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SCREENING OF RICE GENOTYPES (*Oryza sativa* L.) FOR YIELD, GRAIN QUALITY CHARACTERS AND IRON CHLOROSIS ON VERTISOLS

BY

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DISSERTATION

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2014

DEDICATED

to

*I dedicate this thesis
manuscript to My family
especially to my Brother*

RAJAN DHAKAL

*For his encouragement and the
belief that he has on me more
than I have on myself.*

CANDIDATE'S DECLARATION

I, hereby declare that the entire dissertation
or part thereof, has not been
previously submitted by
me for a degree of
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CERTIFICATE-I

This is to certify that **Mr. RAJEEV DHAKAL** has satisfactorily prosecuted his course and research for a period of not less than four semesters and that the dissertation entitled “**SCREENING OF RICE GENOTYPES (*Oryza sativa* L.) FOR YIELD, GRAIN QUALITY CHARACTERS AND IRON CHLOROSIS ON VERTISOLS**” submitted by him is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination.

I also certify that the entire dissertation or part thereof has not been previously submitted by him for a degree of any university.

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CERTIFICATE-II

This is to certify that the thesis entitled “**SCREENING OF RICE GENOTYPES (*Oryza sativa* L.) FOR YIELD, GRAIN QUALITY CHARACTERS AND IRON CHLOROSIS ON VERTISOLS**” submitted by **Mr. RAJEEV DHAKAL** to the Vasantarao Naik Marathwada Krishi Vidyapeeth, Parbhani in partial fulfilment of the requirement for the degree of **MASTER OF SCIENCE** in the subject of **AGRICULTURAL BOTANY (Genetics and Plant Breeding)** has been approved by the student's advisory committee after viva-voice examination in collaboration with the external examiner.

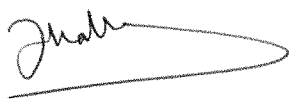


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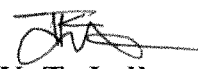


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(Rajeev Dhakal)

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ABBREVIATIONS

/	:	per
%	:	per cent
Σ	:	Summation
σ^2	:	Variance
h^2	:	Heritability
cm	:	Centimeter (s)
CV	:	Coefficient of variation
d.f.	:	Degree of freedom
EMSS	:	Error mean sum of squares
<i>et al.</i>	:	<i>et alia</i> (and others)
etc.	:	Etceteras
Fig.	:	Figure
g	:	Gram (s)
G	:	Genotypic correlation
GM	:	General mean
GCV	:	Genotypic coefficient of variation
PCV	:	Phenotypic coefficient of variation
i.e.	:	Id est (that is)
kg	:	Kilogram (s)
m	:	Meter
ml	:	Milliliter
mm	:	Millimeter
MSS	:	Mean sum of squares
EGA	:	Expected genetic advance
P	:	Phenotypic correlation
No.	:	Number
R	:	Residual effect
r	:	Correlation coefficient
S.E.	:	Standard error
Ch	:	Check
viz.	:	Videlicet (namely)
CD at 5%	:	Critical difference at 5 per cent
CV	:	Coefficient of variance
L:B ratio	:	Length: breadth ratio



INTRODUCTION



CHAPTER-I

INTRODUCTION

Rice belongs to genus *Oryza*, of the family *Gramineae*, and is widely cultivated crop (FAO, 2000; Syed and Khaliq, 2008). Genus *Oryza* contains approximately 23 species, of which 21 are wild type and two; *O. sativa* and *O. glaberrima*, are cultivated world wide (Vaughan, 2003). It is a staple food and more than half of world population depends on its consumption and income generation (Bucheyeki *et. al.*, 2011). About 95 per cent of global output of rice is produced and consumed in developing countries. It is most important food crop for 2.89 billion people in Asia, 40 millions in Africa and 1.3 millions in the Americas (FAO, 2000)

Rice is grown over an area of 163.46 million hectare with production of 718.35 million tonnes and productivity of 4390 kg/ha in the world. In India, rice is cultivated on an area of 43.97 million hectare with production of 104.3 million tones and productivity of 2372 kg/ha (Anonymous, 2014). Rice occupies pivotal role in Indian Agriculture. It is the staple food of more than 70 per cent people and source of livelihood of 120-150 million rural households. It contributes about 43 per cent to total food grain and 53 per cent to cereal production, and thus holds the key to sustain food sufficiency in country (Siddiq *et. al.*, 2004). Forty four per cent of total rice area in India is under rainfed condition, distributed mainly North-East India, North India, Central-Western India, Eastern India and partly in other region (Das, 2006).

In Maharashtra, rice is grown over an area of 15.134 lakh hectares with an annual rice production of 28.78 lakh tones. The average productivity of the state is 1.90 t/ha. Maharashtra ranks 13th place in rice production in country. The average productivity of the Maharashtra state is low as compared to other rice growing states viz., Punjab, Tamil Nadu, Haryana, Andhra Pradesh etc. Maharashtra is classified into four rice growing region viz., Konkan, Western Maharashtra, Marathwada and Vidarbha region. The

highest area under rice crop is in Vidarbha region (7.954 lakh hectares), while the highest productivity is in Konkan region i.e. 2.75 t/ha (3.83 t/ha for rough rice). Marathwada region is the non-traditional rice growing area in Maharashtra. Due to the erratic and less rainfall in Marathwada region, the average productivity of rice crop is lowest i.e. 0.59 t/ha. In Marathwada, area under rice production is 0.122 lakh hectare with production of 0.072 lakh tones (Anonymous, 2014).

It is desirable to study yield and yield contributing traits like number of effective tillers per plant, number of grains per panicle, 1000 grain weight, days to 50% flowering, days to maturity, panicle length and plant height have shown positive association with grain yield per plant (Watoo *et al.*, 2010).

Along with the high yield, better rice grain quality parameters are desirable which gives great value to rice. The traits and parameters used to evaluate grain quality in rice vary across countries. However, four main quality traits are widely used to access quality, namely milling properties, appearance, nutritional value and cooking quality. Milling quality of grain determines the final yield and the broken kernel rate of milled rice (Yu *et al.*, 2008). Appearance is one of the crucial properties appealing consumer after milling. The eating properties, easiness of cooking, as well as firmness and stickiness are associated with cooking quality. Since rice is one of the staple food the nutritive value is also the matter of concern.

Being a major cereal grain, evaluating the nutritional and cooking qualities of rice has been given highest priority (Tan *et al.*, 1999; FAO, 2004; Dong *et al.*, 2007). The cooking quality of rice is largely dependent to a large extent on the properties of starch, mainly amylose content (Juliano, 1985). Cooked rice with low amylose is soft and sticky, while rice with high amylose is firm and fluffy (Juliano, 1971). In India, a long grain with intermediate amylose content and soft gel consistency is preferred since it become soft and fluffy after cooking (Hossain *et al.*, 2009).

Growing rice in upland and non-flooded environment also affects grain quality. A recent study involved several cooking and nutritional quality traits, including amylose content gel consistency, gelatinization temperature and protein content, in the same population grown under upland and lowland conditions. The phenotypic values of all four traits were significantly higher under upland environment than low land (Guo *et. al.*, 2007).

Deficiency of iron is one of the widely known disorders in Vertisols. Iron is indispensable for chlorophyll synthesis. The amount of Fe^{2+} fraction of total iron is believed to make the plant green or chlorotic (De Kock, 1971). In India, calcareous and alkaline soils of Bihar, heavy clay soil of Maharashtra, Karnataka and Andra Pradesh, alkaline soils in Indo-Gangetic alluvial of Uttar Pradesh and Bihar, and manganese rich soils of coastal Karnataka suffers from this malady (Hoan *et. al.*, 1992).

The old varieties of rice grown in Marathwada region were tall in height and tolerant to iron chlorosis but in quality parameters they doesn't satisfied the requirements of consumers like long slender grains and grain quality of basmati type like scent, intermediate amylose content, absence of white belly and soft in cooking. Efforts were made to develop high yielding semi-dwarf varieties of rice with better cooking quality suitable for black cotton soils and series of varieties were evolved like Prabhavati, Sugandha, Parag and Avishkar at Department of Genetics and Plant Breeding and Upland Paddy Research Scheme of Vasantarao Naik Marathwada Krishi Vidyapeeth, Parbhani.

Hence, this investigation was carried out to study the variability for the grain yield, yield contributing characters, nutritional and quality characteristics, correlation and path analysis of different traits along with the reaction of genotypes to iron chlorosis. Thus, this investigation will be very handful in screening the genotypes for yield, quality traits and iron chlorosis on Vertisols. The final result of these investigations will be presented and discussed in the dissertation with the pre-specified objectives.

Objectives:

1. To study the variability for yield and yield contributing characters.
2. To study cooking and eating quality characteristics of rice genotypes.
3. To study the correlation and path analysis for different traits.
4. To screen the rice genotypes for iron chlorosis tolerance on Vertisols.



REVIEW OF LITERATURE



CHAPTER-II

REVIEW OF LITERATURE

Literature in respect of genetic variability, heritability, genetic advance, correlation coefficient, path analysis and iron chlorosis reaction has been reviewed and presented in this chapter.

2.1 Genetic Variability

The success of plant breeding depends upon the extent of genetic variability present in a crop. Genetic variability in the initial breeding material ensures better chances of producing desired forms of a crop. A decisive analysis of genetic variability is a pre-requisite for initiating any crop improvement program and for adopting of apposite selection techniques. Such major variability can be seen in rice crop. We can get remarkable variability in respect of different morphological, floral, grain cooking and quality traits in different cultivars.

The presence of such genetic variability for economic traits is a key factor for improving productivity. Presence of variability aids to selection of suitable parents in hybridization program which is an important step of development of new variety or hybrids in any crops.

Literature in respect to genetic variability of different yield attributing traits and qualitative traits has been presented below.

2.1.1 Genetic variability for quantitative characters

The knowledge and magnitude of genetic variation present in the rice genotypes in respect to quantitative characters like yield and its components are crucial for effective genetic improvement.

Kaul and Kumar (1982) presented genotypic components of variation and observed considerable variability for all traits, highest being for plant height followed by tiller number and grain yield.

Debchoudhary and Das (1998) reported high genotypic coefficient of variation for grain yield and grains per panicle followed by low genotypic and phenotypic coefficient of variation for days to 50% flowering and panicle length.

Vange *et al.*, (1999) studied 10 early duration rice genotypes for grain yield and its components and observed considerable variation. Grain yield ranged from 2 to 4.2 tonnes/ha, 1000 grain weight ranged from 22.4 to 30.9 g, grains per panicle from 116 to 155, panicles per meter from 140 to 233 and flag leaf area from 26.28 to 42.30 cm².

Patil *et al.*, (2003) evaluated 128 aromatic rice genotypes. A wide range of variation for grain yield and yield components like 1000 grain weight (7.03 to 23.65 g), ear bearing tiller per plant (3.50 to 13.90) and panicle length (18.70 to 36.60) was observed.

Singh *et al.*, (2006) estimated genetic variability of 34 genotypes of rice and they reported wide range of genetic variability recorded for grain yield per plant.

Rosamma and Vijaykumar (2007) evaluated 48 hybrid combinations and their reciprocals. It was found that there was significant difference between almost all characters except days to 50% flowering and panicle length.

Waghmare *et al.*, (2008) studied 64 rice genotypes and estimated that genetic diversity is prerequisite for any crop improvement program. The observations were recorded on different morpho-physiological characters viz., days to 50% flowering, plant height, number of effective tillers per plant, panicle length and grain yield per plant.

Bisne *et al.*, (2009) estimated genetic parameters for yield and its correspondent characters in rice in a trial with four CMS lines, 8 testers and 32 hybrids for 13 characters. Low, moderate and high genotypic and phenotypic coefficient of variation were observed, whereas, high GCV and PCV were expressed by harvest index, total number of filled spikelets, 1000-grain weight and spikelet fertility percentage.

Khan *et al.*, (2009) studied the analysis of variance for 25 genotypes indicated highly significant differences for all morphological traits.

Laxuman *et al.*, (2010) observed that, phenotypic coefficient of variation and genotypic coefficient of variation for most of the traits were either high or moderate except productivity trait like days to heading, days to 50% flowering, panicle length and plant height at maturity.

Nadali (2010) revealed that analysis of variance have significant differences among genotypes, crosses, lines, testers and line x tester interactions for tiller number, plant height, days to 50% flowering, panicle length, number of spikelets per panicle, spikelet fertility and grain yield contributing traits.

Pandey *et al.*, (2010) studied the genetic variability of 40 rice genotypes for yield and its components and stated that the analysis of variance revealed highly significant differences for all the characters studied, indicating the presence of substantial genetic variability. The higher magnitude of GCV and PCV was recorded for harvest index, grain yield per hill, plant height and biological yield per hill.

Adeyemi (2011) Studied 25 upland rice cultivars and analysis of variance indicated highly significant differences for plant height and grain weight.

Akinwale *et al.*, (2011) reported that the genotypes tested differed significantly at ($p > 0.001$) for all the traits studied implying the presence of adequate genetic variability in genotypes under study. Moderate to low PCV and GCV were obtained for days to heading, days to maturity, plant height and panicle length. GCV were also found to be lower than the corresponding PCV in all traits studied.

Fukeri *et al.*, (2011) carried out a genetic analysis of yield and other 19 characters and stated that analysis of variance revealed presence of high variability among genotypes for all traits. GCV was high for flag leaf area, plant height, number of tiller per plant, number of ear bearing tillers, number of filled grains/panicle, panicle weight, root length and area, straw weight and

grain yield. Whereas, GCV was low for days to maturity and chlorophyll index and moderate for rest of the characters.

Hasan *et al.*, (2011) studied fourteen genetically diverse CMS lines and revealed that GCV ranged from 1.853 to 47.49 and PCV ranged from 2.963 to 53.258. GCV and PCV did not differ remarkably in tested entry for most of the characters studied, which indicated minimum environmental influence on these traits.

Singh *et al.*, (2011) observed a wide range of variation among 81 genotypes of rice for quantitative characters. Analysis of variance revealed that the difference among genotypes were significant for all characters except flag leaf width. Among all the traits number of spikelets per panicle exhibit high estimates of GCV and PCV followed by harvest index, grain yield per hill and number of panicles.

Selvaraj *et al.*, (2011) studied 21 rice genotypes and analysis of variance revealed that considerable variability was observed among all characters studied. The PVC was slightly greater than GVC for number of tillers per plant followed by plant height and grain yield per plant indicating influence of environment on them.

Idris *et al.*, (2012) studied genetic variability and correlation between yield and yield contributing components in some rice genotypes in seven characters and reported highly significant differences ($p \leq 0.01$) between the most of the characters under study except for percentage of unfilled grains per panicle (%).

Ovung *et al.*, (2012) studied genetic divergence in 70 rice genotypes by considering 13 quantitative characters and revealed the presence of considerable amount of variability among genotypes. High estimates of GCV and PCV were observed for grain yield per hill followed by tillers per hill and harvest index. High heritability with high genetic advance was recorded for spikelets per panicle.

Yaqoob *et al.*, (2012) evaluated ten rice genotypes for yield and yield components and reported the discrepancy among genotypes was found to be significant and highly significant. The mean values for days to heading

ranged from 107.67 to 130.33, plant height from 86.67 to 114.67 cm, panicle length from 21.67 to 27.33 cm, total tiller per plant from 8 to 14.67, productive tiller per plant from 7.67 to 12.67, maturity from 137.33 to 148.33 days, 1000-seed weight from 16.26 to 23.13 g and grain yield from 1.64 to 3.43 ton per hectare.

Bekele *et al.*, (2013) reported significant genotypic differences for all the characters under study in 64 genotypes of rice. The estimates for PCV and GCV were high for zinc concentration, number of tiller per plant, number of productive tiller per plant and grain yield per plant. Remaining characters showed moderate PCV and GCV except days to maturity with low PCV and GCV.

Chakravoty *et al.*, (2013) analyzed the diversity of phenotypic traits of landraces of rice and reported that, analysis of variance showed significant variability in eighteen quantitative traits under study.

Dutta *et al.*, (2013) observed significant variation for all twelve characters among 68 rice genotypes under study. High GCV and PCV were reported for spikelet per panicle, spikelet density, spikelet per plant, grain yield, tillers per plant, days to 50 % flowering, harvest index and 1000-seed weight, while moderate for length of panicle and low for percentage of viable seeds.

Prasad *et al.*, (2013) analyzed the variance among 52 genotypes and result showed significant difference for yield contributing characters except early seedling vigor and spikelet sterility. The result also revealed that PCV in general was higher than GCV for various characters. Highest PCV and GCV were observed for productive tillers and spikelet sterility.

Sanghera *et al.*, (2013) reported that genotypic and phenotypic coefficient were high for grain yield, secondary branches per panicle and panicle weight; moderate for grain number per panicle, grain length and breadth ratio and panicle density. High heritability was found to be accompanied with high to moderate genetic advance for expression of these characters.

Toshimenla (2013) studied seventy four upland rice accessions for evaluation of 13 quantitative characters and reported that maximum phenotypic and genotypic variation were recorded for number of filled grains, plant height, number of unfilled grains, days to 50% flowering and days to maturity. Values of phenotypic and genotypic variation were very close for leaf width and 1000 seed weight indicating the stable nature of these characters.

Tuwar *et al.*, (2013) estimated genetic components of variability in 29 genotypes of rice and revealed a wide range of variation for twelve characters. The plant height exhibit high estimates of GCV and PCV preceded by number of tillers and effective tillers per plant, number of spikelets and number of grains per panicle and grain weight per panicle. The phenotypic coefficient of variance was in general, higher than genotypic coefficient of variance, but the differences between PCV and GCV for many traits was less, suggesting the less influence of environment.

2.1.2 Genetic variability for qualitative characters

Apart from yield, grain quality characters are equally important in rice breeding and improvement of crop. The extent of variability present in respect to qualitative characters such as length breadth ratio, relative density, amylose content, protein content, gel consistency etc. are essential for crop improvement.

Comparison of quality traits showed significant variation among the cultivars in the same environment (Adu-Kwarteng *et al.*, 2003; Cameron and Wang 2005; Kang *et al.* 2006).

Allahgholipour *et al.*, (2006) studied one hundred and sixty seven landraces of rice from twenty three different rice growing countries. They separated those varieties into four groups based on the amylose content and paste viscosity parameters. The four amylose content groups were waxy rice (0-8%), low amylose content (8.1-16%), intermediate amylose content (16.1-24%) and high amylose content (>24.1%).

Nayak (2007) reported that number of principle components are associated with milling, cooking, processing and nutritive quality of rice, some

of them are L:B ratio, grain translucency, relative density, water absorption, gel consistency, protein content and amylose content.

Rathi *et al.*, (2011) determined the grain quality of 100 upland/ahu rice genotypes of Assam. Out of which 15 fell into long grain length (6.6-7.5 mm), 82 into medium grain length (5.51-6.6 mm), 3 into short grain (<5.5 mm) and width vary from 2-3 mm. The starch content varies from 66.0% to 79.5%. The range of amylose content observed from 14% to 25%.

Danbaba *et al.*, (2011) evaluated the cooking and eating quality of Ofada rice. The quality parameters measured were, grain elongation, water absorption, gelatinization temperature and amylose content. The results showed that Ofada rice had high cooked rice volume with length and breadth increase of 152.54% and 87.85% respectively. The highest length and breadth ratio (3.68) was recorded by Ofada 8, while, Ofada 3 had lowest (2.49). The gelatinization temperatures were intermediate. Ofada rice had good cooking and eating quality, hence selection for improvement based on these parameters will be a right direction.

2.1.2.1 Length breadth ratio (L:B)

Binodh *et al.*, (2006) studied the different rice genotypes for length and breadth and they observed range from 4.0 to 7.0 mm and 1.70 to 4.00 mm respectively. The highest length and breadth ratio with long slender grain was observed in hybrids TNRH-55, TNHR-31 and ADTRH-1.

Singh *et al.*, (2011) reported that L:B ratio was important rice quality character which determines the shape of the rice grain, its higher value (3.00) is desirable, three hybrids were identified as slender grains.

Thomas *et al.*, (2013) reported that there was positive correlation ($r=0.66$) between water uptake ratio and length/breadth ratio. The range of L/B ratio was between 2.09 and 3.75.

2.1.2.2 Relative density

Bhattacharya *et al.*, (1972) observed that the bulk density is related to the kernel shape i.e. length/breadth ratio, the more round the kernel, greater the bulk density.

Yadav *et al.*, (2007) evaluated four non-basmati and 2 basmati cultivars for their morphological, physio-chemical and cooking properties and found significant difference in bulk density between Jaya and other cultivars. The bulk densities of various rice cultivars varied between 0.83 to 0.92 g/ml, higher for coarse grains.

Shejul (2012) in her study revealed that relative density ranged from 1.070 to 1.333 g/ml with an average value of 1.194 g/ml. The genotype PBNR 08-01 (1.333 g/ml) was with highest relative density as compare to check Avishkar (1.310 g/ml) and genotype PBNR 04-27 (1.070 g/ml) recorded the lowest relative density.

Thomas *et al.*, (2013) reported that among the different varieties of rice, bulk density was observed to be highest in brown rice (0.86 g/ml), followed by glutinous rice (0.83 g/ml) and Bario rice (0.82 g/ml)

2.1.2.3 Gelatinization temperature

Bhonsle and Krishnan (2011) collected 10 traditionally cultivated varieties and analyzed the physico-chemical characteristics and revealed that low alkali spreading value (ASV) and high gelatinization temperature (GT) were observed in Assgo, Damgo, Kalo korgut, Khochro, Munro and Shiedi. The intermediate ASV and GT were noted in varieties such as Bello, Kalo Damgo, Kalo Novan, and Khochro. The low-intermediate ASV and high-intermediate GT was in variety Korgut.

Subbaiah *et al.*, (2011) studied the extent of variability and genetic parameters with 16 parents and 48 hybrids and reported that the gelatinization temperature ranged from 2.00 – 6.33 with mean 3.69. High PCV and GCV were recorded for gelatinization temperature in parents and as well as in hybrids.

Oko *et al.*, (2012) assessed the cooking quality and physio-chemical characteristics of 15 selected indigenous and five newly introduced hybrid rice varieties. In result, it has been asserted that significant positive correlation was observed between gelatinization temperatures and cooking time, though the r-value was low (0.266).

2.1.2.4 Gel consistency

Cagampang *et al.*, (1973) reported that varieties having same amylose content may be differentiated for tenderness of cooked rice by gel consistency. Gel consistency reflects the combined effects of amylose and amylopectin properties within the same amylose group varieties with softer gel consistency are preferred as cooked rice is tenderer. Most of the intermediate amylose genotypes appear to have soft gel consistency.

Singh and Singh (2005) studied 20 genotypes of rice and they reported that maximum phenotypic and genotypic variances for gel consistency and water absorption. The high values of GCV and PCV suggest that there is possibility of improving these characters through direct selection.

Bajpai and Singh (2010) reported that gel consistency decides either rice is soft (gel consistency >60%) flaky (gel consistency 41-60%) or very flaky (gel consistency < 40%). In his study it was ranged from 60% to 90%.

Rathi *et al.*, (2011) studied 100 rice genotypes for variability in grain quality characters such as gel consistency. The difference between GCV and PCV was very less for this character.

2.1.2.5 Volume expansion

Nayak *et al.*, (2003) studied 200 scented rice varieties and reported that medium values of GCV (10.31) and PCV (12.42) were observed for volume expansion ratio.

Vanaja and and Babu (2006) assessed the genetic variability of 56 high yielding rice genotypes for 10 quality parameters and phenotypic and genotypic coefficients of variation revealed the existence of moderate variability in L/B ratio of grains, milling percentage, amylose content, water uptake and volume expansion. Volume expansion ratio ranged from 1.873 to 3.17.

Umadevi *et al.*, (2010) studied 110 genotypes of rice for 16 grain quality characters and reported that volume expansion ratio ranged from 2.31-4.92 with an average of 3.60. High GCV (23.21) and PCV (23.43) were also observed for this character.

Bhonsle and Krishnan (2011) in their study reported that the volume expansion ratio in traditionally cultivated rice varieties ranged from 1.6 to 4.01 where the highest expansion ratio was recorded in Khocho and lowest in variety Kalo Korgut.

Subbaiah *et al.*, (2011) reported that volume expansion ratio ranged from 1.17 to 1.25 with mean 1.24 with GCV and PCV 2.32 and 2.95 respectively. The heritability was recorded 0.61 and GA was 0.05.

2.1.2.6 Amylose content

Juliano (1979) reported that milled rice may be classified on the basis of amylose content as waxy (1-2%) or non-waxy (more than 2%), very low (2-10%) and low (10-20%).

Pooni *et al.*, (1993) studied 10 rice crosses for inheritance of amylose content and reported that the additive and dominance effects were important in determining the genetic variability in crosses.

Nayak *et al.*, (2003) reported that, the amylose content ranged from 16.10% to 25.47% with mean of 20.49%. The GCV and PCV were recorded to be 11.34 and 11.40 respectively.

Subudhi *et al.*, (2005) evaluated 20 aromatic rice genotypes including one check. Amylose content was intermediate in all genotypes except CRM 839 and CRM 689-116-2.

Binod *et al.*, (2006) amylose content was found to be intermediate in 25 rice varieties and 5 hybrids including the premier quality check variety BPT -5204.

Singh and Singh (2007) evaluated 34 genotypes, the amylose content was estimated and reported that only Pusa Basmati 1 and UPR 840 -31-1 showed optimum (23.30% and 22.74%) amylose content and minimum and maximum amylose content were recorded in improved Indrasam and Nidhi respectively.

Bajpai and Singh (2010) reported that amylose content was in intermediate category and it ranged from 20.6% to 25.5%. Most of the Maharashtrian consumers generally prefer intermediate amylose content (20-

25%). The rice varieties are grouped on the basis of their amylose content into waxy (0-2%), very low (3-9%), low (10-19%), intermediate (20-25%) and high (>25%).

Danbaba *et al.*, (2011) conducted a study of *Odafa* rice and revealed that amylose content ranged from 19.77% to 24.13%, with an average of 21.55%.

Oko *et al.*, (2012) reported that in some physio-chemical characteristics like amylose, amylopectin, gel consistency and gelatinization temperature, highly significant variation was observed. The amylose content among the varieties studied ranged from 19.50% to 25.51% with mean of $22.91 \pm 2.01\%$.

2.1.2.7 Protein content

Among cereals, rice grain protein has been found to be of relatively good quality (rich in lysine, about 4%), Protein content of milled rice is relatively low (about 7%).

Khush and Juliano (1984) selected 6 high protein containing varieties and crossed with IR-8. The results indicated that the resulting lines had only 2/3 of yield potential of IR-8 and there was no line with high protein content.

Shenoy *et al.*, (1991) studied inheritance of protein in rice and they reported overall partial dominance of high protein grain over the low protein grain. Predominance of non-additive gene effect for this character was observed.

Dalal *et al.*, (2003) studied six varieties of rice viz., Gobind, Haryana, Basmati-1, IR-64, Jaya and PR-106 for their crude protein content and it was ranged from 7.2 to 9.1 percent.

Yadav *et al.*, (2007) from his study revealed that protein content in six different rice cultivars ranged from 5.46 to 7.02%. Among these cultivars Jaya cultivar differed significantly from all others, except HKR-120 in protein content.

Banerjee *et al.*, (2011) on their study reported that there was significant variability for grain protein content. Protein content of milled grains among 258 lines ranged from 4.91% to 12.08%. The lysine content varied from 1.73 to 7.13 g/16g of N. The result also revealed that there was presence of wide genetic variability for protein and lysine content in rice landraces those were taken under study.

Thomas *et al.*, (2013) studied six different rice varieties and reported that protein content ranged from 5.96 to 8.16%, while fat content ranged between 0.07 and 1.74%.

2.1.2.8 Water absorption

Subudhi *et al.*, (2005) reported that water uptake values between 250 to 300 ml/100g are acceptable. It was found to range from 130 to 350 ml/100g indicating there was variability for water uptake.

Vanaja and Babu (2006) reported that GCV and PCV were shown relatively high for water uptake. The value for water uptake ranged from 0.37 to 0.95 with mean of 0.56.

Singh and Singh (2007) studied 34 rice varieties analyzed for water uptake and they observed a wide range for uptake from 390 to 500 ml/100g.

Yadav *et al.*, (2007) studied six rice varieties and reported that cultivar HBC-19 showed highest water uptake of 4.63 g/g while cultivar HKR-120 showed the least value of 2.89 g/g.

Shejul *et al.*, (2013) studied 22 genotypes with 2 checks for quality characters of rice and revealed that among all genotypes, the genotype PBNR 03-20 (1.192 mg) had recorded highly significant water absorption followed by PBNR 04-23 (1.185 mg), PBNR 04-28 (1.160 mg), PBNR 04-36 (1.150 mg) and PBNR 08-01 (1.132 mg) as compared to check Avishkar (1.022 mg).

2.1.2.9 Elongation ratio and elongation index

Bhonsle and Krishnan (2011) reported that elongation ratio ranged from 1.03 to 1.66, highest in variety Bello and lowest in Kalo damgo.

Parikh *et al.*, (2012) observed moderate variability for elongation ratio and elongation index with range from 1.25 to 1.80, and 0.75 to 1.40, respectively. Maximum kernel elongation ratio was observed in Barang followed by that in Bantaphool, GangaoBain and Bikoni, whereas highest elongation index was registered by Barabg, Ganga Balu and Chirainikhi.

Srivastava and Jaiswal (2013) studied 24 indigenous aromatic cultivars including indigenous aromatic short grains cultivars, basmati type varieties and 5 high yielding varieties of rice and revealed that elongation index ranged from 0.9 to 1.4, length wise elongation ratio ranged from 1.3 to 1.9 and breadth wise elongation ratio ranged from 1.1 to 1.6.

2.1.2.10 Chalkiness

Singh *et al.*, (2003) studied textural properties of chalky and translucent kernels separated from three rice cultivars and reported that the chalky kernels separated from different cultivars showed higher 1000 kernel weight and bulk density but lower kernel hardness and amylose content than their counterpart translucent kernels. Chalky grains showed higher transition temperatures, enthalpy of gelatinization, peak height index and gelatinization range than the translucent grains. The cooking and textural properties of chalky and translucent kernels differed significantly.

Singh and Singh (2005) evaluated 20 mutants of Pusa Basmati-1 and reported that high values of GCV and PCV for chalkiness of endosperm.

Shejul *et al.*, (2013) studied 22 genotypes with 2 checks and revealed that all the genotypes were having translucent grains including checks.

2.1.2.11 Aroma

Tanchotikul and Hsieh (1991) observed that biochemical basis of aroma was found to be 2-acetyl-1-pyrroline (2AP).

Mittal *et al.*, (1995) studied 322 land races and important basmati cultivars for aroma and reported that analysis of leaf samples indicated, 177 stocks have strong aroma and 28 have mild aroma. One hundred seventeen lines were heterogeneous for aroma.

Khan *et al.*, (2009) studied grain quality characters in six rice genotypes and reported that the genotypes Basmati-2000, Super Basmati and

Basmati-385 were moderately aromatic and statistically similar to each other. The coarse variety KSK-133 was non aromatic and statistically non significant to Liangyoupeijiu and Hua You Guan Kang Zhan. The genotype Hua You Guan Kang Zhan slightly aromatic.

Golam *et al.*, (2010) studied 55 fine rice genotypes to evaluate expression of aroma and kernel elongation after cooking and suggested that, among them aroma was observed in 34 genotypes and in 16 genotypes there was absence of aroma. Out of 34, three of these genotypes performed strong aroma, seven performed moderate aroma and 24 with slight aroma.

2.2 Heritability and genetic advance

Heritability in broad sense refers to the ratio of genotypic variances to the total phenotypic variance. The estimates of heritability acts as a predictive gadget in expressing the reliability of phenotypic value. Therefore high heritability helps in effective selection of particular traits.

Genetic advance is a useful indicator of progress that can be expected as a result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.*, 1955).

2.2.1 Quantitative traits

Genetic variability, broad sense heritability and genetic advance under selection for grain yield and its components were studied in 36 rice genotypes by Chakraborty and Hazarika (1996). The characters *viz.*, grain yield and panicles per plant showed relatively low GCV, indicating the presence of significant influence of environment on these traits. On contrary, high heritability with high GA was found for panicle weight and spikelets per panicle, indicating these traits are mostly due to additive gene action. High heritability associated with moderate to low GA was observed in several characters like plant height and fertility percentage.

Ganesan *et al.*, (1997) carried out an experiment involving F₂ and F₃ generations of three inter varietal crosses with four semi-dwarf rice varieties *viz.*, ASD16, CO33, ADT36 and IR 50. In F₂ generation of ASD16/CO33 cross showed high mean and variability for single plant yield, number of productive

tillers and the cross ASD16/IR50 exhibited higher values for grain number per panicle whereas in F₃, only ASD16/IR50 cross progenies showed higher values for single plant yield. High heritability combined with high genetic advance was observed for single plant yield in F₂ of all the crosses.

High heritability with higher genetic advance and coefficient of genetic variation was observed for spikelet number, grain number and leaf area. Heritability was also high for other characters but expected genetic advance and coefficient of variation were low for these characters. For grain yield, heritability as well as other parameters had low estimates. Number of panicles per plant and grain number per panicle seemed to be reliable criteria for selection and further improvement (Panwar and Gupta, 2000).

Satish *et al.*, (2003) genetic variability, heritability and genetic advance were studied in 200 scented rice genotypes including one non-scented check, Ratna for grain yield and its nine yield contributing characters. High GCV and PCV values were observed for spikelets/panicle, number of grains/panicle and grain yield/plant. High heritability along with high genetic advance was noted for number of spikelets/panicle, number of grains/panicle, grain yield/plant followed by other characters. Emphasis should be given on these characters while selecting rice varieties to improve grain yield.

Shinha *et al.*, (2004) estimated variability, heritability and genetic advance in nineteen local landraces along with IR 36 for yield and yield contributing characters. High genotypic coefficient of variation was observed for grain yield followed by test weight and panicles per plant. High heritability with high genetic advance was found for grain yield followed by test weight and panicles per plant.

Genetic variability and heritability parameters were assessed in 114 genotypes and three checks by Suman *et al.*, (2005). High coefficients of variation were observed for seedling dry weight followed by number of spikelet per panicle, number of filled grains per panicle and biological yield. High values of heritability coupled with high genetic advance as per-cent of mean were observed for the characters *viz.*, number of tillers per plant, productive tillers per plant, number of spikelets per panicle, number of filled

grains per panicle, grain yield per plant, biological yield, harvest index and seedling vigour index.

Singh *et al.*, (2006) genetic variability and correlation studies in rice were conducted during *kharif* 2002 in Khudwani, Anantnag district, Jammu and Kashmir. Thirty-two genotypes were evaluated for days to 50% heading, days to maturity, plant height, panicles per plant, biological yield, grain yield and harvest index. A wide range of variation was recorded for all traits. The highest genotypic and phenotypic coefficients of variation were recorded for grain yield. High heritability coupled with high genetic advance was recorded for plant height, indicating the predominance of additive gene action for this trait. Genotypic and phenotypic correlation studies indicated that biological yield per plant and harvest index were significantly and positively correlated with yield. Thus, selection for these two traits might be helpful in enhancing rice grain yield.

Panwar and Mathur (2007) estimated high heritability with high genetic advance for grain yield per plant and productive tillers per plant indicated that these characters predominantly governed by additive gene action.

Khan and Muhammad (2009) studied a set of 25 genotypes of rice and they observed that heritability was higher for plant height, panicle length and number of grains per panicle.

Babu *et al.*, (2012) studied genetic parameter for yield and yield contributing characters in 21 rice hybrids and reported that characters studied expressed low to high heritability ranging from 25.5 for grain yield per plant to 96.3% for days to 50% flowering. Among yield characters, highest heritability was recorded by days to 50% flowering followed by number of chaffy grains per panicle and number of filled grains per panicle. The highest genetic advance was observed for number of filled grains per panicle followed by days to 50% flowering and lowest for grain yield per plant.

Dhanwani *et al.*, (2013) reported that the characters showing high GCV and PCV were found to be highly heritable coupled with high genetic advance. High estimates of heritability were exhibited for all the characters under study. Plant height (98.65), days to 50% flowering (96.90), grain yield

per plant (95.78) and spikelet sterility percentage (95.29) were found to have high heritability and genetic advance as per mean was highest for biological yield (64.75) followed by grain yield (61.53) and lowest for days to 50% flowering among quantitative characters.

2.2.2 Qualitative traits

Deosarkar (1985) reported high heritability for major quality characters viz., L:B ratio, relative density, water absorption, amylose content, gel consistency, gelatinization temperature and protein content.

Verma *et al.*, (2002) revealed that gel consistency had high estimates of heritability and expected genetic advance and is thus a reliable selection criterion for amylose content in early generations of rice improvement.

Yadav *et al.*, (2002) genetic variability, heritability and expected genetic advance were estimated for length of grain, breadth of grain, L/B ratio, kernel elongation, gel consistency, amylase content and gelatinization in rice. The experimental material included 150 rice germplasm categorized into three groups i.e. long slender, medium slender and short slender. Maximum variability was recorded for test weight in long slender and medium slender groups and for amylase content in medium and short slender groups. Water uptake, volume expansion ratio, kernel elongation and gel consistency appeared to be the useful traits in all the groups because high heritability and high genetic gain were recorded for these characters.

Vanaja and Babu (2006) reported that all quality attributes revealed high heritability and moderate expected genetic advance followed by moderate genotypic coefficient of variation were noted for alkali spreading value, length breadth ratio, milling percentage, amylose content and water absorption.

Nayak (2008) studied the extent of variability and correlation among different quality parameters and revealed high genetic advance for alkali spreading value and grain yield in both seasons, while moderate genetic advance was observed for head rice recovery, kernel length, length breadth ratio and amylose content in both seasons indicated non-additive gene action.

Sabesan *et al.*, (2009) reported high values of heritability along with high genetic advance for grain yield per plant, grains per panicle, grain length, grain breadth and L:B ratio.

Subbaiah *et al.*, (2011) studied 16 parents and 48 hybrids of rice and revealed that high heritability coupled with high genetic advance per cent of mean was recorded for gelatinization temperature, harvest index, total number of productive tillers per plant, number of grains per panicle, kernel length, kernel L/B ratio and grain yield in case of parents and for gelatinization temperature, amylose content, total number of productive tiller per plant, number of grains per panicle and harvest index in case of hybrids.

Parikh *et al.*, (2012) reported high broad sense heritability was observed for all the characters under study. High heritability coupled with genetic advance was recorded for 100-seed weight followed by seed yield per plant and kernel length: breadth ratio, suggesting predominance of additive gene action in the expression of these characters.

Gangashetty *et al.*, (2013) studied 42 genetically diverse genotypes and reported that high heritability was coupled with high genetic advance as per cent of mean in characters like zinc content, iron content, L/B ratio and grain length indicating presence of considerable variation and additive gene effects.

2.3 Correlation

The knowledge on inter-relationship of plant character like yield with other quantitative and qualitative characters is of great importance to breeders. Improvement of quantitative character like yield is complex and not effectively possible by direct selection. The knowledge about correlation and its analysis explicit the direction of selection for such complex characters. Hence, the different reviews about correlation among the different characters of rice are presented below.

2.3.1 Quantitative traits

Abdul and Shafi (1971) studied progenies derived from eight crosses of rice and reported that grain yield per plant was positively correlated with number of panicles per plant. Whereas, grain number per panicle was negatively correlated with grain weight followed by panicle number.

Ajmersingh (1979) reported that grain yield was positively correlated with days to 50% flowering, days to maturity, plant height, panicles per plant, 1000 grain weight but negatively correlated with panicle length.

Kishor *et al.*, (2007) studied 70 rice genotypes, the character association analysis revealed that significantly positive association of grain yield with number of grains per panicle and 1000 grain weight.

Khan *et al.*, (2009) studied 25 rice genotypes and revealed the correlation analysis indicated that plant height had positive and significant association with all morphological traits. Grain yield per plant was positively correlated with plant height, panicle length and number of grains per panicle. Genotypic correlation of plant height with number of tillers per plant was positive.

Sadeghi (2011) found grain yield to be positively and significantly correlated with grains per panicle, days to maturity, panicle weight, the number of productive tillers, days to flowering, plant height, panicle length, flag leaf width and flag leaf length indicating the importance of these characters for yield improvement in particular population.

Selvaraj *et al.*, (2011) observed that characters like plant height, number of tillers per plant, panicle length and test weight had significant association with grain yield.

Idris *et al.*, (2012) studied genetic variability and correlation between yield and yield contributing components in some rice genotypes for seven characters and reported positive phenotypic and genotypic correlation coefficients were detected between grain yield and number of filled grains per panicle, harvest index, panicle length and number of grains per panicle.

Shet *et al.*, (2012) studied the F₂ segregating populations of two crosses viz., cross I (BPT 5204 × JBT 36/14) and Cross II (KMP 148 × JBT

36/14) to assess the genetic variability, correlation and direct and indirect effects among yield and yield components under aerobic condition. The correlation studies of these crosses showed grain yield per plant exhibited highly significant positive association with productive tillers, filled grains per panicle and 1000 seed weight while days to 50 % flowering registered significant negative association with grain yield.

Augustina *et al.*, (2013) observed that correlation coefficient and estimates of heritability of 15 characters associated with grain yield for the combined data showed wide significant genetic variability ($p < 0.0001$) amongst all genotypes. Of all the characters evaluated, only number of grains per plant had the highest and significant correlation with grain yield ($r = 0.7643$). Days to booting and days to 50% flowering had negative but high correlation. All the characters showed high heritability estimates ranging from 93.00 - 99.87%.

Babu *et al.*, (2013) studied 14 genotypes of rice and reported that grain yield was positively correlated with number of productive tillers per plant and number of grains per panicle. A positive correlation between iron and zinc content was observed while a negative correlation between grain iron content and grain yield was recorded. Grain iron content inversely related with grain yield per plant.

Chakravorty *et al.*, (2013) studied 51 landraces of rice and reported that all the traits except ligule length, number of grains per panicle and number of primary branches per panicle exhibited significant and positive correlation coefficients with kernel weight.

Huang *et al.*, (2013) reported that association of grain yield per plant with filled grains per plant, grains per panicle, seed setting rate and 1000-grain weight were positive and significant.

2.3.2 Qualitative traits

Juliano (1979) reported that volume expansion, water absorption and resistant to disintegration of milled rice during cooking were directly related to amylose and amylopectin ratio of starch.

Reddy and Sarala (1979) observed positive correlation between alkali values and amylose content, but negative correlation was found between alkali values and protein content.

Tomar and Nanda (1982) studied correlation between quality traits in rice and reported positive correlation of water uptake with volume expansion, elongation of grain cooked at 77°C, alkali values and amylose content of grain.

Perez *et al.*, (1987) reported that gelatinization temperature correlates positively with grain elongation.

Deosarkar and Nerkar (1994) reported that grain length, L:B ratio and water absorption had positive correlation with kernel elongation. Whereas, grain length has positive correlation with L:B ratio.

Nayak *et al.*, (2003) reported that, kernel length had significant positive correlation with length/breadth ratio, cooked kernel length, amylose content and significant negative correlation with elongation ratio. The kernel length/breadth ratio had significant positive correlation with cooked kernel length, amylose content and significant negative correlation with elongation ratio.

Yadav *et al.*, (2007) studied the morphological, physico-chemical and cooking properties of six Indian rice varieties and reported that water uptake was observed to be positively with L/B ratio and hardness. Highly significant and positive correlations were shown by water uptake and elongation ratio with amylose content. The elongation ratio of cooked kernels showed a highly significant and positive correlation with L/B ratio and hardness of raw kernels.

Golam *et al.*, (2010) studied correlation between kernel elongation ratio and aroma in 10 outstanding aromatic rice genotype and observed highly positive trend between these two traits in grain test.

Umadevi *et al.*, (2010) studied 110 rice genotypes to assess the genetic variability, heritability and correlation among the genotypes for sixteen grain quality characters and grain yield and revealed that the single plant yield

had highly significant and positive association with L/B ratio, water uptake, breadth-wise expansion ratio, gel consistency and amylose content.

Danbaba *et al.*, (2011) reported that there was significant positive correlation between amylose content and water uptake ratio, while significant positive association was observed between length breadth ratio and amylose content.

Thomas *et al.*, (2013) in their study found that cooking time was negatively correlated with amylose content. A positive correlation was recorded for both amylose content and L/B ratio in relation to elongation of cooked rice. Positive correlation between water uptake ratio and L/B ratio was also observed in the study.

2.4 Path analysis

Even though, the knowledge about correlation shows the relationship between yield and yield associated characters, they do not prognosticate about direct and indirect effects of different characters. Path coefficient analysis suggested by Dewey and Lu (1959) specifies the effective measure of direct and indirect causes of association and also depicts the relative importance of each factor involved in contributing the final product like yield. Here, the different literatures regarding path analysis are reviewed and presented below.

Prasad *et al.*, (2001) studied 8 fine grain rice genotypes for genetic variability and selection criteria for some yield contributing characters. Path coefficient analysis revealed that the number of fertile grains per panicle had the highest positive effect on grain yield followed by days to maturity, 1000 grain weight and panicle length.

Khedikar *et al.*, (2004) revealed that 1000 grain weight had the highest positive direct effect on grain yield followed by spikelet density. Effective tillers per plant, panicle length and days to 50% flowering had direct effect on grain yield hence selection through these characters would be more effective.

Natarajan *et al.*, (2005) investigate association among grain yield and yield components, and their direct and indirect influences on the grain

yield of rice. According to direct influences on grain yield, the order of yield components was the number of productive tillers per square meter (0.954) > number of filled grains per panicle (0.0467) > 1000 grain weight (0.0051). The improvement in grain yield will be efficient, if the selection is based on biological yield, the number of productive tillers per square meter and the number of filled grains per panicle under tropical conditions.

Ramkrishnan *et al.*, (2006) observed that number of grains per panicle had direct effect on grain yield, hence it plays an important role in improvement of grain yield in rice.

Kishor *et al.*, (2007) studied path coefficient analysis and revealed that 1000 grain weight, number of grains per panicle, productive tillers per plant, days to 50% flowering and plant height had shown positive direct effect on yield, hence due weightage should be given to these characters during selection in future breeding program.

Nandan *et al.*, (2010) studied 33 genotypes of rice and results of path analysis revealed that number of grains per panicle had maximum direct effect on grain yield per plant followed by days to 50% flowering, plant height, kernel length after cooking, hulling percentage, harvest index and kernel breadth after cooking.

Nandeshwar *et al.*, (2010) studied 25 F₂ progenies of rice for 11 biometrical characters and found that panicle number per plant, imparted maximum direct effect on grain yield, followed by grain number per panicle, 1000-grain weight and panicle length.

Wattoo *et al.*, (2010) studied path analysis, indicated that days to maturity had recorded the highest direct effect on grain yield per plant. Yield components viz., plant height, number of effective tillers per plant and 1000 grain weight had positive direct effect on grain yield.

Selvaraj *et al.*, (2011) studied 21 genotypes; path coefficient analysis revealed that test weight exhibited maximum positive direct effect on grain yield per plant followed by plant height, panicle length and days to 50% flowering.

Cyprien and Kumar (2011) revealed that in path coefficient analysis, panicle number, panicle weight, 1000-grain weight, days to 50% flowering and seed to seed days are considered as causal factors and their direct and indirect effects on grain yield are estimated. The positive effects of panicle number (0.53940), panicle weight (0.30953) and seed to seed days (0.14002) on grain yield were reported. The indirect effects of panicle weight on the grain yield through other characters were negative.

Bhadru *et al.*, (2012) carried out correlation and path coefficient analysis for yield and yield components and reported, number of grains per panicle, days to 50% flowering and panicle length had a significant positive association with yield and also had positive direct effect on grain yield.

Shejul (2012) studied 22 promising genotypes of upland paddy and reported path analysis explicit, qualitative characters viz. L:B ratio and amylose content exerted highest direct effect on grain yield per plant, but protein content showed negative indirect effect on grain yield per plant via number of tillers per plant and number of grains per panicle. While number of effective tillers per plant, number of grains per panicle and days to maturity showed the maximum direct effect on grain yield per plant.

Sanghera *et al.*, (2013) reported that grain yield was positively and significantly correlated with number of tillers per plant, plant density per m² and number of grains per panicle at both genotypic and phenotypic levels. The genotypic path analysis revealed that panicle density had the highest positive direct effect followed by plant height and days to flower at genotypic level.

2.5 Iron chlorosis

Weiss (1943) in soybean and Wann and Hills (1973) in tomato reported single recessive genes for iron chlorosis susceptibility.

Shahi *et al.*, (1975) reported that severe chlorosis observed in year 1974 was due to iron deficiency. They also suggested that plants raised under submerged condition didn't show any chlorosis whereas, those raised without submersed showed severe chlorotic symptoms. The iron chlorosis was overcome by spraying 1% neutralized ferrous sulphate solution.

Nerkar and Misal (1980) reported that the high yielding varieties carrying the Dee-geo-woo-gene (Dgwg) dwarfing gene were susceptible to iron chlorosis, while the local tall cultivars and dwarf mutants induced in them were tolerant.

Nerkar *et al.*, (1984) reported that the release of the rice variety Parbhavati suitable for the cultivation on the Fe-deficiency black soils (Vertisols). It is an induced dwarf mutant of local tall cultivar Ambemohor local obtained through ethyl methylsulphonate (0.2%) treatment of seeds.

Ross (1986) reviewed the breeding and genetic aspects of improving plants for tolerance to iron deficiency and opined that the complexity of inheritance and the mode of reproduction of the plant determine the breeding methodologies. In some instance, pedigree breeding, including back crossing is adequate. In other instance, population improvement may be necessary.

Singh *et al.*, (1986) reported that weight of shoot was reduced in iron chlorosis susceptible genotypes. Leaves of chlorosis tolerant genotypes contained higher levels of reactive Fe^{2+} than those of susceptible genotypes.

Throne (1986) used three general approaches in developing iron chlorosis resistant cultivars of soybean: 1) Screening of advanced breeding lines 2) Selection of parental combinations in which both parents have acceptable levels of resistance and 3) Mass selection in populations derived from resistant x susceptible.

Reddy (1988) studied the genetic control of Fe deficiency tolerance in rice and reported that in all tolerant x sensitive crossed, the F_1 was tolerant. The F_2 plants segregated into 3 tolerant: 1 sensitive ratio indicating a monogenic inheritance in all crosses. This was further confirmed in the backcross generations. Hence he concluded that a major dominant gene 'Fe' is responsible for tolerance of iron chlorosis and its corresponding allele 'fe' for sensitivity in rice.

Deosarkar (1989) reported that iron chlorosis had adverse effect on almost all the characters studied except grain shape (L/B) ratio. Duration

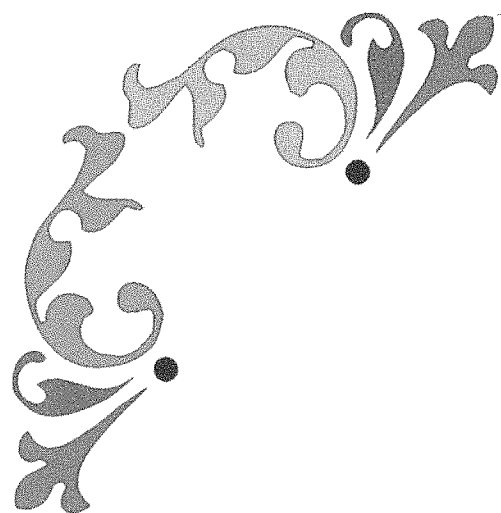
was prolonged with the increase in iron chlorosis grade. Iron chlorosis had significant negative association with grain yield/plant.

Mori *et al.*, (1991), after detailed study, reasoned that high susceptibility of rice seedlings to iron deficiency was due to low secretion of deoxy-mugineic acid (MA), a phytosiderophore.

Hoan *et al.*, (1992), studied the genetics of iron chlorosis in 8 crosses involving parents distinctly different in their level of tolerance and segregating populations were screened under actual stress condition on field and reported that tolerance/moderate tolerance to Fe chlorosis was dominant over susceptibility and was controlled by two sets of non-allelic genes with complementary interaction.

Ahmad *et al.*, (1995) reported, in lentil (*Lens culinaris* Medik.), that resistance to Fe deficiency chlorosis was dominant and also controlled by a single gene.

Toker *et al.*, (2010) studied the inheritance of iron chlorosis in chickpea in F₁ of cross between ICC 6119 x CA 2969 and reported that the resistance was governed by single dominant gene in these genotypes. The most feasible method for alleviating Fe deficiency is the selection of suitable cultivars resistant to Fe deficiency chlorosis.



MATERIAL AND METHODS



CHAPTER-III

MATERIAL AND METHODS

The present investigation entitled “Screening of rice genotypes (*Oryza sativa* L.) for yield, quality characters and iron chlorosis on Vertisols” was conducted during *kharif* 2013.

3.1 Experimental site

This study was carried out at Department of Agril. Botany, Vasantao Naik Marathwada Krishi Vidhyapeeth, Parbhani. Parbhani has subtropical climate and situated above 408-500 m above sea level. It lies between 18° 58' to 20° 2' north latitude and 76° 4' to 77° 42' east longitude. Soil of experimentation site is deep black having well drainage. The average rainfall of Parbhani is 800 to 900 mm received mostly during June to September. The rainfall is assured for *kharif* season. The mean maximum temperature of Parbhani varies from 29° C to 45° C in summer and minimum temperature varies from 11° C to 25° C in winter season. The mean relative humidity ranges from 30 to 90 per cent.

3.2 Experimental material

The material for this present study comprised of 50 promising genotypes of rice among which three genotypes were checks viz., Parag, Basmati-370, and Avishkar. This material was collected from Upland Paddy Research Scheme, Parbhani.

The main object of the study is to screen the advance generation material for grain yield, grain quality characters and tolerant to iron chlorosis in black cotton soil. The list of genotypes is given in Table 1 and experimental site shown in Plate I.

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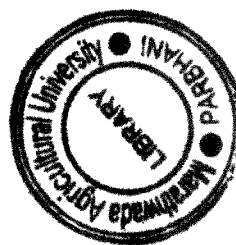


Table 1. List of genotypes

S. No.	Genotypes	S. No.	Genotypes
1.	NDR 1143	2.	CR 3693-1-1
3.	OR 2172-7-1	4.	CR 3635-1-1
5.	RP 5214-18-6-2-1-1-1-B	6.	PBNR-03-10
7.	GK 5022	8.	Rewa 1207-15
9.	PBNR- 04-28	10.	CR 3632-1-2
11.	CRR 599-4-1	12.	CR 2991-1-2-1-1-1
13.	R 2212-RF-75	14.	CRR 452-23-1-1-1-1
15.	CRR 596-8-1	16.	CR 3692-1-1
17.	CB 09 516	18.	TJP 148
19.	CB 10-504	20.	OR 1946-2-1
21.	MAS 946 (RC 2)	22.	RP Bio 4918-166-9
23.	CR 3695-1-1	24.	BAU 408-05
25.	CR 3634-1-3	26.	CR 3690-1-1
27.	CR 3630-1-3	28.	CRR 617-B-47-3
29.	CR 3633-1-3	30.	PBNR- 03 -07
31.	R-RF-48	32.	MAULS-15
33.	PBNR - 08 – 07	34.	CRR 635-3-2
35.	BAU 389-02	36.	CR 3616-2-1-2-1-1
37.	PAU 3832 - 79-4-3-1	38.	RP 5216-13-7-2-1-1-1
39.	R 1700-2240-4-2295-1	40.	CRR 499-11-2-12-1
41.	UPRI 2012-16	42.	Tulasi
43.	CRR 614-4-1	44.	PBNR – 08 – 04
45.	RP 5125-17-6-3-2-1	46.	CRR 451-15-B-A1
47.	PBNR- 03 – 20	48.	Basmati 370 (check)
49.	Parag (check)	50.	Avishkar (check)



General view of experimental field



General view of field for screening genotypes for iron chlorosis
Plate I. Experimental site during *Kharif* 2014

3.3 Experimental details are as given below

Design of experiment	:	Randomized Block Design (RBD)
Replications	:	03
Plot size	:	0.9 X 3 m ²
Spacing	:	30 cm between rows
Seed rate	:	60 kg per hectare
Fertilizer application	:	100 kg N : 50 kg P : 50 kg per ha 50% of N and complete P and K were given at the time of sowing and remaining 50% was applied through two split doses i.e. 45 days and 75 days after sowing
Intercultural operation	:	One hoeing and four weeding
Irrigations	:	Two irrigations were given (28 th of August and 25 th of September) when there was water stress

The experiment was conducted on Vertisols (deep black cotton soil) with 30 cm spacing maintained between two rows. Three rows were sown with 3 m length for each genotype. The weekly weather data and rainfall pattern during the crop season was recorded and is given in Appendix-I.

3.4 Observations recorded

The observations were recorded on quantitative characters viz., plant height, days to 50% flowering, days to maturity, number of effective tillers per plant, effective tillers per meter length, number of grains per panicle, total number of filled grains per panicle, flag leaf area, 1000 grain weight, grain yield per plant and yield per plot. Five random plants were selected from the middle two rows for recording the observations. The average value of each quantitative character was determined from these plants and these values were used for analysis.

The grain quality character studied were viz., L:B ratio, relative density, water absorption , gel consistency, volume expansion, amylose content, crude protein content, gelatinization temperature, kernel elongation ratio, kernel elongation index, chalkiness and aroma. The average value of the grain quality traits was obtained and these values were used for grain quality analysis.

Likewise, for the study of iron chlorosis, the iron chlorosis scores were recorded for each genotype. To find out whether the symptoms on leaves were due to iron chlorosis or some other causes, a confirmatory test was also applied.

3.4.1 Quantitative characters

Observations on following yield and yield contributing characters were recorded.

3.4.1.1 Days to 50% flowering

Number of days required, from sowing, to flowering of approximately 50% plants in each plot from each replication were recorded and average number of days to 50% flowering were worked out.

3.4.1.2 Plant height (cm)

At maturity, from each replication, the average height of five plants from each genotype were measured in centimetres from ground level to the base of panicle on the main tiller and average values were used for analysis.

3.4.1.3 Panicle length (cm)

Length of panicle on main tiller of five plants of each genotype from each replication was recorded in centimetre from the base of panicle to apex of panicle and average values were worked out.

3.4.1.4 Number of effective tillers per plant

Five plants from each plot of each replication were randomly selected for recording observations and numbers of tillers bearing panicle were recorded at the time of maturity.

3.4.1.5 Number of effective tillers per meter length

From three rows of each plot, in each replication the middle row were selected and total number of tillers bearing panicle per meter length was recorded. The border effects were avoided by discarding border plants.

3.4.1.6 Flag leaf area (cm²)

The length of the flag leaf on the main culm was measured in centimetres at heading stage. The width of flag leaf was measured at the widest portion of the blade. The flag leaf area was computed by multiplying product of length and breadth by leaf area constant 0.818 (Jadhav *et. al.*, 2001).

3.4.1.7 Days to maturity

The number of days required for complete maturity of grains in each plots were recorded in each replication and average values were worked out.

3.4.1.8 Number of filled grains per panicle

The number of fertile grains per panicle on a main tiller of five plants of each genotype from each replication was recorded and averages values were worked out.

3.4.1.9 Number of unfilled grains per panicle

The number of unfilled grains per panicle on a main tiller of five plants of each genotype from each replication was recorded and averages values were worked out.

3.4.1.10 One thousand grain weight (g)

A random sample of 1000 well developed, whole grains, dried up to 13 percent moisture content was weighted on a precision electronic balance to obtain 1000 grains weight in grams.

3.4.1.11 Grain yield per plant

Five plants of each genotype from each replication were separated and weight of filled grains per plant was recorded separately and average values were obtained.

3.4.1.12 Grain yield per plot (kg)

The weight of the grains harvested from the net plot was in each replication was recorded in kg and average value was worked out.

3.4.1.12 Straw yield per plot (kg)

The weight of the straw after harvest of grains from the net plot was in each replication was recorded in kg and average value was worked out.

3.4.2 Qualitative characters

3.4.2.1 Elongation ratio and elongation index

A sample comprising of ten whole milled rice kernels were used for the study of this character. Kernel length and breadth of milled rice was measured before cooking by using thickness gauge. After cooking, the length and breadth of cooked samples was measured by placing them on graph. Elongation ratio was computed as length of cooked kernel to length of uncooked kernel and elongation index was computed by the ratio of length: breadth ratio of cooked rice to length: breadth of milled rice as described by Parikh *et al.*, (2012).

3.4.2.2 Length : Breadth ratio

Mean length and breadth of ten grains of each genotype were recorded in mm to determine the L:B ratio. The scale purposed by Kush *et al.*, (1979) was used to classify the grains on the basis of shape as below.

L:B ratio	:	Shape
Over 3.0	:	Slender
2. 1to 3.0	:	Medium
1.1 to 2.0	:	Bold
Less than 1.1	:	Round (short)

3.4.2.3 Volume expansion

The samples used for water absorption were used for the study of volume expansion. After recording weight of uncooked samples, their volume as determined by water displacement method. Similarly, volume of cooked sample was determined after recording their weight. The formula employed for

estimating per unit water expansion was applied in this case by introducing volume instead of weight.

$$\text{Per unit volume expansion} = \frac{V_2 - V_1}{V_1}$$

Where,

V_2 = Volume of sample after cooking

V_1 = Volume of sample before cooking

3.4.2.4 Water absorption

A sample comprising of ten whole milled rice kernels were used for the study of this character. The weight of sample was recorded before and after cooking. The difference in weight was taken as the amount of water absorbed per unit of rice as given below.

$$\text{Water absorption per unit rice} = \frac{W_2 - W_1}{W_1}$$

Where,

W_2 = weight of sample after cooking

W_1 = weight of sample before cooking

Care was taken to remove excess water from the cooked sample with the help of blotting paper. For cooking the rice samples, long test tube were used. The samples were pre-soaked in about 10 ml of water for 5 minutes, then placed over a water bath and maintained at boiling temperature for 15 minutes. Sample tubes were taken out and cooled under running tap water for two minutes.

3.4.2.5 Relative density

The weight and volume of 10 milled rice kernels was recorded and relative density was estimated by using following formula. Water displacement was measured in finely graduated 5ml measuring cylinder.

$$\text{Relative density} = \frac{\text{Weight of rice kernels}}{\text{Weight of water displaced by rice kernels}}$$

3.4.2.6 Protein content

Crude protein was estimated by Micro-kjeldhal method (A.O.A.C., 1965). One gram of fine powdered seed sample was digested with 1 g K_2SO_4 , 0.5 g $CuSO_4 \cdot 5H_2O$ and 25 ml H_2SO_4 and then it was distilled with 40 % NaOH. The distillate was collected in a beaker containing 4 % boric acid. The methyl red and bromocresol green indicator was used. The contents were back titrated with 0.1 N H_2SO_4 until pink colour was obtained. The amount of nitrogen present in grain was estimated and converted to crude protein content by multiplying with the conversion factor 5.95%.

$$\text{Protein \%} = \text{N \%} \times 5.95$$

3.4.2.7 Gel consistency

The milled rice samples of 20 to 25 grains each were ground to fine flour by passing through 100 mesh sieves. Then finely ground samples were stored for at least two days so to ensure a constant moisture content of 12% as suggested by Cagampang *et al.*, (1973). 100 mg samples of each in duplicate were taken in 15 X 100 mm size test tubes and wetted with 0.2 ml of 95% ethanol containing 0.025% thymol blue. After shaking the tubes to prevent clumping, 2.0 ml of 0.2 N KOH was immediately added. The contents were dispersed by stirring. The tubes were then covered with glass balls (marbles) and placed immediately in vigorously boiling water bath for 10 minutes.

The samples removed from water bath were allowed to set in room temperature for five minutes. The tubes then laid horizontally on a glass sheet which had underneath a graph paper graduated in millimetres and provision on top to hold the tube in position. The length of gel was measured from bottom of the test tubes to the gel front after 30 minutes. Using the following scoring scheme of Cagampang *et al.*, (1973), the test were classified into soft (high gel flow), intermediate (intermediate gel flow) and hard (low gel flow) gel consistency types.

25 to 35 mm	: Hard (low gel flow)
36 to 49 mm	: Intermediate (intermediate gel flow)
50 and above	: Soft (high gel flow)

3.4.2.8 Amylose content

Following procedure was carried out in order to compute the amylose content as suggested by Juliano (1971).

Procedure:-

1. Weigh 100 mg of well powdered milled rice samples into 100 ml volumetric flask
2. Add 1 ml of ethanol and 9 ml of 1 N NaOH and leave it to over night
3. Make up the volume to 100 ml
4. Pipette 5 ml of extract from 100 ml into another 100 ml volumetric flask
5. Add 1 ml 1 N acetic acid and then 2 ml iodine solution and make up the volume to 100 ml by distilled water
6. Shake, and stand for 20 minutes and determine per cent transmission at 620 nm using a colorimeter
7. Take 0.2, 0.4, 0.6, 0.8 and 1 ml of standard amylose solution and develop the colour as in case of sample
8. Calculate the amount of amylose present in the sample using standard graph
9. Dilute the iodine reagent to 50 ml distilled water for a blank.
10. Making of amylose standards
 - a. Pipette out 1, 2, 3, 4 and 5 ml of standard amylose into 100 ml volumetric flask in three replications
 - b. Keep one flask as blank without adding anything
 - c. Add 1 ml of 1 N Acetic acid and 2 ml of I-KI solution to all the flasks including blank
 - d. Make up all the flasks to 100 ml using distilled water and cover all flasks with black cloth or aluminium foil to prevent direct light exposure. I-KI disintegrates on exposure

- e. Keep for 20 minutes and take reading at 620 nm in a spectrophotometer
- f. The standards including blank, correspond to 0%, 4%, 8%, 12%, 16% and 20% of amylose
- g. Draw a standard curve using the absorbance reading

Based on the amylose percentage, genotypes were grouped as follows:

Rating of amylose content

Category	Amylose content (%)
Waxy	1-2
Very low amylose	2-9
Low	10-20
Intermediate	20-25
High	>26

3.4.2.9 Gelatinization temperature

Estimation of gelatinization temperature was done according to the method described by Little *et al.*, (1958). Four whole milled rice was evenly placed in a small petri plates containing 10 ml of 1.7% potassium hydroxide (KOH) solution and placed in an incubator maintained at $30^{\circ}\text{C} \pm 1^{\circ}\text{C}$ for 16 hours so as to obtain critical assessment.

The grade rating for gelatinization temperature was as follows:

Rating	Particulars	Class
1.	Completely dispersed and intermingled	Low
2.	Almost completely dispersed and intermingled	
3.	Dispersed with merging collar	
4.	Split or segregating with collar complete and wide	Intermediate
5.	Swollen with collar and wide	
6.	Swollen with complete and narrow	
7.	Swollen	High
8.	Chalky	
9.	Not affected	

3.4.2.10 Grain translucency/ chalkiness

Milled rice grains of each genotype were broken and observed for presence or absence of white belly.

3.4.2.11 Aroma

Aroma, after cooking of sample of each of the genotypes was studied and was scored as strong, mild or absent.

3.4.3 Iron chlorosis

3.4.3.1 Iron chlorosis score

For recording observations on iron chlorosis, 1 to 9 scale adopted by Singh and Singh (1984) was utilized with modification i.e., taking the 1, 3, 5, 7 and 9 grades as 0, 1, 2, 3 and 4 respectively. The individual plants were scored on the basis of visual symptoms observed on leaves.

0 = normal colour

1 = slightly yellow with no visual inter-veinal chlorosis

2 = moderately yellow with inter-veinal chlorosis

3 = severe yellowing with inter-veinal chlorosis and pale whitish yellow

4 = leaves completely turns ivory and tips necrotic

3.4.3.2 Confirmatory test for iron chlorosis symptoms

The confirmatory test for iron chlorosis symptoms was done. To find out whether the symptoms appearing on leaves were due to iron deficiency or some other cause, a confirmatory test was applied as described as following.

Cotton plug was dipped into a freshly prepared ferrous sulphate solution (1%) and rubbed gently on the portion of the leaf where yellowing symptoms appeared and was repeated 2-3 times at 4 hours interval. If the leaf turns to green after 1-2 days, iron chlorosis was confirmed.

In field, iron chlorosis symptoms are usually apparent during 15-20 days after sowing. Therefore, the initial score was recorded at 20 days and another at 60 days after sowing. Confirmatory test for iron chlorosis presented in Plate 2.



Confirmation of iron chlorosis by applying FeSO_4



3 days After application of FeSO_4

Plate II. Confirmatory test for iron chlorosis

3.5 Statistical analysis

The data collected on the above characters was analyzed for genetic parameters of variability, heritability, expected genetic advance, correlation and path analysis. The statistical procedure used in the analysis is given below.

3.5.1 Analysis of variance

The mean values of all the treatments for the character under study were worked out. The replicated observations were analyzed as per Randomized Block Design. The ANOVA of the design is as below.

Source of Variation	Degree of freedom	Mean sum of squares	F ratio
Replications	$r - 1$	Msr	Msr / Mse
Treatments	$t - 1$	Mst	Mst / Mse
Error	$(r - 1)(t - 1)$	Mse	-

Where r = Number of replication t = Number of treatment

The significance of variation among the genotypes was tested by comparing the calculated F with table F value. Standard error and critical difference at 1 % and 5 % level of significance were calculated by using the formula

EMSS

1. Standard Error (S. E.) = -----

No. of replications

2. Critical Difference (C.D.) = S. E. $\times \sqrt{2}$ $\times$ 't' value at 5% level

for error degrees of freedom.

3.5.2 Genetic variability

Various parameters of genetic variability were calculated by using following formula

Treatment MSS - Error MSS

1. Genotypic variance ($\sigma^2 g$) = -----

No. of replications

2. Phenotypic variance ($\sigma^2 p$) = Genotypic variance + error variance

The genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated according to Burton (1952).

$$3. \text{ Genotypic coefficient of variation (GCV)} = \frac{\sigma^2 g}{\bar{X}} \times 100$$

$$4. \text{ Phenotypic coefficient of variation (PCV)} = \frac{\sigma^2 p}{\bar{X}} \times 100$$

Where,

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

$\bar{X}$ = general mean of character

3.5.3 Heritability

Heritability (broad sense) was calculated according to the method suggested by Hanson *et al.*, (1956).

$$\text{Heritability (h}^2\text{) B. S.} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

3.5.4 Genetic advance (GA)

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance.

$$GA = K. \sigma_p h^2 (bs)$$

Where,

GA = Genetic advance

K = Selection differential at 5 % level

h^2 = Heritability

σ_p = Phenotypic standard deviation

Expected genetic advance (EGA) was calculated by the method suggested by Johnson *et al.*, (1955).

$$\text{EGA} = \frac{\text{GA}}{\bar{X}}$$

Where,

GA = genetic advance

$\bar{X}$ = general mean of character

3.5.5 Correlation

Covariances were calculated for all the characters to find out correlation among the characters.

The interrelationships of different yield contributing characters were worked out according to Johnson *et al.*, (1955).

$$r = \frac{\text{Cov. (x. y.)}}{\sqrt{\sigma^2_x \cdot \sigma^2_y}}$$

Where,

r = correlation coefficient between the characters x and y

Cov. (x.y) = Covariance between x and y

σ^2_x and σ^2_y = respective variances of x and y

3.5.6 Path coefficient analysis

The cause and effect relationship is well defined in path coefficient analysis. The path coefficient analysis can be defined as the ratio of the standard deviation of effect due to a given cause to the total standard deviation of the effect, in other words it is simply a standardised partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects, i.e. it measures the direct and indirect contribution of various independent characters on dependent character.

Path coefficient analysis was carried out according to Deway and Lu (1959). The direct path coefficients were calculated by solving the following set of 'P' simultaneous equations by the abbreviated Doolittle technique.

$$P_{01} + P_{02} r_{12} + \dots P_{0p} r_{1p} = r_{01}$$

$$P_{01} r_{12} + P_{02} + \dots P_{0p} r_{2p} = r_{02}$$

$$P_{01} r_{10} + P_{02} r_2 P + \dots P_{0p} = r_{0p}$$

Where,

$P_{01}, P_{02} \dots P_{0p}$ are the path effects of 1, 2, ... P variables on '0' variable.

$r_{12}, r_{13}, \dots r_{1p} \dots r_p$ (P-1) are the possible correlation coefficients between various independent variable and $r_{01}, r_{02} \dots r_{0p}$ are the correlations of independent variables with dependent variable. The different effects of 'i' th variable via 'j' th variable was worked out as ($P_{0j} \times P_{ij}$).

From the simultaneous equation it is clear that the correlation coefficient is the sum of direct and indirect path coefficients.

Residual effect was calculated as under

$$P^2_{0x} = 1 - (P^2_{01} + 2P_{01} P_{02} r_{12} + 2P_{01} P_{03} r_{13} + \dots$$

$$P^2_{02} + 2P_{02} P_{03} r_{23} + \dots P^2_{0p})$$

$$\text{Residual factor} = \sqrt{P^2_{0x}}$$



RESULTS

CHAPTER-IV

RESULTS

In the present study 50 promising genotypes including 3 checks viz., Parag, Basmati- 370 and Avishkar were grown during *Kharif* season of 2013. Observations were recorded on different quantitative, qualitative characters and iron chlorosis. Then the mean data of 50 genotypes (including checks) was analyzed.

The results of present investigations are presented under the following major headings.

1. Analysis of variance
2. Mean performance of genotypes for yield and yield components
3. Mean performance of genotypes for physico-chemical characteristics of rice grain
4. Parameters of genetic variability for grain yield and yield contributing characters
5. Parameters of genetic variability for physico-chemical characteristics of rice grain
6. Reaction of different genotypes for iron chlorosis

4.1 Analysis of variance

Analysis of variance was worked out to assess the variation in the genotypes for grain yield, yield components and grain quality characters. The results of analysis of variance are presented in Table 2 and Table 3.

Table 2. ANOVA for yield and yield contributing characters

Sr. No.	Characters	Mean sum of squares		
		Replication	Treatments	Error
1.	Days to 50% flowering	0.04	137.55**	41.05
2.	Plant height (cm)	34.60	646.06**	54.93
3.	Panicle length (cm)	0.01	8.94**	3.06
4.	No. of tillers/plant	0.07	5.36**	0.15
5.	No. of tillers/meter	2.36	2316.32**	52.42
6.	Flag Leaf Area (cm ²)	11.69	121.96**	4.98
7.	Days to maturity	0.52	173.43**	61.32
8.	No. of filled grains/panicle	6.61	1547.45**	98.03
9.	No. of unfilled grains/panicle	25.01	410.35**	16.18
10.	Test weight (g)	2.49	44.19**	1.18
11.	Grain yield/plant	0.76	120.72**	2.83
12.	Grain yield/plot (kg)	0.005	0.20**	0.01
13.	Straw yield /Plot (kg)	0.01	0.63**	0.01
**Significant at 1% level				

Table 3. ANOVA for grain quality characters

Sr. No.	Characters	Mean sum of squares		
		Replication	Treatments	Error
1.	Elongation ratio	0.0012	0.057**	0.003
2.	Elongation index	0.0002	0.019**	0.006
3.	Length breadth ratio	0.018	1.052**	0.023
4.	Volume expansion	0.0008	1.607**	0.018
5.	Water absorption	0.0021	1.026**	0.018
6.	Relative density (gm/ml)	0.0022	0.241**	0.007
7.	Protein content (%)	0.6378	7.563**	0.610
8.	Gel consistency (mm)	46.512	670.24**	10.18
9.	Amylose content (%)	0.0096	40.566**	2.265
**Significant at 1% level				

The analysis of variance showed that the differences among the genotypes in respect of all the characters viz., plant height, days to 50% flowering, days to maturity, effective tillers per plant, effective tillers per metre length, panicle length, flag leaf area, 1000 grain weight, number of filled grains per panicle, number of unfilled grains per panicle, grain yield per plant, grain yield per plot and straw yield per plot were significant.

The differences among the genotypes with respect to physico-chemical characteristics of rice grain, viz., elongation ratio, elongation index, L:B ratio, volume expansion, gel consistency, relative density (g/ml), water absorption per unit weight of rice, protein content and amylose content were also significant.

4.3 Mean performance

The mean performance of genotypes for different characters is given in Table 4, 5 and 6.

4.3.1 Quantitative characters

4.3.1.1 Days to 50% flowering

Days to 50% flowering was ranged from 78.00 to 104.33 days with an average value of 89.17 days. Among genotypes, CRR 451-15-B-A1 (78.00 days) was early in flowering followed by MAULS-15 (78.33 days). Five genotypes had recorded significantly higher days to 50% flowering over check Basmati-370 (87.33 days).

4.3.1.2 Plant height (cm)

The range for plant height was from 50.63 to 111.56 cm with an average value of 89.17 cm. The genotype PBNR-03-07 (111.56 cm) had recorded significantly superior plant height over checks Basmati-370 (92.26 cm), Avishkar (84.40 cm) and Parag (78.80 cm). Whereas, the genotype PAU 3832-79-4-3-1 recorded lowest plant height (50.63 cm).

4.3.1.3 Panicle length (cm)

Panicle length was ranged from 20.28 to 28.90 cm with an average value of 23.62 cm. Among the genotypes only one culture CR 3690-1-1 (28.90 cm) had recorded significantly superior panicle length over

the checks Basmati-370, Parag and Avishkar and Parag. However, none of the culture had shown significantly superior panicle length over the check Basmati-370 (26.73 cm) except CR 3690-1-1.

4.3.1.4 Number of effective tillers per plant

Effective tillers per plant were ranged from 2.90 to 8.40 with an average value of 4.91 tillers per plant. Six genotypes had recorded significantly superior effective tillers per plant over check Avishkar (5.93) and 12 genotypes over Basmati-370 (5.00). However, the highest number of effective tillers per plant was recorded by genotypes PBNR 04-28 (8.40), followed by PBNR 03-07 (8.00) and lowest was recorded by UPRI-2012-16 (2.90).

4.3.1.5 Effective tillers per metre length

Effective tillers per metre length ranged from 77.00 to 198.66 with an average value of 119.33 tillers per meter length. The genotypes PBNR 04-28 (198.66) had recorded significantly superior number of effective tillers per metre length followed by PBNR 03-07 (184.00), PBNR 03-10 (182.00), as compare to check Parag (166.66). However, seven and eight genotypes were found to be significantly superior over check Avishkar (134.00) and Basmati-370 (127.66) respectively. Lowest number of effective tillers per meter length was recorded by genotype CR 3635-1-1 (77.00).

4.3.1.6 Flag leaf area (cm²)

Flag leaf area was ranged from 19.32 cm² to 45.91 cm² with an average value of 29.38 cm². Two genotypes, PBNR 03-07 (45.91 cm²) and PBNR 08-04 (44.06 cm²) had recorded significantly superior flag leaf area over checks Parag (38.53 cm²) and Avishkar (37.01 cm²). However, ten genotypes were found to have significantly higher flag leaf area than check Basmati-370 (29.18 cm²). The genotype R-RF-48 recorded the lowest flag leaf area (19.32 cm²).

Table 4. Mean values of genotypes for grain yield and yield contributing characters

Sr. No.	Genotypes	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of tillers/plant	No. of tillers/meter	Flag leaf area (cm ²)	Days to maturity
1.	NDR 1143	86.33	77.86	23.33	4.80	120.23	26.29	121.66
2.	CR 3693-1-1	89.33	96.03	21.90	5.93	112.00	38.25	122.66
3.	OR 2172-7-1	93.00	73.66	23.86	3.20	83.66	32.04	128.66
4.	CR 3635-1-1	91.66	68.93	23.46	3.26	77.00	22.43	126.00
5.	RP 5214-18-6-2-1-1-1-B	104.33**	68.23	25.76	4.13	101.33	35.34	142.33**
6.	PBNR-03-10	83.33	94.00	26.83	7.33**	182.00**	37.29	119.33
7.	GK 5022	96.00	52.46	21.96	4.86	118.00	32.17	132.33
8.	Rewa 1207-15	91.00	65.20	22.90	4.13	102.33	28.70	125.33
9.	PBNR- 04-28	86.66	78.30	21.60	8.40**	198.66**	34.58	124.33
10.	CR 3632-1-2	95.00	65.00	23.80	5.26	126.33	26.46	130.33
11.	CRR 599-4-1	85.00	93.40	23.80	5.13	123.00	30.16	122.00
12.	CR 2991-1-2-1-1-1	101.66**	68.36	25.80	3.13	80.33	31.87	138.66*
13.	R 2212-RF-75	85.00	91.86	24.23	3.13	91.66	26.32	120.33
14.	CRR 452-23-1-1-1-1	90.66	71.26	22.65	5.73	105.66	24.37	124.66
15.	CRR 596-8-1	80.00	82.33	23.56	5.93	118.00	27.10	116.33
16.	CR 3692-1-1	94.33	74.60	22.87	4.06	103.33	31.86	130.33
17.	CB 09 516	94.33	61.33	24.53	3.93	99.33	32.17	129.33
18.	TJP 148	81.00	76.73	23.91	5.60	140.33	37.51	115.33
19.	CB 10-504	95.33	66.13	21.30	4.66	114.00	30.78	131.00
20.	OR 1946-2-1	99.66*	61.60	22.54	3.93	93.00	28.76	136.33*
21.	MAS 946 (RC 2)	98.33*	50.80	21.57	5.20	115.66	26.38	135.33*
22.	RP Bio 4918-166-9	94.66	58.86	22.18	4.26	107.00	33.67	128.66
23.	CR 3695-1-1	91.33	56.53	22.66	3.93	104.00	20.54	126.33
24.	BAU 408-05	79.00	84.46	21.75	5.26	127.66	20.96	111.66
25.	CR 3634-1-3	96.66	64.83	22.76	5.20	117.00	24.63	129.66
26.	CR 3690-1-1	97.66	59.13	28.90	6.13	112.00	22.35	133.33
27.	CR 3630-1-3	92.66	66.30	23.91	4.80	121.66	28.48	126.00

Continued

Sr. No.	Genotypes	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of tillers/plant	No. of tillers/meter	Flag leaf area (cm ²)	Days to maturity
28.	CRR 617-B-47-3	81.00	83.13	23.45	4.73	115.00	21.56	114.66
29.	CR 3633-1-3	88.00	87.00	22.65	4.60	108.33	22.42	123.00
30.	PBNR-03-07	84.66	111.56**	27.02	8.00**	184.00**	45.91**	122.00
31.	R-RF-48	93.66	53.20	20.28	4.06	93.33	19.32	131.66
32.	MAULS-15	78.33	85.80	23.93	5.80	135.00	30.15	111.66
33.	PBNR-08-07	85.00	93.43	24.83	6.53	156.33	40.07	120.33
34.	CRR 635-3-2	84.66	94.06	24.33	5.60	127.66	25.32	115.66
35.	BAU 389-02	89.66	72.96	24.10	3.53	97.00	21.00	124.66
36.	CR 3616-2-1-2-1-1	91.66	80.33	24.23	3.53	92.33	29.49	126.00
37.	PAU 3832-79-4-3-1	90.00	50.63	24.47	4.13	101.66	25.41	126.00
38.	RP 5216-13-7-2-1-1-1	93.33	53.03	23.96	4.06	104.33	31.44	129.66
39.	R 1700-2240-4-2295-1	99.00*	46.33	22.26	3.26	113.66	22.82	136.00*
40.	CRR 499-11-2-12-1	88.66	75.00	20.50	4.13	109.33	27.46	124.33
41.	UPRI 2012-16	91.66	71.20	22.20	2.90	87.33	28.17	127.33
42.	Tulasi	79.66	53.26	21.56	4.60	116.33	19.90	108.00
43.	CRR 614-4-1	81.00	89.66	25.66	7.13**	171.33	23.42	114.00
44.	PBNR-08-04	81.33	82.30	25.50	6.93**	164.00	44.06**	116.33
45.	RP 5125-17-6-3-2-1	89.33	73.13	22.36	3.66	102.00	28.31	119.66
46.	CRR 451-15-B-A1	78.00	73.33	22.90	3.60	104.33	27.97	114.00
47.	PBNR-03-20	91.00	87.00	24.60	7.53**	159.66	38.78	119.33
48.	Basmati-370 (ch)	87.33	92.26	26.73	5.00	127.66	29.18	122.33
49.	Parag (ch)	78.66	78.80	24.36	4.93	166.66	38.53	115.33
50.	Avishkar (ch)	79.66	85.40	24.69	5.93	134.00	37.01	117.00
	Mean	89.17	74.022	23.62	4.91	119.33	29.38	124.14
	SE	3.69	4.279	1.01	0.22	4.18	1.28	4.52
	CD 5%	10.38	12.008	2.84	0.64	11.73	3.61	12.69
	CV (%)	7.18	10.012	7.41	8.04	6.06	7.59	6.30
* and ** indicates significant at 5 and 1 per cent level, respectively								

Table 5. Mean values of genotypes for grain yield and yield contributing characters

Sr. No.	Genotypes	Filled grains per panicle	Unfilled grains per panicle	Test weight (g)	Grain yield per plant (g)	Grain yield/plot (g)	Straw yield/plot (g)	Iron chlorosis reaction
1.	NDR 1143	132.56	22.10	18.73	11.80	1.418*	1.788	2
2.	CR 3693-1-1	101.43	21.60	21.66	13.59	0.676	1.207	3
3.	OR 2172-7-1	107.70	14.06	23.40	8.28	0.402	1.049	4
4.	CR 3635-1-1	103.80	17.50	22.13	7.57	0.837	1.150	3
5.	RP 5214-18-6-2-1-1-1-B	102.70	40.33	13.53	5.83	0.463	1.251	4
6.	PBNR-03-10	134.10	31.56	24.53	24.25	1.114	2.477	0
7.	GK 5022	101.56	36.26	14.80	7.250	0.377	1.406	1
8.	Rewa 1207-15	105.40	20.70	18.93	8.283	0.736	1.193	3
9.	PBNR- 04-28	153.80	14.80	17.90	23.04	0.694	2.083	0
10.	CR 3632-1-2	96.70	23.66	17.40	8.72	0.633	1.107	3
11.	CRR 599-4-1	125.96	21.80	17.70	11.51	0.518	0.984	2
12.	CR 2991-1-2-1-1-1	97.66	11.66	20.93	6.33	0.510	1.291	4
13.	R 2212-RF-75	151.10	21.00	20.80	9.61	0.928	1.598	1
14.	CRR 452-23-1-1-1-1	109.40	20.13	18.80	11.70	0.494	0.598	4
15.	CRR 596-8-1	129.30	17.93	19.66	15.04	0.502	0.967	1
16.	CR 3692-1-1	108.93	20.74	21.20	9.38	0.887	1.344	2
17.	CB 09 516	96.10	30.86	14.33	5.33	0.439	1.031	4
18.	TJP 148	125.43	16.73	23.33	16.51	0.849	1.760	0
19.	CB 10-504	153.76	77.30**	15.10	10.90	0.742	1.460	2
20.	OR 1946-2-1	133.03	36.70	13.26	7.03	0.376	0.974	4
21.	MAS 946 (RC 2)	85.96	17.03	20.20	9.15	0.624	1.318	2
22.	RP Bio 4918-166-9	95.80	30.46	12.46	5.18	0.413	1.273	4
23.	CR 3695-1-1	99.10	25.16	21.40	8.29	0.623	1.092	2
24.	BAU 408-05	136.70	17.60	18.46	13.21	0.855	1.112	1
25.	CR 3634-1-3	122.70	15.96	15.46	9.75	0.956	1.331	3
26.	CR 3690-1-1	109.50	26.53	19.06	12.65	0.608	1.067	3
27.	CR 3630-1-3	119.76	24.73	23.80	13.84	0.988	1.316	3

Continued

Sr. No.	Genotypes	Filled grains per panicle	Unfilled grains per panicle	Test weight (g)	Grain yield per plant (g)	Grain yield/plot (g)	Straw yield/plot (g)	Iron chlorosis reaction
28.	CRR 617-B-47-3	85.53	26.60	20.86	8.49	0.544	0.998	3
29.	CR 3633-1-3	111.90	22.90	22.00	11.38	0.986	1.367	2
30.	PBNR- 03 -07	151.06	19.06	25.50	29.63	0.998	2.655	0
31.	R-RF-48	100.66	31.60	19.13	9.19	0.571	0.871	4
32.	MAULS-15	102.60	12.26	25.06	14.75	0.995	1.854	0
33.	PBNR - 08 – 07	150.06	26.63	20.93	19.32	1.012	1.646	0
34.	CRR 635-3-2	99.53	35.33	18.30	10.25	0.802	1.771	2
35.	BAU 389-02	127.60	11.13	19.86	8.85	0.727	1.483	2
36.	CR 3616-2-1-2-1-1	117.90	17.70	21.13	8.87	0.875	1.049	3
37.	PAU 3832 - 79-4-3-1	92.56	11.76	24.93	9.43	0.511	0.857	3
38.	RP 5216-13-7-2-1-1-1	81.70	18.36	13.20	4.49	0.565	1.151	3
39.	R 1700-2240-4-2295-1	121.50	28.83	16.86	6.71	0.618	1.452	2
40.	CRR 499-11-2-12-1	84.20	20.00	14.60	5.17	0.586	1.320	2
41.	UPRI 2012-16	85.86	24.16	20.06	5.02	1.005	1.167	3
42.	Tulasi	119.66	4.23	18.56	10.18	1.141	1.211	2
43.	CRR 614-4-1	122.80	10.93	24.90	22.27	0.921	2.159	0
44.	PBNR – 08 – 04	127.60	17.73	24.53	22.15	1.146	1.846	0
45.	RP 5125-17-6-3-2-1	120.63	25.20	21.60	9.40	0.777	1.081	2
46.	CRR 451-15-B-AI	112.53	21.20	21.00	8.24	0.502	0.670	3
47.	PBNR- 03 – 20	117.26	14.93	24.30	21.32	1.299*	1.900	0
48.	Basmati-370 (ch)	69.36	51.03	20.46	7.29	0.357	1.479	2
49.	Parag (ch)	154.13	11.73	28.53	21.21	1.086	2.724	0
50.	Avishkar (ch)	179.23	12.46	28.53	30.18	1.052	1.601	0
Mean		115.51	23.01	20.05	12.59	0.758	1.391	--
SE ±		5.71	2.32	0.62	0.97	0.062	0.067	--
CD 5%		16.04	6.51	1.76	2.72	0.174	0.188	--
CV %		8.57	17.48	5.42	14.09	14.25	8.37	--

4.3.1.7 Days to maturity

Days to maturity was ranged from 108.00 to 142.33 days with an average of 124.14 days. Five genotypes showed significantly superior over check Basmati-370 for days to maturity but, the genotype Tulasi (108.00 days) was early in maturity followed by MAULS-15 (111.66 days) and BAU 408-05 (111.66 days). Whereas, genotypes RP 5214-18-6-2-1-1-1-B (142.33 days) had recorded late maturity followed by CR 291-1-2-1-1-1 (138.66 days) and OR 1946-2-1 (136.33 days). Genotypes showing early and late maturity shown in Plate III.

4.3.1.8 Number of filled grains per panicle

Filled grains per panicle were ranged from 69.36 to 179.23, with an average value of 151.51. Among the genotypes none of the genotype had recorded significantly superior number of filled grains per panicle over check Avishkar (179.23). The maximum number of grains per panicle were recorded by the check Avishkar (179.23) followed by check Parag (154.13) and PBNR 04-28 (153.80). However, minimum number of filled grains was recorded by check Basmati-370 (69.36).

4.3.1.9 Number of unfilled grains per panicle

Unfilled grains per panicle were ranged from 4.23 to 77.30, with an average value of 23.01. Among the genotypes lowest number of unfilled grains per panicle were recorded by genotypes Tulasi (4.23), followed by CRR 614-4-1 (10.93) and BAU 389-02. The maximum number of unfilled grains per panicle was recorded by the CB 09-516 (77.30) followed by check Basmati-370 (51.03).

4.3.1.10 1000 grain weight (g)

The range for 1000 grain weight was from 12.46 to 28.53 g with average value of 20.05 g. Among all the genotypes, genotype RP Bio 4918-166-9 (12.46 g) had recorded lowest 1000 grain weight followed by RP 5216-13-7-2-1-1-1 (13.20 g) and RP 5214-18-6-2-1-1-1-B (13.53 g).



Early maturing variety: Tulasi (108 days)



Late maturing variety: RP 5214-18-6-2-1-1-B (142days)

Plate III. Genotypes showing early and late maturity

4.3.1.11 Grain yield per plant (g)

Grain yield per plant was ranged from 4.49 g to 30.18 g with an average value of 11.94 g. Significantly superior green yield per plant was recorded by 21 genotypes over check Basmati-370 (7.29 g). The highest grain yield per plant was recorded by check Avishkar (30.18g). However, none of the culture had recorded significantly superior grain yield per plant over the check Avishkar.

4.3.1.12 Grain yield per plot (kg)

The range for grain yield per plot was from 0.357 to 1.418 kg with an average value of 0.758 kg. Significantly superior grain yield per plot had recorded by genotype NDR 1143 (1.418 kg) shown in Plate IV and PBNR 03-20 (1.299 kg) over the checks Parag (1.086 kg) and Avishkar. However, check Basmati-370 (0.357 kg) recorded the minimum grain yield per plot.

4.3.1.13 Straw yield per plot (kg)

The range for straw yield per plot was from 0.598 to 2.724 kg with an average value of 1.391 kg. None of the genotypes were found to record significantly higher straw yield per plot than the check Parag (2.724 kg). However, the highest straw yield per plot had recorded by check Parag followed by PBNR 03-07 (2.655 kg), PBNR 03-10 (2.477 kg).

4.4 Grain quality characters

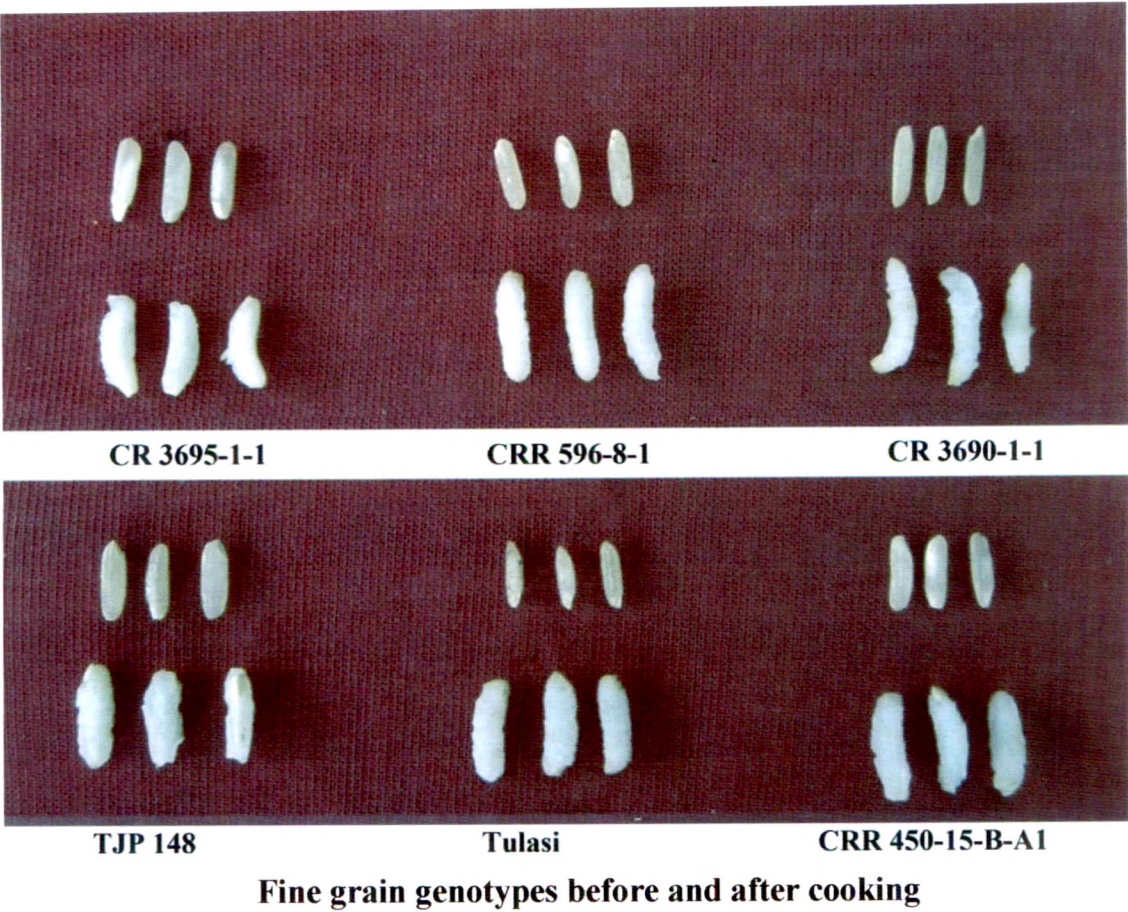
The mean performance of genotypes for grain quality characters is presented in Table 6.

4.4.1 Elongation ratio

The range of elongation ratio was recorded from 1.09 to 1.68 with an average value of 1.27. Among the genotypes, none of the genotype was significantly superior over checks Basmati-370 (1.67) and Avishkar (1.64) whereas, 3 genotypes had recorded significantly higher elongation ratio of grain than check Parag (1.34). However, genotype CRR 596-8-1 (1.68) recorded highest elongation ratio followed by check Basmati-370 and check Avishkar. Fine grain genotypes before and after cooking Plate V.



Plate IV. High yielding genotype NDR 1143



Fine grain genotype CRR 596-8-1



Fine grain genotype Tulasi

Plate V. Fine grain genotypes

4.4.2 Elongation index

The range of elongation index was from 0.75 to 1.09 with an average value of 0.92. Among the genotypes, none of the genotype was significantly superior over checks Basmati-370 (1.09) and Avishkar (1.00). However, highest elongation index was recorded by genotype CRR 596-8-1 (1.13) followed by variety Tulasi (1.07).

4.4.3 L:B ratio

The range of L:B ratio was from 2.39 to 4.61 with an average value of 3.08 mm. Among the genotypes, none of the genotype was significantly superior over check Avishkar (4.61). The distribution of genotypes in each group is given below.

Slender (L:B ratio above 3.0): GK 5022, Rewa 1207-15, PBNR 04-28, CR 3632-1-2, R 2212-RF-75, CRR 596-8-1, CB 09-516, TJP 148, CR 3695-1-1, CR 3634-1-3, CR 3690-1-1, CR 3630-1-3, CRR 617-B-47-3, PBNR 03-07, R-RF-48, MAULS-15, PBNR 08-07, CRR 635-3-2, BAU 389-02, PAU 3832-79-4-3-1, RP 5216-13-7-2-1-1-1, R 1700-2240-42295-1, CRR 499-11-2-12-1, Tulasi, CRR 614-4-1, PBNR 08-04, CRR 451-15-B-A1, Basmati-370 (ch), Parag (ch), Avishkar (ch).

Medium (L:B ratio 2.1 to 3.0): PBNR 03-20, RP 5125-17-6-3-2-1, UPRI 2012-16, CR 3616-2-1-2-1-1, CR 3633-1-3, NDR 1143, CR 3693-1-1, OR 2172-7-1, CR 3635-1-1, RP 5214-18-6-2-1-1-1-B, PBNR 03-10, CRR 599-4-1, CR 2991-1-2-1-1-1, CRR 452-23-1-1-1-1, CR 3692-1-1, CB 10-504, OR 1946-2-1, MAS 946 (RC 2), RP Bio 4918-166-9, BAU 408-05.

Bold (L:B ratio 1.1 to 2.0): None of the genotype

Round (L:B ratio 1 or less) : None of the genotype

4.4.4 Volume expansion

The range of volume expansion was from 0.33 to 3.00 with an average of 1.69. The genotypes RP 5216-13-7-2-1-1-1 (3.00), CB 10-504 (2.89) and CRR 599-4-1 (2.87) had recorded significantly higher over checks Basmati-370, Avishkar and Parag. However, lowest volume expansion was observed for genotype Tulasi.

4.4.5 Water absorption (mg)

Water absorption per unit weight of rice was ranged from 0.52 to 2.91 mg with an average value of 1.67 mg. Among all genotypes, 17 genotypes had recorded highly significant water absorption per unit weight over all three checks Avishkar (1.55 mg), Parag (1.41 mg) and Basmati-370 (1.31 mg). However, the genotype CRR 596-8-1 (2.91 mg) recorded the highest value followed by CRR 452-23-1-1-1-1 (2.77 mg) and CR 3690-1-1 (2.61 mg). The genotype BAU 389-02 (0.52 mg) had lowest water absorption.

4.4.6 Relative density (g/ml)

Relative density was ranged from 0.57 to 1.87 g/ml with an average value of 1.18 g/ml. The genotype CRR 617-b-47-3 (1.87 g/ml) was with highest relative density as compare to check Basmati-370 (1.70 g/ml). However, genotype Tulasi (0.57 g/ml) was with lowest relative density.

4.4.7 Protein content (%)

The range of crude protein content was from 6.54 to 11.82% with an average value of 8.70%. 19 genotypes had recorded significantly higher protein content over all checks Basmati-370 (8.33%), Avishkar (7.45%) and Parag (7.37%). However, the genotype PAU 3832-79-4-3-1 (11.81%) had recorded the highest protein content followed by genotype UPRI 2012-16 (11.59%) and genotype CB 09-513 (11.32%).

Table 6. Mean values of genotypes for grain quality characters of rice

Sr. No.	Genotypes	ER	EI	L/B	VE	WA	RD	PC (%)	GC	AC (%)	GT	WB	AR
1.	NDR 1143	1.27	0.98	2.50	1.55	1.32	0.87	10.83**	78.66	22.33	Intermediate	Absent	Absent
2.	CR 3693-1-1	1.29	0.96	2.57	0.67	1.53	0.94	9.99*	73.33	27.93*	Intermediate	Present	Strong
3.	OR 2172-7-1	1.17	0.90	2.93	2.57	1.55	0.99	7.99	82.66	22.43	Intermediate	Present	Mild
4.	CR 3635-1-1	1.26	0.93	2.98	1.68	2.52**	1.06	8.67	78.66	27.96*	Intermediate	Present	Mild
5.	RP 5214-18-6-2-1-1-1-B	1.21	0.95	2.94	2.44	2.39**	1.17	10.99**	65.33	23.56	High	Absent	Mild
6.	PBNR-03-10	1.27	0.93	2.61	1.38	1.65	1.13	8.26	55.66	20.81	Intermediate	Absent	Mild
7.	GK 5022	1.32	0.85	3.12	2.00	1.75	1.18	9.33	62.66	19.40	Intermediate	Absent	Strong
8.	Rewa 1207-15	1.36	0.87	3.26	1.63	2.60**	0.89	7.17	75.33	22.32	Intermediate	Absent	Mild
9.	PBNR- 04-28	1.20	0.75	3.60	0.72	1.45	1.23	6.84	64.66	24.53	Intermediate	Absent	Strong
10.	CR 3632-1-2	1.17	0.79	3.22	1.22	2.32**	0.92	8.16	75.66	25.37	Intermediate	Absent	Mild
11.	CRR 599-4-1	1.19	0.89	2.82	2.87*	1.46	1.74	7.66	71.00	20.17	Intermediate	Absent	Mild
12.	CR 2991-1-2-1-1-1	1.21	0.98	2.39	1.44	1.34	1.13	7.04	73.00	19.87	High	Present	Mild
13.	R 2212-RF-75	1.16	1.04	3.10	1.80	1.83*	1.19	10.16**	45.66	21.23	Intermediate	Present	Strong
14.	CRR 452-23-1-1-1-1	1.25	0.87	2.99	2.06	2.77**	0.99	7.35	78.66	27.79	Intermediate	Absent	Strong
15.	CRR 596-8-1	1.68	1.13	3.28	2.63	2.91**	1.06	7.04	58.66	25.33	Intermediate	Present	Mild
16.	CR 3692-1-1	1.29	0.99	2.50	1.35	1.66	1.07	8.99	65.66	30.24**	Intermediate	Present	Strong
17.	CB 09 516	1.19	0.99	3.16	1.85	2.59	0.94	11.32**	46.66	32.51**	Intermediate	Absent	Mild
18.	TJP 148	1.31	0.92	3.13	2.00	1.62	1.35	7.33	65.33	28.46**	Intermediate	Absent	Strong
19.	CB 10-504	1.26	0.89	2.84	2.89**	2.59**	1.36	9.83*	62.33	27.05	High	Present	Mild
20.	OR 1946-2-1	1.15	0.87	2.77	1.44	1.22	1.27	9.63*	74.66	30.63**	High	Absent	Mild
21.	MAS 946 (RC 2)	1.15	0.81	2.93	1.28	1.91*	0.95	10.32**	54.33	23.39	Intermediate	Absent	Mild
22.	RP Bio 4918-166-9	1.37	0.99	2.70	2.33	2.47**	1.07	6.67	68.33	20.62	Intermediate	Absent	Mild
23.	CR 3695-1-1	1.29	0.92	3.49	2.67	1.45	1.78	7.03	28.33	29.86**	Intermediate	Present	Mild
24.	BAU 408-05	1.28	0.96	2.80	0.93	1.22	1.08	10.16**	59.33	21.64	Intermediate	Absent	Mild
25.	CR 3634-1-3	1.17	0.90	3.06	0.67	1.07	0.85	7.50	74.66	26.65	Intermediate	Absent	Strong
26.	CR 3690-1-1	1.44	0.96	3.68	1.56	2.61**	0.93	6.83	77.33	24.62	Intermediate	Absent	Absent
27.	CR 3630-1-3	1.32	0.90	3.04	0.53	0.78	1.10	7.54	76.33	26.73	Intermediate	Present	Mild

Continued

28.	CRR 617-B-47-3	1.18	0.91	3.00	1.80	0.61	1.87*	10.33**	26.66	25.68	Intermediate	Absent	Mild
29.	CR 3633-1-3	1.28	0.80	2.58	2.54	1.47	1.56	10.16**	71.33	18.53	Intermediate	Present	Mild
30.	PBNR- 03 -07	1.41	0.80	3.15	1.00	1.22	1.19	6.54	61.33	24.30	Intermediate	Absent	Strong
31.	R-RF-48	1.15	0.86	3.22	1.67	1.65	1.17	11.03**	76.33	29.38**	Intermediate	Present	Mild
32.	MAULS-15	1.19	0.94	3.11	0.50	0.75	0.94	10.32**	58.33	25.83	High	Absent	Mild
33.	PBNR - 08 - 07	1.40	0.86	3.27	1.81	1.88**	1.13	7.22	44.33	19.39	High	Absent	Mild
34.	CRR 635-3-2	1.09	0.92	3.37	2.38	2.20**	1.34	7.13	52.36	30.24**	High	Absent	Strong
35.	BAU 389-02	1.09	0.86	3.20	0.62	0.52	1.26	9.99*	96.33	27.33*	Intermediate	Absent	Absent
36.	CR 3616-2-1-2-1-1	1.32	0.94	2.82	0.60	1.39	0.71	9.66*	69.66	24.33	High	Present	Mild
37.	PAU 3832 - 79-4-3-1	1.22	0.90	3.15	2.60	1.42	1.74	11.82**	57.66	29.50**	Intermediate	Absent	Strong
38.	RP 5216-13-7-2-1-1-1	1.15	0.88	3.52	3.00**	2.29**	1.24	10.83**	58.33	28.40**	Intermediate	Present	Strong
39.	R 1700-2240-4-2295-1	1.13	0.87	3.70	2.17	1.27	1.12	7.21	52.66	20.56	Intermediate	Absent	Mild
40.	CRR 499-11-2-12-1	1.17	0.90	3.15	2.00	2.16**	1.25	8.31	78.33	21.99	High	Absent	Mild
41.	UPRI 2012-16	1.23	1.05	2.43	2.00	1.16	1.76	11.59**	88.66	29.33**	Intermediate	Present	Mild
42.	Tulasi	1.62	1.07	3.34	0.33	1.05	0.57	7.54	24.33	25.63	Intermediate	Present	Strong
43.	CRR 614-4-1	1.26	0.89	3.56	0.60	1.15	0.94	7.66	83.66	19.70	Intermediate	Absent	Mild
44.	PBNR - 08 - 04	1.21	0.96	3.47	1.55	1.49	1.24	8.09	68.33	20.53	Intermediate	Absent	Mild
45.	RP 5125-17-6-3-2-1	1.27	0.94	2.47	1.88	2.15**	1.06	11.16**	73.66	29.03**	High	Present	Mild
46.	CRR 451-15-B-A1	1.36	0.91	3.19	1.71	1.68	1.26	7.38	54.33	25.80	High	Absent	Strong
47.	PBNR- 03 - 20	1.19	0.81	2.55	0.90	1.47	1.16	7.42	46.33	24.83	Intermediate	Absent	Strong
48.	Basmati-370 (ch)	1.67	1.09	3.63	2.60	1.31	1.7	8.33	61.33	20.35	Intermediate	Absent	Strong
49.	Parag (ch)	1.34	0.92	3.24	1.60	1.41	1.28	7.37	72.66	21.14	Intermediate	Absent	Mild
50.	Avishkar (ch)	1.64	1.00	4.61	2.57	1.55	1.53	7.45	65.33	24.80	High	Absent	Strong
	Mean	1.27	0.92	3.08	1.69	1.677	1.18	8.70	64.72	24.80	--	--	--
	SE±	0.03	0.04	0.08	0.07	0.08	0.05	0.45	1.84	0.87	--	--	--
	CD 5%	0.09	0.13	0.24	0.22	0.22	0.14	1.26	5.17	2.44	--	--	--
	CV %	4.62	8.66	4.87	7.94	8.05	7.52	8.98	4.93	6.06	--	--	--

* and ** indicates significant at 5 and 1 per cent level, respectively

ER-elongation ratio, EI-elongation index, L/B-length breadth ratio, WA- water absorption, VE-volume expansion, PC-protein content, RD-relative density, GC-gel consistency, AC-amylase content, GT-gelatinization temperature, WB-chalkiness, AR-aroma.

4.4.8 Gel consistency (mm)

Gel consistency was ranged from 24.33 to 96.33 mm with an average value of 64.72 mm. The genotypes were grouped into three groups according to their score as below (Table 6)

- Hard (below 35 mm) : CR 3695-1-1, CRR 617-B-47-3, Tulasi
- Intermediate (36-49 mm) : PBNR 03-20, PBNR 08-07, CB 09-516,
R 2212-RF-75
- Soft (above 50 mm) : NDR 1143, CR 3693-1-1, OR 2172-7-1 CR
3635-1-1, RP 5214-18-6-2-1-1-1-B, PBNR
03-10, GK 5022, Rewa 1207, PBNR 04-28,
CR 3622-1-2, CRR 599-4-1, CR 2991-1-2-
1-1-1, CRR 452-23-1-1-1-1, CRR596-8-1,
CR 3692-1-1, TJP 148, CB 10-504, OR
1946-2-1, MAS 946 (RC 2), BAU 408-05,
CR 3634-1-3, CR 3690-1-1, CR 3630-1-3,
CR 3633-1-3, PBNR 03-07, R-RF-48,
MAULS-15, CRR 635-3-2, BAU 389-02,
CR 3616-2-1-2-1-1, PAU 3832-79-4-3-1,
RP 5216-13-7-2-1-1-1, R 1700-2240-4-
2295-1, CRR 499-11-2-12-1, UPRI 2012-
16, CRR 614-4-1, PBNR 08-04, RP 5125-
17-6-3-2-1, CRR 451-15-B-A1, Basmati-
370 (ch), Parag (ch), Avishkar (ch).

4.4.9 Amylose content (%)

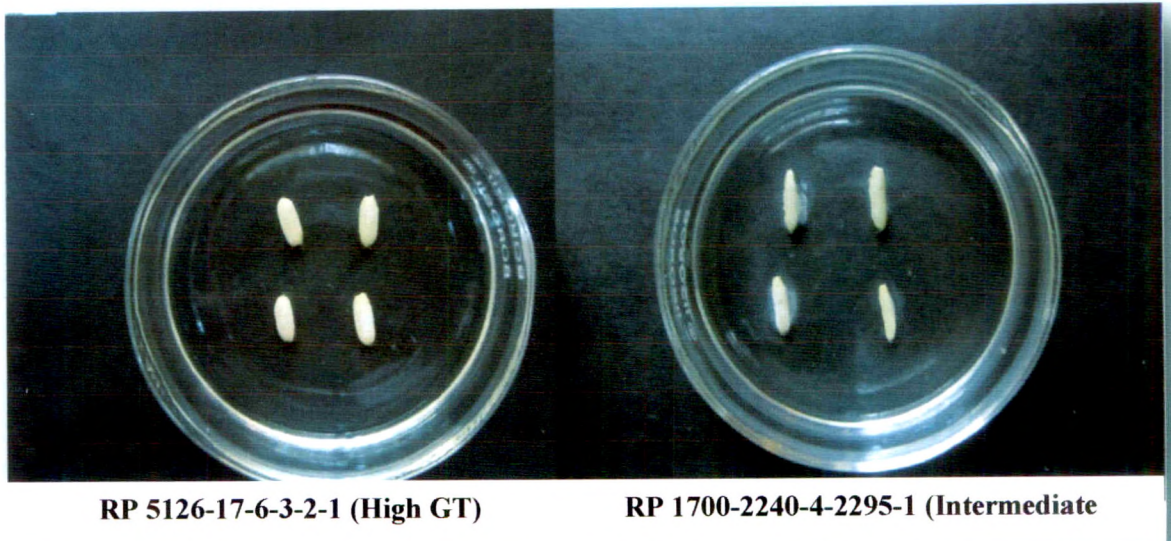
The range of amylose content was from 18.53 to 32.52 % with an average value of 24.80 %. The genotypes falling in classes low, intermediate and high are given below.

- Low (10-20%) : CRR 614-4-1, PBNR 08-07, CR 3633-1-3, GK 5022, CR 2991-1-2-1-1-1
- Intermediate (20-25%): NDR 1143, OR 2172-1-1, RP 5214-18-6-2-1-1-1-B, Rewa 1207-15, PBNR 04-28, CRR 599-4-1, R 2212-RF-75, MAS 946 (RC 2), RP Bio 4918-166-9, BAU 408-05, CR 3690-1-3, PBNR 03-07, CR 3616-2-1-2-1-1, R 1700-2240-4-2295-1, CRR 499-11-2-12-1, PBNR 03-20, Basmati-370 (ch), Parag (ch), Avishkar (ch)
- High (> 25%) : CRR 451-15-B-A1, RP 5125-17-6-3-2-1, PBNR 08-04, Tulasi, UPRI 2012-16, RP 5216-13-7-2-1-1-1, PAU 3832-79-4-3-1, BAU 389-02, CRR 635-3-2, MAULS-15, R-RF-48, CR 3693-1-1, CR 3635-1-1, PBNR 03-10, CR 3632-1-2, CRR 452-23-1-1-1-1, CRR 596-8-1, CR 3692-1-1, CB 09-516, TJP 148, CB 10-504, OR 1946-2-1, CR 3695-1-1, CR 3634-1-3, CR 3630-1-3, CRR 617-B-47-3.

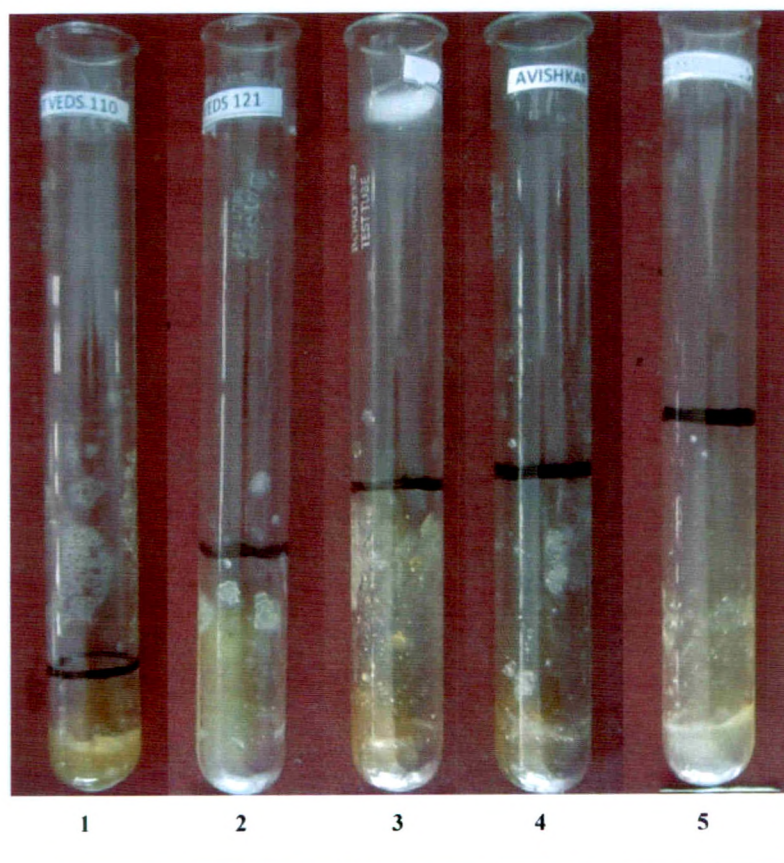
4.4.10 Gelatinization temperature

The genotypes for gelatinization temperature were classified into three classes viz. low, intermediate and high gelatinization temperature depending upon disintegration of grains as given below (Table 6). Gelatinization temperature and gel consistency Plate VI

- Low : None of the genotypes
- Intermediate : NDR 1143, CR 3693-1-1, OR 2172-7-1, CR 3635-1-1, PBNR 03-10, GK 5022, Rewa 1207-15, PBNR 04-08, CRR 599-4-1R 2212-RF-75, CRR 452-23-1-1-1-1, CRR596-8-1, CR 3692-1-1, CB 09-516, TJP-148, MAS 946 (RC 2), RP Bio 4918-166-9, CR 3695-1-1, BAU 408-05, CR 3634-1-3, CR 3690-1-1, CR 3630-1-3, CRR 617-B-47-3, CR 3633-1-3, PBNR 03-07, R-RF-48, BAU 389-



Genotypes showing high and intermediate gelatinization temperature



**Gel consistency of different genotypes: 1 – CRR 617-B-47-3 (hard, 25.68mm),
 2 – R 2212-RF-75 (intermediate, 45.66mm)
 3 – Basmati-370 (soft, 61.33 mm), 4 – Avishkar
 (soft, 65.33 mm) and 5 - Parag (soft, 72.66
 mm)**

Plate VI. Gelatinization temperature and gel consistency

02, PAU 3832-79-4-3-1, RP 5216-13-7-2-1-1-1, R 1700-2240-4-2295-1, UPRI 2012-16, Tulasi, CRR 614-4-1, PBNR 08-04, PBNR 03-20, Basmati-370 (ch), Parag (ch)

High : RP 5214-18-6-2-1-1-1-B, CR 2991-1-2-1-1-1, CB 10-504, OR 1946-2-1, MAULS-15, PBNR 08-07, CRR 635-3-2, CR 3616-2-1-2-1-1, CRR 499-11-2-12-1, RP 5125-17-6-3-2-1, CRR 451-15-B-A1, , Avishkar (ch).

4.4.11 Presence/absence of grain translucency

Presence or absence of grain translucency in the genotypes was noted. The genotypes were categorized into two classes viz., translucent and presence of white belly.

Translucent : NDR 1143, RP 5214-18-6-2-1-1-1-B, PBNR 03-10, GK 5022, Rewa 1207-15, PBNR 04-28, CR 3632-1-2, CRR 599-4-1, CRR 452-23-1-1-1-1, CB 09-516, TJP 148, OR 1946-2-1, MAS 946 (RC2), RP Bio 4918-166-9, BAU 409-05, CR 3634-1-3, CR 3690-1-1, CRR 617-B-47-3, PBNR 03-07MAULS-15, PBNR 08-07, CRR 635-3-2, BAU 389-02, PAU 3832-79-4-3-1, R 1700-2240-4-2295-1, CRR 499-11-2-12-1, CRR 614-4-1, PBNR 08-04, CRR 451-15-B-A1, PBNR 03-20, Basmati-370 (ch), Parag (ch), Avishkar (ch)

White belly : Rp 5125-17-6-3-2-1, Tulasi, UPRI 2012-16, RP 5216-13-7-2-1-1-1, CR3616-2-1-2-1-1, R-RF-48, CR 3633-1-3, CR 3693-1-1, OR 2172-7-1, CR 3635-1-1, CR 2991-1-2-1-1-1, R 2212-RF-75, CRR 596-8-1, CR 3692-1-1, CB 10-504, CR 3695-1-1, CR 3630-3-1.

4.4.12 Aroma

The genotypes for aroma were classified into three classes viz., strong, mild and no aroma as given below (Table 6).

- Strong** : CR 3693-1-1, GK 5022, PBNR 04-28, CRR 452-23-1-1-1-1, CR 3692-1-1, TJP 148, CR 3634-1-3, PBNR 03-07, CRR 635-3-2, PAU 3832-79-4-3-1, RP 5216-13-7-2-1-1-1, Tulasi, CRR 451-15-B-A1, PBNR 03-20, Basmati-370 (ch), Avishkar (ch)
- Mild** : OR 2172-7-1, CR 3635-1-1, RP 5214-18-6-2-1-1-1-B, PBNR 03-10, Rewa 1207-15, CR 3632-1-2, CRR 599-4-1, CR 2991-1-2-1-1-1, R 2212-RF-75, CRR 596-8-1, CB 09-516, CB 10-504, OR 1946-2-1, MAS 946 (RC2), RP Bio 4918-166-9, CR 3695-1-1, BAU 408-05, CR 3630-1-3, CRR 617-B-47-3, CR 3633-1-3, R-RF-48, MAULS-15, PBNR 08-07, CR 3616-2-1-2-1-1, R 1700-2240-4-2295-1, CRR 499-11-2-12-1, UPRI 2012-16, CRR 614-4-1, PBNR 08-04, RP 5125-17-6-3-2-1, Parag (ch)
- No aroma** : NDR 1143, CR 3690-1-1, BAU3 89-02.

4.5 Iron chlorosis reaction

Based on the visual symptoms of iron chlorosis observed on leaf (Plate VII), genotypes are scored 0, 1, 2, 3 and 4 (given in Table 5) and are classified as follows (Table 5)

- Tolerant genotypes** : PBNR 03-10, GK 5022, PBNR 04-28, TJP 148, (0 and 1 score) R 2212-RF-75, CRR 596-8-1, BAU 408-05, PBNR 03-07, MAULS-15, PBNR 08-07, CRR 614-4-1, PBNR 08-04, PBNR 03-20, Parag (ch) and Avishkar (ch).
- Susceptible Genotypes** : NDR 1143, CR 3693-1-1, OR 2172-7-1, (2, 3 and 4 score) CR 3635-1-1, RP 5214-18-6-2-1-1-1-B, Rewa 1207-15, CR 3632-1-2, CRR 599-4-1, CR 2991-1-2-1-1-1, CRR 452-23-1-1-1-1, CB 3692-1-1, CB 09-516, CB 10-504, OR 1946-2-1, MAS 946 (RC 2), RP Bio 4918-166-9, CR 3695-1-1, CR 3634-1-3, CR 3690-1-1, CR



Iron chlorosis grade: 0 and 1 - Tolerant, 2, 3 and 4 – Sensitive



Genotype RP 5214-18-6-2-1-1-1-B showing severe symptom of iron chlorosis

Plate VII. Symptoms of iron chlorosis

3630-1-3, CRR 617-B-47-3, CR 3633-1-3,R-
RF-48,CRR 365-3-2, BAU 389-02,CR 3616-2-
1-2-1-1, PAU 3832-79-4-3-1, RP 5216-13-7-2-
1-1-1, R 1700-2240-4-2295-1, CRR 499-11-2-
12-1, UPRI 2012-16, Tulasi, RP 5125-17-6-3-
2-1, CRR 451-15-B-A1 and Basmati-370 (ch).

4.6 Genotypic and phenotypic coefficient of variation

The phenotypic coefficient of variation was higher in magnitude than that of genotypic coefficient of variation for the characters studied. High phenotypic and genotypic coefficient of variation was recorded for grain yield per plant (54.32 and 52.46) followed by number of unfilled grains per panicle (52.78 and 49.80), grain yield per plot (36.61 and 36.72) and straw yield per plot (33.88 and 32.84) among yield contributing characters. The estimates of phenotypic and genotypic coefficients of variation were moderate for test weight (19.64 and 18.87) and plant height. However, low phenotypic and genotypic coefficient of variation was observed for days to 50% flowering (9.59 and 3.36) followed by panicle length (9.48 and 5.92) and days to maturity (8.00 and 4.92). The data for yield contributing characters is given in Table 7.

Among grain quality characters, volume expansion(43.73 and 43.01), water absorption (35.49 and 34.57), relative density (24.66 and 23.46) and gel consistency (23.44 and 22.91) had recorded the higher GCV and PCV. While, the estimates of GCV and PCV were moderate for protein content (19.66 and 17.49), L: B ratio (19.32 and 18.70) and amylose content (15.63 and 14.40). However, low phenotypic and genotypic coefficient of variation was observed. The data for and grain quality characters is given in Table 8.

4.7 Heritability

Heritability in broad sense estimates were highest for straw yield per plot (93.9%) followed by number of effective tillers per plant (93.5%) ,grain yield per plant (93.3%), 1000 grains weight (92.4%), number

Table 7. Estimates of variability, broad sense heritability and genetic advance for grain yield and yield contributing characters.

Sr. No.	Characteristics	Range	Mean ±SE	σ^2_g	σ^2_p	GCV	PCV	h^2 (broad sense)	G.A. as % of mean (5%)
1.	Days to 50% flowering	78.00 – 104.33	89.17±3.69	32.165	73.220	6.360	9.596	43.9	8.64
2.	Plant height (cm)	50.63 – 111.56	74.02±4.28	197.046	215.977	18.964	21.444	78.2	34.54
3.	Panicle Length (cm)	20.28 – 28.90	23.62±1.01	1.959	5.024	5.925	9.489	39.0	7.62
4.	No. of tiller/plant	2.90 – 8.40	4.91±0.22	1.735	1.891	26.811	27.992	91.7	52.89
5.	No. of tiller/meter	77.00 – 198.66	119.33±4.18	754.635	807.058	23.020	23.807	93.5	45.85
6.	Days to maturity	108.00 -142.33	124.14±4.52	37.369	98.692	4.924	8.002	37.9	6.24
7.	Flag Leaf area (cm ²)	19.32 – 45.91	29.38±1.28	38.992	43.976	21.249	22.566	88.7	41.21
8.	Filled grains/panicle	69.36 – 179.23	151.51±5.71	483.139	581.173	19.028	20.869	83.1	35.73
9.	Unfilled grains/panicle	4.23 – 77.30	23.01±2.23	131.389	147.579	49.802	52.782	89.0	96.80
10.	Test weight (gm)	12.46 – 28.53	20.05±0.62	14.339	15.522	18.878	19.641	92.4	37.37
11.	Grain yield/plant (g)	4.49 – 30.18	12.59±0.972	39.295	42.132	52.465	54.326	93.3	99.05
12.	Grain yield/plot (kg)	0.357 – 1.418	0.754±0.062	0.065	0.076	33.723	36.612	84.8	63.98
13.	Straw yield/plot (kg)	0.598 – 2.724	1.391±0.067	0.209	0.222	33.893	33.880	93.9	65.56

Table 8. Estimates of variability, broad sense heritability and genetic advance for quality characters of rice grain

Sr. No.	Characteristics	Range	Mean ±SE	σ^2_g	σ^2_p	GCV	PCV	h^2 (broad sense)	G.A. as % of mean (5%)
1.	Length breadth ratio	2.39 – 4.61	3.08±0.088	0.343	0.36	18.700	19.32	93.6	37.27
2.	Elongation ratio	1.09 - 1.68	1.27±0.033	0.018	0.021	10.484	11.45	83.7	19.76
3.	Elongation index	0.75 - 1.09	0.92±0.046	0.004	0.01	6.96	11.11	39.2	8.98
4.	Volume expansion	0.33 - 3.00	1.69±0.078	0.530	0.54	43.011	43.73	96.7	87.12
5.	Water absorption	0.52 – 2.91	1.67±0.078	0.336	0.35	34.573	35.49	94.9	69.36
6.	Relative density (g/ml)	0.57 - 1.87	1.18±0.051	0.078	0.086	23.469	24.64	90.7	46.04
7.	Protein content (%)	6.54 - 11.82	8.70±0.451	2.317	2.92	17.491	19.66	79.1	32.05
8.	Gel consistency (mm)	24.33 - 96.33	64.72±1.84	220.017	230.20	22.918	23.44	95.6	46.15
9.	Amylose content (%)	18.53 – 32.52	24.80±1.01	12.767	15.03	14.405	15.63	84.9	27.34

of effective tillers per plant (91.7%), number of unfilled grains per panicle (89.0%), flag leaf area (88.7%), grain yield per plot (84.8%), number of filled grains per panicle (83.1%) and plant height (78.2%) among yield contributing characters, whereas, among grain quality characters volume expansion (96.7%) had recorded highest estimate of broad sense heritability followed by gel consistency (95.6%), water absorption per unit rice (94.9%), L:B ratio (93.6%), relative density (90.7%), amylose content (84.9%) and elongation ratio (79.1%) .

The estimates of heritability were moderate for days to 50% flowering (43.9%) followed by elongation index (39.2%), panicle length (39.0%) and days to maturity (37.9%).

4.8 Genetic advance

Genetic advance as percent of mean were recorded for grain yield and quality traits. The data is given in Table 7 and 8.

Among yield contributing characters, the high expected genetic advance were observed for the characters viz., grain yield per plant (99.05%), number of unfilled grains per panicle (96.80%), straw yield per plot (65.56%), grain yield per plot (63.98%), number of effective tillers per plant (52.89%), number of effective tillers per meter length (45.85%), flag leaf area (41.21%), test weight (37.37%), number of filled grains per panicle (35.73%) and plant height (34.54%) . However, lowest expected genetic advance was observed for days to maturity (6.24%), panicle length (7.62%) and days to 50% flowering (8.64%). Among the quality characters, moderate expected genetic advance was observed in elongation ratio (19.76%) and lowest in elongation index (8.98%)

While among yield contributing characters, high heritability coupled with high expected genetic advance was observed in all the characters under study except days to 50% flowering, panicle length and days to maturity which recorded moderate heritability with low expected genetic advance. In quality characters high heritability coupled with high expected genetic advance was observed for the all the characters under

study except elongation ratio (high heritability with moderate expected genetic advance) and moderate heritability with low expected genetic advance for elongation index.

4.9 Correlation

Correlation was studied in order to find out the inter relationship of different yield contributing and quality characters with grain yield per plant at genotypic and phenotypic levels. The genotypic and phenotypic correlation coefficients for nine characters are presented in Table 9 and Table 10.

4.9.1 Correlations with grain yield

The positive and significant correlations were showed by all the yield contributing characters except iron chlorosis reaction ($G = -0.791$ and $P = -0.754$), days to 50% flowering ($G = -0.661$ and $P = -0.436$) and days to maturity ($G = -0.629$ and $P = -0.357$) which recorded negative and significant association at both genotypic and phenotypic level with grain yield per plant. The characters plant height ($G = 0.628$ and $P = 0.541$), panicle length ($G = 0.475$ and $P = 0.287$), number of effective tillers per plant ($G = 0.829$ and $P = 0.814$), number of effective tillers per meter length ($G = 0.859$ and $P = 0.806$), flag leaf area ($G = 0.576$ and $P = 0.520$), number of filled grains per panicle ($G = 0.710$ and $P = 0.695$), straw yield per plot ($G = 0.672$ and $P = 0.625$) and grain yield per plot ($G = 0.600$ and $P = 0.542$) recorded significant positive association with grain yield per plant at genotypic and phenotypic levels.

Among grain quality characters, elongation index ($G = 0.341$ and $P = 0.299$) showed significant and positive association with grain yield per plant at both genotypic and phenotypic levels. The characters like volume expansion ($G = -0.278$ and -0.272), water absorption ($G = -0.209$ and $P = -0.194$), protein content ($G = -0.428$ and $P = -0.363$) and amylose content ($G = -0.240$ and $P = -0.224$) showed significantly negative correlation with grain yield per plant at both genotypic and phenotypic

levels. Elongation index ($G = -0.2180$ and $P = -0.1393$) was significantly and negatively correlated with grain yield per plant at genotypic level.

4.9.2 Correlations among yield contributing characters

All the yield contributing characters had significant negative correlation with iron chlorosis, days to 50% flowering and days to maturity except panicle length, number of unfilled grains and flag leaf area. Panicle length and flag leaf area showed negative but non-significant association with days to 50% flowering ($G = -0.137$ and $P = -0.083$ respectively) and days to maturity ($G = -0.002$ and $P = -0.072$; $G = -0.062$ and $P = -0.039$ respectively), whereas, positive and significant correlation was recorded by number of unfilled grains per panicle with iron chlorosis ($G = 0.208$ and $P = 0.202$), days to 50% flowering ($G = 0.425$ and $P = 0.274$) and days to maturity ($G = 0.437$ and $P = 0.292$) at genotypic and phenotypic level.

The positive and significant correlation was observed for iron chlorosis with days to 50% flowering ($G = 0.775$ and $P = 0.504$), days to maturity ($G = 0.754$ and $P = 0.453$) at both genotypic and phenotypic level.

The association of flag leaf area was positive and significant at both genotypic and phenotypic level with number of tillers per meter length ($G = 0.549$ and $P = 0.500$), number of filled grains per panicle ($G = 0.356$ and $P = 0.311$), test weight ($G = 0.269$ and $P = 0.249$), straw yield per plant ($G = 0.568$ and $P = 0.511$) and grain yield per plot ($G = 0.247$ and $P = 0.179$). The number of filled grains per panicle ($G = 0.509$ and $P = 0.466$) and test weight ($G = 0.549$ and $P = 0.479$) showed significant positive correlation with grain yield per plot.

4.9.3 Correlations among grain quality characters

Elongation ratio was significantly and positively correlated with elongation index ($G = 0.514$ and $P = 0.546$) and L:B ratio ($G = 0.469$ and $P = 0.479$) but significant negative correlation were observed with characters like protein content ($G = -0.3833$ and $P = -0.346$) and gel consistency ($G = -0.1950$ and $P = -0.1616$) at both phenotypic and genotypic level. Likewise, character elongation index showed significant positive association with L:B ratio ($G = 0.1664$ and $P = 0.2414$).

Table 9. Genotypic and phenotypic correlation of yield contributing characters with grain yield

Characters	PH	PL	ICR	DF	DM	TP	TM	FLA	FGP	UGP	TW	SYP	GYP	GYPL
PH	1	0.493** 0.281**	-0.566** -0.481**	-0.707** -0.455**	-0.729** -0.392**	0.540** 0.470**	0.533** 0.463**	0.462** 0.399**	0.396** 0.347**	-0.077 -0.060	0.489** 0.414**	0.538** 0.461**	0.423** 0.396**	0.628** 0.541**
PL		1	-0.261** -0.153	-0.107 -0.043	-0.002 -0.072	0.411** 0.249**	0.396** 0.219**	0.405** 0.302**	0.119 0.084	-0.064 -0.036	0.471** 0.278**	0.448** 0.297**	0.182* 0.078	0.475** 0.287**
ICR			1	0.775** 0.504**	0.754** 0.453**	-0.672** -0.643**	-0.812** -0.772**	-0.423** -0.402**	-0.595** -0.537**	0.208* 0.202*	-0.538** -0.507**	-0.772** -0.742**	-0.615** -0.553**	-0.791** -0.754**
DF				1	0.802** 0.726**	-0.488** -0.294**	-0.585** -0.408**	-0.137 -0.083	-0.430** -0.320**	0.425** 0.274**	-0.667** -0.422**	-0.419** -0.288**	-0.534** -0.343**	-0.661** -0.436**
DM					1	-0.494** -0.273**	-0.574** -0.339**	-0.062 -0.039	-0.373** -0.239**	0.437** 0.292**	-0.682** -0.359**	-0.381** -0.251**	-0.651** -0.345**	-0.629** -0.357**
TP						1	0.919** 0.851**	0.491** 0.438**	0.403** 0.365**	-0.104 -0.091	0.320** 0.279**	0.611** 0.561**	0.386** 0.330**	0.829** 0.814**
TM							1	0.549** 0.500*	0.501** 0.454**	-0.114 -0.100	0.393** 0.355**	0.811** 0.770**	0.473** 0.438**	0.859** 0.806**
FLA								1	0.356** 0.311**	0.035 0.011	0.269** 0.249**	0.568** 0.511**	0.247** 0.179*	0.576** 0.520**
FGP									1	-0.056 -0.110	0.340** 0.285**	0.494** 0.469**	0.509** 0.466**	0.710** 0.695**
UGP										1	-0.467** -0.425**	-0.093 -0.097	-0.326** -0.294**	-0.260** -0.255**
TW											1	0.453** 0.422**	0.549** 0.479**	0.672** 0.625**
SYP												1	0.607** 0.589**	0.726** 0.687**
GYP													1	0.600** 0.542**
GYPP														1

*-significant at 5% and **-significant at 1% level. Figures in bold indicates genotypic correlation and normal indicates phenotypic correlation. **PH**- Plant height, **PL**- Panicle length, **ICR**- Iron chlorosis reaction, **DF**- Days to 50% flowering, **DM**- Days to maturity, **TP**- No. of effective tillers per plant, **TM**- No. of effective tillers per meter length, **FLA**- Flag leaf area, **FGP**- No. of filled grains per panicle, **UGP**- No. of unfilled grains per panicle, **TW**- Test weight, **SYP**- Straw yield per plot, **GYP**- Grain yield per plot and **GYPP**- Grain yield per plant.

Table 10. Genotypic and phenotypic correlation of grain quality parameters with grain yield

Characters	Elongation ratio	Elongation index	L/B ratio	Volume expansion	Water absorption	Protein content	Relative density	Gel consistency	Amylose content	Grain yield per plant
Elongation ratio	1	0.5140** 0.5466**	0.4693** 0.4799**	0.0704 0.0960	0.1407 0.0988	-0.3833** -0.3464**	-0.0421 -0.0683	-0.1950* -0.1616*	-0.1928* -0.1498	0.3417** 0.2996**
Elongation index		1	0.1664* 0.2414**	0.1639* 0.1682*	0.1213 0.0332	0.1846* -0.0016	0.0284 -0.0558	-0.1785* -0.0885	0.0638 0.0394	-0.2180** -0.1393
L/B ratio			1	0.2089** 0.2136**	-0.0225 -0.0222	-0.2797** -0.2607**	0.2451** 0.2093*	-0.1531 -0.1398	-0.1396 -0.1241	0.1592 0.1507
Volume expansion				1	0.4891** 0.4579**	0.0850 0.0545	0.5984** 0.5509**	-0.1079 -0.0957	-0.0172 -0.0130	-0.2782** -0.2727**
Water absorption					1	-0.0971 -0.0775	-0.2242** -0.2148**	0.0533 0.0402	0.1073 0.144	-0.2094* -0.1946*
Protein content						1	0.1339 0.1180	0.0705 0.0621	0.3377** 0.2752**	-0.4287** -0.3632**
Relative density							1	-0.1557 -0.1424	0.0518 0.0585	-0.0115 -0.0004
Gel consistency								1	-0.0513 -0.0362	-0.0471 -0.0481
Amylose content									1	-0.2404** -0.2242**
Grain yield per plant										1

*-significant at 5% and **-significant at 1% level. Digits in bold indicates genotypic correlation and normal indicates phenotypic correlation.

Volume expansion was also found to have positive and significant correlation with L:B ratio ($G = 0.2089$ and $P = 0.2136$) and relative density ($G = 0.598$ and $P = 0.550$) at both levels. L:B ratio recorded positive association with relative density ($G = 0.245$ and $P = 0.209$) and negative significant correlation with protein content ($G = -0.279$ and $P = -0.260$) at both levels. However, water absorption had significant negative association with relative density ($G = -0.224$ and $P = -0.214$) whereas, amylose content and protein content ($G = 0.337$ and $P = 0.275$) were found to be positively and significantly correlated with each other at genotypic and phenotypic level.

4.10 Path analysis

The correlations do not show the exact picture of direct and indirect effects of yield contributing characteristics on grain yield per plant. Path analysis was carried out to find out the extent and nature of direct and indirect effects of yield contributing characters (Table 11) and grain quality characters (Table 12) on grain yield.

Among yield contributing characters, maximum positive direct effect was recorded by number of effective tiller per meter (0.5695) followed by number of filled grains per panicle (0.3740) and 1000 grains weight (0.3104). The character number of effective tillers per plant also recorded highest indirect positive and negative effect via number of tillers per meter length (0.4850) and iron chlorosis reaction (-0.3665), respectively. The character also recorded higher positive indirect effect via straw yield per plot (0.3196), plant height (0.2681), flag leaf area (0.2495) and number of filled grains per panicle (0.2081) on grain yield per plant.

Among the grain quality characters, elongation ratio (0.0551), volume expansion (0.0252) and L:B ratio (0.0351) showed positive direct effect on grain yield per plant, whereas, only elongation index showed negative direct effect (0.0216) on grain yield per plant. The maximum indirect effect was recorded by elongation ratio via elongation index

(0.0301). However, volume expansion showed negative indirect effect through gel consistency (-0.0024) among grain quality characters.

Likewise, relative density recorded positive indirect effect via volume expansion (0.0262) followed by L:B ratio (0.0099) and protein content (0.0056). While, amylose content showed negative indirect effect through characters like elongation ratio (-0.0032), L:B ratio (-0.0012), gel consistency (-0.0003) and volume expansion(-0.0001) on grain yield per plant.

Table 11. Direct and indirect effect of yield contributing characters on grain yield per plant

Characters	Plant height	Panicle length	Iron Chlorosis reaction	Days to 50% flowering	Days to maturity	Tillers/ plant	Tillers/ meter	Flag leaf area	Filled grains/ panicle	Unfilled grains/ panicle	Test weight	Straw yield/ plot	Grain yield/ plot	Correlation Grain yield/ plant
Plant height	-0.0309	-0.0087	0.0149	0.0141	0.0121	-0.0146	-0.0143	-0.0124	-0.0107	0.0019	-0.0128	-0.0143	-0.0111	0.5412**
Panicle length	-0.0048	-0.0169	0.0026	0.0007	0.0012	-0.0042	-0.0037	-0.0051	-0.0014	0.0006	-0.0047	-0.0050	-0.0013	0.2875**
Iron chlorosis reaction	-0.0435	-0.0138	0.0903	0.0456	0.0409	-0.0581	-0.0698	-0.0364	-0.0486	0.0183	-0.0458	-0.0670	-0.0300	-0.7549**
Days to 50% flowering	0.0080	0.0008	-0.0089	-0.0177	-0.0128	0.0052	0.0072	0.0015	0.0057	-0.0049	0.0075	0.0051	0.0061	-0.4364**
Days to maturity	-0.0054	-0.0010	0.0062	0.0099	0.0137	-0.0037	-0.0046	-0.0005	-0.0033	0.0040	-0.0049	-0.0034	-0.0047	-0.3578**
Tillers/plant	0.2681	0.1421	-0.3665	-0.1677	-0.1556	0.5695	0.4850	0.2495	0.2081	-0.0524	0.1592	0.3196	0.1884	0.8142**
Tillers/meter	-0.0037	-0.0048	0.0062	0.0033	0.0027	-0.0068	-0.0080	-0.0040	-0.0036	0.0008	-0.0028	-0.0062	-0.0035	0.8060**
Flag leaf area	0.0297	0.0225	-0.0299	-0.0062	-0.0029	0.0325	0.0371	0.0742	0.0231	0.0008	0.0185	0.0379	0.0133	0.5200**
Filled grains / panicle	0.1298	0.0318	-0.2012	-0.1197	0.0894	0.1366	0.1700	0.1166	0.3740	-0.0413	0.1068	0.1755	0.1745	0.6953**
Unfilled grains/ panicle	0.0040	0.0024	-0.0134	-0.0182	-0.0194	0.0061	0.0066	-0.0007	0.0073	-0.0663	0.0282	0.0061	0.0195	-0.2559**
Test weight	0.1286	0.0863	-0.1575	-0.1311	-0.1115	0.0868	0.1103	0.0775	0.0886	-0.1320	0.3104	0.1310	0.1487	0.6253**
Straw yield per plot	0.0494	0.0318	-0.0794	-0.0309	-0.0269	0.0601	0.0824	0.0547	0.0502	-0.0098	0.0452	0.1070	0.0630	0.6875**
Grain yield per plot	0.0089	0.0019	-0.0136	-0.0085	-0.0085	0.0081	0.0108	0.0044	0.0115	-0.0072	0.0118	0.0145	0.0246	0.5420**
Residual effect = 0.1719														

** - significant at 1% level. Figures in bold indicates direct effects and normal indicates indirect effects.

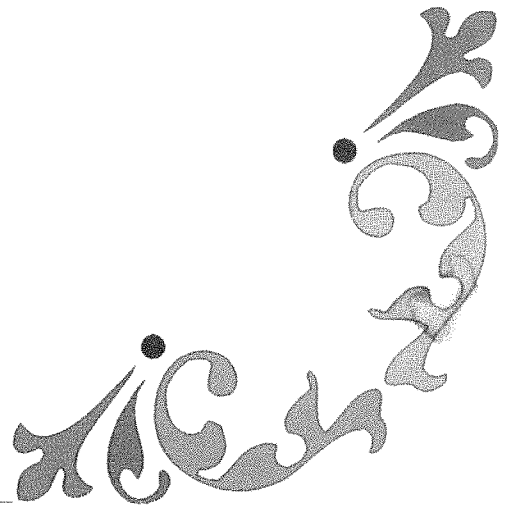
Table 12. Direct and indirect effects of grain quality parameters on grain yield per plant

Characters	Elongation ratio	Elongation index	L/B ratio	Volume expansion	Water absorption	Relative density	Protein content	Gel consistency	Amylose content	Correlation with grain yield per plant
Elongation ratio	0.0551	0.0301	0.0263	0.0053	0.0054	-0.0038	-0.0191	-0.0089	-0.0083	0.2996**
Elongation index	-0.0118	-0.0216	-0.0052	-0.0036	-0.0007	0.0012	0.0000	0.0019	-0.0009	-0.1393
L/B ratio	0.0168	0.0085	0.0351	0.0075	-0.0008	0.0073	-0.0092	-0.0049	-0.0044	0.1507
Volume expansion	0.0024	0.0042	0.0054	0.0252	0.0115	0.0139	0.0014	-0.0024	0.0003	-0.2727**
Water absorption	0.0007	0.0002	-0.0002	0.0031	0.0068	-0.0015	-0.0005	0.0003	0.0007	-0.1946*
Relative density	-0.0032	-0.0026	0.0099	0.0262	-0.0102	0.0475	0.0056	-0.0068	0.0028	-0.0004
Protein content	-0.0096	0.0000	-0.0072	0.0015	-0.0022	0.0033	0.0278	0.0017	0.0077	-0.3632**
Gel consistency	-0.0026	-0.0014	-0.0023	-0.0016	0.0007	0.0023	0.0010	0.0163	-0.0006	-0.0481
Amylose content	-0.0014	0.0004	-0.0012	-0.0001	0.0010	0.0006	0.0026	-0.0003	0.0095	-0.2242**
Residual effect = 0.1719										

*- indicates significant at 5 %, **- indicates significant at 1% level. Figures in bold indicates direct effects and normal indicates indirect effects.



DISCUSSION



CHAPTER-V

DISCUSSION

High yielding rice varieties released for lowland cultivation did not solve the problems of nontraditional areas where rice is cultivated as a drilled crop. High yielding dwarf cultivars like Pusa basmati - 1 show severe symptoms of iron chlorosis when grown as a drilled rainfed crop, on black cotton soil.

Attention should be given to breed fertilizer responsive, high yielding varieties with wide genetic base and having quality attributes which determines the preference of the consumers.

The present investigation was undertaken to screen the extent of variability for different yield and grain quality characters in 50 promising genotypes along with iron chlorosis reaction. The results of which are discussed in this chapter.

5.1 Analysis of variance

The analysis of variance for different characters is presented in Table 2 and 3. The treatments i.e. mean sum of squares due to genotypes showed significant differences for all characters under study, suggesting that the genotypes were genetically divergent. This indicates that there is ample scope for selection of promising genotypes from the present gene pool for grain quality and yield contributing characters. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes. These findings are in accordance with the findings of Babu *et al.*, (2012), Dhanwani *et al.*, (2013) and Shejul *et al.*, (2013), who also observed significant variability for yield and its components and grain quality characters in rice.

5.2 Mean performance of genotypes for different quantitative and qualitative characters

Mean performance of genotypes for different characters are given in Table 4, 5, and 6. The genotype PBNR 03-07 was tall in height and had highest flag leaf area. The genotype CR 3690-1-1 had longest panicle length, whereas, genotype PBNR 04-28 had recorded maximum number of effective tillers per plant and number of effective tillers per meter length. The variety Tulasi recorded early in maturity and minimum number of unfilled grains per panicle. The maximum number of filled grains per panicle was recorded in check Avishkar. The genotype RP Bio 4918-166-9 was with lowest test weight whereas, genotype CR 452-23-1-1-1-1 recorded minimum straw yield per plot. However, maximum grain yield per plot was recorded by genotype NDR 1143.

Among the grain quality characters, genotype CRR 596-8-1 had recorded high elongation ratio along with highest elongation index and absorbed significantly more water. The genotype Tulasi has recorded lowest volume expansion ratio. None of the genotype was observed with bold and round grains. Relative density was highest in genotype CRR 617-b-47-3, whereas, genotype PAU 3832-79-4-3-1 recorded highest protein content.

The most preferred level of grain quality parameters like intermediate amylose content, slender grains, and soft gel consistency were recorded in genotypes PBNR 03-07, PBNR 03-20, PBNR 04-28, PBNR 08-04, CRR 596-8-1, CR 3690-1-1, MAULS-15,R 1700-2240-4-2295-1, and UPRI 499-11-2-12-1. These results are in conformity with findings of Das *et al.*, (1989) and Binod *et al.*, (2006).

5.3 Genetic parameters

Knowledge of genetic variability, heritability and genetic advance is pre-requisite for initiating appropriate breeding procedures in crop improvement programme. The heritable variation marked by non heritable variation which creates difficulty in exercising selection. Hence, it becomes necessary to split overall variability into its heritable and non heritable

components with the help of certain genetic parameters which may enable the breeders to plan out proper breeding programme. The results are given in Table 7 and 8.

Since, any character of economic importance is highly influenced by environmental conditions. Improvement in population is mainly depends upon the magnitude of genetic variability present. Genetic variability among yield and yield components in rice genotypes were reported by Agrawal (2003), Panwar and Mathur (2007).

Estimates of GCV were smaller than of PCV for grain yield per plant suggest that influence of environment on them. Similar findings were reported by Panwar and Mathur (2007). But the differences between PCV and GCV for many traits were less, suggesting the less influence of environment for traits like plant height, number of filled grains per panicle, 1000 grain weight and grain yield per plant. These results were confirmatory with Devi *et al.*, (2006), Prajapati *et al.*, (2011), Tuwar *et al.*, (2013).

High values of genotypic and phenotypic coefficient of variation were recorded for grain yield per plant and number of unfilled grains per panicle, this result was confirmatory with Toshimenla (2013). Similarly, characters like grain yield per plot, number of effective tillers per meter and straw yield also showed high GCV and PCV. This result was in accordance with findings of Deosarkar *et al.*, (1989) and Fukrei *et al.*, (2011) and high GCV and PCV for flag leaf area were also observed by Fukrei *et al.*, (2011). Grain quality characters viz. volume expansion ratio, water uptake and gel consistency were with higher GVC and PCV. Similar finding was reported by Dhanwani *et al.*, (2013).

Moderate PCV and GCV were recorded for characters protein content test weight, L:B ratio, plant height, amylose content, elongation ratio and elongation index. Similar results were observed by Dhanwani *et al.*, (2013) for L:B ratio, elongation ratio and elongation index, Subbaiah *et al.*, (2011)

observed for test weight, elongation ratio and L:B ratio and Kundu *et al.*, (2008) reported for test weight.

Wide range of genotypic variation was observed in number of effective tillers per plant and grain yield per plant which indicates the predominance of additive gene effects. These results are in agreement with earlier results reported by Shukla *et al.*, (1972), Kaul and Kumar (1982), Debchoudhary and Das (1998) and Chauhan (1996).

However, low estimates for GCV and PCV were recorded for days to 50% flowering followed by panicle length and days to maturity. Low GCV and PCV values for these traits were also reported by Shivani and Reddy (2000), Devi *et al.*, (2006), Prajapati *et al.*, (2011), Annand Rao *et al.*, (2011) and Singh *et al.* (2011). Low value for days to 50% flowering and panicle length have also been reported by Sinha *et al.*, (2004) and by Sadeghi (2011) days to 50% flowering. Tuwar *et al.*, (2013) also observed similar result for days to maturity.

High estimates of GCV and heritability for grain yield per plant, number of effective tillers per plant and water absorption was observed. Similar, results were also reported earlier by Durai *et al.*, (2001) and Chaudhari *et al.*, (2007).

Number of effective tillers per plant, number of filled grains per panicle, number of unfilled grains per panicle, gel consistency, flag leaf area, straw yield, grain yield per plot and grain yield per plant showed high estimates of PCV, high heritability with high genetic advance as percent of mean, indicated that role of additive gene effects in the inheritance of traits, these results are in conformity with the findings of Govindswami and Ghosh (1973), Kumari *et al.*, (2003) and Selvaraj *et al.*, (2011). Fukrei *et al.*, (2011) observed high PCV, high heritability and high genetic advance as percent of mean for flag leaf area, straw yield and grain yield while Bisne *et al.*, (2009) observed similar result for number of unfilled grains per panicle.

Low genetic advance as percent of mean was recorded by panicle length, days to 50% flowering and days to maturity coupled with moderate heritability. Similar low genetic advance as percent of mean was noted by Babu *et al.*, (2011), Prajapati *et al.*, (2011) and Singh *et al.*, (2011) for panicle length; Pandey *et al.*, (2010) observed for days to 50% flowering, and Sawarkar and Senapati (2014) for days to % flowering and days to maturity.

In the present investigation appreciable amount of GCV, heritability and EGA was observed for quantitative characters, viz., number of effective tillers per plant, number of effective tillers per meter, flag leaf area, number of grains per panicle, grain yield per plant, grain yield per plot and straw yield per plot. The characters that showed high heritability coupled with high genetic advance are controlled by additive gene action (Panse and Sukhatme, 1957) and can be improved through simple or progeny selection methods. The characters showing high heritability coupled with moderate and low genetic advance can be improved by intermitting superior genotypes of segregating population developed from combination breeding (Samadhia, 2005).

Grain elongation without increase in girth is considered highly desirable in some high quality rice. Basmati rice elongates 100 per cent upon cooking. In the present study elongation ratio exhibited high heritability coupled with moderate EGA which was accordance with the findings of Vanaja and Babu (2006) and Subbaiah *et al.*, (2011). Likewise, gel consistency measures the tendency of the gelatinized starch to retrograde on cooking, varieties with soft gel consistency are preferred. High heritability with high EGA was observed for gel consistency indicating that character is controlled by additive gene action and thus selection would be effective for that character. Similar result was also reported by Babu *et al.*, (2012).

The high heritability coupled with high EGA was observed for water absorption, amylose content, relative density, protein content, volume expansion and L:B ratio. Similar findings were also reported by Chouhan and

Nanda (1983), Hussain *et al.*, (1987) and Nayak *et al.*, (2003) for water absorption and amylose content while Babu *et al.*, (2012) observed for L:B ratio and volume expansion ratio. Vanaja and Babu (2006) observed similar results for L:B ratio, volume expansion, water uptake and amylose content.

In the present study significant differences were observed among the genotypes for protein content, range was from 6.54 to 11.82%. Similar, results were also reported by Dalal *et al.*, (2003). High heritability and high EGA was recorded for protein content, which was in contrary with the result observed by Shenoy *et al.*, (1991).

Amylose is absent in the waxy (glutinous) rice, such rice do not expand in volume, become sticky and remain firm when cooked. Non waxy (non glutinous) rice have high (25 to 30%), low (10 to 20%) or intermediate (20 to 25%) amylose content while all the Japonica varieties of temperate region have low amylose content. Intermediate amylose rice is preferred type in most of the rice growing areas of the world. In the present study variation in amylose content (18.53 – 32.52%) have been reported. These results are in conformity with the findings of Singh *et al.*, (2007), Bajpai and Singh (2010).

5.4 Correlations

Correlation coefficient is an important statistical constant which indicates the degree of association among the various characters. For genetic improvement of yield and other characters in any crop, it is essential to know the nature and extent of association of various component characters with yield. It throws light on the evolutionary trend and the direction of divergence in association among a group of characters and enables breeders to programme their approach in manipulating the expression of characters channelizing towards high yield and desirable grain quality characters. The selection based on performance of yield a polygenically controlled character, is not very efficient, but based on the component characters could be more efficient. The results regarding correlation of are shown in Table 9 and 10.

Positive and significant correlation was found between yield per plant and plant height, panicle length, number of effective tillers per plant, number of effective tillers per meter length, flag leaf area, number of filled grains per panicle, 1000 grain weight, straw yield per plot and grain yield per plot. Similar findings were reported by Khan *et al.*, (2009) who reported significant and positive correlation of grain yield per plant with plant height, flag leaf area, number of grains per panicle and panicle length; Watoo *et al.*, (2010) with plant height, number of grains per panicle and flag leaf area; Sadeghi (2011) with plant height, number of effective tillers per meter, panicle length, grains per panicle and 1000 grains weight; Bhadru *et al.*, (2012) with panicle length and number of effective tillers, and Huang *et al.*, (2013) with filled grains per plant, grains per panicle and 1000 grain weight. Shet *et al.*, (2012) also reported positive and significant correlation of grain yield per plant with number of productive tillers, panicle length, number of filled grains per panicle, straw yield and 1000 seed weight.

Grain yield per plant was negatively and significantly correlated with days to 50% flowering, iron chlorosis reaction and days to maturity. Shet *et al.*, (2012) reported significant negative correlation of grain yield with days to 50% flowering. Similarly, Deosarkar (1989) reported that the correlation between grain yield per plant and iron chlorosis reaction was significant and negative, while he suggested negative correlation of grain yield per plant with days to maturity.

The protein content was negatively correlated with yield per plant. Similar findings were also reported by Nayak (2007) and Shejul (2012). Water absorption, gel consistency and protein content had recorded negative association with grain yield per plant. Similar findings were reported by Deosarkar (1985). While, elongation ratio was found to have significant and positive correlation with grain yield per plant.

Volume expansion and water absorption had positive and significant correlation with each other while, water absorption was negatively

and significantly correlated with relative density, which is accordance with result of Deosarkar (1989). Elongation ratio had significant and positive correlation with water absorption and negative significant correlation with amylose content, which is in line with Juliano and Pascual (1980) and Chauhan *et al.*, (1995). In present investigation L:B ratio showed positive and significant correlation with relative density whereas, significant negative correlation was observed with protein content. Similar result was also reported by Shejul (2012).

5.5 Path analysis

Development of dependent variable is decided by the degree of direct effects of independent variables and the indirect effect exerted via other characters. Under such situation the total correlations are insufficient to explain true association for an effective manipulation of the characters. Path analysis involves effective partitioning of direct effects and the intensity of indirect effects of one attribute via other. Direct and indirect effects of different characters on yield per plant were worked out using correlation coefficient and path analysis. Results of path analysis are presented in Table 11 and 12.

In the present study it was observed that number of effective tillers per plant, number of grains per panicle and 1000 grain weight had maximum direct effect on grain yield per plant. Similar results were also reported by Zia *et al.*, (2005), Kishor *et al.*, (2007) and Watoo *et al.*, (2010). Sadeghi *et al.*, (2011) reported similar findings for 1000 grain weight and grains per panicle.

Almost all of the yield contributing characters exerted negative indirect effect on grain yield per plant via iron chlorosis reaction among which indirect effect of number of tillers per plant was highest followed by filled grains per panicle and 1000 grain weight. These results were accordance with Deosarkar (1989).

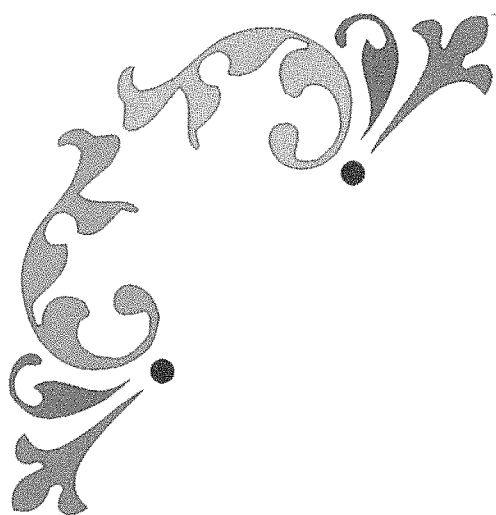
Among quality characters, elongation ratio, L:B ratio and relative density exerted highest positive direct effect on grain yield per plant, whereas direct effect of elongation index was negative. Similar result was reported earlier by Deosarkar (1985), Nandeshwar *et al.*, (2010) and Sanghera *et al.*, (2013) for L:B ratio.

5.6 Conclusions and future line of work

It is presumed that dwarf, high yielding and slender grain rice having quality traits viz., high protein, intermediate amylose and soft gel consistency are the characteristics of rice preferred by people in Maharashtra. The present investigation revealed that genotypes PBNR 03-07, PBNR 03-20, PBNR 04-28, PBNR 08-04, CRR 596-8-1, CR 3690-1-1, MAULS-15, R 1700-2240-4-2295-1, and UPRI 499-11-2-12-1 possess better grain and cooking quality characters including good agronomic traits.

The semi dwarf genotypes Tulasi, NDR 1143, CRR 599-4-1, PBNR 04-28, CRR 3630-1-3, CRR 6614-1-4, PBNR 08-07 and PBNR 03-10 possess maximum number of good attributes and higher grain yield per plant. These genotypes need to be improving for its cooking quality characters. Tall genotypes PBNR 03-07 seemed to be promising but need improvement in some of the quality characters. The genotype NDR 1143 had more yield and protein content than the checks and also possess some good quality characters. The genotypes PAU 3832-79-4-3-1 (11.82%) and UPRI (11.59%) recorded the highest protein content. The promising genotype for yield and grain cooking quality characters requires further study for its confirmation.

Since, most of the traits exhibited high heritability and high expected genetic advance under such situation selection can be effective following intermitting among promising genotypes.



SUMMARY AND CONCLUSION



CHAPTER-VI

SUMMARY AND CONCLUSION

The present investigation was undertaken to test the performance of different promising genotypes for grain yield, yield contributing characters, quality traits and reaction of genotypes to iron chlorosis. The material used for present study comprised of 50 genotypes including 3 check varieties viz., Basmati-370, Parag and Avishkar. The material was raised in Randomized Block Design with three replications, observations were recorded on quantitative character viz., plant height, number of effective tiller per plant, number of effective tillers per metre length, days to 50% flowering, flag leaf area, days to maturity, panicle length, number of filled grains per panicle, number of unfilled grains per panicle, 1000 grain weight, iron chlorosis reaction, grain yield per plant, grain yield per plot and straw yield per plot.

Observations were recorded on quality characteristics of rice grain including elongation index, elongation ratio, L:B ratio, relative density, water absorption, volume expansion ratio, gel consistency, gelatinization temperature, protein and amylose content. The data was analyzed for genotypic and phenotypic coefficient of variation, heritability, expected genetic advance, correlations and path analysis. The results obtained are summarized below.

1. Variability was observed in quantitative traits viz., plant height, number of effective tillers per plant, number of grains per panicle and days to maturity will be very much useful in further breeding program.
2. Analysis of variance among grain quality characters revealed that all the characters studied possess adequate amount of variability for grain quality.
3. The genotype PBNR 04-28 had recorded maximum number of tillers per plant whereas, genotype CR 3690-1-1 had recorded highest panicle length.

4. The variety Tulasi was early in maturity and recorded minimum number of unfilled grains per panicle.
5. High values of genotypic and phenotypic coefficient of variation were recorded for grain yield per plant, number of unfilled grains per panicle, grain yield per plot, number of effective tillers per meter and straw yield.
6. The high GCV and PCV were recorded for grain quality characters viz., volume expansion, water absorption and gel consistency.
7. Number of effective tillers per plant, number of filled grains per panicle, number of unfilled grains per panicle, gel consistency, flag leaf area, grain yield per plant, grain yield per plot and straw yield per plot showed high estimates of PCV and high heritability with high genetic advance as percent of mean, indicated that role of additive gene effects in the inheritance of traits and can be improved through simple or progeny selection methods.
8. Significant differences were observed for all the qualitative characters viz., elongation ratio, elongation index, L:B ratio, relative density, water absorption, gel consistency, protein content and amylose content.
9. High heritability coupled with high to moderate expected genetic advance was observed for elongation ratio and high heritability coupled with high EGA was observed for water absorption, amylose content, relative density, protein content, volume expansion and L:B ratio indicating scope for selection in these grain quality characters.
10. The maximum protein content was recorded in the genotype PAU 3832-79-4-3-1 (11.81%) followed by the UPRI 2012-16 (11.59%) and CB 09-513 (11.32%).

11. The most preferred level of grain quality parameters like intermediate amylose content, slender grains, and soft gel consistency were recorded in genotypes PBNR 03-07, PBNR 03-20, PBNR 04-28, PBNR 08-04, CRR 596-8-1, CR 3690-1-1, MAULS-15, R 1700-2240-4-2295-1, and UPRI 499-11-2-12-1.
12. Genotypic and phenotypic correlation studies revealed that plant height, panicle length, number of effective tillers per plant, number of effective tillers per meter length, flag leaf area, number of filled grains per panicle, 1000 grain weight, grain yield per plot and straw yield per plot showed positive and significant correlation with grain yield per plant. Whereas, significant negative correlation was recorded by days to 50% flowering, days to maturity, iron chlorosis reaction and number of unfilled grains per panicle.
13. The path analysis studies revealed that characters like number of effective tillers per plant and number of grains per panicle had maximum direct effect on grain yield per plant.
14. The genotypes Tulasi, NDR 1143, CRR 599-4-1, PBNR 04-28, CRR 3630-1-3, CRR 6614-1-4, PBNR 08-07 and PBNR 03-10 possess maximum number of good attributes and higher grain yield per plant need to be improved for its grain quality characters.
15. The genotypes like OR 2172-7-1, RP 5214-18-6-2-1-1-1-B, CR 2991-1-2-1-1-1, CB 09-516, RP Bio 4918-166-9 and R-RF-48 showed severe symptoms of iron chlorosis Vertisols.

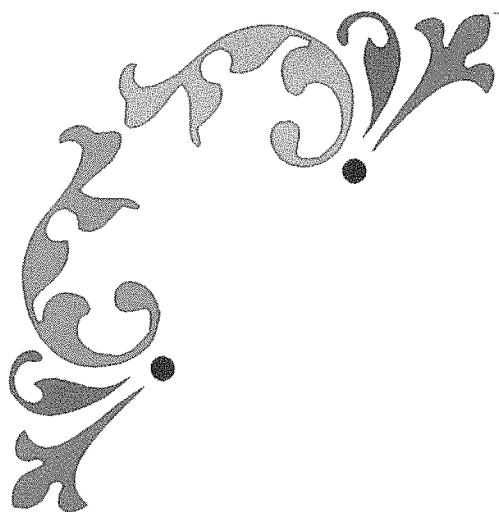
Conclusion

It is presumed that dwarf, high yielding, tolerant to iron chlorosis and slender grain rice having quality traits viz., high protein, intermediate amylose and soft gel consistency are the characteristics of rice preferred by people of Maharashtra. The present investigation revealed that the genotypes PBNR 03-07, PBNR 03-20, PBNR 04-28, PBNR 08-04, CRR 596-8-1, CR 3690-1-1, MAULS-15, R 1700-2240-4-2295-1, and UPRI 499-11-2-12-1, showed grain yield and better cooking characters.

The semi dwarf genotypes Tulasi, NDR 1143, CRR 599-4-1, PBNR 04-28, CRR 3630-1-3, CRR 6614-1-4, PBNR 08-07 and PBNR 03-10 possess maximum number of good attributes for grain yield and these genotypes need to be improved for its grain quality characters. The maximum protein content was recorded in the genotypes PAU 3832-79-4-3-1 (11.81%) followed by UPRI 2012-16 (11.59%) and CB 09-513 (11.32%).

The genotypes like OR 2172-7-1, RP 5214-18-6-2-1-1-B, CR 2991-1-2-1-1-1, CB 09-516, RP Bio 4918-166-9 and R-RF-48 showed severe symptoms of iron chlorosis resulting reduction of grain yield. The tolerant genotypes PBNR 03-10, GK 5022, PBNR 04-28, TJP 148, R 2212-RF-75, CRR 596-8-1, BAU 408-05, PBNR 03-07, MAULS-15, PBNR 08-07, CRR 614-4-1, PBNR 08-04 and PBNR 03-20 can be used in breeding program.

Since, most of the traits exhibited high heritability and high expected genetic advance under such situation selection can be effective following intermitting among promising genotypes.



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LITERATURE CITED

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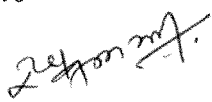
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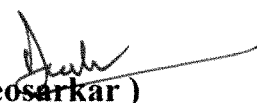
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THESIS ABSTRACT

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- b) Name of student : Rajeev Dhakal
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ABSTRACT

The present investigation was under taken on, "Screening of rice genotypes (*Oryza sativa* L.) for yield, quality characters and iron chlorosis on Vertisols". The experiment consisted of 50 promising genotypes along with standard checks viz., Basmati-370, Parag and Avishkar were grown in randomized block design with three replications.

Observations were recorded for ten yield contributing characters, iron chlorosis reaction and physio-chemical characters. The correlations were carried out to study the association between yield components with grain yield per plant and path analysis was worked out to study the direct and indirect effects of these characters on grain yield.

The analysis of variance revealed that there were significant differences among the genotypes for all the characters studied. Additive gene effects were predominant for characters number of effective tillers per plant, number of filled grains per panicle, number of unfilled grains per panicle, gel consistency, flag leaf area, straw yield, grain yield per plot and grain yield per plant.

The genotypes PBNR 03-10, GK 5022, PBNR 04-28, TJP 148, R 2212-RF-75, CRR 596-8-1, BAU 408-05, PBNR 03-07, MAULS-15, PBNR 08-07, CRR 614-4-1, PBNR 08-04 and PBNR 03-20 showed tolerant reaction to iron chlorosis.

The genotypes PBNR 03-07, PBNR 03-20, PBNR 04-28, PBNR 08-04, CRR 596-8-1, CR 3690-1-1, MAULS-15, R 1700-2240-4-2295-1, and UPRI 499-11-2-12-1 were having preferred level of grain quality parameters like intermediate amylose content and soft gel consistency. The maximum protein content was recorded in genotypes PAU 3832-79-4-3-1, UPRI 2012-16 and CB 09-513.

The study of correlation revealed that plant height, panicle length, number of effective tillers per plant, number of effective tillers per meter length, flag leaf area, number of filled grains per panicle and 1000 grain weight had positive and significant association with grain yield per plant, however, significant negative correlation was recorded by days to 50% flowering, days to maturity, iron chlorosis reaction and number of unfilled grains per panicle.

Whereas, path analysis indicated that number of effective tillers per plant exerted the highest positive direct effect on grain yield per plant followed by number of grains per panicle.

APPENDIX – I**WEEKLY WEATHER DATA 2013**

WK	Period	Rainfall (mm)	R.D.	Temperature °C		Humidity (%)	
				Max.	Min.	AM	PM
22	28-03 June	0.0	0.0	40.4	27.6	52	25
23	04-10 June	107.5	4.0	34.9	23.3	86	55
24	11-17 June	29.2	2.0	31.4	22.9	86	66
25	18-24 June	24.0	1.0	33.3	23.0	85	61
26	25-01 July	41.8	3.0	30.1	22.5	85	64
27	02-08 July	80.1	4.0	32.1	22.6	92	62
28	09-15 July	96.4	4.0	29.2	22.7	90	79
29	16-22 July	154.0	5.0	26.7	22.0	93	84
30	23-29 July	50.5	2.0	29.4	22.6	86	65
31	30-05 Aug	77.5	3.0	28.3	21.8	91	75
32	06-12 Aug	19.7	2.0	29.8	22.5	89	67
33	13-19 Aug	59.8	4.0	30.5	22.7	91	65
34	20-26 Aug	9.3	2.0	28.5	21.7	89	71
35	27-02 Sept	0.0	0.0	31.0	22.9	82	59
36	03-09 Sep	29.8	1.0	33.1	22.6	85	61
37	10-16 Sep	84.5	5.0	32.0	22.2	92	63
38	17-23 Sep	150.6	5.0	30.2	22.4	93	67
39	24-30 Sep	0.0	0.0	32.2	22.0	86	53
40	01-07 Oct.	40.8	4.0	31.5	22.8	89	64
41	08-14 Oct.	66.2	5.0	30.7	21.7	93	70
42	15-21 Oct.	0.0	0.0	32.5	19.5	83	46
43	22-28 Oct.	10.3	2.0	30.8	21.2	85	56
44	29-04 Nov.	0.0	0.0	31.7	15.0	78	37
45	05-11 Nov.	0.0	0.0	30.4	13.3	71	36
46	12-18 Nov.	0.0	0.0	29.2	12.1	79	35
47	19-25 Nov.	14.0	2.0	30.4	14.5	81	41
48	26-02 Dec.	0.0	0.0	30.7	15.9	75	43
49	03-09 Dec.	26.6	1.0	29.0	12.3	84	35
Total		1172.6	61	—	—	—	—