



E-ISSN: 2278-4136  
P-ISSN: 2349-8234  
JPP 2017; 6(6): 75-80  
Received: 14-09-2017  
Accepted: 15-10-2017

**Atul Kumar Pachauri**  
Department of Genetics & Plant  
breeding Indira Gandhi Krishi  
Vishwavidyalaya Raipur,  
Chhattisgarh, India

**AK Sarawgi**  
Department of Genetics & Plant  
breeding Indira Gandhi Krishi  
Vishwavidyalaya Raipur,  
Chhattisgarh, India

**S Bhandarkar**  
Department of Genetics & Plant  
breeding Indira Gandhi Krishi  
Vishwavidyalaya Raipur,  
Chhattisgarh, India

**GC Ojha**  
Department of Genetics & Plant  
breeding Indira Gandhi Krishi  
Vishwavidyalaya Raipur,  
Chhattisgarh, India

**Correspondence**  
**Atul Kumar Pachauri**  
Department of Genetics & Plant  
breeding Indira Gandhi Krishi  
Vishwavidyalaya Raipur,  
Chhattisgarh, India

## Agro-morphological characterization and morphological based genetic diversity analysis of Rice (*Oryza sativa* L.) germplasm

Atul Kumar Pachauri, AK Sarawgi, S Bhandarkar and GC Ojha

### Abstract

The present study was carried out to characterize one hundred twenty four rice germplasm accessions on the basis of nineteen morphological and eleven agronomical traits. Most of the morphological characters showed variation in different accessions except leaf: ligule and leaf: shape of ligule. A significant amount of variation was displayed for most of the agronomical traits examined. After evaluation of 124 accessions for eleven quantitative characters, on the basis of mean values, top ten accessions were identified for the yield ancillary traits. Principal Component Analysis was used to analyze quantitative data. The 72.48% of the total variation. The PC1 showed first four principal components explained about 37.12%, while PC2, PC3 and PC4 exhibited 13.56, 11.04 and 10.76% variability, respectively results of PCA revealed that the traits such as No. of effective tillers, 100 grain weight were the principal discriminatory traits.

Thus the results of principal component analysis used in the study have revealed the high level of genetic variation and the traits contributing for the variation was identified. Hence this population panel can be utilized for trait improvement in breeding programs for the traits contributing for major variation.

**Keywords:** Agro-morphological characters, germplasm, phenotypic component analysis, rice

### 1. Introduction

Any crop improvement program depends on the utilization of germplasm stock available in different research organization or institutes. Due to rapid growth of the population, rice yield is urgently required to increase to meet the food demand. In order to meet the demand there is a necessity of development of high yielding varieties along with good quality traits. Agro-morphological characterization of germplasm is fundamental in order to provide information for plant breeding programs (Das and Ghosh., 2011) [5].

The landraces are valuable as they possess a huge treasure of genetic material which may prove valuable in future crop development and improvement programs. Our information about them is incomplete and is therefore urgent to collect and conserve these landraces of rice (Sinha and Mishra 2012). Green revolution has considerably improved production of food grains in our country and its role in achieving status of self-sufficiency in food grain is beyond any doubt (Maji and Saibu., 2012) [10]. But high yielding varieties, which are the back bone of green revolution, have indirectly stimulated erosion of landraces and wild varieties of rice. Presently more than 90% of rice cultivation is being done using high yielding variety only. Obviously landraces are disappearing fast (Sajid *et al.*, 2012) [14]. Importance of landraces can never be denied in agriculture system, because improvement in existing variety depends upon desirable genes which are possibly present in landraces and wild varieties only (Jiang *et al.*, 2013). Landraces offer a valuable gene pool for future breeding program (Rabbani *et al* 2010) [13]. Assessment of genetic diversity is very important in rice breeding from the standpoint of selection, conservation of different land races variety of rice and proper utilization (Jayasudha. and Sharma 2010) [7]. The main objective of the present study was to characterize 124 landraces of rice of using eleven agro-morphological characters to provide useful information to facilitate the choice of genitors for rice plant breeding programs. Principal Component Analysis (PCA) can be used to uncover similarities between variable and classify the cases (genotypes), while cluster analysis on the other hand is concerned with classifying previously unclassified materials. Statistical method of classification is usually by multivariate methods as it has extensive use in summarizing and describing the inherent variation among crop genotypes. Principal Component Analysis (PCA) is a multivariate technique that analyzes a data table in which observations are described by several inter-correlated quantitative dependent variables.

Its goal is to extract the important information from the table, to represent it as a set of new orthogonal variables called principal components, and to display the pattern of similarity of the observations and of the variables as points in maps. 'Proper values' measure the importance and contribution of each component to total variance, whereas each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated.

### Materials and Methods

The material for the present investigations consisted of 118 rice germplasm accessions received from NBPGR New Delhi. These genotypes were evaluated in augmented design (Federer, 1961) with six national checks viz., Pusa Basmati-1, Jaya, NDR 97, Annada, Swarna and IR64 during *Kharif* 2014 at Research cum Instructional farm, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh. Each entry was sown in a plot comprising three rows having three meter length at spacing of 20 cm between rows and 15 cm between plants. The recommended agronomical practices were followed to raise good crop in the season. Observations were recorded on five randomly chosen plants of each accession for thirty morphological and agronomical traits. The traits studied were Early plant vigour, Coleoptile color Basal leaf sheath colour, Leaf blade color, Leaf Pubescence, Panicle exertion, Stigma color, Apiculus color, Panicle type, Awning, Seed coat color, Hull Color, Threshability, Flag Leaf Angle Leaf senescence, Sterile lemma, Auricle colour and Aroma. Frequency distribution was computed to categorize the accession into different classes. Simple statistics (means, ranges) was calculated to have an idea of the level of variation.

### Results and Discussion

#### (A) Agro-Morphological characterization

Qualitative characters are important for plant description and mainly influenced by the consumers preference, socio-economic scenario and natural selection (Das and Ghosh., 2011) [5]. Frequency distribution for 19 qualitative traits is depicted in Table 1 and its graphical representation of frequency distribution showed in Figure 1. A majority of accessions were found to possess Basal leaf: sheath colour (81% green), Leaf blade colour (37% dark green) Leaf Pubescence (67% Intermediate), Panicle exertion (76% well exerted), Stigma color (76% white), Apiculus color (91% straw), Panicle type (17% compact), Awning (96% Absent), Seed coat color (85% white), Hull Color (67% straw), Threshability (81% green), Flag Leaf Angle (75% open), Leaf senescence (47% medium), Sterile lemma (80% straw), and Auricle colour (90% light green) Similar type of work was also reported by Bisne and Sarawgi (2008) [8], Sarawgi *et al* (2013) and Sinha and Mishra. (2013) [9]. Based on the morphological descriptors 118 accessions were classified for 19 characters. Some of the unique accessions with distinct features are presented in Table 2.

#### (B) Agronomical characterization

Rice accessions were evaluated for agronomical traits viz., Leaf length (cm), Leaf width (cm), Days to 50% flowering (days), Stem length (cm), Panicle length (cm), No. of effective tillers/plant (cm), Time of maturity, Grain: weight of 100 fully developed grains, Grain: length, Grain: width from five competitive plants of middle row of each entry.

**Time to 50% heading:** It had mean value of 85 days and a wider range of 66-110 days. Almost 50% of the lines fall in the range of medium to late group (Fig. 2), whereas IC 464013 and IC 577310 accessions were found to be very early in duration with days to 50% heading of 66 and 70 days, respectively.

**Plant height:** It had wider range (70-184 cm) of variation with a mean value of 151.15 cm. (Maji and Shaibu., 2012) [10]. Have observed relatively greater range in plant height than the other characters. Plant height in rice is a complex character and is the end product of several genetically controlled factors called internodes (Sarawgi *et al.*, 2015). IC453690 (76.00 cm) IC453697 (88.20cm.) IC 576902 (89.00cm.) IC453707 (73.40cm.) IC123063 (70.00cm.) IC123174 (76.80cm.) and IC123216 (79.20 cm) were the eight accessions which falls under very dwarf group. More than 50% accessions were having plant height in the range of 131-150 cm and can be grouped as tall. Very few accessions exhibited semi dwarf nature and about 79 accessions showed very tall stature. Reduction in plant height may improve their resistance to lodging and reduce substantial yield losses associated with this trait Pachauri, *et al* (2016),

**Panicle length:** It exhibited reasonable amount of variation with range values of 15-34 cm. The average panicle length was 25.58 cm long. Most of the accessions fall under the range of 26-30 cm panicle length. The maximum panicle length was observed in IC 460174X. Although it contributes positively yet maximum panicle length is not the only factor responsible for higher grain yield Sinha and Mishra (2012), So panicle length alone does not determine the high grain yield as traits such as grain size, grain shape, higher number of tillers/plant, longer panicles and greater number of grains/panicle ultimately contribute to higher grain yield (Sajid *et al.*, 2015).

**Number of productive tillers per plant:** It is another yield attributing trait (Sajid *et al.*, 2015). A great variability with high range (5-26) and mean value of 8.20 was exhibited for number of productive tillers/plant. IC 453885 had maximum value (26) followed by IC453707 (26) IC123242 (25) IC455312 (24).

**Days to maturity:** It also exhibited high range (86-130 days) with a mean of 111.33 days IC123216 had shorter maturity period (86 days) representing earliness. Minimum value for days to maturity represents that the variety has a benefit of early ripening. Most of the lines fall under mid early followed by medium and late duration.

**100-grain weight:** It is also a yield-attributing trait (Khare *et al.*, 2014) [8]. Most of the lines were in the range of 2.1 – 2.5 g. Lines with high grain weight (> 3g) were also observed in this set of germplasm (Fig.2). IC 463274 had maximum 100 grain weight (4.32 g).

**Grain length: breadth ratio** Grain length is an important quality parameter. Rice grain can be classified as extra-long, long, medium and short (Bisne *et al.* 2006) [3]. It exhibited high range (2.40-4.65mm) with mean of 3.28` mm. In the present material, more than 80% accessions falls in short to medium group, whereas few of the accessions were observed with long grain. IC134218 was observed with maximum grain length (4.65 mm).

### Principal Component Analysis

The result of PCA explained the genetic diversity of the rice germplasm accession. In the present investigation PCA was performed for agro morphological traits in rice accession in presented in table 2. As per the criteria set by Brejeda *et al.*, (2000) [4], the PCA with eigen values >1 and which explained at least 5% of the variation in the data were considered. The PC with higher eigen values and variables, which had high factor loading were considered as best representative of system attributes. Out of twenty only four PCs exhibited more than 1 eigen value, and showed about 72.48% cumulative variability among the traits studied. So these four PCs were given due importance for further explanation. The PC1 showed 37.12% while PC2, PC3 and PC4 exhibited 13.56, 11.00 and 10.76% variability, respectively among the accession for the traits under study (Table 3). The first PC accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible.

Within each PC, only highly loaded factors or traits (having absolute values within 10% of the highest factor loading) were retained for further explanation. Rotated component matrix revealed that the PC 1 which accounted for the highest variability (37.12%) was mostly related with traits such as plant height (0.82) grain yield per plant (0.81) and panicle length (0.61) days to 50% flowering (0.67) (Table 3). The second principal component accounted for 13.56% of total

variance. Variables highly and positively related correlated with PC2 grain length breadth ratio (0.42). As a result the first two components differentiate rest of the accession on the basis of yield attributing traits. The third principle components which accounted 11.04% of the variability was highly loaded with two traits leaf length leaf width both are (0.37). The PC 4 was positively more related with seeding height (0.62). From the first and fourth PCs, it is clear that the PC1, PC3 mostly related to yield attributing traits characters, while PC2 and PC4 associated only single traits.

The PCA revealed that traits such as No. of effective tillers, 100 grain weight were the principal discriminatory characteristics. The prominent character coming together in different principal components and contributing towards explaining the variability has the tendency to remain together, which may be kept into consideration during utilisation of these character in breeding programme. Through PCA we could identify the number of plant characters, which are responsible for the observed genotypic variation within a group. Our result are agreement with the finding of Sinha and Mishra (2013) [9]; Kumar *et al.*, (2013) [9]. Nachimuthu *et al.*, (2014) [11]; Shaibu and Ugaru., (2017). Tuhina-Khatun *et al.*, (2015) identified four principal components with eigen value greater than >1 and that explained 72.1% of the total cumulative variance within the axes further strengthen current result.

**Table 1:** Top ranking accessions for yield ancillary traits.

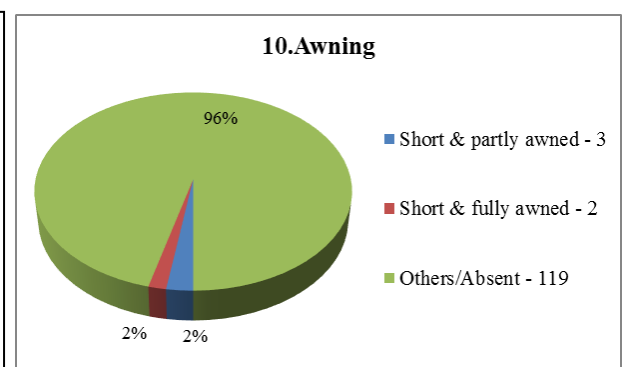
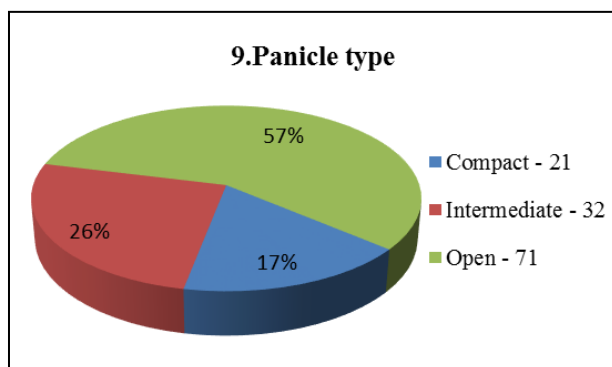
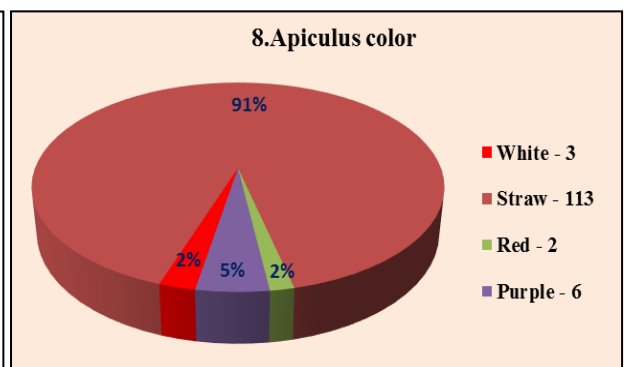
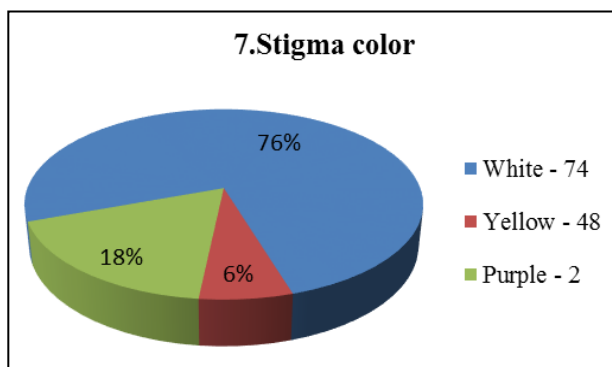
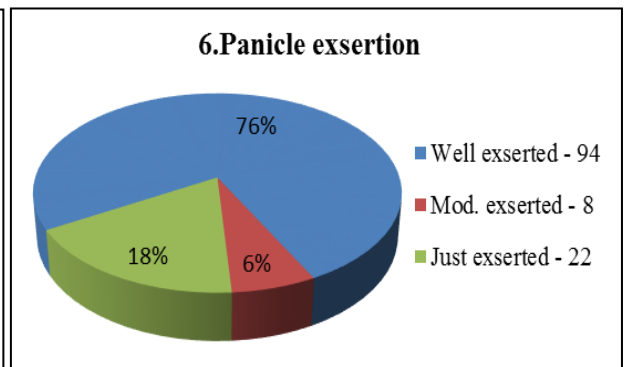
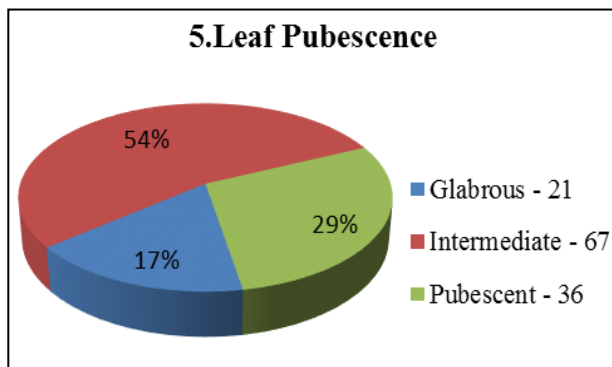
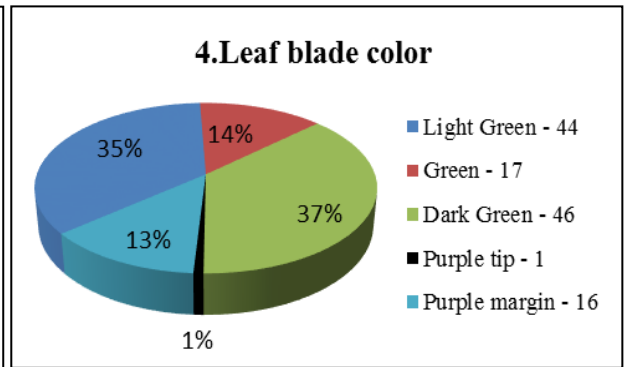
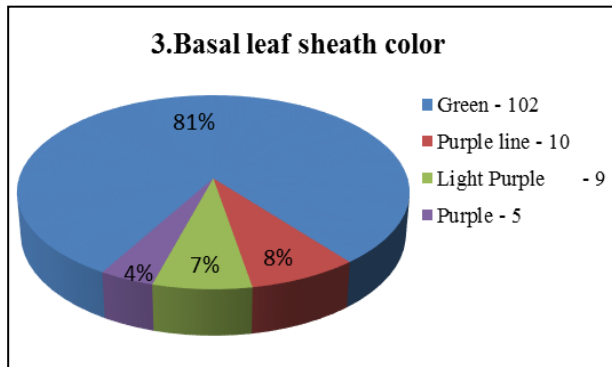
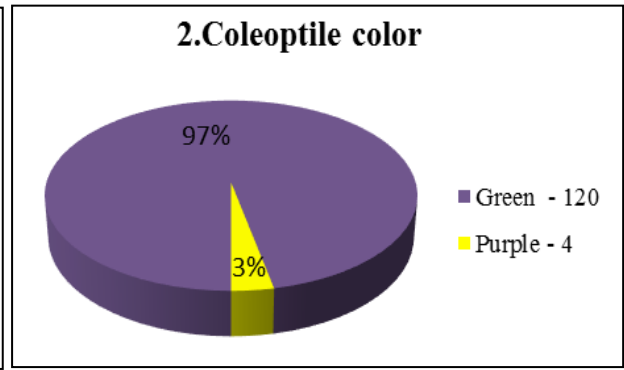
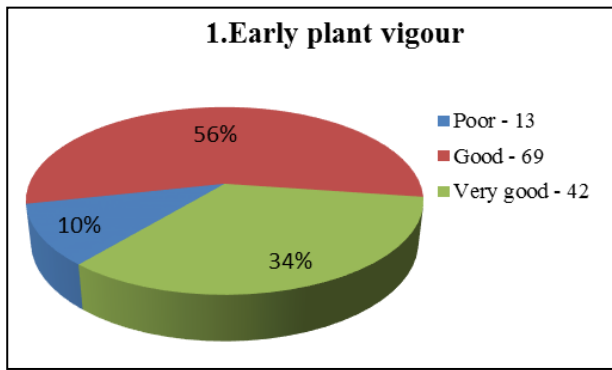
S No.	Panicle length (cm.)	Plant height (cm.)	Number of effective tillers	Grain length: breadth ratio(mm)	100 grain wt. (gm.)
1	IC460174X (34.22)	IC123216 (79.20)	IC453885 (27)	IC124448 (3.57)	IC134218 (4.65)
2	IC133071 (32.00)	IC123747 (79.26)	IC453707 (26)	IC389332 (3.30)	IC134252 (4.55)
3	IC134879 (31.96)	IC453691 (88.20)	IC123242 (25)	IC1333448 (3.29)	IC124476 (4.43)
4	IC453693 (30.00)	IC453697 (88.38)	IC455312 (24)	IC124430 (3.20)	IC124377 (4.38)
5	IC460158X (30.82)	IC453707 (89.00)	IC453910 (23)	IC124460 (3.16)	IC124357 (4.33)
6	IC133049 (30.00)	IC123242 (94.60)	IC123063 (22)	IC123837 (3.12)	IC123925 (4.14)
7	IC1333442 (29.32)	IC453676 (107.40)	IC460174X (13)	IC124357 (3.10)	IC124119 (4.20)
8	IC123435 (29.20)	IC453788 (100.40)	IC124446 (12)	IC123242 (3.10)	IC125790 (3.96)
9	IC133368 (29.06)	IC123218 (117.40)	IC125267 (12)	IC134376 (3.10)	IC124286 (3.95)
10	IC124364 (29.04)	IC459147 (125.00)	IC123067 (11)	IC134143 (3.00)	IC123435 (3.95)

**Table 2:** List of unique accessions for different morphological traits.

S. No	Morphological characters	Colour pattern/ type	Unique accessions
1	Basal leaf: sheath colour	Purple	IC459147 IC125025 IC125437 IC133090 IC134180
2	Leaf: shape of ligule	Acute	IC123128 IC123901 IC123925 IC124119 IC124163 IC124409
3	Spikelet: colour of stigma	purple	IC124430, IC124458
4	Lemma and palea: colour	Brown town	IC453691 IC453697 IC123067 IC123435 IC124554
5	Decorticated grain: colour	Red	IC123064 IC123071 IC124119 IC124225 IC124409

**Table 3:** Eigen value, contribution of variability and factor loading for the principal component axis in rice genotypes

	F1	F2	F3	F4
Eigen value	4.08	1.49	1.21	1.18
Variability (%)	37.12	13.56	11.04	10.76
Cumulative %	37.12	50.68	61.72	72.48
	Factor loading value			
Seedling Height (cm)	0.002	0.017	0.105	0.624
Leaf length (cm)	0.320	0.027	0.375	0.068
Leaf width (cm)	0.118	0.114	0.373	0.005
Days to 50% flowering	0.679	0.067	0.143	0.052
No. of effective tillers	0.020	0.378	0.021	0.039
Plant Height (cm)	0.825	0.028	0.001	0.012
Panicle length (cm)	0.615	0.050	0.000	0.025
Days to maturity	0.660	0.069	0.152	0.051
Grain length breadth ratio	0.026	0.425	0.044	0.011
100 grain weight	0.000	0.298	0.003	0.292
Grain yield per plant (gm)	0.818	0.020	0.001	0.002



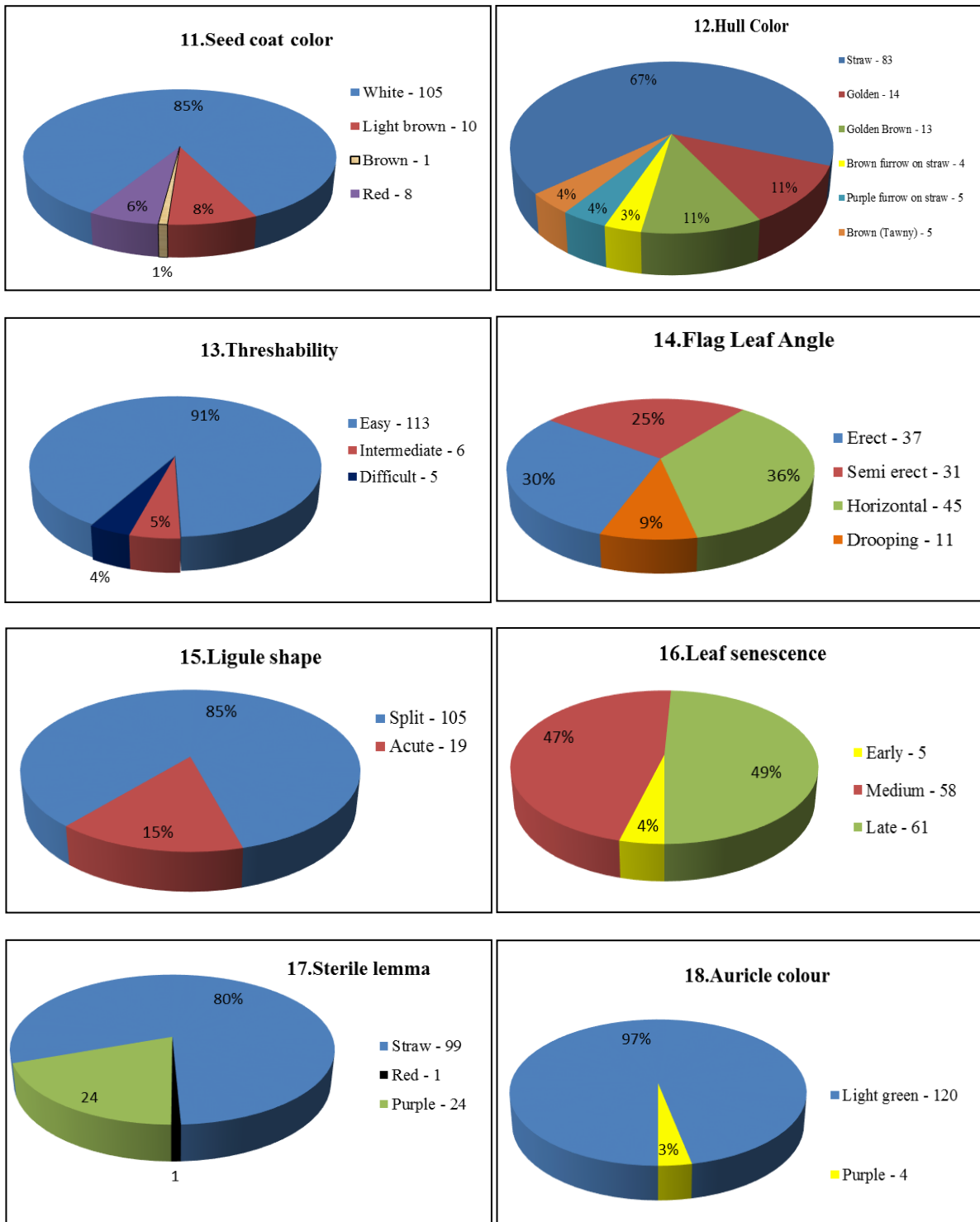


Fig 1: Frequency distribution of important morphological characters

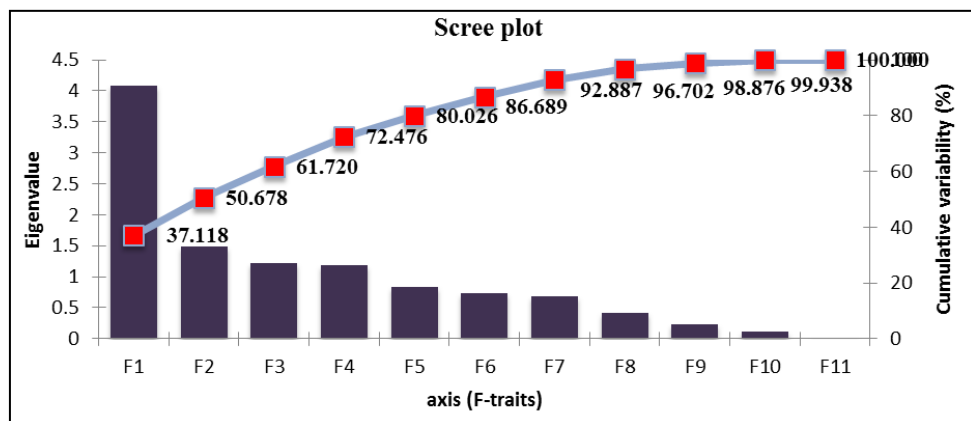


Fig 2: Scree plot showing Eigen value and percentage of cumulative variability in rice genotypes

### Conclusion

After evaluation of 124 accessions for five quantitative characters, on the basis of mean values, top ten accessions were identified for the yield ancillary traits (Table 3). IC 453885 (27) had the highest number of effective tillers per plant followed by IC 453707 (26). Similarly, IC 134218 (4.65 g) had the highest rank for 100 grain weight followed by IC 134252 (4.55 g). Identifying germplasm accessions for different agronomical characters in phenotypically divergent sources would help in pre-breeding and breeding programs.

### Acknowledgement

Authors articulate honest gratitude to the, Ministry of Science and Technology, Indian Council Of Agriculture Research (ICAR) New Delhi for provided that the pecuniary support to the ICAR Network Project "Consortium Research Platform on Agrobiodiversity on Germplasm characterization and evolution".

### Reference

1. Ashfaq M, Khan AS, Khan SH, Ahmad R. Association of various morphological traits with yield and genetic divergence in rice (*Oryza sativa* L.) International journal of Agriculture and Biology. 2012; 14:55-62.
2. Bisne R, Sarawgi AK. Morphological and quality characterization of Badsahbhog group from aromatic rice germplasm of Chhatisgarh. Bangladesh J Agric. Res. 2008; 33(4):479-492.
3. Bisne R, Motiramani NK, Sarawgi AK. Association analysis and variability analysis in rice. Mysore J. Agric. Sci., 2006; 40(3):375-380.
4. Brejda JJ, Moorman TB, Karien DL, Dao TH. Identification of regional soil quality factors and indicators. I. Central and Southern High Plains, Soil Science society of America Journal. 2000; 64:2115-2124.
5. Das S, Ghosh A. Characterization of rice germplasm of West Bengal. *Oryza*. 2011; 47(3):201-205.
6. Ekka RE, Sarawgi AK, Kanwar RR. Correlation and Path Analysis in Traditional Rice Accessions of Chhatisgarh. *J. Rice Res.*, 2011; 4(1, 2):11-18.
7. Jayasudha S, Sharma D. Genetic parameter of variability, correlation and path coefficient for grain yield and physiological trait in rice (*Oryza sativa* L) under shallow lowland situation. Electronic J. Plant Breed. 2010; 1(5):33-38.
8. Khare R, Singh AK, Eram S, Singh PK. Genetic variability, association and diversity analysis in upland rice (*Oryza sativa* L) SAARC J. Agri. 2014; 12(2):40-51
9. Kumar V, Koutu GK, Mishra DK, Singh SK. Principal component analysis of inter sub specific RILs of rice for the important traits responsible for yield and yield quality. JNKVV Research Journal. 2013; 47(2):185-190.
10. Maji AT, Shaibu AA. Application of principal component analysis for rice germplasm characterization and evaluation Journal of Plant Breeding and Crop Science. 2012; 4(6):87-93.
11. Nachimuthu VV, Robin S, Sudhakar D, Raveendran M, Rajeswari S, Manonmani S. Evaluation of Rice Genetic Diversity and Variability in a Population Panel by Principal Component Analysis Indian Journal of Science and Technology. 2014; 7(10):1555-1562,
12. Pachauri AK, Sarawgi AK, Bhandarkar S, Ojha GC. Genetic variability and association study for yield contributing traits of promising core rice germplasm accessions (*Oryza sativa* L.) Res. on Crops. 2017; 18(1):133-138
13. Rabbani MA, Masood MS, Shinwari ZK, Yamaguchi-Shinozaki K. Genetic Rice Sci. 2010; 27:359-364.
14. Sajid M, Khan AS, Khurshid H, Javed I, Muhammad A, Saleem N *et al.* Characterization of Rice (*Oryza sativa* L.) Germplasm through Various Agro-Morphological Traits *Scientia agriculture*. 2012; 8(6):287-293.
15. Sarawgi AK, Rastogi NK. Genetic diversity in traditional aromatic rice accessions from Madhya Pradesh. Indian J. Plant Genet. Resour. 2000; 13:138-146.
16. Sharma AK, Sharma RN. Genetic variability and character association in early maturing rice. *Oryza*. 2007; 44(4):300-303.
17. Singh AK, Nandan R, Singh PK. Genetic variability and association analysis in rice germplasm under rainfed system. Crop Res. 2014; 47(1-3):7-11.