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Genetic variability of quality, yield and yield related traits in germplasm of rice (*Oryza sativa* L.)

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Abstract

Qualitative traits are considered as morphological markers in the identification of genotypes of rice because they are less influenced by environment. Thus, characterization of germplasm accessions establishes distinctiveness among rice genotypes. Coleoptile colour, anthocyanin coloration of leaf, intensity of anthocyanin colouration, pubescence of blade surface, density of pubescence of lemma, lemma and palea colour, colour of awns, attitude of branches of panicle, and decorticated grain shape showed maximum variation among accessions.

The analysis of variance indicated that the mean sum of square due to genotypes were significant for all the qualitative and quantitative characters. This indicates the presence of considerable variability among the accessions. Highest genotypic and phenotypic coefficient of variation was shown by head rice recovery percentage followed by Kernel length Breadth Ratio and Flag leaf width. High heritability coupled with high genetic advance as percent of mean was observed for head rice recovery, cooked kernel L/B ratio, kernel L/B ratio, grain L/B ratio, 1000 grain weight and elongation index, indicating that selection for these traits is likely to be effective accumulation due to more additive genes leading to further improvement in their performance.

Keywords: genetic variability, yield related traits, germplasm of rice, qualitative traits

Introduction

Rice (*Oryza sativa* L.) belonging to family Poaceae is one of the world's most important food crops. It is grown in 115 countries in different parts of the world and provides staple food to more than half of the world's population. India has largest area under rice in the world and ranks second in production next to China. In India, total production is 105.48 million tones with productivity 3020 kg/ha (Anonymous, 2015 a) [1]. Chhattisgarh popularly known as "Rice Bowl of India" occupies an area around 3.64 million hectares with the production of 7.65 million tones and productivity 1517 kg/ha (Anonymous, 2015 b) [2]. In Chhattisgarh, rice is mainly grown under rainfed ecosystem, which covers about 74, 97 and 95 per cent cropped area of Chhattisgarh plain, Bastar plateau and Northern hill zones, respectively.

Genetic diversity probably serves as an insurance against crop failure (Subba Rao *et al.* 2001) [17]. Landraces and wild species possess immense potential of most valuable genes which can be effectively utilized in the present day breeding programmes to evolve miracle varieties in rice that possess not only high yield potential and quality, but also resistant to biotic and abiotic stresses (Saxena *et al.* 1988) [13]. Collection and characterization of the germplasm is not only important for utilizing the appropriate attribute based on donors in breeding programmes, but is also essential in the present era for protecting the unique rice.

The Amount of genetic variation in germplasm accessions and genetic relationships between genotypes are important considerations for designing effective breeding programme. In crop improvement programme, genetic variability for agronomic traits as well as quality tests in almost all the crops is important, since this component is transmitted to the next generation. Study of genetic divergence among the plant materials is a vital tool to the plant breeders for an efficient choice of parents for plant improvement. Biometrical techniques are useful to the plant breeder in the assessment of genetic variability present in a population. The statistical parameters *viz.* mean, range, variance, phenotypic coefficient of variation, genotypic coefficient of variation, and genetic divergence measure the component characters on which selection can be based for genetic improvement of yield and other characters. The knowledge of parameters of variability is helpful for developing superior varieties with high yield

potential. For effective breeding programmes it is important to know the association of yield with its component traits, direct and indirect effects on yield contributing components on yield by correlation coefficient and path-coefficient, respectively.

Materials and methods

The present investigation was carried out during the *Kharif* 2015. The experimental materials comprised forty seven lines of germplasm accessions of rice including five checks namely, Danteshwari, Indira Aerobic-1, Rajeshwari, Durgeshwari and Safri-17. The details of germplasm accessions of rice has been given in Table 1.

Twenty-six day old seedlings were subsequently transplanted in to the field in Randomized Block Design. The experimental material was planted in three replications and each replication comprised 47 genotypes including five checks. Each entry was transplanted in a single row at spacing of 20 cm between rows and 15 cm between plants. Gap filling was done within a week in order to maintain uniform plant population. The standard agronomic practices were adopted for normal crop growth. Crop was raised following recommended package of practices. The observations on various agro-morphological including qualitative and quantitative characters were recorded.

Table 1: Germplasm accessions of rice along with checks

S. No.	CGR No	IC No.	Name of Genotypes	District
1.	CGR: 1735	IC-132668	Lali Ajan	Bastar
2.	CGR: 1737	IC-132671	Ajaniya	Bastar
3.	CGR: 1760	IC-132694	Badshah Bhog (B)	Durg
4.	CGR: 1761	IC-132695	Badshah Bhog	Raigarh
5.	CGR: 1768	IC-132702	Badshah Bhog (IT)	Shahadol
6.	CGR: 1774	IC-132708	Jogi Bhog	Mahasamud
7.	CGR: 1795	IC-132732	Vishnu Bhog	Surguja
8.	CGR: 1803	IC-132740	Angur Guchcha	Durg
9.	CGR: 1809	IC-132746	Anjan (II)	Shahadol
10.	CGR: 1810	IC-132747	Anjan (I)	Mandla
11.	CGR: 1811	IC-132748	Anjani	Mandla
12.	CGR: 1813	IC-132750	Anjan	Mungeli
13.	CGR- 1972	IC-132920	Dhabli Banko (I)	Raipur
14.	CGR- 1987	IC-132935	Lal Banko	Raipur
15.	CGR- 1990	IC-132398	Mudi Banko	Sarguja
16.	CGR- 1991	IC-132939	Raj Banko	Bastar
17.	CGR- 1994	IC-132942	Surgujihi Banko	Bilaspur
18.	CGR- 2009	IC-132957	Banskupi	Shahdol
19.	CGR- 3653	IC-135043	Luchai	Mandla
20.	CGR- 3738	IC-135128	Peeleeluchai	Balaghat
21.	CGR- 3741	IC-135131	Peeleeluchai	Balaghat
22.	CGR- 3808	N.A.	Mahuwadeta Lal	Mandla
23.	CGR- 3819	IC-135209	Mauhakuchi	Raipur
24.	CGR- 3831	IC-135221	Makado	Bastar
25.	CGR- 3863	IC-135253	Malpa (I)	Raipur
26.	CGR- 3866	IC-135256	Mancha	Bastar
27.	CGR- 4336	N.A.	Patel 27 Type Four	Durg
28.	CGR- 4378	IC-135769	Dadamphool	Bastar
29.	CGR- 4464	IC-135855	Rajniti (A)	Shahdol
30.	CGR- 4521	IC-214037	Ram Karoni	Balaghat
31.	CGR: 4909	IC-214410	Surmatia	Bastar
32.	CGR: 4971	NA	X:5 Bhairamgarh/Bastar	Bastar
33.	CGR: 5123	IC-124706	Anjan (A)	Raipur
34.	CGR: 5737	IC-113998	Barangi	Bastar
35.	CGR: 5740	IC-113999	Barangi	Raipur
36.	CGR: 5817	IC-114049	Moti basmati	Seoni
37.	CGR: 5818	IC-114050	Baspan	Raipur
38.	CGR: 1854	IC-114073	Bauwara	Raipur
39.	CGR: 5897	IC-114093	Bhaya	Raigarh
40.	CGR: 5988	NA	Bhujani	Durg
41.	CGR: 6046	NA	Bhurkund	Raigarh
42.	CGR: 6261	IC-125488	Chitarboti	Bastar
	C-1		Danteshwari	Raipur (IGKV)
	C-2		Indira aerobic 1	Raipur (IGKV)
	C-3		Rajeshwari	Raipur (IGKV)
	C-4		Durgeshwari	Raipur (IGKV)
	C-5		Safri 17	Raipur (IGKV)

Results and discussion

A. Agro-morphological and quality characterization

Any variety can be identifying through its distinguished stable morphological traits. These traits may be monogenic or polygenic. The stable morphological traits can be used as reliable morphological markers for identification of variety. Each variety must have certain novel diagnostic features which will distinguish a variety from others. Such diagnostic characters should uniformly present in the population and should be inherited in next generation then only the character is supposed to be stable and can be used as morphological marker traits to distinguish that variety. The 42 germplasm accessions of rice and five checks were characterized on the basis of agro-morphological and quality characters. Frequency distribution and percentage value of agro-morphological and quality characters of 42 germplasm accessions of rice along with five checks are presented in Table 2. Some of the characters are unique. In case of Basal leaf sheath colour- Out of 47 accessions, 29 accessions were recorded green basal leaf sheath colour including checks danteshwari, indira aerobic 1, rajeshwari, and safri 17, 4 accessions and check durgeshwari were recorded light purple, 12 were uniform purple and only one accession (surmatiya) was recorded purple lines colour. According to leaf intensity of green colour- 31 accessions and check Indira Aerobic 1 were recorded medium intensity of green colour, 14 accessions including checks Danteshwari, Rajeshwari and Durgeshwari were recorded dark. Light green colour intensity was not found in any accession. Check Safri 17 exhibits light intensity of green colour. Leaf blade pubescence were recorded in 47 accessions out of 21 were recorded medium, 12 were strong, eight were weak and only one (X: 5Bhairamgarh/Bastar) was recorded very strong pubescent. The checks were also recorded variation on pubescence characteristics. Danteshwari and Safri 17 have medium leaf blade, Indira Aerobic 1, and Rajeshwari exhibits weak pubescent. Curvature of main axis grouped into different

classes, 10 accessions were grouped into straight, 32 accessions, including Indira Aerobic 1 grouped into semi-straight, check Danteshwari, check Rajeshwari and check Durgeshwari grouped into deflexed. Whereas, Safri 17 had drooping curvature. On the basis of lemma colour, 25 genotypes including check Indira Aerobic 1 into white color, check Danteshwari and check Safri 17 into yellowish colour, check Rajeshwari and check Durgeshwari into brown, only one genotype was recorded red, niether genotypes into black. Whereas, 16 genotypes grouped into into purple.

Those 47 genotypes were also classified on the basis of lemma and palea colour as, 18 genotypes including checks into straw color, six genotypes into gold and gold furrows on straw, three genotypes into brown spots on straw, 12 genotypes into brown furrows on straw, three genotypes into brown, four genotypes into reddish to light purple. Whereas, only one genotype (Angur guchcha) into black. In case of colour of awns, six genotypes had yellowish brown colour, two genotypes had reddish brown colour, only one genotype (Moti Basmati) had light purple, two genotypes had red awn colour. None of the genotypes found yellowish white, light red, black and purple awn colour. Whereas, check Rajeshwari and Durgeshwari had brown awns. Out of 47 genotypes studied, 34 genotypes were awnless, eight genotype including check Durgeshwari had very short awns, four genotypes including check Rajeshwari had short awns and only one genotype (Baspan) had long awns. None of the genotype found medium and very long awns. The genotypes were also classified according to distribution of awns. Nine genotypes including check Rajeshwari and check Durgeshwari had awns distributed on tips only, three had awns on upper half only and only one genotype (Baspan) had awns on whole length. In case of leaf senescence, 47 accessions, were grouped into five classes based on attitude of branches. In which 40 accessions including check Indira Aerobic 1 were grouped into medium, six accessions including check Rajeshwari, Durgeshwari and Safri 17 were late, only one accession was found early.

Table 2: Frequency distribution and percentage value of Agro-morphological and quality of 47 germplasm accessions of rice

S. No.	Characters	Categories of types	No. of accessions	Frequency (%)
1.	Coleoptile colour	1-colourless	20	43
		2- Green	19	40
		3- purple	8	17
2.	Basal leaf: sheath colour	1- Green	29	62
		2-Light purple	5	11
		3-Purple lines	1	2
		4-Uniform purple	12	25
3.	Leaf: intensity of green colour	3-Light	1	2
		5-Medium	32	68
		7-Dark	14	30
4.	Leaf: Anthocyanin colouration	1-Absent	30	64
		9-Present	17	36
5.	Leaf: Distribution of Anthocyanin colouration	1&2- On tips and margins	7	44
		1-On tips only	1	6
		2-On margins only	6	37
		3-In blotches only	2	13
		4-Uniform	0	0
6.	Leaf sheath: Anthocyanin Colouration	1-Absent	29	62
		9-Present	8	38
7.	Leaf Sheath: intensity Anthocyanin Colouration	1-Very weak	5	21
		3-Weak	2	8
		5-Medium	0	0
		7-Strong	7	29
		9-Very strong	10	42
8.	Leaf: Pubescence of blade surface	1-Very weak	0	0
		3-Weak	11	23

		5-Medium 7-Strong 9-Very strong	23 12 1	49 26 2
9.	Leaf: Auricles	1-Absent 9-Present	0 47	0 100
10.	Leaf: Anthocyanin Colouration of auricles	1-colourless 2- Green 3- purple	36 2 9	77 4 19
11.	Leaf: Collar	1-Absent 9-Present	0 47	0 100
12.	Leaf: Anthocyanin Colouration of collar	1-Absent 9-Present	29 18	62 38
13.	Leaf: Ligules	1-Absent 9-Present	0 47	0 100
14.	Leaf: shape of Ligules	1-Truncate 2-Acute 3-Split	0 0 47	0 0 100
15.	Leaf: colour of ligules	1-White 2-Light purple 3-Purple	29 2 16	62 4 34
16.	Culm: attitude	1-Erect 3-Semi-erect 5-Open 7-Spreading	16 31 0 0	34 66 0 0
17.	Flag leaf: Attitude of blade	1-Erect 3-Semi-erect 5-Horizontal 7-Drooping	40 6 0 0	85 13 0 2
18.	Density of Pubescence of lemma	1-Absent 3-weak 5-Medium 7-Strong 9-Very strong	4 16 12 13 2	8 34 26 28 4
19.	Male sterility	1-Absent 9-Present	0 47	0 100
20.	Lemma: Anthocyanin Colouration of keel	1-Absent/very weak 3-Weak 5-Medium 7-Strong 9-Very strong	26 7 4 6 4	55 15 8 13 9
21.	Lemma: Anthocyanin Colouration of apex	1-Absent/very weak 3-Weak 5-Medium 7-Strong 9-Very strong	26 8 5 3 5	55 17 11 6 11
22.	Lemma: Anthocyanin Colouration of area below apex	1-Absent/very weak 3-Weak 5-Medium 7-Strong 9-Very strong	27 3 4 8 5	57 6 9 17 11
23.	Stigma colour	1-White 2-Light green 3-Yellow 4-Light purple 5- Purple	32 0 0 0 15	68 0 0 0 32
24.	Anthocyanin colouration of nodes	1-Absent 9-Present	26 11	70 30
25.	Intensity of Anthocyanin colouration of nodes	3-Weak 5-Medium 7-Strong	2 7 2	18 64 18
26.	Anthocyanin colouration of internodes	1-Absent 9-Present	26 11	70 30
27.	Panicle: Curvature of main axis	1-Straight 3-Semi straight 5-Deflexed 7-Drooping	10 33 3 1	21 70 7 2
28.	Colour of tip of lemma	1-White 2-Yellowish 3-Brown 4-Red	26 2 2 1	56 4 4 2

		5-Purple 6-Black	16 0	34 0
29.	Lemma and palea colour	1-Straw 2-Gold and gold furrows on straw 3-Brown spots on straw 4-Brwon furrows on straw 5-Brown 6-Reddeish to light purple 7-Purple spots/furrows on straw 8-Purple 9-Black	18 6 3 12 3 4 0 0 1	39 13 6 26 6 9 0 0 2
30.	Panicle awns	1-Absent 9-Present	34 13	72 28
31.	Colour of awns	1-Yellowish white 2-Yellowish brown 3-Brown 4-Reddish brown 5-Light red 6-Red 7-Light purple 8-Purple 9-Black	0 6 2 2 0 2 1 0 2	0 46 16 15 0 15 8 0 0
32.	Length of longest awn	1-Absent/very weak 3-Weak 5-Medium 7-Strong 9-Very strong	8 4 0 1 0	61 31 0 8 0
33.	Distribution of awns	1-Tips only 3-Upper half only 5-Whole length	9 3 1	69 23 8
34.	Panicle: Presence of secondary branching	1-Absent 9-Present	0 47	0 100
35.	Panicle: secondary branching	1-Weak 2-Strong 3-Clustered	29 15 3	62 32 6
36.	Panicle: Attitude of branches	1-Erect 3-Erect to Semi-erect 5-Semi-erect 7-Semi-erect to spreading 9-Spreading	15 11 9 4 8	32 23 19 9 17
37.	Panicle: exertion	3-Partly exerted 5-Mostly exerted 7-Well exerted	0 20 27	0 57 43
38.	Leaf: senescence	3-Early 5-Medium 7-Late	1 40 6	2 85 6
39.	Sterile lemma colour	1-Straw 2-Gold 3-Red 4-Purple	40 3 2 2	85 7 4 4
40.	Decorticated grain shape	1-Short slender 2-Short bold 3-Medium slender 4-Long bold 5-Long slender 6-Extra-long slender	0 11 16 14 6 0	0 23 34 30 13 0
41.	Decorticated grain colour	1-White 2-Light brown 3-Variogated brown 4-Dark brown 5-Light red 6-Red 7-Variogated purple 8-Purple 9-Dark purple	31 16 0 0 0 0 0 0 0	66 34 0 0 0 0 0 0 0
42.	Endosperm: presence of amylase	1-Absent 9-Present	0 47	0 100
43.	Decorticated grain aroma	1-Absent 9-Present	39 8	83 17

B. Analysis of variance of different yield characters

The analysis of variance for 23 quantitative characters presented in Table 4.2. The analysis of variance indicated that the mean sum of squares due to replication were significant

for panicle number per plant, grain breadth, and grain length breadth ratio. Whereas, genotype were significant for all the characters. The analysis of variance for different characters is presented in Table 3.

Table 3: Analysis of variance for different yield and quality Characters in 47 germplasm accessions

Source of Variance		Mean Sum of Square		
S. No.	Degree of Freedom	Replication	Treatment	Error
		2	3	4
1.	Flag leaf length (cm)	0.295	132.08**	2.41
2.	Flag leaf Width (cm)	0.003	0.23**	0.01
3.	Days to 50% Flowering	0.475	119.34**	0.34
4.	Plant height (cm)	1.385	20.06**	0.05
5.	Panicle number per plant	2.370*	5.98**	0.49
6.	1000 grain weight (g)	0.263	1481.43**	7.19
7.	Days to maturity	0.532	55.08**	1.00
8.	Grain yield per plant (g)	1.577	123.80**	0.50
9.	Grain length (mm)	0.015	51.40**	2.60
10.	Grain breadth (mm)	0.048**	3.23**	0.01
11.	Grain length-breadth ratio	0.037*	0.23**	0.01
12.	Kernel length (mm)	0.002	0.68**	0.01
14.	Kernel breadth (mm)	0.002	3.21**	0.10
15.	Kernel Length- breadth ratio	0.000	0.24**	0.00
16.	Kernel Length after cooking (mm)	0.003	1.50**	0.00
17.	Kernel breadth after cooking (mm)	0.001	0.17**	0.00
18.	Cooked Kernel Length- breadth ratio	0.000	0.61**	0.00
19.	Kernel Elongation Ratio	0.000	3.16**	0.00
20.	Elongation Index	0.000	0.20**	0.00
21.	Hulling %	0.877	0.34**	0.00
22.	Milling %	0.606	0.13**	0.00
23.	Head Rice Recovery %	0.274	0.09**	0.00
24.	Amylose content	0.414	33.17**	0.22

** Significant at 1% level of probability, *Significant at 5% level of probability

C. Heritability

Heritability in the broad sense was calculated for each character and expressed in terms of percentage as given in Table 4. The high heritability estimates (>70%) were observed for all the 23 characters studied in which head rice recovery % and kernel length after cooking has highest heritability.

Similar type of results are reported by Sinha *et al.* (2004) [16] for grain yield, test weight and panicles per plant and Karad and Pol (2008) [8] for 1000 grain weight and plant height. Heritability is the heritable portion of phenotypic variance and it is a good index of the transmission of characters from parents to the offspring. Present study revealed that head rice recovery percentage and kernel length after cooking was highly heritable characters among all and plant breeder can select the germplasm having high rice recovery percentage and high kernel length after cooking as the character is highly heritable followed by milling percentage, kernel length, kernel L: B ratio, and grain length etc.

D. Genetic Advance

Highest genetic advance as percentage of mean were recorded for the characters like head rice recovery, kernel L/B ratio, flag leaf width, grain L/B ratio and elongation index. The moderate genetic advance as per cent of mean (20-30%) was recorded for 1000 grain weight, flag leaf length, kernel elongation index, plant height, cooked kernel L/B ratio, grain yield per plant, kernel length, kernel length after cooking, grain length, panicle number per plant, kernel breadth, and milling percentage. Similar type of results was also reported by Rahman *et al.* (2014) [12] for 1000 grain weight and

Nandeshwar *et al.* (2010) [11] for panicle numbers per plant and plant height.

High magnitude of genetic advance indicates that the characters governed by additive genes and selection will be rewarded. Moderate genetic advance indicates the existence of additive as well as non-additive gene action for the traits. The low genetic advance indicates that the characters are governed by non-additive genes and heterosis breeding may be exploited for the traits.

The low genetic advance as percentage of mean (<20%) under present investigation was recorded by amylose content, grain breadth, kernel breadth after cooking, days to 50% flowering, days to maturity and hulling %.

High genetic advance as per cent of mean was observed for 100 seed weight and which is similar to the findings of Chandra and Pradhan (2003) [4], Choubey and Singh (1994) [5], Balan *et al.* (1999) [3], Choudhary and Motiramani (2003) [6], Sharma and Bhuyan (2004) [14] and Shukla *et al.* (2004). Since broad sense heritability includes both additive and epistatic effects it will be reliable only when accompanied by high genetic advance. Heritability estimates along with genetic advance is more useful than heritability alone in predicting the effectiveness of selection. In the present study, the characters which showed high heritability associated with high genetic advance were head rice recovery, cooked kernel L/B ratio, kernel L/B ratio, grain L/B ratio, 1000 grain weight and elongation index, indicating that selection for these traits is likely to accumulate more additive genes leading to further improvement. High heritability with high genetic advance as per cent of mean recorded by Mohammad *et al.* (2002) [9] for L: B ratio, grain breadth and 1000 grain weight.

E. Genotypic and phenotypic coefficient of variation

The estimates of phenotypic and genotypic coefficient of variation for different quantitative characters of 47 genotypes in the present study are presented in Table 4. The Phenotypic coefficient of variation was higher in magnitude than that of genotypic coefficient of variation for all the characters studied. This reveals that observed variation are result of both genotype and influence of environment.

Among the characters studied, highest genotypic coefficient of variation (>20%) was shown by head rice recovery percentage (34.84). Higher GCV was earlier recorded for 1000 grain weight and plant height by Rahman *et al.* (2014)^[12] and Karad and Pal (2008)^[8]; grain yield per plant by Dhurai *et al.* (2014)^[7]; plant height and effective tillers per plant by Tuwar *et al.* (2013)^[18], grain yield per plant and effective tillers by Medhi *et al.* (2004)^[10].

Moderate genotypic coefficient of variations (10-20%) were recorded for kernel length: breadth ratio followed by flag leaf width, grain length: breadth ratio, elongation index, 1000 grain weight, grain yield per plant, flag leaf length, kernel elongation ratio, plant height, cooked kernel length: breadth ratio, kernel length, kernel length after cooking, grain length, panicle number per plant, amylose content and kernel breadth.

Whereas, Vanaja and Babu (2006)^[19] found moderate genotypic coefficient of variation for length: breadth ratio of grain, milling percentage, amylose content. On the other hand, low magnitude of genotypic coefficient of variation (<10%) in present study was recorded for milling percentage, followed by grain breadth, kernel breadth after cooking, days to 50% flowering, days to maturity, and hulling percentage.

High magnitude (>20%) of phenotypic coefficient of variation (PCV) was recorded for head rice recovery percentage. Moderate phenotypic coefficient of variations (10-20%) were recorded for kernel length: breadth ratio, followed by flag leaf width, grain length: breadth ratio, elongation index, grain yield per plant, 1000 grain weight, flag leaf length, kernel elongation index, plant height, cooked kernel length: breadth ratio, kernel length, Panicle number per plant, kernel length after cooking, grain length, amylose content, kernel breadth, and grain breadth. Vanaja and Babu (2006)^[19] found moderate phenotypic coefficient of variation for length: breadth ratio of grain, milling percentage, amylose content. On the other hand, low magnitude of phenotypic coefficient of variation (<10%) in present study was recorded for Milling Percentage, followed by kernel breadth after cooking, days to flowering, days to maturity and hulling percentage.

Table 4: Estimates of Genetic parameters for different yield and quality characters.

S. No.	Characters	Range			GCV%	PCV%	H ² %(bs)	GA as % of mean
		Min.	Max.	Mean				
1.	FLL (cm)	26.63	57.96	46.38	14.18	14.57	94.71	28.42
2.	FLW (cm)	1.10	2.24	1.51	17.94	18.58	93.21	35.68
3.	DTF	88.33	112.00	102.07	6.17	6.20	99.16	12.66
4.	PH (cm)	88.65	207.25	162.76	13.64	13.74	98.56	27.89
5.	PNPP	8.01	13.83	11.09	12.20	13.73	78.93	22.33
6.	1000 GW (g)	17.26	31.00	23.90	14.94	15.35	94.74	29.97
7.	DTM	116.00	141.00	131.44	4.88	4.91	98.80	9.99
8.	GYPP (g)	19.59	36.37	28.23	14.29	15.39	86.22	27.33
9.	GL (mm)	5.40	10.54	8.34	12.43	12.47	99.47	25.55
10.	GB (mm)	2.27	3.41	2.84	9.67	10.05	92.56	19.16
11.	GLBR	2.01	4.09	2.96	15.95	16.18	97.10	32.37
12.	KL (mm)	3.60	6.83	5.37	13.17	13.19	99.64	27.08
13.	KB (mm)	1.81	2.91	2.29	10.44	10.53	98.41	21.34
14.	KLBR	1.45	3.56	2.38	18.85	18.89	99.57	38.74
15.	KLAC (mm)	5.06	9.81	8.12	12.63	12.64	99.87	26.00
16.	KBAC (mm)	2.58	4.05	3.25	7.95	8.07	97.09	16.13
17.	CKLBR	1.74	3.07	2.51	13.43	13.51	98.91	27.52
18.	KER	1.14	2.07	1.53	13.76	13.81	99.38	28.27
19.	EI	0.68	1.42	1.08	15.67	15.84	97.53	31.95
20.	Hull %	66.66	79.33	73.00	4.54	4.59	98.00	9.26
21.	Mill %	38.86	69.04	61.12	9.87	9.88	99.73	20.30
22.	HRR %	12.15	58.57	34.13	34.84	34.86	99.87	71.72
23.	AC (%)	20.32	30.84	25.33	10.72	11.88	81.39	19.92

FLL-flag leaf length, FLW-flag leaf width, DTF-days to 50% flowering, PH-plant height, PNPP-panicle number per plant, 1000 grain weight, DTM-days to maturity, GYPP-grain yield per plant, GL-grain breadth, GLBR-grain length breadth ratio, KL-kernel length, KB-kernel breadth, KLBR-kernel length breadth ratio, KLAC-kernel length after cooking, KBAC-kernel breadth after cooking, CKLBR-cooked kernel length breadth ratio, KER-kernel elongation ratio, EI-elongation index, Hull % -hulling percentage, Mill % -milling percentage, HRR % -head rice recovery %, AC -amylose content.

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