

**GENETIC EVALUATION FOR CYTOPLASMIC
INHERITANCE OF MORPHOMETRIC TRAITS
AND GRAIN QUALITY PARAMETERS IN
RECIPROCAL CROSSES OF RICE (*Oryza sativa* L.)**

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**DEPARTMENT OF GENETICS AND PLANT BREEDING
UNIVERSITY OF AGRICULTURAL SCIENCES
BANGALORE**

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Thesis submitted to the

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In partial fulfillment of the requirements

for the award of the Degree of

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Affectionately
Dedicated to
My Beloved Parents,
Brothers, Sisters
and Farmers

**DEPARTMENT OF GENETICS AND PLANT BREEDING
UNIVERSITY OF AGRICUTURAL SCIENCES
BANGALORE**

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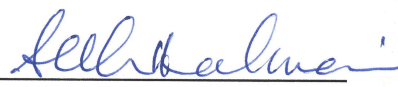
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February, 2021


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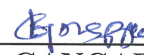
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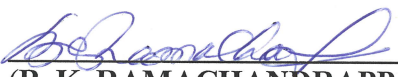
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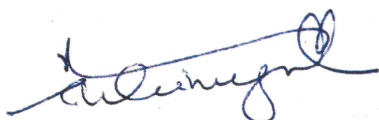
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(Yallappa Harijan)

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YALLAPPA HARIJAN

ABSTRACT

Reciprocal crosses play an important role in identification of cytoplasmic effect and to choose right breeding programme for population improvement and development of new hybrids to meet global demand for food. In the present study, F₂ and F₃ population of straight (BPT-5204 × HPR-14) and reciprocal (HPR-14 × BPT-5204) crosses along with parents were evaluated for growth and yield-attributing traits, disease resistance and grain nutrient traits. Significant differences between mean performance of 50% flowering, number of productive tillers, biomass, grain iron and carbohydrate content in straight and reciprocal F₂ and F₃ population were revealed cytoplasmic effect. Higher transgressive segregants for yield attributing and grain nutrient traits was observed in straight F₂ and F₃-populations compared to reciprocal crosses. Straight F₂ and reciprocal F₃ populations showed higher GCV and PCV for most of the traits. Number of tillers, number of productive-tillers, biomass and harvest index exhibited high PCV, GCV coupled with high-heritability and GAM. Inter-generation association indicated that grain yield plant⁻¹ exhibited significant positive correlation with plant height, productive tillers, panicle length and grain zinc content in both the crosses. Panicle exertion and grain carbohydrate content showed highest positive direct effect on grain yield⁻¹ in reciprocal F₂ and F₃ populations. Genetic basis of anthocyanin pigmentation of basal leaf sheath colour and spikelets tip revealed monogenic inheritance (3:1) and leaf blade colour as inhibitory gene action (3:13). Most of F₂ and F₃-populations with less infestation of brown spot, sheath blight and sheath rot diseases. Fifteen mitochondrial and chloroplast specific SSRs showed polymorphism between parents, which could be utilized further to check cytoplasmic effects in the progenies. Multitrait selection index identified superior RIL's (top ranked F₃ families) in straight (1,2,6,18,21) and in reciprocal (10,87,96,98,100) crosses for all the traits and those families could be utilized for developing breeding lines for improvement of the traits.

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ಭತ್ತದ (ಒರೈಜಾ ಸಟ್ವೆವಾ ಎಲ್.) ವ್ಯತ್ಯಮ ಸಂಕರಣ ತಳಿಗಳಲ್ಲಿ ಬಾಹ್ಯರೂಪ ಲಕ್ಷಣಗಳು ಮತ್ತು ಧಾನ್ಯಗಳ ಗುಣಮಟ್ಟ ಸ್ಥಿರರಾಶಿಗಳಿಗೆ ಸಂಬಂಧಿಸಿದ ಕೋಶದ್ರವ್ಯದ ವಂಶವಾಹಿ ಗುರುತಿಸುವಿಕೆ ಮತ್ತು ಅನುವಂಶಿಕ ಮೌಲ್ಯ ಮಾಪನ ಬಗ್ಗೆ ಅಧ್ಯಯನ

ಯಲ್ಲಪ್ಪ ಹರಿಜನ

ಸಾರಾಂಶ

ಕೋಶದ್ರವ್ಯದ ಪರಿಣಾಮವನ್ನು ಗುರುತಿಸುವಲ್ಲಿ ಸರಿಯಾದ ತಳಿ ಅಭಿವೃದ್ಧಿ ಕಾರ್ಯಕ್ರಮವನ್ನು ಆಯ್ಕೆಮಾಡಲು ಮತ್ತು ಆಹಾರಕ್ಕಾಗಿ ಜಾಗತಿಕ ಬೇಡಿಕೆಯನ್ನು ಪೂರೈಸಲು ಹೊಸ ಮಿಶ್ರತಳಿ ಅಭಿವೃದ್ಧಿಗೆ ವ್ಯತ್ಯಮ ಸಂಕರಣ ತಳಿಗಳು ಪ್ರಮುಖ ಪಾತ್ರವಹಿಸುತ್ತವೆ. ಪ್ರಸ್ತುತ ಸಂಶೋಧನೆಯಲ್ಲಿ, ಎಫ್-೨ ಮತ್ತು ಎಫ್-೩ ಒಟ್ಟು ಜೀವಗುಂಪುಗಳನ್ನು ಮೂಲ ತಳಿಗಳ ಜೊತೆಗೆ ನೇರ (ಬಿಪಿಟಿ-೫೨೦೪ × ಹೆಚ್‌ಪಿಆರ್-೧೪) ಮತ್ತು ವ್ಯತ್ಯಮ (ಹೆಚ್‌ಪಿಆರ್-೧೪ × ಬಿಪಿಟಿ-೫೨೦೪) ಸಂಕರಣಗಳನ್ನು ಬೆಳೆವಣಿಗೆ ಮತ್ತು ಇಳುವರಿ ಗುಣಲಕ್ಷಣಗಳು, ರೋಗ ನಿರೋಧಕತೆ ಮತ್ತು ಧಾನ್ಯ ಪೋಷಕಾಂಶಗಳಿಗಾಗಿ ಮೌಲ್ಯಮಾಪನ ಮಾಡಲಾಗಿದೆ. ೫೦ ಪ್ರತಿಶತ ಹೂಬಿಡುವಿಕೆ, ಉತ್ಪಾದಕ ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ, ಜೈವಿಕರಾಶಿ, ಧಾನ್ಯಗಳ ಕಬ್ಬಿಣಾಂಶ ಮತ್ತು ಶರ್ಕರ ಪಿಷ್ಟಗಳ ಸರಾಸರಿ ಕಾರ್ಯಕ್ರಮತೆಯ ನಡುವಿನ ಗಮನಾರ್ಹ ವ್ಯತ್ಯಾಸವು ಎಫ್-೨ ಮತ್ತು ಎಫ್-೩ ಒಟ್ಟು ಜೀವಗುಂಪುಗಳಲ್ಲಿ ಕೋಶದ್ರವ್ಯದ ಪರಿಣಾಮವನ್ನು ಬಹಿರಂಗ ಪಡಿಸಿದೆ. ವ್ಯತ್ಯಮ ಸಂಕರಣಗಳಿಗೆ ಹೋಲಿಸಿದರೆ ಇಳುವರಿ ಮತ್ತು ಧಾನ್ಯ ಪೋಷಕಾಂಶಗಳ ಗುಣಲಕ್ಷಣಗಳಿಗಾಗಿ ಹೆಚ್ಚಿನ ಅತಿಕ್ರಮೀ ಪೃಥಕ್ರಣಗಳನ್ನು ನೇರ ಎಫ್-೨ ಮತ್ತು ಎಫ್-೩ ಒಟ್ಟುಜೀವಗುಂಪುಗಳಲ್ಲಿ ಹೆಚ್ಚಿನ ಗುಣಲಕ್ಷಣಗಳಿಗೆ ಅಧಿಕ ವಂಶವಾಹಿ ಮತ್ತು ದೃಶ್ಯರೂಪಿ ವ್ಯತ್ಯಸ್ಥ ಸಹಗುಣಾಂಕಗಳನ್ನು ತೋರಿಸಿದೆ. ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ, ಉತ್ಪಾದಕ ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ, ಜೈವಿಕರಾಶಿ ಮತ್ತು ಸುಗ್ಗಿಯ ಸೂಚ್ಯಂಕವು ಹೆಚ್ಚಿನ ವಂಶವಾಹಿ ಮತ್ತು ದೃಶ್ಯರೂಪಿ ವ್ಯತ್ಯಸ್ಥ ಸಹಗುಣಾಂಕಗಳ ಜೊತೆಗೆ ಹೆಚ್ಚಿನ ಅನುವಂಶಿಕತೆ ಮತ್ತು ಸರಾಸರಿ ವಂಶವಾಹಿ ಮುಂಗಡವನ್ನು ಪ್ರದರ್ಶಿಸಿದೆ. ಅಂತರಪೀಳಿಗೆ ಕೂಡಿಕೆಯ ಪ್ರಕಾರ, ಧಾನ್ಯದ ಇಳುವರಿ ಜೊತೆಗೆ ಸಸ್ಯದ ಎತ್ತರ, ಉತ್ಪಾದಕ ತೆಂಡೆಗಳು, ಪುಷ್ಪಗುಚ್ಚದ ಉದ್ದ ಮತ್ತು ಧಾನ್ಯದ ಸತುವು ಎರಡೂ ಸಂಕರಣಗಳಲ್ಲಿ ಗಮನಾರ್ಹ ಸಕಾರಾತ್ಮಕ ಸಂಬಂಧವನ್ನು ಹೊಂದಿದೆ. ಪುಷ್ಪಗುಚ್ಚದ ಹೊರನುಲಿಕೆ ಮತ್ತು ಧಾನ್ಯದ ಶರ್ಕರ ಪಿಷ್ಟವು ವ್ಯತ್ಯಮ ಎಫ್-೨ ಮತ್ತು ಎಫ್-೩ ಒಟ್ಟು ಜೀವಗುಂಪುಗಳಲ್ಲಿ ಧಾನ್ಯದ ಇಳುವರಿ ಮೇಲೆ ಹೆಚ್ಚಿನ ಸಕಾರಾತ್ಮಕ ನೇರ ಪರಿಣಾಮವನ್ನು ತೋರಿಸಿದೆ. ಸಸ್ಯತಳದ ಎಲೆಪೊರೆ ಬಣ್ಣ ಮತ್ತು ಉಪಗುಚ್ಚದ ತುದಿಯ ಆಂಥೋಸಯಾನಿನ್ ವರ್ಣದ್ರವ್ಯದ ಅನುವಂಶಿಕ ಆಧಾರವು ಏಕವಂಶವಾಹಿ ಅನುವಂಶಿಕತೆಯನ್ನು (೩:೧) ಮತ್ತು ಎಲೆಯಲಗುವಿನ ಬಣ್ಣವನ್ನು ಪ್ರತಿಬಂಧಕ ವಂಶವಾಹಿ ಕ್ರಿಯೆಯಾಗಿ ಬಹಿರಂಗಪಡಿಸಿದೆ (೩:೧೩) ಹೆಚ್ಚಿನ ಎಫ್-೨ ಮತ್ತು ಎಫ್-೩ ಒಟ್ಟು ಜೀವಗುಂಪುಗಳಲ್ಲಿ ಕಡಿಮೆ ಕಂದುಚುಕ್ಕೆ, ಕವಚ ಅಂಗಮಾರಿ ಹಾಗೂ ಎಲೆ ಕವಚ ಕೊಳೆರೋಗಗಳಿಂದ ಕೂಡಿದೆ. ಹದಿನೈದು ಸೂತ್ರಕಣಿಕಾ ಮತ್ತು ಹರಿದ್ರೇಣು ನಿರ್ದಿಷ್ಟಸರಳ ಅನುಕ್ರಮ ಪುನರಾವರ್ತಿಸಿ (ಎಸ್‌ಎಸ್‌ಆರ್) ಬಳಸಿಕೊಂಡು ಮೂಲ ತಳಿಗಳ ನಡುವೆ ಬಹುರೂಪತೆಯನ್ನು ತೋರಿಸಿವೆ. ಇವುಗಳನ್ನು ಸಂತತಿಗಳಲ್ಲಿ ಕೋಶದ್ರವ್ಯ ಪರಿಣಾಮವನ್ನು ಪರೀಕ್ಷಿಸಲು ಬಳಸಿಕೊಳ್ಳಬಹುದು. ಬಹುಗುಣಲಕ್ಷಣ ಆಯ್ಕೆ ಸೂಚ್ಯಂಕವು ಉನ್ನತ ಮರುಸಂಯೋಗ ಒಳಸಂಕರಣ ಸಾಲಿಗಳನ್ನು (ಉನ್ನತ ಶ್ರೇಯಾಂಕಿತ ಎಫ್-೩ ಕುಟುಂಬಗಳು) ನೇರ (೧, ೨, ೯, ೧೮, ೨೧) ಮತ್ತು ವ್ಯತ್ಯಮ (೧೦, ೮೩, ೯೬, ೯೮, ೧೦೦) ಸಂಕರಣಗಳಲ್ಲಿ ಗುರುತಿಸಲಾಗಿದೆ ಮತ್ತು ಅವುಗಳನ್ನು ಗುಣಲಕ್ಷಣಗಳ ಸುಧಾರಣೆಯೊಂದಿಗೆ ತಳಿ ಅಭಿವೃದ್ಧಿ ಪಡಿಸಲು ಬಳಸಿಕೊಳ್ಳಬಹುದು.

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ಬೆಂಗಳೂರು-೫೬೦೦೬೫

ಡಾ|| ಶೈಲಜಾ ಹಿತ್ತಲಮನಿ
(ಮುಖ್ಯ ಸಲಹೆಗಾರರು)

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I INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important crop plants that feed more people than any other plant species occurring in the world. Asia is considered as the ‘Rice Bowl’ of the world as more than 90 % of rice is produced and consumed in Asia. In developing countries, rice accounts for 715 kcal/capita/day, 27 *per cent* of dietary energy supply, 20 *per cent* of dietary protein and 3 *per cent* of dietary fat. More than 80% daily calorie and 75% required protein is obtained from rice in Asia. World rice production is around 498.65 million metric tons grown in over 163.51 mha with productivity of 4.55 tonnes ha⁻¹ (USDA, 2019). In India rice is cultivated in over an area of 44.50 mha with a production of 115.63 million metric tons with an average of around 3.90 tonnes ha⁻¹ (USDA, 2019). Andhra Pradesh, Bihar, West Bengal, Tamil Nadu, Punjab Uttar Pradesh and Karnataka are important rice growing states in India. At the current rate of population growth in India, it is estimated that net rice production should be around 135 to 140 million tonnes by 2020. So it is critical to produce high yielding cultivars with high quality by inbreeding methods (Jondhale *et al.*, 2018).

Rice is rich in genetic diversity and known to have more than 1,27,000 germplasm in the world (IRRI, 2017). Landraces provides a vast genetic variability for the present day rice improvement programme. Though domesticated, un-adapted landraces possess several undesirable agronomic traits leading to low yield. Diverse plant types are immediately valuable for shaping new varieties and this forms the basic wealth on which plant breeders can operate for reconstructing the existing genotypes (Sujay, 2007). To meet the increasing demand, rice production must be increased with less land, less water using less pesticide in a sustainable way (Anandan *et al.*, 2009). Among the different options available to increase yield, exploiting the variability present in segregating populations is important for improving plant types through selection.

To increase the present levels of grain yield, quality and other traits there is ample need to identify and utilize genetically divergent parents for inter and intra sub specific and reciprocal crosses in rice. Among the many factors for rice production, cytoplasmic gene effect or maternal gene effect is more useful in three-line hybrid seed production in

rice where cytoplasmic genes control male sterility, where information on the inheritance of polygenic and oligogenic traits is useful for planning and executing a breeding strategy leading to their genetic improvement. So, identification of maternal effect in reciprocal crosses also helpful to identify some traits which are controlled by cytoplasmic genes and useful for development of new high yielding cultivars.

Reciprocal crosses play an important role in choosing the right breeding programme for population improvement and development of new hybrids in the crop. Both female and male parents contribute genes to their offspring, but the influence of female parent often extends beyond simple genetic transmission (Munganyinka *et al.*, 2015). The reciprocal effect for a trait is based on the assumption that the F_2 plants from direct crosses and reciprocal crosses have same mean value for the trait under study. If the difference exists between F_2 and its reciprocal F_2 population, it likely indicates the maternal effects and this contributes accordingly for the design and interpretation of genetic studies (Mosjidis and Yermanos, 1984). Using reciprocal crosses, maternal effects have been reported for many characters in rice, including filled-grains and grain weight (Toa *et al.*, 2011), grain quality trait (Asfaliza *et al.*, 2012), milling quality traits (Shi and Zhu 1995), protein content (Shi *et al.*, 1996), hybrid vigor (Virmani, 1994) and crossability (IRRI, 1993). In disease resistance studies, the maternal effects were reported to direct the inheritance of resistance to rice bacterial blight in some combinations (Habarurema *et al.*, 2012). Diversity of the germplasm has been disclosed to be related to the manifestation of cytoplasmic differences in the expression of various characters (Kalsy and Sharma, 1972).

Rice is affected by many diseases and cause significant yield losses i.e. 25-30 % per annum in many rice growing areas (Jha *et al.*, 2012). Among all the diseases of rice, the most common and severe diseases are blast and sheath blight (Wopereis *et al.*, 2009). Sheath blight fungus can reduce yield by up to 50 % under favourable environmental conditions (Richa *et al.*, 2016). It has been documented that rice cultivation under aerobic conditions resulted in 27.5% yield reduction over flooded rice due to brown spot disease (Patel *et al.*, 2010). All the diseases can be managed by the use of fungicides, resistant cultivars, agronomic practices and biotechnological methods (Ribot *et al.*, 2008).

However, the use of resistant cultivars is the most economical and environment friendly method for the management of rice diseases (Waheed *et al.*, 2009).

DNA markers are useful tools in identification of desired trait in plants or organisms. They help to find out association if any for selection (Hittalmani *et al.*, 1995) and help in pyramiding of the traits. Mitochondrial markers may help to find out there is any cytoplasmic inheritance for the traits under study. Further, they could also be useful for selection for traits. The use of chloroplast (cp) DNA and / or mitochondrial (mt) DNA polymorphisms to investigate evolutionary phenomena requires a knowledge of the mode of organellar inheritance. For example, the frequent occurrence of uniparental inheritance of organellar genomes results in a characteristic decrease in the expected level of standing organellar variation in a population (as compared to the biparental case; Birky *et al.*, 1989). In addition, to the extent that they are uniparentally inherited. Organellar polymorphisms can provide insights into phenomena such as sex-biased gene flow (McCauley, 1994) and the directionality of introgression in populations of hybrid origin (Edwards-Burke *et al.*, 1997).

Considering above criteria, the present investigation entitled “Genetic evaluation for cytoplasmic inheritance of morphometric traits and grain quality parameters in reciprocal crosses of rice (*Oryza sativa* L.)” was undertaken with following objectives

1. To identify the genetic variation among the reciprocal crosses for morphological characters and grain nutrient traits.
2. To estimate the inter-generation association for grain nutrient and yield attributing traits in reciprocal crosses.
3. To identify desirable RILs for grain quality, disease and yield attributing traits in F₂ and F₃ generation.
4. To validate mitochondrial and chloroplast specific SSRs in parents BPT 5204 & HPR-14.

II REVIEW OF LITERATURE

Crop improvement depends on the available genetic variability and the extent to which the traits are heritable. A wide survey of genetic variability and a thorough understanding of genetic makeup of the crop with the help of biometrical tools are indispensable for initiating an effective breeding programme. Variation in an individual's phenotype maybe determined not only by the genotype and environment of that individual but also by maternal effects, *i.e.* the contribution of the maternal parent to the phenotype of its progenies beyond the equal chromosomal contribution expected from each parent. Maternal effects will increase the amount of environmental noise and thus slow the response to selection. Cytoplasmic or nuclear genetic maternal effects will inflate the amount of genetic variance but may slow the response to selection if the trait is completely under maternal control. Based on these facts available, there felt an immense need to study and understand the phenomenon of cytoplasmic inheritance in rice. In order to improve the efficiency of breeding for rice nutrient quality, understanding variation of gene expression in different organelles is necessary.

The available literature pertaining to the objectives outlined for the present study were comprehensively reviewed and presented under the following headings.

- 2.1 Assessment of genetic variability in rice
- 2.2 Genetic correlation and association studies for grain yield & other related traits.
- 2.3 Assessment of intergeneration correlation for yield and related traits in rice.
- 2.4 Screening for diseases resistance in segregating populations of rice.
- 2.5 Estimation of protein and other grain quality parameters.
 - 2.5.1 Estimation of phytic acid content in rice.
- 2.6 Identification of reciprocal differences among the segregating generation of rice.
- 2.7 Identification or validation of organelle specific markers in reciprocal crosses of rice.

2.1 Assessment of genetic variability in rice.

The basic requirement of plant breeding is the presence of genetic variability. Importance of genetic variability in any breeding material is a prerequisite as it provides not only a basis for selection but also some valuable information regarding selection of diverse parents for use in hybridization programme. Variability in rice, before it became a subject of study by plant breeder was the concern of taxonomists such as Linnaeus (who gave the generic name '*Oryza*'), De Candolle (1886), Camus (1920), Roschevich (1932) and Chatterjee (1947).

Venkataramana and Hittalmani (1999) evaluated two F_2 crosses of rice and observed high GCV for grain yield, total tillers and productive tillers per plant and high phenotypic and genotypic variability (51.89 and 44.10 %) for grain yield per plant, productive tillers per plant (52.78 and 43.25) and for panicle exertion (39.71 and 32.00 %) respectively.

Genetic variability and estimates of broad sense heritability observed in F_2 population of rice were reported to be significant by Ali *et al.* (2000) for plant height, spikelet density, number of spikelets per panicle, number of grains per panicle, 100 grain weight and grain yield per plant. Heritability estimates were also maximum for plant height, 100 seed weight, number of tillers per plant, panicle length and spikelet density but maximum genetic gain relative to the mean was expected for number of tillers per plant, plant height and spikelet density.

Verma *et al.* (2000) reported that the higher magnitude of GCV and PCV were observed for number of sterile and total spikelets per panicle, grain yield, biological yield, number of productive and total tillers per plant.

Rao *et al.* (2001) revealed that panicle number followed by grains per panicle exhibited high coefficient of variation, whereas, days to maturity and plant height showed least coefficient of variation.

Singh *et al.* (2002) conducted experiment on variability study of quantitative characters in 52 genotypes of lowland rice. The genotypic and phenotypic variances were high for grain yield per plant, panicle weight, number of grains per panicle and number of branches per panicle, grains per panicle and 100 seed weight and low for panicle length.

Shanthi and Singh (2002) evaluated sixteen F₆ progenies of induced mutants of rice and reported high heritability in broad sense (more than 80%) for plant height, panicle length, number of grains per panicle, 1000-grain weight with the exception of grain yield per plant (78.99%) and number of tillers per plant (63.04%). High heritability coupled with high genetic advance was observed for plant height, number of grains per panicle and 1000-grain weight indicating that these characters were governed mainly by additive genetic effects.

In a study of 10 parents and their nine F₂ populations, Suresh and Reddy (2002) reported moderate to high GCV and PCV values for productive tillers per plant, grains per panicle and grain yield per plant. High heritability coupled with high genetic advance was observed for plant height.

Mishra and Verma (2002) studied 16 rice parental cultivars and 72 F₁ progenies. They reported that the PCV was higher than the GCV for twenty quality characters. Kernel elongation ratio recorded the highest magnitude of GCV followed by biological yield per plant and grain yield per plant. Genetic advance as percentage of the mean was highest for kernel elongation ratio and lowest for grain yield per plant. Plant height, 100-grain weight, head rice recovery percentage, spikelet density, kernel breadth after cooking and kernel elongation ratio showed high heritability coupled with high genetic advance, indicating the role of additive genetic variance in the expression of these traits.

Agrawal (2003) in a study of seven parental lines and their 21 F₂ populations in rice observed highest GCV and PCV for yield per plant. Further, high heritability with high genetic advance was noticed for grain weight per panicle, yield per plant and number of grains per panicle suggesting that improvement in these characters may be possible by direct selection. However, days to flowering, days to maturity, tillers per

plant and panicle length exhibited high heritability but low genetic advance indicating that selection for these characters must be made in advance generations.

Khedikar *et al.* (2003) studied genetic variability for seven characters viz., days to 50 *per cent* flowering, plant height, effective tillers per plant, panicle length, testweight, head rice recovery and grain yield per plant in 20 scented rice genotypes grown under three different environments. The PCV was higher than GCV among all characters, indicating that the variation among them is not only due to genetic content but also due to the influence of environment.

Chaudhary and Motiramani (2003) evaluated 54 traditional aromatic rice accessions. A wide range of variation was recorded for most of the characters. The highest phenotypic coefficient of variation was observed for spikelets sterility *per cent* followed by 100 seed weight, biological yield and grain yield per plant, fertile spikelets per panicle and effective tillers per plant.

Sharma and Bhuyan (2004) studied the genetic variation in 58 rice genotypes, consisting mostly of indigenous and improved. They reported highest PCV and GCV being exhibited by the number of grains per panicle followed by grain yield per plant and number of effective panicles per plant.

Raju *et al.* (2004) evaluated F₂ population of 21 crosses of rice and reported high PCV, GCV and heritability for productive tillers per plant and 100 grain weight coupled with high genetic advance.

Hasib *et al.* (2004) reported good correspondence between phenotypic and genotypic coefficient of variation for plant height, tillers per plant, panicle length, filled grains per panicle, grain length, 1000-grain weight and grain yield per plant. While, Sharma and Bhuyan (2004) revealed highest genotypic as well as phenotypic coefficient of variation by the grains per panicle, followed by grain yield per plant and effective panicles per plant.

Sanjeev Kumar *et al.* (2005) in a study of F₁ and F₂ generation of rice cross reported moderate genotypic coefficient of variation but high heritability in broad sense and genetic advance for 100 grain weight.

Mall *et al.* (2005) revealed highly significant differences among the 35 genotypes for all the characters studied. A wide range of variation was observed for mean values of plant height, days to panicle initiation, days to 50 *per cent* flowering, number of tillers per plant, number of panicles per plant, number of spikelets per panicle, panicle length, flag leaf length and flag leaf width.

Bisne *et al.* (2006) observed high GCV for filled spikelets per panicle, chaffy spikelets per panicle, spikelet fertility percentage, 100 grain weight, harvest index and grain yield per plant.

In seven F₂ populations of inter sub-specific crosses of rice evaluated by Vaithiyalingan and Nandarajan (2006), grain yield showed high genotypic coefficient of variation followed by spikelet fertility *per cent*, productive tillers per plant and number of grains per panicle. The grain yield per plant and productive tillers possessed high genetic advance with high heritability.

Verma *et al.* (2006) observed high estimates of narrow-sense heritability for grain yield per plant and panicle length and days to 50 *per cent* flowering in F₂ generation of a rice cross.

Veni *et al.* (2006) reported that kernel length, kernel breadth and length breadth ratio showed higher variability estimates in hybrids than in parents both at genotypic and phenotypic level.

Bharadwaj *et al.* (2007) reported significant genetic variability between the F₂ generations of three crosses of rice for days to maturity, plant height, panicle length, 1000-grain weight, productive tillers per plant and grain yield per plant. High heritability estimates coupled with high genetic advance as *per cent* of mean was also noticed in all the crosses for days to 50 *per cent* flowering, days to maturity, plant height, panicle

length and 1000-grain weight. Spikelets per panicle and filled grains per panicle had moderate heritability and high genetic advance. Productive tillers per plant and grain yield per plant had low to moderate heritability coupled with low to moderate genetic advance as *per cent* mean.

In F₂ population of rice, Thirugnana Kumar *et al.* (2007) observed high PCV, GCV coupled with high heritability estimates and high genetic advance as percentage of mean for number of filled grains per panicle, 100 grain weight, biomass per plant and grain yield per plant. Similarly, high genetic parameters for number of productive tillers per plant and grain yield per plant was observed in the F₃ population.

Sarkar *et al.* (2007) evaluated 41 genotypes of rice for different quality parameters of grains to assess the genetic variability and revealed that genotypic and phenotypic coefficient of variations were maximum for cooked kernel L/B ratio and 1000-grain weight.

In F₂ populations of six cross combinations of rice, Hasib and Kole (2008) noticed high estimates of PCV, GCV, heritability and genetic advance for panicle weight and spikelet number per panicle, whereas grain yield per panicle had low genetic gain with high heritability indicating predominant role of non-additive gene action.

Moderate to high genetic variability and high genetic advance were observed by Nayak (2008) for plant height, ear bearing tiller, panicle length, spikelets per panicle, 100 grain weight and single plant yield in F₂ generation of two crosses of rice viz., 'Gourav × Ratna' and 'Kasturi × Ratna'.

Padmaja *et al.* (2008) revealed highly significant differences for all the characters except leaf width and 1000-seed weight among the genotypes. The estimates of genotypic and phenotypic coefficients of variation were high for all the characters except days to 50 *per cent* flowering and panicle length.

Sabu *et al.* (2009) reported highest variability for grains per panicle. The coefficient of variation over seasons was moderate to high for the progenies for all traits except panicle length and 1000-seed weight.

Sahidullah *et al.* (2009) observed enormous variations in majority of characters viz., grain length, grain breadth, kernel weight, milling yield, kernel length and L/B ratio of kernel.

High heritability estimates for spikelets per main panicle and 100- grain weight and medium to low heritability for grain yield and low heritability for panicles per plant was reported by Mukul Kumar *et al.* (2009a) in F₃ and F₄ generations of a rice cross.

Bisne *et al.* (2009) found that low, moderate and high genotypic and phenotypic coefficient of variation were expressed by harvest index, total number of filled spikelets per panicle, 100-grain weight and spikelet fertility percentage.

Yadav *et al.* (2010) studied on genetic variability in 20 rice genotypes. The highest phenotypic and genotypic coefficient of variation was observed for number of tillers per hill and number of spikelets per panicle.

Nandeshwar *et al.* (2010) studied two F₂ progenies derived from the crosses 'IR-62 x Samba Mashuri' and 'Kunti x Dudheswar' and observed high GCV and PCV for grain yield per plant, panicle number per plant and panicle weight. High heritability was also recorded for plant height, panicle number per plant, panicle length, fertility percentage, grain length, grain length breadth ratio, 1000-grain weight and grain yield per plant. Grain yield per plant showed maximum genetic advance as percentage of mean followed by panicle number per plant, plant height and panicle weight respectively.

Laxuman *et al.* (2010) observed that the PCV and GCV for most of the traits were either high or moderate except for productivity trait like days to heading, days to 50 *per cent* flowering, panicle length and plant height at maturity. RILs exhibited high heritability (>60%) coupled with high genetic advance (> 20%) for all the characters

under study except in case of days to heading, days to 50 *per cent* flowering, plant height at maturity, panicle length and grain yield per plant for which it was moderate to low.

Nadali *et al.* (2010) revealed that analysis of variance has significant differences among genotypes, crosses and lines for tiller number, plant height, days to 50 *per cent* flowering, panicle length, number of spikelets per panicle, spikelet fertility and grain yield traits.

Pankaj and Singh (2011) studied genetic variability for 17 yield and quality traits in 48 genotypes of rice (*Oryza sativa* L.). Both phenotypic and genotypic coefficients of variation were high for grains per panicle, grain yield per plant and gel consistency. Hence, direct selection of these traits will prove effective. Total tillers per plant and effective tillers per plant at maturity had moderate PCV and GCV.

Subbaiah *et al.* (2011) studied variability and genetic parameters with 16 parents and 48 hybrids for yield and its components and twenty-five quality characters. High genotypic coefficient of variation and phenotypic coefficient of variation were recorded for harvest index, total number of productive tillers per plant and gelatinization temperature in parents and for total number of productive tillers per plant, number of grains per panicle, gelatinization temperature and amylose content in hybrids.

Babu *et al.* (2012) studied on genetic parameters for yield, yield attributing, quality and nutritional characters in twenty-one rice hybrids. The characters *viz.*, number of filled grains per panicle, number of chaffy grains per panicle and iron content exhibited high GCV and PCV.

Idris *et al.* (2012) estimated genotypic coefficients of variation and phenotypic coefficient of variation for grain yield, number of filled grains per panicle, harvest index, panicle length and number of grains per panicle. The highest values of phenotypic and genotypic variance were recorded by yield kg ha⁻¹.

Sravan *et al.* (2012) studied thirty-six exotic breeding lines for genetic variation and interrelationship of grain yield and its component traits. High genotypic coefficient of variation was exhibited for grain yield followed by harvest index and flag leaf length.

Singh *et al.* (2012) reported that high heritability coupled with high genetic advance as *per cent* of mean were recorded for number of spikelets per panicle, plant height and biological yield per hill. Among the quality traits, high GCV and PCV were found for L/B ratio, kernel breadth before cooking and kernel length before cooking, while rest of the characters showed low magnitude of GCV and PCV. High heritability was observed for all the quality traits studied, while none of the character exhibited high heritability along with high genetic advance as *per cent* of mean.

Ghosh and Sharma (2012) revealed that high heritability along with high genetic advance as *per cent* of mean for grain yield per plant, pollen fertility (%), sterile spikelets per panicle, fertile spikelets per panicle, spikelets fertility (%), head rice recovery (%), 1000-seed weight and spikelets per panicle. Therefore, the improvement of these traits through selection is the most important way to achieve the genetic gain generation after generation.

Basavaraja *et al.* (2013) recorded high coefficients of variation for number of productive tillers per plant, grain yield per plant, number of tillers per plant, panicle number, plant height, panicle length, test weight and number of spikelet per panicle. The maximum genotypic co-efficient of variability and phenotypic co-efficient of variability were observed for test weight, number of productive tillers per plant, number of spikelet per panicle, amylose per cent and grain yield per plant.

Jain *et al.* (2013) exhibited productive tillers per plant with highest GCV and PCV estimates followed by kernel breadth, yield per plant and 1000-grain weight indicating that greater amount of variability prevailed for these traits within the F₅ population.

Sharma (2013) reported high estimates of PCV and GCV for culm length, plant height, total spikelets, filled spikelets, grain yield, 1000-seed weight, biological yield per plant, spikelet density and panicle weight.

Toshimenla and Sapu (2013) observed significant difference among seventy-four upland rice accessions for 13 quantitative traits. Maximum genotypic and phenotypic variances were observed for days to 50 *per cent* flowering, days to maturity, plant height, leaf length, number of filled grains and yield per plant.

Shrivastava *et al.* (2014) assessed the high GCV and PCV for the traits unfilled spikelets per panicle, filled spikelets per panicle, seed yield per plant, pollen viability, total spikelets per panicle, effective tillers per plant, panicle weight per plant, tillers per plant, spikelet density, spikelet fertility, biological yield per plant, harvest index, flag leaf length and culm length. Similarly, maximum variability for spikelet density and minimum for elongation ratio was observed by Kumar *et al.* (2014).

Rajput *et al.* (2014) noted high heritability coupled with high genetic advance for number of spikelets/panicle, biological yield per hill and plant height. This indicates the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance hence, amenable of simple selection.

Singh *et al.* (2014) characterized forty-eight upland rice germplasm accessions for quantitative and qualitative traits. Analysis of variance revealed that existence of significant variation among accessions for all the quantitative traits. High genotypic and phenotypic coefficient of variation, heritability and genetic advance as *per cent* of mean was recorded for total number of grains per panicle, fertile spikelets per panicle, number of effective tillers per plant, leaf width and grain yield per plant. Among the qualitative traits, variation was found to be high for leaf blade colour, leaf blade pubescence, ligule shape, panicle shattering, leaf senescence and sterile lemma colour.

On the basis of frequency distribution Sarawgi *et al.* (2014) reported various frequency for eighteen qualitative traits of 408 rice germplasm accessions and such genotypes possessed green basal leaf sheath colour (87.25 %), green leaf blade colour (89.70 %), pubescent leaf (48.03 %), well panicle exertion (57.10 %), white stigma colour (65.93 %), compact panicle type (55.63 %), white seed coat (82.84 %), straw hull colour (70.34%), erect flag leaf angle (57.59 %) and medium leaf senescence (67.15 %).

Das (2015) observed maximum GCV and PCV for flag leaf area, grain yield, number of effective tillers per plant, number of fertile grains per panicle, 100-seed weight and harvest index indicating selection for such characters would be more reliable.

Aravind *et al.* (2015) noticed high heritability for plant height and days to 50% flowering, moderate heritability was recorded for number of tillers, number of panicles, panicle length, biomass yield and total number of grains per panicle under both rain fed and aerobic conditions while, grain yield and harvest index showed low heritability under aerobic conditions and high heritability under rain fed condition.

Sajid *et al.* (2015) recorded 32 different agro-morphological traits. The rice germplasm exhibited sufficient genetic variation for most of the qualitative and quantitative traits. Variation was observed for all the qualitative traits except anther color and ligule shape. Highly significant differences ($p < 0.01$) were observed for the flag leaf length, flag leaf breadth, culm length, days to 50% flowering, panicle length, length of primary branches per panicle, secondary branches per panicle, grain length, grain width, awn length and percent leaf lesion while, significant differences ($p < 0.05$) were observed for peduncle length and primary branches per panicle.

Shaikh *et al.* (2017) estimated high heritability in broad sense for number of filled grains per panicle and plant height. High heritability along with high genetic advance as *per cent* of mean was recorded for yield per plant, effective tillers per square meter, total number of grains per plant, effective tillers per plant, 1000 grain weight.

Shet *et al.* (2017) evaluated *Indica* rice accessions under aerobic condition for quantitative traits to examine the nature and magnitude of variability and genetic divergence. Among all traits, grain yield per plant exhibited highest estimate of PCV and GCV followed by productive tillers/ plant and filled grains/panicle. Broad sense heritability was highest for 50% flowering by 1000 seed weight and filled grains/panicle.

Savita *et al.* (2017) revealed *per se* performance in both F_2 and F_3 generations. Among the six crosses studied, IR 72 x Veeradangan and ADT 39 x Kavuni exhibited superior *per se* performance in both F_2 and F_3 generations for almost all the biometrical

characters studied including yield. The F₂ and F₃ populations of the IR 72 x Veeradangan and ADT 39 x Kavuni showed moderate PCV, GCV coupled with high heritability estimates and high genetic advance as percentage of mean for number of productive tillers per plant, number of filled grains per panicle and single plant yield.

Prabhu *et al.* (2017) observed the highest GCV and PCV in number of grains per panicle for the cross (BPT 5204 X JGL 1798) X BPT 5204 & (BPT 5204 X JGL 1798) X JGL 1798 and Number of productive tillers in (BPT 5204 X ADT 45) X ADT 45 and also grain yield per plant in all the crosses. High heritability coupled with moderate genetic advance was observed for number of productive tillers per plant and grain yield per plant for all the crosses. Among the different populations studied, (BPT 5204 X ADT 45) X ADT 45 recorded high mean yield coupled with earliness.

Irappa *et al.* (2018) observed high heritability coupled with high predicted genetic advance for the traits like plant height, panicle exertion, number of spikelet per panicle, number of grains per panicle, test weight, L/B ratio and grain yield per plant. High values of PCV, GCV coupled with high heritability and genetic advance as *per cent* of the mean was observed for panicle exertion, the number of spikelets per panicle and number of grains per panicle. Highly significant positive correlation of grain yield was observed with days to 50 *per cent* flowering, days to maturity, plant height and test weight at both genotypic and phenotypic level.

2.2 Genetic correlation and association studies for grain yield & other related traits

The nature of association between different yield components and yield in a plant, as revealed through correlation estimates is being frequently used in planning selection for increased yield. Also, knowledge of the existence of correlation between the important and auxiliary characters reveals that some of the latter are useful as indicators of one or more of the characters. It is observed very often that correlation values between yield and its components are misleading due to interrelationships existing between the components. As a result, the direct contribution of each component to the yield and the indirect effects it has through its association with other components cannot be discerned from mere correlation studies. Degree of association between grain yield and its

components which can be expressed as correlation coefficients can be further partitioned into direct and indirect effects. The path coefficient analysis suggested by Wright (1921) offers a solution to this problem and unveils the direct and indirect paths of the components with yield. The various correlation and path analysis studies in rice is reviewed and presented below:

Venkataramana and Hittalmani (1999a) in F_2 populations of three intra-varietal crosses of rice observed positive correlation of grain yield with panicle exertion, total tillers per plant, production tillers per plant, panicle weight per plant, 1000-grain weight, panicle fertility and harvest index and negative association with plant height and maturity.

Highest positive direct effect of harvest index and highest negative direct effect of plant height on grain yield and positive indirect effect of harvest index *via* productive tillers per plant and grain weight was also reported by Venkataramana and Hittalmani (2000) in three F_2 segregating populations of rice.

Tomar *et al.* (2000), Nayak *et al.* (2001), Chakraborty (2001), Satyanarayana *et al.* (2005), Shashidhar *et al.* (2005) and Sabu *et al.* (2009) reported grain yield per plant was positively associated with plant height, effective tillers per plant, panicle length, grains per panicle, harvest index, biological yield per plant and days to 50 *per cent* flowering. While, Islam *et al.* (2002) found that grain yield per plant was positively correlated with plant height, days to maturity and 1000 seed weight and negatively correlated with flowering time.

Janardhanam *et al.* (2002) observed direct effect of plant height, spikelets per panicle, and grains per panicle on plant yield. The effects of these characters were further increased by positive indirect effect of plant height through spikelets and grains per panicle, productive tillers per plant, panicle length through plant height, spikelets per panicle, and grains per panicle, spikelets per panicle through plant height and grains per panicle.

Chaudhary *et al.* (2003) reported grain yield per plant indicated significant positive correlation of grain yield per plant with effective tillers per plant and biological yield per plant. While, Chand *et al.* (2004) observed positive significant correlations of grain yield with grains per panicle and grain length. Whereas, Sinha *et al.* (2004) observed significant positive genotypic correlations of panicles per plant and 1000 seed weight with grain yield per plant. Similarly, Souroush *et al.* (2004) observed significantly positive results of genotypic and phenotypic correlations of panicle per plant, filled grains per panicle, panicle weight, days to 50 *per cent* flowering and maturity with yield.

Surek *et al.* (2003) reported biological yield and harvest index had the highest positive direct effects on grain yield. In addition, the yield components had positive direct effects on grain yield. According to the magnitude of the direct effects on grain yield per plant, the order of yield components was filled grain per panicle > productive tillers per square meter > 1000 seed weight.

Haul Surek and Necmi Beser (2003) noticed positive and significant associations between grain yield and number of grains per panicle in F₃, F₄ and F₅ populations of rice.

Rajeswari and Nadarajan (2004) worked out the correlation coefficients and association in the F₄ to F₅ generations of rice and reported positive and significant correlation of grain yield per plant with plant height, days to 50 *per cent* flowering, number of productive tillers per plant, panicle length, number of grains per panicle and 100 grain weight and negative correlation between grain yield per plant and panicle exertion.

Raju *et al.* (2004) in a study of F₂ populations of twenty one crosses of rice reported significant correlation of productive tillers per plant and 100 grain weight with grain yield per plant, in addition to exhibiting direct effect on it.

Khedikar *et al.* (2004) revealed that the 1000 seed weight had the highest positive direct effect on grain yield followed by spikelet density, effective tillers per plant, panicle length and days to 50 *per cent* flowering and hence direct selection through these characters would be more effective. Whereas, Nayak *et al.* (2001) revealed that, panicle

number per plant, grains per panicle and 1000 seed weight contributed to the grain yield. However, Vaithiyalingan *et al.* (2005) reported grains per panicle had the highest positive direct effect on yield followed by productive tillers per plant.

In F₂ generation of twenty-three crosses of rice, grain yield was reported to be positively and significantly associated with tiller number, panicle length, total spikelets per panicle and test weight at both genotypic and phenotypic level and plant height had a very poor association and very low direct effect on grain yield while net effective tillers had a high positive relationship along with very high direct effect (Krishnaveni and Shobha Rani, 2005).

A significant and positive correlation was present between plant height and number of grains per panicle. A non-significant and negative association was observed between number of tillers per plant and grain yield per plant as reported by Zahid *et al.* (2006) while, significant and positive association between grain breadth and grain yield was reported by Girish *et al.* (2006).

Highest positive direct effect towards grain yield per plant was contributed by 100-grain weight, number of effective tillers per plant, harvest index, flag leaf length and number of grains per panicle reported by Gazafrodi *et al.* (2006).

Narinder (2006) reported positive direct effect of days to maturity, plant height, number of productive tillers per plant, panicle weight per plant, panicle index, number of spikelets per panicle, number of filled grains per panicle, biological yield per plant and harvest index on grain yield per plant.

Agahi *et al.* (2007) reported that, the productive tillers per plant had the highest positive direct effect on grain yield per plant followed by the number of grains per panicle and 1000-seed weight, respectively.

Bhagat (2007), Rao (2007) and Rani (2007) reported days to maturity was positively associated with panicle length, panicle index and negatively correlated with plant height, number of tiller, panicle weight, biological yield per plant, 100 grain weight

and grain yield per plant. Single plant yield was positively and significantly correlated with plant height, ear bearing tiller and panicle length in F₂ generations of two crosses of rice viz., ‘Gourav × Ratna’ and ‘Kasturi × Ratna’ (Nayak, 2008).

Mukul Kumar *et al.* (2009b) in early generations of rice observed significant and positive associations of grain yield per plant with spikelets per main panicle but non-significant and positive association with 100-grain weight. Further, spikelets per main panicle followed by 100-grain weight had direct contribution in their magnitude to grain yield as revealed by path coefficient analysis.

In two F₂ progenies derived from the crosses ‘IR-62 x Samba Mashuri’ and ‘Kunti x Dudheswar’, grain yield per plant possessed significant positive correlation with panicle numbers per plant, panicle weight and grain number per panicle while it had significant negative correlation with plant height. Panicle number per plant imparted maximum direct effect on grain yield followed by grain number per panicle, 1000-grain weight and panicle length (Nandeshwar *et al.*, 2010).

Yogameenakshi and Vivekanandan (2010) observed negative and significant association noticed between grain yield and days to flowering in F₂ generation of rice.

Nandan *et al.* (2010) observed path analysis and indicated that the number of grains per panicle had maximum direct effect on grain yield per plant followed by days to 50 % flowering, hulling percentage, plant height and harvest index.

Madakemoheker (2011) observed positive significant association of grain yield per plant with biological yield per plant, harvest index, number of tillers per plant, number of panicle per plant, plant height, seed length, panicle length and 1000 grain weight at both genotypic and phenotypic level while, flag leaf area showed highly negative association with grain yield per plant in RIL's of rice derived from *indica* and *japonica* crosses.

Rajamadhan *et al.* (2011) reported that the grain yield per plant exhibited positive direct effect on number of productive tillers, panicle length, number of grains per panicle,

grain breadth and 1000-grain weight. While, Basavaraja *et al.* (2011) revealed that days to 50% flowering, plant height, panicle length, panicle number, number of productive tillers per plant, spikelet fertility percent and amylose *per cent* had positive direct effect on grain yield. Hence, selection based on these traits could help to bring simultaneous improvement of yield.

Bekele *et al.* (2013) showed highly significant and positive correlation between grain yield per plant with plants height (0.379), number of tillers per plant with number of productive tillers per plant (0.906). Significant correlations between different traits can be used to conduct indirect selection of a desired trait.

Soni *et al.* (2013) reported highly positive and significant correlation between grain yield per plant and biological yield per plant, productive tillers per plant, spikelet fertility, panicle length, 1000-grain weight, grains per panicle, panicle weight, flag leaf length, spikelet per panicle, flag leaf area, kernel length, flag leaf width, days to 50% flowering and harvest index.

Singh *et al.* (2013) reported that the grain yield per plant showed positive correlation with productive tillers per plant and test weight. Path coefficient analysis showed that the productive tillers per plant and test weight contribute to grain yield per plant through direct effect. The parent off-spring regression was high for all the characters under study suggesting improvement of these characters by mere selection.

Dongre *et al.* (2014) reported that number of tillers per plant, culm height, plant height, biological yield per plant, panicle index and harvest index were positively correlated with grain yield.

Rahman *et al.* (2014) reported that grain yield per plant of newly developed advanced fine rice lines and check showed positive association in respect of number of effective tillers hill (0.308), number of filled spikelets per panicle (0.110) and weight of 1000-grains (0.109), whereas significant negative association with panicle length (-0.609), number of unfilled spikelets per panicle (-0.542) and non-significant negative association with plant height (-0.136) and number of ineffective tillers per hill (-0.304).

Kumar *et al.* (2014) suggested that the traits viz., panicles weight per plant, number of spikelets per panicle, panicle index, number of leaves per plant, plant height, days to heading, average panicle weight, flag leaf width, grain length and hulling *per cent* exhibited significant positive correlation with grain yield per plant as well as positive direct effect on grain yield per plant.

Nagle *et al.* (2014) revealed the characters viz., number of grains per panicle, biological yield per plant and harvest index had positive and high direct effect on grain yield while, 1000-grain weight, number of effective tillers per plant, spikelet sterility percentage, days to 50 % flowering and spikelet fertility percentage and spikelet density had positive and very low direct effects.

Hossain *et al.* (2015) showed that days to flowering had maximum direct effect on yield followed by number of effective tillers and number of unfilled grains per panicle, while the lowest direct effect on grain yield was exhibited by root weight followed by number of filled grain per panicle. The highest negative indirect effects on grain yield were obtained by number of root hair.

Islam *et al.* (2015) revealed that the days to maturity, days to 50% flowering, plant height, number of filled grains per panicle and grain length had direct positive effect on yield, indicating these are the main contributors to yield.

Huan-he *et al.* (2016) analysed late-maturity type of Yongyou *Japonica/ Indica* hybrids series and obtained yield of HYYS was mainly attributed to larger sink size due to more spikelets per panicle. Significant positive correlations were recorded between duration from heading to maturity stage and grain yield, and also between whole growth periods and grain yield.

Grain yield per plant had highest significant positive association with filled seeds per panicle, plant height, flag leaf length, effective tillers, flag leaf width and panicle length indicating importance of these characters for yield improvement, while head rice recovery was found to be significantly and positively correlated with milling *per cent* and hulling *per cent*. Path analysis revealed that test weight (3.48), effective tillers (1.57), and

filled grains per panicle (1.41) had positive direct effect on grain yield per plant. Among the quality traits kernel length followed by milling *per cent* and kernel elongation ratio had direct effect on head rice recovery (Rukmini Devi *et al.*, 2017).

Jayaprakash *et al.* (2017) revealed that the significant positive correlation of number of filled grains per panicle, spikelet fertility, total number grains per panicle, number of productive tillers per plant and 1000-grain weight with grain yield. Path analysis indicated maximum positive direct effect of total number of grains per panicle followed by spikelet fertility on grain yield, while protein content had direct negative phenotypic effect on grain yield and its correlation with grain yield was also negative and non-significant.

The studies by Madhukar *et al.* (2017) under aerobic situation indicated that grain yield is primarily contributed by filled grains per panicle and 1000 seed weight. Highly significant correlation was noticed between panicle length and plant height and also between panicle length and grains per panicle, stature of plant. The path analysis indicated that among several yield components in rice, number of filled grains per panicle play a key role for better yields under aerobic situation.

Haridari and Hittalmani (2017) showed significant positive association of rice grain yield per plant with productive tillers per plant, filled spikelet per panicle and harvest index and significant negative association with days to flowering and days to maturity at both genotypic (rg) and phenotypic (rp) levels. Path coefficient analysis exhibited the positive direct effect on grain yield per plant *via* days to flowering, productive tillers per plant, spikelet fertility and 100 grain weight. The productive tillers per plant, filled spikelets per panicle, spikelet fertility and harvest index showed highly significant positive correlation coefficients along with high direct effects on grain yield per plant.

2.3 Assessment of intergeneration correlation for yield and related characters

Inter generation correlation studies by using parent-offspring regression helps in estimating the extent of transferring the genetic potentials of the character from one

generation to other generation. Extent of genetic segregation expected in later generations of crosses dependent largely on the heritable nature of character for which selection pressure would be effective.

Lush (1949) proposed parent offspring regression method, which involves regressing the mean value of a character in the progeny upon the value of the same character on the parent. This technique is useful to determine the influence of environment on different character in progenies obtained from individual selection from early generations and to study the real genetic potentiality of progenies inherited from their parents. The heritability in narrow sense as the ratio of additive variance to the total variance. As only additive genetic variability was inherited in next generation, heritability in narrow sense was more reliable. The heritability in broad sense is the ratio of genetic variance to the total variance (Hanson *et al.*, 1956)

Yamamoto and Toriyama (1971) practiced truncation selection in F₄ and F₅ lines derived from F₂ population of rice plant to compare the expected with observed genetic gains. The expected and observed direct responses to selection were substantially large in all traits *viz.*, culm length, panicle length, panicle number per m², panicle weight per m², grain number per panicle and grain weight per m² measured. Correlated responses obtained in all traits measured were smaller than direct responses. There was comparatively good agreement between the expected and observed responses. It is estimated that an expected genetic gain is available to develop an effective selection method in the rice breeding programme.

The composition of the genetic variance has a limited influence on the optimal size of the progenies. If epistatic variance is important, then the number of F₂ lines has to be reduced and the number of F₃ and F₄ families must be increased. The same is true for non-genetic variance (Webber, 1982).

Subrahmanyam *et al.* (1986) estimated the heritability in nine rice populations (three crosses and three methods of selection). In F₃ and F₄ itself, 1000-seed weight and number of grains per panicle had given high heritability (almost 90%), showing that these

characters got established even in early generations. For other characters viz., plant height, panicle length, ear-bearing tillers, and yield heritability (almost 80%) estimates increased from F_1 to F_6 generations.

Sardana *et al.* (1989) reported a high estimate of heritability along with low genetic advance for number of grains per panicle and tiller number per plant in rice. In the F_3 , the variability was moderated for yield per plant and low for other characters while days to panicle emergence showed high heritability (broad sense) and low genetic advance (Ganeshan and Subramanian, 1990).

Mishra *et al.* (1994) worked out effectiveness of different selection methods (pedigree, bulk and SSD) in segregating population of rice cross ARC 10372 X IR 36 under different environments, viz., selected and tested in irrigated conditions, selected in upland and tested in irrigated conditions, selected in irrigated and tested in upland conditions and selected and tested in upland conditions. Substantial variability for yield and its components in F_2 gradually declined with the increase of mean values in subsequent generations and varied from method to method and selection in different environments. Heritability values gradually increased with the advancement of generation. Bulk and SSD methods were superior in retaining and maintaining the high yielding lines in comparison to pedigree method of breeding.

Ganeshan *et al.* (1998) analyzed transfer of genetic potential from F_2 to F_3 generation using parent-offspring regression in six crosses of rice. Significant positive correlation and regression was observed in crosses ASD 1/ IR 50 and ASD 16/ IR 50 at mean 1 Standard deviation(SD) level and in ASD 16/ADT 36 at mean level between F_3 means corresponding F_2 values, indicating that selection of single plants for yield at those levels would be effective in respective crosses. The observed intergeneration correlation and regression were non-significant but positive in other level of selection *via* Mean- 1 SD for ASD 16/ ADT36 and mean level for ASD 1/ IR50, indicating the chances of selecting high yielding genotypes at these levels also. There were equal chances of selecting high yielding genotypes at mean, mean+ 1SD, mean- 1 SD levels for early selection.

Prom-u-thai and Rerkasen (2004) compared expected genetic gain with observed genetic gain in F₄ and F₅ generation from F₂ population of rice. The expected and observed direct responses to selection were substantially large in all traits measured like panicle length, grain weight and culm length. Correlated responses obtained in all the traits were smaller than direct responses.

Surek and Baser (2005) estimated the correlation of grain yield with yield components in the different segregating generations (F₃, F₄ and F₅) of rice. And also determined the response to selection for high and low grain yield and yield components. The results indicated that selections for grain weight and the number of grains per panicle were effective in early generations. There were positive and significant associations between grain yield and the number of grains per panicle in all populations in both years. High heritability estimated for 1000 grain weight. The estimated narrow sense and realized heritability were similar in terms of magnitude.

Habib *et al.* (2005) evaluated ten local varieties in rice for variability and genetic association for grain yield and its component characters. The highest genetic variability was obtained in flag leaf area and filled grains per panicle. High heritability associated with high genetic advance was observed in filled grains per panicle, 1000 grains weight, harvest index and grain yield.

Kato *et al.* (2008) examined selection efficiency of rice grain size, narrow sense heritability from parent to offspring correlation and selection response in segregating generation using five cultivars of rice. The average heritability was 0.8 for grain length, 0.56 for grain width from parent offspring correlation. The average heritability estimated for grain length obtained from selection response was 0.679. The narrow sense heritability estimated for grain length and grain width were high in general as compared with heritability for other agronomic traits in rice. The estimates for grain length and grain width did not fluctuate drastically with generation advancement from F₂ to F₄.

Mukul Kumar *et al.* (2009b) studied effectiveness of plants selected in early segregating populations of rice crosses, Jhona 349 X IET-12944 and Narendra 80 X

Lalmati. Both the F_2 and F_3 selected plants showed consistency in increment of response to selection and realized heritability in their corresponding F_3 and F_4 generation for grain yield per plant and 100-grain weight, whereas these estimates were inconsistent for spikelets per main panicle and in undesirable direction for panicle per plant. Among intergeneration correlations, the F_2 selected plants showed inconsistent significant correlation with their F_3 progenies over crosses for all the characters, while F_3 selected plants had significant correlations with their F_4 progenies for 100-grain weight and grain yield per plant in both the crosses. The higher estimates of selection parameters like response to selection and realized heritability as well as significant correlation for grain yield per plant and 100-grain weight in F_4 generation suggested that selection for these two polygenic traits should preferably be started from F_3 generation.

Kanbar *et al.* (2011) studied the comparative efficiency of three selection methods, viz., pedigree, modified bulk and single seed descent (SSD) in F_3 , F_4 , F_5 and F_6 generations of a cross combination Moroberekan/IR20 of rice. Bulk population showed superiority over pedigree for grain yield, panicle length, number of panicles, number of tillers and harvest index in F_3 generation. Pedigree method was found to be superior over bulk and SSD for grain yield per plant in F_4 and F_5 generations. In the three breeding methods, mean values of grain yield showed directional shift across the generations. In F_6 generation, the pedigree-derived lines showed higher superiority over mean value than lines derived from SSD and modified bulk for grain yield, number of panicles and harvest index. Inter-generation correlation coefficients were significant and positive between all the generations for grain yield, number of tillers and number of panicles.

Barman and Borah (2012) estimated expected response to selection in F_4 and F_3 generations compared to previous generations. F_3 generations showed significant positive selection response for plant height, number of panicles per plant, grain density and days to 50 % flowering, thus indicating the effectiveness of selection for these characters. Grain yield showed non-significant response in F_2 generation which indicates straight selection for this character during early generation may not be effective. F_4 generation showed positive selection response for all the above characters. This indicates the effectiveness of selection for these characters in F_3 or later generation. The regression

coefficient between F₂ and F₃ generation and F₃ and F₄ generation was significant for all the characters. Selection for plant height, number of panicles per plant and days to 50 per cent flowering can be made in the early segregating generation. Grain yield per plant and grain density is effective for selection in later generation.

Suwarto *et al.* (2015) showed that F₃ generation has significant positive selection response for plant height, number of grains per panicle, panicle length and days to 50% flowering, thus indicating the effectiveness of selection for these characters. The correlation and regression coefficient between F₂ and F₃ generation was significant for these characters. But, grain yield per clump showed non-significant response in F₃ generation. The correlation and regression coefficient between F₂ and F₃ generation was non-significant for grain yield per clump, which indicates straight selection for this character during early generation (F₂) may not be effective.

Govindraju *et al.* (2017) practiced the effectiveness of early generation selection in bacterial blight resistance genes introgressed F₂ and F_{2:3} population of the cross CB 174 R × IRBB 60 in rice. F₂ Selection have been proved to be robust and effective tool in crop improvement program. Selection differential was positive for all studied traits. Selection response was high for number of grains, thus indicating the effectiveness of selection for these character. Realized heritability was found high for number of grains and thousand grain weight, suggested that direct selection was effective. Expected selection response and predicted genetic gain was high for number of grains. Parent-offspring correlation showed low but significance association for number of productive tillers ($r=0.47^{**}$, $P<0.01$), single plant yield ($r=0.35^{**}$, $P<0.01$) and ($r=0.30^{*}$, $P<0.05$) panicle length in F₂ and F_{2:3} generation indicated that selection was fruitful in early generation. Statistically regression coefficient was not significant linear dependence of the mean of F₂ and F_{2:3} generation.

2.4 Screening for diseases resistance in segregating population rice

Chandrashekar *et al.* (2008) revealed that, none of the genotypes was found immune to *Pyricularia oryzae*. However, eight genotypes viz., Rasi, Sasyasree, Nidhi, Calaro, Tetep, HRI-155 (Hybrid), CSAR- 840 and MTUHR-2091 (Hybrid) were found

resistant to leaf blast. Similarly, 18 genotypes were found resistant to neck blast. Another 138 genotypes were moderately resistant to leaf blast and 82 genotypes were moderately resistant to neck blast. However, only one entry namely, Sasyshree was found resistant to both leaf and neck blast. The susceptible check (HR-12) showed highly susceptible reaction for both leaf and neck blast.

Usman *et al.* (2009) screened rice germplasm against *Pyricularia oryzae*, cause of rice blast disease. The screening revealed that none of the test lines were immune or highly resistant. One line IR-70181-1-1-1 of course type was found to be resistant. Nine lines of the course type displayed moderately resistant response, while none of the fine type lines showed this response. Seventy-seven lines of both course (35) and fine (42) rice were found to be moderately susceptible. Twenty-four lines of fine rice showed susceptible to highly susceptible response. This indicated prevalence of the resistance against rice blast pathogen was more common in the course as compared to the fine germplasm lines of rice.

Waheed *et al.* (2009) screened 11 rice genotypes to assess the losses in yield and yield components by bacterial leaf blight disease under natural field condition. Significant differences were observed for all the traits studied viz., days to 50 *per cent* flowering, plant height, number of tillers, spike length, number of grains per panicle, straw yield and grain yield. Among all the genotypes, PARC-298, PARC-299 and PARC-301 showed resistance to bacterial leaf blight and out yielded in grain yield.

Banito *et al.* (2012) evaluated 21 rice varieties and near isogenic lines under screen house with inoculation of 13 *X. oryzae* *pv.* *oryzae* strains from Togo. The results revealed differential reactions of these genotypes in disease expression. AMMI analysis identified three groups of genotypes: resistant group made up of 12 lines (IRBB1, IRBB2, IRBB3, IRBB4, IRBB7, IRBB8, IRBB10, IRBB11, IRBB13, IRBB14, IRBB21 and IR24), medium resistant group made up of three cultivars (NERICA4, NERICA8 and NERICA14) grown in Togo and one cultivar (Giganté) from Africa Rice and susceptible group including five genotypes TGR203 and IR841 from ITRA, NERICA19 and TOG5681 from Africa Rice and the line IRBB5.

Santosh Kumar *et al.* (2013) screened eighty-seven rice genotypes consisting of new breeding lines as well as some local check varieties against bacterial leaf blight and brown spot diseases. Significant differences were observed for resistance to both the diseases among genotypes. The screening revealed that none of the breeding lines of rice were immune or highly resistant against both the diseases. The three genotypes IR 83387-B-B-109-4-89-3, IR 84887-B-155-40-1-1 and IR 83867-B-B-250-3-1-1 showed resistance to brown spot and bacterial blight and out yielded in grain yield. The grain yield was significantly and positively correlated with harvest index, biomass, tiller number and test weight under aerobic conditions.

Mwendo *et al.* (2014) screened 100 tested rice lines to identify new source of resistance to brown spot disease in F₂ progenies of specific crosses for segregating pattern of reaction to brown spot disease. Among the hundred tested rice lines, eighteen lines were rated as highly resistant, fifty-two resistant, twenty-seven moderately resistant and three lines were susceptible. The results revealed that there was significant variation for brown spot resistance among genotypes tested.

Dar *et al.* (2015) screened rice germplasm consisting of 9 parents, 27 crosses to determine resistance intensity in rice germplasm against rice blast disease under natural epiphytotic conditions and the results revealed that none of the test lines was immune or highly resistant. Four crosses namely, K-08-60 x IR-68888A, K-08-61 x SKAU-11A, K-08-61 x IR-68888A, PS-5 x SKAU-11A and one parent PS-5 were found to be resistant. Seven hybrids and four parents displayed moderately resistant response. Three crosses and equal number of parents were found to be moderately susceptible. Rest of the crosses and parents showed susceptible to highly susceptible response.

Magar (2015) conducted a field experiment on fourteen rice varieties to determine the level of resistance against brown leaf spot disease. Disease severity and total area under disease progress curve (AUDPC) value ranged from 21.73% to 58.07% and 614.8 to 1827 respectively. None of these varieties were found either resistant or highly resistant to disease. Only HJ-G1 and HJ-G2 were moderately resistant with grain yield of

5.10 t/ha and 4.25 t/ha respectively. HJ-G1 variety had the highest grain yield 5.10 t/ha and lowest disease severity (21.73%) as well as total AUDPC value (614.8).

Alam *et al.* (2016) screened 25 varieties against brown leaf spot of rice in three conditions i.e. laboratory, pot and field. The results were four varieties recorded viz., NDR-359, CR-1, CR-2 and N-18 in highly resistant. Seven varieties were recorded viz. PR-103, IR-36, Prasad, Narendra-2, IR-597, OC-1339 and Cross-116 in resistant. Six varieties were recorded viz., IET-849, Pusa NR-381, Narendra-80, Narendra Dhan-97, Jalnidhi and Jallahari in moderately resistant. Three varieties were recorded viz., Rupali, MTU-7029 and Sweta in moderately susceptible. IET-2969 and Annapurna was recorded in susceptible. Three varieties were recorded viz., Nagina-22, CR-126 and Cauvery highly susceptible in all three screening conditions.

Mubassir *et al.* (2016) carried out both morphological and molecular screening for identifying Bacterial leaf blight (BLB) resistant cultivars in rice. Among the rice varieties, BR-26, BRRI Dhan31, IRBB5, IRBB21, IRBB60, IRBB65, and Kumragur were recorded as resistant where BR-11, Binadhan-8, and Binadhan-10 were found highly susceptible to BLB. In case of RFLP marker based analysis, confirmed that IRBB5 and IRBB 60 varieties had *xa5* and *xa13* genes respectively.

Chandra *et al.* (2016) screened 108 germplasm under natural as well as under artificial inoculated condition for sheath blight disease. In natural condition, none of the entries were found immune or resistant, 45 entries were found moderately resistant, 37 moderately susceptible and 14 were observed susceptible. Rest of the entries showed highly susceptible reaction. Under artificial inoculated condition, out of 82 entries, none of the entry was found resistant. Only 2 entries viz., Baigani black and Prasada showed moderately resistant reaction, 17 were moderately susceptible and 27 entries were susceptible. Rest of the entries was found highly susceptible.

Santosh Kumar *et al.* (2017) conducted experiment to identify sheath blight and bacterial leaf blight disease resistance rice genotypes under submergence condition in middle Indo Gangetic Plain. The disease incidence was observed at maturity stages

during *Kharif* season 2016. The incidence of sheath blight and bacterial leaf blight of paddy ranged from 18.6 to 39.0% and 15.3 to 34.0%, respectively. Among the rice genotypes, the minimum disease incidence of sheath blight was recorded in IR 96321-1447-521-B-2-1-2; minimum bacterial leaf blight disease incidence was recorded in IR96321-1099-227-B-3-1-3.

Pavani *et al.* (2018) carried out screening experiment with 196 germplasm lines under natural conditions after inoculation with virulent isolate of *R. solani* (RS 49). None of the entries were found immune or resistant. Fifty-seven entries were found moderately resistant, moderately susceptible and rest of the entries showed highly susceptible reaction.

2.5 Estimation of protein and other grain nutrient parameters

The inheritance study of amylose content was reported as monogenic with modifiers (incompletely dominant) by Seetharaman (1959), Kahlon (1965), Bollich and Webb (1973), Somrith (1974), Chang and Li (1981), Chauhan and Nanda (1983). It was controlled by two complimentary genes by Stansel (1966) and digenic with partial dominance of high over low Heda and Reddy (1986), and also as a dosage effect of genes by Kumar and Khush (1986), Heu and Park (1976), Okuno (1983), Okuno and Yano (1984).

He-jian Hua *et al.* (2000) studied nutritional characteristics of rice grain and brown rice in 18 cultivars. The average dry matter in rice grain and brown rice was 87.24 and 87.39 respectively, crude protein was 8.85 and 10.35, respectively. The amino acid content of rice grain and brown rice are 0.29% and 0.44% for lysine, 0.10% and 0.18% for methionine and 0.26% and 0.30% for threonine.

Gregorio *et al.* (2000) in a study on comparison of Fe content at different polishing times for high-iron traditional varieties (red pericarp) with IR64 and IR68144-3B-2-2-3 (white pericarp), reported a strong interaction between genotype and time of milling. Grain color seemed to be associated with the amount of iron content.

Singh *et al.* (2001) reported that excessive polishing results in a considerable loss of protein content in the milled rice (2.48 – 4.43%) depending on variety at 8 - 11 *per cent* degree of polish. Dipti *et al.* (2002) reported that the highest protein (8.6%) among the six fine rice varieties was found in BRR1, dhan 28 followed by Badshabhog and Superfast. Entire varieties contain more or less standard rate 7% of protein.

A high iron trait can be combined with high yielding traits. A cross of a high yielding variety (IR72) and a tall traditional variety (Zawa Bonday) from India, from which IRRI identified an improved line (IR68144-3B-2-2-3) with high concentration of grain iron content in brown rice (Gregorio, 2002).

Ghadi *et al.* (2003) in their study of chemical analysis of 12 promising rice cultivars (RTN-1, RTN-2, RTN-68-1, PLG-1, RTN-3, KJT-2, KJT-3, KJT-4, PNL-1, PNL-2, Sahyadri and KJT-1) reported considerable genetic variation with respect to proximate composition, protein quality and mineral composition. KJT-1 recorded the highest protein content (9.05%), while RTN-3 contained the highest tryptophan (1.85 g 100-1 g protein) in its grain protein.

Asaduzzaman *et al.* (2004) evaluated thirty high yielding and low yielding rice varieties cultivated in Bangladesh for phytic acid, iron, zinc and calcium, contents. Among the high yielding varieties, BR11 (Mukta), BRRI dhan29, BR8 (Asha) and BRRI dhan28 were suitable varieties for consumption as these varieties contained low content of phytic acid and high content of minerals, especially iron and zinc. Likewise, Chinigura, Kalijira, Sazoni and Bashmoti were suitable among the low yielding varieties.

Koutroubas *et al.* (2004) conducted an experiment to assess the variation in grain quality traits among rice lines. Grain protein content (PC) ranged from 4.8 to 11.9%. protein content was greater in tall and late maturing lines than in short and early maturing ones.

White and Broadley (2005) reported that the bioavailability of iron and zinc is associated with the presence of antinutrients and/or the lack of promoter substances for micronutrients. Saluja *et al.* (2005) characterized land races of rice for protein, lysine and

micronutrients. The analysis of 4000 accessions for protein content in polished rice varied from 4.15% to 9.90% and lysine from 3.23 to 6.80 gm/16 gm of nitrogen.

Chandel *et al.* (2005) screened 1100 accessions of rice for protein, lysine, iron and zinc content. This study revealed wide range of variation for protein and lysine accumulation in the endosperm of rice grains. Low level of variation for iron (3-10 ppm) was recorded in the polished grain of rice.

Neng *et al.* (2006) showed that protein content was ranged from 6.3 to 15.7% in indica and 6.0 to 13.6% in japonica rice. Classifying the rice protein content into high (11%), middle (8%-11%) and low (8%) groups, 73% of the rice cultivars belonged to the middle group, while 14% belonged to the high group and 13% belonged to the low protein content group. For indica rice, the protein content was negatively correlated to gel consistency and amylose content with a significant coefficient of -0.093 and - 0.17, respectively, and positively related to translucency (grade) with a significant coefficient of 0.154. High protein rice was usually preferred over poor translucency, hard gel consistency and low amylose content rice.

Kohli and Diwan (2006) analyzed micronutrient (Zn, Mn and Cu) contents in seeds of different rice cultivars (Ananda, IR-36, Kalinga-3, Kranti, Mahamaya, Masuri, Purnima, Safri, Shyamla and Rasi) and evaluated its relationship with seed quality characters. Results showed significant variation in micronutrient contents of seeds of different cultivars.

Martinez *et al.* (2006) revealed a great variability in grain iron and zinc levels among 12 rice genotypes. The grain iron concentrations were in range of 7.2 to 14.5 ppm with one wild rice having 30.4 ppm grain iron concentration. The range of grain zinc concentration was from 17.3 to 25.6 ppm with an average of 21 ppm.

Liang *et al.* (2007) studied the variation of phytic acid, iron and zinc levels in 56 varieties of Chinese rice. Iron levels showed the biggest variation and zinc showed a moderate variability which was narrower than for iron, while broader than for phytic acid.

Lee *et al.* (2007) analyzed 494 rice cultivar for grain iron and zinc concentration using ICP-OES (inductively coupled argon plasma technique) at IRRI and reported that grain iron and zinc concentration ranged from 2 to 12.0 $\mu\text{g/g}$ (average 4.3 $\mu\text{g/g}$) and 10.0 to 33.0 $\mu\text{g/g}$ (average 22.8 $\mu\text{g/g}$). They identified cultivars Suweon 464 and Joryeongbeo to have significantly higher grain iron and zinc concentration.

Shashidhara *et al.* (2008) reported that clear cut segregation for total grain protein content ranged from 8.73 to 20.59 *per cent* of crude protein. The crude protein percentage showed high heritability coupled with high genetic advance.

Habibi (2008) noticed highest protein content (20.59%) crude grain protein content in F_2 generation of a cross between BPT 5204 x HPR 14. Crude protein showed high heritability coupled with high genetic advance.

The wide variability for grain Fe and Zn content of 46 accessions of rice were analyzed by Banerjee *et al.* (2010) and recorded more variations in micronutrient level which ranged from 4.82 to 22.69 $\mu\text{g/g}$ and 13.95 to 41.73 $\mu\text{g/g}$ for grain Fe and Zn content, respectively. Anandan *et al.* (2011) reported that zinc concentration ranged from 3.00 to 38.60 mg/kg with a mean value of 15.84 mg/kg among 202 rice genotypes.

Ravi *et al.* (2011) analyzed 156 local land races, for protein content ranging from 5.45- 14.08 with an average of 7.84%. The highest protein per cent of 14.08 was recorded by purple putt following Bisagohra (12.38%), Bidar Local-2 (11.09%) and Pooja (10.95%) as compared to Vani (5.47%). High acquisition of protein was observed in six local land races (10.11-14.08%) followed by 64 locals (7.81-10.10) and 86 locals (5.45-7.80 %).

Anuradha *et al.* (2012) evaluated 126 accessions of rice for Fe and Zn concentration and reported that Iron concentration ranged from 6.2 to 71.6 ppm and zinc from 26.2 to 67.3 ppm in brown rice. The wild accessions had the highest Fe and Zn concentration compare to cultivated, thus wild species may be used for biofortification of popular rice cultivars.

Lu *et al.* (2013) showed that half of the total Zn, two thirds of the total Fe, and most of the total K, Ca and Mn were removed by the milling process if the hull and bran were thoroughly polished.

Ravindra Babu *et al.* (2013) evaluated twenty-one popular rice hybrids for the protein content. High amounts of protein content was found to be observed in hybrids of DRRH-2 (9.79%) and Sahyadri-2 (9.45%) while lowest value was obtained for PSD-3 (5.74%). The mean protein content among the hybrids was found to be 7.95 %.

Nachimuthu *et al.* (2014) estimated iron and zinc in the brown rice of 192 germplasm lines and found positively correlated implying the chance for concurrent selection for both the micro nutrients. Iron concentration ranged from 6.6 to 16.7 $\mu\text{g/g}$ and zinc concentration from 7.1 to 32.4 $\mu\text{g/g}$ in brown rice.

Roy and Sharma (2014) reported the nutritional values of mineral contents of iron and zinc estimated in all cultivars by Atomic Absorption Spectrophotometric method. Iron concentration varies from 0.25 to 34.8 $\mu\text{g/g}$ and zinc from 0.85 to 195.3 $\mu\text{g/g}$ in the landraces. Highest iron containing rice was Swetonunia with 34.8 $\mu\text{g/g}$ and highest amount of zinc was found in Nepali Kalam which was 195.3 $\mu\text{g/g}$.

Renuka *et al.* (2015) estimated Iron, Zinc, Calcium, Magnesium, Copper and b-carotene contents in 39 aromatic indica rice (*Oryza sativa* L.) cultivars. The b-carotene contents were ranging from 1.23 to 9.9 $\mu\text{g/g}$ in brown and 0.08 to 1.99 $\mu\text{g/g}$ in milled rice. Among the mineral contents, Magnesium was found ranging from 855 $\mu\text{g/g}$ to 1636 $\mu\text{g/g}$ followed by Iron in 32 $\mu\text{g/g}$ to 218 $\mu\text{g/g}$, Copper content from 2 $\mu\text{g/g}$ to 1004 $\mu\text{g/g}$, Zinc content from 25 to 165 $\mu\text{g/g}$ and Calcium ranged from 14 $\mu\text{g/g}$ to 67 $\mu\text{g/g}$.

Ramya *et al.*, 2017 revealed that the grain yield per plant showed significant positive association with number of productive tillers per plant, panicle length, number of filled grains per panicle and grain iron concentration. Path coefficient analysis revealed that the traits 1000-grain weight, numbers of filled grains per panicle, number of productive tillers per plant, grain iron concentration, grain zinc concentration, days to 50% flowering and plant height were directly influencing the grain yield per plant. Sriram

et al. (2017) reported that grain Fe content had strong positive significant association with grain Zn content.

2.5.1 Estimation of phytic acid content in rice

Larson *et al.* (1999) showed the nonlethal mutation rice *lpa11* reduces the phytic acid portion of seed phosphorous from 71 to 39% and increases the inorganic portion of seed phosphorous from 5 to 32%, with little effect on total seed P. This rice *lpa1* mutation was mapped to a 2.2cM interval on chromosome 2L. Although this myoinositol1phosphate synthase (MIPS) gene may be an appropriate target for controlling seed phytic acid synthesis, modifications of other genes (e.g., maize *lpa2*, barley *lpa1*, barley *lpa2*, and rice *lpa1*) may also be useful in reducing grain phytic acid and improving the nutritional value of cereal grains and/or milling byproducts.

Feng and Yoshida (2004) attempted to reduce the phytic acid content of seeds through manipulation of the expression of the Ins(3)P1 synthase gene *RINO1* using antisense RNA method. This led to increase in inorganic phosphate (1.5 to 2 fold) and dry weight of transgenic rice seeds without reduction in seed total P levels. This suggested a molar equivalent phytic acid decrease in seeds of transgenic rice.

Ahn *et al.* (2004) compared the antioxidant activities of irradiated phytic acid and commonly used antioxidants viz., ascorbic acid, tocopherol and butylated hydroxyl anisole (BHA). The phytic acid (800 µM) irradiated at 20 kGy showed the highest antioxidative ability among other antioxidants during storage due to significantly higher 2, 2-diphenyl-1-picrylhydrazyl (DPPH) radical scavenging capacity.

Andya and Tai (2005) observed the rice low phytic acid mutation *lpa1* results in a 45% reduction in seed phytic acid with a molar equivalent increase in inorganic P. The *Lpa1* locus was mapped to the long arm of chromosome 2 between the markers RM3542 and RM482, which encompass a region of 135 kb.

Bryant *et al.* (2005) estimated that the reduction in whole grain phytic acid P in rice *lpa1-1* is accompanied by a 5- to 10-fold increase in grain inorganic P, and this

increase was observed in both whole grain and milled products. Phytic acid P was also reduced by 45% in bran obtained from *lpa1-1* grain, and this was accompanied by a 10-fold increase in inorganic P. Therefore, while the block in the accumulation of phytic acid in *lpa1-1* seed has little effect on whole grain total P and mineral concentration, it greatly alters the chemistry of these seed constituents, alters their distribution between germ, central endosperm and aleurone.

Ren *et al.* (2007) showed that the concentration of phytate P (PA-P) was significantly reduced in rice (*Oryza sativa* L.) mutant *HIPi1* grains. The low phytate mutation could not only potentially increase the bioavailability but also the amount of most important micronutrient elements, i.e., Fe, Zn and Ca, in the edible part of rice grains.

Zhao *et al.* (2008a) observed LPA mutant lines in rice with reduction in phytic acid-P (33.8% to 63.6%), reduction in grain yield (12.5–25.6%), grain weight (5.4% to 10.7%), and inferior seed viability to their corresponding wild type parent varieties.

Zhao *et al.* (2008b) identified the effects of grain phytic acid (PA) mutant on rice (*Oryza sativa* L.) grain filling and grain weight, the accumulating patterns of grain PA, total starch contents and also in relation with the carbohydrate translocation in different organs (leaf, culm, and sheath) and the activities of some enzymes using 2 early *indica* genotypes differing in grain PA content-namely Xieqingzao and its low PA mutant (*Os-lpa1*). Compared with Xieqingzao, *os-lpa1* had higher starch content and more carbohydrate accumulations in flag leaf, culm, and sheath, but much lower activities of ADPG pyrophosphorylase (*ADPG-Ppase*) and starch phosphorylase (*SPase*) in grains at filling stage, leading relatively decreasing grain weight, low grain starch accumulation and poor plumpness for *os-lpa1*.

Frank *et al.* (2009) investigated the influence of mutational breeding on the contents of nutritionally relevant minerals in low phytic acid (*lpa*) mutants compared to their wild-types. Three *lpa* rice (*Os-lpa-XQZ-1*, *Os-lpa-XS110-1*, *Os-lpa-XS110-2*) were analyzed regarding their contents of phytic acid. The phytic acid reduction in *lpa* rice was

consistently more pronounced in *Os-lpa- XS110-1* than in *Os-lpa-XQZ-1* and *Os-lpa-XS110-2*. However, only for *Os-lpa-XQZ-1*, levels of calcium, iron and zinc were found to be consistently increased, whereas the cadmium level was shown to be predominantly decreased compared to the wild-type. This indicates *lpa* mutations do not result in systematic increases or decreases of mineral contents in rice. However, on the basis of the molar ratios of phytate/minerals in *lpa* rice were considered as predictive parameters and improved bioavailability of minerals in the *lpa* mutants.

Liang *et al.* (2009), tested the effect of soaking and phytase treatment on phytic acid and other minerals with the aim to maximise phytic acid removal and minimise losses of dry matter and minerals in rice of variety Kenjian 90-31. The products were soaked in demineralized water at 10°C (SDW), NaAc buffer of pH 3.5 at 10 °C (SAB), and 500 U L⁻¹ phytase of pH 5.5 at 50°C (SPS). In whole kernels and flour of white rice, phytic acid removal was 100%, losses of dry matter, Ca, Fe, and Zn were 2–5%, 12–63%, 9–10%, and apparent gain of 63–72%, respectively. In whole brown rice, SAB removed 75% phytic acid, and SPS 100% from flour; dry matter, Ca, Fe, and Zn losses were 1–16%, 26–56%, 39– 45%, and 23–24%. In rice bran, SPS removed 92% phytic acid, and SAB 50%; dry matter, Ca, Zn, and Fe losses were 20%, 48%, 63%, and apparent gain of 5%, respectively.

Zhao *et al.* (2013) identified the rice low phytic acid (*lpa*) mutant *Os-lpa- XS110-1*(*XS-lpa*) has ~45 % reduction in seed phytic acid (PA) compared with the wild-type cultivar Xiushui 110. They observed a single recessive gene mutation was shown to be responsible for the *lpa* phenotype and was mapped to a region of chromosome 3 near *OsMIK* (*LOC_Os03g52760*) and *OsIPK1* (*LOC_Os03g51610*), two genes involved in PA biosynthesis.

Li *et al.* (2014a) conducted experiment to produce agronomically competitive rice with nutritionally superior, environmentally safe phytic acid (PA) levels, hairpin RNA (hpRNA)- and artificial microRNA (amiRNA)-mediated gene silencing approaches were explored to reduce both myo-inositol kinase gene (*OsMIK*) expression and PA accumulation in rice seeds. *Ole 18*-driven *OsMIK* transcripts were significantly reduced

in both transgenic amiMIK and hpMIK seeds, which had phytic acid levels reduced by 14.9–50.2 and 38.1–50.7 %, respectively. No correlation between seed PA contents and decreased rates of seed germination and seedling emergence.

Li *et al.* (2014b) used the *OsMRP5* mutant gene to reduce seed PA as well as seed yield and viability, was down-regulated specifically in rice seeds by using an artificial microRNA driven by the rice seed specific promoter *Ole18*. Seed PA contents were reduced by 35.8–71.9 % in brown rice grains, lower seed weights (up to 17.8 %) accompanied by reductions of seed germination and seedling emergence in transgenic plants compared non transgenic plants. It was observed that the silencing of the *OsMRP5* gene increased the inorganic P(Pi) levels (up to 7.5 times) in amounts more than the reduction of PA-P in brown rice.

Sakai *et al.* (2015) studied the role of phytic acid in the dynamic accumulation and distribution patterns of mineral elements during seed development using two independent low phytic acid (*lpa*) mutants of rice (*Oryza sativa* L.). The reduced phytic acid in *lpa* seeds did not affect the translocation of mineral elements from vegetative organs into seeds, because the total amounts of phosphorus and the other mineral elements in *lpa* seeds were identical to those in the wild type (WT). However, the reduced phytic acid caused large changes in mineral localization within *lpa* seeds. Phosphorus and potassium in the aleurone layer of *lpa* greatly decreased and diffused into the endosperm. Zinc and copper, which were broadly distributed from the aleurone layer to the inner endosperm in the WT, were localized in the narrower space around the aleurone layer in *lpa* mutants.

2.6 Identification of reciprocal differences among the segregating generation of rice

Chandraratna and Sakai (1960) found matroclinous inheritance for grain weight in *indica* varieties. The coefficient of maternal effect in grain-weight inheritance in the cross reported was 32 *per cent*. The difference between reciprocal crosses was 0.39 g in the F₁; it was 0.12 g in the F₂. The effect of these cytoplasm-borne determinants is to shift the phenotypic expression of the progeny towards that of the female parent. In presence of complete maternal effect, the heritability was zero exactly as in a homozygous line but in

absence of maternal effect it was 28.6 *per cent* for 100 grain weight. The maternal effects for heterosis of protein and lysine content in indica hybrid rice was observed by Shi *et al.* (1999a).

Murayama *et al.* (1985) found reciprocal difference in plant height of many F₁ seedlings of rice. The plant height of F₁ obtained from the cross combinations whose maternal variety showed a tendency that it was taller than that from the reverse cross combinations.

Young and Virmani (1990) studied reciprocal differences between AxR and RxB crosses to find the effect of cytoplasm on heterosis for agronomic traits in rice and observed that the cytoplasm affected heterosis for plant height, days to flowering and grain yield.

Chang *et al.* (1991) studied meiotic behavior, pollen and spikelets fertility of parents and F₁ reciprocal hybrids. They commonly observed chromosomal aberrations in the 146 F₁ reciprocal hybrids such as loose pairings, univalents, chains-of-four, straggling chromosomes and laggards, bridges and fragments, and deficiency loops in low frequencies. Pollen fertility values showed more stability within a variety-group because they were less subject to environmental influences than spikelet fertility values. Eight crosses were showed significant differences (19–48%) for pollen fertility with their reciprocal crosses.

Shi *et al.* (1996) reported that nutrient quality traits of *Indica* rice (*Oryza sativa* L.). like lysine content, lysine index, and the ratio of lysine content to protein content were controlled by cytoplasmic and maternal effects. Cytoplasmic effects accounted for 2.41–20.80% of the total genetic variation and were significant for all nutrient quality traits.

Chen *et al.* (1998) observed the percentage of brown rice, milled rice recovery, grain length and chalkiness score were predominantly governed by maternal additive effects. The genetic variations of grain width and length/width ratio were mainly assigned to maternal additive× environment effect.

The cytoplasmic effects were observed for brown rice length, brown rice width, brown rice thickness, ratio of length to width of brown rice and ratio of length to thickness of brown rice of indica rice in different environments. All apparent quality traits were mainly affected by maternal X environment interaction effects (Shi *et al.*, 1999b).

Zhang *et al.* (2004) observed significant genetic correlations of seed additive, seed dominance, cytoplasm, maternal additive and maternal dominance between grain characteristics such as 100 grain weight, grain length, grain width, grain shape and mineral elements Fe, Zn, Mn and P contents.

The significant effect of cytoplasm and its interaction with nucleus on yield, width of flag leaf and low temperature tolerance along with some important agronomic traits in *japonica* rice was observed by Tao *et al.* (2004). The significant cytoplasmic effect on grain weight and filled grain ratio were detected in indica rice (Tao *et al.*, 2011).

The endosperm additive and maternal additive effects were predominant for the development of brown rice width from early to late stage of the grain development, but the endosperm dominant effect together with maternal effect and cytoplasmic effect became the major factor determining the brown rice width at the ripening stage (Zhang *et al.*, 2006).

Roy *et al.* (2010) observed reciprocal effect for days to 50% flowering, panicle length. Both negative and positive reciprocal effect was observed for days to maturity, number of primary branches per panicle and harvest index.

Yamagata *et al.* (2010) studied about hybrid incompatibility to show the reciprocal loss of duplicated genes encoding mitochondrial ribosomal protein L27 causes hybrid pollen sterility in F₁ hybrids of the cultivated rice (*Oryza sativa*) and its wild relative (*O. glumaepatula*). Functional analysis revealed that this gene is essential for the later stage of pollen development, and distribution analysis suggested that the gene duplication occurred before the divergence of the AA genome species.

The characters like percentage of brown rice, percentage of milled rice, kernel length, percentage of chalky grain, amylose content, gelatinization temperature, percentage of head rice and chalkiness were simultaneously controlled by seed genetic effects and maternal genetic effects (Qiang *et al.*, 2011). The gel consistency (mm) was mainly controlled by maternal genetic effects (Shi *et al.*, 1994).

Thirugnanakumar *et al.* (2011) studied the mean number of days to first flowering was lesser in the F_1 's of $P_1 \times P_2$ than its parents and reciprocal cross F_1 's. The F_2 and F_3 progenies of $P_2 \times P_1$ came to first flowering earlier than its homozygous and heterozygous parents as well as its direct cross. The mean and median were lesser than mode in the F_2 's and F_3 's of $P_1 \times P_2$, indicating the distribution was negatively skewed, whereas the reverse was true in the F_2 's and F_3 's of its reciprocal cross, indicating the distribution was positively skewed. Hence, selection for earliness can be practiced well in the F_2 's and F_3 's of $P_1 \times P_2$ than in its reciprocal F_2 and F_3 populations.

Asfaliza *et al.* (2012) conducted experiment to determine the combining ability and heritability of rice grain quality traits in crossed, reciprocal and parental lines. Where, reciprocal effect was significant for eight combinations for grain quality traits. Dhaliwal and Sharma (1990) have reported that maternal effect, have important role in plant height.

Abdul Rahim *et al.* (2013) studied the inheritance of blast disease resistance using local cultivars by making normal and reciprocal crosses between resistance variety Pongsu Seribu 2 (*Oryza sativa* L. subsp. *indica*) and susceptible variety Mahsuri (*Oryza sativa* L. subsp. *indica*). A total of 2560 F_2 plants from normal crosses and 3182 from reciprocal crosses were challenged with pathotype P7.2. A 3:1 (R:S) segregation ratio was observed in both types of crosses using the chi-square test, indicating the maternal effect which showed resistance to the blast disease caused by pathotype P7.2 is most likely controlled by a single nuclear gene.

Kiani *et al.* (2013) reported significant cytoplasmic effects as regard tiller number in Sang-e-Tarrom $\times$ Gerdeh and tiller number, flag leaf length and 1000 grain weight in

IRRI2×IR229. Similar results were obtained by Sasmal and Banerjee (1986). In addition, maternal effects were significant on plant height, panicle length, total grain number in panicle and 1000 grain weight in both crosses while flag leaf length in Sang-e-Tarrom × Gerdeh cross and flag leaf width and primary panicle in IRRI2×IR229 were significant.

Takai *et al.* (2014) demonstrated that the reciprocal chromosome segment substitution lines (CSSLs) were a useful tool for understanding the genetic mechanisms underlying yield potential in the high yielding indica rice cv. Takanari.

Mungayinka *et al.* (2015) crossed nine parents in a full diallel manner and evaluated for maternal genetic effects for resistance to rice yellow mottle virus disease. In the F₂ generation evaluated, eight out of the 14 reciprocal crosses showed significant reciprocal effects. The results revealed that cytoplasmic gene effects played a role in modifying resistance to RYMV with enhanced resistance when the resistant parent was used as female. Parental lines Gigante, Nerica 4 and Nerica 6 as the female produced progenies with better resistance than when they were used as the male parent. Segregation patterns generally suggested the presence of one or two genes with modifications beyond Mendelian ratios. This also revealed that the resistance to RYMV was affected by a very complex interaction of cytoplasm and nuclear genes.

Razzaque *et al.* (2017) studied to discover physiological and transcriptional variation associated with salt tolerance in reciprocal populations of rice. The cytoplasmic effect of the Horkuch (saline tolerance rice landrace of Bangladesh) background in leaves under stress showed functional enrichment for signal transduction, DNA-dependent regulation and transport activities. In contrast, the cytoplasmic effect of IR29 showed upregulation of apoptosis and down regulation of phosphorylation across tissues relative to Horkuch.

2.7 Identification or validation of organelle specific markers in reciprocal crosses of rice

Wolfe *et al.* (1987) Compared plant mitochondrial (mt), chloroplast (cp) and nuclear (n) DNA sequences and shown that the silent substitution rate in mtDNA is less

than one-third that in cpDNA, which in turn evolves only half as fast as plant nDNA. The slower rate in mtDNA than in cpDNA is probably due to a lower mutation rate. In cpDNA, the rate of substitution both at synonymous sites and in noncoding sequences in the inverted repeat is greatly reduced in comparison to single-copy sequences. The rate of cpDNA evolution appears to have slowed in some dicot lineages following the monocot/dicot split, and the slowdown is more clearly visible at nonsynonymous sites than at synonymous sites.

Taberalet *et al.* (1991) studied in order to find out whether chloroplast DNA primers were universal or not by using various plant species. The primers worked for most species tested including algae, bryophytes, pteridophytes, gymnosperms and angiosperms. The amplification in chloroplast DNA non-coding regions over a wide taxonomic range indicates that these primers may be used to study the population biology and evolution of plants.

McCauley (1995) proved that numerous species of plants have shown that intraspecific variation in chloroplast DNA is often sufficiently abundant to serve as a marker for studies of gene flow. The estimates of population structure based on cpDNA polymorphism should be especially sensitive to the impact of seed movement on gene flow, because cpDNA is often maternally inherited.

Demesure *et al.* (1995) studied the genetic information present in the plant mitochondrial DNA and chloroplast DNA is of great interest in phylogeny and in population genetics, largely because of the non mendelian mode of inheritance of these genomes. The circular DNA molecules has been shown to be highly conserved in structure. This has led to the design of pairs of universal primers which can amplify non-coding regions separating two coding sequences in most of the plants. Such non-coding sequences can then be explored in order to detect informative polymorphisms at a variety of taxonomic level.

Provan *et al.* (1996) detected intraspecific chloroplast variability. Diversity indices varied between 0.07 and 0.72. The length variation detected at multiple,

physically linked sites was used to identify 15 unique haplotypes with an overall diversity index of 0.90. This level of polymorphism is sufficiently high to allow chloroplast variability to be studied at the intraspecific level. The distribution of these haplotypes is described in relation to isozyme groupings and subspecies differentiation.

Provan *et al.* (1997) showed chloroplast DNA variability in wild and cultivated rice (*Oryza* spp.) revealed by polymorphic chloroplast simple sequence repeats. Diversity values ranged from 0.5224 ± 0.0845 (SE) to 0.8298 ± 0.0085 in the wild accessions, which was higher than that detected in the *O. sativa* accessions. Both intra- and inter-specific polymorphism was detected, and the extent of chloroplast genomic differentiation based on chloroplast simple sequence repeat (cpSSR) assays was quantified to trace the origin of rice polyploid species.

Ishii *et al.* (2001) used simple sequence length polymorphism to reveal the microsatellite variation and to clarify the phylogenetic relationships among A genome species of rice. For chloroplast microsatellites, the average number of alleles per locus and the average PIC value were 2.9 and 0.38, respectively. While the magnitude of diversity was much greater for nuclear microsatellites than for chloroplast microsatellites, they showed parallel patterns of differentiation for each taxonomic group. For both nuclear and chloroplast microsatellites, *O. sativa* showed the highest similarity values to *O. rufipogon*, and *O. glaberrima* was most similar to *O. barthii*. These data support previous evidence that these cultivars originated from the corresponding wild ancestral species.

Notsu *et al.* (2002) showed that sequences derived from plastid and nuclear genomes make up 6.3% and 13.4% of the mitochondrial genome, respectively. The degree of conservation of plastid sequences in the mitochondrial genome ranged from 61% to 100%, suggesting that sequence migration has occurred very frequently. Three plastid DNA fragments that were incorporated into the mitochondrial genome were subsequently transferred to the nuclear genome. This indicates frequent and independent DNA sequence flow to and from the mitochondrial genome during the evolution of

flowering plants, and this may account for the range of genetic variation observed between the mitochondrial genomes of higher plants.

Nishikawa *et al.* (2005) reported first phylogenetic analysis among plant species in the genus *Oryza*, based on mitochondrial and chloroplast SSR and their flanking sequences. The CC genome is suggested to be the maternal parent for the two BBCC genome species (*O. punctata* and *O. minuta*) and the CCDD species *O. latifolia*, based on the high level of sequence conservation between the diploid CC genome species and these allotetraploid species. Chloroplast SSR were more informative due to their higher sequence diversity.

Rajendrakumar *et al.* (2006) identified rice mitochondrial DNA sequence, possessing a repeat motif that is polymorphic between the wild abortive (WA)-CMS lines and their cognate isonuclear maintainer lines of rice. The PCR assay was able to precisely detect the impurities in a commercial seed lot of a popular CMS line, IR58025A. There is possibility of utilizing mitochondrial specific marker as a replacement for the morphology-based (grow-out test) GOT in accurate detection of contaminants in CMS seed stocks.

Tian *et al.* (2006) assembled rice (*Oryza sativa*) mitochondrial genomes for two cultivars, 93-11 (an indica variety) and PA64S (an indica-like variety with maternal origin of japonica), which are paternal and maternal strains of an elite super hybrid rice LYP-9, respectively. They identified 96 SNPs (0.02%) and 25 indels (0.006%) sequence variations as inter subspecific polymorphisms which is nearly 2.5 and 3 times lower than that of their chloroplast counterparts and 21 and 38 times lower than corresponding rates of the rice nuclear genome, respectively. The intra varietal polymorphism rates among analyzed mitochondrial genomes such as 93-11 and PA64S are 1.26% and 1.38% for SNPs and 1.13% and 1.09% for indels, respectively. Based on the total number of SNPs between the two mitochondrial genomes, we estimate that the divergence of indica and japonica mitochondrial genomes occurred approximately 45,000 to 250,000 years ago.

Rajendrakumar *et al.* (2007) identified and validated SSRs in both organellar genomes of rice and they identified 2528 SSRs in the mitochondrial genome and average 870 SSRs in the chloroplast genomes. About 8.7% of the mitochondrial and 27.5% of the chloroplast SSRs were observed in the genic region. The *rps* and *nad* gene clusters of mitochondria had the maximum repeats, while the *rpo* and *ndh* gene clusters of chloroplast had the maximum repeats.

Rajendrakumar *et al.* (2008) studied the organization of microsatellites in the coding and non-coding regions of organellar genomes of major cereals viz., rice, wheat, maize and sorghum. About 5.8-14.3% of mitochondrial and 30.5-43.2% of chloroplast microsatellites were observed in the coding regions. About 83.8-86.8% of known mitochondrial genes had at least one microsatellite while this value ranged from 78.6-82.9% among the chloroplast genomes. Dinucleotide repeats were the most abundant in coding and non-coding regions of the mitochondrial genome while mononucleotides were predominant in chloroplast genomes (Rajendrakumar *et al.*, 2007).

Kumagai *et al.* (2010) studied the genetic diversity and evolutionary relationships in genus *Oryza* revealed by using highly variable regions of chloroplast DNA using an in silico pre-analysis of the whole chloroplast genome and subsequent nucleotide sequencing of the regions with the greatest number of variant sites. They compared the complete chloroplast sequences of *Oryza sativa* japonica, *O. sativa* indica, and *O. nivara*, and identified regions containing many variant sites and also the maternal relationships among *Oryza* species.

Zhang *et al.* (2012) studied organelle genomes of Hassawi rice, a landrace resistance to salinity and drought and its hybrid. They discovered 16 InDels but no SNP and 48 InDels and 26 SNPs in the two Hassawi chloroplast and mitochondrial genomes, respectively. Microsatellite sequence analysis showed there are more SSRs in the genic regions of both cp and mt genomes in the Hassawi rice than in the other rice varieties. The frequent DNA rearrangement in the Hassawi mt and cp genomes indicate ongoing dynamic processes to reach genetic stability under strong environmental pressures.

III MATERIAL AND METHODS

The details of plant material used and methods adapted in the experiments were described here under the following headings

- 3.1 Details of plant material in the experiments
- 3.2 Details of methodologies adopted for the present investigation
- 3.3 Method of sampling and recording of observations
 - 3.3.1 Observations on growth traits
 - 3.3.2 Observations on yield attributing traits
 - 3.3.3 Observation on qualitative traits
- 3.4 Screening for disease resistance
 - 3.4.1 Brown spot disease
 - 3.4.2 Sheath blight disease
 - 3.4.3 Sheath rot disease
- 3.5 Estimation of protein and other grain nutrient traits
 - 3.5.1 Protocol for phytic acid estimation by Wade reagent method
 - 3.5.2 Standard curve for phytic acid estimation from Sodium phytate
- 3.6 Descriptive statistical analysis
- 3.7 Validation of organelle specific SSRs on parents for cytoplasmic effect

3.1 Details of plant material in the experiments

The field experiment was conducted under aerobic condition at experimental plots of Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru located at an altitude of 924 meters above mean sea level, with geographical co-ordinates of 13° 05" North latitude and 77° 34" longitude East, and falls into the Agro-climatic Zone-V of Karnataka. Most of these soils are red sandy loam soil and are characterized by low water and nutrient holding capacities and thus are low in productivity. The soil pH is around

6.5. The annual rainfall of Zone-V ranges from 528 mm to 1374.4 mm with the mean of 915.8 mm.

The experimental materials for the present study comprised the reciprocal crosses previously developed by Mahadevaiah and Hittalmani (2015) were obtained from Marker Assisted Selection laboratory, UAS, GKVK, Bengaluru. It composed of 479 straight cross (BPT 5204 × HPR-14) and 487 individual plants of reciprocal cross (HPR-14 × BPT 5204) of F₂ population. The BPT 5204 is a very popular variety grown in irrigated conditions in South India is known to fetch high price for its excellent cooking and milling quality. The HPR 14 is a local land race, purple pigmented, not popular and not cultivated on commercial scale but having high protein content. Salient features of parents are given below (Plate 1).

Table 1: Salient features of parents (BPT-5204&HPR-14) selected for the present study

Traits	BPT-5204	HPR-14
Plant stature	Medium tall (60-70 cm), Erect and compact	Tall (>90 cm) Medium spreading
Colour of plant, leaf & sheath	Green	Purple
Duration	Late (160 days)	Early (120 days)
Tillering ability	High (20)	Low (10)
No. of panicles	High (15-18) compact	Low (8-10)
Grain yield	4 ton/ ha	2.5 ton/ ha
Grain type	Short fine	Short bold
Total protein content	7-8%	13-14%



Plant type



Flowering time



Presence of Spikelet pigmentation (HPR-14)



Absence of Spikelet pigmentation (BPT5204)



Grain type



Grain type after dehusking

Plate 1: Variability for plant type, flowering time, spikelets pigmentation and grain type of parents BPT 5204 & HPR 14

Table 2: Observations recorded on F₂ individuals and F₃ families derived from straight and reciprocal crosses.

Growth traits	Yield attributing traits	Qualitative traits	Grain nutrient traits	Diseases
- Days to 50% flowering - Plant height at maturity(cm) - Total number of tillers - Total number of productive tillers - Physiological maturity (days)	- Number of fertile grains panicle⁻¹ - Number of chaffy grains panicle⁻¹ - Total number of grains panicle⁻¹ - Test weight (g) - Flag leaf length (cm) - Panicle length (cm) - Panicle exertion (cm) - Grain weight panicle⁻¹ (g) - Grain weight plant⁻¹ (g) - Biological yield (g) - Harvest index (%) - Grain length (cm) - Grain breadth (cm) - L/B ratio.	- Leaf blade colour - Spikelet's tip pigmentation - Node colour - Internode stem colour - Basal leaf sheath colour - Flag leaf type	- Protein (%) - Iron (ppm) - Zinc (ppm) - Amylose (%) - Carbohydrate (%) - Moisture (%) - Phytic acid (mg/100g)	- Brown spot - Sheath blight - Sheath rot

3.2 Details of methodologies adopted for the present investigation

The segregating plants of F₂ and F₃ straight (BPT 5204 × HPR 14) and reciprocal crosses (HPR 14 × BPT 5204) along with parents as checks were evaluated for growth and yield attributing traits, disease resistance and grain nutrient traits.

The experiment was laid out in augmented design and the observations were recorded on all the individual plants and used for statistical analysis. The straight and reciprocal F₂ population along with parents were sown on 18th July, 2015. The best two hundred lines were selected from F₂ population and forwarded to F₃ generation. After 21 days' nursery seedlings were transplanted in main experimental field with spacing of 30 cm × 20 cm at the experimental plots of Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru. In F₃ families, five plants were maintained (Plate 2 and 3). Recommended cultural practices for aerobic rice was carried out to ensure uniform crop stand as per the package of practices.

3.3 Method of sampling and recording of observations

The observations were recorded on all F₂ individuals & F₃ families from both straight and reciprocal crosses under aerobic conditions. The details of the observation recorded on various traits are presented below.

3.3.1 Observations on growth traits

3.3.1.1 Days to 50 *per cent* flowering (days)

The total number of days from sowing to the emergence of panicle in 50 *per cent* of the total plants in each plot was recorded.

3.3.1.2 Plant height at maturity (cm)

Height of the plant at maturity from the base of the plant to the tip of the main panicle was measured and expressed in centimeters.

3.3.1.3 Total number of tillers per plant

The total number of tillers in each plant was counted at the time of maturity.



Plate 2: Transplantation of F_3 progenies



Plate 3: General view of F_3 segregating population

3.3.1.4 Number of productive tillers per plant

The total number of productive panicle bearing tillers in each plant was counted at the time of maturity.

3.3.1.5 Physiological maturity (days)

Total number of days taken by each individual from sowing to physiological maturity of plant was recorded.

3.3.2 Observations on yield attributing traits

3.3.2.1 Panicle length (cm)

The length of the main panicle measured from the base to tip and was expressed in centimeters.

3.3.2.2 Panicle exertion (cm)

The total length between the flag leaf collar and the base of the panicle was measured to indicate the extent of panicle exertion. Depending on whether, the panicle base was above, below or in line with the flag leaf collar, the exertion was given positive, negative and zero values, respectively.

3.3.2.3 Flag leaf length (cm)

The length of the flag leaf measured from base to the tip and expressed in centimeters.

3.3.2.4 Total number of grains per panicle

The number of total grains from a single representative panicle per plant were counted and recorded.

3.3.2.5 Chaffy grains per panicle

The number of total chaffy or unfilled grains from a single representative panicle per plant were counted and recorded.

3.3.2.6 Test weight or 100 grain weight (g)

Weight of one hundred randomly selected filled grains was measured and recorded in grams.

3.3.2.7 Grain weight per panicle (g)

The weight of the grains per panicle was recorded in grams.

3.3.2.8 Grain yield per plant (g)

The weight of the grains per plant was recorded in grams after threshing, cleaning and drying.

3.3.2.9 Biological yield (g/plant)

Sun dried weight of each plants after harvesting from ground level (excluding roots) was recorded in grams.

3.3.2.10 Harvest index (%)

The ratio of grain yield per plant (economic yield) to the total biological yield was worked out and expressed in *per cent*.

3.3.2.11 Length of paddy grain (cm)

Ten paddy grains of each line were arranged lengthwise, for the cumulative measurement of length in centimeters of ten grains. Average length of the paddy grains was recorded as paddy grain length.

3.3.2.12 Breadth of the paddy grain (cm)

Ten paddy grains of each line were arranged breadthwise, for the cumulative measurement of breadth in centimeters of ten grains. Average breadth of the paddy grains was recorded as paddy grain breadth.

3.3.2.13 Length to Breadth (L/B) ratio of paddy grain

The ratio of length to breadth (L/B) of paddy grain was obtained by dividing the length of each grain by its corresponding breadth.

3.3.3 Observation on qualitative traits

3.3.3.1 Plant type / leaf blade colour

Number of plants were counted based on colour of the plant of leaf blade by giving score either as a green (1) or purple colour (2).

3.3.3.2 Spikelet's tip pigmentation

The anthocyanin pigmentation present within the pericarp on tip of the spikelets was scored as present (1) or absent (2).

3.3.3.3 Node colour

The colour of the node was recorded on each plant either as green (1) or purple (9). Within purple intensity of colour was varied and recorded as purple (9), strong purple (7), medium purple (5) and weak purple (3).

3.3.3.4 Internode colour

The colour of the internode was recorded on each plant as green (1), light gold (2), purple line (3) and purple (4).

3.3.3.5 Basal leaf sheath colour

The colour of the basal leaf sheath was recorded on each plant either as green (1), purple line (2), light purple (3) and purple (4).

3.3.3.6 Flag leaf type

The type of the flag leaf based on the attitude of blade, recorded either as erect (1), semi erect (3), horizontal (5) and deflexed (7).

3.4 Screening for disease resistance

The disease scoring in individual plants of both straight and reciprocal crosses of F₂& F₃ generation in aerobic rice under natural condition was carried out at different growth stages for different diseases by following 0-9 scale of standard evaluation system for rice of IRRI (2002).

3.4.1 Brown spot [*Bipolaris oryzae* (syn. *Helminthosporium oryzae*)]

Symptoms: Typical leaf spots are small, oval or circular and dark brown. Larger lesions usually have the same color on the edges but have a pale, usually grayish center. Most spots have a light yellow halo around the outer edge. Scoring was done at 60 days after transplanting.

Table 3: Method of scoring for brown spot disease

Scale	Percentage of affected leaf area
0	No incidence
1	Less than 1%
2	1 - 3%
3	4 - 5%
4	6 - 10%
5	11 - 15%
6	16 - 25%
7	26 - 50%
8	51-75%
9	76-100%

Source: IRRI (2002)

3.4.2 Sheath blight (*Rhizoctonia solani*)

Symptoms: Grayish-green lesions may enlarge and coalesce with other lesions, mostly on lower leaf sheaths, but occasionally on the leaves (The relative lesion height is the average vertical height of the uppermost lesion on leaf or sheath expressed as a percentage of the average plant height). Scoring was done at 60 days after transplanting.

Table 4: Method of scoring for sheath blight disease

Scale	Infection based on relative lesion height	Reaction
0	No infection observed	Immune
1	Lesions limited to lower 20% of the plant height	Resistant
3	20-30%	Moderately resistant
5	31-45%	Moderately susceptible
7	46-65%	Susceptible
9	More than 65%	Highly susceptible

Source: IRRI (2002)

3.4.3 Sheath rot (*Sorocladium oryzae*)

Symptoms: Oblong or irregular brown to grey lesions on the leaf sheath near panicle; sometimes coalescing to prevent emergence of panicle. Scoring was done at 85 days after transplanting.

Table 5: Method of scoring for sheath rot disease

Scale	Incidence of severely affected tillers	Reaction
0	No incidence	Immune
1	Less than 1 %	Resistant
3	1-5%	Moderately resistant
5	6-25%	Moderately susceptible
7	26-50%	Susceptible
9	51-100%	Highly susceptible

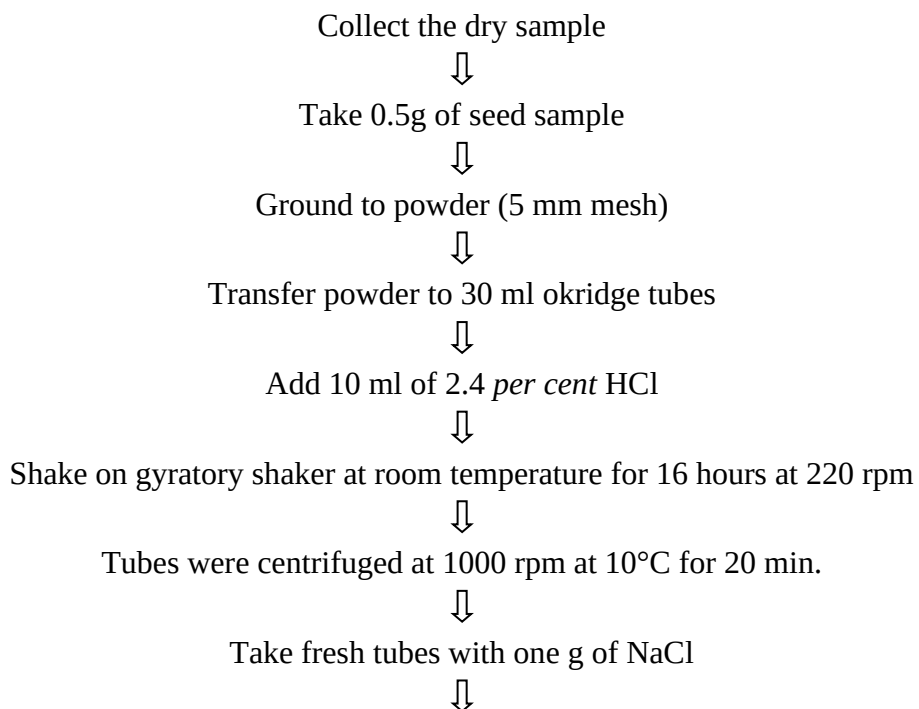
Source: IRRI (2002)

3.5 Estimation of protein and other grain nutrient traits

The Near Infrared Reflectance spectroscopy (NIR system, FOSS, Denmark) system was used for the estimation of total protein, iron, zinc, amylose, carbohydrates and moisture present in the grain. NIR is a fast and non-destructive technique that provides multi-constitute estimates. It works on the principle of detection and measurement of chemical composition of biological materials which was based on vibrational responses of chemical bonds to NIR radiations.

The phytic acid content present in the parents and two crosses of F₂& F₃ population was estimated by following the standard protocol of Gao *et al.*, 2007 and results were expressed as a percentage of dry weight (mg/100g). Using the standard protocol, 400 samples from two crosses were estimated and developed the standard spectra for phytic acid content in Near Infrared Reflectance spectroscopy (NIR system, FOSS, Denmark) system and remaining samples (F₂& F₃ population) were analyzed for phytic acid content using NIR. The SPSS version 16.0 software was used to obtain frequency distribution curves for grain nutrients traits.

3.5.1 Protocol for phytic acid estimation by Wade reagent method (Gao *et al.*, 2007)



Collect the supernatant in those fresh tubes
 ↓
 Shake for 20 min at 350 rpm in room temperature
 ↓
 Mixture was allowed to settle at 4°C for one hour or -20 °C for 20 min
 ↓
 Centrifuge at 1000 rpm at 10°C for 20 min.
 ↓
 Collect the treated supernatant and used for color development with wade reagent
 ↓
 Take one ml of supernatant + 24 ml of distilled de ionized water
 ↓
 3 ml of supernatant diluted + One ml of Wade reagent
 ↓
 Mix the mixture on vortex for 5-10 seconds
 ↓
 Centrifuge at 1000 rpm at 10°C for 10 min
 ↓
 Absorbance will be measured at 500 nm in spectrophotometer

Reagents

1. Wade reagent: 0.03 % FeCl₃.6 H₂O + 0.3 % sulfosalicylic acid
2. 2.4 % HCl: HCl supplied in lab is of 35 % (11.5 N/M)

$$N_1 V_1 = N_2 V_2$$

$$\text{Need} = 2.4 \%$$

So,

$$35\% \times V_1 = 2.4\% \times 100\text{ml}$$

$$V_1 = \frac{2.4\% \times 100\text{ml}}{35\%} = 6.857 \text{ ml of HCl in 100 ml water gives 2.4 \% HCl}$$

3.5.2 Standard curve for phytic acid estimation from Sodium phytate

Dissolve 0.4 g of sodium phytate in 100 ml water (4 mg/ml) (Stock 1)



Take one ml from this stock



Dilute it to 100 ml (Stock 2)



One ml contains 0.04 mg/ml (or 40 µg/ml)



Prepare the standard containing series of 3 to 30 µg of PA/ml

$$N_1 V_1 = N_2 V_2$$

$$40 \text{ µg/ml} \times V_1 = 3 \text{ µg/ml} \times 4 \text{ ml}$$

$$V_1 = \frac{3 \text{ µg/ml} \times 4 \text{ ml}}{40 \text{ µg/ml}} = 0.3 \text{ ml or } 300 \text{ µl}$$

So,

300 µl of stock 2 contains – 3 µg of PA

600 µl of stock 2 contains – 6 µg of PA

900 µl of stock 2 contains – 9 µg of PA

1.2 ml of stock 2 contains – 12 µg of PA

1.5 ml of stock 2 contains – 15 µg of PA

3.6 Descriptive statistics analysis

The statistical analysis of RILs were carried out on the mean values of five randomly selected plants from each F₃ families of the straight and reciprocal crosses for individual characters using WINDOSTAT (version 8.5) statistical package. For F₂ population, the statistical analysis was carried out on individual plants using SPSS 23.0 version and WINDOSTAT (version 8.5). The following descriptive statistics were calculated as per Sundararaj *et al.* (1972).

Table 6: Preparation of standard solution for phytic acid estimation in rice.

Sl. No.	PA concentration (µg/ml)	Amount of stock 2 to be taken (ml)	Amount of distilled water (ml)	Wade reagent to be added (ml)	Final volume(ml)
1	0	0.0	3.0	1.0	4.0
2	3	0.3	2.7	1.0	4.0
3	6	0.6	2.4	1.0	4.0
4	9	0.9	2.1	1.0	4.0
5	12	1.2	1.8	1.0	4.0
6	15	1.5	1.5	1.0	4.0
7	18	1.8	1.2	1.0	4.0
8	21	2.1	0.9	1.0	4.0
9	24	2.4	0.6	1.0	4.0
10	27	2.7	0.3	1.0	4.0
11	30	3.0	0.0	1.0	4.0

3.6.1 Mean

On the basis of individual plant observations, the population mean for each character was computed as follows.

$$\bar{X} = \left[\frac{(\sum_{i=1}^n X_i)}{n} \right]$$

Where,

X= population mean

X_i= individual value

n= number of observations

The trait means of segregating populations were compared with parental trait mean values.

3.6.2 Range

Range for each trait was estimated as difference between highest and lowest trait mean value.

3.6.3 Variance

Variance is defined as the average of the squared deviations of individual observation from the mean or it is the square of the standard deviation. It is expressed as the sum of squares of the deviations of all observations of a sample from its mean and divided by (n-1), where n is the number of observations.

3.6.4 Test of normality and nature of frequency distribution

Frequency distribution of genotypes for growth and yield attributing, grain nutrient traits was constructed using SPSS 23.0 version. Skewness, the third degree statistics and kurtosis, the fourth degree statistics were estimated as per Snedecor and Cochran (1974) to understand the nature of distribution of segregating generation for growth and related traits under aerobic condition. The mean values of quantitative traits of above cross was used to estimate coefficients of skewness and kurtosis using 'SPSS' 23.0 version software program. Kurtosis indicates the relative number of genes controlling the traits (Robson, 1956). Three types of kurtosis are recognized based on the kurtosis value which depends on distribution curve.

If kurtosis value = 3 = Normal curve = Mesokurtic

If kurtosis value > 3 = Leaping curve = Leptokurtic

If kurtosis value < 3 = Flat curve = Platykurtic

Similarly, the lack of symmetry *i.e.*, skewness was recognized based on the coefficient of skewness values which range from -3 to +3. The type of distribution based on the skewness values are as follows.

If skewness value is zero = symmetrical distribution

If skewness value is negative = negatively skewed distribution

If skewness value is positive = positively skewed distribution

The Shapiro-Wilk Test For Normality

The Shapiro-Wilk test for normality (Shapiro and Wilk, 1965) has highest power of statistics to discriminate the departure of population from normality due to skewness and kurtosis. Statistics 'W' ranges from zero to one where smaller values indicate rejection from normality whereas higher value of 'W' indicates normality of population. Test of normality for all the traits recorded was carried out using 'SPSS 23.0 version'.

3.6.5 Identification of transgressive segregants

The individuals surpassing their parental limits were identified for all traits by direct counting and expressed as observed frequency of transgressive segregants (*per cent*).

$$\text{Transgressive segregants} = \frac{\text{Number of individuals surpassing better parent}}{\text{Total number of individuals}} \times 100$$

3.6.6 Estimation of genetic variability parameters

3.6.6.1 Coefficients of Variation

The co-efficient of variability both at phenotypic and genotypic levels for all the characters were computed by applying the formula as suggested by Burton and Devane (1953).

Phenotypic and Genotypic coefficient of variation (PCV and GCV)

The phenotypic and genotypic coefficient of variation for traits were estimated by using formula Burton and Devane (1953).

$$\text{PCV (\%)} = \frac{\sigma_P}{\bar{X}} \times 100$$

$$\text{GCV(\%)} = \frac{\sigma_g}{\bar{X}} \times 100$$

Where,

σ_P = Phenotypic standard deviation

σ_g = Genotypic standard deviation

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

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

PCV and GCV were classified according to Robinson *et al.*, (1949). 0-10% was considered as low, 10-20% as moderate and 20% and above as high value.

3.6.6.2 Heritability (%)

Broad sense Heritability estimate as *per cent* mean was calculated using the formula (Hanson *et al.*, 1956).

$$h^2(\%) = \frac{V_g}{V_p} \times 100$$

Where,

$h^2\%$ = Heritability percentage

V_g = Genotypic variance

V_p = Phenotypic variance

Heritability percentage was categorized as follows (Robinson *et al.*, 1949)

0-30% was considered as low,

30-60% was considered as moderate

60% and above as high.

3.6.6.3 Genetic advance (GA)

The extent of genetic advance expected through selection for each character was estimated by using the following formula given by Johnson *et al.* (1955).

$$\text{Genetic advance (GA)} = K h^2 \sigma_p$$

Where,

K = Selection differential which is equal to 2.06 at 5 *per cent* selection intensity

h^2 = Broad sense heritability estimated.

σ_p = Phenotypic standard deviation

Further, the GA as *per cent* of mean (GAM) was estimated by using the following formula,

$$\text{GS as per cent mean (GAM)} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where, GA = genetic advance estimated

$\bar{X}$ = mean of the population

The genetic advance as *per cent* of mean was categorized as suggested by Johnson *et al.* (1955) and the same is given below.

Low (0-10%); Moderate (10.1-20%) and High (>20%).

3.6.7 Estimation of correlation coefficients

To determine the degree of association of component traits with the dependent trait like grain yield, the correlation coefficients were computed as shown below using the formula given by Al-Jobourie *et al.* (1958) and Sunderaraj *et al.* (1972).

$$r_{(xy)} = \frac{\text{COV}(x,y)}{\sqrt{v(x) \cdot v(y)}}$$

Where, $r_{(xy)}$ = Phenotypic correlation coefficient between characters 'x' and 'y'

$V(x)$ = Phenotypic variance of character 'x'

$V(y)$ = Phenotypic variance of character 'y'

$\text{COV}(x, y)$ = phenotypic covariance of characters 'x' and 'y'

Significance of correlation coefficients, i.e., the calculated value of 'r' was compared against the table 'r' value with (n-2) degrees of freedom at 5% and 1% significance levels, where 'n' refers to number of pairs of observations.

3.6.8 Path coefficient analysis

Path coefficient analysis was carried out using phenotypic coefficient to ascertain the direct and indirect effect of the yield components on yield as suggested by Wright (1921) and Dewey and Lu (1959).

Standard path coefficients which are the standard partial regression coefficients were obtained by solving the set of 'p' simultaneous equations through the use of "Doolittle Technique" as described by Goulden (1959).

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

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

↓

$$P_{01} r_{1p} + P_{02} r_{2p} + \dots + P_{0p} = r_{0p}$$

Where $P_{01}, P_{02}, \dots, P_{0p}$ are the direct path coefficients of variables 1, 2, ..., p on the dependent variable 0, $r_{12}, r_{13}, \dots, r_{1p}, \dots, r_{p(p-1)}$ are the possible correlation coefficients between various independent variables, $r_{01}, r_{02}, r_{03}, \dots, r_{0p}$ are the correlation between dependent and independent variables.

The indirect effect of the i^{th} variable via j^{th} variable is attained as $P_{0j} \times r_{ij}$. The contribution of remaining unknown factor is measured as the residual factor, which is calculated as given below

$$P_{0X}^2 = 1 - (P_{01}^2 + 2P_{01}P_{02}r_{12} + 2P_{01}P_{03}r_{13} + \dots + P_{02}^2 + 2P_{02}P_{03}r_{23} + \dots + P_{0p}^2)$$

$$r_{13} + \dots + P_{0p}^2)$$

$$\text{Residual factor} = P_{0X}^2$$

The direct and indirect effects are rated as given below following the method of Lenka and Mishra (1973).

0.00 – 0.09 = Negligible

0.10 – 0.19 = Low

0.20 – 0.29 = Moderate

0.30 – 1.00 = High

>1.00 = Very high.

3.6.9 Chi-square test of goodness of fit

The differences between observed and expected number of plants in F₂ population anthocyanin pigmentation classes were examined using chi square (χ^2) test of goodness of fit as given by

$$\chi^2 = \sum_{i=1}^n \frac{(O_i - E_i)^2}{E_i}$$

The test statistic follows χ^2 distribution with (n-1) degrees of freedom

Where,

O_i=Observed number of accessions within ith qualitative trait class

E_i= Expected number of accessions within ith qualitative trait class

n= Number of classes

3.6.10 Finding relationship between plant pigmentation of leaves, spikelets, flag leaf, stem internode, basal leaf sheath with yield attributing traits in straight and reciprocal F₂'s derived from crosses between BPT-5204 and HP-14

The difference in the quantitative trait means between purple pigmented and non-pigmented trait mean was tested using two sample 't' test assuming unequal variances.

The test statistics was computed as,

$$t = \frac{\bar{x}_p - \bar{x}_g}{\sqrt{sp^2 \left(\frac{1}{n_p} - \frac{1}{n_g} \right)}}$$

Where,

X_p=trait mean in purple pigmented genotypes

X_g= trait mean in non pigmented genotypes

sp²= (n_p-1) sp²+ (n_g-1) sg²/n_p+n_g-2

n_p=number of purple pigmented genotypes

n_g=number of non pigmented genotypes

3.7 Validation of organelle specific SSRs on parents for cytoplasmic effect

3.7.1 DNA Isolation protocol

Both the parents (BPT 5204 & HPR 14) were used for validation of cytoplasmic effect in rice. Parental leaves were harvested from seedlings and genomic DNA was isolated as per the modified Cetyl trimethyl ammonium bromide (CTAB) method (Cao and Oard, 1997). The step-wise methodology detail is given below;

- One gram of fresh leaves was taken in 2ml tubes for DNA extraction.
- The leaves were crushed in liquid nitrogen to make fine powder.
- DNA extraction buffer was added and kept in water bath for 45 minute at 65⁰C with intermittent shaking.
- After 45 minutes, samples were taken out from water bath and 1 ml of chloroform: Isoamyl alcohol (24:1) was added and mixed well.
- The solution was centrifuged at 10,000 rpm for 10 minutes and supernatant was transferred to fresh eppendorf tube.
- Supernatant was mixed with equal volume (500 µl) of phenol: chloroform solution and centrifuged at 10,000 rpm for 10 min.
- Supernatant was collected and transferred to new 1.5 ml Eppendorf tube. Then 700 µl of isopropanol and 50 µl sodium acetate was added and kept at -20⁰C overnight for precipitation.
- Afterwards, tubes were removed from the deep freezer and kept outside to attain room temperature. Then centrifuged at 10,000 rpm for 10 minutes.
- Supernatant was decanted without disturbing the pellet. Added 70% alcohol and centrifuged for 10,000 rpm for 10 minutes. Pellet was dried and suspended in 50 µl of 1 X T10E1 buffer.
- RNase was added (1 mg/ml) to the DNA and incubated at 37⁰C in water bath for half an hour.
- The DNA was stored at -20⁰C.

3.7.2 Quantification of DNA using Nano Drop

DNA purity and quantity was determined using Nano DropTM spectrophotometer. The ratios between the reading at 260 nm and 280 nm provide an estimate of DNA purity. Pure DNA samples will have a ratio of 1.8. If the sample is contaminated by protein the ratio will be significantly less. Ratio of 2.0 or more indicates a high proportion of RNA in the sample. DNA has maximum absorbance at 260 nm. One μL of DNA isolated from rice leaves were fed to the sample pedestal and the absorbance at 260 and 280 nm were recorded against a buffer blank. A 260/280 nm ratio for all the samples was calculated to check the purity. DNA was quantified using the formula

$$\mu\text{g ds DNA}/\mu\text{L} = (\text{A}_{260} * 40)/2$$

Further all the samples were diluted to a final concentration of 10 - 20 ng/ μL .

3.7.3 DNA quantification on agarose gel

Submersible agarose gel electrophoresis was used to separate the DNA based on size. Genomic DNA was electrophoresed in 0.8 % agarose. Details are as follows.

- 0.8 g of agarose was weighed and taken in a clean 100 ml conical flask. To this 100ml of 1x TE buffer (0.89 M Tris base, 0.02 MEDTA, pH = 8) was added. And then the agarose was dissolved by heating. After agarose completely melts, it was cooled to 60°C and 3.5 μL of ethidium bromide was added (10 mg/ml) and mixed.
- The ends of gel casting trays were sealed with tapes. Agarose was poured; comb was inserted and allowed to solidify. After solidification the tape on either side was removed and the gel was immersed in electrophoresis tray having 1X TE buffer. Then the comb was removed.
- Two μL of DNA samples and 2 μL of 6X loading dye was mixed well and loaded into the well. 2 μL of standard uncut lambda DNA was used as marker.
- Electrophoresis was carried out at 100 V for 2 hours until the bromophenol blue dye migrated to the two-third of the gel. The gel tray was removed and the gel was observed under UV trans illuminator and documented using BioRad Gel Doc system.

The quantity of the DNA was determined based on the intensity of the band relative to lambda uncut band.

3.7.4 PCR Reaction mixture

The microsatellites reaction mixture consisted of 10 ng of template DNA, 10 μ M/ μ l of each of forward and reverse primer (Research Genetics, USA), 100 μ M of dNTPs, 1 U of Taq DNA polymerase (Bangalore Genei, India) and 10x PCR buffer (10 mM Tris pH 8.0, 50 mM KCl, 1.8 mM MgCl₂ and 0.01 mg/ml gelatin) in a volume of 10 μ l. The PCR mixture for one reaction is given below.

SSR reaction mixture	1x
Template DNA (10 ng)	2.0 μ l
Primer mix (forward and reverse)	1.0 μ l
dNTP mix (1mM)	1.0 μ l
Taq buffer (10X)	1.0 μ l
Taq polymerase (5U/ μ l)	0.3 μ l
Sterile water	4.7 μ l
Total	10.0 μ l

The amplification profile was as follows:

- | | | | | |
|-------------------------------------|---|-------|---|---------|
| 1. Initial denaturation temperature | : | 94° C | - | 5 min |
| 2. Denaturation | : | 94° C | - | 1 min |
| 3. Primer annealing | : | 56° C | - | 0.5 min |
| 4. Primer extension | : | 72° C | - | 1 min |

The above three stages were repeated 35 times

- | | | | | |
|------------------------------|---|-------|---|---------------|
| 5. Complete primer extension | : | 72° C | - | 5 min |
| 6. Soak temperature | : | 4° C | - | until removed |

3.7.5 Parental polymorphism

A total of 20 different universal mitochondrial (mt) DNA specific primers primarily used by Khera *et al.*, 2012 (Table 2) and a total of 21 chloroplast DNA specific primers used by Provan *et al.*, 1996 (Table 3) synthesized by Eurofins Genomics India Pvt. Ltd., Bengaluru were used in this study. These universal mt DNA primers were designed based on consensus mt DNA (Petit *et al.*, 1998; Wu *et al.*, 1998) derived from the various mitochondrial genes. The parental polymorphism on MultiNa (Microchip Electrophoresis System for DNA/RNA Analysis, Shimadzu Biotech, Tokyo, Japan) was carried out using 20 mitochondrial and 21 chloroplast specific simple sequence repeats (SSRs). The protocol of MultiNa is given below.

1. PCR products were prepared using DNA of parents for different SSR primers.
2. A 100 µl solution of SYBR GOLD using 1 µl SYBR GOLD (Invitrogen) and 99 µl 1X TE buffer was prepared in 2ml eppendorf tube.
3. About 2500 µl mixture of Separation buffer DNA-500 from Shimadzu with 2475 µl and 25 µl solution of SYBR GOLD was prepared in 2ml eppendorf tube.
4. About 200 µl Marker solution DNA-500 (Shimadzu) was taken in 2 ml eppendorf tube.
5. DNA ladder 25bp (Invitrogen) solution of 50 µl was prepared with 1 µl DNA ladder 25bp and 49 µl 1X TE buffer in 2ml eppendorf tube.
6. The PCR product in a plate with 96 samples was loaded in the MultiNA along with all other solutions.
7. The MultiNA was run for 210 minutes with four chips for reading the samples.
8. Gel images and graphs of DNA amplifications were saved.

Table 7: List of mitochondrial DNA specific microsatellite primers

Sl. No.	Primer name	Primer Sequence 5' to 3'	Annealing Temp.(°C)
1	Nad1 F	GCATTACGATCTGCAGCTCA	57.3
	Nad1 R	GGAGCTCGATTAGTTTCTGC	57.3
2	Nad4ex1 F	CAGTGGGTTGGTCTGGTATG	59.4
	Nad4ex1 R	TCATATGGGCTACTGAGGAG	57.3
3	Nad4ex2 F	TGTTTCCCGAAGCGACACTT	57.3
	Nad4ex2 R	AACCAGTCCATGACTTAACA	53.2
4	rpS14 F	CACGGGTCGCCCTCGTTCCG	67.6
	rpS14 R	GTGTGGAGGATATAGGTTGT	55.3
5	coxII F	AATCCAATCCCGCAAAGGATT	55.9
	coxII R	AGAAGATGATCCAGAATTGGG	55.9
6	Rrna F	GTGTTGCTGAGACATGCGCC	61.4
	Rrna R	ATATGGCGCAAGACGATTCC	57.3
7	alp F	TTTGCCAGCGGTGTTAAAGG	57.3
	alp R	CTTCGCCATATTGTGCCAATTC	58.4
8	Atp6 F	GGAGGTGGAAATTCAGTTCCAA	58.4
	Atp6 R	TAGCATCATTCAAGTAAATACA	50.9
9	Cob F	AGTTATTGGTGGGGGTTCCG	59.4
	Cob R	CCCCAAAAGCTCATCTGACCCC	64.0
10	coxIa F	GGTGCCATTGCTGGAGTGATGG	64.0
	coxIa R	TGGAAGTTCCTTAAAAGTATG	49.1
11	coxIb F	GGCTTTTCTCCACTAACCACAA	58.4
	coxIb R	GGAGGGCTTTGTACCATCCATTC	62.4
12	cox2 F	GATGCTGCTGAACCTTGGA	59.4
	cox2 R	TCCGATACCATTGATGTCC	54.5
13	cox3 F	GTAGATCCAAGTCCATGGCCT	59.8
	cox3 R	GCAGCTGCTTCAAAGCC	55.2
14	Nad1A F	CTAGCTGAACGTAAAGTAATGGC	58.9
	Nad1A R	CCAACCTGCTATAATTATTCC	54.0
15	Nad3 F	AATTGTCGGCCTACGAATCTG	57.9
	Nad3 R	TTCATAGAGAAATCCAATCGT	52.0
16	Nad3A F	AATTGTCGGCCTAGGAATGTG	57.9
	Nad3A R	GCTCGTGTACGGTCTGTGGG	63.5
17	Nad4A F	ATACGATTGATTTCGGTCTGTG	55.9
	Nad4A R	TGAACTGGTACCATAGGCACTTT	58.9
18	Nad5A F	GAAATCTTTGATGCTTCTTGGG	56.5
	Nad5A R	ACCAACATTGGCATAAAAAAAGT	53.5
19	Nad5D F	ATAAGTCAACTTCAAAGTGGA	52.0
	Nad5D R	CATTGCAAAGGCATAATGAT	51.2
20	Rps14 F	ATACGAGATCACAAACGTAGA	54.0
	Rps14 R	CCAAGACGATTTTTTTTATGCC	54.0

Table 8: List of chloroplast DNA specific microsatellite primers

Sl.No.	Primer name	Primer sequence (5'-3')	Tm (°C)
1	Oscp3536 F	TCCATAACATCCTTTTCAATCC	55.7
	Oscp3536 R	GCTGGTTTTCTATGAAGTAGACC	48.5
2	Oscp29138 F	CAAAAATTTGTGCACCGTTAC	50.5
	Oscp29138 R	AATATCTCTCATTTCGACGC	50.5
3	Oscp43899 F	GGATCTAGGCATAATTCCCAA	50.5
	Oscp43899 R	GAGCATAGGGATCGATTGAT	52.4
4	Oscp49274 F	TTGGTCAAGTAGGGGAAACTC	48.5
	Oscp49274 R	TAGTTTATGCATGGCGAAAAG	46.8
5	Oscp75969 F	GGAATTTGGACATTTTCGC	50.5
	Oscp75969 R	AAGACAGGGGTAATCTTTCGA	49.5
6	Oscp76221 F	GGAAAAAATAAGTCTCTTTGTTGA	52.4
	Oscp76221 R	AGACTCGAAGGATACCGAAGA	52.4
7	Oscp76527 F	GCTTCCATAACTAAACCCTCG	52.4
	Oscp76527 R	CCCAAATTCTATCTTGAACCTCC	51.7
8	Oscp78412 F	GGAAAGGTTAGGGTTTTTAATATTG	51.1
	Oscp78412 R	CCGCGATGCAATAAGAGTAAA	50.5
9	Oscp80599 F	GTCATAAATAAGGTTATTCCCCG	51.7
	Oscp80599 R	GGATACTAAATCTCGTCGTAACTG	54.4
10	Oscp89568 F	TTCATTTGGAATCTGGGCT	46.8
	Oscp89568 R	CGCTGTACCTAGAGGATAGGG	56.3
11	Oscp124451 F	ATAGAGGAAGAGGGAAAAATCG	51.1
	Oscp124451 R	CTCGGTATCAATCCCCTTG	51.1
12	Oscp134510 F	GGAATTCGTACCAACTCGG	51.1
	Oscp134510 R	GAAAGGAAAGCTAGAAATACCCA	51.7
13	Ctrn1 F	ACGGGAATTGAACCCGCGCA	55.9
	Ctrn1 R	CCGACTAGTTCGGGGTTCGA	55.9
14	Ctrn2 F	GGGTTGCCCGGGACTCGAAC	60.0
	Ctrn2 R	CAACGGTAGAGTACTCGGCTTTTA	55.7
15	Ctrn3 F	CCAGTTCAAATCTGGGTGTC	51.8
	Ctrn3 R	GGGATTGTAGTTCAATTGGT	47.7
16	Ctrn4 F	ACCAATTGAACTACAATCCC	47.7
	Ctrn4 R	CTACCACTGAGTTAAAAGGG	49.7
17	Ctrn5 F	GGTCGTGACCAAGAAACCAC	53.8
	Ctrn5 R	GGTTCGAATCCCTCTCTCTC	53.8
18	Ctrn6 F	GAGAGAGAGGGATTCTGAACC	53.8
	Ctrn6 R	CATAACCTTGAGGTCACGGG	53.8
19	Ctrn7 F	ACTTCTGGTTCCGGCGAACGAA	56.7
	Ctrn7 R	AACCACTCGGCCATCTCTCCTA	56.7
20	Ctrn8 F	CGAGGGTTTCAATCCCTCTC	55.9
	Ctrn8 R	AGAGCATCGCATTGTGAATG	47.7
21	Ctrn9 F	TGCTTTCATACGGCGGGAGT	53.8
	Ctrn9 R	GCTTTAGTCTCTGTTTGTGG	49.7

IV RESULTS AND DISCUSSION

Rice is a staple food crops that is consumed by more than 65% of global population; it occupies a position of overwhelming importance in Asian agriculture and constitutes the bulk of the Asian diet too. To feed the growing population and to achieve food security in the country, current production levels need to be increased. Hence, it is critical to produce high yielding cultivars with high quality of rice. The presence of adequate genetic variability is pre requisite factor for rice improvement. Among the different options, exploiting the variability present in segregating populations is essential for improvement through selection and identification of maternal effect in reciprocal crosses helps to identify some traits which are controlled by cytoplasmic genes and useful for development of new high yielding cultivars. Reciprocal crosses play an important role in the selection of any breeding programme for population improvement and development of new hybrids in the crop. Reciprocal differences prevail in nature mainly due to unequal contribution of cytoplasmic determinants from male and female gametes to the zygote. Both the parents contribute genes to their offspring, but the influence of female parent often extends beyond simple genetic transmission. In the present study, estimation of cytoplasmic and maternal effects in rice and their adequacy in describing the observed reciprocal differences based on study of the parents, F_2 s, F_3 s and reciprocal cross progenies was carried out. The experimental results obtained from the present investigation has been presented below under the following sub headings.

4.1 Genetic variability studies for growth, yield attributing and grain nutrient traits

4.1.1 Effect of reciprocal cross differences on mean performance of straight and reciprocal F_2 and F_3 populations

4.2 Observed probabilities of transgressive segregants

4.3 Effect of reciprocal cross differences on genetic variability on straight and reciprocal F_2 and F_3 populations.

4.3.1 Effect of reciprocal cross difference on range

4.3.2 Effect of reciprocal cross difference on GCV and PCV

- 4.3.3 Effect of cross difference on heritability and genetic advance as *per cent* mean (GAM)
- 4.4 Association of yield attributing and grain nutrient traits and their reciprocal differences in straight and reciprocal F₂ and F₃ populations
- 4.5 Genetics of quantitative and qualitative traits in straight and reciprocal F₂ and F₃ populations
 - 4.5.1 Number of genes controlling quantitative traits inferred from third and fourth degree statistics
 - 4.5.2 Frequencies of quantitative characters in straight and reciprocal F₂ populations
 - 4.5.3 Segregation of anthocyanin pigmentation in straight and reciprocal F₂ populations
- 4.6 Reciprocal differences on qualitative traits in straight and reciprocal F₂ populations
 - 4.6.1 Cytoplasmic effect of leaf blade colour
 - 4.6.2 Cytoplasmic effect of spikelet's pigmentation
 - 4.6.3 Cytoplasmic effect of flag leaf type
 - 4.6.4 Cytoplasmic effect of stem internodes colour
 - 4.6.5 Cytoplasmic effect of basal leaf sheath pigmentation
- 4.7 Parents offspring correlation and regression in straight and reciprocal F₂ and F₃ populations
- 4.8 Screening for disease reactions in straight and reciprocal F₂ and F₃ populations
- 4.9 Identification of superior RIL's (top ranked F₃ families) for quantitative, grain nutrient traits and disease response in straight and reciprocal F₂ and F₃ populations
- 4.10 Validation of organelle specific SSRs on parents BPT-5204 and HPR-14 for cytoplasmic effect

4.1 Genetic variability studies for growth, yield attributing and grain nutrient traits

4.1.1 Effect of reciprocal cross differences on mean performance of straight and reciprocal F₂ and F₃ populations

Significant differences between mean performance of straight and reciprocal F₂ and F₃ for yield and yield attributing traits were strong evidence to conclude for presence of reciprocal difference (Table 9; Plate 4, 5, 6, 7 and 8).

Mean performance of number of productive tillers per plant was high in straight F₂ population (average of 12.62 when HPR-14 used as male parent) as compared to its reciprocal F₂ population (average of 10.95 when HPR-14 as a female parent) followed by biomass per plant.

Mean performance of chaffy grains per plant was high in straight F₃ families (average of 25.63 when HPR-14 used as male parent) as compared to its reciprocal F₃ families (average of 23.33 when HPR-14 used as female parent) followed by number of productive tillers per plants.

In both F₂ and F₃ population, mean performance of yield & yield attributing traits were affected by the parents (BPT-5204 & HPR-14) when used as male and female parents and *vice versa*. This would be an evidence to conclude that cytoplasm of BPT-5204 and HPR-14 has undesirable effect and moderately interferes with manifestation of yield & yield attributing traits similarly, cytoplasm influence of same parents for sheath rot disease (Mahadevaiah *et. al.*, 2015).

Significant differences between mean performances of straight and reciprocal F₂ and F₃ populations was also observed. The mean performance of grain iron content in rice was high in straight F₂ (average 11.87) when HPR-14 was used as male and straight F₃ (Average 11.76) as compared to its reciprocal F₂ population (average 11.29) and F₃ families (average 11.21) when HPR-14 was used as female parent. The same trend was followed for carbohydrates content in rice grain. This significant differences in respect of grain nutrient traits showed evidences for reciprocal difference (Table 10).

Table 9: Estimates of traits mean performance of F₂& F₃ generation in straight and reciprocal crosses of rice

Traits	F ₂			F ₃			Parents	
	SC	RC	Two sample t test P value/ t statistics (assuming unequal variance)	SC	RC	Two sample t test P value/ t statistics (assuming equal variance)	BPT 5204	HPR 14
DF	96.59	94.61	2.97**	96.56	97.49	-1.05	104.06	101.94
PH	88.15	90.82	-2.97**	91.76	96.35	-3.72***	97.75	107.41
NT	15.01	14	3.07**	15.47	15.12	0.94	14.22	10.24
NPT	12.62	10.95	4.95***	12.76	12.04	2.09*	12.06	7.88
DM	127.1	125.51	2.38*	127.12	128.67	-1.76	133.44	131.71
PL	20.2	19.99	-0.41	20.19	19.67	1.36	19.97	22.32
PE	0.14	0.65	-2.13*	0.41	0.95	-1.56	1.88	5.19
FLL	26.55	27.29	-2.39*	27.39	28.36	-2.17*	21.08	32.64
TGPP	142.61	137.74	2.21*	144.84	141.94	1.12	149.89	167.12
FGPP	117.44	113.54	1.85	119.22	118.51	0.35	122.61	133.76
CGPP	25.17	24.2	0.77	25.63	23.33	2.18*	27.28	33.35
SFP	81.86	82.4	-0.63	82.03	83.59	-2.25*	79.17	79.04
GWPP	2.26	2.24	0.58	2.39	2.3	1.85	1.87	2.72
TW	1.81	1.86	-3.26**	1.92	1.96	-2.06	1.42	1.97
GYPP	15.14	14.19	1.63	16.49	17.07	-0.87	23.3	17.5
BM	27.41	24.09	4.34***	29.16	28.95	0.24	45.69	29.76
HI	0.53	0.56	-1.8	0.56	0.59	-2.23*	0.51	0.59
GL	7.14	7.34	-8.46***	7.13	7.33	-4.59***	7.03	6.78
GB	2.35	2.33	1.32	2.31	2.35	-1.96	2.11	2.45
LBR	3.06	3.19	-6.16***	3.13	3.15	-0.83	3.36	2.8

* Significant at 5 per cent

** Significant at 1 per cent

*** Significant at 0.1 per cent

SC: Straight Cross (BPT 5204 × HPR-14); **RC:** Reciprocal Cross (HPR-14 × BPT 5204)

DF=50 % flowering

PH= Plant height (cm)

NT: Number of tillers

NPT= Number of productive tillers

DM= Days to maturity

PL= Panicle length(cm)

PE= Panicle exertion (cm)

FLL= Flag leaf length (cm)

TGPP= Total grains per panicle

FGPP= Fertile grains per panicle

CGPP= Chaffy grains per panicle

SFP: Seed fertility percentage

GWPP= Grain weight per panicle (g)

TW= Test weight (g)

GYPP= Grain yield per plant (g)

BM= Biomass (g)

HI: harvest index (%)

GL= Grain length (cm)

GB= Grain breadth (cm)

LBR: L/B ratio of paddy grain



Plate 4: Variability for grain type in straight F₂ population (BPT 5204 × HPR 14) along with parents



Plate 5: Variability for grain type in reciprocal F₂ population (HPR 14 × BPT 5204) along with parents

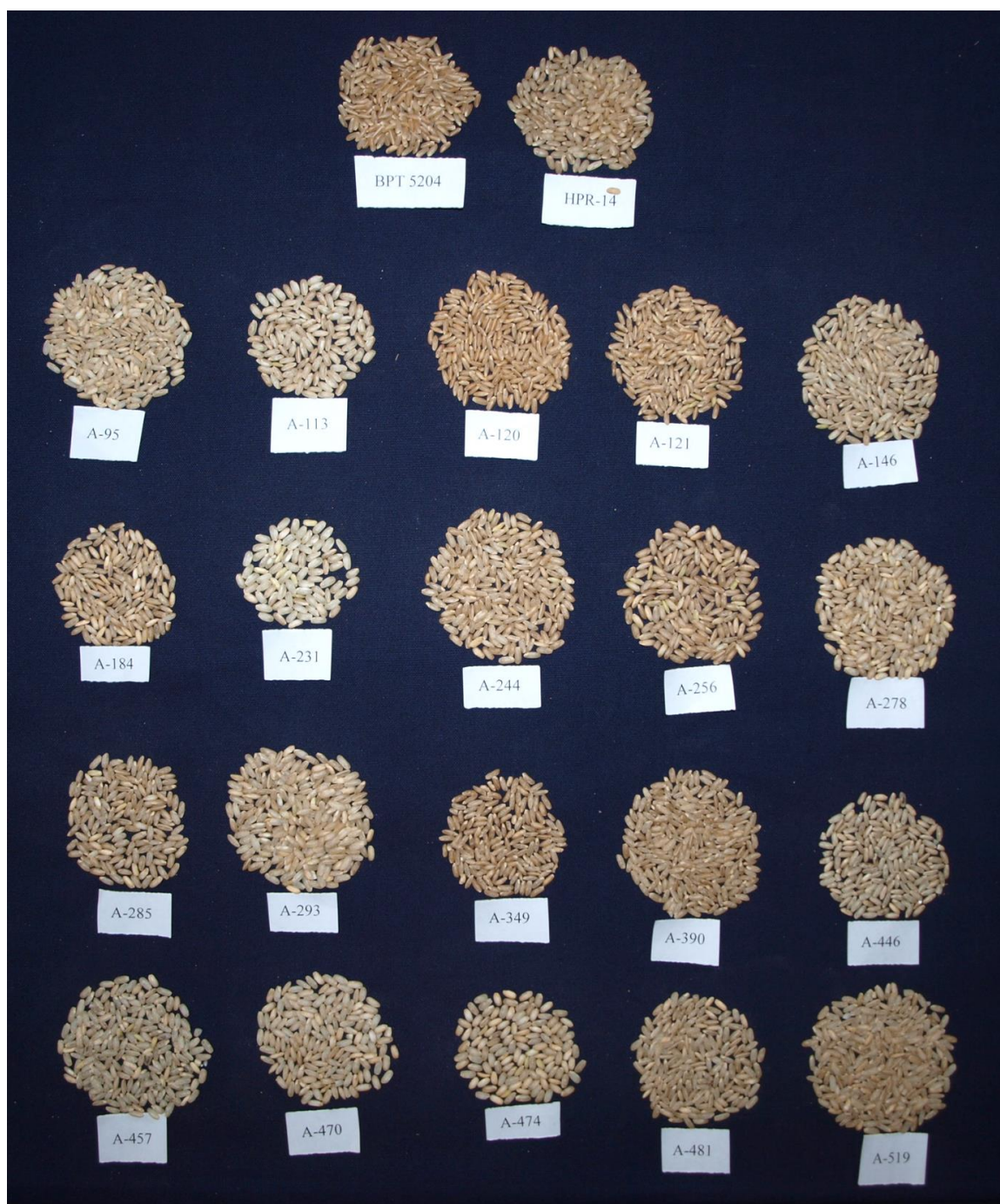


Plate 6: Variability for grain type in straight F₂ population (BPT 5204 × HPR 14) along with parents after dehusking.

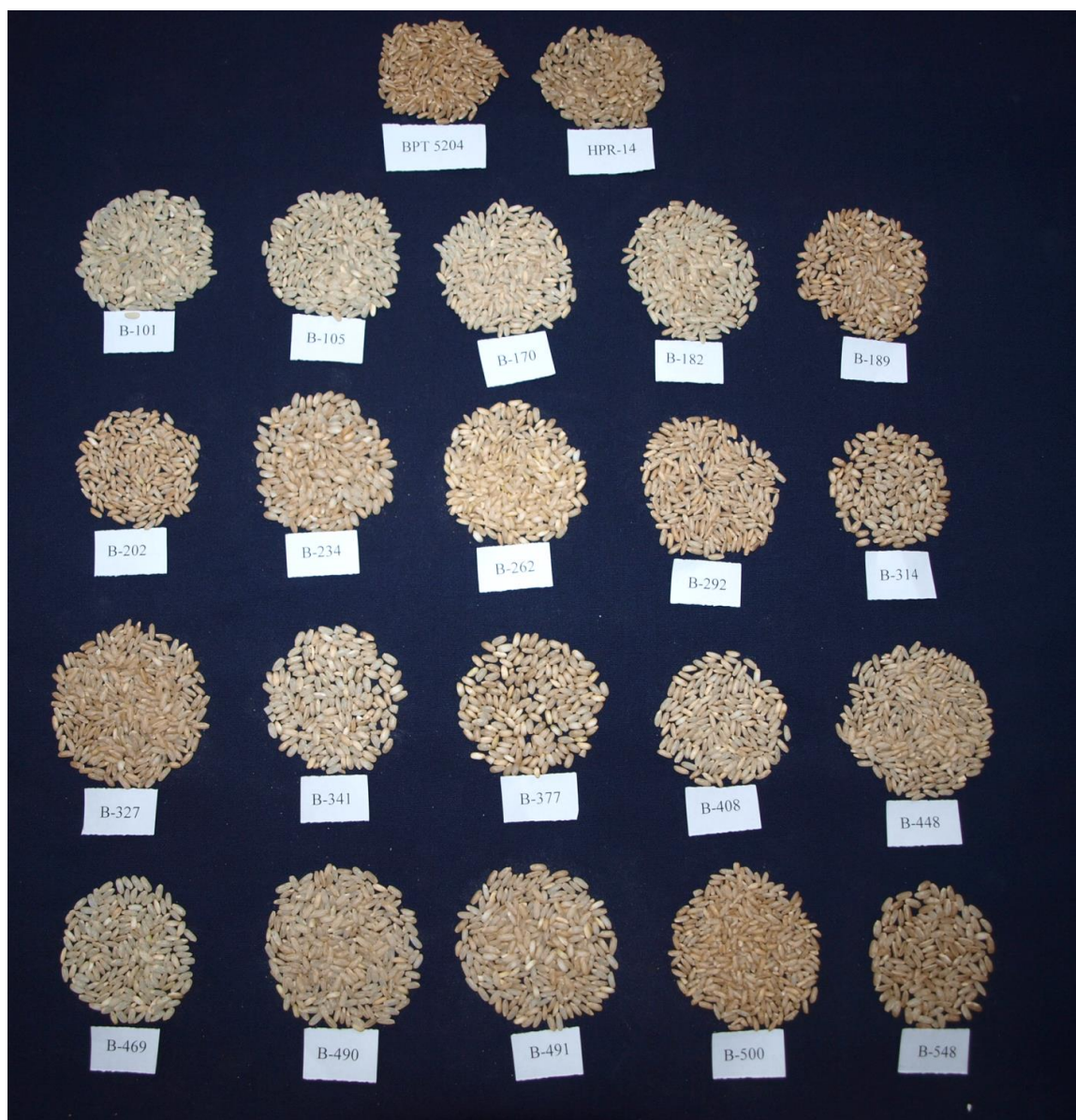


Plate 7: Variability for grain type in reciprocal F₂ population (HPR 14 × BPT 5204) along with parents after dehusking.



Plate 8: The variability present at field in F₃ segregating generation.

Table 10: Estimates of grain nutrient traits mean performance of F₂& F₃ generation in straight and reciprocal crosses of rice

Grain nutrient traits	F ₂			F ₃			Parents	
	SC	RC	Two sample t test P value/ t statistics (assuming unequal variance)	SC	RC	Two sample t test P value/ t statistics (assuming equal variance)	BPT5204	HPR 14
P	9.71	9.54	1.59	9.62	9.54	0.55	8.12	12.35
Fe	11.87	11.29	12.23***	11.76	11.21	7.29***	11.66	12.68
Zn	28.92	30.36	-19.01***	29.15	30.38	-9.97***	28.14	30.23
Am	28.86	34.4	-11.68***	29	34.38	-6.95***	27.14	28.01
CHO	83.05	80.47	8.53***	82.43	80.09	4.98***	79.6	84.57
PA	736.09	724.9	1.47	732.02	720.02	1.29	848.06	636.59

* Significant at 5 per cent ** Significant at 1 per cent *** Significant at 0.1 per cent

SC: Straight Cross (BPT 5204 × HPR-14); **RC:** Reciprocal Cross (HPR-14 × BPT 5204)

P: Protein (%)

Am: Amylose (%)

Fe: Iron (ppm)

CHO: Carbohydrate (%)

Zn: Zinc (ppm)

PA: Phytic acid (mg/100g)

4.2 Observed probabilities of transgressive segregants

Transgressive segregation produces hybrid progeny phenotypes that are superior to the parental phenotypes. Such plants are produced by accumulation of favourable genes from both the parents as a consequence of segregation and recombination, unlike heterosis, extreme phenotypes caused by transgressive segregation are heritably stable. Kshirsagar *et al.* (2013) suggested that transgressive segregation can be exploited for development of genotypes with positive characters from both the parents. Estimates of observed probability of segregants for yield and its components traits, and grain nutrient traits in straight and reciprocal crosses of F_2 and F_3 populations were summarized in table 11 and 12.

In straight F_2 population, traits like number of productive tillers (63.44), panicle length (85.87), panicle exertion (64.60), flag leaf length (27.66), seed fertility percentage (99.32), grain yield per plant (86.07), and harvest index (83.56) were higher observed probabilities of transgressive segregants compared to reciprocal F_2 population (Table 11).

In straight F_3 population, plant height (70.50), number of tillers (68.50), number of productive tillers (64.50), days to maturity (96.0), panicle length (54.50), panicle exertion (59.50), flag leaf length (17.00), grain yield per panicle (75.0), biomass per panicle (67.0), harvest index (81.0) and grain breadth (37.0) were observed higher than reciprocal F_3 population. Observed probabilities of transgressive segregation were higher for all the grain nutrient traits in reciprocal crosses of F_2 and F_3 populations except protein and moisture content (Table 12).

F_2 and F_3 populations surpassed the parental limits in both straight and reciprocal crosses for all the traits. Occurrences of such transgressions is possibly due to accumulation of complimentary alleles from both the parents at multiple loci in certain F_2 population (Tansley, 1993) and unmasking of recessive deleterious alleles due to inbreeding (Rick & Smith, 1953). Reddy (2008) reported transgressive segregants over both the parents for many traits this clearly indicates the parents had different alleles and gene governing yield and its component traits.

Table 11: Frequency of transgressive segregants in F₂& F₃ population of straight and reciprocal crosses of rice

Characters	Parental criteria	Transgressive segregants (%)			
		F ₂		F ₃	
		SC	RC	SC	RC
DF	>BPT 5204	21.08	18.20	19.00	15.00
	< HPR 14	69.05	78.24	74.50	79.50
PH	<BPT 5204	70.60	64.91	65.00	51.00
	> HPR 14	5.22	11.63	5.50	15.50
NT	>BPT 5204	48.36	43.90	57.00	59.00
	< HPR 14	21.47	26.45	11.50	2.00
NPT	>BPT 5204	43.71	35.27	52.00	45.00
	<HPR 14	19.73	25.56	12.50	8.00
DM	>BPT 5204	24.56	19.32	23.00	20.00
	<HPR 14	66.15	75.98	3.00	74.00
PL	<BPT 5204	40.42	41.84	49.50	42.00
	>HPR 14	45.45	11.44	5.00	1.50
PE	<BPT 5204	61.31	52.92	58.00	50.00
	>HPR 14	3.29	4.52	1.50	1.50
FLL	<BPT 5204	14.31	10.51	6.00	4.00
	>HPR 14	13.35	15.76	11.00	11.50
TGPP	<BPT 5204	61.12	65.85	57.50	63.00
	>HPR 14	22.82	19.51	21.50	20.00
FGPP	<BPT 5204	56.28	59.85	57.50	57.50
	>HPR 14	28.82	25.33	27.00	26.00
CGPP	<BPT 5204	63.44	66.79	63.50	74.50
	>HPR 14	25.14	26.27	16.50	15.00
SFP	>BPT 5204	66.92	67.17	74.50	81.50
	<HPR 14	32.88	31.71	24.50	18.50
GWPP	<BPT 5204	24.76	25.14	13.00	15.00
	>HPR 14	21.28	20.45	36.00	19.00
TW	<BPT 5204	9.09	4.69	0.00	0.00
	>HPR 14	29.21	35.83	42.00	43.00
GYPP	>BPT 5204	19.15	14.45	17.50	15.00
	<HPR 14	66.92	69.23	57.50	59.50
BM	>BPT 5204	9.28	3.56	9.00	3.50
	<HPR 14	65.18	74.29	58.00	62.50
HI	<BPT 5204	42.94	33.96	40.00	21.50
	>HPR 14	40.62	48.22	41.00	48.00
GL	>BPT 5204	53.19	75.61	60.00	79.00
	<HPR 14	18.37	6.38	16.00	9.00
GB	<BPT 5204	20.31	29.83	13.50	2.00
	>HPR 14	37.91	31.14	23.50	22.00
LBR	>BPT 5204	17.02	36.77	19.00	21.50
	<HPR 14	21.86	16.88	11.50	9.00

DF=50 % flowering
 PH= Plant height (cm)
 NT: Number of tillers
 NPT= Number of productive tillers
 DM= Days to maturity
 PL= Panicle length(cm)
 PE= Panicle exsertion (cm)

FLL= Flag leaf length (cm)
 TGPP= Total grains per panicle
 FGPP= Fertile grains per panicle
 CGPP= Chaffy grains per panicle
 SFP: Seed fertility percentage
 GWPP= Grain weight per panicle (g)
 TW= Test weight (g)

GYPP= Grain yield per plant (g)
 BM= Biomass (g)
 HI: harvest index (%)
 GL= Grain length (cm)
 GB= Grain breadth (cm)
 LBR: L/B ratio of paddy grain

Table 12: Frequency of transgressive segregants of grain nutrient traits in F₂ & F₃ population of straight and reciprocal crosses of rice.

Grain nutrient traits	Parental criteria	Transgressive segregants (%)			
		F ₂		F ₃	
		SC	RC	SC	RC
Protein (%)	<BPT 5204	17.33	15.81	17.50	14.50
	> HPR 14	7.93	3.49	6.00	1.00
Iron (ppm)	<BPT 5204	37.79	72.28	46.50	80.50
	> HPR 14	14.61	4.11	9.50	3.00
Zinc (ppm)	<BPT 5204	24.22	7.39	14.00	4.50
	> HPR 14	12.94	62.22	15.50	59.50
Amylose (%)	<BPT 5204	49.06	12.32	41.00	9.50
	>HPR 14	46.55	85.83	54.50	89.00
Carbohydrates(%)	<BPT 5204	25.68	46.82	26.50	51.00
	>HPR 14	36.32	15.81	29.50	16.50
Moisture (%)	>BPT 5204	17.12	16.02	5.50	9.00
	<HPR 14	34.03	29.36	48.00	40.00
Phytic Acid (mg/100g)	>BPT 5204	7.72	10.06	7.00	10.00
	<HPR 14	11.89	18.48	11.00	17.50

< BPT 5204 =The genotypes having value less than the parent BPT 5204 and expressed in percentage

<HPR 14 =The genotypes having value more than the parent HPR 14 and expressed in percentage

SC: Straight Cross (BPT 5204 × HPR-14); RC: Reciprocal Cross (HPR-14 × BPT 5204)

Hence, polygenic inheritance and high frequencies of favourable transgressive segregants for yield and its component traits indicates, there is a lot of scope to bring in beneficial alleles in to single genotype through rigorous selection in later generations and identification of plants with many desirable traits are of great contributions to increasing to rice yield potential (Reddyamini *et al.*, 2019).

4.3 Effect of reciprocal cross differences on genetic variability on straight and reciprocal F₂ and F₃ populations

Estimates of GCV, PCV, heritability and genetic advance for straight and reciprocal F₂ and F₃ populations were presented in table 13 and 14.

4.3.1 Effect of reciprocal cross difference on range

Wider range of variability for some important traits viz., days to 50 *per cent* flowering (78 to 136), plant height (51 to 136 cm), number of productive tillers (2 to 36), panicle length (12.6 to 27.0 cm), test weight (0.39 to 3.20g), grain yield (0.40 to 10.60 g), grain length (5.6 to 9.0 cm) and grain breadth (1.20 to 3.10 cm) were observed in straight F₂ population as compared to reciprocal F₂ population viz., days to 50 *per cent* flowering (77 to 136), plant height (50 to 128 cm), number of productive tillers (1 to 29), panicle length (9.5 to 21 cm), test weight (0.89 to 3.08 g) and grain yield per plant (0.20 to 41.50 g). Similarly, for plant height (55.20 to 121 cm) number of productive tillers (4.40 to 24.40), panicle length (16 to 38.60 cm), grain length (5.94 to 8.46 cm) and grain breadth (1.60 to 2.92 cm) were observed higher range in straight F₃ population as compared to reciprocal F₃ population viz., plant height (64.50 to 127.50 cm) number of productive tillers (6.80 to 21.40), panicle length (14.82 to 22.67 cm), grain length (6.36 to 8.30 cm) and grain breadth (1.90 to 2.98 cm) (Table 13).

Table 13: Estimates of components of quantitative traits' variability in straight and reciprocal crosses in F₂& F₃ populations of rice

Characters	Generation	Range		Phenotypic coefficient of variation (%)		Genotypic coefficient of variation (%)		Heritability % (broad sense)		Expected genetic advance over mean	
		SC	RC	SC	RC	SC	RC	SC	RC	SC	RC
DF	F ₂	78-136	77-136	14.60	13.46	12.20	10.30	69.90	58.60	21.01	16.24
	F ₃	74.60-122.80	80.40-117.33	10.55	11.81	10.07	10.99	91.10	86.70	19.50	21.07
PH (cm)	F ₂	51-136	50-128	16.32	16.54	8.74	16.26	70.81	72.29	23.82	24.22
	F ₃	55.20-121.00	64.50-127.50	11.68	12.78	4.09	5.19	52.30	56.07	12.59	14.77
NT	F ₂	4-37	3-32	44.55	43.12	36.88	33.45	68.60	60.20	62.91	53.46
	F ₃	7.20-27.20	9.60-24.20	34.95	29.05	27.34	19.24	61.20	43.90	44.04	26.25
NPT	F ₂	2-36	1-29	49.15	46.89	46.13	43.53	88.10	86.20	89.17	83.27
	F ₃	4.40-24.40	6.80-21.40	35.08	25.20	32.05	22.41	83.50	79.10	60.34	41.05
DM	F ₂	108-167	109-167	9.49	8.03	9.31	7.85	96.20	95.60	18.82	15.82
	F ₃	96.20-152.40	93.25-148.60	7.77	5.89	7.62	5.76	96.20	95.80	15.40	11.62
PL (cm)	F ₂	12.60-27	9.5-21	19.66	44.61	10.10	41.92	26.40	88.30	10.69	81.15
	F ₃	16.00-38.60	14.82-22.67	18.22	14.68	9.95	5.79	29.80	15.60	11.20	4.70
PE (cm)	F ₂	-9.6 -10.00	-9.0 -12.0	2812.13	561.54	2751.86	501.27	69.79	65.87	4043.47	99.07
	F ₃	-8.04-6.00	-6.90-10.30	325.66	793.12	265.39	732.85	53.77	57.95	360.73	946.85
FLL (cm)	F ₂	10.00-43.00	14.70-45.0	20.82	19.36	19.52	18.34	87.90	89.70	37.69	35.78
	F ₃	16.40-39.50	17.10-43.04	17.14	17.13	15.89	15.42	86.00	81.12	30.36	28.60
TGPP	F ₂	40-268	30-263	24.49	25.29	24.44	25.24	99.60	99.60	50.25	51.89
	F ₃	57.20-213.00	71.00-219.40	19.59	18.83	19.54	18.78	99.50	99.45	40.15	38.58
FGPP	F ₂	6-236	4-200	30.02	29.30	29.59	28.84	97.20	96.90	60.11	58.47
	F ₃	38.40-192.80	52.60-193.40	22.72	20.18	22.28	19.71	96.20	95.36	45.00	39.64
CGPP	F ₂	0-133	0-145	68.65	82.70	24.13	38.19	39.35	54.82	55.64	93.40
	F ₃	10.50-62.40	6.25-70.20	43.01	55.79	38.05	51.83	78.30	86.30	69.36	99.19

Characters	Generation	Range		Phenotypic coefficient of variation (%)		Genotypic coefficient of variation (%)		Heritability % (broad sense)		Expected genetic advance over mean	
		SC	RC	SC	RC	SC	RC	SC	RC	SC	RC
SFP (%)	F₂	6.90-100	6.06-100	16.17	17.47	15.40	16.64	90.70	90.70	30.21	32.65
	F₃	60.46-93.63	54.77-94.26	19.06	16.16	18.73	15.67	96.60	94.03	37.93	31.30
GWPP (g)	F₂	0.20-25	0.20-5.30	155.8	163.74	29.00	27.97	3.50	2.90	11.12	9.84
	F₃	1.08-3.96	0.96-3.44	164.95	153.36	20.53	31.19	1.50	4.14	5.26	13.07
TW (g)	F₂	0.39-3.20	0.89-3.08	24.72	23.45	15.39	15.57	38.80	44.00	19.75	21.28
	F₃	1.42-2.50	1.42-2.94	15.97	22.63	9.45	10.89	35.00	23.17	11.51	10.80
GYPP (g)	F₂	0.40-60.60	0.20-41.50	65.88	59.62	28.77	22.51	41.91	19.21	56.87	23.59
	F₃	6.33-35.46	7.94-37.66	37.11	43.16	3.89	6.05	44.15	14.02	33.75	12.46
BM (g)	F₂	5.17-105.50	3.60-76.60	49.70	46.24	48.34	44.64	94.6	93.2	96.86	88.79
	F₃	12.15-67.55	14.68-54.36	30.76	36.79	3.08	6.02	52.90	18.40	33.53	13.95
HI (%)	F₂	0.05-0.99	0.01-0.98	52.43	33.99	32.50	14.06	85.13	67.93	91.95	47.56
	F₃	0.27-0.88	0.38-0.91	19.93	20.71	3.10	0.78	16.50	13.50	6.78	5.76
GL (cm)	F₂	5.60-9.0	6.0-8.90	6.49	6.02	1.01	0.53	33.36	27.29	4.46	3.38
	F₃	5.94-8.46	6.36-8.30	5.54	13.33	5.43	13.30	96.03	99.63	10.95	27.35
GB (cm)	F₂	1.20-3.10	1.90-3.30	29.92	30.14	9.79	10.69	10.70	12.60	6.60	7.81
	F₃	1.60-2.92	1.90-2.98	28.11	42.79	8.86	7.73	9.94	3.26	5.75	2.88
L/B ratio	F₂	2.0-6.0	2.32-4.10	14.29	14.49	11.13	11.12	60.60	58.80	17.85	17.56
	F₃	2.13-4.30	2.44-3.69	12.95	20.03	10.11	19.21	60.92	92.02	16.25	37.96

SC: Straight Cross (BPT 5204 × HPR-14); **RC:** Reciprocal Cross (HPR-14 × BPT 5204)

DF=50 % flowering

PH= Plant height (cm)

NT: Number of tillers

NPT= Number of productive tillers

DM= Days to maturity

PL= Panicle length(cm)

PE= Panicle exsertion (cm)

FLL= Flag leaf length (cm)

TGPP= Total grains per panicle

FGPP= Fertile grains per panicle

CGPP: Chaffy grains per panicle

SFP: Seed fertility percentage

GWPP= Grain weight per panicle (g)

TW= Test weight (g)

GYPP= Grain yield per plant (g)

BM= Biomass (g)

HI: harvest index (%)

GL= Grain length (cm)

GB= Grain breadth (cm)

LBR: L/B ratio of paddy grain

For grain nutrient traits, wider range of variability for protein (5.65 to 15.82%), iron (8.53 to 14.625ppm), carbohydrate (68.87 to 87.05%) and phytic acid (389.97 to 1072.43mg/100g) in reciprocal F₂ population as compared to straight F₂ population where protein (5.16 to 14.75%), iron (9.47 to 14.87 ppm), carbohydrate (69.96 to 86.95%) and phytic acid (492.21 to 1061.66 mg/100g). Similarly, protein (5.8 to 14.94%), iron (8.67 to 14.16 ppm), zinc (25.03 to 34.27 ppm), carbohydrate (69.19 to 96.29%) and phytic acid (465.06 to 1035.93 mg/100g) were observed higher in reciprocal F₃ population as compared to straight F₃ population (Table 14).

4.3.2 Effect of reciprocal cross difference on GCV and PCV

F₂ population: Estimates of GCV and PCV for most of the yield attributing traits and grain nutrient traits were high in straight F₂ population as compared to reciprocal F₂ population. Days to 50 *per cent* flowering (12.20, 14.60), number of tillers (36.88, 4.55), number of productive tillers (46.13, 49.15), days to maturity (9.31, 9.49), panicle exertion (2751.86, 2812.13), flag leaf length (19.52, 20.82), grain yield per plant (28.77, 65.88), biomass (48.34, 49.70), harvest index (32.50, 52.43), grain length (1.01, 6.49), grain breadth (9.79, 29.92), protein (17.77, 27.34), amylase (28.10, 28.28) and carbohydrates (5.75, 6.69) were high GCV and PCV respectively, in straight F₂ population compared to reciprocal F₂ population (Table 13 and 14).

F₃ population: Estimates of GCV and PCV for most of yield attributing traits and grain nutrient traits were high in reciprocal F₃ population as compared to straight F₃ population. Days to 50 *per cent* flowering (10.99, 11.81), plant height (5.19, 12.78), panicle exertion (732.85, 793.12), chaffy grains per panicle (51.83, 55.79), test weight (10.89, 22.63), grain yield per plant (6.05, 43.16), biomass (6.02, 36.79), grain length (13.30, 13.33), L/B ratio (19.21, 20.03), iron (6.47, 6.61), zinc (4.26, 5.10), carbohydrate (8.50, 6.55) and phytic acid (13.15, 13.15) were high GCV and PCV respectively, in reciprocal F₃ population compared straight F₃ population (Table 13 and 14). Very narrow differences were observed between estimates of GCV and PCV in both straight and reciprocal F₂ and F₃ populations indicate minimal role of environment.

Table 14: Estimates of components of variability of grain nutrient traits in straight and reciprocal cross derived F₂ population & F₃ families of rice

Grain nutrient traits	Generation	Range		Phenotypic coefficient of variation (%)		Genotypic coefficient of variation (%)		Heritability % (broad sense)		Expected genetic advance over mean	
		SC	RC	SC	RC	SC	RC	SC	RC	SC	RC
P	F ₂	5.16-14.75	5.65-15.82	27.34	26.14	17.77	15.64	42.25	35.80	23.80	19.28
	F ₃	5.63-13.81	5.8-14.94	29.22	29.15	12.25	15.16	70.18	79.89	42.25	48.09
Fe	F ₂	9.47-14.87	8.53-14.62	6.47	6.97	6.39	6.91	97.65	98.05	13.02	14.09
	F ₃	9.98-13.7	8.67-14.16	6.33	6.61	6.18	6.47	95.20	95.90	12.42	13.07
Zn	F ₂	25.10-31.85	26.37-32.98	4.80	5.01	3.75	4.09	61.10	66.71	6.04	6.89
	F ₃	23.99-31.45	25.03-34.27	4.55	5.10	3.52	4.26	59.70	70.20	5.59	7.36
Am	F ₂	10.92-59.13	15.03-57.03	28.28	19.88	28.10	19.66	98.72	97.82	57.52	40.05
	F ₃	13.65-53.45	20.17-53.10	23.63	17.72	23.44	17.45	98.40	97.10	47.89	35.43
CHO	F ₂	69.96-86.91	68.87-87.05	6.69	6.56	5.75	5.72	73.92	76.04	10.18	10.28
	F ₃	70.85-91.88	69.16-96.29	6.11	6.55	5.22	8.50	72.80	78.50	9.17	10.59
PA	F ₂	492.21-1016.66	389.97-1072.43	11.51	13.39	11.47	13.35	99.67	99.75	23.71	27.58
	F ₃	499.02-1023.89	465.06-1035.93	11.75	13.15	11.75	13.15	100.00	100.00	24.20	27.09

P: Protein (%)

Am: Amylose (%)

Fe: Iron (ppm)

CHO: Carbohydrate (%)

Zn: Zinc (ppm)

PA: Phytic acid (mg/100g)

SC: Straight Cross (BPT 5204 × HPR-14); RC: Reciprocal Cross (HPR-14 × BPT 5204)

4.3.3 Effect of cross difference on heritability and genetic advance as *per cent* mean (GAM)

Variability of phenotype traits partitioned into heritable and non-heritable components with suitable genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA). Higher value of broad sense heritability attributed to lesser difference between PCV and GCV values. High heritability values resulted in higher values of expected GAM.

F₂ population: Highest heritability was observed for total grain per panicle (99.60%), phytic acid (99.67%) and lowest was observed for grain weight per particle (3.50%) in straight F₂ population. Similarly, heritability was ranged from 2.90 to 99.75% for grain weight per panicle and phytic acid content respectively, in reciprocal F₂ population. The lowest genetic advances as per cent mean (GAM) was observed for zinc content (6.04%) and highest was observed for panicle exsertion (4043.47%) in straight F₂ population compared to reciprocal F₂ population where lowest genetic advance per cent mean was observed for grain length (3.38%) and highest was observed for panicle exsertion (99.07%).

F₃ population: Highest heritability was observed for phytic acid (100%) and lowest was for grain weight per panicle (1.50%) in straight F₃ population. Similarly, heritability was ranged from 3.26 to 100% for grain breadth and phytic acid content respectively, in reciprocal F₂ population. The lowest genetic advance as per cent mean (GAM) was observed for grain weight per panicle (5.26%) and highest was observed for panicle exsertion (360.73%) in straight F₃ population compared to reciprocal F₃ population. Where lowest genetic advance per cent mean was observed for grain breadth (2.88%) and highest was observed for panicle exsertion (945.85%) (Table 13). Similar results of high heritability for panicle exsertion and plant height were reported by *Das et al.* (2001) *Kuldeep et al.* (2004) *Uttam et al.* (2005). Whereas, high GA as per cent mean was observed for plant height at maturity and moderate to low was observed for other characters which are similar to results reported by *Prajapati et al.* (2011).

High PCV, GCV coupled with high heritability and GAM observed for number of tillers, number of productive tillers, biomass and harvest index. High heritability and GA per cent mean was observed for plant height, amylose and phytic acid content in straight and reciprocal F₂ and F₃ populations. Similar results were observed by Thirunganana kumar *et al.* (2007); Basavaraja *et al.* (2013); Arvind *et al.* (2015) and Irappa *et al.* (2018). Moderate to high inheritability coupled with high genetic advance per cent mean for protein in the present study is supported by Habibi (2008) and Shashidhara *et al.* (2008). The results indicated the major genes with additive gene action governing these traits, which offers scope for further improvement through selection which were agreement with Sala (2012); Verma *et al.* (2000); Ashwini samak *et al.* (2011); Shashidhar *et al.* (2013) and Roy (2000). The success in a crop improvement program depends by the ability of the breeder to define and assemble the required genetic variability and select for yield indirectly through yield associated and highly heritable characters after eliminating the environmental components of phenotypic variation (Mathew, 1949). Therefore, it is necessary to have information on both PCV, GCV to estimate heritability, which helps the breeder to predict the expected grains through selection.

4.4 Association of yield attributing and grain nutrient traits and their reciprocal differences in straight and reciprocal F₂ and F₃ populations

The correlation coefficient estimates the degree and direction of association between pair of characters and helps simultaneous improvement of the correlated traits through selection. High magnitude of positive correlation coefficient at genotypic level indicates strong linkage at genetic level, but high values at phenotypic level may not always show strong association and it may be broken up with change in environment. The development of a high yielding genotype through breeding rice requires a thorough knowledge of the association of yield components. Grain yield in rice is a complex character quantitative in nature and an integrated function of a number of component traits. Therefore, selection for yield *per se* may not be much regarding unless yield components are taken into consideration.

Correlation studies for yield attributing and grain nutrients traits in straight and reciprocal F_2 and F_3 population were presented in table 15 and 16; Appendix I and II. Grain yield per plant exhibited significant positive correlations with plant height, number of productive tillers, panicle length in both straight and reciprocal F_2 and F_3 populations. But non-significant positive correlation for panicle exertion and test weight in reciprocal F_2 and F_3 populations. Grain yield per plant had non-significant and negative correlation with days to 50 *per cent* flowering in both straight reciprocal F_2 and F_3 populations (except straight F_3 population). This indicates the relative utility of all these traits for selection with respect to grain yield. Plant height showed positive and significant association with number of productive tillers (except reciprocal F_3 population) panicle length and panicle exertion in both straight and reciprocal F_2 and F_3 populations. Association of remaining traits in straight and reciprocal F_2 and F_3 populations were presented in Appendix I and II. The observed positive correlation of grain yield with various traits was supported by earlier workers *viz.*, Islam *et al.* (2002); Basavaraj *et al.* (1997); Nayak *et al.* (2001); Sathyanarayana *et al.* (2005) and Shashidhar *et al.* (2005) for plant height, Chakravarty *et al.* (2001); Rajeshwari and Nandarajan (2004) Gazafrodi *et al.* (2006); Agahi *et al.* (2007) for test weight. In the present study, significant positive association of panicle length with grain yield was in agreement with the findings of Bhagat (2007); Rao (2007); Rani (2007) and Nandeshwar *et al.* (2010), indicating that this character can also be considered to be achieve better results for improving grain yield.

Correlation studies for grain yield per plant and grain nutrient traits in straight and reciprocal F_2 and F_3 crosses revealed that grain yield had positive significant correlation with zinc (0.2436, 0.1062) in straight and reciprocal F_2 population respectively. But, zinc had non-significant negative and positive correlation in straight and reciprocal F_3 population respectively. Grain yield had negative non-significant (except straight F_3 population) with protein and significant with phytic acid (except straight F_3 population). Straight F_2 and F_3 population for amylose had negative association with grain yield compared to reciprocal crosses where positive association was observed (Table 16).

Table 15: Estimates of phenotypic correlation coefficient of straight and reciprocal derived F₂ and F₃ population crosses of rice

Traits	Generation	DF		PH		NPT		PL		PE		TW	
		Cross											
		SC	RC	SC	RC	SC	RC	SC	RC	SC	RC	SC	RC
DF	F ₂	1	1										
	F ₃												
PH	F ₂	0.0152	-0.0106	1	1								
	F ₃	0.1357*	0.2239**										
NPT	F ₂	-0.0255	0.0138	0.1325**	0.1906***	1	1						
	F ₃	0.0142	0.0334	0.1149	-0.0299								
PL	F ₂	-0.1808***	-0.1075*	0.5761***	0.5704***	0.2651***	0.2450***	1	1				
	F ₃	-0.0246	-0.0669	0.3316***	0.4678***	0.1326	0.135						
PE	F ₂	-0.0123	-0.0582	0.6351***	0.6321***	-0.0461	-0.0214	0.2652***	0.2659***	1	1		
	F ₃	0.0815	0.0357	0.7972***	0.5977***	0.0312	-0.1404*	0.1698*	0.3322***				
TW	F ₂	-0.3936***	-0.3557***	-0.0095	0.0709	0.0247	-0.0339	0.1762***	0.1073*	-0.0139	0.0703	1	1
	F ₃	-0.2488***	-0.3932***	-0.0225	-0.0041	0.0225	-0.0737	0.0582	0.0709	-0.0369	-0.0124		
GYPP	F ₂	-0.023	-0.045	0.3008***	0.3236***	0.7502***	0.8114***	0.3764***	0.3443***	0.1088*	0.0749	0.1579**	0.0267
	F ₃	0.0868	-0.0526	0.3300***	0.2155***	0.7641***	0.6620***	0.2176***	0.2515***	0.2205**	0.0802	0.1538**	0.1111

* Significant at 5 per cent ** Significant at 1 per cent *** Significant at 0.1 per cent

SC: Straight Cross (BPT 5204 × HPR-14); **RC:** Reciprocal Cross (HPR-14 × BPT 5204)

DF=50 % flowering

PL= Panicle length(cm)

PH= Plant height (cm)

PE= Panicle exsertion (cm)

NPT= Number of productive tillers

TW= Test weight (g)

GYPP= Grain yield per plant (g)

Table 16: Estimates of phenotypic correlation coefficient of grain nutrient traits in straight and reciprocal derived F₂ and F₃ population crosses of rice

Traits	Generation	P		Fe		Zn		Am		CHO		PA	
		Cross											
		SC	RC	SC	RC	SC	RC	SC	RC	SC	RC	SC	RC
P	F ₂ F ₃	1	1										
Fe	F ₂ F ₃	-0.245*** -0.4898***	-0.0765 0.0062	1	1								
Zn	F ₂ F ₃	-0.1148* -0.0287	0.0276 0.0411	-0.2891*** -0.0213	- 0.5010*** -0.2793***	1	1						
Am	F ₂ F ₃	-0.0549 -0.0126	-0.0084 -0.0227	-0.4138*** -0.3905***	-0.5803*** -0.4688***	0.3914*** 0.2665***	0.3480*** 0.3062***	1	1				
CHO	F ₂ F ₃	-0.507*** -0.7199***	-0.7120*** -0.7291***	0.3953*** 0.5217***	0.2960*** 0.2575***	-0.2528*** -0.0664	-0.5265*** -0.3608***	-0.0098 -0.0026	-0.1333** -0.1728*	1	1		
PA	F ₂ F ₃	-0.0907* -0.0645	0.1319** 0.0815	0.0051 0.0454	0.1278** 0.1991**	-0.0877 -0.0901	-0.3388*** -0.3087***	-0.0084 -0.0085	-0.1664*** -0.1839**	0.1339** 0.1213	0.1654*** 0.2003**	1	1
GYPP	F ₂ F ₃	-0.0865 -0.1275**	-0.0640 -0.0357	0.0449 0.1860**	-0.0548 -0.0255	0.2436*** -0.1749	0.1062* 0.0155	-0.0536 -0.1444**	0.0714 0.0095	-0.0502 0.1110*	-0.0738 -0.0019	-0.1103* -0.0894	-0.2293** -0.1840**

* Significant at 5 per cent ** Significant at 1 per cent *** Significant at 0.1 per cent

SC: Straight Cross (BPT 5204 × HPR-14); **RC:** Reciprocal Cross (HPR-14 × BPT 5204)

P: Protein (%)

CHO: Carbohydrate (%)

Fe: Iron (ppm)

PA: Phytic acid (mg/100g)

Zn: Zinc (ppm)

GYPP: Grain yield per plant (g)

Am: Amylose (%)

Phytic acid had significantly positive and negative correlation in reciprocal F₂ and F₃ populations with iron and zinc respectively. Carbohydrates had negative significant correlation with protein, zinc and amylose content but positive significant with iron content in both straight and reciprocal F₂ and F₃ populations. Amylose content had significant positive and negative correlation with zinc and iron respectively. Protein had significantly negative association in straight F₂ and F₃ population as compared to reciprocal were positive non-significant correlation was observed with zinc content. Grain iron content had negative correlation with grain used in reciprocal F₂ and F₃ populations in accordance with Nagesh *et al.* (2013) and positive significant correlation with given zinc content is similar to Kalmeshwar Gouda Patil (2018). Where grain iron content had significantly negative correlation with grain zinc content these findings are in contradicting with Steangoulis *et al.* (2007) and Jeom *et al.* (2008) and Kalmeshwar Gouda Patil (2008).

The path coefficient analysis was carried out to discern direct and indirect effects of yield attributing traits on grain yield were presented in table 17; Appendix III, IV, V and VI. The relationship between yield and yield components may be negative or positive but it is the net result of direct effect of that particular trait and indirect effect *via* other traits. Hence, it is necessary to determine the path coefficient which partition the observed correlation into direct and indirect effect and also reveals the cause and effect relationship exist between yield and their related traits. Highest positive direct effect on yield was shown by number of productive tillers (0.0971) in straight F₃ population and zinc (0.2617, 0.2176) in straight F₂ and F₃ populations respectively. Panicle exertion (0.0219) and carbohydrates (0.0388) had highest positive direct effect on reciprocal F₂ and F₃ population respectively. Thus, choosing number of productive tillers for yield will be best for selection process. Kavita and Upadhaya (2001); Rajeshwari and Nandarajan (2004); Suman *et al.* (2005); Ambili and Radhakrishana (2011), Rangare *et al.* (2012); Naseem *et al.* (2014); Sarawagi *et al.* (2016) and Rashmi *et al.* (2010) also reported high positive direct effect of number of productive tillers on plant on grain yield. Plant height and amylose content had lowest and highest negative direct effect in straight F₂ and F₃ populations respectively. Phytic acid had highest negative direct effect in reciprocal F₂ and F₃ populations.

Table 17: Estimation of correlation coefficient and direct effect of easily assayable traits on grain yield in straight and reciprocal cross derived F₂ population & F₃ families of rice

Traits		Correlation coefficient (r)		Direct effect	
		SC	RC	SC	RC
Days to 50% flowering	F ₂	-0.0014	0.0044	0.0604	-0.0981
	F ₃	0.0012	0.0001	0.0140	-0.0021
Plant height (cm)	F ₂	-0.0004	-0.0138	-0.0014	-0.0427
	F ₃	-0.0002	-0.0014	-0.0005	-0.0067
Number of productive tillers	F ₂	-0.0159	-0.0295	-0.0212	-0.0363
	F ₃	0.0742	0.0109	0.0971	0.0165
Panicle length (cm)	F ₂	-0.0052	-0.0053	-0.0139	-0.0154
	F ₃	-0.0020	-0.0046	-0.0093	-0.0184
Panicle exsertion (cm)	F ₂	0.0029	0.0016	0.0266	0.0219
	F ₃	0.0026	0.0006	0.0120	0.0069
Protein (%)	F ₂	0.0097	0.0120	-0.1121	-0.1868
	F ₃	0.0069	-0.0002	-0.0542	0.0043
Iron (ppm)	F ₂	0.0026	-0.0001	0.0570	0.0012
	F ₃	0.0131	0.0007	0.0704	-0.0263
Zinc (ppm)	F ₂	0.0638	-0.0080	0.2617	-0.0753
	F ₃	0.0381	-0.0004	0.2176	-0.0245
Amylose (%)	F ₂	0.0078	0.0025	-0.1448	0.0356
	F ₃	0.0253	-0.0003	-0.1751	-0.0340
Carbohydrate (%)	F ₂	0.0037	0.0156	-0.0730	-0.2115
	F ₃	0.0062	-0.0001	0.0560	0.0388
Phytic acid (mg/100g)	F ₂	0.0098	0.0435	-0.0893	-0.1899
	F ₃	0.0076	0.0384	-0.0847	-0.2048

Similar results of zinc content had highest positive direct effect was supported by Nagesh *et al.* (2013). These negative relation and effects obstacles the selection of particular traits (Nagesh *et al.*, 2013). If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects appear to be the cause of that positive correlation. In such circumstances, the other factors are to be considered simultaneously for selection. However, if the correlation coefficient is negative but direct effect is positive and high, a restriction has to be imposed to nullify the undesirable indirect effects in order to make use of direct effect.

4.5 Genetics of quantitative and qualitative traits in straight and reciprocal F₂ and F₃ populations

4.5.1 Number of genes controlling quantitative traits inferred from third and fourth degree statistics

Shapiro Wilk ‘W’ test is the preferred test of normality because of its high statistics power as compared to a wide range of alternative tests. If the ‘W’ statistics is significant, then the population is not normally distributed. The results of the ‘Shapiro-Wilks ‘W’ test for straight and reciprocal F₂ population and F₃ families was presented in table 18 and 19.

Shapiro-Wilk ‘W’ test showed non-normal distribution for all the growth and yield attributing traits except total grains per panicle, fertile grains per panicle and grain weight per panicle in both straight and reciprocal F₂ population (Figure 1a, 1b, 1c, 1d, 1e, 1f and 1g). In F₃ population, number of tillers, number of productive tillers, flag leaf length, total grains per panicles, fertile grains per panicle, grain weight per panicle, test weight, harvest index, grain length, L/B ratio showed normal distribution in both straight and reciprocal crosses (Figure 2a, 2b, 2c, 2d, 2e, 2f and 2g). In addition to plant height in reciprocal and grain breadth in straight cross F₃ population showed normal distribution (Table 18). For grain nutrient traits except amylose content, all the traits followed normal distribution in F₂ and F₃ population. In reciprocal F₂ population, protein, moisture and phytic acid content followed normal distribution compared to reciprocal F₃ population whereas, protein carbohydrate and phytic acid showed normal distribution (Table 8).

Table 18: Test for normality for growth and yield related traits in F₂ and F₃ populations of straight and reciprocal crosses of rice

Traits	Shapiro Wilk's test for normality															
	F ₂								F ₃							
	SC				RC				SC				RC			
	W	P<W	Skewness	Kurtosis	W	P<W	Skewness	Kurtosis	W	P<W	Skewness	Kurtosis	W	P<W	Skewness	Kurtosis
DF	0.9244	<0.0001	0.83	0.38	0.8826	<0.0001	1.24	1.28	0.9308	<0.0001	0.87	0.34	0.9091	<0.0001	1.01	0.56
PH	0.9702	<0.0001	-0.32	-0.38	0.9706	<0.0001	-0.48	-0.22	0.9556	<0.0001	-0.72	0.29	0.9815	0.0099	-0.43	0.39
NT	0.9596	<0.0001	0.79	0.71	0.9850	<0.0001	0.34	-0.18	0.9782	0.0033	0.46	-0.05	0.9823	0.0128	0.34	-0.35
NPT	0.9540	<0.0001	0.84	0.76	0.9845	<0.0001	0.36	-0.03	0.9840	0.0226	0.39	-0.13	0.9789	0.0042	0.46	-0.05
DM	0.9303	<0.0001	0.79	0.30	0.8894	<0.0001	1.24	1.35	0.9336	<0.0001	0.73	0.56	0.8943	<0.0001	0.43	2.59
PL	0.9904	<0.0001	-0.27	0.69	0.1382	<0.0001	-0.79	2.70	0.6874	<0.0001	4.52	36.67	0.9398	<0.0001	-1.09	3.34
PE	0.9171	<0.0001	-0.70	-0.10	0.9227	<0.0001	-0.77	-0.04	0.8699	<0.0001	-1.02	0.01	0.9000	<0.0001	-0.85	0.52
FLL	0.9827	<0.0001	0.44	0.15	0.9914	<0.0001	0.34	0.15	0.9901	0.1877	0.24	-0.20	0.9728	0.0006	0.33	0.79
TGPP	0.9945	0.0586	0.18	0.29	0.9947	0.0611	0.12	0.55	0.9949	0.7293	0.05	-0.16	0.9884	0.1029	0.21	0.08
FGPP	0.9953	0.1166	0.03	0.46	0.9935	0.0220	-0.25	0.26	0.9936	0.5367	0.18	0.27	0.9942	0.6325	0.16	0.32
CGPP	0.8911	<0.0001	1.62	4.81	0.8568	<0.0001	1.71	4.39	0.9228	<0.0001	1.16	1.77	0.8894	<0.0001	1.52	3.23
SFP	0.8810	<0.0001	-1.67	4.58	0.8741	<0.0001	-1.57	3.59	0.9466	<0.0001	-0.92	0.83	0.9101	<0.0001	-1.31	2.33
GWPP	0.9887	0.0005	-0.07	0.89	0.9870	0.0001	-0.09	1.01	0.9872	0.0672	0.26	-0.24	0.9858	0.0423	0.14	-0.01
TW	0.9635	<0.0001	-0.40	2.64	0.8704	<0.0001	0.37	2.92	0.9955	0.8191	-0.01	-0.09	0.9700	0.0003	0.66	2.12
GYPP	0.9233	<0.0001	1.15	1.75	0.9587	<0.0001	0.74	0.39	0.9437	<0.0001	0.63	-0.35	0.9366	<0.0001	0.92	0.60
BM	0.9238	<0.0001	1.26	2.77	0.9426	<0.0001	1.08	2.42	0.9548	<0.0001	0.74	0.26	0.9529	<0.0001	0.82	0.48
HI	0.5719	<0.0001	-0.42	-0.36	0.9769	<0.0001	-0.51	-0.17	0.9879	0.0857	0.10	-0.53	0.9900	0.1802	0.27	-0.29
GL	0.9832	<0.0001	0.21	0.59	0.9823	<0.0001	-0.17	0.41	0.9764	0.0019	0.50	1.15	0.9915	0.2940	-0.04	-0.21
GB	0.9563	<0.0001	0.37	1.35	0.9407	<0.0001	0.66	0.13	0.9768	0.0022	0.31	0.55	0.9256	<0.0001	1.17	2.41
LBR	0.9317	<0.0001	1.35	10.54	0.9894	0.0007	-0.04	-0.59	0.9802	0.0064	-0.13	1.33	0.9864	0.0513	-0.34	-0.15

SC: Straight Cross (BPT 5204 X HPR-14); **RC:** Reciprocal Cross (HPR-14 X BPT 5204)

DF=50 % flowering

PH= Plant height (cm)

NT= Number of tillers

NPT= Number of productive tillers

DM= Days to maturity

PL= Panicle length(cm)

PE= Panicle exertion (cm)

FLL= Flag leaf length (cm)

TGPP= Total grains per panicle

FGPP= Fertile grains per panicle

CGPP: Chaffy grains per panicle

SFP: Seed fertility percentage

GWPP= Grain weight per panicle (g)

TW= Test weight (g)

GYPP= Grain yield per plant (g)

BM= Biomass (g)

HI: harvest index (%)

GL= Grain length (cm)

GB= Grain breadth (cm)

LBR: L/B ratio of paddy grain

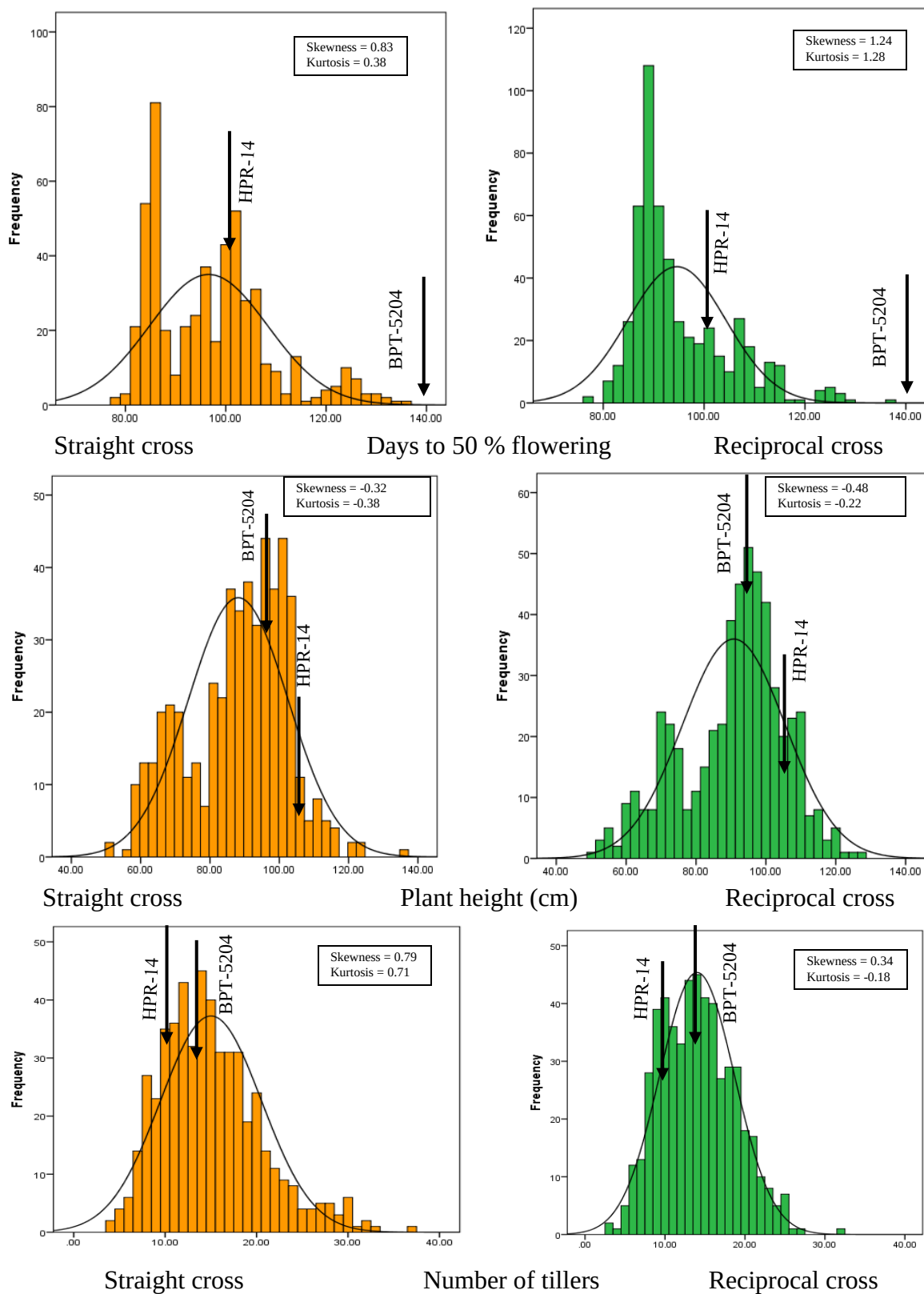
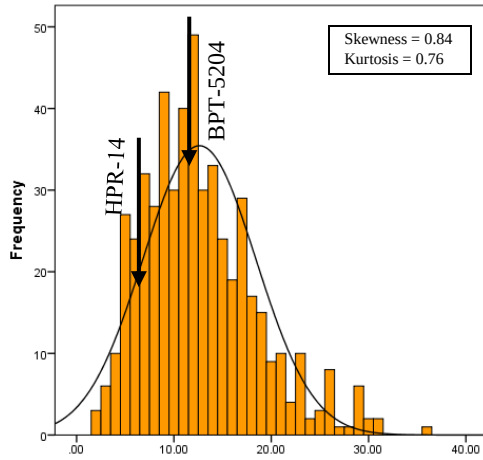
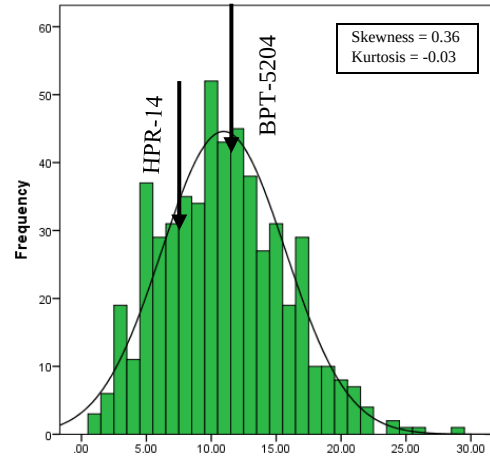


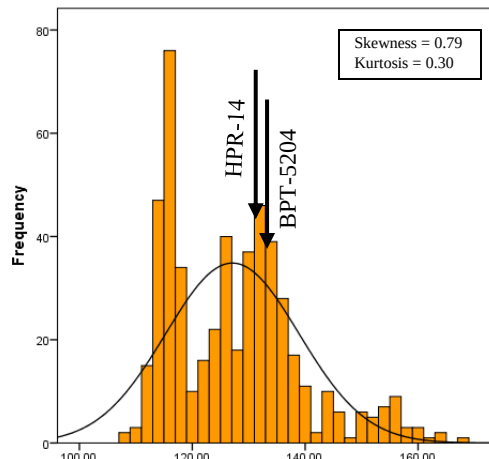
Fig. 1A: Frequency distribution of days to 50% flowering, plant height & number of tillers in straight and reciprocal F₂'s derived from BPT 5204 & HPR 14 crosses in rice



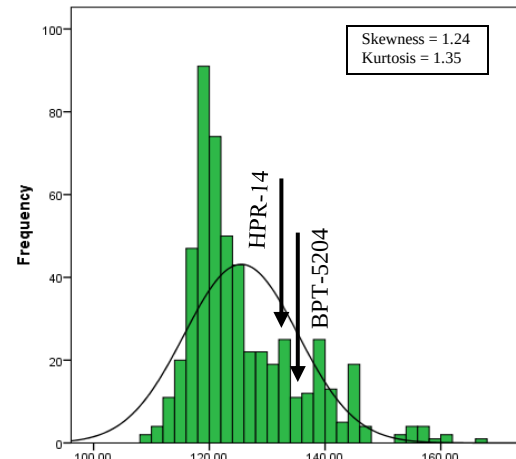
Straight cross



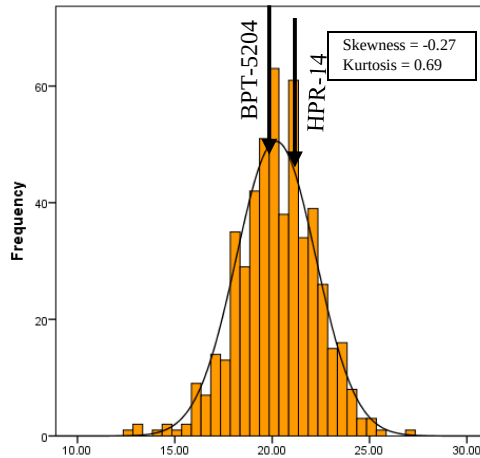
Reciprocal cross



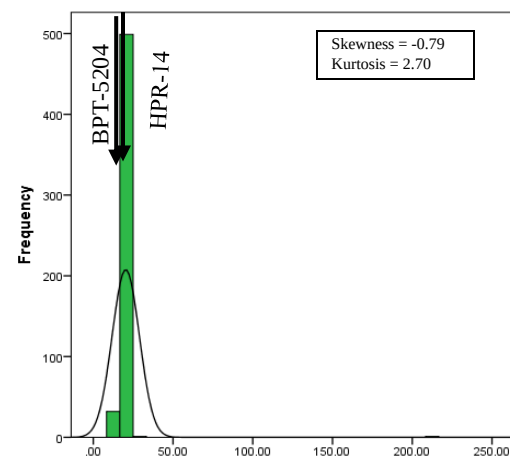
Straight cross



Reciprocal cross

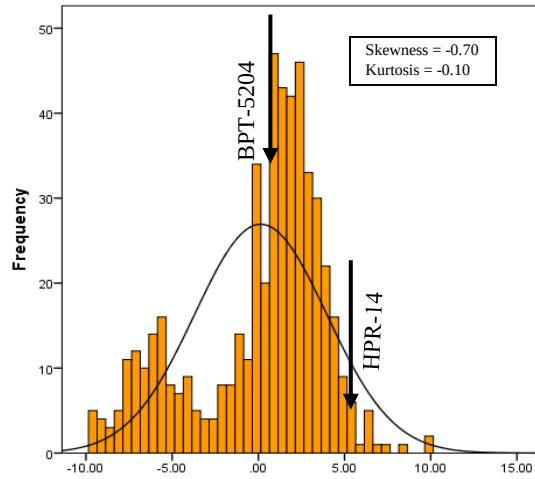


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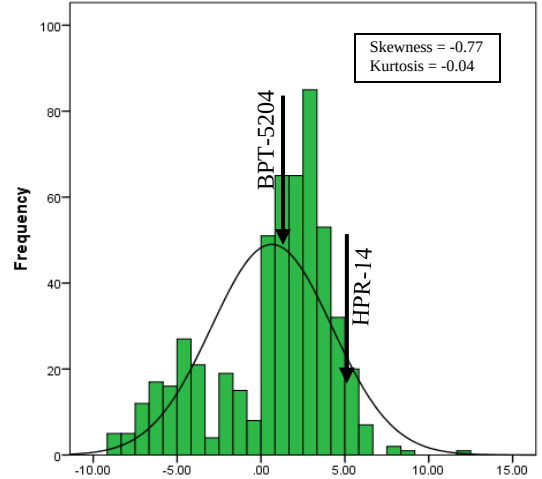


Reciprocal cross

Fig. 1B: Frequency distribution of number of productive tillers, days to maturity & panicle length in straight and reciprocal F₂'s derived from BPT 5204 & HPR 14 crosses in rice

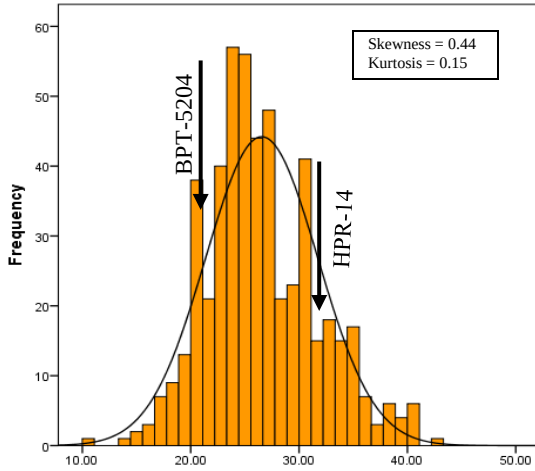


Straight cross

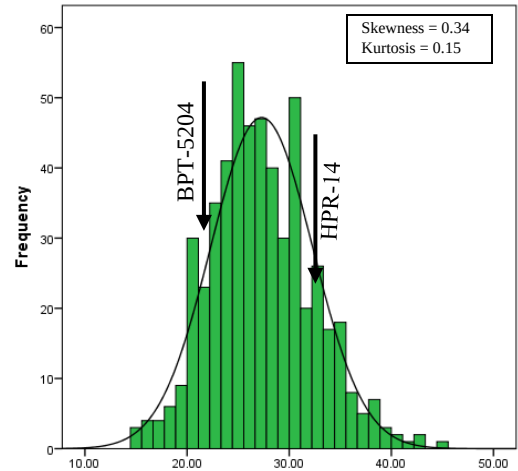


Panicle exertion (cm)

Reciprocal cross

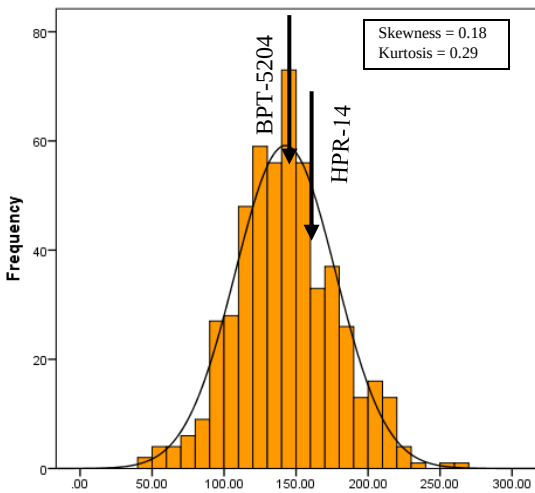


Straight cross

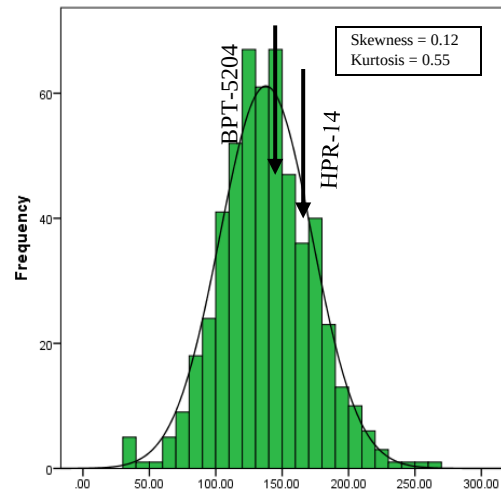


Flag leaf length (cm)

Reciprocal cross



Straight cross



Total grains per panicle

Reciprocal cross

Fig. 1C: Frequency distribution of panicle exertion, flag leaf length & total grains per panicle in straight and reciprocal F₂'s derived from BPT 5204 & HPR 14 crosses in rice

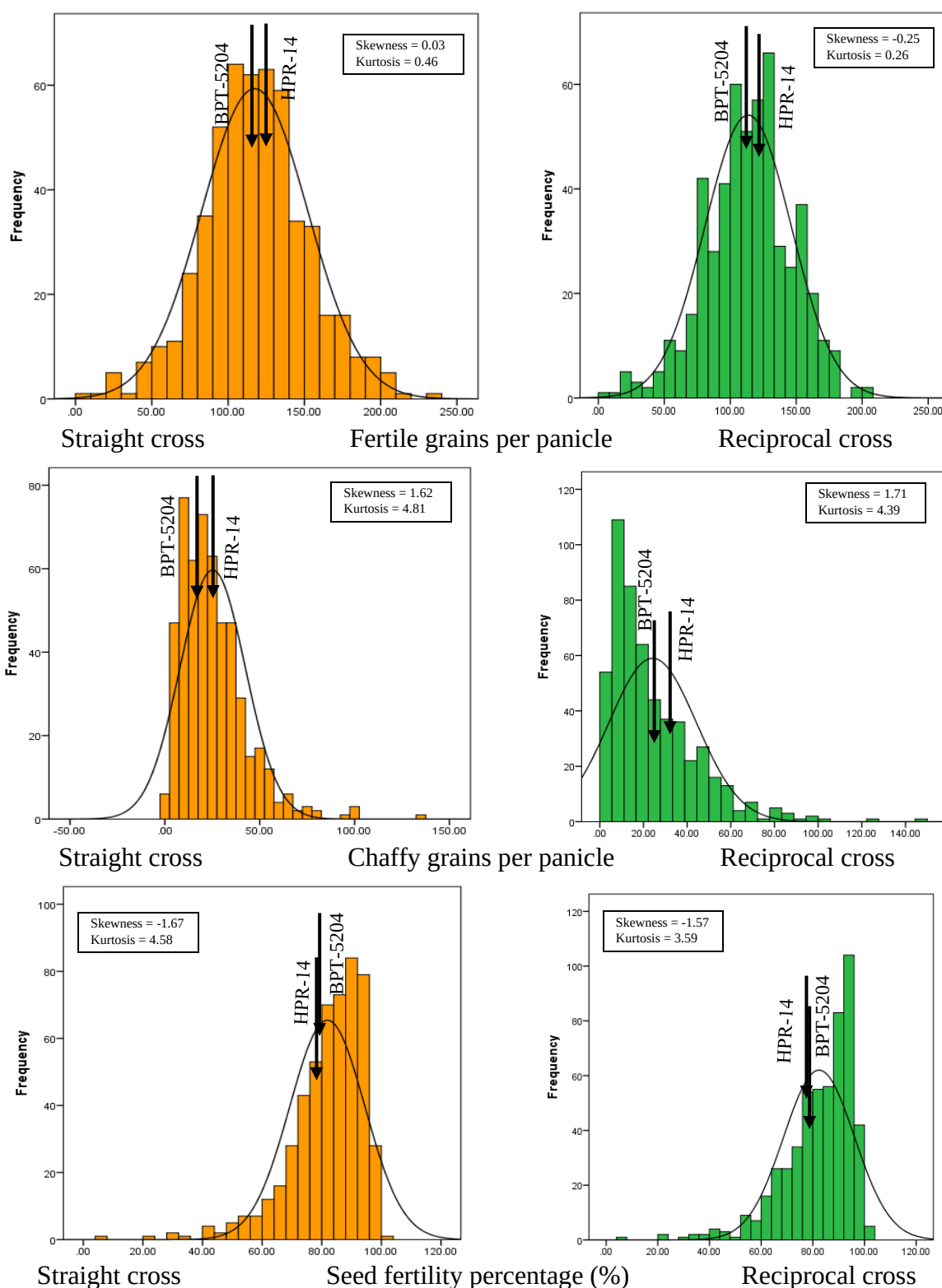


Fig. 1D: Frequency distribution of fertile grains per panicle, chaffy grains per anile & seed fertility percentage in straight and reciprocal F₂'s derived from BPT 5204 & HPR 14 crosses in rice

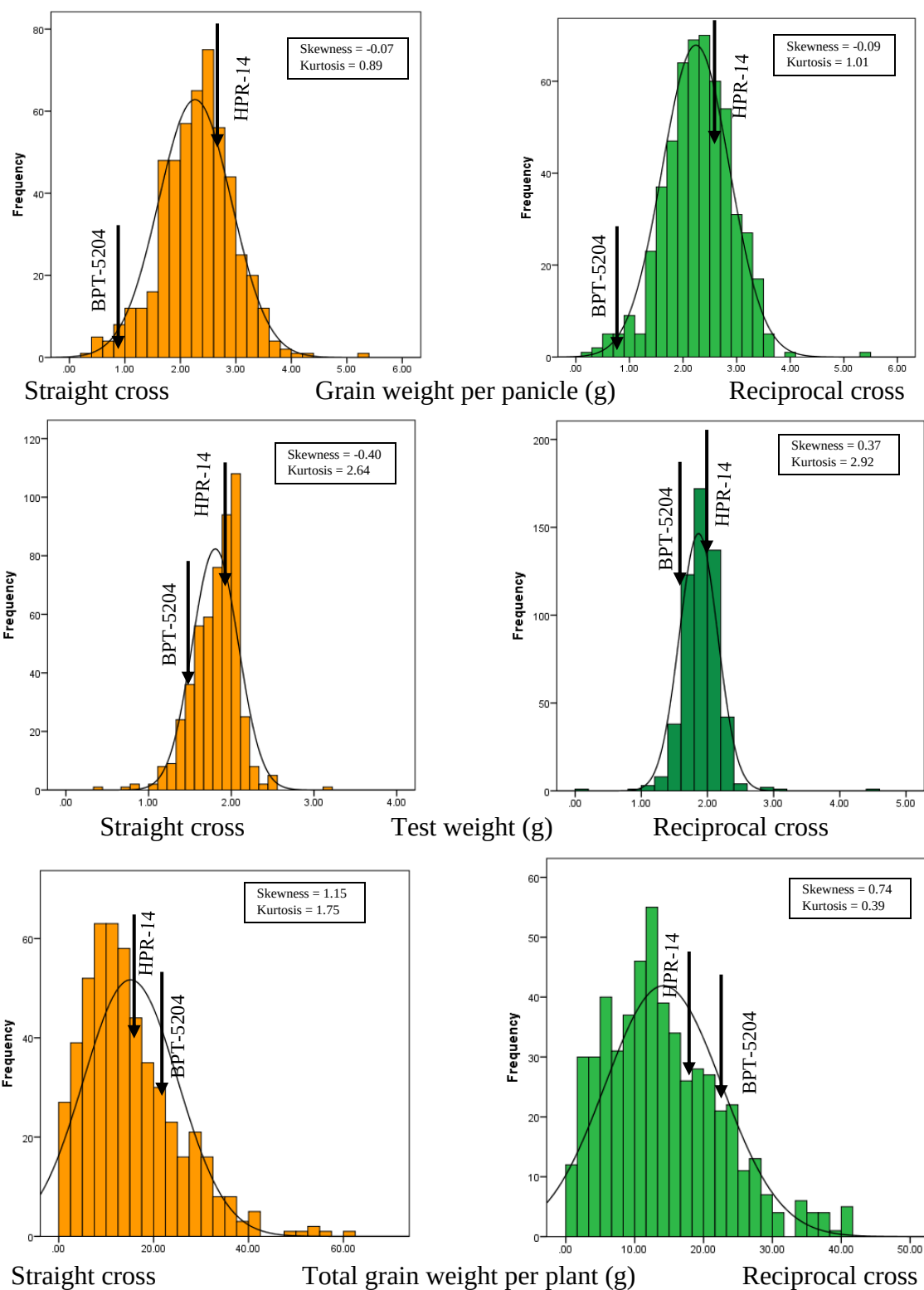
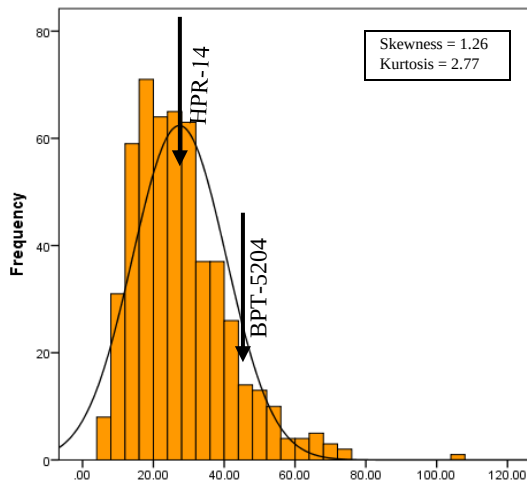
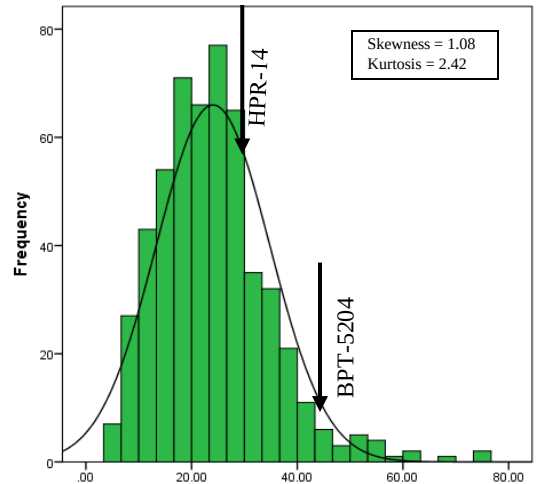


Fig. 1E: Frequency distribution of grain weight per panicle, test weight and total grain weight per plant in straight and reciprocal F_2 's derived from BPT 5204 & HPR 14 crosses in rice

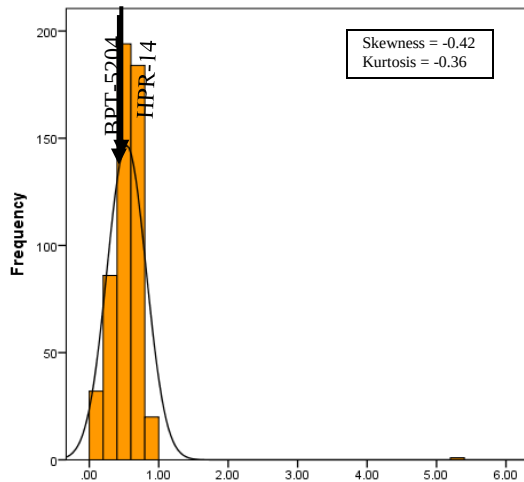


Straight cross

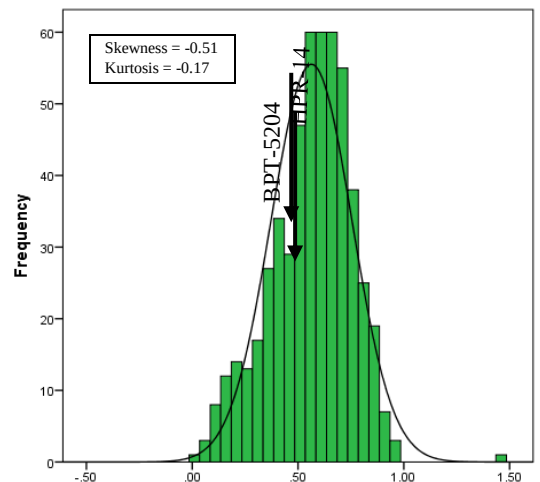


Biomass (g)

Reciprocal cross

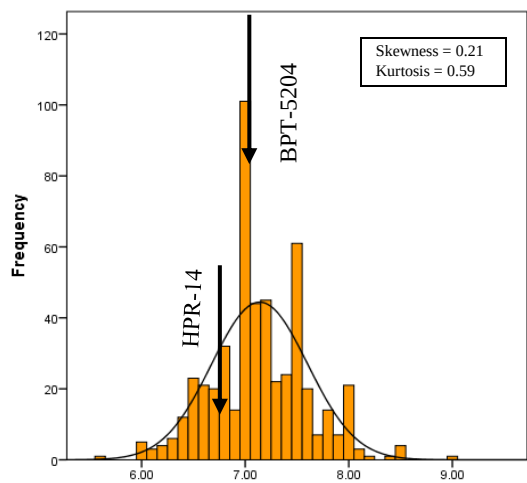


Straight cross

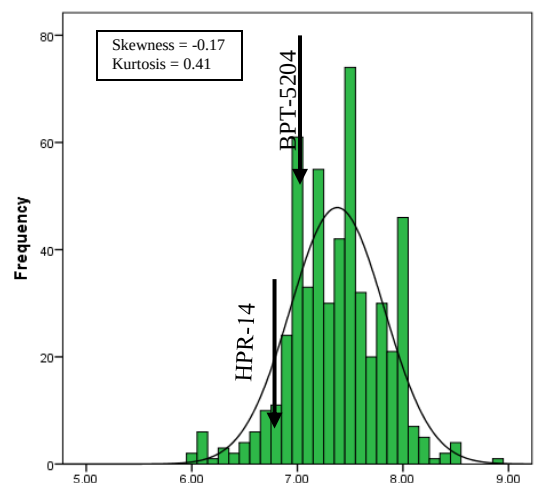


Harvest index

Reciprocal cross



Straight cross



Grain length (cm)

Reciprocal cross

Fig. 1F: Frequency distribution of biomass, harvest index & grain length in straight and reciprocal F_2 's derived from BPT 5204 & HPR 14 crosses in rice

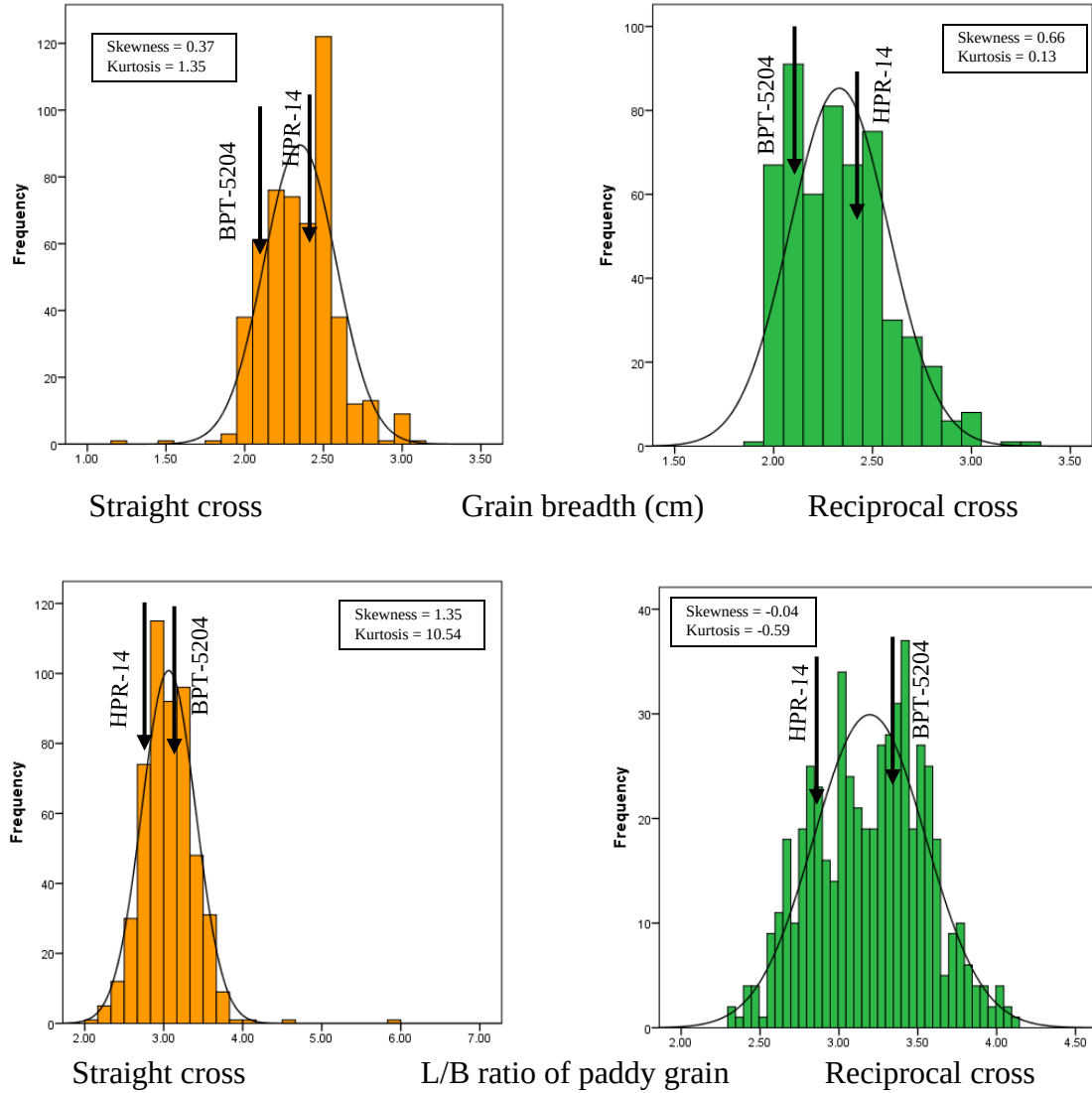


Fig. 1G: Frequency distribution of grain breadth & L/B ratio in straight and reciprocal F_2 's derived from BPT 5204 & HPR 14 crosses in rice.

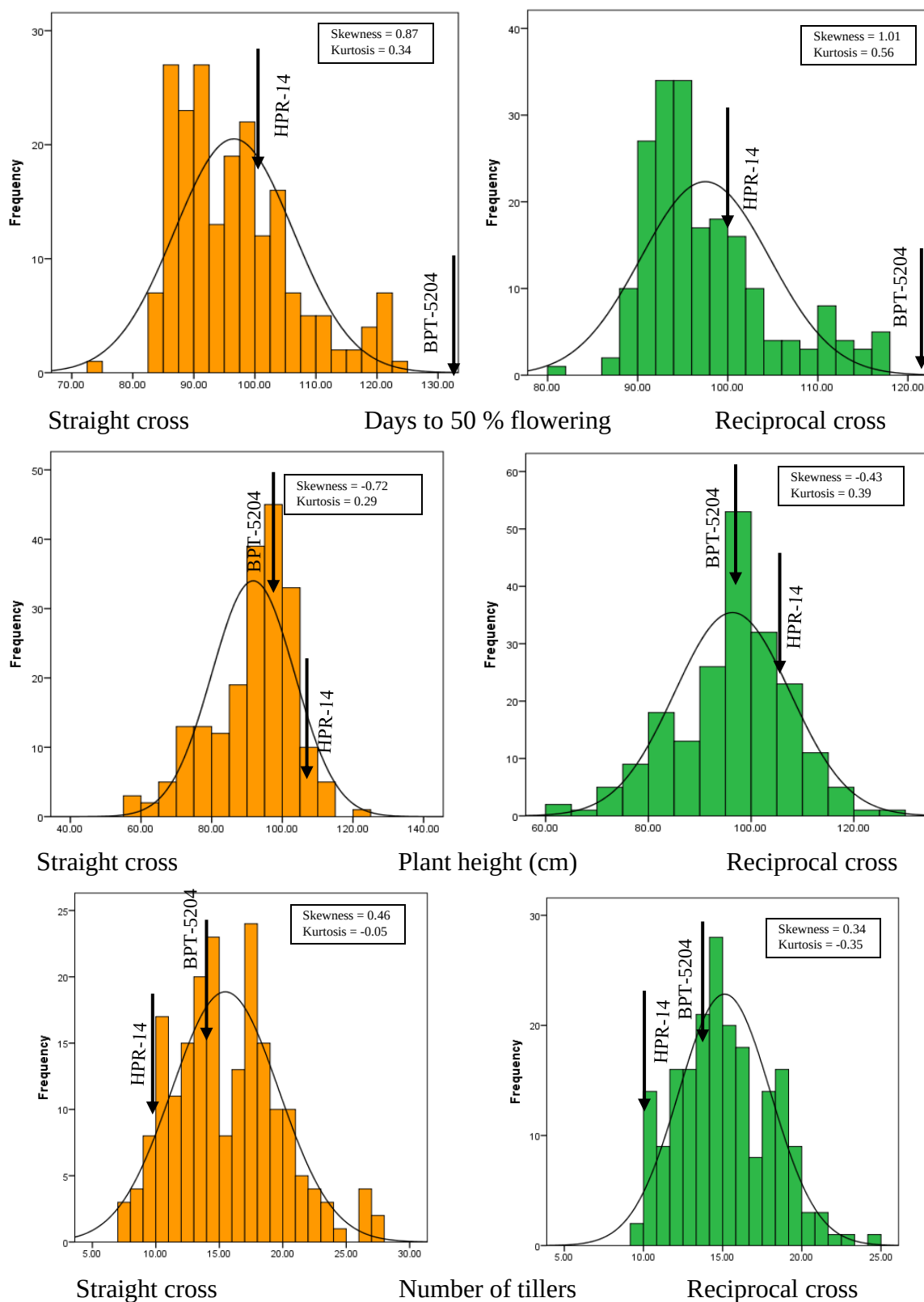


Fig. 2A: Frequency distribution of days to 50% flowering, plant height & number of tillers in straight and reciprocal F_3 's derived from BPT 5204 & HPR 14 crosses in rice

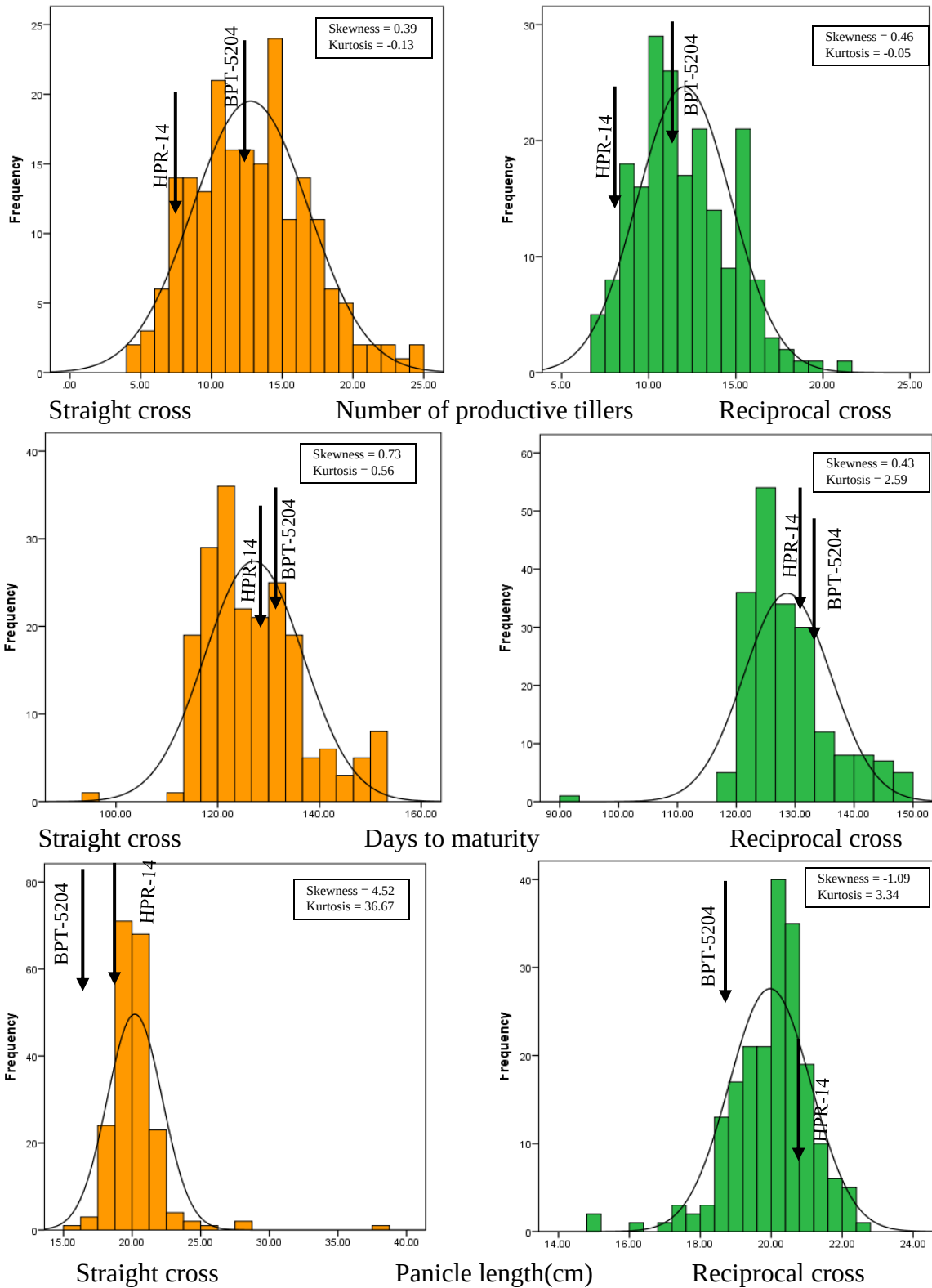


Fig. 2B: Frequency distribution of number of productive tillers, days to maturity & panicle length in straight and reciprocal F_3 's derived from BPT 5204 & HPR 14 crosses in rice

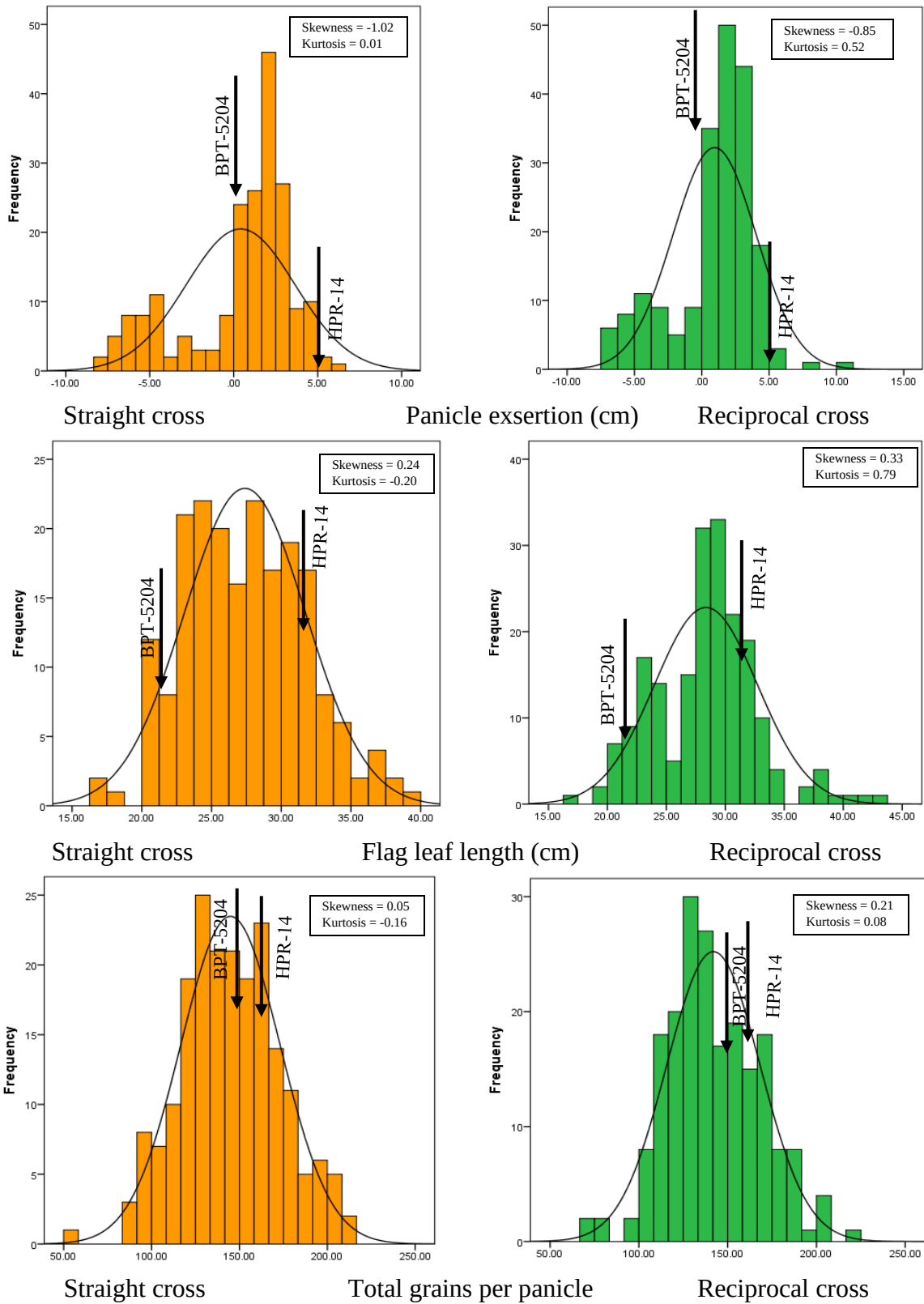


Fig. 2C: Frequency distribution of panicle exertion, flag leaf length & total grains per panicle in straight and reciprocal F_3 's derived from BPT 5204 & HPR 14 crosses in rice

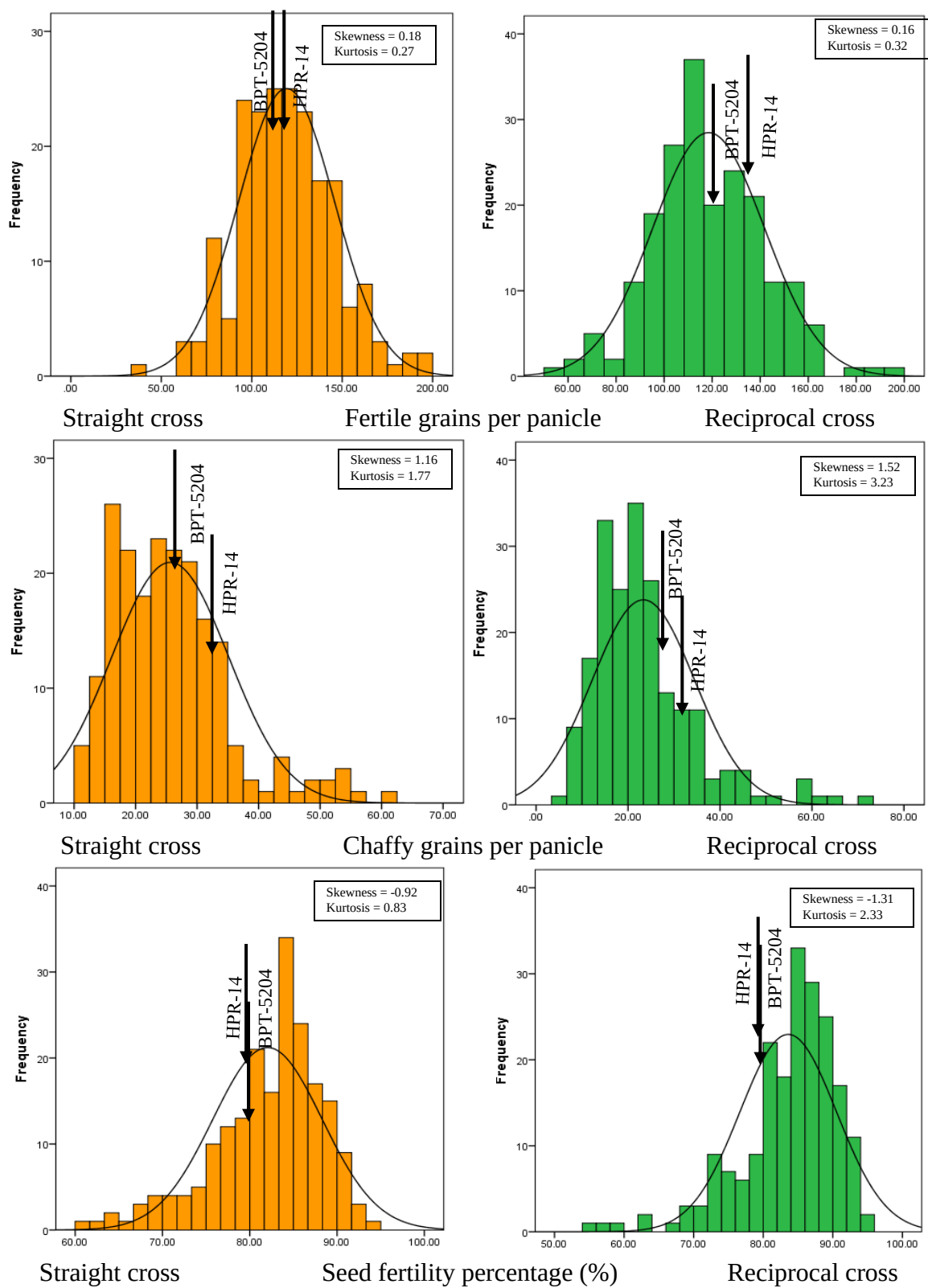


Fig. 2D: Frequency distribution of fertile grains per panicle, chaffy grains per anile & seed fertility percentage in straight t and reciprocal F_3 's derived from BPT 5204 & HPR 14 crosses in rice

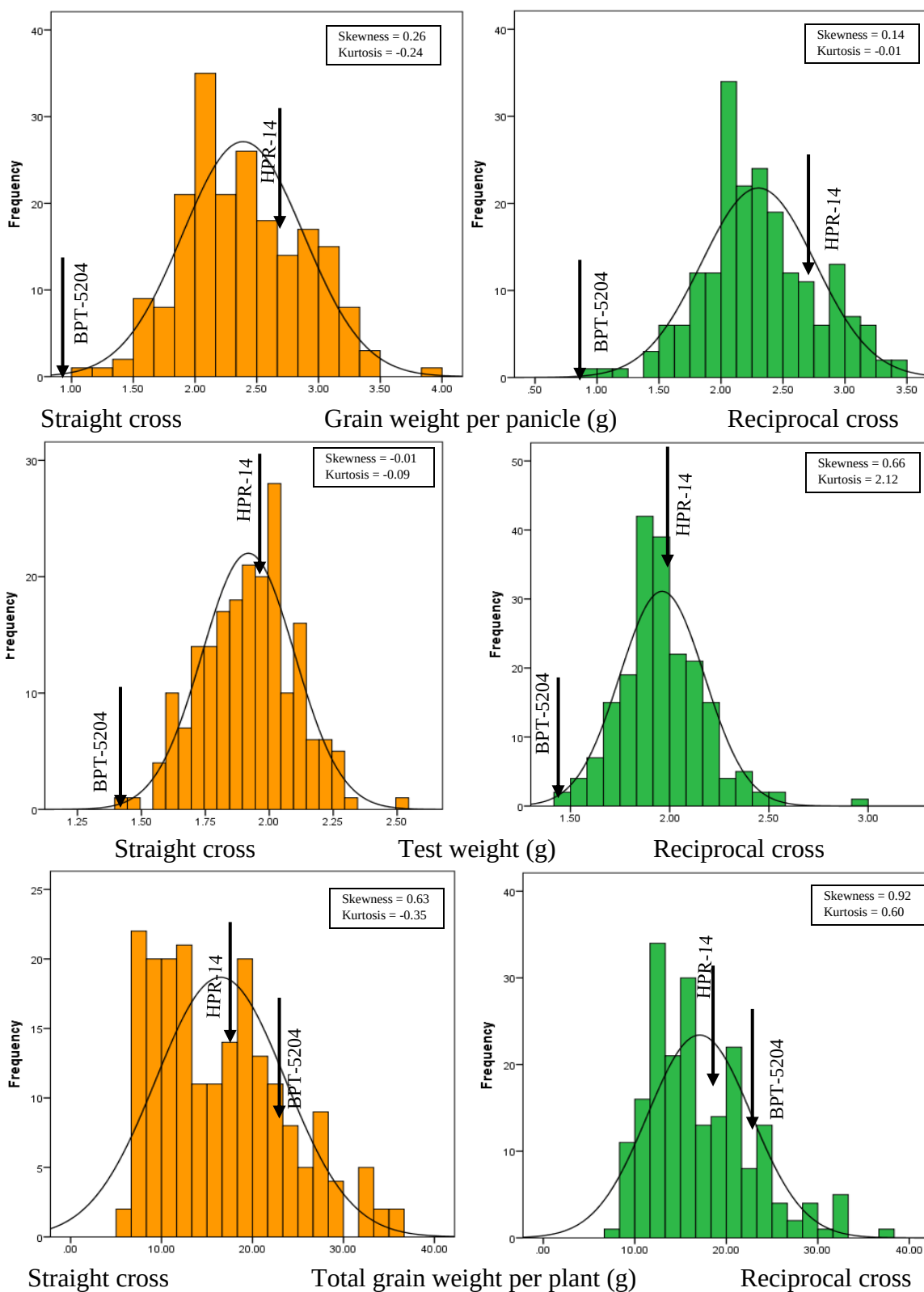


Fig. 2E: Frequency distribution of grain weight per panicle, test weight and total grain weight per plant in straight and reciprocal F_3 's derived from BPT 5204 & HPR 14 crosses in rice

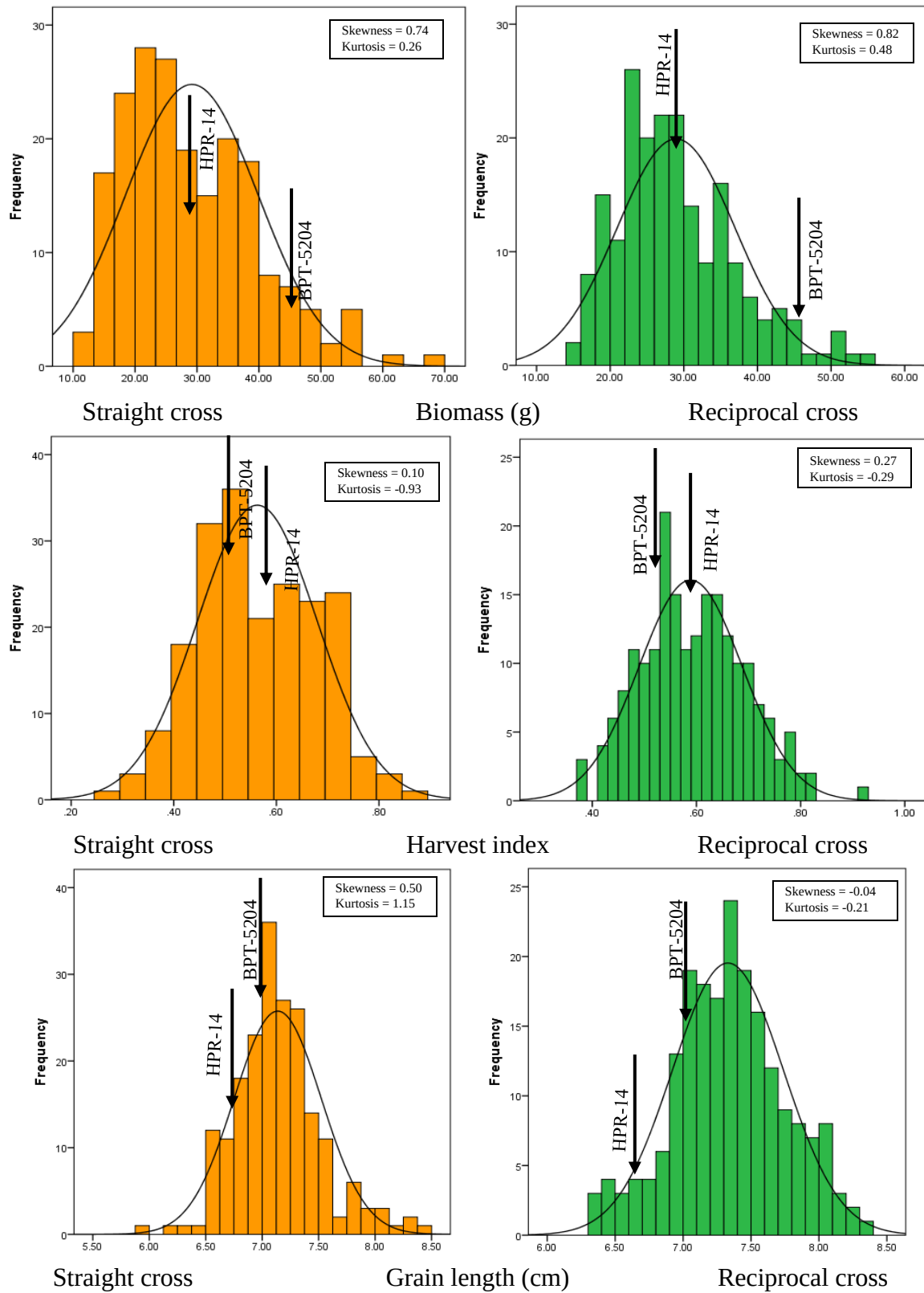


Fig. 2F: Frequency distribution of biomass, harvest index & grain length in straight and reciprocal F_3 's derived from BPT 5204 & HPR 14 crosses in rice

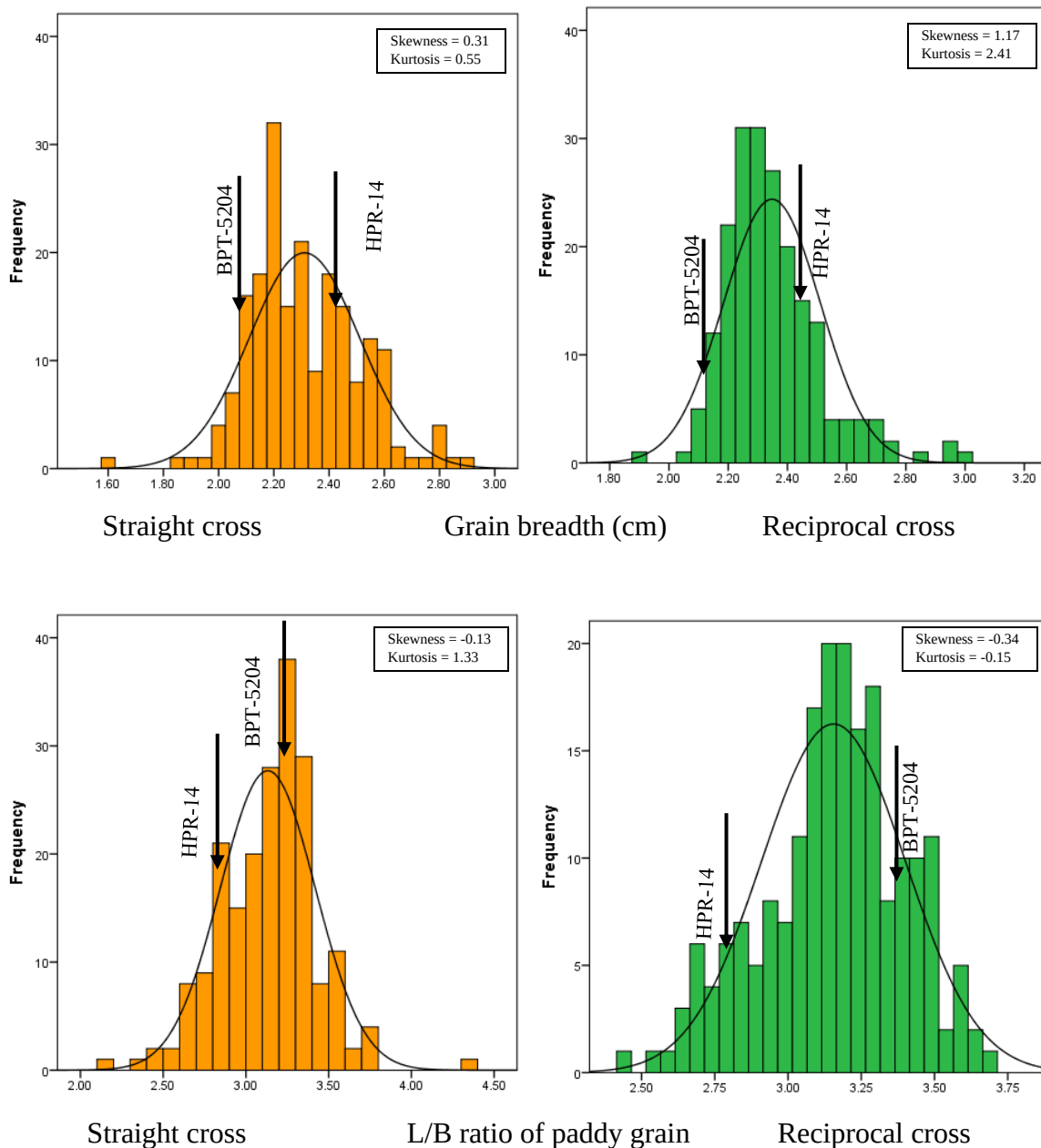


Fig. 2G: Frequency distribution of grain breadth & L/B ratio in straight and reciprocal F_3 's derived from BPT 5204 & HPR 14 crosses in rice.

Table 19: Test for normality for grain nutrient traits in F₂ and F₃ populations of rice in straight and reciprocal crosses of rice

Traits	Shapiro Wilk's test for normality															
	F ₂								F ₃							
	SC				RC				SC				RC			
	W	P<W	Skewness	Kurtosis	W	P<W	Skewness	Kurtosis	W	P<W	Skewness	Kurtosis	W	P<W	Skewness	Kurtosis
P	0.9947	0.0918	0.17	0.12	0.9887	0.0006	0.36	0.73	0.9920	0.3455	0.14	-0.20	0.9895	0.1530	0.14	0.93
Fe	0.9930	0.0219	0.25	0.61	0.9765	<0.0001	0.36	1.94	0.9912	0.2627	0.09	0.14	0.9494	<0.0001	0.32	3.06
Zn	0.9862	0.0001	0.29	-0.17	0.9425	<0.0001	-0.91	0.64	0.9693	0.0002	-0.54	2.27	0.9332	<0.0001	-1.05	2.88
Am	0.9672	<0.0001	0.71	0.39	0.9792	<0.0001	0.55	0.41	0.9543	<0.0001	0.81	0.53	0.9642	<0.0001	0.64	0.37
CHO	0.9924	0.0130	0.29	0.03	0.9734	<0.0001	0.67	0.91	0.9906	0.2196	0.03	-0.40	0.9783	0.0034	0.58	0.39
M	0.9889	0.0009	-0.42	0.49	0.9973	0.5688	-0.11	-0.02	0.9675	0.0001	-0.63	0.28	0.9314	<0.0001	-1.14	5.51
PA	0.9960	0.2451	0.04	0.37	0.9892	0.0009	0.36	0.66	0.9878	0.0833	-0.21	0.58	0.9780	0.0032	0.50	0.79

SC: Straight Cross (BPT 5204 X HPR-14); **RC:** Reciprocal Cross (HPR-14 X BPT 5204)

P: Protein (%)

CHO: Carbohydrate (%)

Fe: Iron (ppm)

M: Moisture content (%)

Zn: Zinc (ppm)

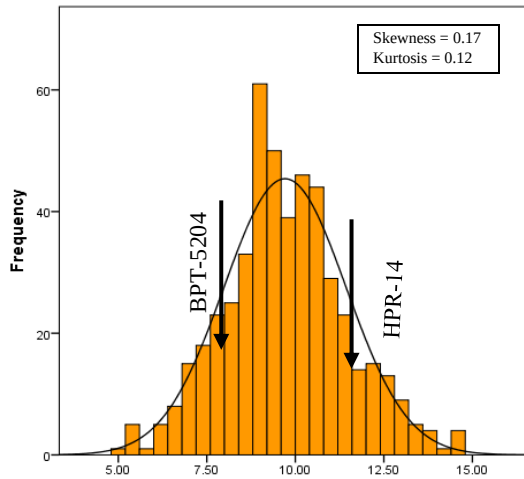
PA: Phytic acid (mg/100g)

Am: Amylose (%)

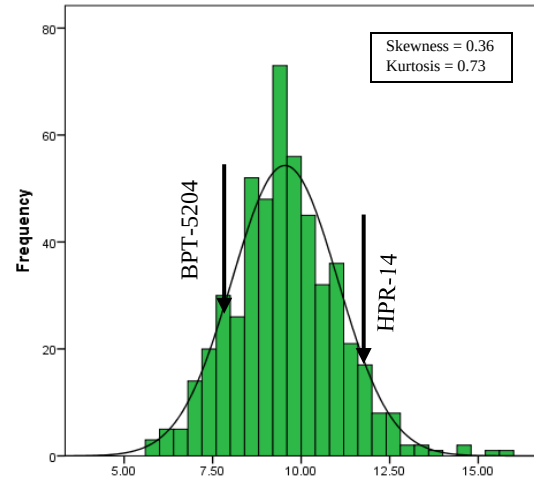
Frequency distribution of all the traits in straight and reciprocal crosses F_2 and F_3 populations were presented in figure 3a, 3b, 3c, 4a, 4b and 4c. The skewness is measure of the extent to which the distribution of the respective variable is skewed to the left (negative value) or right (positive value) relative to the standard normal distribution (skewness ranges between -0.25 to +0.25). Majority of the traits showed skewed distribution in straight and reciprocal F_2 populations. Traits like days to 50 *per cent* flowering, number of tillers, number of productive tillers, days to maturity, grain yield per plant, biomass per plant and grain breadth showed positively skewed distribution in straight and reciprocal crosses of F_2 and F_3 population, negatively skewed distribution was observed for plant height, particle exertion, seed fertility percentage, panicle length (except straight F_3 population), harvest index (except reciprocal F_3 population) and zinc (except straight F_2) in both straight and reciprocal F_2 and F_3 populations.

Kurtosis, the fourth degree statistics depicts degree of peakedness of distribution. ‘Platykurtic kurtosis’ has kurtosis value less than three, mesokurtic distribution has near zero (-0.25 to +0.25) kurtosis value and leptokurtic distribution kurtosis value more than three. Most of the growth and yield attributing traits and all the grain nutrient traits showed platykurtic distribution in both straight and reciprocal F_2 and F_3 population. Traits like chaffy grains per panicle and seed fertility percentage and L/B ratio (except reciprocal F_2 ’s) in straight and reciprocal F_2 population panicle length and chaffy grains per panicle (except straight F_3 population) showed leptokurtic distribution suggesting that few genes governing these traits.

In F_2 population it is composed of heterozygous heterogeneous plants and trait variation manifested by both additive $\times$ additive, additive $\times$ dominance and dominance $\times$ dominance epistatic gene action (Xu, 2010). Kurtosis indicates the relative number of genes controlling the trait under investigation (Robson, 1956). Fisher *et al.* (1932) outlined the theoretical basis of usefulness of skewness for explaining the genetic causes for variation in quantitative traits. Skewness and kurtosis which reveals interaction of genetic effects are more powerful than first and second degree statistics (Choo and Reinbergs, 1982). The skewed distribution of a trait in general suggest that trait is under the control of non-additive gene action, especially epistasis and is influenced by

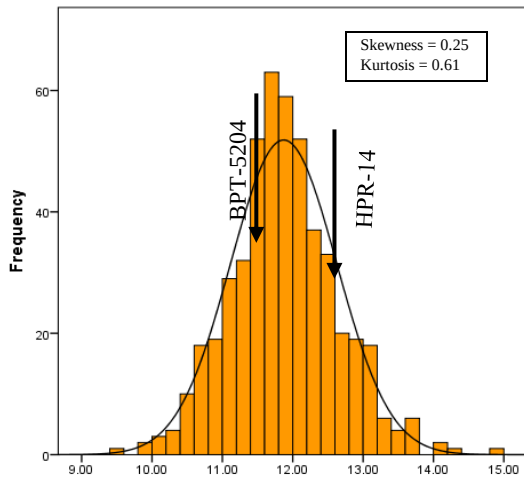


Straight cross

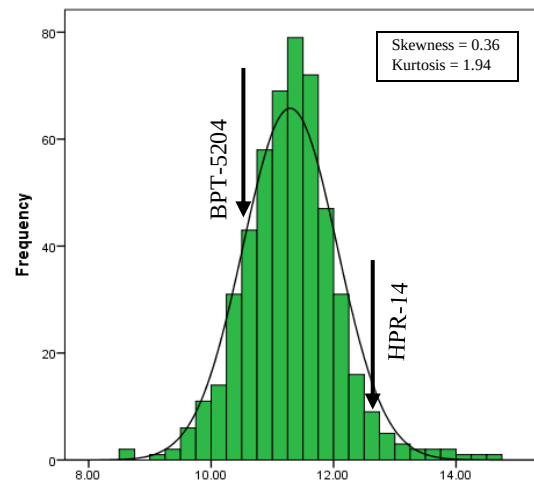


Protein (%)

Reciprocal cross

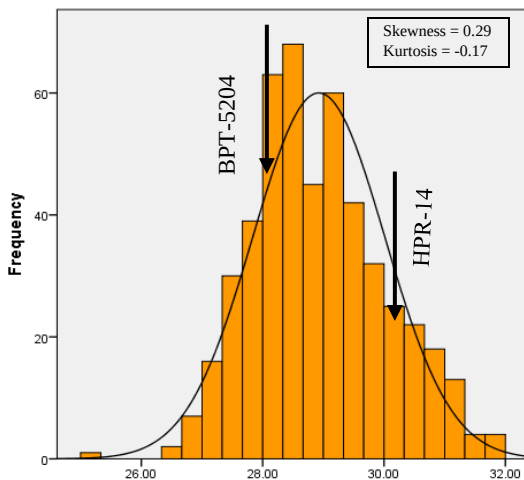


Straight cross

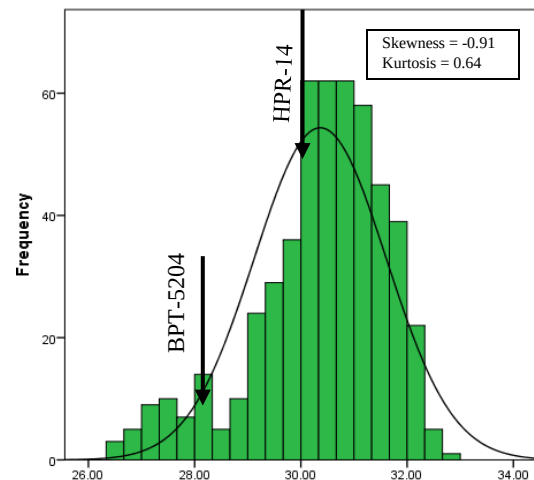


Iron (ppm)

Reciprocal cross



Straight cross



Zinc (ppm)

Reciprocal cross

Fig 3a: Frequency distribution protein, iron & zinc in straight and reciprocal F_2 's derived from BPT 5204 & HPR 14 crosses in rice

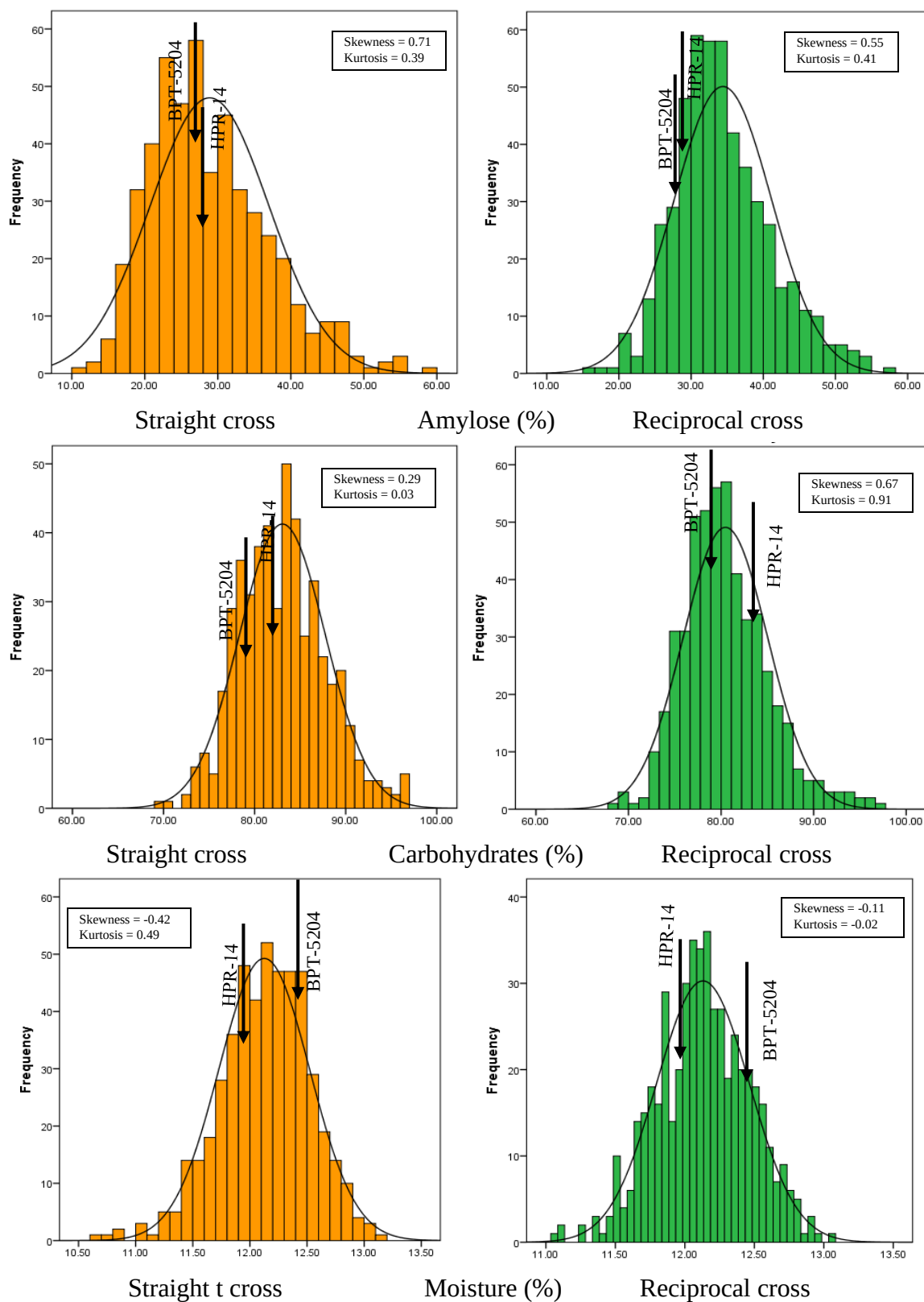


Fig 3b: Frequency distribution of amylose, carbohydrates & moisture in straight and reciprocal F_2 's derived from BPT 5204 & HPR 14 crosses in rice.

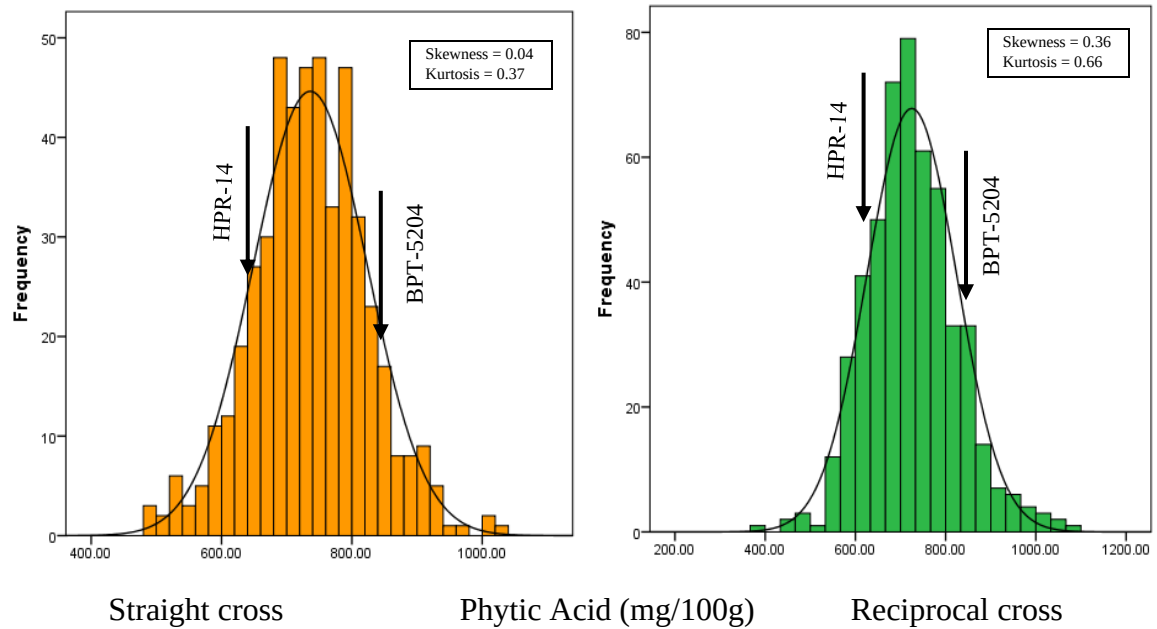


Fig 3c: Frequency distribution of phytic acid in straight and reciprocal F₂'s derived from BPT 5204 & HPR 14 crosses in rice.

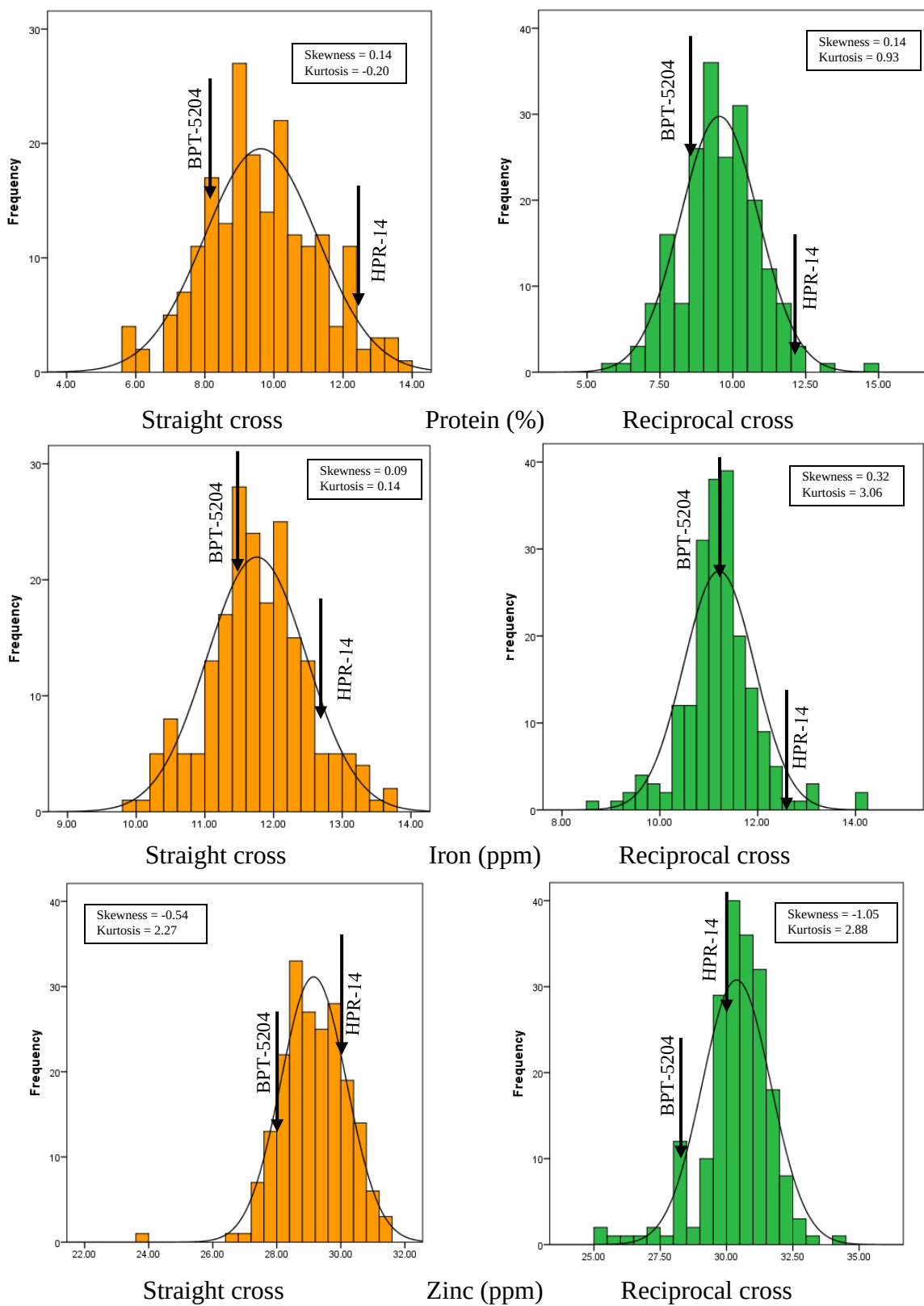


Fig. 4A: Frequency distribution protein, iron & zinc in straight and reciprocal F_3 's derived from BPT5204 & HPR 14 crosses in rice.

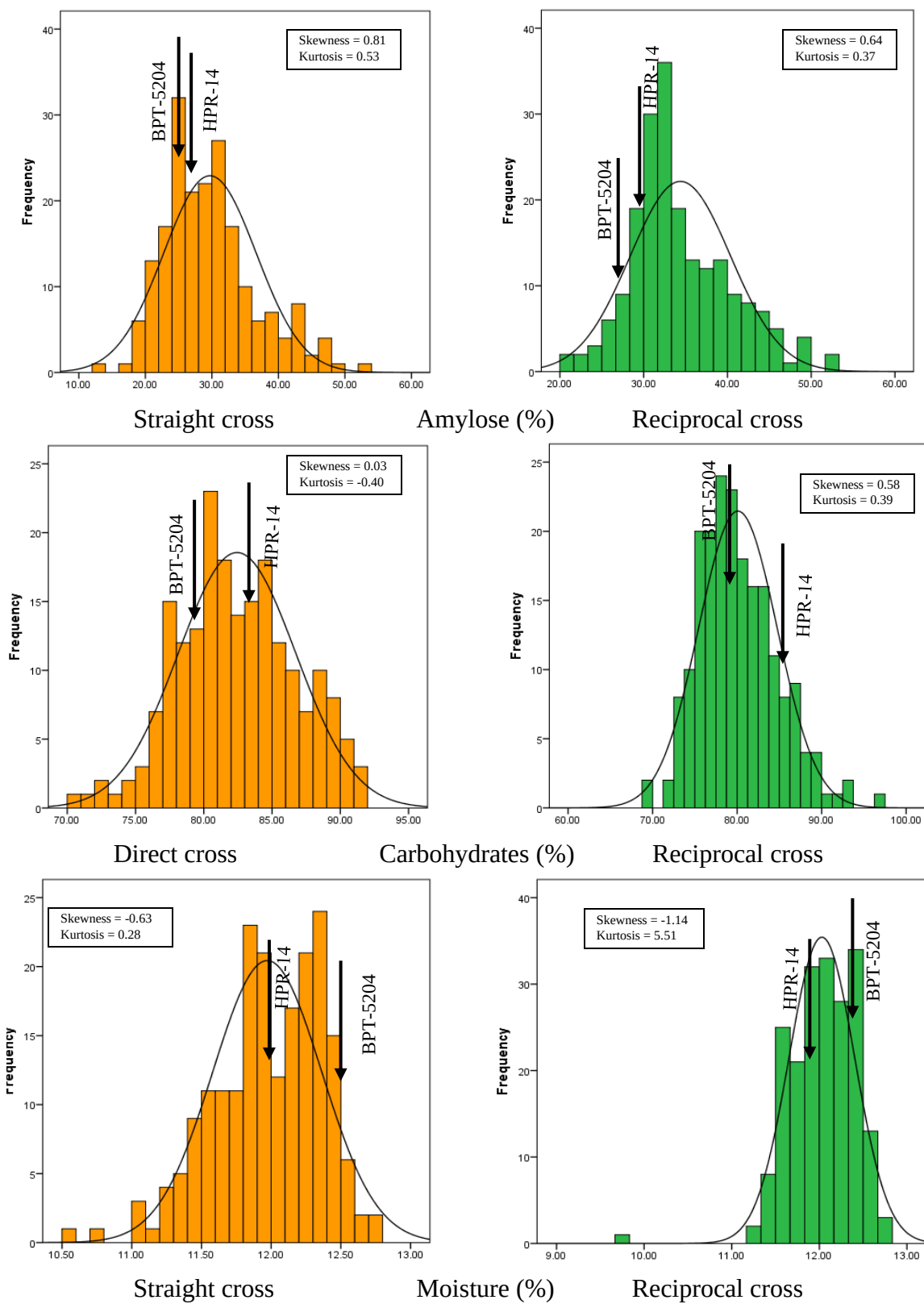
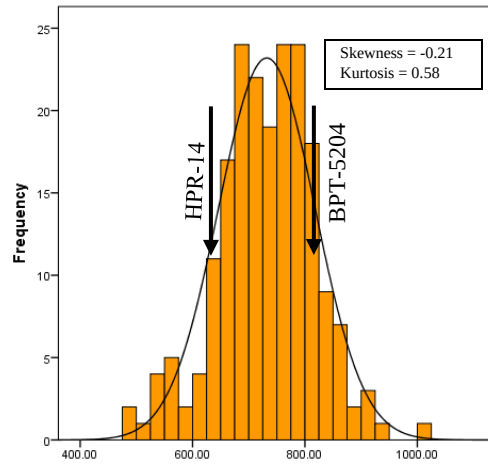
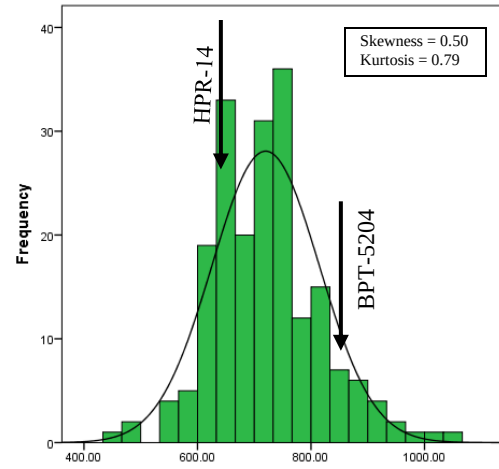


Fig. 4B: Frequency distribution of amylose, carbohydrates & moisture in straight and reciprocal F_3 's derived from BPT 5204 & HPR 14 crosses in rice.



Straight cross

Phytic Acid (mg/100g)



Reciprocal cross

Fig. 4C: Frequency distribution of phytic acid in straight and reciprocal F₃'s derived from BPT 5204 & HPR 14 crosses in rice.

environmental variables (Pooni *et al.*, 1977; Kimbeng and Bingham, 1988; Roy, 2000). Positive skewness is caused by complementary gene interactions, while negative skewness is caused by duplicate gene interactions predominantly in the same directions (Snape and Rizzs, 1975). Complete ambi-directional epistasis however produces kurtosis while distribution stays symmetrical around mean (Pooni *et al.*, 1977). The genes controlling the traits with skewed distribution tend to be predominantly dominant irrespective of whether they have increasing or decreasing effect on the expression of trait.

Positively skewed leptokurtic distribution for chaffy grain per panicle, L/B ratio (straight F₂'s), and panicle length in straight and reciprocal F₃ population in the present study suggested that traits were influenced by fewer genes with complimentary gene action. Positively skewed mesokurtic distribution flag leaf length (straight and reciprocal F₂'s), grain breadth (reciprocal F₂'s) and total grains per panicle (reciprocal F₃ population), protein and carbohydrates (straight F₂'s) and iron (straight F₃ population) suggests that traits were governed by moderate number of genes with complimentary gene action. Negatively skewed mesokurtic distribution for panicle length (straight F₂'s), plant height and harvest index (reciprocal F₂'s), panicle exertion and test weight (straight F₃'s), grain length and L/B ratio (reciprocal F₃'s) in the present investigation suggests that traits were governed by large number of genes with additive gene action.

4.5.2 Frequencies of quantitative characters in straight and reciprocal F₂ populations

A total of 517 straight and 533 reciprocal F₂ individuals were classified based on stem internode colour as green, light gold, purple line, purple and flag leaf type as erect, semi-erect, horizontal and deflexed type. Since, parents BPT-5204 (green, semi-erect) and HPR- 14 (purple, erect) were in contrast to each other.

Among straight F₂ population, 201 were green, 92 were light gold, 144 were purple line, and 80 were purple type of stem internodes were observed compared to reciprocal F₂ population where, 211 were green, 35 were light gold, 225 were purple line and 62 were purple type of stem internode. Among straight F₂ population, 324 were erect

and 193 were semi-erect type of flag leaf as compared to reciprocal cross where 211 were erect and 322 were semi-erect but none of the individuals were horizontal and deflexed type of flag leaf in both straight and reciprocal F₂ populations (Table 20).

4.5.3 Segregation of anthocyanin pigmentation in straight and reciprocal F₂ populations

The occurrence as well as distribution of anthocyanin pigmentation in different part of the rice plant are very variable and are striking features of the crop. Such morphological variant with distinct phenotypic expression and simple inheritance pattern can be used to establish linkages and for indirect selection is found associated with useful traits (Reddy *et al.*, 2008). Present study investigated genetic basis of anthocyanin pigmentation of three qualitative characters; basal leaf sheath colour, leaf blade colour and spikelets tip pigmentation (Table 21).

Spikelet's tip pigmentation: The 517 straight and 533 reciprocal F₂ population of BPT-5204 (absence of tip pigmentation) and HPR-14 (presence of tip pigmentation) was studied for mode of inheritance of anthocyanin tip pigmentation on spikelets. The straight and reciprocal F₂ plants segregating in ratio of 3 present: 1 absent of tip pigmentation on spikelets, which suggested monogenic inheritance is that presence of tip pigmentation dominant over absence of tip pigmentation.

Basal leaf sheath colour: The straight (BPT-5204 × HPR-14) and reciprocal (HPR-14 × BPT-5204) had purple basal leaf sheath indicating this trait to be dominant over green leaf sheath. The 517 straight F₂ and 533 reciprocal F₂ populations were suggested in 3:1 ratio for basal leaf sheath colour revealing the presence of a single dominant gene in HPR-14 variety. Monogenic inheritance of basal leaf sheath colour was also reported by earlier workers Sathyanarayanaiah and Reddy, 1973 and Majumdar, 1985. Mizro (1981) designated this gene as *Psh*. However, contrasting reports with monogenic, digenic (Pavda and Mohapatra, 1997), trigenic (Pavithram *et al.*, 1995 and Shukla, 1999) and tetragenic (Singh *et al.*, 1990) control for this character have also been reported earlier in different crosses. These varied genetics may be due to multiple set of gene conferring the character in different source material used in these studies.

Table 20: Frequencies of qualitative characters in F₂ generation in straight and reciprocal crosses of rice

Characters	Descriptions	Score	Observed frequency		BPT-5204	HPR-14
			Straight cross (517)	Reciprocal cross (533)		
Stem internode Color	Green	1	201 (38.89%)	211 (39.59%)	Green	Purple
	Light gold	2	92 (17.79%)	35 (6.57%)		
	Purple line	3	144 (27.85%)	225 (42.21%)		
	Purple	4	80 (15.47%)	62 (11.63%)		
Flag leaf type	Erect	1	324 (62.67%)	211 (39.59%)	Semi erect	Erect
	Semi erect	3	193 (37.33%)	322 (60.41%)		
	Horizontal	5	0	0		
	Deflexed	7	0	0		

Table 21: Genetics or segregation of anthocyanin pigmentation in straight and reciprocal F₂ population

Traits	Criteria	Observed frequency		Expected frequency		Expected ratio		Chi-square statistics		Prob. chi-square	
		SC	RC	SC	RC	SC	RC	SC	RC	SC	RC
Leaf blade colour	Green	436	461	420.06	433.06	13:3	13:3	3.22	9.61	0.07248	0.00193
	Purple	81	72	96.94	99.94						
Spikelets tip pigmentation	Present	376	378	387.75	399.75	3:1	3:1	1.41	4.73	0.23271	0.02958
	Absent	141	155	129.25	133.25						
Basal leaf sheath color	Purple	362	387	387.75	399.5	3:1	3:1	6.84	1.62	0.00891	0.49490
	Green	155	146	129.25	133.25						

SC: Straight Cross (BPT 5204 × HPR-14); **RC:** Reciprocal Cross (HPR-14 × BPT 5204)

Leaf blade colour: Mode of inheritance of anthocyanin pigmentation on leaf blade was studied in 517 straight and 533 reciprocal F₂ populations. The F₂ plants segregating in the ratio of 3 purple: 13 green leaf blade, which suggested inhibitory gene control with single major gene for green leaf. Further this gene has been designated as *PI* (Kinoshita and Markawal, 1985). Effect of *PI* gene was inhibited by the inhibitory gene *I-PI* when presented along with it and resulted in green colour (Nagao *et al.*, 1962) other workers (Qian *et al.*, 1995; Tomar *et al.*, 2000) also reported similar gene action for expression of purple pigmentation on leaf blade.

Pigmentation of various parts of the rice plant involves a complicated system of the gene interaction, ranging from epistasis to pleiotropic effects (Chang, 1960). Our results also indicated involvement of one to three genes with various interactions determining pigmentation of basal leaf sheath, leaf blade and spikelets tip pigmentation.

4.6 Reciprocal differences on qualitative traits in straight and reciprocal F₂ populations

4.6.1 Cytoplasmic effect of leaf blade colour

Straight and reciprocal F₂ populations were categorized based on leaf blade pigmentation. viz., purple and green leaves. Significant difference between purple and green categories for anthocyanin pigmentation in leaf blade in straight and reciprocal crosses was carried out using paired 't' test assuring unequal variance (Table 22). Significant difference for most of the yield and yield attributing traits were observed between purple and green pigmented categories in straight F₂ population.

The mean performance of days to 50 *per cent* flowering, number of tillers., number of productive tillers, days to maturity and biomass per plant were comparatively higher in green leaf blade category as compared to purple leaf blade categories. The results suggested that green pigmented leaf blade was significantly associated with many traits in rice. However, purple pigmentation of leaf blade was found lesser and non-significant for most of the traits in reciprocal F₂ population (when HPR-14 used as female) and it could be attributed to undesirable or modifier effect of cytoplasm. Similar

results were used as morphological markers for sheath rot diseases attributing traits by Mahadevaiah *et al.* (2015).

Table 22: Cytoplasmic effect of leaf blade colour with different traits in straight and reciprocal crosses derived F₂ population of rice

Traits	Leaf blade colour					
	Green		't' statistics	Purple		't' statistics
	SC (436)	RC (461)		SC (81)	RC (72)	
Days to 50 % flowering	97.34	95.08	2.95**	92.51	91.58	0.60
Plant height (cm)	88.09	90.92	-2.79**	88.44	90.14	-0.95
Number of tillers	15.88	14.67	3.74***	10.35	9.6	1.22
Number of productive tillers	13.41	11.51	5.39***	8.35	7.36	1.84
Days to maturity	127.88	126.00	2.38*	122.86	122.32	0.38
Flag leaf length (cm)	26.53	27.30	-2.12*	26.69	27.28	-0.71
Test weight (g)	1.82	1.87	-2.55*	1.75	1.82	-1.65
Biomass (g)	29.04	25.30	4.66***	18.22	16.14	2.09*
Grain length (cm)	7.15	7.39	-7.54***	7.09	7.28	-2.51*
Grain breadth (cm)	2.35	2.33	2.32*	2.35	2.34	0.54
L/B ratio of paddy grain	3.07	3.20	-6.29***	3.05	3.14	-2.13*
Brown spot	2.33	3.11	-6.44***	1.26	1.99	-2.43*

SC: Straight Cross (BPT 5204 × HPR-14); **RC:** Reciprocal Cross (HPR-14 × BPT 5204)

* Significant at 5 per cent

** Significant at 1 per cent

*** Significant at 0.1 per cent

4.6.2 Cytoplasmic effect of spikelet's pigmentation

Straight and reciprocal F₂ populations were categorized based on spikelet's pigmentation viz., presence and absence of spikelet's pigmentation. Significant difference between present and absent for straight and reciprocal crosses was carried out using paired 't' test between assuming unequal variance (Table 23). Significance difference for most of the yield and yield attributing traits were observed between straight and reciprocal crosses for presence and absence of spikelet's pigmentation in F₂ population.

Table 23: Cytoplasmic effect of spikelets pigmentation with different traits of straight and reciprocal crosses derived F₂ population of rice

Traits	Spikelet's pigmentation					
	Present		't' statistics	Absent		't' statistics
	SC (376)	RC (378)		SC (141)	RC (155)	
Days to 50 % flowering	96.33	94.39	2.29*	97.27	95.14	1.89
Plant height (cm)	89.25	90.36	-1.05	85.21	91.93	-3.55**
Number of tillers	14.74	13.42	3.51**	15.73	15.45	0.61
Number of productive tillers	12.35	10.40	4.93***	13.34	12.30	1.71
Flag leaf length (cm)	26.70	27.08	-1.01	26.16	27.82	-2.77**
Total grains per panicle	142.30	133.92	3.24**	143.43	147.08	-1.29
Fertile grains per panicle	117.61	111.05	2.59**	116.98	119.59	-0.79
Test weight (g)	1.80	1.87	-3.63***	1.82	1.84	-0.53
Grain yield per plant (g)	14.65	13.28	2.03*	16.45	16.40	-0.05
Biomass (g)	26.74	22.92	4.42***	28.97	26.83	1.49
Harvest index (%)	0.53	0.55	-0.96	0.55	0.60	-2.57**
Grain length (cm)	7.14	7.38	-6.88***	7.14	7.36	-4.13***
L/B ratio of paddy grain	3.06	3.19	-5.26***	3.08	3.21	-3.29**
Brown spot	2.06	2.81	-5.60***	2.42	3.34	-3.83***

SC: Straight Cross (BPT 5204 × HPR-14); **RC:** Reciprocal Cross (HPR-14 × BPT 5204)

* Significant at 5 per cent ** Significant at 1 per cent *** Significant at 0.1 per cent

The mean performance of days to 50 *per cent* flowering (96.33), number of tillers (14.74), number of productive tillers (12.35) total grains per plant (142.30) fertile grains per panicle (117.61), grain yield per plant (14.65) and biomass per plant (26.74) was higher comparatively reciprocal F₂ when spikelet's pigmentation was present. The mean performance of days 50 *per cent* flowering (97.27), number of tillers (15.73), number of productive tillers (13.34), grain yield per plant (16.45g) and biomass per plant (28.97g) was higher as compared to reciprocal F₂'s when spikelet's pigmentation was absent. The

results suggested that presence of spikelet's pigmentation was found non-significant for most of the traits studied. These differences could be attributed to undesirable or modifier effect of cytoplasm.

4.6.3 Cytoplasmic effect of flag leaf type

Straight and reciprocal F₂ populations were categorized based on flag leaf type viz., Erect and semi-erect type of flag leaf. Significance between straight and reciprocal populations for erect and semi-erect was carried out using paired 't' test assuring unequal variances (Table 24). The significance differences for most of the yield and yield attributing traits was observed between straight and reciprocal crosses for flag leaf type in F₂ population.

Table 24: Cytoplasmic effect of flag leaf type different traits of straight and reciprocal crosses derived F₂ population of rice

Traits	Flag leaf type					
	Erect		't' statistics	Semi erect		't' statistics
	SC (324)	RC (211)		SC (193)	RC (322)	
Number of tillers	14.60	14.11	1.28	15.66	13.94	4.41***
Number of productive tillers	12.13	11.00	2.54**	13.38	10.92	5.78***
Panicle exsertion (cm)	-0.70	-0.61	-1.40	1.59	1.47	2.24*
Fertile grains per panicle	114.71	107.75	1.74	122.44	117.33	2.32*
Test weight (g)	1.78	1.84	-2.17*	1.85	1.88	-0.93
Grain yield per plant (g)	14.19	13.69	0.16	16.78	14.51	2.93**
Biomass (g)	25.44	23.08	1.86	30.43	24.70	5.08***
Grain length (cm)	7.12	7.35	-3.56***	7.18	7.40	-6.43***
Grain breadth (cm)	2.36	2.34	0.68	2.35	2.32	3.31**
L/B ratio of paddy grain	3.05	3.17	-2.68**	3.08	3.21	-6.66***
Brown spot	2.00	3.08	-9.52***	2.44	2.89	-2.75**
Sheath rot	1.67	1.99	-0.47	0.74	0.86	-2.11*

SC: Straight Cross (BPT 5204 × HPR-14); **RC:** Reciprocal Cross (HPR-14 × BPT 5204)

* Significant at 5 per cent

** Significant at 1 per cent

*** Significant at 0.1 per cent

The mean performance of number of tillers (15.66), number of productive tillers (13.38), panicle exertion (1.59cm), fertile grains per panicle (122.44), grain yield per plant (16.78g) biomass per plant (30.43g) and grain breadth (2.35cm) were significantly higher comparatively reciprocals F_2 's population in semi-erect type of flag leaf. Whereas, the mean performance of the number of productive tillers per plant (12.13) was shown significantly high comparatively reciprocal F_2 's in erect type of flag leaf. The results suggested that semi-erect type of flag leaf was significantly associated with many yield and yield attributing traits in straight cross population of rice. However, erect type of flag leaf was found non-significance for most of traits between straight and reciprocal F_2 populations. This could be attributed to undesirable or modifier effect of cytoplasm.

4.6.4 Cytoplasmic effect of stem internodes colour

Straight and reciprocal F_2 populations were categorized based on stem internodes colour viz., Green, light gold, purple line and purple. Significance between straight and reciprocal populations for stem internodes colour was carried out using paired 't'test assuming unequal variances (Table 25). The significance difference for most of traits were observed between straight and reciprocal crosses for stem internodes colour F_2 populations.

The mean performance of days to 50 *per cent* flowering (97.43) number of tillers (15.80), number of productive tillers (13.36), days to maturity (127.91) and grain breadth (2.52cm) were significantly higher in straight F_2 population comparatively reciprocal F_2 population. In light gold type of stem internodes, the mean performance of traits like number of tillers (10.92), number of productive tillers (8.27), grain yield per plant (12.88g) and biomass per plant (23.47g) found significantly higher in straight cross compared to reciprocal cross.

In purple line stem internodes, most of traits viz., number of tillers (16.10), number of productive tillers (13.58), total grains per panicle (145.34), fertile grains per panicle (123.24), grain weight per panicle (2.41g), grain breadth (2.36cm) were significantly higher in straight F_2 population. In purple stem internode, only number of productive tillers (10.95) was significantly high in the straight cross compared to reciprocal crosses of rice.

Table 25: Cytoplasmic effect of internode colour with different traits of straight and reciprocal crosses derived F₂ population of rice

Traits	Stem internode colour											
	Green		‘t’ statistics	Light gold		‘t’ statistics	Purple line		‘t’ statistics	Purple		‘t’ statistics
	SC (201)	RC (211)		SC (92)	RC (35)		SC (144)	RC (225)		SC (80)	RC (62)	
DF	97.43	94.36	3.14**	95.40	92.94	0.94	97.47	95.09	1.92	94.23	96.03	0.26
PH	83.08	88.82	-3.82**	88.45	90.90	-1.53	92.80	92.05	0.07	92.14	94.80	-1.07
NT	15.80	14.66	2.12*	13.05	10.90	3.62***	16.10	14.54	3.25**	13.34	12.11	1.39
NPT	13.36	11.53	3.29**	10.92	8.27	4.21***	13.58	11.45	4.00***	10.95	9.03	2.18*
DM	127.91	125.30	2.62**	126.02	123.68	0.92	127.92	126.03	1.49	124.81	126.63	0.24
PE	-0.93	0.15	-2.48**	-0.03	-0.17	-0.50	1.09	1.24	-0.43	1.28	1.16	0.05
FLL	25.71	27.22	-3.15**	26.71	27.75	-1.42	27.38	27.15	0.39	27.01	27.90	-0.53
TGPP	141.18	141.97	-0.51	145.02	135.24	1.76	145.34	134.92	3.29**	138.49	134.80	0.57
FGPP	113.86	115.51	-0.69	117.33	109.37	1.46	123.24	114.08	2.65**	116.13	105.51	0.99
GWPP	2.20	2.26	-1.25	2.21	2.18	0.37	2.41	2.26	2.20*	2.24	2.06	0.70
TW	1.81	1.87	-1.87	1.74	1.86	-2.91**	1.84	1.86	-1.32	1.80	1.83	-1.19
GYPP	15.71	15.32	0.26	12.88	10.59	2.19**	16.56	14.58	2.03*	13.75	11.24	0.89
BM	27.58	25.07	1.94	23.47	18.17	3.83***	30.60	25.16	4.01***	25.34	21.28	1.30
HI	0.57	0.59	-0.89	0.52	0.56	-1.32	0.52	0.55	-1.31	0.51	0.50	-0.14
GL	7.12	7.36	-5.66***	7.10	7.37	-2.03*	7.15	7.40	-5.96***	7.22	7.36	-2.19*
GB	2.36	2.31	2.52*	2.32	2.28	0.61	2.36	2.35	3.61***	2.35	2.41	-1.39
LBR	3.05	2.31	-5.19***	3.08	3.26	-2.13*	3.06	3.18	-7.33***	3.09	3.09	0.16
BS	2.30	3.37	-5.99***	1.80	2.32	-2.66**	2.47	2.85	-1.24	1.68	2.34	-2.19*

* Significant at 5 per cent ** Significant at 1 per cent *** Significant at 0.1 per cent

SC: Straight Cross (BPT 5204 × HPR-14); RC: Reciprocal Cross (HPR-14 × BPT 5204)

DF: 50 % flowering

PH: Plant height (cm)

NT: Number of tillers

NPT: Number of productive tillers

DM: Days to maturity

PE: Panicle exertion (cm)

FLL: Flag leaf length (cm)

TGPP: Total grains per panicle

FGPP: Fertile grains per panicle

GWPP: Grain weight per panicle(g)

TW: Test weight (g)

GYPP: Grain yield per plant (g)

BM: Biomass (g)

HI: harvest index (%)

GL: Grain length (cm)

GB: Grain breadth (cm)

LBR: L/B ratio of paddy grain

BS: Brown spot disease

These results suggested that purple line stem internode was significantly associated with most of traits in straight F₂ population. However, purple stem internode was found non-significance with most of traits studied between straight and reciprocal F₂ populations. This could be attributed to undesirable or modifier effect of cytoplasm.

4.6.5 Cytoplasmic effect of basal leaf sheath pigmentation

Based on purple pigmentation of basal leaf sheath, straight and reciprocal F₂ populations were categorized into purple sheath, light purple sheath, purple line and non-pigmented or green colour sheath. Significant difference between straight and reciprocal populations for these types of basal leaf sheath pigmentation was carried out using paired 't' test assuming unequal variance. The significance differences for most of the yield and yield attributing traits were observed between straight and reciprocal crosses for based leaf sheath pigmentation types in F₂ population (Table 26).

The mean performance of number of tillers (15.94), productive tillers (13.45) were significantly higher in straight F₂ comparatively reciprocal F₂ population in non-pigmented or green type of basal leaf sheath. In purple line type, grain breadth (2.36cm) was significantly higher in straight cross compared to reciprocal F₂'s. Most of the traits viz., day to 50 *per cent* flowering (94.83), plant height (87.92cm), number of tillers (15.98), numbers of productive tillers (13.74), panicle length (20.48cm), total grains per panicle (145.14) fertile grains per plant (16.68) and biomass per plant (28.87g) found significantly higher in straight F₂ population as compared to reciprocal F₂ population for light purple type of basal leaf sheath pigmentation.

The mean performance of days to 50 *per cent* flowering (97.30) number of tillers (11.89), number of productive tillers (9.75), days to maturity (127.91) and biomass per plant (22.31g) were significantly higher in straight F₂'s comparatively reciprocal F₂ population. These results suggested that light purple basal leaf sheath type was significantly associated with many yield and yield attributing traits in straight F₂ population of rice. However, green and purple leaf type found non-significance for most of the traits between straight and reciprocal F₂ population. This could be attributed to undesirable or modifier effect of cytoplasm.

Table 26: Cytoplasmic effect of basal leaf sheath colour with different traits of straight and reciprocal crosses derived F₂ population of rice

Traits	Basal leaf sheath colour											
	Green		't' statistics	Purple line		't' statistics	Light purple		't' statistics	purple		't' statistics
	SC (155)	RC (146)		SC (83)	RC (151)		SC (169)	RC (155)		SC (110)	RC (81)	
DF	96.43	94.79	1.48	99.49	96.93	0.75	94.83	92.61	2.19*	97.30	93.78	2.10*
PH	84.69	91.91	-4.57***	90.30	94.24	-2.36*	87.92	84.73	2.02*	91.75	94.12	-1.45
NT	15.94	14.89	1.63	15.43	14.74	1.62	15.98	14.14	2.89**	11.89	10.78	2.07*
NPT	13.45	11.81	2.43*	12.58	11.68	1.87	13.74	10.91	4.17***	9.75	8.15	2.92**
DM	126.92	125.79	0.93	130.01	127.81	0.51	125.30	123.52	1.83	127.91	124.49	2.08*
PL	19.91	20.22	-1.30	19.95	21.58	-1.06	20.48	19.44	4.91***	20.37	20.04	1.04
PE	-0.46	0.64	-2.59*	1.31	1.57	-0.08	-0.21	-0.17	-0.50	0.63	0.47	0.12
FLL	25.90	27.84	-46.94***	26.28	27.76	-1.92	26.72	26.00	1.36	27.41	27.95	-1.11
TGPP	141.03	147.08	-1.17	136.46	137.73	0.19	145.14	128.44	5.16***	145.58	138.74	0.97
FGPP	115.60	120.05	-0.87	113.45	114.56	0.12	122.56	107.90	4.54***	115.17	110.67	0.71
GWPP	2.23	2.32	-1.15	2.21	2.28	-0.12	2.41	2.18	3.83**	2.14	2.14	-0.10
TW	1.82	1.84	-0.72	1.80	1.85	-1.40	1.86	1.93	-2.19*	1.71	1.84	-3.15**
GYPP	16.27	16.06	-0.90	14.09	15.00	-0.35	16.68	13.59	2.92**	11.97	10.44	1.37
BM	28.87	26.18	1.62	28.05	26.18	1.21	28.87	22.84	4.38***	22.31	18.62	2.62**
HI	0.54	0.60	-2.56**	0.47	0.55	-2.51*	0.58	0.56	0.79	0.51	0.54	-1.06
GL	7.15	7.37	-4.40**	7.09	7.36	-4.44**	7.18	7.42	-4.51***	7.10	7.35	-2.28*
GB	2.35	2.31	1.91	2.36	2.34	4.09**	2.36	2.33	1.59	2.33	2.35	-0.43
LBR	3.07	3.22	-3.87**	3.03	3.18	-6.51**	3.07	3.21	-4.93***	3.07	3.16	-1.19
BS	2.45	3.46	-4.86**	2.65	3.01	-0.89	1.99	2.86	-4.54***	1.65	2.17	-2.28*
SR	1.79	1.29	2.23*	0.83	0.98	-0.66	1.61	1.95	-1.04	0.57	0.73	-0.49

* Significant at 5 per cent ** Significant at 1 per cent *** Significant at 0.1 per cent

SC: Straight Cross (BPT 5204 × HPR-14); RC: Reciprocal Cross (HPR-14 × BPT 5204)

DF: 50 % flowering

PH: Plant height (cm)

NT: Number of tillers

NPT: Number of productive tillers

DM: Days to maturity

PL: Panicle length

PE: Panicle exertion (cm)

FLL: Flag leaf length (cm)

TGPP: Total grains per panicle

FGPP: Fertile grains per panicle

GWPP: Grain weight per panicle(g)

TW: Test weight (g)

GYPP: Grain yield per plant (g)

BM: Biomass (g)

HI: harvest index (%)

GL: Grain length (cm)

GB: Grain breadth (cm)

LBR: L/B ratio of paddy grain

BS: Brown spot disease

SR: Sheath rot disease

4.7 Parents offspring correlation and regression in straight and reciprocal F₂ and F₃ populations

Inter-generation correlation co-efficient were estimated to study the relationship between F₂ and F₃ generations for yield attributing and grain nutrient traits in straight and reciprocal F₂ population (Table 27). Inter-generation correlations were positive and significantly higher in most of the traits viz., days to 50 *per cent* flowering (0.96), plant height (0.90), number of tillers (0.97), number of productive tillers (0.97), days to maturity (0.97), biomass per plant (0.97), harvest index (0.93), grain length (0.92) and L/B ratio of paddy grain (0.81) in straight F₂ population compared to reciprocal F₂ population. Intergeneration correlation for grain nutrient traits were positive and significantly higher for the traits viz., zinc (0.72), amylase (0.96), carbohydrate (0.96) and phytic acid (0.99) in reciprocal F₂ population as compared to straight F₂ population. Therefore, the performance of the plant in F₂ generation is a reliable indicator of the performance of its progeny in subsequent generations in both straight and reciprocal crosses. Similar conclusions were drawn by Mishra *et al.*, 1994 in rice.

Further, it was also observed that the regression coefficient for days to 50 *per cent* flowering (0.79), plant height (0.75), numbers of tiller (0.82), number of productive tillers (0.75), days to maturity (0.79), panicle length (0.61), panicle exertion (0.83), total grains per panicle (0.82), and fertile grains per panicle (0.79). grains weight per panicle (0.76), grain yield per plant (0.83), biomass per plant (0.81), harvest index (0.74), grain breadth (0.61), L/B ratio (0.59) and grain zinc content (0.72) showed higher regression co-efficient between F₂ and F₃ generation in straight cross than reciprocal crosses. From these observations, it can be said that selection for above said traits can be made in the early segregating generations keeping aside such characters showed lesser correlation and regression between F₂ and F₃ generations. Similar results were also observed by Barman *et al.* (2012), Dhanraj *et al.* (1987) and Jangale *et al.* (1987) Kumar *et al.* (2009). Simultaneous selection of plants with higher yield and average grain weight might be performed in early generation with higher levels of heterozygotes.

Table 27: Parents offspring correlation and regression in F₂& F₃ populations of straight and reciprocal crosses for growth, yield attributing and grain nutrient traits in rice

Traits	Straight cross		Reciprocal cross	
	Correlation F ₂ -F ₃	Regression F ₂ -F ₃	Correlation F ₂ -F ₃	Regression F ₂ -F ₃
Growth and yield attributing traits				
Days to 50 % flowering	0.96	0.79	0.90	0.69
Plant height (cm)	0.90	0.75	0.89	0.69
Number of tillers	0.97	0.82	0.93	0.66
Number of productive tillers	0.96	0.75	0.93	0.61
Days to maturity	0.94	0.79	0.87	0.65
Panicle length(cm)	0.60	0.61	0.79	0.51
Panicle exertion (cm)	0.97	0.83	0.91	0.79
Flag leaf length (cm)	0.95	0.79	0.95	0.83
Total grains per panicle	0.92	0.82	0.95	0.76
Fertile grains per panicle	0.92	0.79	0.92	0.70
Chaffy grains per panicle	0.87	0.47	0.92	0.51
Seed fertility percentage (%)	0.88	0.49	0.91	0.51
Grain weight per panicle (g)	0.89	0.76	0.92	0.75
Test weight (g)	0.82	0.62	0.87	0.65
Grain yield per plant (g)	0.97	0.83	0.95	0.74
Biomass (g)	0.97	0.81	0.91	0.79
Harvest index	0.93	0.74	0.78	0.53
Grain length (cm)	0.92	0.75	0.90	0.81
Grain breadth (cm)	0.70	0.61	0.74	0.52
L/B ratio of paddy grain	0.80	0.59	0.74	0.57
Grain nutrient traits				
Protein (%)	0.99	0.91	0.99	1.09
Iron (ppm)	0.94	0.94	0.89	1.00
Zinc (ppm)	0.71	0.72	0.72	0.68
Amylose (%)	0.93	0.80	0.96	1.05
Carbohydrates (%)	0.94	0.88	0.96	1.02
Phytic Acid (mg/100g)	0.96	0.95	0.99	1.03

Therefore, it is advisable that selection in rice should be practiced as early as in F₃ generation for test weight as well as for complex characters like yield was emphasized by Benin *et al.* (2005) Sneepe (1977) and Cooper (1981). Shesbeshki (1967) suggested that for the identification of superior gene contributions even in the heterozygote certainly some point of view the proportion of the plant with most desirable gene combination decreases rapidly with the advancement of generation and if these were not selected in the early generations even if heterozygote condition, these would be lost. The present results get supported with the suggestion of Shebeshki (1967) as higher number of alleles governed individual were recovered when early selection in F₂ was practiced.

4.8 Screening for disease reactions in straight and reciprocal F₂ and F₃ populations

The rice (*Oryza sativa*) is known to suffer from number of diseases caused by fungal, bacterial and viral origins. These changes may be due to change over from the cultivars, most of them even though high yielding are susceptible to diseases. Among all the diseases of rice the most common and severe diseases are blast, sheath blight and sheath rot (Woperers *et al.*, 2009) that causes economic loss to the rice crop in the country. Therefore, in the present investigation 517 F₂ straight cross, 533 F₂ reciprocal cross, 200 families derived from straight and reciprocal crosses were screened for identification of disease reaction, since parent had differentially rank to all the diseases (BPT-5204 was susceptible parent and HPR-14 was resistant parent).

Among straight F₂ population 175 individuals (33.85%) were with no incidence, 132 individuals (25.33%) were less than 4 to 5 *per cent* incidence and none of the individuals were highly susceptible is 50 *per cent* incidence to the brown spot disease. In reciprocal F₂ population 54 individuals (10.13%) with no incidence, 181 individuals (33.96%) were with 4.5 *per cent* incidence, 103 individuals were with 19.07% incidence and none of the individuals were highly susceptible (>50 *per cent* incidence). Among 200 F₃ families of straight cross, 10 families (5%) with no incidence, 117 families (58.50%) were with 4 to 5% incidence and none of the families exhibited more than 25 *per cent* incidence and similarly in reciprocal families, 14 families (7%) were with no incidence,

105 families (52.50%) were with 4 to 5% incidence and none of the families showed more than 50 *per cent* incidence of brown spot disease (Table 28 and Figure 5).

Among 517 straight cross F₂ population, 330 individuals (63.83%) were immune, 24 (4.64%) were resistant, 87 (16.83%) were moderately resistant, 65 (12.57%) were moderately susceptible, 11 (2.13%) were susceptible and none of the individuals were highly susceptible to the sheath rot disease. Among 533 reciprocal cross F₂ population, 347 individuals (65.10%) were immune, 37 (6.94%) were resistant, 72 (13.51%) were moderately resistant, 55 (10.32%) were moderately susceptible 19 (3.56%) were susceptible and 3 (0.56%) were highly susceptible for sheath rot disease. Among 200 F₃ families straight cross, none of the families were immune as well as highly susceptible, 3 families were resistant, 42 were moderately resistant and 155 families were moderately susceptible compared to 200 reciprocal F₃ families. Where, 4 were immune, 4 were resistant 35 were moderately resistance 157 were moderately susceptible and none of the families were susceptible & highly susceptible to the sheath rot disease (Table 29 and Figure 6).

Among 517 straight cross F₂ population, 508 individuals were immune, 7 were resistant, 2 were moderately resistant and none of the individuals were susceptible and highly susceptible to the sheath blight disease compared to 533 reciprocal F₂ population. Where, 528 individuals were immune, 5 were moderately resistant and none of individuals were resistant, susceptible and highly susceptible to the sheath blight disease. Among 200 F₃ families of straight cross, 5 families were immune, 194 were resistant, one family was moderately resistant and none of the families were susceptible and highly susceptible to the sheath blight disease compared to reciprocal F₃ families whereas, all the families were resistant to the sheath blight disease (Table 30 and Figure 7).

Table 28: Grouping of F₂ plants and F₃ families based on brown spot disease reaction in rice under natural condition

Scale	<i>Per cent</i> leaf area affected	Number of F ₂ individuals affected				Number of F ₃ families affected			
		Straight cross		Reciprocal cross		Straight cross		Reciprocal cross	
		Number of plants affected	<i>Per cent</i> of disease incidence	Number of plants affected	<i>Per cent</i> of disease incidence	Number of families affected	<i>Per cent</i> of disease incidence	Number of amilies affected	<i>Per cent</i> of disease incidence
0	No incidence	175	33.85	54	10.13	10	5.00	14	7.00
1	Less than 1%	39	7.48	86	15.92	33	16.50	56	28.00
2	1 - 3%	47	9.02	26	4.81	117	58.50	105	52.50
3	4 - 5%	132	25.53	181	33.96	25	12.50	16	8.00
4	6 - 10%	44	8.44	53	9.81	14	7.00	6	3.00
5	11 - 15%	62	11.90	103	19.07	1	0.50	1	0.50
6	16 - 25%	16	3.07	29	5.37	0	0.00	1	0.50
7	26 - 50%	2	0.38	1	0.18	0	0.00	1	0.50
8	51-75%	0	0.00	0	0.00	0	0.00	0	0.00
9	76-100%	0	0.00	0	0.00	0	0.00	0	0.00

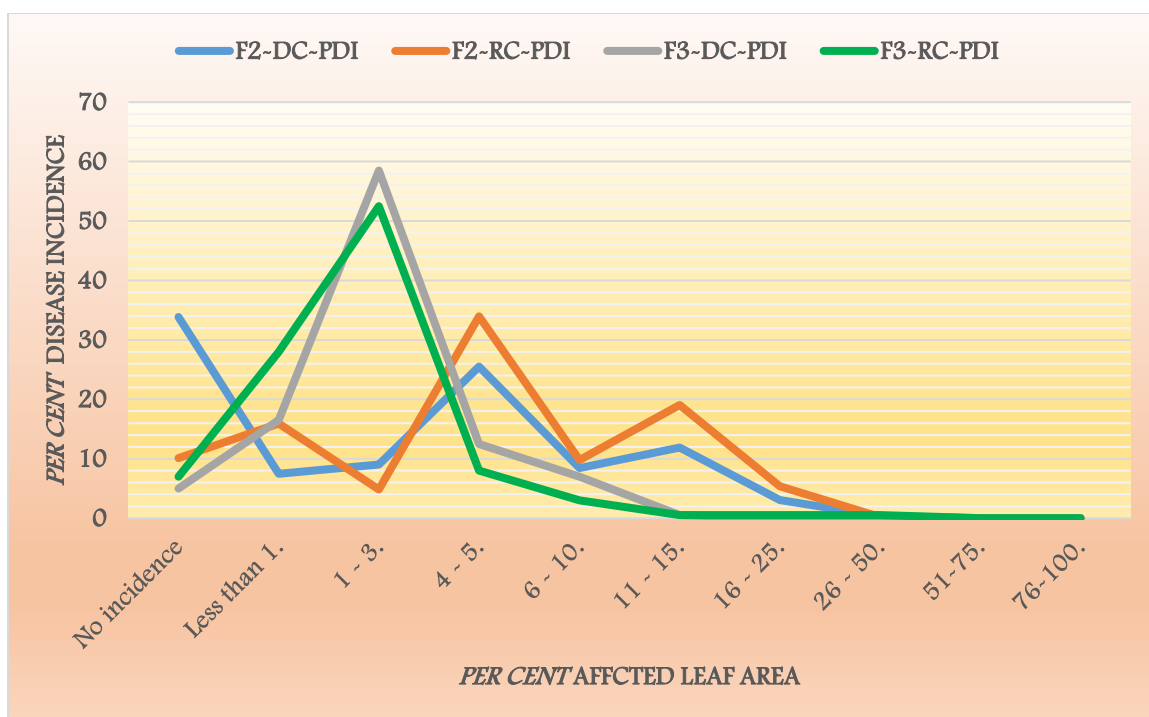


Fig. 5: Graph depicting the *per cent* disease incidence of brown spot of rice in straight and reciprocal F₂ and F₃ populations

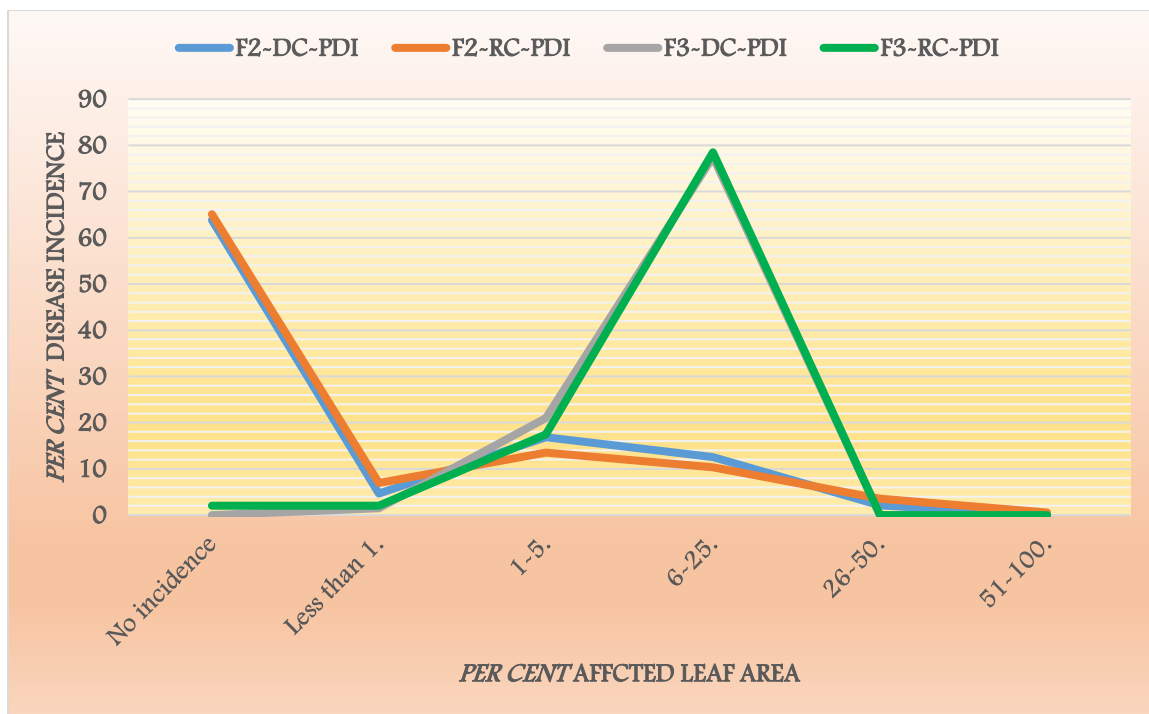


Fig. 6: Graph depicting the *per cent* disease incidence of sheath rot of rice in straight and reciprocal F₂ and F₃ population

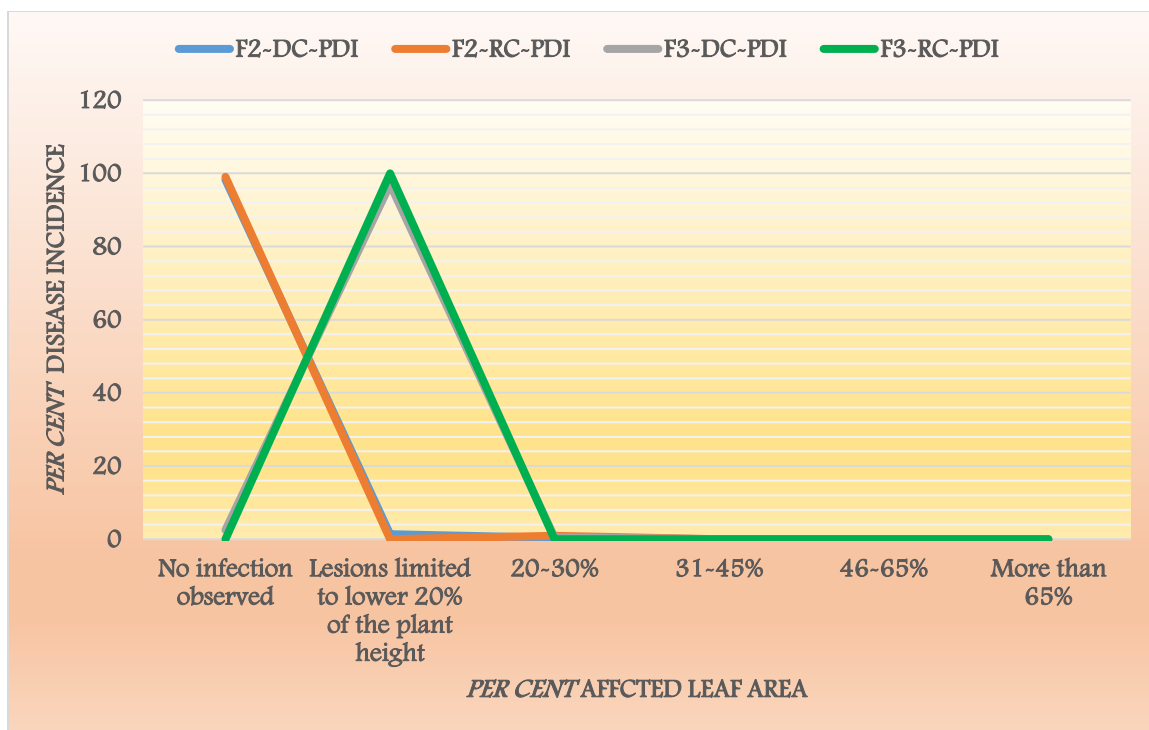


Fig. 7: Graph depicting the *per cent* disease incidence of sheath blight of rice in straight and reciprocal F_2 and F_3 populations.

Table 29: Grouping of F₂ plants and F₃ families based on sheath rot disease reaction in rice under natural condition.

Scale	<i>Per cent</i> leaf area affected	Number of F ₂ individuals affected				Number of F ₃ families affected			
		Straight cross		Reciprocal cross		Straight cross		Reciprocal cross	
		Number of plants affected	<i>Per cent</i> of disease incidence	Number of plants affected	<i>Per cent</i> of disease incidence	Number of families affected	<i>Per cent</i> of disease incidence	Number of families affected	<i>Per cent</i> of disease incidence
0	No incidence	330	63.83	347	65.10	0	0.00	4	2.00
1	Less than 1 %	24	4.64	37	6.94	3	1.50	4	2.00
3	1-5%	87	16.83	72	13.51	42	21.00	35	17.50
5	6-25%	65	12.57	55	10.32	155	77.50	157	78.50
7	26-50%	11	2.13	19	3.56	0	0.00	0	0.00
9	51-100%	0	0.00	3	0.56	0	0.00	0	0.00

Table 30: Grouping of F₂ plants and F₃ families based on sheath blight disease reaction in rice under natural condition

Scale	<i>Per cent</i> leaf area affected	Number of F ₂ individuals affected				Number of F ₃ families affected			
		Straight cross		Reciprocal cross		Straight cross		Reciprocal cross	
		Number of plants affected	<i>Per cent</i> of disease incidence	Number of plants affected	<i>Per cent</i> of disease incidence	Number of plants affected	<i>Per cent</i> of disease incidence	Number of plants affected	<i>Per cent</i> of disease incidence
0	No infection observed	508	98.26	528	99.06	5	2.50	0	0.00
1	Lesions limited to lower 20% of the plant height	7	1.35	0	0.00	194	97.00	200	100.00
3	20-30%	2	0.39	5	0.94	1	0.50	0	0.00
5	31-45%	0	0.00	0	0.00	0	0.00	0	0.00
7	46-65%	0	0.00	0	0.00	0	0.00	0	0.00
9	More than 65%	0	0.00	0	0.00	0	0.00	0	0.00

4.9 Identification of superior RIL's (top ranked F₃ families) for quantitative, grain nutrient traits and disease response in straight and reciprocal F₂ and F₃ populations

Response of F₃ families for quantitative traits grain nutrients and disease response under natural condition was done by multitrait selection index. Where individual trait was ranked separately followed by sums of ranks of all the traits and finally arranged by ascending order of rank for all the traits along with parents was presented in table 31 for straight cross and table 32 for reciprocal cross. Identity numbers 1 in F₃ families secured top rank for all growth, yield attributing and grain nutrient traits and disease responses followed by identify 2 and 6 in F₃ families.

Many of the top ranked F₃ families performed lesser than the parental (BPT-5204 & HPR-14) since these ranks based on overall performance of all the traits. Further, these top superior F₃ families will be used for developing breeding lines for improvement of the traits.

Best F₃ families derived from straight cross for grain yield, protein, iron and zinc content was presented in table 33 and for reciprocal cross in table 34. The F₃ family number, 295 was superior in grain yield per plant followed by 182, 324, 171 and 118 F₃ families and also performed better than the parents (BPT-5204 and HPR-14) in straight cross. Best F₃ family 376 was superior in protein content followed by 137, 410, 268 and 47 F₃ families in straight cross. In reciprocal cross, best F₃ family 255 was superior in grain yield per plant followed by 248, 60, 122 and 208 F₃ families. For protein content, F₃ family 123 was higher followed by 542, 156, 225 and 311 F₃ families. These best F₃ families can be utilized for improvement of respective traits.

4.10 Validation of organelle specific SSRs on parents BPT-5204 and HPR-14 for cytoplasmic effect

Molecular markers are often used to select suitable genotype in plant breeding. Twenty mitochondrial specific markers (Khera *et al.*, 2012) and twenty-one chloroplast specific markers (Provan *et al.*, 1996) were already mapped.

Table 31: Quantitative traits, grain nutrient and disease response of top ranking F₃ families derived from straight cross of rice

Sl. No.	F ₃ families	Growth and yield attributing traits							Grain nutrient traits				Disease Response		
		DF	PH	NPT	DM	PL	PE	GY	P (%)	Fe (ppm)	Zn (ppm)	PA (mg/100g)	BS	SR	SB
1	1	84.00	97.20	22.80	114.40	21.94	-1.56	19.54	12.28	12.22	29.62	882.95	R	HR	R
2	2	85.80	91.60	18.40	116.60	21.00	1.64	21.12	10.18	10.45	28.89	653.23	R	R	HR
3	6	92.80	77.20	17.60	120.20	25.10	1.18	19.82	10.85	12.09	28.16	640.12	MR	MR	MR
4	18	84.80	85.00	17.00	114.80	19.80	-0.30	23.63	10.38	11.99	29.62	714.26	R	MR	MR
5	21	86.40	91.10	21.60	117.20	21.80	0.72	29.17	10.40	13.18	29.71	627.86	HR	R	R
6	35	91.40	79.60	19.40	122.20	19.52	-4.88	23.10	10.92	11.75	30.93	764.16	HR	MS	MR
7	43	85.00	57.83	24.33	116.33	18.37	-6.53	25.88	9.47	12.04	31.23	713.07	R	MR	R
8	46	74.60	100.00	17.20	119.40	19.90	1.14	21.31	10.38	11.51	30.75	632.04	R	R	MR
9	47	85.40	66.20	14.40	96.20	19.26	-2.00	10.81	12.98	9.99	30.50	651.36	MR	HR	MR
10	50	87.60	97.40	14.40	118.40	21.36	0.44	25.94	9.01	12.42	29.33	683.66	R	HR	R
11	55	85.40	95.80	17.60	116.00	20.06	1.22	28.57	8.82	12.06	29.90	907.89	MR	HR	HR
12	65	86.20	102.60	17.00	116.80	22.20	1.90	23.26	8.49	11.47	29.49	734.13	MR	R	HR
13	66	84.20	80.20	10.80	115.00	21.02	1.80	19.10	8.11	11.30	29.88	671.52	R	R	R
14	74	86.80	98.70	13.00	117.40	21.72	1.30	13.73	12.31	10.83	29.64	680.65	MS	R	MR
15	81	88.60	105.00	16.20	119.80	21.96	1.98	27.11	7.62	11.93	29.46	568.33	HR	MR	R
16	84	84.40	75.60	18.40	115.40	19.10	-7.00	16.89	11.42	11.45	29.47	704.79	MR	MS	R
17	128	85.80	94.90	16.60	117.00	20.62	-0.08	14.47	10.99	12.09	29.76	695.20	MR	R	MR
18	178	98.80	77.00	16.40	129.40	19.70	-4.40	18.44	12.26	12.21	30.15	502.40	HR	MS	R
19	206	89.40	100.60	13.00	119.80	20.40	1.94	18.43	5.91	13.32	29.81	499.81	R	HR	MR
20	293	93.00	97.10	17.80	124.00	20.30	2.24	27.69	10.22	12.44	28.74	682.57	R	R	R
Parents	BPT-5204	104.06	97.50	12.06	133.44	19.97	1.88	23.30	8.12	11.66	28.14	848.06	S	S	S
	HPR-14	101.94	107.41	7.88	131.71	22.32	5.19	17.50	12.35	12.68	30.23	636.59	HR	HR	R

DF: 50 % flowering

PH: Plant height (cm)

NPT: Number of productive till

DM: Days to maturity

PL: Panicle length

PE: Panicle exertion (cm)

GY: Grain yield per plant (g)

P: Protein (%)

Fe:Iron (ppm)

Zn:Zinc (ppm)

PA: Phytic acid (mg/100g)

BS: Brown spot

SR: Sheath rot

SB: Sheath blight

Table 32: Quantitative traits, grain nutrient and disease response of top ranking F₃ families derived from reciprocal cross of rice

Sl. No.	F ₃ families	Growth and yield related parameters							Grain nutrient traits				Disease Response		
		DF	PH	NPT	DM	PL	PE	GY	P (%)	Fe (ppm)	Zn (ppm)	PA (mg/100g)	BS	SR	SB
1	10	91.00	109.00	19.20	122.80	21.20	5.06	22.21	9.38	11.16	29.91	745.44	HR	R	R
2	87	86.33	98.00	11.33	117.67	21.67	0.57	24.77	10.94	11.44	29.47	736.63	HR	R	HR
3	96	89.00	97.75	11.75	119.75	20.38	3.03	20.03	9.16	11.54	30.86	703.64	HR	R	MR
4	98	92.00	83.40	14.80	122.80	18.46	-3.58	21.04	10.11	11.29	30.62	645.10	R	R	MR
5	100	89.60	91.00	14.40	120.20	19.04	2.38	21.18	9.55	9.58	30.74	498.07	R	R	R
6	155	101.00	114.40	17.00	132.00	21.16	7.96	23.44	10.90	9.72	31.83	556.38	HR	R	R
7	160	90.00	83.75	17.50	122.50	20.55	-6.48	24.25	10.36	10.46	34.27	728.29	HR	MR	R
8	162	90.00	103.00	13.00	122.00	22.33	2.70	21.38	7.36	10.94	33.30	623.04	R	R	MR
9	185	89.00	104.00	8.50	93.25	20.90	3.00	12.10	10.48	10.69	32.17	603.12	MR	MR	MR
10	225	93.00	73.20	15.80	124.00	18.74	-6.84	18.39	12.05	11.72	31.27	671.62	R	MR	MR
11	248	90.20	108.60	15.60	121.80	20.68	-0.58	32.52	10.19	11.90	30.69	627.57	R	HR	HR
12	259	94.20	97.60	16.00	125.00	21.70	4.14	23.55	9.31	11.04	29.63	627.57	R	R	HR
13	287	89.40	91.20	12.80	121.00	21.36	4.32	15.51	11.24	11.12	30.09	592.39	R	R	MR
14	291	90.80	96.80	16.20	122.40	20.95	1.40	29.17	9.35	10.91	32.10	645.66	R	R	MR
15	306	93.00	99.60	15.60	124.40	20.30	3.10	21.75	8.81	12.00	30.18	637.30	HR	R	R
16	309	96.20	80.00	13.00	127.60	20.66	-4.76	16.33	11.92	11.77	30.56	660.94	MR	MR	R
17	311	91.40	110.40	15.20	123.80	21.04	3.80	25.47	12.01	11.10	31.06	813.95	MR	R	R
18	320	90.60	99.00	21.40	123.00	21.90	2.28	31.68	10.59	11.19	29.85	638.02	HR	HR	R
19	322	94.40	76.40	18.60	126.00	19.36	-3.80	24.42	10.54	11.34	31.25	629.22	R	R	R
20	335	90.75	75.25	11.50	121.00	20.38	0.60	12.74	9.00	11.03	31.93	637.73	R	R	R
Parents	BPT-5204	104.06	97.50	12.06	133.44	19.97	1.88	23.30	8.12	11.66	28.14	848.06	S	S	S
	HPR-14	101.94	107.41	7.88	131.71	22.32	5.19	17.50	12.35	12.68	30.23	636.59	HR	HR	R

DF: 50 % flowering

PH: Plant height (cm)

NPT: Number of productive tillers

DM: Days to maturity

PL: Panicle length

PE: Panicle exertion (cm)

GY: Grain yield per plant (g)

P: Protein (%)

Fe:Iron (ppm)

Zn:Zinc (ppm)

PA: Phytic acid (mg/100g)

BS: Brown spot

SR: Sheath rot

SB: Sheath blight

Table 33: Best F₃ families derived from straight cross for grain yield, protein, iron and zinc content

Sl. No.	F ₃ family identity	Grain yield per plant (g)	F ₃ family identity	Protein%	F ₃ family identity	Iron (ppm)	F ₃ family identity	Zinc(ppm)
1	295	35.46	376	13.81	318	13.77	306	31.45
2	182	35.05	137	13.27	435	13.60	31	31.37
3	324	34.92	410	13.27	393	13.51	43	31.23
4	171	34.21	268	13.22	421	13.39	379	31.18
5	118	32.86	47	12.98	151	13.37	100	31.05
Parents	BPT 5204	23.30	BPT 5204	8.12	BPT 5204	11.66	BPT 5204	28.14
	HPR-14	17.50	HPR-14	12.35	HPR-14	12.68	HPR-14	30.23

Table 34: Best F₃ families derived from reciprocal cross for grain yield, protein, iron and zinc content

Sl. No.	F ₃ family identity	Grain yield per plant (g)	F ₃ family identity	Protein%	F ₃ family identity	Iron (ppm)	F ₃ family identity	Zinc(ppm)
1	255	37.66	123	14.94	118	14.16	160	34.27
2	248	32.52	542	13.15	109	14.13	162	33.30
3	60	32.32	156	12.17	149	13.07	374	32.69
4	122	32.17	225	12.05	16	13.06	129	32.57
5	208	32.01	311	12.01	130	13.01	383	32.55
Parents	BPT 5204	23.30	BPT 5204	8.12	BPT 5204	11.66	BPT 5204	28.14
	HPR-14	17.50	HPR-14	12.35	HPR-14	12.68	HPR-14	30.23

These universal mtDNA primers were designed based on consensus mtDNA (Petit *et al.*, 1998; We *et al.*, 1998) derived from various mitochondrial genes. These two sets of markers were screened on BPT 5204 & HPR 14 rice varieties. The parental polymorphism on MultiNa was carried out using 20 mitochondrial & 21 chloroplast specific markers. Out of 41 markers, 6 mitochondrial & 12 chloroplast specific markers showed polymorphism on MultiNa (Plate 9 and 10). Majority of the primers analysed were monomorphic in nature. This might be attributed to the conservative nature of mitochondrial DNA (Fuji *et al.*, 2010 & Khera *et al.*, 2012) across the species and varieties. These polymorphism markers could be utilised further to see the effect of cytoplasm in the progenies of both the crosses.

Six primers of mitochondrial (*Nad1*, *Cob*, *cox1B*, *cox2*, *cox3*, *Nad5A* & *Nad5D*) and ten primers of Chloroplast (*Oscp43899*, *Oscp124451*, *Oscp134510*, *Ctrn1*, *Ctrn2*, *Ctrn3*, *Ctrn5*, *Ctrn6*, *Ctrn7* & *Ctrn9*) exhibited conspicuous polymorphism (Plate 11 and 12). The complete cp and mt genome demonstrate the gene content, order, and organization are highly conserved and their inheritance is always maternal, which is different from nuclear genomes. Recombination of mt genomes is prevalent in rice and results in complex genome rearrangements and much larger than the cp genome (Zhang *et al.*, 2012).

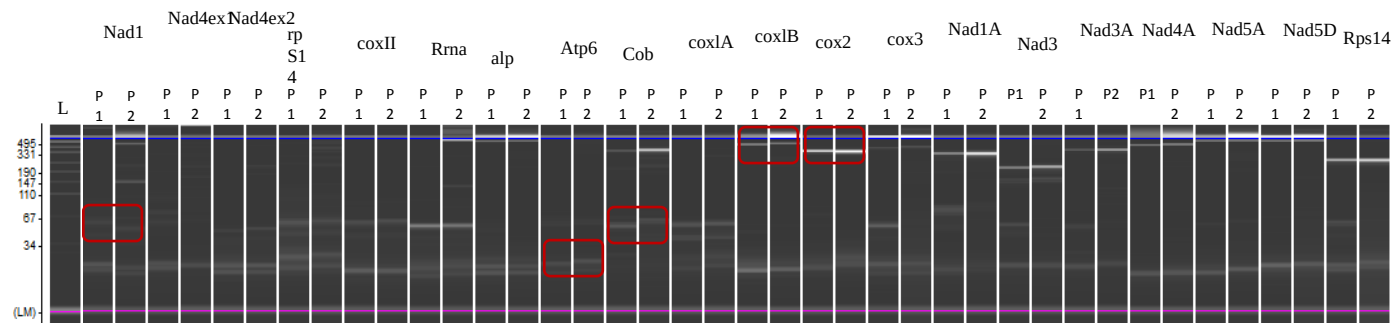


Plate 9: Mitochondrial specific SSR markers showing polymorphism between BPT 5204 & HPR-14

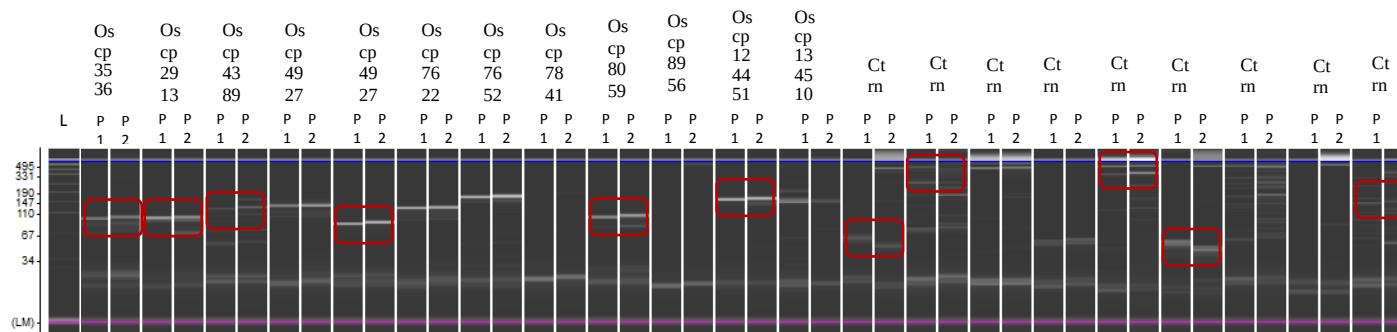


Plate 10: Chloroplast specific SSR markers showing polymorphism between BPT 5204 & HPR-14

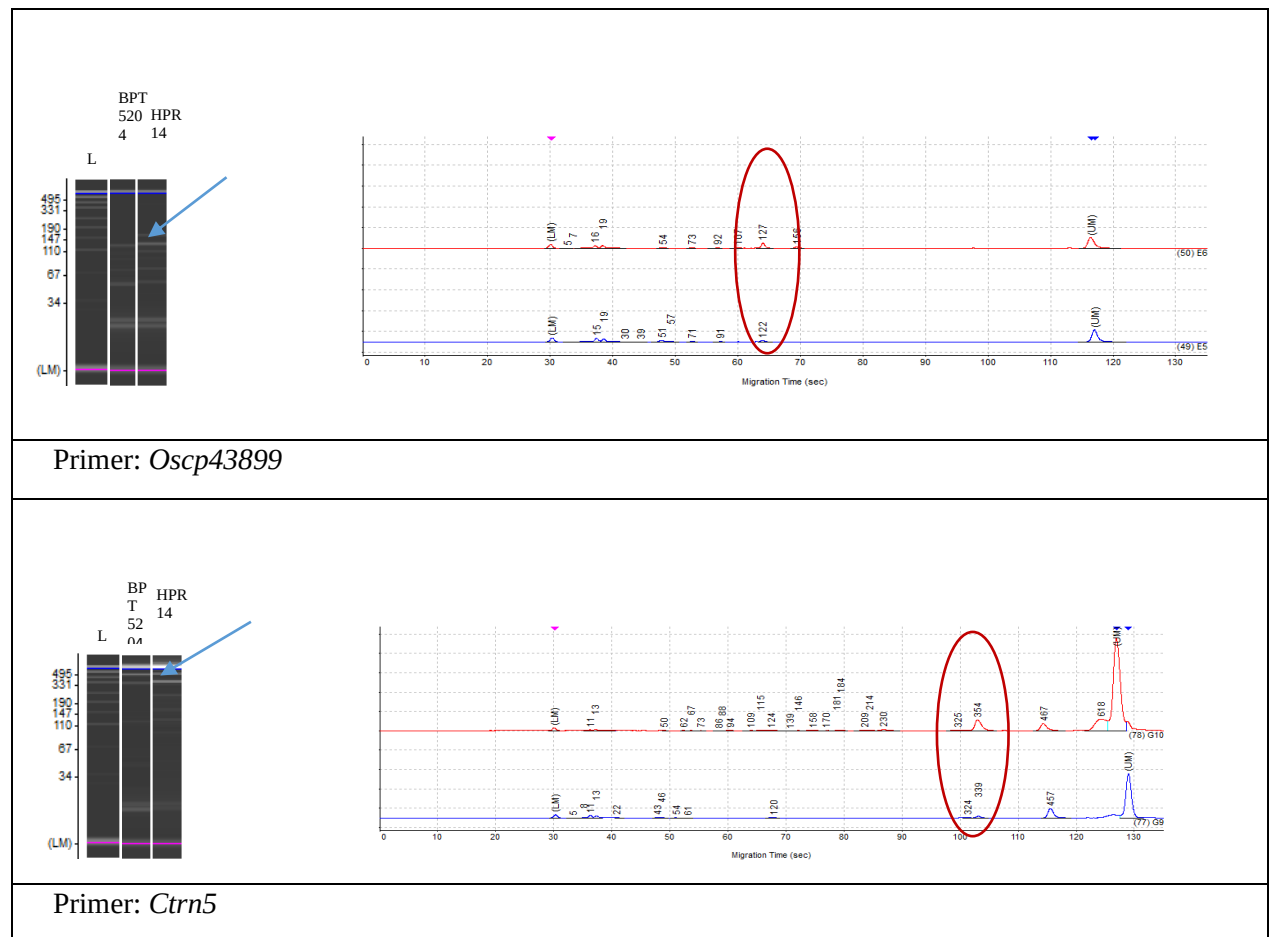


Plate 12: Chloroplast SSR markers (*Oscp43899* & *Ctrn5*) showing polymorphism between parents BPT 5204 and HPR 14

V SUMMARY

Rice crop provides a vast genetic variability for the present day improvement programme. Though domesticated, un-adapted landraces possess several undesirable agronomic traits that leads to low yield. Diverse plant types are immediately valuable for shaping new varieties and this forms the basic wealth on which plant breeders can operate for reconstructing the existing genotypes. To increase the present levels of production in terms of grain yield, quality and other traits there is ample need to identify and utilize genetically divergent parents for inter and intra sub specific and reciprocal crosses in rice. Among the many factors for rice production, cytoplasmic gene effect or maternal gene effect is one the most important factors. Reciprocal crosses play an important role in the selection of any breeding programme for population improvement and development of new hybrids in the crop. Hence, the identification of maternal effect in reciprocal crosses also helps to identify some traits which are controlled by cytoplasmic genes and useful for development of new high yielding cultivars.

Considering above criteria, present investigation entitled as “Genetic evaluation for cytoplasmic inheritance of morphometric traits and grain quality parameters in reciprocal crosses of rice (*Oryzasativa* L.)” was carried out at field and laboratory facilities of Department of Genetics and plant breeding, University of Agricultural Sciences, Bangalore during 2015 and 2016. The experimental material consisted of a straight (BPT 5204 $\times$ HPR 14) and reciprocal (HPR 14 $\times$ BPT 5204) F₂ population of BPT-5204 and HP-14. The Augmented design was adopted for evaluation of the segregating plants of F₂ and F₃ of straight and reciprocal crosses along with parents for growth and yield attributing traits, disease resistance and grain nutrient traits. Observations were recorded on various parameters and experimental results were summarized hereunder as follows.

Highly significant differences were observed for mean performances of most of the traits like days to 50 *per cent* flowering, number of tillers, number of productive tillers, biomass per plant, chaffy grains per plants, grain iron and carbohydrate content in

straight and reciprocal F_2 and F_3 populations revealed reciprocal differences or undesirable effect of cytoplasm.

Observed probability of transgressive segregants for yield and its components traits were higher in straight F_2 and F_3 populations compared to reciprocal crosses. For grain nutrient traits, observed probabilities of transgressive segregants for all the traits were higher except protein in both reciprocal crosses of F_2 and F_3 populations. Both straight and reciprocal crosses the populations surpassed the parental limits which favours identification of plants with desirable traits and are of great contributions to increase yield potential by bringing beneficial alleles in to single genotype through rigorous selection.

Estimates of GCV and PCV for most of the yield attributing traits and grain nutrient traits were higher in straight F_2 population and reciprocal F_3 population. Very narrow differences were observed between estimates of GCV and PCV in both straight and reciprocal F_2 and F_3 populations that indicated minimal role of environment. High PCV, GCV coupled with high heritability and GAM observed for number of tillers, number of productive tillers, biomass and harvest index. High heritability and GA *per cent* mean was observed for plant height, amylose and phytic acid content in straight and reciprocal F_2 and F_3 populations. These indicated the major genes with additive gene action governing these traits, which offers scope for further improvement through selection.

Positively skewed distribution was observed for days to 50 *per cent* flowering, number of tillers, number of productive tillers, days to maturity, grain yield per plant, biomass per plant and grain breadth in straight and reciprocal crosses of F_2 and F_3 population revealed that traits governed by complementary gene action and slow gain was expected with mild selection. Negatively skewed distribution was observed for plant height, panicle exertion, seed fertility percentage, panicle length, harvest index and zinc in both straight and reciprocal F_2 and F_3 populations suggested that traits governed by additive gene action and rapid gain was expected with mild selection.

Grain yield per plant exhibited significant positive correlations with plant height, number of productive tillers, panicle length and grain zinc content in both straight and reciprocal F_2 and F_3 populations. Phytic acid had significantly positive and negative correlation in reciprocal F_2 and F_3 populations with iron and zinc, respectively. Highest positive direct effect on grain yield was observed in number of productive tillers and zinc in straight F_3 population. Panicle exertion and carbohydrates had highest positive direct effect on reciprocal F_2 and F_3 population. Thus, choosing these traits for grain yield will be best for selection process.

Genetic basis study of anthocyanin pigmentation of three qualitative characters viz., basal leaf sheath colour, leaf blade colour and spikelets tip pigmentation revealed that, the straight and reciprocal F_2 plants segregating in ratio of 3 present: 1 absent of tip pigmentation on spikelets and ratio of 3 purple:1 green basal leaf sheath colour was found which indicated monogenic inheritance of those traits. Genetic analysis of straight and reciprocal F_2 population segregating in 3 purple: 13 green leaf blade, which suggested inhibitory gene control with single major gene for green leaf. Therefore, purple pigmentation of basal leaf sheath and leaf blade shall be considered as morphological markers for some traits.

Significant difference for most of the yield and yield attributing traits were observed for leaf blade colour, spikelet's pigmentation, flag leaf, stem internode colour and basal leaf sheath colour in straight and reciprocal F_2 population. This could be attributed to undesirable or modifier effect of cytoplasm.

Positive and significantly high parents offspring correlation for most of the yield attributing traits in straight and grain nutrient traits in reciprocal F_2 and F_3 populations revealed that performance of the plant in F_2 generation is reliable indicator of the performance of their progeny in subsequent generations. The regression co-efficient for most of the traits between F_2 and F_3 populations were higher in straight than reciprocal crosses indicates that selection for such traits can be made in the early segregating generations.

Screening of straight and reciprocal F_2 and F_3 populations for brown spot, sheath blight and sheath rot diseases were done along with parents BPT-5204 and HPR-14. The results revealed that, most of the F_2 individuals and F_3 families were less infestation of all the diseases could be utilized for disease resistance breeding programme.

Fifteen mitochondrial and chloroplast specific SSRs showed polymorphism between parents BPT-5204 and HPR-14. Majority of organelle specific SSRs analysed were monomorphic in nature which might be attributed to the conservative nature of mitochondrial and chloroplast DNA across the species and varieties.

Future line of work

F_3 families 1, 2, 6, 18 and 21 in straight cross and F_3 families 10, 87, 96, 98 & 100 in reciprocal crosses were found top ranked for growth, yield attributing, grain nutrients traits and resistant to diseases. Therefore, those families could be used for overall improvement of traits.

In the present study, identified best F_3 families for grain yield, protein, iron and zinc content separately in both straight and reciprocal crosses. Those could be used further for crop improvement programme and/or improvement of specific traits.

Validated polymorphic mitochondrial and chloroplast specific SSRs might be utilised in progenies of straight and reciprocal crosses to check the influence cytoplasmic effect.

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APPENDIX 1: Estimates of phenotypic correlation coefficient of straight and reciprocal derived F₂ crosses of rice

Traits		NT	DM	FLL	TGPP	FGPP	CGPP	SFP	GWPP	BM	HI	GL	GB	LBR
NT	SC	1												
	RC	1												
DM	SC	-0.005	1											
	RC	0.026	1											
FLL	SC	0.105*	-0.084	1										
	RC	0.090*	-0.114**	1										
TGPP	SC	0.342***	0.045	0.410***	1									
	RC	0.410***	0.124**	0.315***	1									
FGPP	SC	0.365***	-0.127**	0.477***	0.877***	1								
	RC	0.419***	-0.131**	0.375***	0.826***	1								
CGPP	SC	-0.045	0.346***	-0.132**	0.253***	-0.243***	1							
	RC	0.020	0.430***	-0.065	0.386***	-0.202***	1							
SFP	SC	0.194***	-0.370***	0.307***	0.160***	0.592***	-0.867***	1						
	RC	0.146***	-0.409***	0.211***	0.007	0.544***	-0.878***	1						
GWPP	SC	0.362***	-0.290***	0.483***	0.769***	0.869***	-0.198***	0.52***	1					
	RC	0.386***	-0.263***	0.397***	0.699***	0.863***	-0.196***	0.490***	1					
BM	SC	0.818***	0.026	0.212***	0.410***	0.470***	-0.119**	0.265***	0.467***	1				
	RC	0.861***	-0.014	0.232***	0.462***	0.552***	-0.100*	0.275***	0.527***	1				
HI	SC	0.330***	-0.105*	0.171***	0.394***	0.407***	-0.024	0.214***	0.459***	0.279***	1			
	RC	0.382***	-0.068	0.086*	0.431***	0.453***	0.008	0.192***	0.446***	0.317***	1			
GL	SC	0.021	-0.231***	0.039	-0.109*	-0.030	-0.159***	0.131**	0.037	-0.053	-0.022	1		
	RC	0.071	-0.173***	0.072	-0.079	0.012	-0.157***	0.158***	0.072	0.073	0.020	1		
GB	SC	-0.026	-0.139**	0.085	-0.049	0.009	-0.118**	0.101	0.132**	-0.014	0.079	0.188***	1	
	RC	-0.021	-0.135**	-0.019	-0.064	-0.056	-0.019	-0.001	0.082	-0.024	-0.052	0.135**	1	
LBR	SC	0.051	0.007	-0.057	-0.022	-0.028	0.012	-0.015	-0.092*	-0.014	-0.073	0.406***	-0.794***	1
	RC	0.054	0.029	0.054	0.017	0.059	-0.068	0.088*	-0.031	0.057	0.046	0.419***	-0.836***	1
GYPP	SC	0.754***	-0.026	0.224***	0.463***	0.517***	-0.106*	0.278***	0.542***	0.862***	0.677***	-0.049	0.03	-0.042
	RC	0.799***	-0.043	0.169***	0.523***	0.596***	-0.066	0.267***	0.562***	0.872***	0.699***	0.049	-0.049	0.066

* Significant at 5 per cent

** Significant at 1 per cent

*** Significant at 0.1 per cent

NT: Number of tillers

DM= Days to maturity

FLL= Flag leaf length (cm)

TGPP= Total grains per panicle

FGPP= Fertile grains per panicle

CGPP: Chaffy grains per panicle

SFP: Seed fertility percentage

GWPP= Grain weight per panicle (g)

GYPP= Grain yield per plant (g)

BM= Biomass (g)

HI: harvest index (%)

GL= Grain length (cm)

GB= Grain breadth (cm)

LBR: L/B ratio of paddy grain

APPENDIX 2: Estimates of phenotypic correlation coefficient of straight and reciprocal derived F₃ crosses of rice

		NT	DM	FLL	TGPP	FGPP	CGPP	SFP	GWPP	BM	HI	GL	GB	LBR
NT	SC	1												
	RC	1												
DM	SC	-0.008	1											
	RC	0.019	1											
FLL	SC	0.094	-0.042	1										
	RC	-0.049	-0.115	1										
TGPP	SC	0.455***	0.078	0.332***	1									
	RC	0.185**	0.174*	0.316***	1									
FGPP	SC	0.486***	-0.010	0.391***	0.942***	1								
	RC	0.191**	0.023	0.391***	0.899***	1								
CGPP	SC	-0.004	0.260***	-0.101	0.347***	0.011	1							
	RC	0.035	0.35***	-0.074	0.466***	0.034	1							
SFP	SC	0.298***	-0.242***	0.325***	0.224**	0.531***	-0.806***	1						
	RC	0.031	-0.339***	0.218**	-0.084	0.353***	-0.003***	1						
GWPP	SC	0.337***	-0.079	0.425***	0.749***	0.806***	-0.078	0.416***	1					
	RC	0.147*	-0.195**	0.461***	0.668***	0.815***	-0.113	0.410***	1					
BM	SC	0.754***	0.108	0.223**	0.521***	0.576***	-0.056	0.366***	0.509***	1				
	RC	0.703***	0.020	0.169*	0.306***	0.382***	-0.068	0.198**	0.366***	1				
HI	SC	0.296***	0.013	0.083	0.335***	0.351***	0.016	0.159*	0.268***	0.091	1			
	RC	0.088	-0.116	0.038	0.208**	0.243***	-0.020	0.113	0.349***	0.024	1			
GL	SC	0.040	-0.276***	0.128	-0.053	0.005	-0.173*	0.182**	0.050	0.017	-0.058	1		
	RC	-0.078	-0.159*	-0.084	-0.165*	-0.098	-0.175*	0.149*	0.023	-0.067	0.062	1		
GB	SC	-0.067	-0.155*	0.064	-0.055	-0.001	-0.160*	0.102	0.142*	0.030	-0.016	0.154*	1	
	RC	-0.091	-0.129	-0.041	-0.006	0.033	-0.083	0.116	0.102	-0.117	0.023	0.145*	1	
LBR	SC	0.099	-0.011	0.009	0.022	0.005	0.051	0.008	-0.094	-0.003	-0.025	0.419***	0.825***	1
	RC	0.012	-0.005	-0.023	-0.110	-0.097	-0.052	0.006	-0.069	0.040	0.013	0.585***	-0.701	1
GYPP	SC	0.761***	0.100	0.234**	0.589***	0.643***	-0.041	0.378***	0.559***	0.864***	0.553***	-0.024	0.025	-0.024
	RC	0.650***	-0.042	0.151*	0.368***	0.451***	-0.068	0.225**	0.487***	0.866***	0.505***	-0.036	-0.085	0.028

* Significant at 5 per cent

** Significant at 1 per cent

*** Significant at 0.1 per cent

NT: Number of tillers

DM= Days to maturity

FLL= Flag leaf length (cm)

TGPP= Total grains per panicle

FGPP= Fertile grains per panicle

CGPP: Chaffy grains per panicle

SFP: Seed fertility percentage

GWPP= Grain weight per panicle (g)

GYPP= Grain yield per plant (g)

BM= Biomass (g)

HI: harvest index (%)

GL= Grain length (cm)

GB= Grain breadth (cm)

LBR: L/B ratio of paddy grain

APPENDIX 3: Genotypic direct (diagonal) and indirect effects of growth and yield attributing traits in straight cross of F₂ generation of rice

Traits	DF	PH	NT	NPT	DM	PL	PE	FLL	TGPP	FGPP	CGPP	SFP	GWPP	TW	BM	HI	GL	GB	LBR
DF	0.0604	0.0009	-0.0002	-0.0015	0.0601	-0.0109	-0.0007	-0.0054	0.0025	-0.0078	0.0208	-0.0224	-0.0175	-0.0238	0.0018	-0.0065	-0.0140	-0.0087	0.0010
PH	0.0000	-0.0014	-0.0002	-0.0002	0.0000	-0.0008	-0.0009	-0.0007	-0.0006	-0.0007	0.0002	-0.0005	-0.0006	0.0000	-0.0006	0.0000	0.0000	0.0000	0.0000
NT	-0.0001	0.0060	0.0418	0.0410	-0.0002	0.0116	-0.0015	0.0044	0.0143	0.0153	-0.0019	0.0081	0.0151	0.0015	0.0342	0.0138	0.0009	-0.0011	0.0021
NPT	0.0005	-0.0028	-0.0208	-0.0212	0.0006	-0.0056	0.0010	-0.0022	-0.0069	-0.0074	0.0010	-0.0040	-0.0072	-0.0005	-0.0170	-0.0074	-0.0004	0.0008	-0.0012
DM	-0.0649	-0.0012	0.0003	0.0018	-0.0652	0.0114	0.0003	0.0055	-0.0029	0.0083	-0.0225	0.0241	0.0189	0.0257	-0.0017	0.0068	0.0150	0.0091	-0.0005
PL	0.0025	-0.0080	-0.0039	-0.0037	0.0024	-0.0139	-0.0037	-0.0093	-0.0084	-0.0091	0.0014	-0.0053	-0.0093	-0.0024	-0.0052	-0.0037	-0.0012	-0.0004	-0.0003
PE	-0.0003	0.0169	-0.0009	-0.0012	-0.0001	0.0071	0.0266	0.0093	0.0030	0.0080	-0.0102	0.0112	0.0060	-0.0004	0.0049	-0.0019	-0.0007	-0.0005	-0.0007
FLL	0.0000	0.0001	0.0000	0.0000	0.0000	0.0001	0.0000	0.0001	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
TGPP	0.0108	0.1124	0.0896	0.0855	0.0117	0.1593	0.0292	0.1075	0.2620	0.2297	0.0664	0.0420	0.2014	-0.0115	0.1074	0.1033	-0.0287	-0.0129	-0.0058
FGPP	0.0303	-0.1184	-0.0853	-0.0816	0.0297	-0.1539	-0.0705	-0.1112	-0.2046	-0.2333	0.0567	-0.1380	-0.2028	-0.0172	-0.1097	-0.0950	0.0071	-0.0022	0.0066
CGPP	-0.0935	0.0419	0.0122	0.0123	-0.0938	0.0271	0.1041	0.0356	-0.0688	0.0659	-0.2715	0.2354	0.0537	0.0641	0.0323	0.0065	0.0433	0.0321	-0.0033
SFP	0.0657	-0.0599	-0.0344	-0.0338	0.0655	-0.0679	-0.0745	-0.0543	-0.0284	-0.1048	0.1537	-0.1772	-0.0934	-0.0421	-0.0470	-0.0379	-0.0233	-0.0180	0.0026
GWPP	-0.0055	0.0087	0.0068	0.0064	-0.0055	0.0126	0.0042	0.0091	0.0145	0.0164	-0.0037	0.0099	0.0188	0.0081	0.0088	0.0087	0.0007	0.0025	-0.0017
TW	0.0009	0.0000	-0.0001	-0.0001	0.0009	-0.0004	0.0000	-0.0003	0.0001	-0.0002	0.0005	-0.0005	-0.0010	-0.0023	-0.0002	-0.0005	-0.0003	-0.0006	0.0003
BM	0.0215	0.2920	0.5863	0.5738	0.0185	0.2702	0.1317	0.1522	0.2939	0.3371	-0.0852	0.1900	0.3347	0.0537	0.7168	0.2002	-0.0377	-0.0074	-0.0098
HI	-0.0525	0.0148	0.1620	0.1718	-0.0513	0.1307	-0.0350	0.0841	0.1933	0.1997	-0.0118	0.1049	0.2254	0.1044	0.1370	0.4904	-0.0108	0.0388	-0.0356
GL	0.0076	0.0010	-0.0007	-0.0006	0.0076	-0.0029	0.0009	-0.0013	0.0036	0.0010	0.0052	-0.0043	-0.0012	-0.0047	0.0017	0.0007	-0.0327	-0.0062	-0.0133
GB	-0.0073	-0.0018	-0.0013	-0.0019	-0.0071	0.0015	-0.0010	0.0043	-0.0025	0.0005	-0.0060	0.0051	0.0067	0.0124	-0.0005	0.0040	0.0096	0.0508	-0.0404
LBR	0.0009	-0.0004	0.0029	0.0034	0.0004	0.0012	-0.0015	-0.0033	-0.0013	-0.0017	0.0007	-0.0008	-0.0053	-0.0072	-0.0008	-0.0042	0.0236	-0.0462	0.0582
GYPP	-0.0230	0.3008	0.7542	0.7502	-0.0258	0.3764	0.1088	0.2240	0.4627	0.5168	-0.1062	0.2776	0.5425	0.1579	0.8622	0.6773	-0.0495	0.0300	-0.0419
r	-0.0014	-0.0004	0.0315	-0.0159	0.0017	-0.0052	0.0029	0.0000	0.1212	-0.1206	0.0288	0.0492	0.0102	0.0004	0.6180	0.3322	0.0016	0.0015	-0.0024

Residual effect= 0.214; R Square= 0.9542

DF=50 % flowering
 PH= Plant height (cm)
 NT= Number of tillers
 NPT= Number of productive tillers
 DM= Days to maturity

PL= Panicle length(cm)
 PE= Panicle exsertion (cm)
 FLL= Flag leaf length (cm)
 TGPP= Total grains per panicle
 FGPP= Fertile grains per panicle

CGPP= Chaffy grains per panicle
 SFP= Seed fertility percentage
 GWPP= Grain weight per panicle (g)
 TW= Test weight (g)
 GYPP= Grain yield per plant (g)

BM= Biomass (g)
 HI= harvest index (%)
 GL= Grain length (cm)
 GB= Grain breadth (cm)
 LBR= L/B ratio of paddy grain

APPENDIX 4: Genotypic direct (diagonal) and indirect effects of growth and yield attributing traits in reciprocal cross F₂ generation of rice under aerobic condition

Traits	DF	PH	NT	NPT	DM	PL	PE	FLL	TGPP	FGPP	CGPP	SFP	GWPP	TW	BM	HI	GL	GB	LBR
DF	-0.0981	0.0010	-0.0019	-0.0014	-0.0973	0.0106	0.0060	0.0116	-0.0123	0.0132	-0.0429	0.0410	0.0259	0.0349	0.0017	0.0062	0.0169	0.0124	-0.0019
PH	0.0005	-0.0427	-0.0083	-0.0081	0.0004	-0.0243	-0.0269	-0.0216	-0.0156	-0.0221	0.0092	-0.0160	-0.0203	-0.0030	-0.0199	-0.0019	-0.0012	0.0025	-0.0029
NT	-0.0002	-0.0020	-0.0105	-0.0102	-0.0003	-0.0026	0.0002	-0.0009	-0.0043	-0.0044	-0.0003	-0.0015	-0.0040	0.0003	-0.0090	-0.0040	-0.0007	0.0002	-0.0006
NPT	-0.0005	-0.0069	-0.0353	-0.0363	-0.0007	-0.0089	0.0008	-0.0029	-0.0150	-0.0154	-0.0009	-0.0054	-0.0141	0.0012	-0.0308	-0.0156	-0.0026	0.0009	-0.0021
DM	0.0760	-0.0007	0.0020	0.0014	0.0767	-0.0082	-0.0043	-0.0088	0.0096	-0.0100	0.0330	-0.0314	-0.0202	-0.0274	-0.0011	-0.0052	-0.0132	-0.0103	0.0022
PL	0.0017	-0.0088	-0.0039	-0.0038	0.0016	-0.0154	-0.0040	-0.0095	-0.0084	-0.0088	-0.0001	-0.0034	-0.0092	-0.0016	-0.0059	-0.0034	-0.0015	0.0003	-0.0011
PE	-0.0013	0.0138	-0.0004	-0.0005	-0.0012	0.0058	0.0219	0.0075	0.0015	0.0061	-0.0074	0.0087	0.0054	0.0015	0.0042	-0.0024	0.0007	0.0003	0.0002
FLL	0.0024	-0.0105	-0.0019	-0.0016	0.0024	-0.0129	-0.0071	-0.0208	-0.0065	-0.0078	0.0014	-0.0044	-0.0083	-0.0018	-0.0048	-0.0018	-0.0015	0.0004	-0.0011
TGPP	-0.0510	-0.1483	-0.1668	-0.1678	-0.0507	-0.2228	-0.0270	-0.1282	-0.4068	-0.3359	-0.1570	-0.0028	-0.2847	0.0553	-0.1881	-0.1753	0.0323	0.0259	-0.0068
FGPP	-0.0636	0.2452	0.1981	0.2003	-0.0618	0.2723	0.1315	0.1772	0.3904	0.4728	-0.0953	0.2573	0.4080	0.0132	0.2611	0.2141	0.0056	-0.0264	0.0280
CGPP	0.0556	-0.0273	0.0034	0.0030	0.0547	0.0012	-0.0432	-0.0083	0.0491	-0.0256	0.1272	-0.1116	-0.0249	-0.0358	-0.0127	0.0010	-0.0200	-0.0024	-0.0086
SFP	0.0622	-0.0558	-0.0218	-0.0220	0.0609	-0.0331	-0.0594	-0.0315	-0.0010	-0.0810	0.1308	-0.1489	-0.0730	-0.0370	-0.0410	-0.0286	-0.0236	0.0000	-0.0132
GWPP	0.0126	-0.0226	-0.0183	-0.0184	0.0125	-0.0284	-0.0118	-0.0189	-0.0333	-0.0410	0.0093	-0.0233	-0.0475	-0.0156	-0.0250	-0.0212	-0.0034	-0.0039	0.0015
TW	0.0014	-0.0003	0.0001	0.0001	0.0014	-0.0004	-0.0003	-0.0004	0.0005	-0.0001	0.0011	-0.0010	-0.0013	-0.0040	0.0000	-0.0003	-0.0005	-0.0008	0.0005
BM	-0.0138	0.3680	0.6793	0.6680	-0.0109	0.3029	0.1522	0.1827	0.3646	0.4354	-0.0789	0.2169	0.4153	0.0096	0.7886	0.2503	0.0576	-0.0186	0.0449
HI	-0.0306	0.0211	0.1859	0.2085	-0.0332	0.1092	-0.0535	0.0417	0.2096	0.2202	0.0039	0.0933	0.2167	0.0392	0.1544	0.4864	0.0098	-0.0204	0.0222
GL	-0.0045	0.0007	0.0019	0.0018	-0.0045	0.0026	0.0008	0.0019	-0.0021	0.0003	-0.0041	0.0042	0.0019	0.0035	0.0019	0.0005	0.0263	0.0035	0.0110
GB	0.0074	0.0035	0.0012	0.0015	0.0080	0.0012	-0.0009	0.0012	0.0038	0.0033	0.0011	0.0000	-0.0049	-0.0119	0.0014	0.0025	-0.0080	-0.0591	0.0494
LBR	-0.0011	-0.0037	-0.0030	-0.0033	-0.0016	-0.0041	-0.0004	-0.0030	-0.0009	-0.0033	0.0038	-0.0049	0.0017	0.0063	-0.0032	-0.0025	-0.0232	0.0463	-0.0554
GYPP	-0.0450	0.3236	0.7999	0.8114	-0.0434	0.3443	0.0745	0.1688	0.5229	0.5958	-0.0664	0.2667	0.5625	0.0267	0.8718	0.6987	0.0498	-0.0492	0.0660
r	0.0044	-0.0138	-0.0084	-0.0295	-0.0033	-0.0053	0.0016	-0.0035	-0.2127	0.2817	0.0084	0.0397	0.0267	0.0001	0.6876	0.3398	0.0013	0.0029	-0.0037

Residual effect= 0.1892; R Square= 0.9642

DF=50 % flowering

PH= Plant height (cm)

NT= Number of tillers

NPT= Number of productive tillers

DM= Days to maturity

PL= Panicle length(cm)

PE= Panicle exsertion (cm)

FLL= Flag leaf length (cm)

TGPP= Total grains per panicle

FGPP= Fertile grains per panicle

CGPP= Chaffy grains per panicle

SFP= Seed fertility percentage

GWPP= Grain weight per panicle (g)

TW= Test weight (g)

GYPP= Grain yield per plant (g)

BM= Biomass (g)

HI= harvest index (%)

GL= Grain length (cm)

GB= Grain breadth (cm)

LBR: L/B ratio of paddy grain

APPENDIX 5: Genotypic direct (diagonal) and indirect effects of growth and yield attributing traits in straight cross F₃ generation of rice under aerobic

Traits	DF	PH	NT	NPT	DM	PL	PE	FLL	TGPP	FGPP	CGPP	SFP	GWPP	TW	BM	HI	GL	GB	LBR
DF	0.0140	0.0019	-0.0001	-0.0002	0.0137	-0.0003	0.0011	-0.0008	0.0011	-0.0002	0.0037	-0.0035	-0.0011	-0.0035	0.0014	0.0000	-0.0039	-0.0022	-0.0001
PH	-0.0001	-0.0005	-0.0001	-0.0001	-0.0001	-0.0002	-0.0004	-0.0003	-0.0002	-0.0002	0.0001	-0.0002	-0.0002	0.0000	-0.0002	0.0000	0.0000	0.0000	0.0000
NT	0.0008	-0.0094	-0.0796	-0.086	0.0006	-0.0111	-0.0021	-0.0074	-0.0362	-0.0387	0.0003	-0.0237	-0.0268	-0.0033	-0.0600	-0.0236	-0.0032	0.0054	-0.0079
NPT	0.0014	0.0112	0.0959	0.0971	-0.0013	0.0129	0.0030	0.0096	0.0430	0.0467	0.0026	0.0308	0.0313	0.0022	0.0728	0.0300	0.0049	-0.0069	0.0105
DM	-0.0041	-0.0007	0.0000	0.0001	-0.0042	0.0001	-0.0004	0.0002	-0.0003	0.0000	-0.0011	0.0010	0.0003	0.0010	-0.0005	-0.0001	0.0012	-0.0007	0.0000
PL	0.0002	-0.0031	-0.0013	-0.0012	0.0002	-0.0093	-0.0016	-0.0033	-0.0034	-0.0036	0.0000	-0.0021	-0.0030	-0.0005	-0.0018	-0.0012	-0.0001	0.0005	-0.0005
PE	0.0010	0.0096	0.0003	0.0004	0.0011	0.0020	0.0120	0.0057	0.0028	0.0043	-0.0035	0.0055	0.0036	-0.0004	0.0035	-0.0007	0.0000	0.0001	-0.0003
FLL	-0.0005	0.0048	0.0008	0.0009	-0.0004	0.0031	0.0042	0.0088	0.0029	0.0034	-0.0009	0.0029	0.0037	0.0018	0.0020	0.0007	0.0011	0.0006	0.0001
TGPP	0.0126	-0.0691	-0.0760	-0.0740	-0.0130	-0.0611	-0.0397	-0.0556	-0.1672	-0.1575	0.0580	-0.0380	-0.1254	0.0022	-0.0872	-0.0560	0.0089	0.0092	-0.0037
FGPP	0.0026	0.0810	0.0811	0.0803	-0.0017	0.0649	0.0595	0.0652	0.1572	0.1669	0.0019	0.0887	0.1345	0.0057	0.0961	0.0586	0.0009	-0.0002	0.0009
CGPP	0.0101	-0.0047	-0.0001	-0.0010	0.0098	0.0000	-0.0109	-0.0038	0.0131	0.0004	0.0377	-0.0304	-0.0007	-0.0051	-0.0021	0.0006	-0.0065	-0.0060	0.0019
SFP	0.0064	-0.0096	-0.0075	-0.0080	0.0061	-0.0056	-0.0115	-0.0082	-0.0057	-0.0134	0.0203	-0.0253	-0.0105	-0.0038	-0.0092	-0.0040	-0.0046	-0.0026	-0.0002
GWPP	0.0010	0.0051	0.0042	0.0040	-0.0010	0.0040	0.0037	0.0052	0.0093	0.0100	-0.0002	0.0052	0.0124	0.0040	0.0063	0.0033	0.0006	0.0018	-0.0012
TW	0.0058	-0.0005	0.0009	0.0005	-0.0057	0.0013	-0.0009	0.0047	-0.0003	0.0008	-0.0031	0.0035	0.0075	0.0232	0.0017	0.0034	0.0033	0.0066	-0.0039
BM	0.0786	0.3224	0.6001	0.5964	0.0856	0.1577	0.2337	0.1775	0.4147	0.4581	-0.0447	0.2913	0.4054	0.0589	0.7956	0.0720	0.0135	0.0241	-0.0022
HI	0.0001	-0.0050	0.1394	0.1451	0.0063	0.0605	-0.0260	0.0392	0.1576	0.1653	0.0074	0.0751	0.1263	0.0697	0.0426	0.4707	-0.0274	-0.0077	-0.0116
GL	0.0366	0.0015	-0.0052	-0.0065	0.0358	-0.0014	-0.0004	-0.0167	0.0069	-0.0007	0.0224	-0.0236	-0.0065	-0.0184	-0.0022	0.0075	-0.1298	-0.0199	-0.0544
GB	-0.0309	0.0017	-0.0131	-0.013	-0.0300	-0.0106	0.0020	0.0124	-0.0106	-0.0002	-0.0311	0.0198	0.0276	0.0552	0.0059	-0.0032	0.0298	0.1940	-0.1600
LBR	0.0019	-0.0066	0.0207	0.0226	-0.0024	0.0106	-0.0051	0.0018	0.0047	0.0011	0.0107	0.0016	-0.0196	-0.0352	-0.0006	-0.0052	0.0876	-0.1723	0.2089
GYPP	0.0868	0.3300	0.7606	0.7641	0.0996	0.2176	0.2205	0.2344	0.5892	0.6428	-0.0407	0.3784	0.5588	0.1538	0.8642	0.5532	-0.0237	0.0250	-0.0237
r	0.0012	-0.0002	-0.0605	0.0742	-0.0004	-0.0020	0.0026	0.0021	-0.0985	0.1073	-0.0015	-0.0096	0.0070	0.0036	0.6876	0.2604	0.0031	0.0048	-0.0050

Residual effect= 0.1545 ; R Square= 0.9761

DF=50 % flowering

PH= Plant height (cm)

NT= Number of tillers

NPT= Number of productive tillers

DM= Days to maturity

PL= Panicle length(cm)

PE= Panicle exertion (cm)

FLL= Flag leaf length (cm)

TGPP= Total grains per panicle

FGPP= Fertile grains per panicle

CGPP= Chaffy grains per panicle

SFP= Seed fertility percentage

GWPP= Grain weight per panicle (g)

TW= Test weight (g)

GYPP= Grain yield per plant (g)

BM= Biomass (g)

HI= harvest index (%)

GL= Grain length (cm)

GB= Grain breadth (cm)

LBR: L/B ratio of paddy grain

APPENDIX 6: Genotypic direct (diagonal) and indirect effects of growth and yield attributing traits in reciprocal cross F₃ generation of rice under aerobic condition

Traits	DF	PH	NT	NPT	DM	PL	PE	FLL	TGPP	FGPP	CGPP	SFP	GWPP	TW	BM	HI	GL	GB	LBR
DF	-0.0021	-0.0005	0.0000	0.0001	-0.0019	0.0001	-0.0001	0.0003	-0.0003	0.0000	-0.0008	0.0007	0.0005	0.0008	0.0000	0.0002	0.0003	0.0002	0.0000
PH	-0.0015	-0.0067	0.0001	0.0002	-0.0013	-0.0032	-0.0040	-0.0031	-0.0018	-0.0024	0.0008	-0.0017	-0.0019	0.0000	-0.0023	0.0010	0.0008	0.0005	0.0002
NT	0.0000	0.0000	-0.0014	-0.0014	0.0000	-0.0002	0.0002	0.0001	-0.0003	-0.0003	0.0000	0.0000	-0.0002	0.0001	-0.0010	-0.0001	0.0001	0.0001	0.0000
NPT	0.0006	-0.0005	0.0161	0.0165	-0.0001	0.0022	-0.0023	-0.0007	0.0030	0.0033	0.0002	0.0009	0.0026	-0.0012	0.0116	0.0018	-0.0010	-0.0015	0.0005
DM	-0.0044	-0.0009	-0.0001	0.0000	-0.0047	0.0003	-0.0001	0.0005	-0.0008	-0.0001	-0.0017	0.0016	0.0009	0.0019	-0.0001	0.0005	0.0008	0.0006	0.0000
PL	0.0012	-0.0086	-0.0024	-0.0025	0.0013	-0.0184	-0.0061	-0.0104	-0.0083	-0.0096	0.0005	-0.0045	-0.0088	-0.0013	-0.0052	-0.0010	0.0012	-0.0006	0.0011
PE	0.0002	0.0041	-0.0009	-0.0010	0.0002	0.0023	0.0069	0.0025	0.0009	0.0020	-0.0022	0.0029	0.0017	-0.0001	0.0010	-0.0007	-0.0006	0.0007	-0.0011
FLL	0.0013	-0.0038	0.0004	0.0004	0.0009	-0.0046	-0.0030	-0.0081	-0.0026	-0.0032	0.0006	-0.0018	-0.0038	-0.0012	-0.0014	-0.0003	0.0007	0.0003	0.0002
TGPP	-0.0108	-0.0177	-0.0121	-0.0120	-0.0114	-0.0297	-0.0083	-0.0207	-0.0655	-0.0588	-0.0305	0.0055	-0.0438	0.0099	-0.0201	-0.0136	0.0108	0.0004	0.0072
FGPP	0.0009	0.0334	0.0176	0.0183	0.0021	0.0483	0.0272	0.0360	0.0828	0.0921	0.0031	0.0325	0.0747	-0.0031	0.0352	0.0224	-0.0091	0.0030	-0.0089
CGPP	0.0072	0.0023	-0.0007	-0.0003	-0.0070	0.0005	0.0063	0.0014	-0.0091	-0.0007	-0.0196	0.0177	0.0022	0.0056	0.0013	0.0004	0.0034	0.0016	0.0010
SFP	0.0187	-0.0132	-0.0016	-0.0028	0.0181	-0.0130	-0.0225	-0.0117	0.0045	-0.0189	0.0483	-0.0534	-0.0219	-0.0141	-0.0106	-0.0060	-0.0080	-0.0062	-0.0003
GWPP	-0.0023	0.0030	0.0016	0.0017	-0.0021	0.0051	0.0026	0.0050	0.0072	0.0087	-0.0012	0.0044	0.0107	0.0033	0.0039	0.0038	0.0002	0.0011	-0.0007
TW	0.0014	0.0000	0.0003	0.0003	0.0014	-0.0003	0.0000	-0.0005	0.0005	0.0001	0.0010	-0.0009	-0.0011	-0.0036	-0.0002	-0.0004	-0.0005	-0.0005	0.0001
BM	0.0052	0.2890	0.5913	0.5929	0.0170	0.2361	0.1283	0.1424	0.2578	0.3214	-0.0575	0.1670	0.3083	0.0585	0.8412	0.0201	-0.0565	-0.0987	0.0335
HI	-0.0531	-0.0688	0.0419	0.0516	-0.0552	0.0262	-0.0469	0.0180	0.0988	0.1158	-0.0097	0.0537	0.1660	0.0555	0.0113	0.4756	0.0294	0.0106	0.0062
GL	-0.0080	-0.0076	-0.0050	-0.0041	-0.0103	-0.0043	-0.0056	-0.0055	-0.0107	-0.0064	-0.0113	0.0097	0.0015	0.0097	-0.0043	0.0040	0.0647	0.0094	0.0379
GB	0.0093	0.0061	0.0072	0.0074	0.0102	-0.0024	-0.0083	0.0032	0.0004	-0.0026	0.0066	-0.0092	-0.0081	-0.0115	0.0093	-0.0018	-0.0114	-0.0791	0.0554
LBR	0.0008	0.0027	-0.0022	-0.0034	0.0005	0.0064	0.0160	0.0024	0.0115	0.0101	0.0054	-0.0006	0.0072	0.0018	-0.0041	-0.0013	-0.0610	0.0730	-0.1042
GYPP	-0.0526	0.2123	0.6500	0.6620	-0.0424	0.2515	0.0802	0.1511	0.3680	0.4505	-0.0680	0.2245	0.4868	0.1111	0.8656	0.5045	-0.0359	-0.0850	0.0280
r	0.0001	-0.0014	-0.0009	0.0109	0.0002	-0.0046	0.0006	-0.0012	-0.0241	0.0415	0.0013	-0.0120	0.0052	-0.0004	0.7281	0.2399	-0.0023	0.0067	-0.0029

Residual effect= 0.1236 ; R Square= 0.9847

DF=50 % flowering

PH= Plant height (cm)

NT= Number of tillers

NPT= Number of productive tillers

DM= Days to maturity

PL= Panicle length(cm)

PE= Panicle exertion (cm)

FLL= Flag leaf length (cm)

TGPP= Total grains per panicle

FGPP= Fertile grains per panicle

CGPP: Chaffy grains per panicle

SFP: Seed fertility percentage

GWPP= Grain weight per panicle (g)

TW= Test weight (g)

GYPP= Grain yield per plant (g)

BM= Biomass (g)

HI: harvest index (%)

GL= Grain length (cm)

GB= Grain breadth (cm)

LBR: L/B ratio of paddy grain

Identification of Cytoplasmic Influence on Grain Quality and Micro-nutrient Traits Using Reciprocal Crosses and Mitochondrial Marker Based Polymorphism in Rice (*Oryza sativa* L.)

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ABSTRACT

The data on plant, grain quality and nutrient traits were recorded to study genetic variability, heritability, genetic advance, correlation and path coefficient in both direct and reciprocal F_2 crosses of rice involving BPT-5204 and HPR-14 parents. The objective was to observe the effect of cytoplasmic influence on these traits. On the basis of mean performance, protein, iron, carbohydrates, phytic acid contents and grain yield per plant was higher in direct cross compared to its reciprocal cross. The percentage of transgressive segregants obtained in reciprocal cross for iron, zinc, amylose contents and grain yield per plant was higher than the direct cross. Both the crosses showed high heritability with low PCV, GCV and genetic advance for iron, zinc, carbohydrate and phytic acid contents. For grain yield per plant, moderate heritability with high PCV, GCV was observed. Zinc content in grain exhibited maximum positive direct effect on grain yield compared to iron content. Phytic acid had negative correlation with protein, zinc and amylose content in both crosses. In the parental polymorphism effort using 20 mitochondrial markers, 13 markers indicated similarity for both parents and mostly showed monomorphism.

Keywords: cytoplasmic-inheritance, reciprocal-crosses, protein, zinc and iron, phytic acid and mitochondrial DNA markers

RICE (*Oryza sativa* L.) is India and South Asia's staple food. India is the second largest producer of rice and most of it is consumed in the country. It is rich in energy sources like carbohydrate but deficient in nutrients of protein, zinc and Fe hence, most rice eating population suffers from micronutrient deficiency and leading to diseases in children and elderly persons from the lower strata of the society. It is estimated that more than 3.5 billion people in the world are deficient in vitamin A, iodine, iron and zinc (Virk *et al.*, 2007). Also World Health Organization (2011) reported approximately 1.62 billion people suffer from Iron deficiency (Anemia) and more than half the world suffering from Zinc deficiency. Zinc is an essential trace element for microorganisms, plants and animals. For humans, sufficient zinc is needed to maintain health and plays a role in many major metabolic pathways (Hanamareddy Biradar *et al.*, 2007).

Rice is a crop rich in genetic diversity, and known to have more than 1,27,000 germplasm in the world (IRRI, 2017). From among these, some donor genotypes with higher nutritional value could contribute

to development of rice varieties that are high in nutrients and with higher yield.

Cytoplasmic effects can contribute substantially to the phenotype of an individual, despite evidence that maternal effects can have a large influence on offspring phenotype. Variation in an individual's phenotype may be determined not only by the genotype and environment of that individual but also by maternal effects, *i.e.*, the contribution of the maternal parent to the phenotype of its progenies beyond the equal chromosomal contribution expected from each parent. Maternal effects will increase the amount of environmental noise and thus slow the response to selection. Cytoplasmic or nuclear genetic maternal effects will inflate the amount of genetic variance but may slow the response to selection if the trait is completely under maternal control. Molecular and quantitative genetic studies have shown that cytoplasmic factors contribute to heritable variation in both qualitative and quantitative traits in plants. (Alexander and Wulff, 1985).

DNA markers are useful tools in identification of desired trait in plants or organisms. They help to find out if any association exists for selection (Hittalmani *et al.*, 1995 and 1997) and help in pyramiding of the traits. Mitochondrial markers may help to find out there is any cytoplasmic inheritance for the traits under study. Further, they could also be useful for selection for traits. The use of chloroplast (cp) DNA and / or mitochondrial (mt) DNA polymorphisms to investigate evolutionary phenomena requires a knowledge of the mode of organellar inheritance. For example, the frequent occurrence of uniparental inheritance of organellar genomes results in a characteristic decrease in the expected level of standing organellar variation in a population (as compared to the biparental case; Birky *et al.*, 1989). In addition, to the extent that they are uniparentally inherited. Organellar polymorphisms can provide insights into phenomena such as sex-biased gene flow (McCauley, 1994) and the directionality of introgression in populations of hybrid origin (Edwards-Burke *et al.*, 1997).

Using reciprocal crossing, maternal effects have been reported for several traits in rice, including grain weight and filled-grain ratio (Toa *et al.*, 2011), grain quality trait (Asfaliza *et al.*, 2012), protein content (Shi *et al.*, 1996) and milling quality traits (Shi and Zhu, 1995). The reciprocal effect for a trait is based on the assumption that if the difference exists between F_2 and its reciprocal F_2 population, they would be expected to be due to maternal effects and this contributes consequently for the design and interpretation of genetic studies (Mosjidis and Yermanos, 1984). Phytic acid (PA; myo-inositol hexaphosphate) is a ubiquitous biomolecule present abundantly in plants wherein PA phosphorus constitutes the major portion of total phosphorus in several seeds and grains (Harland and Overleas, 1987). It accounts for 50–80 per cent of the total phosphorus in different cereals (Raboy, 2003; Stangoulis *et al.*, 2007). However, the presence of certain forms of a particular nutrient can hinder the uptake of other nutrients especially micronutrients.

The present study was conducted to find out if there exists any variation for observed traits in the progenies of reciprocal crosses due to cytoplasmic

inheritance involving a superior grain quality popular variety BPT 5204 and a local donor for micronutrients and protein HPR 14 and Further, explore the possibility of selecting desired combination by testing them using genetic-statistical parameters.

MATERIAL AND METHODS

The experiment was carried out during *Kharif*, under aerobic condition representing the eastern dry zone which is located at the latitude of 12° 58' North; longitude 77° 35' East and altitude of 930 meters above mean sea level. The reciprocal crosses previously developed by Mahadevaiah and Shailaja Hittalmani (2015) were obtained from Marker Assisted Selection laboratory, UAS, GKVK, Bengaluru for the present study. It composed of 479 direct cross (BPT 5204 x HPR-14) and 487 individuals plants of reciprocal cross (HPR-14 x BPT 5204) of F_2 population. The BPT 5204 is a highly popular variety grown in irrigated conditions in South India is known to fetch high price for its excellent cooking and milling quality. The HPR 14 is low yielder, short duration for growth, bold grain type, low tillering ability and having high protein content of 13-14 per cent.

The Near Infrared Reflectance spectroscopy (NIR system, FOSS, Denmark) system was used for the estimation of total protein, iron, zinc, amylose, carbohydrates and moisture present in the grain. The phytic acid content present in the parents and two crosses of F_2 population were estimated by following the standard protocol of Gao *et al.*, 2007 and results were expressed as a percentage of dry weight (mg /100 g). Using the above procedure 400 samples across two crosses were estimated and developed the standard spectra for phytic acid content in Near Infrared Reflectance spectroscopy (NIR system, FOSS, Denmark) system and remaining samples were analyzed for phytic acid content using NIR. Correlation and path analysis were done for grain quality and micronutrients in both the crosses using software, INDOSTAT version 8.5. The SPSS version 16.0 software was used to obtain frequency distribution curves for grain nutrients traits.

A total of 20 different universal mitochondrial (mt) DNA specific primers primarily used by Khera *et al.*, 2012 (Table I) synthesized by Eurofins

TABLE I
List of mitochondrial DNA specific primers

Primer Name	Primer Sequence 5' to 3'	Annealing Temp. (°C)
Nad1 F	GCATTACGATCTGCAGCTCA	57.3
Nad1 R	GGAGCTCGATTAGTTTCTGC	57.3
Nad4ex1 F	CAGTGGGTTGGTCTGGTATG	59.4
Nad4ex1 R	TCATATGGGCTACTGAGGAG	57.3
Nad4ex2 F	TGTTTCCCGAAGCGACACTT	57.3
Nad4ex2 R	AACCAGTCCATGACTTAACA	53.2
rpS14 F	CACGGGTCGCCCTCGTTCCG	67.6
rpS14 R	GTGTGGAGGATATAGGTTGT	55.3
coxII F	AATCCAATCCCGCAAAGGATT	55.9
coxII R	AGAAGATGATCCAGAATTGGG	55.9
Rrna F	GTGTTGCTGAGACATGCGCC	61.4
Rrna R	ATATGGCGCAAGACGATTCC	57.3
alp F	TTTGCCAGCGGTGTTAAAGG	57.3
alp R	CTTCGCCATATTGTGCCAATTC	58.4
Atp6 F	GGAGGTGGAAATTCAGTTCCAA	58.4
Atp6 R	TAGCATCATTCAGTAAATACA	50.9
Cob F	AGTTATGGTGGGGTTCGG	59.4
Cob R	CCCCAAAAGCTCATCTGACCCC	64.0
coxIA F	GGTGCCATTGCTGGAGTGATGG	64.0
coxIA R	TGGAAGTTCCTTAAAAGTATG	49.1
coxIB F	GGCTTTTCTCCACTAACCACAA	58.4
coxIB R	GGAGGGCTTTGTACCATCCATTC	62.4
cox2 F	GATGCTGCTGAACCTTGCCA	59.4
cox2 R	TCCGATACCATTGATGTCC	54.5
cox3 F	GTAGATCCAAGTCCATGGCCT	59.8
cox3 R	GCAGCTGCTTCAAAGCC	55.2
Nad1A F	CTAGCTGAACGTAAAGTAATGGC	58.9
Nad1A R	CCAACCTGCTATAATTATTC	54.0
Nad3 F	AATTGTCGGCTACGAATCTG	57.9
Nad3 R	TTCATAGAGAAATCCAATCGT	52.0
Nad3A F	AATTGTCGGCTAGGAATGTG	57.9
Nad3A R	GCTCGTGTACGGTCTGTGGG	63.5
Nad4A F	ATACGATTGATTGGTCTGTG	55.9
Nad4A R	TGAACTGGTACCATAGGCACTTT	58.9
Nad5A F	GAAATCTTTGATGCTTCTTGGG	56.5
Nad5A R	ACCAACATTGGCATAAAAAAGT	53.5
Nad5D F	ATAAGTCAACTTCAAAGTGGA	52.0
Nad5D R	CATTGCAAAGGCATAATGAT	51.2
Rps14 F	ATACGAGATCACAAACGTAGA	54.0
Rps14 R	CCAAGACGATTTTATGCC	54.0

Genomics India Pvt. Ltd., Bengaluru were used in this study. These universal mt DNA primers were designed based on consensus mt DNA (Petit *et al.*, 1998; Wu *et al.*, 1998) derived from the various mitochondrial genes. The parental polymorphism on 3 per cent agarose gel electrophoresis and 6 per cent polyacrylamide gel electrophoresis was carried out using 20 mitochondrial specific simple sequence repeats (SSRs) following the methods described by (Sambrook *et al.*, 1989).

RESULTS AND DISCUSSION

The mean performance of grain nutrient traits like protein (9.70 %), iron (11.86 ppm), carbohydrates (83.05 %), phytic acid (733.44 mg / 100 g) and grain yield per plant (15.10 g) was higher in direct cross compare to its reciprocal cross (Table II). Frequency distribution was normal for grain nutrient traits and grain yield per plant both in direct and reciprocal crosses (Fig. 1). The present investigation lead to the identification of superior promising individual plants for the traits under observation in F_2 segregating generations in the two crosses. The percentage of transgressive segregants obtained in reciprocal cross for iron were 76.39 per cent, zinc 69.61 per cent, amylose 98.15 per cent and phytic acid 28.54 per cent in reciprocal cross. For grain yield per plant 95.49 per cent of transgressive segregants were observed in reciprocal cross and which was higher than direct cross (94.15 %). The transgressive segregants were lesser for protein 19.30 per cent and moisture content, 45.38 per cent in reciprocal cross compared to direct cross. The *per cent* of transgressive segregants in respect of carbohydrates was almost same in both the crosses *i.e.* 62 per cent (Table III).

The percentage of phenotypic and genotypic coefficients of variation for iron, zinc and carbohydrate were low in both the crosses. High heritability coupled with low genetic advance were observed for iron (97.65 %, 1.54%), zinc (61.10%, 1.75%) and carbohydrate content (73.92%, 8.46%) in direct cross, respectively. Similar results of high heritability and low genetic advance were obtained in reciprocal cross as well. *i.e.*, iron (98.05 %, 1.59 %), zinc (66.71 %, 2.09 %) and carbohydrate contents (76.04 %, 8.27 %), respectively. For amylose content, the percentage of

TABLE II
Comparison of various grain nutrient traits in direct and reciprocal crosses in F_2 generation of rice under aerobic condition

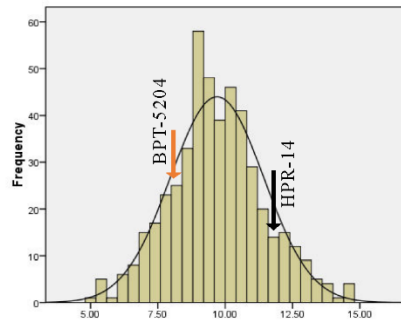
Grain nutrient traits	Parameters	BPT 5204 X HPR - 14	HPR - 14 X BPT 5204	Parents	
		Direct cross	Reciprocal cross	BPT 5204	HPR 14
Protein (%)	Mean	9.70	9.56	8.12	12.35
	Range	5.16-14.75	5.65-15.82		
Iron (ppm)	Mean	11.86	11.29	11.66	12.68
	Range	9.47-14.87	8.53-14.62		
Zinc (ppm)	Mean	28.92	30.37	28.14	30.23
	Range	25.10-31.85	26.37-32.98		
Amylose (%)	Mean	28.82	34.34	27.14	28.01
	Range	10.92-59.13	15.03-57.03		
Carbohydrate (%)	Mean	83.05	80.39	79.6	84.57
	Range	69.96-86.91	68.87-87.05		
Moisture (%)	Mean	12.12	12.13	12.48	11.97
	Range	10.69-13.15	11.06-13.04		
Phytic Acid (mg/100g)	Mean	733.44	720.80	848.06	636.59
	Range	492.21-1016.66	389.97-1072.43		
Grain yield per plant (g)	Mean	15.10	14.41	14.63	13.52

high PCV, GCV, heritability and genetic advance were noticed in both crosses. For phytic acid high heritability (99.67 %, 99.75 %) with high genetic advance as *per cent* of mean (23.71 %, 27.58 %) were recorded in both crosses, respectively. For grain yield per plant, the highest PCV (89.80 %, 89.92 %) and GCV (66.03 %, 58.36 %) were recorded in direct and reciprocal crosses, respectively (Table IV). Indicating the presence of ample variation for these traits in the present material. This implies that the trait was controlled by additive gene action, which offers scope for further improvement through selection which were in agreement with Sala., 2012; Verma *et al.*, 2000; Ashwini Samaket *et al.*, 2011 and Shashidhar *et al.*, 2013.

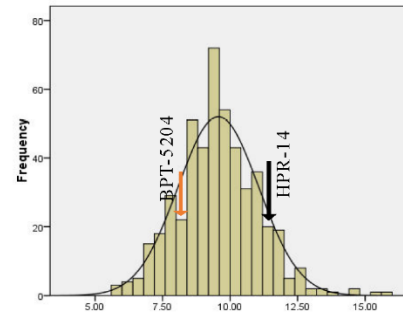
Correlation studies for grain yield per plant and grain nutrient traits in F_2 population of direct and

reciprocal crosses revealed that, grain yield had positive non-significant correlation with the zinc (0.2436), iron (0.0449), moisture contents (0.1347) while protein (-0.0865), amylose (-0.0536), carbohydrate (-0.0502) and phytic acid (-0.1103) had negative correlation in direct cross. In reciprocal cross, grain yield per plant had non-significant negative correlation with iron and positive non-significant correlation with amylose content (0.0717) (Table V & VI). These results were in accordance with the Nagesh *et al.* (2012) and Sala and Geetha (2015).

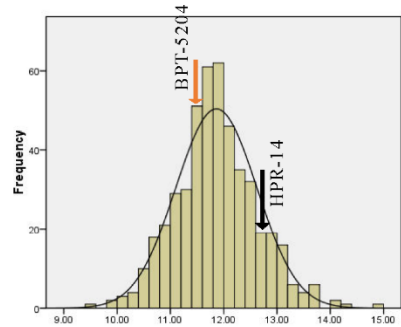
Phytic acid had significant negative correlation with protein (-0.0907) and significant positive correlation with the carbohydrate (0.01339) in direct cross whereas, protein (0.1319), iron (0.1278), carbohydrate (0.1654) had significant positive correlation and zinc (-0.3388), amylose (-0.1664) had



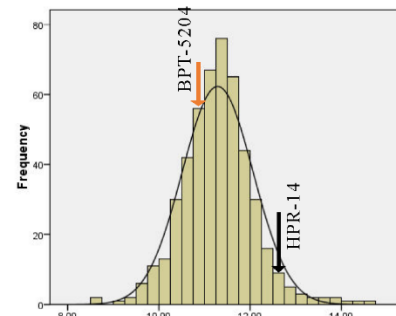
1(a). Protein content (%) Direct cross



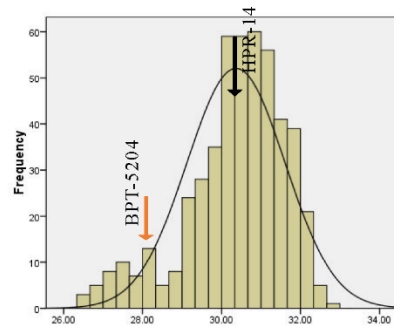
Protein content (%) Reciprocal cross



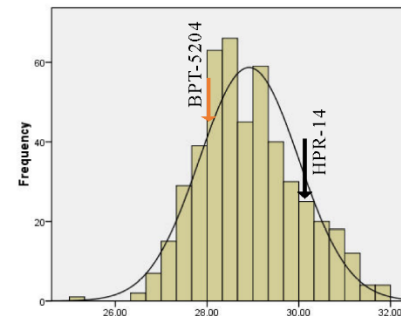
1(b). Iron (ppm) Direct cross



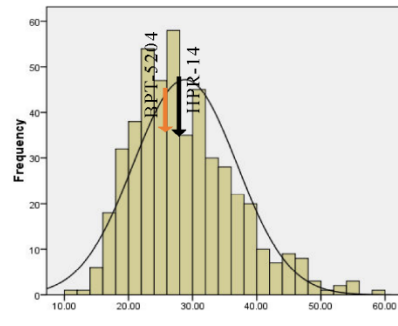
Iron (ppm) Reciprocal cross



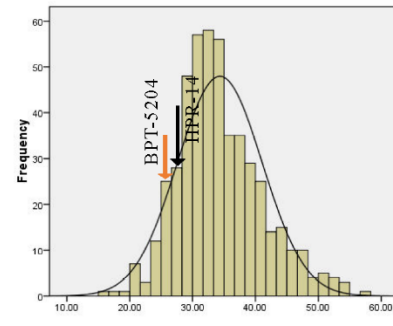
1(c). Zinc (ppm) Direct cross



Zinc (ppm) Reciprocal cross



1(d). Amylose (%) Direct cross



Amylose (%) Reciprocal cross

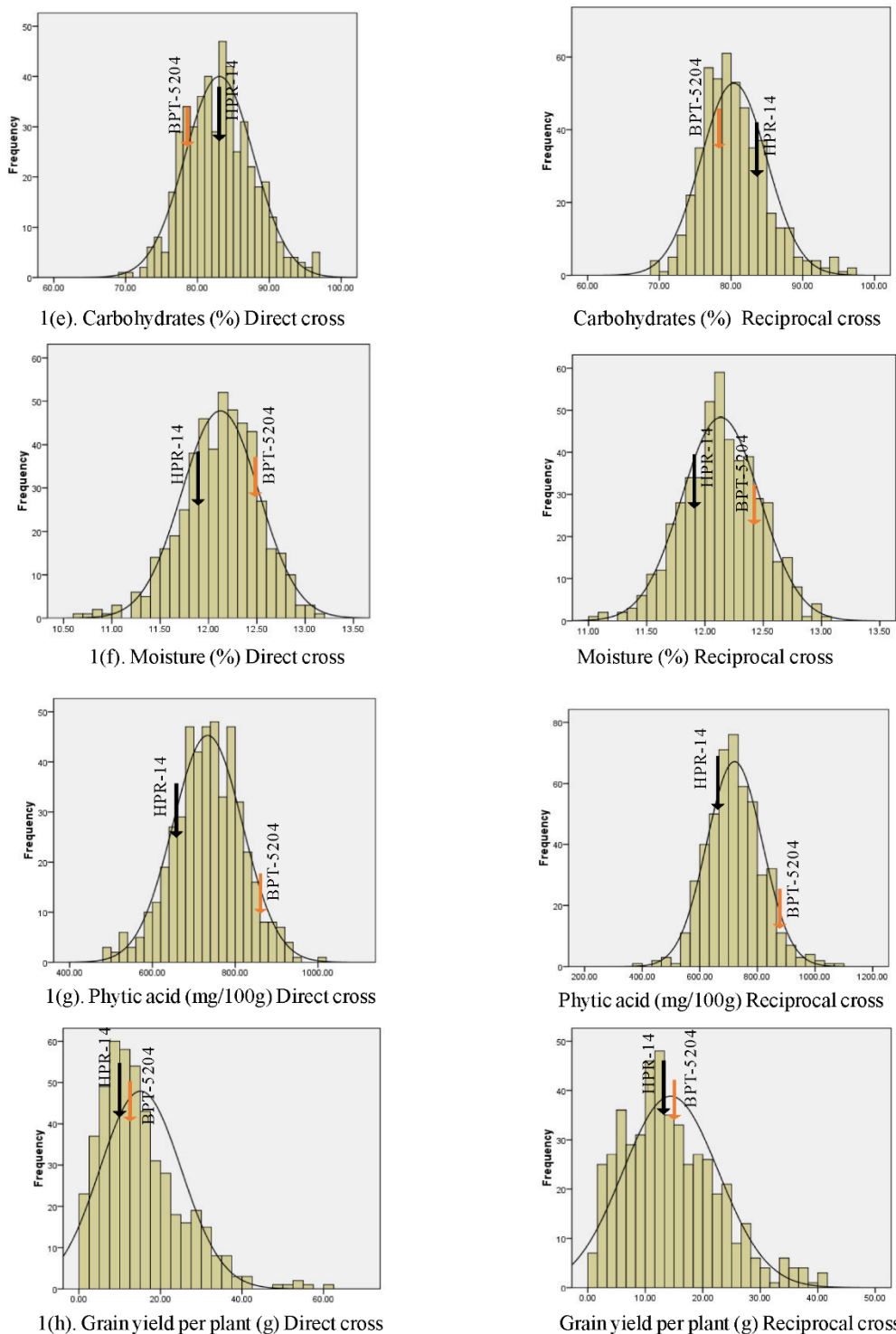


Fig. 1: Comparison of frequency distribution curve for grain quality parameters in direct and reciprocal crosses of F_2 generation in rice under aerobic condition.

TABLE III

Estimates of observed probability and transgressive segregants of F_2 population of direct and reciprocal crosses for grain nutrient traits in rice under aerobic condition.

Characters	Parental criteria	Observed probability (%)		Transgressive segregants (%)	
		Direct Cross	Reciprocal Cross	Direct Cross	Reciprocal Cross
Protein (%)	<BPT 5204	17.33	15.81	25.26	19.30
	>HPR 14	7.93	3.49		
	Intermediate	74.74	80.69		
Iron (ppm)	<BPT 5204	37.79	72.28	52.40	76.39
	>HPR 14	14.61	4.11		
	Intermediate	47.59	23.61		
Zinc (ppm)	<BPT 5204	24.22	7.39	37.16	69.61
	>HPR 14	12.94	62.22		
	Intermediate	62.84	30.39		
Amylose (%)	<BPT 5204	49.06	12.32	95.61	98.15
	>HPR 14	46.55	85.83		
	Intermediate	4.38	1.85		
Carbohydrates (%)	<BPT 5204	25.68	46.82	62.00	62.63
	>HPR 14	36.32	15.81		
	Intermediate	37.99	37.37		
Moisture (%)	>BPT 5204	17.12	16.02	51.15	45.38
	<HPR 14	34.03	29.36		
	Intermediate	48.85	54.62		
Phytic Acid (mg/100g)	>BPT 5204	7.72	10.06	19.61	28.54
	<HPR 14	11.89	18.48		
	Intermediate	80.37	71.46		
Grain yield per plant (g)	>BPT 5204	42.17	43.33	94.15	95.49
	<HPR 14	51.98	52.16		
	Intermediate	5.84	4.51		

<BPT 5204 = The genotypes having value less than the parent BPT 5204 and expressed in percentage

<HPR 14 = The genotypes having value more than the parent HPR 14 and expressed in percentage

Intermediate = The value between the two parents BPT 5204 & HPR 14 and expressed in percentage

TABLE IV
Estimates of PCV, GCV, heritability (broad sense) genetic advance and genetic advance per cent mean in direct and reciprocal rice crosses of F_2 generation under aerobic condition.

Characters	PCV (%)		GCV (%)		h^2 (broad sense)		Genetic advance (%)		Genetic advance over mean (%)	
	Direct Cross	Reciprocal Cross	Direct Cross	Reciprocal Cross	Direct Cross	Reciprocal Cross	Direct Cross	Reciprocal Cross	Direct Cross	Reciprocal Cross
Protein (%)	27.34	26.14	17.77	15.64	42.25	35.80	2.31	1.84	23.80	19.28
Iron (ppm)	6.47	6.97	6.39	6.91	97.65	98.05	1.54	1.59	13.02	14.09
Zinc (ppm)	4.80	5.01	3.75	4.09	61.10	66.71	1.75	2.09	6.04	6.89
Amylose (%)	28.28	19.88	28.10	19.66	98.72	97.82	16.58	13.75	57.52	40.05
Carbohydrates (%)	6.69	6.56	5.75	5.72	73.92	76.04	8.46	8.27	10.18	10.28
Moisture (%)	17.04	16.74	3.29	2.76	3.74	2.72	0.16	0.11	1.31	0.94
Phytic Acid (mg/100g)	11.51	13.39	11.47	13.35	99.67	99.75	173.91	198.78	23.71	27.58
Grain yield per plant (g)	89.80	89.92	66.03	58.36	54.07	42.13	15.10	11.20	100.02	78.03

PCV (%) = Phenotypic coefficient of variation (%)

GCV (%) = Genotypic coefficient of variation (%)

h^2 = Heritability

TABLE V
Phenotypic correlations among grain nutrient traits in direct cross (BPT 5204 X HPR-14) of F_2 generations under aerobic condition.

	X1	X2	X3	X4	X5	X6	X7
X1	1						
X2	-0.245 ***	1					
X3	-0.1148 *	-0.2891 ***	1				
X4	-0.0549	-0.4138 ***	0.3914 ***	1			
X5	-0.507 ***	0.3953 ***	-0.2528 ***	-0.0098	1		
X6	0.0049	0.0247	0.1781 ***	0.0528	-0.0805	1	
X7	-0.0907 *	0.0051	-0.0877	-0.0084	0.1339 **	0.0010	1
X8	-0.0865	0.0449	0.2436	-0.0536	-0.0502	0.1347	-0.1103

X1= Protein (%), X2= Iron (ppm), X3= Zinc (ppm), X4= Amylose (%), X5= Carbohydrates (%), X6= Moisture (%), X7= Phytic Acid (mg/100g) and X8= Grain yield per plant (g)

* Significant at 5 per cent, ** Significant at 1 per cent, *** Significant at 0.5 per cent

TABLE VI
Phenotypic correlations among traits in reciprocal cross (HPR-14 X BPT 5204) of F_2 generations under aerobic condition.

	X1	X2	X3	X4	X5	X6	X7
X1	1						
X2	-0.0765	1					
X3	0.0276	-0.5010 ***	1				
X4	-0.0084	-0.5803 ***	0.3480 ***	1			
X5	-0.7120 ***	0.2960 ***	-0.5265 ***	-0.1333 **	1		
X6	0.0379	0.0499	0.1088 *	-0.1712 ***	-0.1130 *	1	
X7	0.1319 **	0.1278 **	-0.3388 ***	-0.1664 ***	0.1654 ***	-0.0623	1
X8	-0.0640	-0.0548	0.1062	0.0714	-0.0738	0.0066	-0.2293

X1= Protein (%), X2= Iron (ppm), X3= Zinc (ppm), X4= Amylose (%), X5= Carbohydrates (%), X6= Moisture (%), X7= Phytic Acid (mg/100g) and X8= Grain yield per plant (g)

* Significant at 5 per cent, ** Significant at 1 per cent, *** Significant at 0.5 per cent

significant negative correlation with the phytic acid content in reciprocal cross. Grain zinc content had significant negative correlation with iron in both direct and reciprocal crosses. Among the traits studied, zinc had highest direct effect on grain yield per plant followed by moisture and iron. The amylose content (-0.1448) had highest negative effect in direct cross and this amylose had highest direct effect (0.0356)

followed by iron (0.0012) on grain yield per plant and carbohydrate had highest negative direct effect in reciprocal cross (Table VII & VIII). Since, there was no significant correlation between grain nutrients under study and grain yield per plant suggests that simultaneous selection or breeding can be taken up to enhance iron, zinc contents and grain yield per plant.

TABLE VII

Genotypic direct (diagonal) and indirect effects of different grain nutrient traits in direct cross of rice F_2 generation under aerobic condition.

	X1	X2	X3	X4	X5	X6	X7
X1	-0.1121	0.0308	0.0129	0.0062	0.0841	-0.0006	0.0102
X2	-0.0156	0.0570	-0.0165	-0.0236	0.0225	0.0014	0.0003
X3	-0.0301	-0.0757	0.2617	0.1024	-0.0662	0.0466	-0.0230
X4	0.0080	0.0599	-0.0567	-0.1448	0.0014	-0.0076	0.0012
X5	0.0548	-0.0289	0.0185	0.0007	-0.0730	0.0059	-0.0098
X6	0.0004	0.0022	0.0159	0.0047	-0.0072	0.0891	0.0001
X7	0.0081	-0.0005	0.0078	0.0007	-0.0120	-0.0001	-0.0893
r	0.0097	0.0026	0.0638	0.0078	0.0037	0.0120	0.0098

Residual effect= 0.944

R square = 0.109

X1= Protein (%), X2= Iron (ppm), X3= Zinc (ppm), X4= Amylose (%), X5= Carbohydrates (%), X6= Moisture (%), X7= Phytic Acid (mg/100g), X8= Grain yield per plant (g) and r= partial R^2

TABLE VIII

Genotypic direct (diagonal) and indirect effects of different grain nutrient traits in reciprocal cross of rice F_2 generation under aerobic condition

	X1	X2	X3	X4	X5	X6	X7
X1	-0.1868	0.0143	-0.0052	0.0016	0.1330	-0.0071	-0.0246
X2	-0.0001	0.0012	-0.0006	-0.0007	0.0003	0.0001	0.0001
X3	-0.0021	0.0377	-0.0753	-0.0262	0.0396	-0.0082	0.0255
X4	-0.0003	-0.0207	0.0124	0.0356	-0.0047	-0.0061	-0.0059
X5	0.1506	-0.0626	0.1114	0.0282	-0.2115	0.0239	-0.0350
X6	-0.0003	-0.0004	-0.0008	0.0013	0.0009	-0.0078	0.0005
X7	-0.0250	-0.0243	0.0643	0.0316	-0.0314	0.0118	-0.1899
r	0.0120	-0.0001	-0.0080	0.0025	0.0156	-0.0001	0.0435

Residual effect= 0.9667

R square = 0.0655

X1= Protein (%), X2= Iron (ppm), X3= Zinc (ppm), X4= Amylose (%), X5= Carbohydrates (%), X6= Moisture (%), X7= Phytic Acid (mg/100g), X8= Grain yield per plant (g) and r= partial R^2

DNA marker validation: Molecular markers are often used to select suitable genotype in plant breeding. Twenty mitochondrial specific markers have been already mapped by Khera *et al.*, 2012. These 20 mt specific SSR markers were screened on BPT 5204 and HPR-14 genotypes. The amplified products were resolved on 3 per cent agarose and 6 per cent PAGE gel. About 65 per cent of mitochondrial SSRs or 13 SSR markers indicated similarity for both parents and showed monomorphism on 3 per cent agarose. Out of 20 markers, none of markers showed polymorphic on 3 per cent agarose (Fig. 2) and 3 markers were polymorphic on 6 per cent PAGE (Fig. 3). Majority of

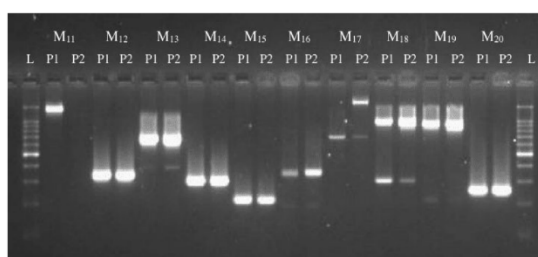


Fig. 2: Parental polymorphism on BPT 5204 (P_1) and HPR-14 (P_2) genotypes using mitochondrial specific SSRs. L=100bp Ladder; M=Mitochondrial specific SSR markers

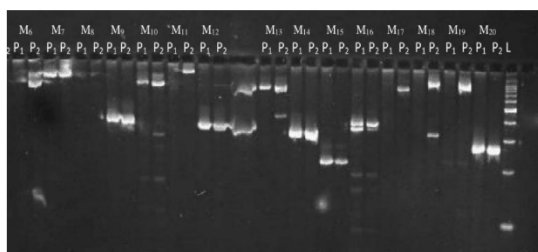


Fig. 3 : Parental polymorphism on BPT 5204 (P_1) and HPR-14 (P_2) genotypes using mitochondrial specific SSRs. L = 100bp Ladder; M= Mitochondrial specific SSR markers

primers analyzed were monomorphic in nature. This might be attributed to the conservative nature of mitochondrial DNA (Fuji *et al.*, 2010; Khera *et al.*, 2012) across species and varieties. 15 per cent of polymorphism was observed on 6 per cent PAGE gel. These polymorphic markers could be utilized further to see the effect of cytoplasm in the progenies of both the crosses.

Total grain protein is quantitatively inherited and is sensitive to environmental conditions like the level

of nitrogen fertilizers and normal distribution for total grain protein (Harshiya Banu *et al.*, 2013; Uday *et al.*, 2014). Symmetric variation suggested complete ambi-directional tends to normality due to interaction of between epistatic gene action and $G \times E$ interaction effect. The study of distribution using skewness and kurtosis provides information about nature of gene action and number of genes controlling traits, respectively. (Ashwini Samak *et al.*, 2011; Mahadevaiah *et al.*, 2015). Since, no skewness in both the crosses for all micronutrient traits indicating that those traits are governed by large number of genes and quantitatively controlled.

High transgressive segregants for iron, zinc, amylose and phytic acid in reciprocal cross compared to direct cross is mainly due to the combination of favourable genes (positive alleles) from different parents and additive gene action. Low heritability and low genetic advance in reciprocal cross for protein, amylose, moisture and grain yield per plant indicating the involvement of large number of loci in the inheritance of these traits and the major role of non-additive genes. For such characters high proportion of phenotypic coefficient of variation as compared to genotypic coefficient of variation is mainly responsible for reduced heritability and selection could be ineffective.

Grain quality is an economically important character in rice varieties. Any knowledge of the genetic mechanism of rice grain quality will be of benefit to rice breeders. Therefore, the major and minor genes affecting rice grain quality should accelerate the process of breeding new rice varieties with both a higher yield and a better quality. Quality traits are dependent not only on the genotypic but also on an environmental influence, and are controlled by some minor genes with additive effects. The inheritance of grain quality is complicated due to epistasis, cytoplasmic effects, and the triploid nature of endosperm (Pooni *et al.*, 1992). Some of the plants in the above two crosses may be further advanced to later generations so as to select the best segregants for high single plant yield coupled with more nutritive content and grain quality. This implies that the trait was controlled by additive gene action, which offers scope for further improvement through selection.

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To,
**Yallappa Harijan, Ashvinkumar Katral, Mahadevaiah C, Hanumareddy Biradar,
Jagadeesh Hadimani and Shailaja Hittalmani**

Manuscript titled "Genetic analysis of reciprocal differences for yield and yield attributing traits in segregating populations of rice (*Oryza sativa* L.)" is very well written and has been accepted for publication.

Corresponding author: Yallappa Harijan

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Genetic analysis of reciprocal differences for yield and yield attributing traits in segregating populations of rice (*Oryza sativa* L.)

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Abstract: Reciprocal differences prevail in nature mainly due to unequal contribution of cytoplasmic determinants from male and female gametes to the zygote, but the influence of female parent often extends beyond simple genetic transmission. In this report, we estimate the cytoplasmic and maternal effects in rice and their adequacy in describing the observed reciprocal differences based on study of the parents, F₂s, F₃s and reciprocal cross progenies. Our study revealed that significant differences were observed for majority of yield & yield attributing traits between mean performance of straight & reciprocal F₂ & F₃ populations derived by crossing BPT-5204 & HPR-14 indicating the presence of reciprocal differences. High PCV, GCV coupled with high heritability & GAM observed for number of tillers, number of productive tillers, biomass & harvest index. High heritability & high GAM was observed for plant height in straight & reciprocal F₂ & F₃ populations. The variability by Shapiro-Wilk 'W' normality test revealed normal distribution for total grains, fertile grains per panicle & grain weight per panicle in F₂ population, whereas number of productive tillers, flag leaf length, total grains per panicles, fertile grains per panicle, grain weight per panicle, test weight, harvest index & grain length in both straight and reciprocal F₃ population. Multi trait selection index was performed to evaluate F₃ families for quantitative traits & selected top 20 F₃ families in both straight & reciprocal crosses. Best F₃ families showed grain yield of 41% to 52% gain over the better parent BPT-5204 in straight & 37% to 61% gain in reciprocal crosses indicating the effect of cytoplasmic differences among the parents in the derived crosses. Further, these top performing superior F₃ families can be utilized for developing breeding lines for improvement of the traits.

Key words: straight cross, reciprocal cross, cytoplasmic effect, normality test, F₃ families

Introduction

Maximum human food is derived from cereal crop plants and major share is from wheat and rice, are supplying more than 65% human food requirement throughout globe. Global demand for these staple crops is on the rise and making these crops ideal targets for improving nutrition through biofortification. Among these, rice is a staple food crop that is consumed by more than 65% of global population (Kalyan *et al.*, 2017); it occupies a position of overwhelming importance in Asian agriculture and constitutes the bulk of the Asian diet too. It is largely grown in Asia (90% area) under diverse conditions of soil, climate, hydrology and topography (Mahapatra and Behera, 2011). For many people in the poor countries, rice is a main source of energy and plays an important role in providing livelihood. To feed the growing population and to achieve food security in the country, current production levels need to be increased minimum by two million tonnes every year (Singh *et al.*, 2018); hence it is critical to produce high yielding cultivars with high quality of rice.

To meet the increasing demand, rice production must be increased with less land, less water using less pesticide in a sustainable way (Anandan *et al.*, 2009). The presence of adequate genetic variability is pre requisite factor for rice improvement. Among the different options, exploiting the variability present in segregating populations is essential for improvement through selection and identification of maternal effect in reciprocal crosses helps to identify some traits which are controlled by cytoplasmic genes and useful for development of new high yielding cultivars. Reciprocal crosses play an important role in the selection of any breeding programme for population improvement and development of new hybrids in the crop. Reciprocal differences prevail in nature mainly due to unequal contribution of cytoplasmic determinants from male and female gametes to the zygote (Valluri *et al.*, 2016). Both the parents contribute genes to their offspring, but the influence of female parent often extends beyond simple genetic transmission (Munganyinka *et al.*, 2015).

The reciprocal effect for a trait is based on the assumption that the F_2 plants from direct crosses and reciprocal crosses have same mean value for the trait under study. If the difference exists between F_2 and its reciprocal F_2 population, likely to indicates the

maternal effects and this contributes accordingly for the design and interpretation of genetic studies (Mosjidis and Yermanos, 1984). Using reciprocal crosses, maternal effects have been reported for many characters in rice, including filled-grains and grain weight (Toa *et al.* 2011), grain quality trait (Asfaliza *et al.* 2012), milling quality traits (Shi & Zhu, 1995), protein content (Shi *et al.* 1996), hybrid vigor (Virmani, 1994) and crossability (IRRI, 1993). Diversity of the germplasm has been disclosed to be related to the manifestation of cytoplasmic differences in the expression of various characters (Kalsy & Sharma, 1972). The significant genetic differences among the straight & reciprocal crosses for the sheath rot disease (Mahadevaiah & Shailaja, 2015). In this context, the study was conducted to evaluate the straight & reciprocal F_2 & F_3 populations for their yield & yield attributing traits; to identify best performing RILs based on multitrait evaluation and existence of any reciprocal difference among segregating populations.

Material and methods

The experiment was conducted during *kharif*-2015 & *rabi*-2016 using augmented design. The experimental material for the present study comprised the straight and reciprocal crosses previously developed by Mahadevaiah and Shailaja Hittalmani (2015) was obtained from Marker Assisted Selection laboratory, UAS, GKVK, Bengaluru. It composed of 517 straight cross (BPT-5204 $\times$ HPR-14) & 533 individual plants of reciprocal cross (HPR-14 $\times$ BPT-5204) of F_2 population. The BPT-5204 is a highly popular variety grown in irrigated conditions in South India is known to fetch high price for its excellent cooking and milling quality. The HPR-14 is a local land race, purple pigmented, not popular and not cultivated on commercial scale but having high protein content. Salient features of parents used to derive the material for the study are presented in table 1. Nursery seedlings were transplanted after 21 DAS in main experimental field with spacing of 0.3 m $\times$ 0.2 m and maintained with recommended cultural practices. The best two hundred lines based on yield were selected from F_2 population and forwarded to F_3 generation in both straight & reciprocal crosses. In F_2 & F_3 segregating populations, straight & reciprocal crosses along with parents were evaluated for growth & yield attributing traits. Observations were recorded on all F_2 individual plants & F_3 families

(five plants per family) from both straight & reciprocal crosses under aerobic conditions. Statistical analysis was done using WINDOSTAT (version 8.0) for genetic variability and 'SPSS 23.0 version' for Shapiro Wilks 'W' normality test. The top performing families in both straight & reciprocal crosses among F_3 families have been quantified by "Duncan's multiple range test (DMRT)" through 'agricolae' package in R version 4.0.2 statistical software.

Results and Discussion

The inheritance study of quantitative characters in various crosses will help breeders to choose appropriate breeding methods (Singh *et al.*, 2018). The pattern of inheritance of different yield contributing and quantitative traits in rice has been reported by Kamara *et al.*, 2017. Diverse plant types are immediately valuable for shaping new varieties and forms the basic wealth on which plant breeders can operate for reconstructing the existing genotypes. To increase the present levels of production in terms of grain yield, quality & other traits there is ample need to identify & utilize genetically divergent parents for inter- and intra-sub specific and reciprocal crosses in rice. Among the many factors for rice production, cytoplasmic gene effect or maternal gene effect is one the most important factors & it can contribute to heritable variation in both quantitative and qualitative traits in plants (Alexander and Wulff, 1985; Singh *et al.*, 2018).

Significant differences were observed between mean performance of straight & reciprocal F_2 & F_3 populations for majority of yield & yield attributing traits. The traits like plant height, flag leaf length, seed fertility percentage, test weight, grain length & L/B ratio of paddy grain were found higher mean value in reciprocal cross compared to straight cross in both F_2 & F_3 populations (Table 2). The mean performances of these traits were affected by the parents when used as male and female parents and vice versa. This showed that cytoplasm of BPT-5204 & HPR-14 have an undesirable effect & moderately interferes with manifestation of yield & yield attributing traits. A result indicates the presence of reciprocal differences among straight & reciprocal F_2 & F_3 populations. The cytoplasmic influence of same parents (BPT-5204 & HPR-14) for sheath rot disease was reported (Mahadevaiah, 2015). The similar kind of reciprocal

differences for seed size in maize was reported by Roach & Wulff, 1987; Zhang *et al.*, 2016. Even the reciprocal difference clearly reported from Valluri *et al.*, 2016 in pearl millet under in-vitro conditions via. embryogenic callus quantity & regeneration frequency.

Wide range variability was observed for important traits like plant height, number of productive tillers, panicle length, grain length & grain breadth in straight cross compared to reciprocal cross in both F_2 & F_3 populations. The estimates of GCV & PCV was higher for most of the yield & yield attributing traits viz., days to 50% flowering, number of tillers, number of productive tillers, days to maturity, panicle exertion, flag leaf length, grain yield per plant, biomass, harvest index, grain length & grain in straight F_2 population as compared to reciprocal F_2 population. But in F_3 population, higher GCV & PCV was observed in reciprocal cross compared to straight cross for most of traits like days to 50 % flowering, plant height, panicle exertion, chaffy grains per panicle, test weight, grain yield per plant, biomass, grain length & L/B ratio. Very narrow differences were observed between estimates of GCV & PCV in both straight & reciprocal F_2 & F_3 populations indicate minimal role of environment on the performance of the genotypes. The heritability was ranged from 2.90 % (grain weight per plant) to 99.60% (total grain per plant) in F_2 population & 1.50% to 99.50% for the same traits in F_3 population. The higher heritability for days to 50% flowering, number of productive tillers, days to maturity, flag leaf length, total grain per plant, fertile grains per plants & seed fertility percentage and lower heritability for grain breadth, grain weight per plant & panicle length (except reciprocal F_2) was observed in both crosses of F_2 & F_3 populations. The lowest genetic advance per cent over mean (GAM) was observed for grain length (F_2 population), grain breadth (F_3 population) & highest for panicle exertion in both crosses of F_2 & F_3 populations (Table 3). Similar results of high heritability for panicle exertion and plant height were reported by Das *et al.* (2001); Kuldeep *et al.* (2004); Uttam *et al.* (2005). Whereas, high GAM was observed for plant height at maturity and moderate to low was observed for other characters which are similar to results reported by Prajapat *et al.* (2011).

Higher value of broad sense heritability attributed to lesser difference between PCV & GCV values. High heritability values resulted in higher values of expected GAM. High PCV, GCV coupled with high heritability & GAM observed for number of tillers, number of productive tillers, biomass & harvest index. High heritability & high GAM was observed for plant height in straight & reciprocal F₂ & F₃ populations. Similar results were observed by Thirunganana kumar *et al.* (2007); Basavaraja *et al.* (2013); Arvind *et al.* (2015) and Irappa *et al.* (2018). The results indicated the major genes with additive gene action governing these traits, which offers scope for further improvement through selection which were agreement with Sala (2013); Verma *et al.* (2000); Ashwini Samak *et al.* (2011); Roy (2000). The success in any crop improvement program depends by the ability of the breeder to define & assemble the required genetic variability & select for yield indirectly through yield associated and highly heritable characters after eliminating the environmental components of phenotypic variation (Mather, 1949). Therefore, it is necessary to have information on both PCV, GCV to estimate heritability, which helps the breeder to predict the expected grains through selection.

Shapiro Wilk 'W' test is the preferred test of normality due to its high statistical power as compared to a wide range of alternative tests. Results showed that non-normal distribution for all the growth and yield attributing traits except total grains per panicle, fertile grains per panicle and grain weight per panicle in both straight & reciprocal F₂ population. In F₃ population, number of tillers, number of productive tillers, flag leaf length, total grains per panicles, fertile grains per panicle, grain weight per panicle, test weight, harvest index, grain length and L/B ratio showed normal distribution in both straight & reciprocal crosses (Table 4). Majority of the traits showed skewed distribution in straight & reciprocal F₂ populations. Traits like days to 50 % flowering, number of tillers, number of productive tillers, days to maturity, grain yield per plant, biomass per plant and grain breadth showed positively skewed, whereas plant height, particle exertion, seed fertility percentage, panicle length (except straight F₃ population) and harvest index (except reciprocal F₃ population) showed negatively skewed distribution in both crosses of F₂ & F₃ populations (Table 4). The skewed distribution of a trait in general suggests that trait is under the control of non-additive gene action, especially epistasis & is influenced by environmental variables (Pooni *et al.*, 1977; Kimbeng &

Bingham, 1998; Roy, 2000). Positive skewness is caused complementary gene interactions, while negative skewness is caused by duplicate gene interactions predominantly in the same directions (Snape & Rizzs, 1975). The genes controlling the traits with skewed distribution tend to be predominantly dominant irrespective of whether they have increasing or decreasing effect on the expression of trait. Most of the growth & yield attributing traits showed platykurtic distribution in both straight & reciprocal F_2 & F_3 population. Traits like panicle length, seed fertility percentage, L/B ratio (except reciprocal F_2 's) & chaffy grains per panicle (except straight F_3 population) in both crosses of F_2 & F_3 populations showed leptokurtic distribution suggesting that few genes governing these traits (Table 4). Kurtosis indicates the relative number of genes controlling the trait under investigation (Robson, 1956).

Positively skewed leptokurtic distribution was observed for chaffy grain per panicle, L/B ratio (straight F_2 's), and panicle length in straight & reciprocal F_3 population indicated that traits were influenced by fewer genes with complimentary gene action. Positively skewed mesokurtic distribution flag leaf length (straight & reciprocal F_2 's), grain breadth (reciprocal F_2 's) and total grains per panicle (reciprocal F_3 population) indicated that traits were governed by moderate number of genes with complimentary gene action. Negatively skewed mesokurtic distribution for panicle length (straight F_2 's), plant height & harvest index (reciprocal F_2 's), panicle exertion & test weight (straight F_3 's), grain length and L/B ratio (reciprocal F_3 's) indicated that traits were governed by large number of genes with additive gene action.

Multi trait selection index was performed using Duncon's Multiple Range Test (DMRT) through "agricolae" package in "R" version 4.0.2 software to evaluate F_3 families for quantitative traits. Individual trait was ranked separately followed by sums of ranks of all the traits & finally arranged by ascending order of rank for all the traits along with parents. The top performing 20 F_3 families in both straight & reciprocal crosses derived from BPT-5204 & HPR-14 was presented in Table 5 & 6. Best F_3 families showed grain yield of 41% to 52% gain over the better parent BPT-5204 in straight and 37% to 61% gain in reciprocal crosses indicating the effect of cytoplasmic differences among the parents in the derived crosses (Table 7 & Fig.1). The significant cytoplasmic effect of reciprocal cross for grain yield was reported in rice (Singh *et al.* 2018). Further,

these top performing superior F₃ families can be utilized for developing breeding lines for improvement of the traits.

Conclusion: In the present study, significant differences were observed for majority of yield & yield attributing traits between mean performance of straight & reciprocal F₂ & F₃ populations derived by crossing BPT-5204 & HPR-14 indicating the presence of reciprocal differences. The performance of F₃ families for yield & yield attributing traits indicated that the majority of the traits not exhibited differences among the straight & reciprocal crosses but performance of reciprocal cross for grain yield found to be higher, indicating the influence of cytoplasmic differences on the expression of the trait. Best F₃ families showed 37% to 61% gain in grain yield per plant. The F₃ family 295 & 255 were identified as superior for grain yield per plant in straight & reciprocal crosses, respectively. The best performing F₃ families for various traits can serve as potential genotypes for various economical traits as per the need & can be utilized in the future crop improvement programme.

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Table 1: Salient features of parents (BPT-5204 & HPR-14) selected for the present study

Traits	BPT-5204	HPR-14
Plant stature	Medium tall (60-70 cm), Erect and compact	Tall (>90 cm) Medium spreading
Colour of plant, leaf & sheath	Green	Purple
Duration	Late (160 days)	Early (120 days)
Tillering ability	High (20)	Low (10)
No. of panicles	High (15-18) compact	Low (8-10)
Grain yield	4 ton/ ha	2.5 ton/ ha
Grain type	Short fine	Short bold
Total protein content	7-8%	13-14%

Table 2: Estimates of traits mean performance of F₂ and F₃ generations in straight and reciprocal crosses of rice

Traits	F ₂			F ₃			Parents	
	SC	RC	Two sample t test P value/ t statistics (assuming unequal variance)	SC	RC	Two sample t test P value/ t statistics (assuming equal variance)	BPT 5204	HPR 14
DF	96.59	94.61	2.97**	96.56	97.49	-1.05	104.06	101.94
PH	88.15	90.82	-2.97**	91.76	96.35	-3.72***	97.75	107.41
NT	15.01	14	3.07**	15.47	15.12	0.94	14.22	10.24
NPT	12.62	10.95	4.95***	12.76	12.04	2.09*	12.06	7.88
DM	127.1	125.51	2.38*	127.12	128.67	-1.76	133.44	131.71
PL	20.2	19.99	-0.41	20.19	19.67	1.36	19.97	22.32
PE	0.14	0.65	-2.13*	0.41	0.95	-1.56	1.88	5.19
FLL	26.55	27.29	-2.39*	27.39	28.36	-2.17*	21.08	32.64
TGPP	142.61	137.74	2.21*	144.84	141.94	1.12	149.89	167.12
FGPP	117.44	113.54	1.85	119.22	118.51	0.35	122.61	133.76
CGPP	25.17	24.2	0.77	25.63	23.33	2.18*	27.28	33.35
SFP	81.86	82.4	-0.63	82.03	83.59	-2.25*	79.17	79.04
GWPP	2.26	2.24	0.58	2.39	2.3	1.85	1.87	2.72
TW	1.81	1.86	-3.26**	1.92	1.96	-2.06	1.42	1.97
GYPP	15.14	14.19	1.63	16.49	17.07	-0.87	23.3	17.5
BM	27.41	24.09	4.34***	29.16	28.95	0.24	45.69	29.76
HI	0.53	0.56	-1.8	0.56	0.59	-2.23*	0.51	0.59
GL	7.14	7.34	-8.46***	7.13	7.33	-4.59***	7.03	6.78
GB	2.35	2.33	1.32	2.31	2.35	-1.96	2.11	2.45
LBR	3.06	3.19	-6.16***	3.13	3.15	-0.83	3.36	2.8

* Significant at 5 % ** Significant at 1 % *** Significant at 0.1 %

SC: Straight Cross (BPT 5204 × HPR-14); **RC:** Reciprocal Cross (HPR-14 × BPT 5204)

DF=50 % flowering	FLL= Flag leaf length (cm)	GYPP= Grain yield per plant (g)
PH= Plant height (cm)	TGPP= Total grains per panicle	BM= Biomass (g)
NT: Number of tillers	FGPP= Fertile grains per panicle	HI: harvest index (%)
NPT= Number of productive tillers	CGPP: Chaffy grains per panicle	GL= Grain length (cm)
DM= Days to maturity	SFP: Seed fertility percentage	GB= Grain breadth (cm)
PL= Panicle length(cm)	GWPP= Grain weight per panicle (g)	LBR: L/B ratio of paddy grain
PE= Panicle exertion (cm)	TW= Test weight (g)	

Table 3: Estimates of components of quantitative traits' variability in straight and reciprocal crosses in F₂ & F₃ populations of rice

Traits	Generation	Range		Phenotypic coefficient of variation (%)		Genotypic coefficient of variation (%)		Heritability % (broad sense)		Expected genetic advance over mean	
		SC	RC	SC	RC	SC	RC	SC	RC	SC	RC
DF (days)	F ₂	78-136	77-136	14.60	13.46	12.20	10.30	69.90	58.60	21.01	16.24
	F ₃	74.60-122.80	80.40-117.33	10.55	11.81	10.07	10.99	91.10	86.70	19.50	21.07
PH (cm)	F ₂	51-136	50-128	16.32	16.54	8.74	16.26	70.81	72.29	23.82	24.22
	F ₃	55.20-121.00	64.50-127.50	11.68	12.78	4.09	5.19	52.30	56.07	12.59	14.77
NT	F ₂	4-37	3-32	44.55	43.12	36.88	33.45	68.60	60.20	62.91	53.46
	F ₃	7.20-27.20	9.60-24.20	34.95	29.05	27.34	19.24	61.20	43.90	44.04	26.25
NPT	F ₂	2-36	1-29	49.15	46.89	46.13	43.53	88.10	86.20	89.17	83.27
	F ₃	4.40-24.40	6.80-21.40	35.08	25.20	32.05	22.41	83.50	79.10	60.34	41.05
DM (days)	F ₂	108-167	109-167	9.49	8.03	9.31	7.85	96.20	95.60	18.82	15.82
	F ₃	96.20-152.40	93.25-148.60	7.77	5.89	7.62	5.76	96.20	95.80	15.40	11.62
PL (cm)	F ₂	12.60-27	9.5-21	19.66	44.61	10.10	41.92	26.40	88.30	10.69	81.15
	F ₃	16.00-38.60	14.82-22.67	18.22	14.68	9.95	5.79	29.80	15.60	11.20	4.70
PE (cm)	F ₂	-9.6 -10.00	-9.0 -12.0	2812.13	561.54	2751.86	501.27	69.79	65.87	4043.47	99.07
	F ₃	-8.04-6.00	-6.90-10.30	325.66	793.12	265.39	732.85	53.77	57.95	360.73	946.85
FLL (cm)	F ₂	10.00-43.00	14.70-45.0	20.82	19.36	19.52	18.34	87.90	89.70	37.69	35.78
	F ₃	16.40-39.50	17.10-43.04	17.14	17.13	15.89	15.42	86.00	81.12	30.36	28.60
TGPP	F ₂	40-268	30-263	24.49	25.29	24.44	25.24	99.60	99.60	50.25	51.89
	F ₃	57.20-213.00	71.00-219.40	19.59	18.83	19.54	18.78	99.50	99.45	40.15	38.58
FGPP	F ₂	6-236	4-200	30.02	29.30	29.59	28.84	97.20	96.90	60.11	58.47
	F ₃	38.40-192.80	52.60-193.40	22.72	20.18	22.28	19.71	96.20	95.36	45.00	39.64
CGPP	F ₂	0-133	0-145	68.65	82.70	24.13	38.19	39.35	54.82	55.64	93.40
	F ₃	10.50-62.40	6.25-70.20	43.01	55.79	38.05	51.83	78.30	86.30	69.36	99.19
SFP (%)	F ₂	6.90-100	6.06-100	16.17	17.47	15.40	16.64	90.70	90.70	30.21	32.65
	F ₃	60.46-93.63	54.77-94.26	19.06	16.16	18.73	15.67	96.60	94.03	37.93	31.30
GWPP (g)	F ₂	0.20-25	0.20-5.30	155.8	163.74	29.00	27.97	3.50	2.90	11.12	9.84
	F ₃	1.08-3.96	0.96-3.44	164.95	153.36	20.53	31.19	1.50	4.14	5.26	13.07
TW (g)	F ₂	0.39-3.20	0.89-3.08	24.72	23.45	15.39	15.57	38.80	44.00	19.75	21.28
	F ₃	1.42-2.50	1.42-2.94	15.97	22.63	9.45	10.89	35.00	23.17	11.51	10.80
GYPP (g)	F ₂	0.40-60.60	0.20-41.50	65.88	59.62	28.77	22.51	41.91	19.21	56.87	23.59
	F ₃	6.33-35.46	7.94-37.66	37.11	43.16	3.89	6.05	44.15	14.02	33.75	12.46
BM (g)	F ₂	5.17-105.50	3.60-76.60	49.70	46.24	48.34	44.64	94.6	93.2	96.86	88.79
	F ₃	12.15-67.55	14.68-54.36	30.76	36.79	3.08	6.02	52.90	18.40	33.53	13.95
HI (%)	F ₂	0.05-0.99	0.01-0.98	52.43	33.99	32.50	14.06	85.13	67.93	91.95	47.56
	F ₃	0.27-0.88	0.38-0.91	19.93	20.71	3.10	0.78	16.50	13.50	6.78	5.76
GL (cm)	F ₂	5.60-9.0	6.0-8.90	6.49	6.02	1.01	0.53	33.36	27.29	4.46	3.38
	F ₃	5.94-8.46	6.36-8.30	5.54	13.33	5.43	13.30	96.03	99.63	10.95	27.35
GB (cm)	F ₂	1.20-3.10	1.90-3.30	29.92	30.14	9.79	10.69	10.70	12.60	6.60	7.81
	F ₃	1.60-2.92	1.90-2.98	28.11	42.79	8.86	7.73	9.94	3.26	5.75	2.88
L/B ratio	F ₂	2.0-6.0	2.32-4.10	14.29	14.49	11.13	11.12	60.60	58.80	17.85	17.56
	F ₃	2.13-4.30	2.44-3.69	12.95	20.03	10.11	19.21	60.92	92.02	16.25	37.96

Table 4: Test for normality for growth and yield related traits in F₂ and F₃ populations of straight and reciprocal crosses of rice

Traits	Shapiro Wilk's test for normality															
	F ₂								F ₃							
	SC				RC				SC				RC			
	W	P<W	Skewness	Kurtosis	W	P<W	Skewness	Kurtosis	W	P<W	Skewness	Kurtosis	W	P<W	Skewness	Kurtosis
DF	0.9244	<0.0001	0.83	0.38	0.8826	<0.0001	1.24	1.28	0.9308	<0.0001	0.87	0.34	0.9091	<0.0001	1.01	0.56
PH	0.9702	<0.0001	-0.32	-0.38	0.9706	<0.0001	-0.48	-0.22	0.9556	<0.0001	-0.72	0.29	0.9815	0.0099	-0.43	0.39
NT	0.9596	<0.0001	0.79	0.71	0.9850	<0.0001	0.34	-0.18	0.9782	0.0033	0.46	-0.05	0.9823	0.0128	0.34	-0.35
NPT	0.9540	<0.0001	0.84	0.76	0.9845	<0.0001	0.36	-0.03	0.9840	0.0226	0.39	-0.13	0.9789	0.0042	0.46	-0.05
DM	0.9303	<0.0001	0.79	0.30	0.8894	<0.0001	1.24	1.35	0.9336	<0.0001	0.73	0.56	0.8943	<0.0001	0.43	2.59
PL	0.9904	<0.0001	-0.27	0.69	0.1382	<0.0001	-0.79	2.70	0.6874	<0.0001	4.52	36.67	0.9398	<0.0001	-1.09	3.34
PE	0.9171	<0.0001	-0.70	-0.10	0.9227	<0.0001	-0.77	-0.04	0.8699	<0.0001	-1.02	0.01	0.9000	<0.0001	-0.85	0.52
FLL	0.9827	<0.0001	0.44	0.15	0.9914	<0.0001	0.34	0.15	0.9901	0.1877	0.24	-0.20	0.9728	0.0006	0.33	0.79
TGPP	0.9945	0.0586	0.18	0.29	0.9947	0.0611	0.12	0.55	0.9949	0.7293	0.05	-0.16	0.9884	0.1029	0.21	0.08
FGPP	0.9953	0.1166	0.03	0.46	0.9935	0.0220	-0.25	0.26	0.9936	0.5367	0.18	0.27	0.9942	0.6325	0.16	0.32
CGPP	0.8911	<0.0001	1.62	4.81	0.8568	<0.0001	1.71	4.39	0.9228	<0.0001	1.16	1.77	0.8894	<0.0001	1.52	3.23
SFP	0.8810	<0.0001	-1.67	4.58	0.8741	<0.0001	-1.57	3.59	0.9466	<0.0001	-0.92	0.83	0.9101	<0.0001	-1.31	2.33
GWPP	0.9887	0.0005	-0.07	0.89	0.9870	0.0001	-0.09	1.01	0.9872	0.0672	0.26	-0.24	0.9858	0.0423	0.14	-0.01
TW	0.9635	<0.0001	-0.40	2.64	0.8704	<0.0001	0.37	2.92	0.9955	0.8191	-0.01	-0.09	0.9700	0.0003	0.66	2.12
GYPP	0.9233	<0.0001	1.15	1.75	0.9587	<0.0001	0.74	0.39	0.9437	<0.0001	0.63	-0.35	0.9366	<0.0001	0.92	0.60
BM	0.9238	<0.0001	1.26	2.77	0.9426	<0.0001	1.08	2.42	0.9548	<0.0001	0.74	0.26	0.9529	<0.0001	0.82	0.48
HI	0.5719	<0.0001	-0.42	-0.36	0.9769	<0.0001	-0.51	-0.17	0.9879	0.0857	0.10	-0.53	0.9900	0.1802	0.27	-0.29
GL	0.9832	<0.0001	0.21	0.59	0.9823	<0.0001	-0.17	0.41	0.9764	0.0019	0.50	1.15	0.9915	0.2940	-0.04	-0.21
GB	0.9563	<0.0001	0.37	1.35	0.9407	<0.0001	0.66	0.13	0.9768	0.0022	0.31	0.55	0.9256	<0.0001	1.17	2.41
LBR	0.9317	<0.0001	1.35	10.54	0.9894	0.0007	-0.04	-0.59	0.9802	0.0064	-0.13	1.33	0.9864	0.0513	-0.34	-0.15

Table 5: Quantitatively top performing F₃ families derived from straight cross of rice for yield and yield attributing characters

Rank	F ₃ Family	DF	PH	NPT	DM	PL	PE	FLL	FGPP	SFP	GWPP	TW	GYPP	BM	HI	GL	GB	LBR
1	15	122.80	70.60	20.80	149.60	19.84	-4.60	23.30	134.40	79.89	3.02	2.22	32.68	46.37	0.70	7.18	1.60	4.30
2	21	86.40	91.10	21.60	117.20	21.80	0.72	31.80	117.40	87.55	2.40	1.94	29.17	50.10	0.58	7.34	2.18	3.39
3	22	120.00	101.60	19.40	150.40	20.20	0.50	20.46	118.80	87.83	1.66	1.64	31.69	53.34	0.60	6.90	2.02	3.43
4	38	99.80	91.60	17.60	130.80	19.50	2.08	33.80	171.20	83.49	2.62	1.86	27.54	40.26	0.68	6.54	2.40	2.75
5	41	91.20	93.30	18.20	122.00	19.90	0.82	31.66	143.20	84.55	3.16	1.98	27.07	36.74	0.74	7.14	2.32	3.09
6	55	85.40	95.80	17.60	116.00	20.06	1.22	30.10	147.60	84.28	3.20	2.26	28.57	35.62	0.80	7.04	2.46	2.89
7	79	105.60	104.40	21.20	134.40	20.90	2.20	22.70	148.20	82.65	3.10	2.04	28.31	54.87	0.52	6.88	2.10	3.29
8	81	88.60	105.00	16.20	119.80	21.96	1.98	32.40	162.60	89.79	3.14	1.88	27.11	38.88	0.70	7.28	2.26	3.24
9	109	108.80	84.00	18.00	139.20	19.00	-5.68	30.00	143.60	74.25	2.52	2.12	32.84	40.82	0.81	6.40	2.32	2.76
10	118	96.20	93.50	12.00	126.80	18.90	0.02	23.10	125.40	86.43	2.46	2.20	32.86	48.29	0.68	7.40	2.56	2.92
11	153	88.60	104.60	16.20	119.00	21.16	0.66	34.70	143.80	86.39	2.86	2.08	27.00	60.36	0.45	7.48	2.40	3.16
12	171	104.00	106.50	11.00	135.00	22.00	3.07	31.67	151.33	86.75	3.40	2.50	34.21	46.22	0.74	7.13	2.80	2.56
13	182	100.25	105.00	19.75	131.00	20.88	2.13	28.38	148.50	83.82	3.13	1.93	35.05	46.69	0.75	7.63	2.73	2.81
14	193	98.60	102.30	16.00	129.20	22.90	2.76	21.10	192.80	91.60	3.06	1.74	29.75	38.40	0.77	6.78	2.58	2.71
15	207	98.60	102.20	17.40	130.40	21.90	4.34	33.36	120.20	84.48	2.28	2.14	28.48	40.10	0.71	7.28	2.56	2.86
16	293	93.00	97.10	17.80	124.00	20.30	2.24	26.40	147.80	82.19	3.32	2.00	27.69	36.38	0.76	6.98	2.12	3.31
17	295	104.60	112.00	24.40	135.40	20.36	3.90	26.98	108.80	82.66	2.06	1.78	35.46	55.08	0.64	6.96	2.18	3.21
18	318	103.60	110.00	17.60	133.80	21.50	3.44	36.30	162.40	87.52	3.02	1.92	27.33	42.20	0.65	6.72	2.60	2.61
19	324	103.00	112.00	15.40	133.20	21.90	4.60	37.10	192.40	93.63	3.96	2.10	34.92	67.55	0.52	6.90	2.80	2.47
20	387	96.33	112.33	16.67	127.00	24.17	2.67	39.50	160.67	83.40	3.50	1.87	31.78	38.07	0.84	7.00	2.17	3.24
Parents	BPT-5204	104.06	97.75	12.06	133.44	19.97	1.88	21.08	122.61	79.17	1.87	1.42	23.30	37.23	0.46	7.03	2.11	3.36
	HPR-14	101.94	107.41	7.88	131.71	22.32	5.19	32.64	133.76	79.04	2.72	1.97	17.50	33.73	0.59	6.78	2.45	2.80

Table 6: Quantitatively top performing F₃ families derived from reciprocal cross of rice for yield and yield attributing characters

Rank	F ₃ Family	DF	PH	NPT	DM	PL	PE	FLL	FGPP	SFP	GWPP	TW	GYPP	BM	HI	GL	GB	L/B
1	60	99.80	105.80	13.20	130.20	20.64	3.84	32.40	161.60	87.19	2.98	1.88	32.32	51.80	0.62	7.30	2.34	3.14
2	87	86.33	98.00	11.33	117.67	21.67	0.57	29.00	119.67	87.00	2.83	2.50	24.77	27.33	0.91	7.43	2.30	3.23
3	113	114.00	105.75	16.00	145.50	20.38	2.68	26.25	122.00	80.88	2.20	1.79	26.01	40.66	0.64	7.40	2.25	3.31
4	122	98.20	110.40	14.60	128.80	18.90	0.72	24.00	149.80	87.52	3.44	2.58	32.17	42.83	0.75	7.54	2.22	3.41
5	170	95.40	90.20	15.80	126.80	20.00	1.36	28.16	115.80	88.53	2.32	2.08	29.42	43.73	0.67	7.32	2.26	3.26
6	208	105.80	98.60	14.00	136.40	20.48	2.04	30.94	184.40	89.68	3.38	2.00	32.01	44.48	0.72	7.60	2.38	3.19
7	248	90.20	108.60	15.60	121.80	20.68	-0.58	32.30	155.00	91.30	3.28	2.30	32.52	52.62	0.62	7.50	2.38	3.18
8	249	102.60	111.60	15.00	134.80	22.14	3.74	38.26	193.40	88.26	3.16	1.74	28.06	50.97	0.55	7.00	2.26	3.12
9	255	94.20	109.80	18.00	125.40	20.50	0.70	29.20	141.60	80.46	3.04	1.78	37.66	47.61	0.79	6.90	2.50	2.79
10	256	97.00	103.20	13.40	128.20	21.40	1.54	29.88	160.80	85.99	3.28	1.90	27.49	41.03	0.67	7.44	2.32	3.21
11	290	101.40	91.40	15.20	132.60	20.50	1.48	21.72	134.80	85.34	2.18	1.68	26.54	39.06	0.68	7.22	2.22	3.27
12	291	90.80	96.80	16.20	122.40	20.95	1.40	31.84	121.40	87.57	2.60	2.14	29.17	42.25	0.69	7.72	2.44	3.20
13	311	91.40	110.40	15.20	123.80	21.04	3.80	31.96	124.80	85.06	2.34	1.92	25.47	49.00	0.52	7.38	2.30	3.23
14	320	90.60	99.00	21.40	123.00	21.90	2.28	34.10	135.80	89.48	3.02	1.94	31.68	50.79	0.62	6.38	2.36	2.72
15	322	94.40	76.40	18.60	126.00	19.36	-3.80	21.12	104.40	87.98	1.90	1.80	24.42	36.95	0.66	8.04	2.32	3.49
16	383	89.40	93.00	16.00	121.60	19.20	3.12	27.50	129.60	88.94	2.66	2.06	28.58	40.38	0.71	7.32	2.28	3.24
17	398	96.00	63.00	13.75	127.75	20.00	-2.38	30.75	125.25	78.70	2.53	1.90	26.29	34.24	0.77	7.88	2.20	3.60
18	423	102.60	100.80	13.60	135.60	20.34	3.56	24.90	140.60	84.62	2.62	1.60	24.42	34.01	0.72	7.04	2.28	3.11
19	434	94.00	101.40	14.40	125.00	20.20	1.42	31.80	132.80	87.96	3.02	2.10	28.51	54.36	0.52	7.76	2.40	3.29
20	481	93.40	97.10	15.60	124.20	19.70	1.12	30.80	120.00	89.75	2.42	2.06	30.77	44.61	0.69	7.18	2.38	3.03
Parents	BPT-5204	104.06	97.75	12.06	133.44	19.97	1.88	21.08	122.61	79.17	1.87	1.42	23.30	37.23	0.46	7.03	2.11	3.36
	HPR-14	101.94	107.41	7.88	131.71	22.32	5.19	32.64	133.76	79.04	2.72	1.97	17.50	33.73	0.59	6.78	2.45	2.80

DF=50 % flowering

PH= Plant height (cm)

NPT= Number of productive tillers

DM= Days to maturity

PL= Panicle length(cm)

PE= Panicle exsertion (cm)

FLL= Flag leaf length (cm)

FGPP= Fertile grains per panicle

SFP: Seed fertility percentage

GWPP= Grain weight per panicle (g)

TW= Test weight (g)

GYPP= Grain yield per plant (g)

BM= Biomass (g)

HI: harvest index (%)

GL= Grain length (cm)

GB= Grain breadth (cm)

LBR: L/B ratio of paddy grain

Table 7: Best F₃ families derived from straight and reciprocal cross for grain yield

Sl. No.	Straight cross			Reciprocal cross		
	F ₃ family identity	Grain yield per plant (g)	% gain over BPT-5204	F ₃ family identity	Grain yield per plant (g)	% gain over BPT-5204
1	295	35.46	52.18	255	37.66	61.63
2	182	35.05	50.43	248	32.52	39.57
3	324	34.92	49.87	60	32.32	38.71
4	171	34.21	46.82	122	32.17	38.07
5	118	32.86	41.03	208	32.01	37.38
Parents	BPT 5204	23.30		BPT 5204	23.30	
	HPR-14	17.50		HPR-14	17.50	

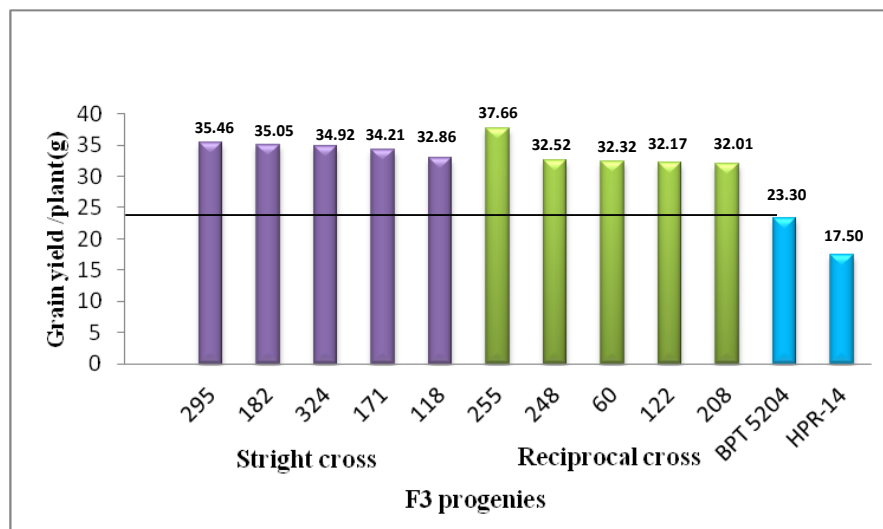


Fig. 1: Grain yield performance of best F₃ families derived from stright & reciprocal crosses