



Genetic analysis of indigenous rice (*Oryza sativa* L.) genotypes of Bastar Plateau

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Abstract

The investigation entitled “Genetic analysis of indigenous rice (*Oryza sativa* L.) genotypes of Bastar Plateau” was carried out at Research cum Instructional Farm, S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, Bastar, Chhattisgarh, India. Molecular studies were performed at Plant Molecular Biology laboratory, S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur. Study was carried out to study 94 rice accessions, along with 3 checks, on the basis of 16 qualitative and 20 quantitative characters. Analysis of variance for quantitative characters showed differences for different characters. From the result of major rice insect's incidence, it was concluded that out of 97 genotypes tested against different insect-pests, 55, 69 and 3 genotypes were categorized at most promising entries against gall midge, stem borer and leaf folder. And major rice disease incidence, it was concluded that out of 97 genotypes tested against leaf blast and brown spot disease, 7 and 15 genotypes were categorized at most promising entries against leaf blast and brown spot disease. High coefficient of variation in the entire genotypes was observed for grain yield per plant (27.4 %), number of effective tillers per plant (22.37 %), test weight (21.14 %) and kernel length breadth ratio (20.59 %). Correlation analysis revealed positive and highly significant correlation of total number of filled grains per panicle, total number of grains per panicle, plant height and number of effective tiller per plant; harvest index, test weight, flag leaf length and days to maturity had positive highly significant correlation with grain yield per plant. Principal Component Analysis revealed, out of 20, only 7 principal components (PCs) exhibited more than 1.00 eigen value, and showed about 77.42 % variability among the traits studied. So, these 7 PCs were given due importance for further explanation. Component matrix revealed that the PC1 was mostly related to quality characters while PC2, PC3, PC4, PC5, PC6 and PC7 mostly associated with yield related traits. Cluster analysis performed by UPGMA method using Euclidean distance as dissimilarity measure divided the 97 genotypes of rice into ten clusters. The cluster III constituted of 48 genotypes, forming the largest cluster followed by cluster VI (22 genotypes), cluster V (10 genotypes), cluster II (5 genotypes) and cluster VIII (4 genotypes), cluster I, IV and VII (two genotypes each), cluster IX and X had (only one genotypes each). Quality analysis performed for 97 rice genotypes revealed wide range of genetic variability for most of the quality traits. Total of 12 SSR markers (primers) were used for molecular characterization and discrimination of 28 genotypes of rice. After analyzing the data generated from 12 microsatellite markers (SSR), a total of 22 alleles were detected in 28 rice genotypes. The number of alleles per locus generated by each marker ranged from 1 to 3 alleles with an average of 1.8 alleles per locus. Out of 12 SSR markers, 6 markers showed polymorphic reaction with polymorphism information content (PIC) values of 0.53 in RM125, 0.6 in RM161 and 0.75 in RM152, 0.84 in OCR13, 0.88 in RM413 and 0.89 in RM408. Genetic similarity of genotypes of rice under study the genetic similarity coefficient (Jaccard coefficient) ranged from 0.51-1.00 as revealed by UPGMA cluster analysis using the 12 SSR markers. A total of five distinct groups resulted at a cut-off similarity coefficient of 0.683 among the 28 rice genotype.

Introduction

- Rice is one of the Staple foods for more than half of the world's population and influences the livelihoods and economies of several billion people.
- Chhattisgarh the central eastern state is also called as the “Rice bowl of India”. The total estimated area of Rice in Chhattisgarh is 3.70 million ha, production is 7.44 million tonnes and productivity is 1322 Kg/ ha. (Anonymous, 2017).
- Some indigenous rice genotypes of Bastar contain special quality characters like iron and zinc content and some rice genotypes contain delicious scent, exportable grain texture or size, cooking quality or rich in vitamins.
- In the rice cultivation major problem is insect pest tolerance; availability of large genetic variability may be helpful to develop new insect resistant varieties for which proper identification and study of indigenous rice genotypes is required.
- The Rice Germplasm Section at Indira Gandhi Krishi Vishwavidyalaya, Raipur maintains a collection of more than 23,250 accessions, which is biggest in India and second largest in the world after International Rice Research Institute, Philippines.
- And also the Germplasm Section at Shaheed Gundadhoo College of Agriculture & Research Station Kumhrawand, Jagdalpur maintains a collection of more than 390 accessions, which is biggest in Bastar. The collection was collected and conserved as biological treasure from overall Bastar division.
- Keeping in view the above facts, the investigation entitled “Genetic analysis of indigenous rice (*Oryza sativa* L.) genotypes of Bastar Plateau” is very important for exploration of hidden beneficial genetic characters of indigenous rice of Bastar.
- The old and existing landraces are important genetic resources of region having the quality for climate resilient agriculture in consideration of moisture stress, insects, diseases etc. The diversity among land races of any crop is required for improvement of the crop.
- This investigation may be helpful for researchers to identify the gene in combating biotic and abiotic stresses which is needed in the near future to achieve food security.
- Keeping these points in view, to find out suitable genotypes or donor to meet any current or future demand for improvement of the rice crop, various indigenous rice genotypes are taken to study the following objectives:

Objectives:

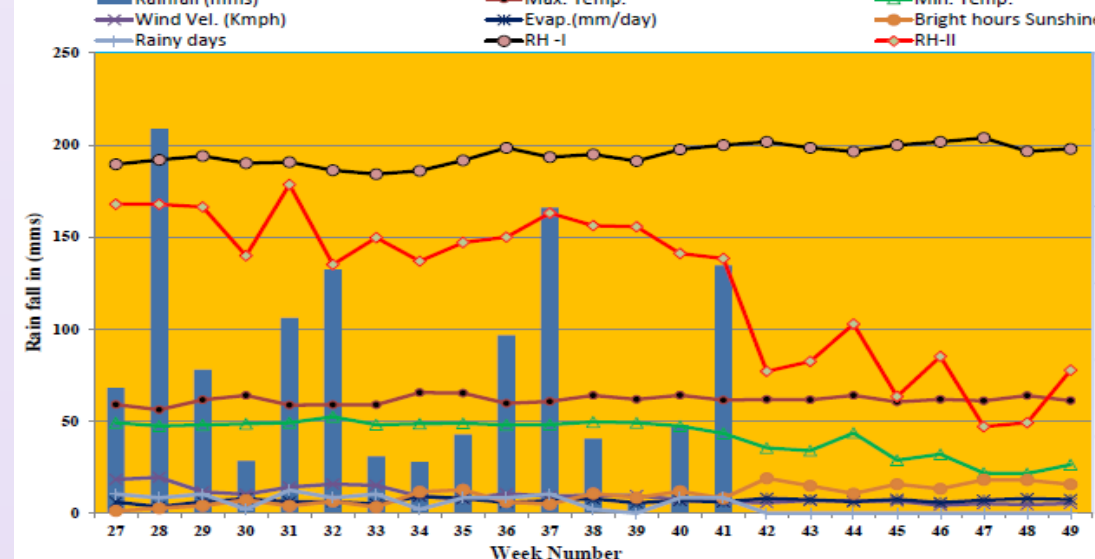
- To study the variation in morphological and yield attributing characters.
- To study quality parameters of selected rice germplasm.
- To understand correlations between yield and yield attributing traits.
- Genetic Diversity analysis of selected genotypes.

Material and methods

Experimental site:

Field work and Molecular studies, were performed at, S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, Bastar, Chhattisgarh, India.

Experimental season and weather:



Experimental material:

The experimental materials comprised of ninety four local landraces of rice and three popular standard checks namely MTU-1010, Danteshwari and CR-40

Experimental Methods:

Randomized Block Design in ten blocks and each block comprised of 10 genotypes and three checks.



Observations recorded:

- Agro-morphological Characters,
- Incidence of major insect and disease of rice

Molecular characterization: On the basis of yield performance twenty five Genotypes and three checks were selected for molecular analysis.

Genomic DNA isolation



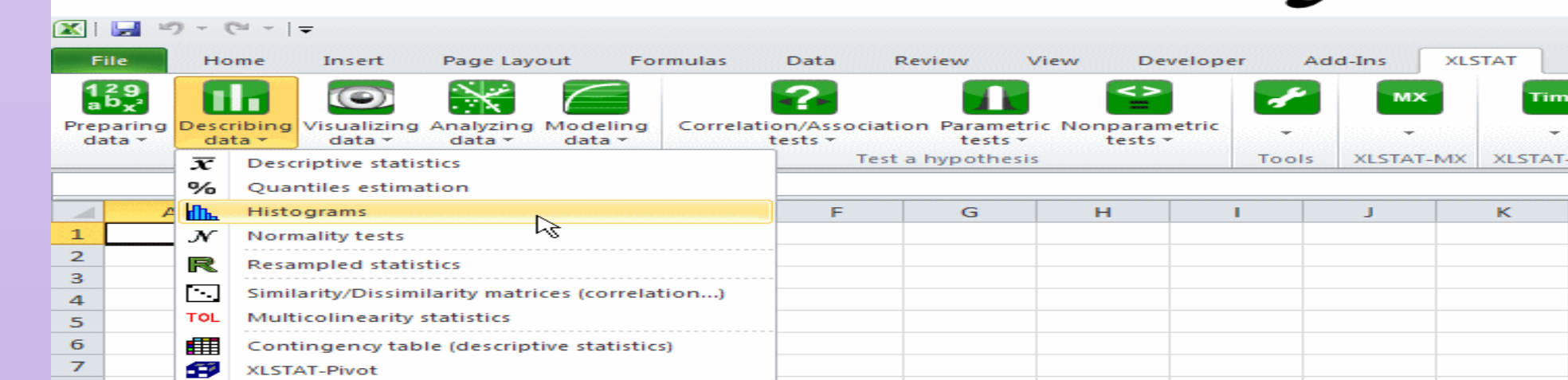
PCR amplification using SSR Primers:

S. No.	SSR Primers	Chromosome number	S. No.	SSR Primers	Chromosome number
1	RM413	5	7	RM484	10
2	RM161	5	8	RM277	12
3	RM162	6	9	RM338	3
4	RM125	7	10	RM152	3
5	RM408	8	11	RM154	2
6	RM44	8	12	OSR 13	3

Statistical Analysis

The data recorded on ninety four local landraces of rice and three popular standard checks for different quantitative characters and quality characters were subjected to the following analysis. Analysis of variance, Assessment of Genetic variability, Association analysis, Genetic divergence analysis: Cluster analysis, Principal Component Analysis.

Statistical Analysis



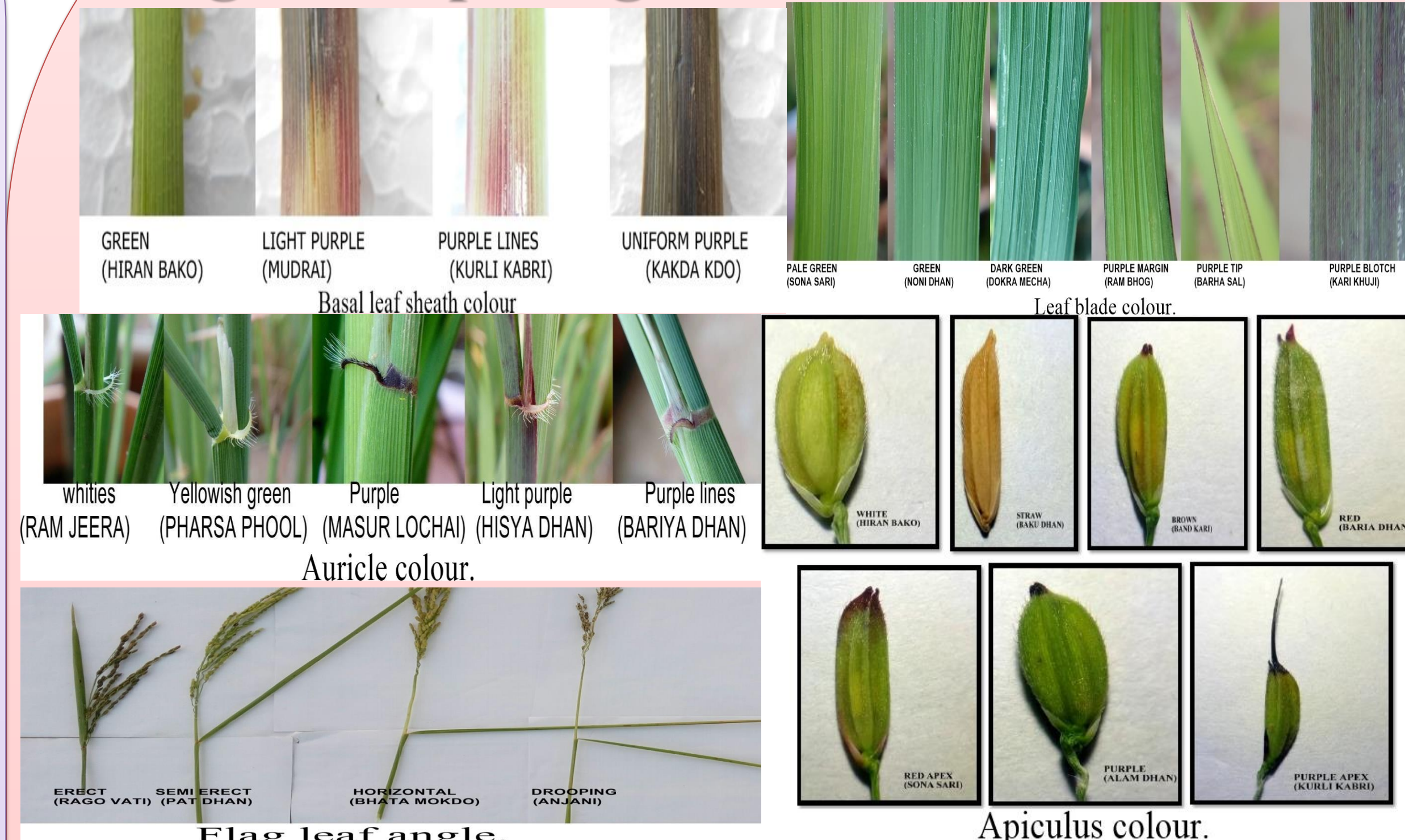
Statistical Analysis using XLSTAT 2017 software.

ACKNOWLEDGEMENTS

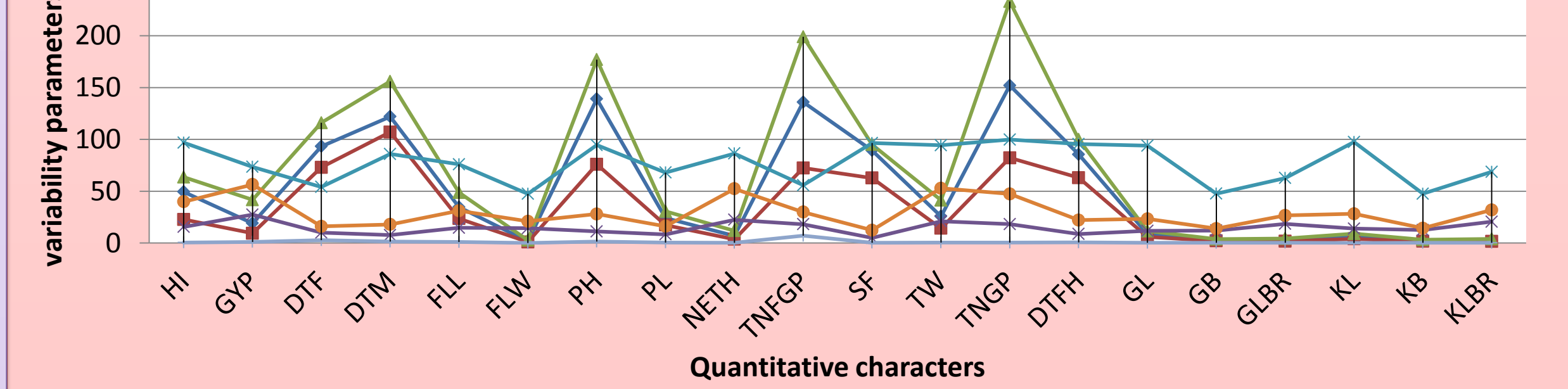
The author is thankful to the Department of Genetics and Plant Breeding S G College of Agriculture and Research Station Kumhrawand, Jagdalpur, (C.G.) IGKV.

HI=Harvest Index, GYP=grain yield/plant, DTF= days to 50%flowering, DTM =days to maturity, FLL=flag leaf length, FLW=flag leaf width, PH= plant height, PL=panicle length, NETH= no. of effective tillers/plant, TNFGP= total no. of grain /panicle, SF spikelet fertility, TW=test weight, TNFGP=total no. of filled grains/panicle, DTFH=date of first heading, GB=grain breadth, GL= grain length, GLGR=grain length breadth ratio, KB=kernel breadth, KL=kernel length, KLBR= kernel length breadth ratio.

Agro-morphological characterization



Mean and variability parameters for different quantitative characters



Path coefficients showing direct and indirect effects of different characters on grain yield per plant.

Character	DTF	DTFH	DTM	GB	GL	GLBR	KB	KL	KLBR	Correlation with GYP
TNFGP	0.00	0.00	0.05	-0.01	-0.19	0.16	0.05	0.00	-0.10	0.34**
DTF	0.00	0.00	0.04	-0.04	-0.29	0.20	0.07	0.00	-0.12	0.34**
SF	0.01	0.00	-0.02	0.09	0.04	-0.13	-0.07	0.00	0.04	-0.011
PH	-0.01	0.01	0.01	-0.01	0.20	-0.20	-0.08	0.01	0.07	0.25**
NETH	0.00	0.00	0.01	0.22	-0.08	0.27	-0.24	0.06	0.17	0.27**
FLW	0.00	0.00	0.00	-0.01	0.09	-0.07	-0.10	-0.02	0.06	0.120
DTM	0.00	0.00	0.02	0.05	0.04	-0.06	-0.04	-0.07	0.11	0.29**
TW	-0.01	0.01	0.00	-0.01	0.12	0.12	0.12	0.12	0.12	0.27**
FL	0.00	0.00	0.00	0.01	0.06	0.03	0.00	0.04	-0.06	0.20**
DTFH	0.00	0.00	0.01	0.14	0.14	0.05	0.17	-0.04	0.13	0.27**
DTM	-0.06	0.02	0.10	-0.06	0.26	0.12	0.01	-0.06	0.06	0.078
DTFH	-0.05	0.02	0.09	-0.06	0.26	0.12	0.01	-0.06	0.06	0.078
DTM	-0.04	0.01	0.08	-0.04	0.26	0.12	0.01	-0.06	0.06	0.078
DTFH	-0.04	0.01	0.08	-0.04	0.26	0.12	0.01	-0.06	0.06	0.078
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