaver diversity index of 0.67. Moreover, among studied rice genotypes 58% were erect, 31% were intermediate and 11 % were horizontal (Figure 6). Similar to with the current study, Ghimire et al. (2018) & Pathak (2020) reported polymorphic of the flag leaf angle.

Ligules color

Among the studied rice genotypes, 99% showed white and only 1 % (G18 = ROJOMENA271/10) showed purple lines ligules color which showed dimorphic with small evenness (Figure 7; Table 2, 3). Similarly, Mondal et al. (2014) reported dimorphic of the ligules color.

Culm Angle and ligules shape

All the tested rice genotypes had same erected culm angle and truncate ligules shape with Shannon Weaver diversity index of 0 (Figure 8; Table 2). This implies that the studied genotypes didn't show polymorphic for these two traits.

Table 2a. Phenotypic classes, proportion and diversity index for 100 rice genotypes using qualitative traits

S. No.	Traits	Measuring time	Number of phenotypic classes	Scale	Number of genotypes	Proportion of a phenotypic class	Shannon Weaver diversity index (H')
1	Leaf senescence	At harvest	Very early	1	35	35	0.57
			Early	3	57	57	
			Intermediate	5	7	7	
			Late	7	1	1	
			Very late	9	0	0	
2	Panicle exertion	Dough growth stage	Enclosed	1	18	18	0.92
			Partly exerted	3	12	12	
			Just exerted	5	16	16	
			Moderately well exerted	7	42	42	
			Well exerted	9	12	12	
3	Panicle Threshability	At harvest	Difficult (less than 1%)	1	11	11	0.80
			Moderately difficult (1-5%)	3	3	3	
			Intermediate (6-15%)	5	8	8	
			Loose (26-50%)	7	36	36	
			Easy (51-100%)	9	42	42	
4	Leaf blade pubescence	Heading stage	Glabrous	1	31	31	0.56
			Intermediate	2	69	69	
			Pubescent	3	0	0	
5	Leaf blade color	Booting stage	Light green	1	19	19	0.45
			Green	2	72	72	
			Dark green	3	8	8	
			Purple tips	4	0	0	
			Purple margins	5	1	1	
			Purple mixed with green	6	0	0	
			Purple	7	0	0	
6	Basal leaf sheath anthocyanin coloration	Stem elongation stage	Absent	1	98	98	0.08
			Weak	3	0	0	
			Medium	5	1	1	
			Strong	7	1	1	
7	Leaf angle	Booting stage	Erect	1	66	66	0.58
			Intermediate	3	34	34	
			Horizontal	5	0	0	
8	Flag leaf angle	Booting stage	Erect	1	58	58	0.67
			Intermediate	3	31	31	
			Horizontal	5	11	11	
			Descending	7	0	0	
9	Ligules color	Booting stage	Absent	0	0	0	0.04
			White	1	99	99	
			Purple lines	2	1	1	
			Purple	3	0	0	
10	Culm angle	Dough growth stage	Erect (<30°)	1	100	100	0.00
			Intermediate (~45°)	3	0	0	
			Open (~60°)	5	0	0	
			Spreading (>60°)	7	0	0	
			Procumbent	9	0	0	
11	Ligules Shape	Stem elongation stage	Absent	0	0	0	0.00
			Acute to acuminate	1	0	0	
			Cleft	2	100	100	
			Truncate	3	0	0	
12	Collar color	Booting stage	Absent (collarless)	0	0	0	0.04
			Light green	1	99	99	
			Green	2	0	0	
			Purple	3	1	1	
13	Auricle Color	Stem elongation stage	Absent (no auricles)	0	0	0	0.05
			Light green	1	99	99	
			Purple	2	1	1	
14	Culm internodes color	Dough growth stage	Green	1	31	31	0.48
			Light gold	2	68	68	
			Purple lines	3	1	1	
			Purple	4	0	0	

Table 2b. Phenotypic classes, proportion and diversity index for 100 rice genotypes using qualitative traits

S. No.	Traits	Measuring time	Number of phenotypic classes	Scale	Number of genotypes	Proportion of a phenotypic class	Shannon Weaver diversity index (H')
15	Panicle type	Dough growth stage	Compact	1	32	32	1.00
			Intermediate	2	34	34	
			Open	3	34	34	
16	Panicle curvature of main axis	Maturity stage	Upright	1	1	1	0.54
			Semi-upright	3	33	33	
			Slightly drooping	5	65	65	
			Strongly drooping	7	1	1	
17	Awning	Dough growth stage	Absent	0	88	88	0.27
			Short and partly awned	1	10	10	
			Short and fully awned	5	1	1	
			Long and partly awned	7	0	0	
			Long and fully awned	9	1	1	
18	Awn color	Dough growth stage	Awnless	0	88	88	0.25
			Straw	1	8	8	
			Gold	2	0	0	
			Brown (tawny	3	0	0	
			Red	4	4	4	
			Purple	5	0	0	
			Black	6	0	0	
19	Apiculus color	Dough growth stage	White	1	0	0	0.4
			Straw	2	68	68	
			Brown (tawny)	3	0	0	
			Red	4	0	0	
			Red apex	5	28	28	
			Purple	6	1	1	
			Purple apex	7	3	3	
20	Lemma and Palea Color	Maturity stage	Straw	0	0	0	0.37
			Gold and gold furrows on straw background	1	50	50	
			Brown spots on straw	2	0	0	
			Brown furrows on straw	3	0	0	
			Brown (tawny)	4	46	46	
			Reddish to light purple	5	1	1	
			Purple spots on straw	6	0	0	
			Purple furrows on straw	7	3	3	
			Purple	8	0	0	
			Black	9	0	0	
21	Lemma and Palea Pubescence	Maturity stage	Glabrous	1	14	14	0.58
			Hairs on lemma keel	2	0	0	
			Hairs on upper portion	3	1	1	
			Short hairs	4	64	64	
			Long hairs (velvety)	5	21	21	
22	Chalkiness of endosperm	After harvest	None	0	32	32	0.93
			Small (less than 10%)	1	40	40	
			Medium (11% to 20%)	5	15	15	
			Large (more than 20%)	9	13	13	
23	Brown rice length	After harvest	Extra-long (>7.5 mm)	1	3	3	0.75
			Long (6.61 to 7.5 mm)	3	27	27	
			Medium (5.51 to 6.6 mm)	5	57	57	
			Short (5.5mm or less)	7	13	13	
24	Brown rice shape	After harvest	Slender – ratio (Over 3.0)	1	25	25	0.69
			Medium – ratio (2.1 to 3.0)	3	59	59	
			Bold – ratio(1.1 to 2.0)	5	16	16	
			Round – ratio(Less than 1.1)	7	0	0	
25	Seed coat (bran) color	After harvest	White	1	91	91	0.16
			Light brown	2	0	0	
			Speckled brown	3	0	0	
			Brown	4	0	0	
			Red	5	9	9	
			Variable purple	6	0	0	
			Purple	7	0	0	

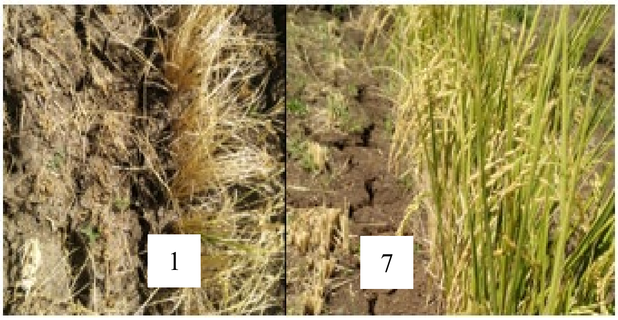

Figure 2. Leaf senescence scale 1 and 7 (Table 2): photos were taken in our experiment in 2021

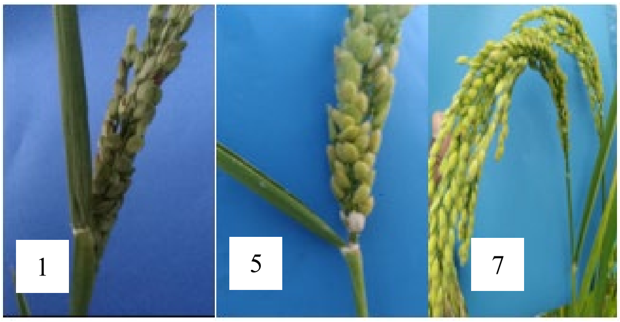

Figure 3. Panicle exertion scale 1, 5 and 7 (Table 2): photos were taken in our experiment in 2021

Figure 4. Basal Leaf Sheath anthocyanin coloration scale 1, 5 and 7 (Table 2): photos were taken in our experiment in 2021

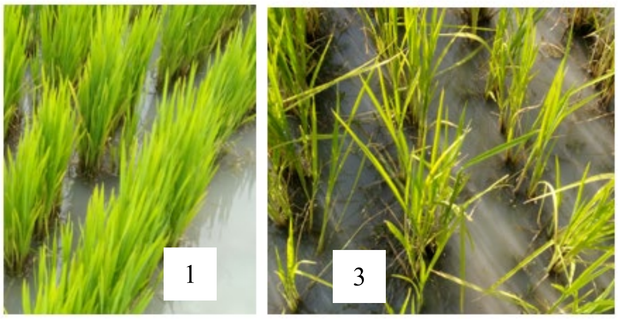

Figure 5. Leaf angle scale 1 and 3 (Table 2): photos were taken in our experiment in 2021

Figure 6. Flag leaf angle scale 3 and 5 (Table 2): photos were taken in our experiment in 2021

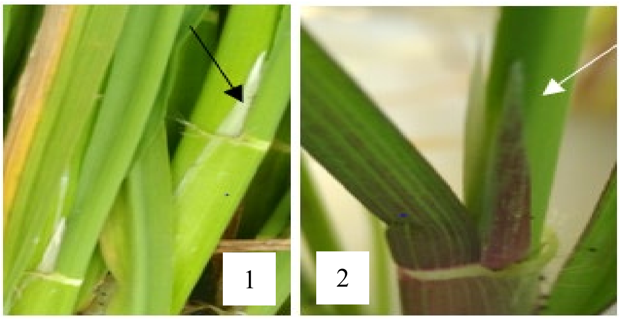

Figure 7. Ligules color scale 1 and 2 (Table 2): photos were taken in our experiment in 2021

Therefore, culm angle and ligules shape are not important traits to characterize the FNRRTC genotypes. Similarly, Mondal et al. (2014) reported that ligules shape were non-polymorphic. Similarly, Sinha & Mishra (2013) reported the non-polymorphic of ligules shape; while, they reported polymorphic for culm angle.

Collar and auricle color

Both collar and auricle color showed dimorphic with very small evenness of Shannon Weaver diversity index of 0.04 and 0.05, respectively (Table 2). Moreover, 99% the studied genotypes scored light green and 1% (G31 = SIM2 SUMADEL) scored purple collar color (Figure 9; Table 2, 3). In different to the present study result, Pathak (2020) reported polymorphic for collar color.

Culm internodes color

It revealed polymorphic with Shannon Weaver diversity index of 0.48 (Table 2). Among 100 rice genotypes considered 31% were green, 68% were light gold and 1% was purple lines (Figure 10; Table 2). In different to the present study, Ghimire et al. (2018) reported dimorphic of culm internodes with Shannon Weaver diversity index of 0.14 and 95.3% of their studied rice accessions were light gold and the other 4.7% were of purple lines. The other scholars Nascimento et al. (2011) and Pathak (2020) also reported different results to the present findings that their studied rice genotypes showed non-polymorphic for culm internodes color. This indicates that the genotypes in our study had appreciable amount of variation on culm internode color.

Panicle type and curvature of main axis

The Shannon Weaver diversity index of panicle type was 1, perfect evenness which implies the studied genotypes were fairly distributed in the three phenotypic classes (Table 2). In contrary, Nascimento et al. (2011) reported non-polymorphic of panicle type (all 146 accessions were intermediate). For panicle curvature of main axis of the studied genotypes which were upright (1%), semi-upright (33%), slightly drooping (65%) and strongly drooping (1%) with the index of 0.53 (Figure 11; Table 2). In line with the present study, Mondal et al. (2014) reported polymorphic of panicle curvature of main axis and similarly Pathak (2020) reported polymorphic of panicle type.

Awning

As indicated in Figure 12 & Table 2, awning showed polymorphic with small evenness and Shannon Weaver diversity index of 0.27 which awning absent (88%), short and partly owned (10%), short and fully awned (1%) plus long and fully awned (1%). Similarly, Sinha & Mishra (2013) reported polymorphic of awning. On the other hand, Mondal et al. (2014) reported dimorphic for awning. In the present study, 1% of genotypes were long and fully awned (Table 2). Sahu et al. (2018) reported that expression of long and fully awned trait advocated the presence of two independent genes; one dominant and another one recessive. As well as 10% of the present study genotypes were short and partly awned. Sahu et al. (2018) reported that partially awned trait was expressed by three gene interaction of two dominant genes either of which being capable to complement with another dominant gene.

Awn color

It indicated polymorphic with small evenness and Shannon Weaver diversity index of 0.25 (Table 2). Among 100 studied rice genotypes, 88%, 8% and 4% were Awnless, Straw and red awn color, respectively (Figure 13; Table 2). In agreement with the present study, Sinha & Mishra (2013) and Mondal et al. (2014) reported polymorphic for awn color.

Apiculus color

As indicated in Table 2, apiculus color confirmed polymorphic by small evenness with Shannon Weaver diversity index of 0.4. Apiculus color that indicated straw (68%), red apex (28%), purple (1%) and purple apex (3%) are illustrated in Figure 14. In agreement to the present study, Nethra et al. (2005) reported polymorphic for apiculus color. The result the present studied genotypes on apiculus color can be used as phonological markers for future breeding work to identify distinctiveness and uniformity of a given genotypes or variety at dough growth stage.

Lemma and palea Color

As indicated in Table 2, lemma and palea color revealed polymorphic with small evenness and Shannon Weaver diversity index of 0.37. Lemma and palea color that scored gold (50%), brown (tawny) (46%), reddish to light purple (1%) and purple furrows on straw (3%) are illustrated in Figure 15. In agreement to the present result, Mondal et al. (2014) & Pathak (2020) reported polymorphic for lemma and palea color.

Lemma and palea pubescence

It showed polymorphic with Shannon Weaver diversity index of 0.58 (Table 2). Among 100 studied rice genotypes 14% were glabrous, 1% were hairs on upper portion, 64% were short hairs and 21% were long hairs (Figure 16; Table 2). In line with the present study, Mondal et al. (2014) demonstrated polymorphic for lemma and palea pubescence.

Chalkiness of endosperm

It showed polymorphic with Shannon Weaver diversity index of 0.93. Among 100 studied rain fed rice genotypes, 32%, 40%, 15%, and 13% were translucent (no chalkiness), small chalkiness, medium chalkiness and large chalkiness, respectively (Figure 17; Table 2). Those 32% of studied rain fed rice genotypes are opportunities for breeders for selection as well as for hybridization because as translucent increases rice quality also increases (Sharma & Khanna, 2019).

Brown rice length and shape

Both brown rice length and shape showed polymorphic with Shannon Weaver diversity index of 0.75 and 0.69, respectively. Among the studied rice genotypes, slender (25%), medium (59%), and bold (16%) brown rice shape (Table 2). In the study area, people who consume rice in the form of 'Injera' may not concern for rice shape while people who live in urban areas that used for table rice prefer slender shape.

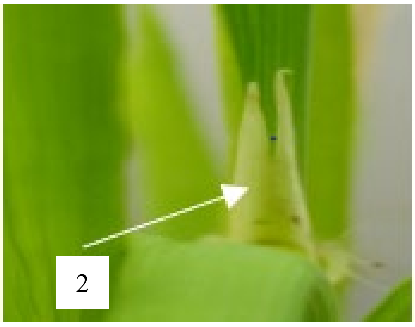

Figure 8. Ligules shape scale 2 (Table 2): photo was taken in our experiment in 2021

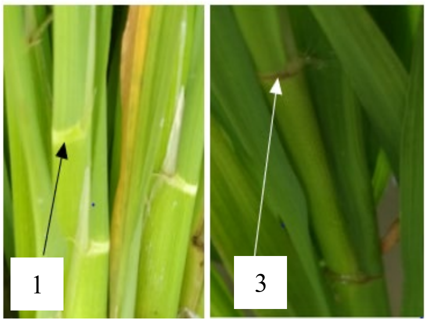

Figure 9. Collar color scale 1 and 3 (Table 2): photos were taken in our experiment in 2021

Figure 10. Culm internodes color scale 1, 2 and 3 (Table 2): photos were taken in our experiment in 2021

Figure 11. Panicle curvature of main axis scale 1, 3, 5 and 7 (Table 2): photos were taken in our experiment in 2021

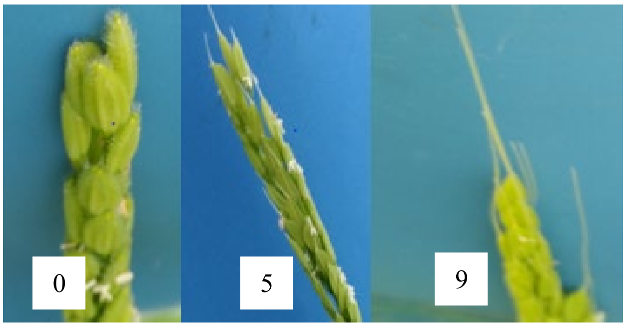

Figure 12. Awning scale 0, 5 and 9 (Table 2): photos were taken in our experiment in 2021

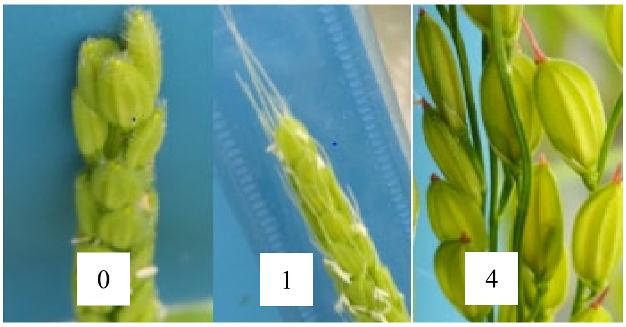

Figure 13. Awn color scale 0, 1 and 4 (Table 2): photos were taken in our experiment in 2021

Figure 14. Apiculus color scale 2, 5, 6 and 7 (Table 2): photos were taken in our experiment in 2021

Figure 15. Lemma and palea color scale 1, 4, 5 and 7 (Table 2): photos were taken in our experiment in 2021

Figure 16. Lemma and palea pubescence scale 1, 3, 4 and 5 (Table 2): photos were taken in our experiment in 2021

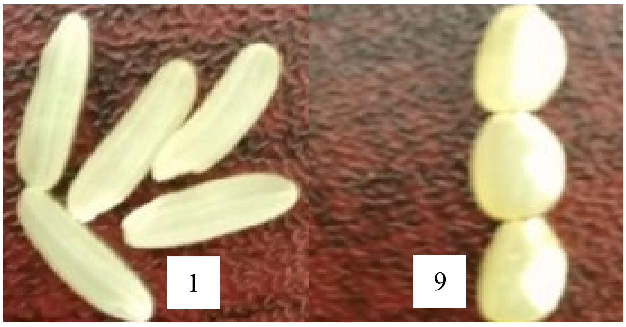

Figure 17. Chalkiness of endosperm scale 1 and 9 (Table 2): photos were taken in our experiment in 2021

Figure 18. Seed coat color scale 1 and 5 (Table 2): photos were taken in our experiment in 2021

Seed coat color

It showed very small evenness with Shannon Weaver diversity index of 0.16 (Table 2). Among 100 studied genotypes, 91% had white and 9% had red seed coat color (Figure 18; Table 2). These 91% of studied genotypes that showed white seed coat color are opportunities for breeders because farmers of the study area prefer white seed coat color. In general the detail of each 100 genotypes for each 23 di/polymorphic qualitative morphological characteristics are presented in Supplementary Table 1.

Multivariate Analysis

Clustering analysis

As illustrated in Figure 20 and Table 3, the current studied 100 rain fed rice genotypes were grouped into four clusters based on their similarities on 13 quantitative morphological traits with the cutting point of 0.97 distances. Cluster I was the largest cluster which consisted of 58 genotypes followed by clusters II, III and IV with 28, 12 and 2 genotypes, respectively. This result indicated that the existence of genetic divergence among the studied genotypes which implies that genotypes within a cluster are genetically less different from each other than genotypes found in different clusters .

Similar to the present results, many researchers reported the existence of genetic diversity in their studied genotypes. Worede et al. (2014) reported two hierarchical clusters with additional subgroups in each groups for 24 rice genotypes that were done in Thailand. Tejaswini et al. (2016) studied 121 rice genotypes and reported 12 clusters. The other researchers Rashid et al. (2013) and Dhakal et al. (2020) reported 6 clusters for 20 and 30 rice landraces, respectively. In addition, Fentie et al. (2021) reported 4 clusters for 30 studied rain fed rice genotypes.

Cluster distance and mean analysis

As presented in Table 4, the maximum average inter cluster distance was found between clusters II and IV ($D^2 = 49.96$) followed by between clusters III and IV ($D^2 = 32.76$) which showed that the genotypes found in these clusters are genetically more diversified than other clusters. These results are opportunities for breeders to hybridize and would bring maximum heterosis to generate promising segregantes for grain yield and other important traits. In line with the present study, many researchers found maximum average inter cluster distances between their reported clusters. Dhakal et al. (2020) reported maximum average inter cluster distances for their studied genotypes.

On the other hand, the minimum average inter cluster distances were found among cluster I and III, while that distance was big as compared with intra cluster distances. Crossing of genotypes from cluster I and III might not give higher heterotic value in F1 generation. From 10 released and commonly cultivated varieties, nine were in cluster I and only one (selam) was in cluster III. Therefore, according to the present results, hybridization between these 10 released varieties would not give heterosis in F1 generation. Therefore to get heterosis F1 generation of these10 released varieties, it is better to cross with genotypes that found in cluster II and IV. The chi-square test among all inter clusters were significant ($p < 0.01$), which implies that categorical traits for clustering were highly correlated for each genotypes under each of those significant inter clusters. While, the chi-square test between clusters I and III were not significant which revealed that the traits used for clustering of genotypes were not correlated in cluster I and III based on Chi-square test of independence interpretation by Turhan (2020).

Cluster mean of 13 quantitative of the studied rice genotypes are presented in Table 5. Considerable differences were found among 13 quantitative traits of inter-clusters.

Cluster I comprised 58 genotypes (Table 3). This cluster had characteristics of low number of fertile tillers, short panicle length, low number of unfilled spikelets, early heading, early mature, low adjusted grain yield, low harvest index and heavy 1000 seed weight as compared to other clusters (Table 5). In agreement to the present findings, Abebe (2016) reported same characteristics of early heading, relatively early maturing period, lowest biomass yield and heavy 1000 grain weight in the same cluster. The other researchers Dejen Bekis et al. (2021) reported similar short panicle length, low number of filled spikelets and high thousand grain weight in one cluster. Besides, the present study of cluster I had moderate maximum tillering ability, fertile tillers per panicle, plant height, filled spikelets per panicle and biomass yield. Similar to the present study, Abebe (2016) found same characteristics of moderate number of filled spikelets and fertile tillers in the same cluster. In agreement to the current study, Fentie et al. (2021) also reported similar characteristics of moderate fertile tiller per plant, plant height, panicle length and biomass yield in the same cluster.

Table 3. Distribution of 100 rice genotypes into 4 clusters based on genetic divergence analysis

Cluster	No. of Genotypes	Proportion in (%)	Genotypes
I	58	58	G2, G7, G8, G9, G12, G16, G17, G19, G20, G21, G22, G23, G25, G26, G28, G29, G30, G51, G52, G53, G56, G57, G58, G59, G60, G61, G62, G63, G64, G65, G66, G67, G69, G70, G71, G72, G73, G74, G77, G78, G79, G80, G81, G82, G83, G84, G85, G86, G87, G92, G93, G94, G95, G96, G97, G98, G99 and G100
II	28	28	G5, G11, G13, G14, G15, G24, G31, G32, G33, G34, G35, G36, G37, G38, G39, G40, G41, G42, G43, G44, G46, G47, G48, G49, G50, G54, G75 and G76
III	12	12	G1, G3, G4, G6, G10, G27, G45, G55, G88, G89, G90 and G91
IV	2	2	G18 and G68

Table 4. Pair-wise generalized intra - (bolded diagonal) and inter-cluster distances (off-diagonal)

Cluster	1	2	3	4
1	4.33			
2	27.79**	3.64		
3	19.72^{ns}	30.04**	3.77	
4	30.34**	49.96**	32.76**	4.36

** Significant > χ^2 value 26.22($p < 0.01$) and ns = non-significant < χ^2 value 21.03($p < 0.05$)

Table 5. Four cluster mean values of 13 quantitative traits

	Clusters			
Traits	I	II	III	IV
MTA	2.10	3.22^{H}	2.04^{L}	2.69
FTP	1.61	2.22^{H}	1.52^{L}	1.92
NFT	0.57^{L}	1.09^{H}	0.58	0.83
PH	78.31	61.66^{L}	82.42	111.35^{H}
PL	17.87^{L}	18.77	19.11	22.63^{H}
FSP	81.81	81.70^{L}	109.16^{H}	104.23
UFS	7.21^{L}	13.02^{H}	9.07	8.53
DM	136.57^{L}	148.37^{H}	145.92	143.33
DH	102.76^{L}	114.50^{H}	109.92	109.33
BYD	8.67	8.58	8.55^{L}	10.89^{H}
AGY	2.85^{L}	3.61	4.00	4.05^{H}
HI	33.52^{L}	42.28	46.94^{H}	37.37
ATW	29.10^{H}	22.96^{L}	25.55	24.36

‘L’ and ‘H’ are the lowest and highest value of cluster mean, respectively. MTA = Maximum tillering ability; FTP = Number of fertile tillers per plant; NFT = Number of Non-fertile tillers per plant; PH = Plant height (cm); PL = Panicle length; FSP = Number of filled spikelets per panicle; UFS = Number of unfilled spikelets per panicle; DM = Days to 85% maturity; DH = Days to 50% heading; BYD = Above ground biomass yield (ton/ha); AGY = Adjusted grain yield (kg/ha) at 14% moisture content; HI = Harvest Index %; ATW = Adjusted thousand grain weight (g) at 14% moisture content

Table 6. Eigenvectors, variance explained and Eigen values of the first four PCs

Traits	Eigen vectors			
	PC-1	PC-2	PC-3	PC-4
MTA	0.36	-0.10	0.38	-0.15
FTP	0.30	-0.05	0.49	-0.13
NFT	0.35	-0.14	0.20	-0.08
PH	-0.18	0.47	0.09	0.00
PL	0.19	0.40	-0.03	0.29
FSP	0.06	0.48	-0.27	0.04
UFS	0.29	-0.13	-0.23	0.27
DM	0.36	0.01	-0.18	0.30
DH	0.36	0.00	-0.11	0.34
BYD	-0.03	0.39	0.51	0.29
AGY	0.26	0.40	0.02	-0.39
HI	0.28	0.16	-0.31	-0.59
ATW	-0.32	0.03	0.16	-0.09
EV	5.38	2.52	1.34	1.03
EXV	41.38	19.38	10.31	7.92
CV	41.38	60.76	71.07	78.99

MTA = Maximum tillering ability; FTP = Number of fertile tillers per plant; NFT = Number of Non-fertile tillers per plant; PH = Plant height (cm); PL = Panicle length; FSP = Number of filled spikelets per panicle; UFS = Number of unfilled spikelets per panicle; DM = Days to 85% maturity; DH = Days to 50% heading; BYD = Above ground biomass yield (ton/ha); AGY = Adjusted grain yield (kg/ha) at 14% moisture content; HI = Harvest Index %; ATW = Adjusted thousand grain weight (g) at 14% moisture content; EV = Eigen value; EXV = Explained variance; CV = Cumulative variance (%) (%)

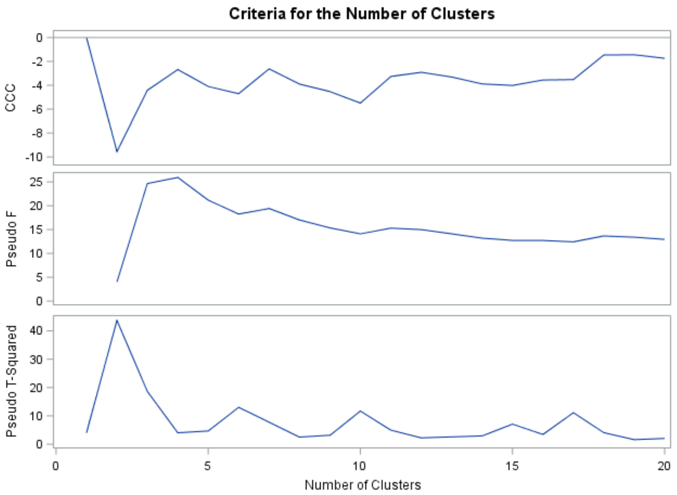

Figure 19. Criteria for the number of clusters

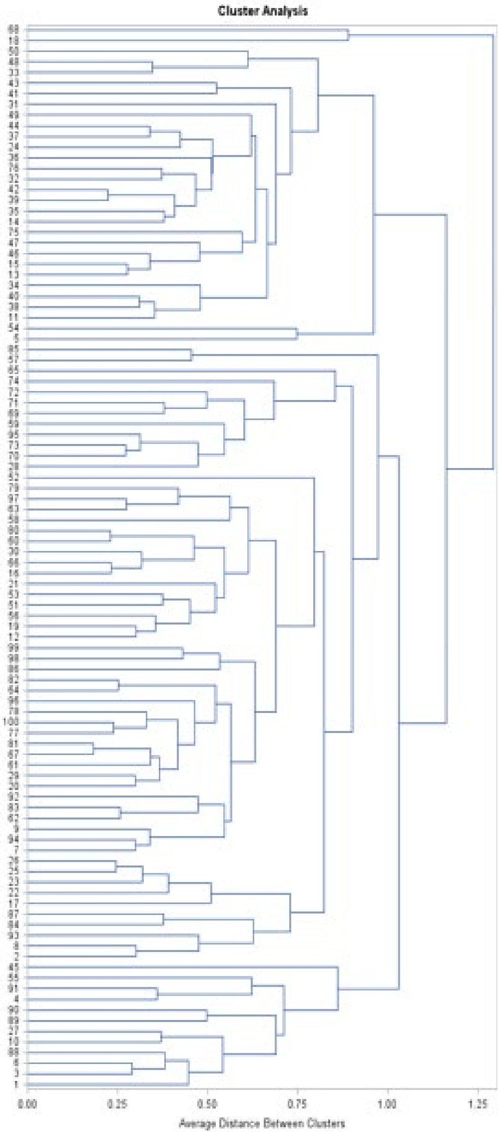

Figure 20. Dendrogram that showing relationships among 100 rain fed rice genotypes

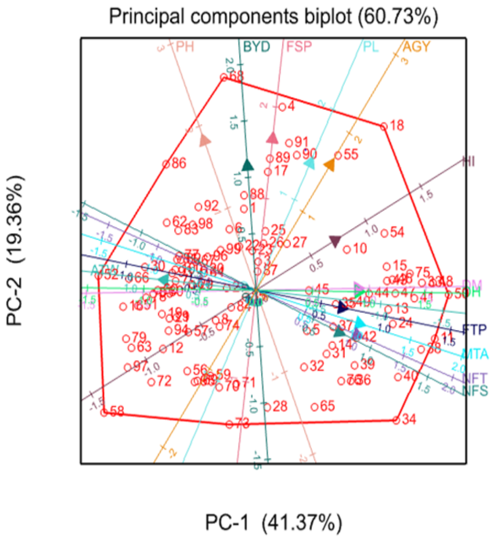

Figure 21. Biplot of PC1 and PC2 showing the relationships of genotypes by traits
The traits abbreviations are expanded in Table 6 and genotype designations are depicted in Table 1.

Cluster II included 28 genotypes (Table 3). It had features of high maximum tillering ability, fertile tiller per plant and unfilled spikelets per panicle, late heading and maturing. Moreover, cluster II had characteristics of short plant height, low filled spikelets per panicle and 1000 seed weight. In addition, cluster II had characteristics of relatively moderate panicle length, biomass yield, grain yield and harvest index (Table 5). In agreement to this study, Tiruneh et al. (2019) reported high tillering ability, fertile tillers/plant and number of unfilled grains/panicle in the same cluster. The other researchers Alamir Ayenew et al. (2020) reported short plant height, moderate panicle length, late heading and maturing in the same cluster.

Cluster III consisted of 12 genotypes (Table 3). This cluster had characteristics of low maximum tillering ability, fertile tiller/plant and biomass yield. Moreover, cluster III had high filled spikelets per panicle and harvest index. In addition, cluster III had feature of moderate plant height, panicle length, non - filled spikelets per panicle, heading, maturing, grain yield and 1000 seed weight (Table 5). In corresponding to the present study, Abebe (2016) reported similar high filled spikelets/panicle and harvest index in the same cluster.

Cluster IV comprised only two genotypes (G18 = ROJOMENA271/10 and G68 = PCT-11\0\0\2, Bo\2\1>487-1-6-2-3-3-M). It had also its own characteristics of long plant height and panicle length, high biomass yield and grain yield (Table 5). Moreover, the other traits of this cluster had moderate mean values. Similarly, Tiruneh et al. (2019) reported long plant height and panicle length, high biomass yield and grain yield in the one cluster. The other researcher Birhanu (2020) scored high biomass yield and grain yield in the same cluster.

Principal component analysis

The result of the principal component analysis (PCA) is represented in Figure 21 and Table 6. The study was carried out using 100 rain fed rice genotypes with 13 quantitative traits. Among 13 principal components (PC), the first four PC with Eigen value >1 were maintained. These 4 PC contributed to 78.99% of the total variance. PC1accounted for the highest variance (41.38%) followed by PC2 (19.38%), PC3 (10.31%) and PC4 (7.92%). Similarly, many researchers reported that most of the total variation was explained by the first three to five PC. Ayenew et al. (2020) reported that 64.16% variability was described by the first three PC. The other researchers Abebe (2016) reported that 79.23% variation was explained by the first four PC. Moreover, Worede et al., (2014), Tiruneh et al. (2019), Birhanu (2020), Dhakal et al. (2020), and Kashyap & Yadav (2020) reported 89.68%, 75.20%, 75.56%, 84.67% and 80.03% of the total variation was explained by the first five PC, respectively; among different studied rice genotypes.

According to Raji (2003), traits having coefficients of the Eigen vectors value greater than 0.3 were considered as important effects on the overall variation. Moreover, the direction of Eigen vectors value (±) represents across which principal axis the data is mostly distributed and the magnitude signifies the amount of variance (Jolliffe, 2002). Based on these evidences, the first four PC of the present study are discussed as follows:

Supplementary Table 1a. Qualitative characterization for 100 rice genotypes in Ethiopia

GEN	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	R	S	T	U	V	Y	Z
G1	3	7	1	2	2	1	1	3	1	1	1	2	1	5	0	0	2	4	4	5	5	5	1
G2	3	7	7	1	3	1	1	1	1	1	1	2	1	3	0	0	2	4	4	1	7	5	1
G3	3	7	1	1	2	1	1	1	1	1	1	2	1	3	0	0	2	4	4	1	7	5	1
G4	3	9	7	2	2	1	1	3	1	1	1	2	1	3	0	0	2	4	4	5	7	5	1
G5	1	7	1	1	2	1	1	1	1	1	1	2	2	3	0	0	2	4	4	5	7	5	1
G6	3	7	3	2	2	1	1	1	1	1	1	1	1	3	0	0	2	4	4	1	7	5	1
G7	3	7	1	2	2	1	1	1	1	1	1	2	1	3	0	0	2	4	5	0	5	3	1
G8	3	7	7	1	2	1	1	1	1	1	1	2	1	3	0	0	2	4	4	5	7	5	1
G9	3	7	1	1	2	1	1	1	1	1	1	2	1	3	0	0	2	4	4	0	7	5	1
G10	3	3	9	1	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	1	5	3	1
G11	3	1	9	2	2	1	1	1	1	1	1	1	2	3	0	0	2	1	4	0	5	1	1
G12	3	5	9	2	2	1	3	3	1	1	1	2	1	3	0	0	2	4	5	5	5	3	1
G13	3	3	9	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	5	1	1
G14	3	3	9	1	2	1	3	3	1	1	1	2	3	5	0	0	2	1	4	1	3	3	1
G15	3	3	9	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	5	1	1
G16	3	7	9	2	2	1	3	3	1	1	1	2	1	3	0	0	2	4	5	5	5	3	1
G17	1	7	3	2	1	1	3	1	1	1	1	2	2	3	0	0	2	1	4	1	3	1	1
G18	1	9	7	2	5	7	1	1	2	1	1	3	3	3	0	0	7	1	4	1	5	3	1
G19	1	7	9	2	3	1	1	3	1	1	1	2	2	5	1	1	2	4	4	9	5	3	1
G20	3	7	5	1	3	1	1	1	1	1	1	2	2	5	0	0	5	1	1	1	3	3	1
G21	5	5	9	2	2	1	3	1	1	1	1	2	1	5	1	1	2	4	5	9	3	3	1
G22	3	7	9	2	1	1	3	1	1	1	1	2	3	3	0	0	2	4	4	1	5	3	5
G23	1	7	7	2	1	1	3	1	1	1	1	2	3	3	0	0	2	4	4	1	5	3	5
G24	1	1	9	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	3	1	1
G25	3	7	7	2	1	1	3	1	1	1	1	2	3	3	0	0	2	4	4	1	5	3	5
G26	1	7	7	2	1	1	3	1	1	1	1	2	3	3	0	0	2	4	4	1	5	3	5
G27	3	7	1	1	2	1	3	1	1	1	1	1	1	3	0	0	2	4	4	5	7	5	1
G28	3	5	1	1	2	1	1	1	1	1	1	1	2	3	0	0	2	4	4	1	5	3	1
G29	5	7	7	1	3	1	1	1	1	1	1	2	2	5	0	0	5	1	1	0	3	1	1
G30	3	7	7	2	2	1	3	3	1	1	1	2	1	5	0	0	5	4	5	9	5	3	1
G31	1	3	9	2	2	5	1	1	1	3	2	2	3	5	0	0	7	4	4	0	5	1	1
G32	3	3	7	2	1	1	1	1	1	1	1	1	3	5	1	1	2	1	4	1	3	3	1
G33	7	1	7	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	5	3	1
G34	1	1	9	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	5	3	1
G35	1	1	9	2	1	1	1	1	1	1	1	2	3	5	0	0	2	1	4	0	3	1	1
G36	1	1	7	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	5	1	1
G37	1	3	9	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	1	5	3	1
G38	1	1	9	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	5	1	1
G39	1	1	9	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	5	1	1
G40	1	1	9	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	1	5	1	1
G41	1	1	9	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	5	1	1
G42	1	1	9	2	1	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	5	1	1
G43	1	3	9	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	3	1	1
G44	1	1	9	2	2	1	1	1	1	1	1	1	3	5	1	1	2	1	4	1	5	3	1
G45	3	5	9	1	3	1	1	1	1	1	1	1	3	3	0	0	2	1	4	0	5	3	1
G46	1	3	9	2	2	1	1	1	1	1	1	2	3	5	0	0	2	1	4	1	3	1	1
G47	3	1	7	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	3	1	1
G48	1	1	9	2	2	1	1	3	1	1	1	1	3	5	0	0	2	1	4	0	3	1	1
G49	1	1	9	2	3	1	1	1	1	1	1	1	3	5	0	0	2	1	4	1	5	1	1
G50	1	1	9	2	1	1	1	1	1	1	1	1	3	5	1	1	2	1	4	0	3	1	1
G51	3	9	5	2	2	1	3	3	1	1	1	2	1	5	0	0	5	4	5	9	5	5	1
G52	3	7	5	2	1	1	3	3	1	1	1	2	1	5	0	0	5	4	5	9	5	5	1
G53	3	9	5	2	2	1	3	3	1	1	1	2	1	5	0	0	5	4	5	9	5	3	1
G54	1	7	7	2	1	1	1	1	1	1	1	2	3	5	0	0	2	1	4	1	5	3	5
G55	1	7	9	2	1	1	1	1	1	1	1	2	3	3	0	0	2	1	4	5	5	3	1
G56	1	7	9	1	2	1	1	3	1	1	1	2	2	5	1	1	2	4	4	5	5	3	1
G57	3	9	9	1	2	1	3	5	1	1	1	2	2	5	0	0	5	1	1	1	5	3	1
G58	1	5	5	2	1	1	3	3	1	1	1	2	1	3	0	0	2	4	5	5	3	3	1
G59	3	5	7	2	2	1	3	3	1	1	1	2	1	1	0	0	2	4	4	5	5	3	1
G60	3	7	7	2	2	1	1	3	1	1	1	1	1	5	0	0	5	4	4	5	3	3	1
G61	3	5	7	1	3	1	1	3	1	1	1	2	2	5	1	4	5	1	1	0	1	1	1
G62	3	7	7	2	2	1	3	3	1	1	1	2	1	5	0	0	5	4	5	1	5	3	1
G63	3	7	7	2	2	1	3	3	1	1	1	2	1	5	0	0	5	4	5	9	5	3	1
G64	3	7	7	2	1	1	3	3	1	1	1	2	1	5	0	0	5	4	5	5	5	3	1
G65	1	1	7	1	2	1	1	1	1	1	1	1	2	3	0	0	2	4	4	0	7	5	1
G66	3	7	9	2	1	1	3	3	1	1	1	2	1	3	0	0	2	4	5	1	5	3	1
G67	3	7	7	2	2	1	1	1	1	1	1	2	2	5	0	0	5	4	5	0	3	3	1
G68	1	9	1	2	1	1	3	5	1	1	1	2	2	7	0	0	2	5	3	1	5	3	1
G69	3	5	9	1	2	1	1	1	1	1	1	1	2	5	0	0	5	1	1	0	3	3	1
G70	3	5	9	2	2	1	1	3	1	1	1	2	2	3	0	0	2	1	4	1	3	3	1
G71	3	5	9	1	2	1	1	5	1	1	1	2	2	3	0	0	2	1	1	1	5	3	1
G72	3	5	9	2	2	1	1	3	1	1	1	1	2	5	0	0	2	1	4	1	5	3	1
G73	5	5	9	2	2	1	1	5	1	1	1	2	2	3	0	0	2	1	4	0	5	3	1
G74	5	3	7	2	2	1	1	5	1	1	1	2	2	3	0	0	2	1	4	1	3	3	1
G75	1	3	7	2	2	1	1	1	1	1	1	1	3	5	0	0	2	1	4	0	1	1	1
G76	1	1	9	2	1	1	1	1	1	1	1	1	3	5	0	0	2	1	4	1	3	3	1

Supplementary Table 1b. Qualitative characterization for 100 rice genotypes in Ethiopia

GEN	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	R	S	T	U	V	Y	Z
G77	3	7	7	2	2	1	1	1	1	1	1	2	2	5	0	0	5	4	5	1	5	3	1
G78	3	3	9	2	2	1	3	3	1	1	1	2	2	5	0	0	5	4	4	1	5	3	1
G79	3	5	7	2	2	1	3	1	1	1	1	2	1	3	0	0	5	4	5	9	5	3	1
G80	3	7	1	1	2	1	1	3	1	1	1	2	1	5	9	1	2	4	4	5	3	3	1
G81	3	7	7	2	2	1	3	3	1	1	1	2	1	5	0	0	5	4	4	1	3	3	1
G82	3	7	7	2	2	1	3	3	1	1	1	2	1	5	0	0	5	4	5	1	5	3	1
G83	3	7	7	2	2	1	1	1	1	1	1	2	1	5	0	0	5	4	5	1	5	3	1
G84	1	7	9	2	2	1	1	5	1	1	1	2	2	5	1	4	5	1	4	1	3	3	5
G85	3	9	9	1	2	1	3	5	1	1	1	2	2	5	1	4	5	1	1	0	5	3	1
G86	5	7	7	2	2	1	3	3	1	1	1	2	1	5	0	0	5	4	5	0	3	3	1
G87	1	7	7	1	2	1	3	5	1	1	1	2	2	5	1	4	5	1	4	1	5	3	5
G88	1	9	7	1	2	1	1	1	1	1	1	2	1	5	0	0	2	4	4	9	7	5	1
G89	3	7	1	1	2	1	1	3	1	1	1	2	2	3	0	0	2	7	4	5	7	5	1
G90	3	7	1	2	2	1	1	3	1	1	1	2	2	3	0	0	2	7	4	9	5	3	1
G91	3	9	7	1	2	1	1	1	1	1	1	2	1	5	0	0	2	4	4	9	7	5	1
G92	3	9	3	1	2	1	1	5	1	1	1	2	2	5	0	0	7	1	1	1	7	3	5
G93	1	9	5	1	2	1	1	5	1	1	1	2	2	5	0	0	6	7	1	1	5	3	5
G94	3	7	5	1	2	1	3	1	1	1	1	2	2	5	0	0	5	1	1	1	1	1	1
G95	5	5	5	1	1	1	3	3	1	1	1	2	2	3	5	1	2	1	1	0	3	3	1
G96	3	7	7	1	2	1	1	1	1	1	1	2	2	5	0	0	5	1	1	1	3	1	1
G97	3	5	9	2	2	1	3	3	1	1	1	2	1	3	0	0	2	4	5	9	5	3	1
G98	5	5	7	1	2	1	3	1	1	1	1	2	2	5	0	0	2	1	1	0	3	1	1
G99	3	9	9	2	1	1	3	5	1	1	1	2	2	5	0	0	5	4	5	9	5	5	1
G100	3	7	7	1	3	1	1	1	1	1	1	2	2	5	0	0	5	1	1	0	5	3	1

GEN: Genotypes, A: Leaf Senescence, B: Panicle Exertion, C: Panicle Threshability, D: Leaf Blade Pubescence, E: Leaf Blade Color, F: Basal Leaf Sheath Anthocyanin Coloration, G: Leaf Angle, H: Flag Leaf Angle, I: Ligules Color, J: Collar Color, K: Auricle Color, L: Culm Internodes Color, M: Panicle Type, N: Curvature of Main Axis, O: Awning, P: Awn Color, R: Apiculus Color, S: Lemma and Palea Color, T: Lemma and Palea Pubescence, U: Chalkiness of Endosperm, V: Brown Rice Length, Y: Brown Rice Shape and Z: Seed Coat Color

The first principal component (PC1), major contributor traits were maximum tillering ability (0.36), days of maturity (0.36), days of heading (0.36), number of non-fertile tillers (0.35), thousand grain weight (-0.32) and number of fertile tillers (0.30). In corresponding to the current study, Abebe (2016) found same traits of days of maturity, days of heading, number of fertile tillers contributed positively and 1000 seed weight contributed negatively in PC1. Similarly, Kashyap & Yadav (2020) reported same traits of days of heading contributed positively and 1000 seed contributed negatively in PC1.

The second principal component (PC2), main provider traits were number of filled spikelets per panicle (0.48), plant height (0.47), grain yield (0.40), panicle length (0.40), and biomass yield (0.39) in the respective order. In agreement, Abebe (2016) found plant height and panicle length that contribute positively in PC2. The other researchers Mahendran et al., (2015) also reported similar traits, biomass yield and grain yield that contribute positively in PC2. Differently, Worede et al., (2014) reported plant height and panicle length were important traits in PC1.

The third principal component (PC3), major provider traits were biomass yield (0.51), number of fertile tillers (0.49), maximum tillering ability (0.38), and harvest index (-0.31) in the respective order. In agreement, Tiruneh et al. (2019) reported biomass yield and harvest index that contribute positively in PC3. Moreover, Kashyap & Yadav (2020) reported similar positive contribution of number of fertile tillers in PC3.

In fourth principal component (PC4), most important contributor traits were harvest index (-0.59), grain yield (-0.39), days to 50% heading (0.34), and days of 85% maturity (0.30). Differently, Tiruneh et al. (2019) and Birhanu (2020) found that harvest index contributed positively in PC4.

As illustrated in Figure 21, the bi-plot represents more than 60.73% of the total variance and gave more opportunity to assess which genotypes were good for which traits. Convex of the hull showing the outliers was occupied by G18 (ROJOMENA271/10), G50 (IR99637-6-1-1), G11 (GSR IR1-12-D10-S1-D1), G34 (IR-72593-B-B-2-3-14P1), G73 (PCT-4\0\0\1>295-2-3-1-3-3-M), G58 (Trakya), G52 (MET-HE-17-14), G86 (SCRID186-72-1-1-2) and G68 (PCT-11\0\0\2, Bo\2\1>487-1-6-2-3-3-M). Those outlier genotypes could be due to their unique gene expression than other genotypes and give opportunities for future variety development through selection as well as through hybridization. Especially for hybridization, those nine genotypes are the most recommended in 13 studied quantitative traits of rice genotypes; because hetrosis in F1 generation might be generated between those outlier genotypes. According to Dehghani et al. (2008), the correlation among two traits is approached by the cosine of the angle between their vectors. Accordingly, the present study traits of panicle length, harvest index and number of filled spikelets/panicle were positively correlated with grain yield.

In general, among four principal components of major contributing traits, maximum tillering ability, days of maturity, days of heading, thousand grains weight and number of fertile tillers in PC1 were major influential for clustering than traits found in other components. In agreement to Chahal and Gosal (2002) those traits having the highest |~1| for the first principal component influence clustering more than those with a lower absolute value closer to zero.

Conclusions and Recommendations

The Shannon Weaver diversity index of the present studied traits varied from 0 to 1. Among 25 qualitative traits, 23 were showed polymorphic except culm angle and ligules shape. Based on breeders' objective, these 23 qualitative traits had unique genotypes. For example, if breeder's interest is to have late leaf senescence, G33 (IR-63275-B-1-1-13-2) is the recommended donor parent for future crossing work to improve early leaf senescence genotypes.

Based on the clustering result, the studied 100 genotypes were grouped into four distinct clusters. According to genetic divergence, it is better to cross cluster I and IV genotypes to get early maturing and moderate grain yield variety for moisture stress area. Moreover, it is better to cross cluster III and IV genotypes to get medium matured, high filled spikelet/panicle, optimized harvest index, biomass and grain yield variety for rain fed with irrigation supplemented areas.

According to principal component result, nine genotypes {G18 (ROJOMENA271/10), G50 (IR99637-6-1-1), G11 (GSR IR1-12-D10-S1-D1), G34 (IR-72593-B-B-2-3-14P1), G73 (PCT-4\0\0\1>295-2-3-1-3-3-M), G58 (Trakya), G52 (MET-HE-17-14), G86 (SCRID186-72-1-1-2) and G68 (PCT-11\0\0\2, Bo\2\1>487-1-6-2-3-3-M)} are recommended for hybridization parents because those genotypes are genetically divergent to have hetrosis F1s.

Declarations

Author Contributions

Assaye Berie; initiated the research idea, collected, organized, analyzed and interpreted the data and wrote the manuscript. Tiegist Dejene; supervised the research, suggested the research methods, structured the paper and edited the manuscript.

Fund Statement

This work was funded by Ethiopian Institute of Agricultural Research.

Competing Interests

The authors declare that there is no competing of interests

Acknowledgments

The authors would like to express our deepest gratitude to Ethiopian Institute of Agricultural Research for material allocation and financing this research through Rice Program in Fogera National Rice Research and Training Center. We appreciate Mrs. Seged Aychew for her daily assistance. We also appreciate Dr. Taddesse Lakew and Dr. Fisseha Worede for their valuable comments. We extend our gratefulness for Mr. Endalew Gete and Mrs. Sewunet Mengistie for their effective weed and bund management.

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