Genetic Analysis and Characterization of Inter-subspecific Cross Derived Genotypes for Yield and Quality Traits in Rice

THESIS

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In partial fulfilment of the requirement for the Degree of

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In

AGRICULTURE

(Genetics and Plant Breeding)

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2015

CERTIFICATE- I

This is to certify that the thesis entitled ***"Genetic Analysis and Characterization of Inter-subspecific Cross Derived Genotypes for Yield and Quality Traits in Rice"*** *submitted in partial fulfillment of the requirement for the degree of* ***MASTER OF SCIENCE (Ag.) in (Genetics and Plant Breeding)*** *of Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur is a record of the bonafide research work carried out by Ms. Ruchika Mishra under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of Instruction.*

All the assistance and help received during the course of the investigation has been acknowledged by her.

Dr. G.K. Koutu
Chairman of Advisory Committee

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This is to certify that the thesis entitled ***"Genetic Analysis and Characterization of Inter-subspecific Cross Derived Genotypes for Yield and Quality Traits in Rice"*** *submitted by Ms. Ruchika Mishra to the Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, in partial fulfillment of the requirement for the degree of Master of Science in* ***Agriculture*** *in the Department of* ***Plant Breeding and Genetics, JNKVV, Jabalpur,*** *after evaluation has been approved by the Student's Advisory Committee and the External Examiner and by the student's Advisory Committee after an oral examination on the same.*

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Place : Jabalpur

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CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF ABBREVIATIONS

Amyl	Amylose
ASV	Alkali spreading value
BY/Pl	Biological yield per plant
DFF	Days to 50 % flowering
DSL	Decorticated seed length
DSW	Decorticated seed width
DTM	Days to maturity
FSp/Pa	Fertile spikelets per panicle
FLL	Flag Leaf Length
FLW	Flag Leaf Width
GL	Grain length
GT	Gelatinization temperature
GW	Grain width
GYld	Grain yield per plant
H%	Hulling per cent
HI	Harvest index
HRR	Head Rice Recovery
LB Ratio	Length Breadth ratio
M%	Milling percent
No.Sp/ Pa	Number of spikelets per panicle
Pa/Pl	Panicle number per plant
PaWt/Pl	Panicle weight per plant
PCA	Principal Component Analysis
PH	Plant height
PI	Plant index
PL	Panicle length
PT/P	Productive tillers per plant
SD	Spikelet density
SF	Spikelet fertility per cent
SL	Stem length
SSp/Pa	Sterile spikelet per panicle
ST	Stem thickness
TT/P	Total tillers per plant
TGW	1000 grain weight

%	:	Percentage
±	:	Plus or minus
√	:	Square root
Σ	:	Summation
^{0}C	:	Celsius
^{0}	:	Degree
µl	:	Micro liter
CD	:	Critical Difference
et al.,	:	And others
g	:	Gram
df	:	Degree of freedom
i.e.,	:	That is
N	:	Nitrogen
NaCl	:	Sodium chloride
NaOH	:	Sodium Hydroxide
P_2O_5	:	Phosphorus
K_2O	:	Potassium
x^{-1}	:	Per
e.g.	:	Example
M.P.	:	Madhya Pradesh
G X E	:	Genotype and environment interaction
Hrs: min	:	Hours and Minute
Max.	:	Maximum
Min.	:	Minimum
mm	:	Millimeter
cm	:	Centimeter
ml	:	Milliliter
No.	:	Number
CMS	:	Cytoplasmic Male Sterile
SD	:	Standard Deviation
SE	:	Standard Error
viz;	:	Namely
h^2_b	:	Broad sense heritability

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This is to certify that Ms. Ruchika Mishra has prepared the thesis entitled "Genetic Analysis and Characterization of Inter-subspecific Cross Derived Genotypes for Yield and Quality Traits in Rice" as per the specification given in "Guidelines for Thesis Preparation" prescribed by the Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur.

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INTRODUCTION

Rice is a cereal crop, belongs to genus *Oryza* of Poaceae family. The genus *Oryza* has twenty two wild and two cultivated species namely; *Oryza sativa* and *Oryza glaberrima*, representing 10 genomic types (AA, BB, CC, BBCC, CCDD, EE, FF, GG, HHJJ and HHKK) (Brar and Khus, 1986). All the germplasm found in Asia, America and Europe belongs to *Oryza sativa,* and while in West Africa belongs to *Oryza glaberrima*. *Oryza sativa* is a cultivated diploid species having 24 chromosomes. The *sativa* rice germplasm of the world are commonly divided into three sub-species i.e. *Indica, Japonica* and *Javanica.* Rice is a short day self-pollinated crop, needs a hot humid climate with an average temperature of 21 to 37^0C throughout the life period of the crop *(Oryza sativa* L*)*. It is an extensively consumed cereal crop that serves as a major source of carbohydrate in human diet.

Rice is grown, particularly in India with a wide range of agro climatic situations, from high altitude Himalayan valleys to the tropical coastal areas of Kerala. There is a wide spectrum of varieties cultivated with differential response to climatic factors such as highlands, valleys and lowlands. The principal systems of rice cultivation followed in India are dry, semidry and wet. However, wet system is commonly followed and is most productive. This is practiced in areas of adequate water supply either by rainfall or irrigation. Dry and semidry system of cultivation are mainly confined to tracts which depend on rain and do not have supplementary irrigation facilities and grown under conditions where water does not impound in the field particularly in upland situation. It is cultivated in 114 countries, over an area of 161.4 million ha with the production of 466.7 million tons, approximately 90 per cent of the world's rice is grown in Asia continent and constitutes a staple food of 2.7 billion people worldwide.

Among the rice growing countries, India ranks first in the world in area of rice cultivation with 43.97 million ha and second in production with 104.32 million tonns (Anonymous 2013). In order to improve the productivity level, a breakthrough is required by way of increasing the productivity of new varieties and by increasing the biological efficiency through hybridization programme.

Perhaps there is no other single crop possessing an enormous variation as in rice. Varietal and cultural diversity in rice is enormous and its improvement is therefore a challenging task.

Enhancing crop yield is one of the top most priorities in crop breeding programmes. In the past half century, rice yield has benefitted from two major genetic improvements: improved harvest index and plant architecture through use of semi-dwarf genes, and production of hybrids that exploit heterosis. Results have indicated that an effective way to develop super rice lines first in developing the new plant type and strong vigor by crossing *indica* with *japonica* subspecies, and then consolidating the two advantages by optimizing the combination of desirable traits via multiple crossing and backcrossing (Cheng et al. 2001).

Characterization is the most basic and important step in the process of evaluation and cataloguing of germplasm. It is essential for its evaluation, judicious use and protection against illegal utilization. Generally germplasm accessions are evaluated for morphological, physiological, biochemical, plant pathological, entomological and other features. Characterization of several agro-morphological traits is helpful in tracing correlation and linkages between different traits. The characters assessed must be related to the need of the breeders for its proper utilization in breeding programmes.

Yield of paddy is a complex quantitative character controlled by many genes interacting with the environment and is the product of many factors called yield components. Selection of parents based on yield alone is often misleading. Hence, the knowledge about relationship between yield and its contributing characters is needed for an efficient selection strategy for the plant breeders to evolve an economic variety. The nature and relationship between yield and its component traits and also among yield components seem to provide information, which would be of greater value at the time of practicing selection for improving yield. Correlation studies provide better understanding of yield components. For fixation of the characters that are contributing towards yield, the knowledge regarding relative contribution of individual trait to yield is very

important and this can be accomplished by partitioning the correlation coefficient into direct and indirect effects. The quantitative traits are under polygenic control and are considerably influenced by an environment to which the individual is exposed. Simple correlation studies do not provide adequate information about the contribution of each factor towards yield. Therefore, the technique of path-coefficient analysis is utilized to have an idea of the magnitude of contribution of a trait on yield, directly as well as indirectly via other traits.

Besides yield, quality traits are also very important. The desired quality traits may vary from one ethnic group or geographical region to another and may also vary from country to country. The quality in rice therefore, may be considered from viewpoint of milling efficiency, grain size, shape, appearance and cooking characteristics. As countries, reach self-sufficiency in rice production, the demand by the consumer for better quality rice has increased. Traditionally, plant breeders concentrated on breeding for high yield and pest resistance. Recently the trend has changed to incorporate preferred quality characteristics that increase the total economic value of rice. The grain quality is not just dependent on the variety of rice, but also depends on the crop production environment, harvesting, processing and milling system. Thus, the grain quality can be improved genetically through the improvement of grain quality components (Khan et al., 2009).

Molecular marker is a new approach based on DNA polymorphism among tested genotypes, and thus, applicable to biological research. Molecular markers are valuable as genetic markers because, they cover whole genome with random distribution throughout the genome and, therefore, are much larger in quantity. SSRs are the most promising molecular marker because PCR based methods are readily automated and require a small amount of DNA and facilitate many QTL mapping studies in crop plants. QTLs affecting a wide range of traits in rice have been identified and mapped. (Yang et al., 2006; You et al., 2006). In rice, it has been observed that derivatives of *indica* x *japonica* crosses have higher yield vigor than either *indica* x *indica* or *japonica* x *japonica* derivatives. Therefore identifying the chromosomal locations influencing yield and yield related traits in inter-sub specific derivatives is useful for rice improvement. Exploitation of inter sub-specific *indica* x *japonica* diversity is conceptualized as

New Plant Type and utilized in pedigree breeding, has been suggested as a possible means for breaking genetic ceiling to yield in rice(Khush, 2000).

In rice first generation New Plant Type (NPT) was having low tillering capacity with few unproductive tillers, sturdy stems, erect leaves, a vigorous root system and increased harvest index (Peng et al., 1994). In 1995, development of second generation NPT lines was initiated by crossing first generation tropical *japonica* NPT lines with elite *indica* parents, to increase tillering capacity and to improve biomass production. Genes from *indica* parents have effectively reduced panicle size and increased tillering capacity and also improved other NPT attributes such as grain quality, disease and insect resistance. (Peng et al., 2004). The high heterosis level for yield in *indica*/tropical *japonica* crosses seems to be promising and prospects for large scale adoption of this technology in India appears to be bright. Jawaharlal Nehru Kirshi Vishwa Vidyalaya have also developed New Plant Types i.e. Jawahar New Plant Type (JNPT) of rice by crossing *indica* with tropical *japonica.*

In the light of above information, the present study was initiated to obtain the precise information on the “Genetic Analysis and Characterization of Inter-subspecific Cross Derived Genotypes for Yield and Quality Traits in Rice”. To achieve such goals the investigation was conducted with the following objectives:

- To characterize the JNPT lines based on morphological and quality traits.
- To estimate genetic variability among yield, yield components and quality traits.
- To assess character association among all the traits.
- To estimate direct and indirect effects of traits under study on seed yield.
- To rank the genotypes based on principle component analysis for combination of phenotypic traits.
- To validate the reported SSR markers on selected rice lines for yield related traits.

REVIEW OF LITERATURE

The present investigation entitled “Genetic analysis and Characterization of Inter-subspecific Cross Derived Genotypes for Yield and Quality Traits in Rice” was carried out during the Kharif season of 2014.The review of the work done earlier is reviewed here at two major levels:

(A) Field level

(B) Molecular level

The nature and extent of genetic variability present in the population is the basic requirement for any crop improvement programme. The large spectrum of genetic variability in segregating populations depends on the level of genetic diversity present among genotypes which offers better scope for selection. Success of any crop improvement programme through recombination breeding depends largely on genetic constitution of parent and important pattern of the traits. The development of a new variety in any crop species mainly depends on the availability of genetic variability which is of great interest to the plant breeder as it plays a vital role in planning a successful breeding programmes.

(A) Field level

2.1 Characterization

Germplasm provides the base material for crop improvement. A need for germplasm collection, evaluation and cataloguing is of utmost importance to have a dynamic crop improvement programme. Characterization of cultivars is based on different agro-morphological traits which is the most important step in the genetic improvement of varieties.

Motiramani et al. (2001) characterized 480 accessions of early duration rice germplasm of Madhya Pradesh and Chhattisgarh for 15 morphological and 12 quantitative characters. A good amount of variation was observed for all the characters studied.

Rao et al. (2001) studied 123 native cultivars and landraces from Bastar region for 11 morphological and 9 agronomic traits. A majority of

cultivars were found to possess green basal leaf sheath (65%), green leaf blade (38%), light green auricle (59%), straw coloured apiculus (57%), white stigma (57%), panicle exertion (79%) and open type of panicle, however horizontal flag leaf are other traits that were encountered in majority of cultivars.

Sharma (2013) studied 120 NPT lines from JNKVV, Jabalpur. Majority of the NPT lines had medium culm length (100 cm or more), greater culm diameter, lower relative internodes elongation, short erect leaves of medium width, high tillering capacity and panicles were bunchy.

Sajid et al. (2015) studied 30 accessions of indigenous rice germplasm. Variation was observed for all the qualitative traits except anther color and ligule shape. Highly significant differences ($p<0.01$) were observed for the traits of flag leaf length, flag leaf breadth, culm length, days to 50% flowering, panicle length, length of primary branches panicle^{-1}, secondary branches panicle^{-1}, grain length, grain width, awn length and percent leaf lession while significant differences ($p<0.05$) were observed for peduncle length and primary branches panicle^{-1}. Rice accession 6531 took minimum days (95) in reaching to 50% flowering while accession 6512 displayed maximum panicle length (35.37 cm). Rice accession 6508 showed the highest values for flag leaf length (59.95 cm), primary branches panicle^{-1} (13), secondary branches panicle^{-1} (51), spikelets panicle^{-1} (240), and grain width (3.06 mm). The genetic potential of accessions 6508, 6547, 6512 and 6531 on account of excellent performance for various traits can be used in future rice breeding programs.

2.2 Genetic variability

The 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.

Verma et al. (2000) reported magnitude of genotypic and phenotypic coefficients of variation for sterile spikelets panicle^{-1}, grain yield plant^{-1}, biological yield plant^{-1} and productive tillers plant^{-1}. While, Islam et al. (2002) observed variances due to environments who's genotypic environment

interaction was highly significant. However, Mishra and Verma (2002) observed that, the phenotypic coefficient of variation was higher than the genotypic coefficient of variation. Kernel elongation ratio recorded the highest magnitude of genotypic coefficient of variation, followed by biological yield plant^{-1} and grain yield plant^{-1}.

Chakraborty et al. (2001) studied to access the genetic variability for eight morphological characters like days to 50% flowering, plant height, flag leaf length, flag leaf breadth, effective tillers per hill, panicle length, sterility percentage and grain yield per hill. Very small difference between GCV and PCV was observed for the characters like days to 50% flowering and flag leaf breadth. Wide difference between GCV and PCV was observed for the characters like plant height, flag leaf length, effective tillers per hill, panicle length, sterility percentage and yield per plant.

Nayak et al. (2002) obtained high estimates of genotypic and phenotypic coefficients of variation for number of panicles, spikelets panicle^{-1}, grains panicle^{-1} and grain yield plant^{-1}.

Chand et al. (2004) showed that all genotypes differed significantly with respect to plant height, number of tillers hill^{-1}, days to maturity, panicle length, filled grains panicle^{-1}, 1,000 seed weight, effective tillers plant^{-1}, grain length, grain breadth, and grain yield plant^{-1}. Genotypic and phenotypic coefficient of variation were high for grains panicle^{-1} and grain yield plant^{-1}.

Hasib et al. (2004) reported good correspondence between phenotypic and genotypic coefficient of variation in plant height, tillers plant^{-1}, panicle length, filled grains panicle^{-1}, grain length, 1000 seed weight and grain yield plant^{-1}. While (Sharma and Bhuyan, 2004) revealed highest genotypic as well as phenotypic coefficient of variation by the grains panicle^{-1}, followed by grain yield plant^{-1} and effective panicles plant^{-1}.

Saxena et al. (2005) reported high GCV and PCV for number of unfilled spikelets, seed yield per plant, biological yield per plant, number of filled spikelets, total number of spikelets and L/B ratio of rough rice.

Bhaskar (2006) observed low magnitudes of PCV and GCV for plant height, days to 50% flowering, grain length / width ratio, panicle length, 100 grain weight and panicle index.

Padmaja et al. (2008) revealed highly significant differences for all the characters except leaf width and 1,000 seed weight among the genotypes. The estimates of genotypic and phenotypic coefficients of variation were high for all the characters except days to fifty per cent flowering and panicle length.

Sabu et al. (2009) reported highest variability for grains panicle^{1}. The coefficient of variation over seasons was moderate to high for the progenies for all traits except panicle length and 1,000 seed weight.

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

Selvaraj et al. (2011) revealed considerable variability among genotypes for characters like, plant height, number of tiller, number of productive tillers, panicle length, and filled grain per panicle and test weight.

Tiwari et al. (2011) reported high estimates of genotypic coefficient of variation for grain yield per hill, spikelets per panicle, plant height, flag leaf width and number of tillers per hill.

Singh et al. (2012) investigated twenty-five rice (*Oryza sativa* L.) genotypes. The analysis of variance showed highly significant differences among genotypes for all the quantitative traits studied except flag leaf width, while physical and cooking quality traits showed significant differences only for hulling percentage, milling percentage and head rice recovery. High GCV and PCV were recorded for number of spikelets per panicle, number of productive tillers per hill and grain yield per hill.

Khan et al. (2012) evaluated forty rice genotypes on the basis of various morphological traits in a field experiment. They found significant variation for all the traits studied among the genotypes. The results indicated

that the highest genetic variability was observed in plant height followed by spikelets per panicle, panicle length, days to heading and days to maturity.

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

Singh et al. (2013) evaluated that ample amount of genetic variability was observed for the characters, plant height, tillers/plant, kernel length, kernel breath and L/B ratio.

2.3 Heritability

Heritability in broad sense refers to the ratio of genotypic variance to the total phenotypic variance. The estimates of heritability help the plant breeders in selection of elite genotypes from diverse genetic population and also a good index of the transmission of characters from parents to their offspring. Brief reviews of heritability for different characters by various workers are as under.

High heritability for grain yield plant^{-1} was reported by Durai et al. (2001), Mishra and Verma (2002), Elayaraja et al. (2004), Madhavilatha et al. (2005), Girish et al. (2006), Kole et al. (2008) and Selvaraj et al. (2011).

High heritability for number of effective tillers plant^{-1} was reported by Mishra and Verma (2002), Narinder (2006), Bhagat (2007), Nandan et al. (2010) and Selvaraj et al. (2011).

High heritability for grain length and grain width was reported by Manna and Sasmal (2000). However high heritability was also reported for L/B ratio by Vanaja and Luckins (2006) and Nandan et al. (2010)

Thakur et al. (2000), Narinder (2006) and Abdul Fiyaz et al. (2011) observed high heritability for biological yield per plant. However, high heritability for sterility % and spikelet density was elucidated by Mishra and Verma (2002) while, the same for days to maturity was reported by Narinder (2006).

High heritability for panicle length was observed by Mishra and Verma (2002), Hasib et al. (2004), Saxena et al. (2005), Ananthi et al. (2006),

Narinder (2006), for number of grains panicle^{-1} by Durai et al. (2001), Saxena et al. (2005), Narinder (2006), Bhagat (2007), Kole et al. (2008), Chandra et al. (2009) and Nandan et al. (2010). Similarly, high heritability for days to 50 % flowering was reported by Durai et al. (2001), Ananthi et al. (2006).

High heritability for 1000 grain weight was recorded by (Mishra and Verma, 2002), Narinder (2006), Kole et al. (2008), Nandan et al. (2010) and Abdul Fiyaz et al. (2011) while, the same for plant height was reported by Mishra and Verma (2002), Elayaraja et al. (2004), Girish et al. (2006), Narinder (2006), Kole et al. (2008), Chandra et al. (2009) and Selvaraj et al. (2011).

Saxena et al. (2005), Girish et al. (2006) and Abdul Fiyaz et al. (2011) reported high heritability for total number of spikelets per panicle.

Mishra and Verma, (2002), Hasib et al. (2004), Panwar (2005), Narinder (2006) and Bhagat (2007) reported high heritability for number of filled grains panicle^{-1}.

Mishra and Verma, (2002) and Hasib et al. (2004) reported high heritability for grain width.

The entire yield contributing characters showed high heritability was elucidated by Tyagi et al. (2004) and Narinder (2006).

High heritability for harvest index was observed by Elayaraja et al. (2004), Madhavilatha et al. (2005) and Girish et al. (2006) while Madhavilatha et al. (2005) reported high heritability for spikelet fertility %.

Selvaraj et al. (2011) reported high heritability coupled with high genetic advance and high genotypic variation for number of tillers, number of productive tillers per plant, plant height and grain yield per plant. The same was also reported by Tiwari et al. (2011) for flag leaf width, flag leaf length, spikelet per panicle and no. of tillers per hill.

Asfaliza et al. (2012) reported that Broad sense heritability for amylose had the lowest value. The grain length showed moderate value while grain width, length width ratio and head rice recovery were the highest. The narrow sense heritability for grain physical properties was higher than grain

chemical properties. The highest heritability was observed for length width ratio, head rice recovery, grain width and grain 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 breath before cooking and kernel length before cooking, while rest 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.

Dongre et al. (2014) found that high heritability coupled with high genetic advance was exhibited for characters viz., number of tillers/plant, number of filled grains/panicle, number of unfilled spikelets/panicle, number of spikelets/panicle, grain yield/plant, panicle index and harvest index in Japonica x Indica derived F10 RILs. Number of tiller/plant, culm height, plant height, biological yield/plant, panicle index and harvest index were positively correlated with grain yield and also had positive direct effect and therefore these traits should be given due importance while practicing selection, aimed for improvement of grain yield.

2.4 Genetic Advance

Genetic advance refers to the improvement in the genetic value of the selected single plants over the base population. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection from heritability alone.

Grain yield plant^{-1} recorded high genetic advance was reported by Mishra and Verma (2002), Agrawal (2003), Chand et al. (2004), Panwar (2005), Girish et al. (2006), Chandra et al. (2009), Nandan et al. (2010) and Selvaraj et al. (2011). However, Saleem et al. (2008) reported high genetic advance for characters *viz.,* spikelet density, flag leaf area and grain yield plant^{-1}.

High genetic advance for 1000 grain weight was reported by Rao (2000), Sinha et al. (2004), Nandan et al. (2010) and Abdul Fiyaz et al.

(2011). Similarly, high genetic advance observed for plant height was reported by Elayaraja et al. (2004), Saleem et al. (2008) and Selvaraj et al. (2011), for number of effective tillers plant^{-1} reported by Mishra and Verma (2002), Chaudhary et al. (2004), Girish et al. (2006), Nandan et al. (2010) and Selvaraj et al. (2011) and for number of tillers plant^{-1} reported by Kumari et al. (2003) and Girish et al. (2006).

Number of grains panicle^{-1} recorded high genetic advance was reported by Rao (2000), Agrawal (2003), Panwar (2005), Madhavilatha et al. (2005) and Chandra et al. (2009) while, the same for panicle weight plant^{-1} was reported by Thakur et al. (2000) and Chand et al. (2004).

Low genetic advance for days to 50 % flowering and panicle length were reported by Agrawal (2003), Chand et al. (2004) and Padmaja et al. (2008) while, low genetic advance for number of tillers plant^{-1} was reported by Agrawal (2003) and Chand et al. (2004). Number of grains panicle^{-1}, days to 50 % flowering and 1000 grain weight recorded low genetic advance was elucidated by Satyanarayana et al. (2005). However, Satyanarayana et al. (2005), Madhavilatha et al. (2005), and Chandra et al. (2009) recorded low genetic advance for spikelet fertility %.

High genetic advance for panicle length was reported by Chaudhary et al. (2004) and Hasib et al. (2004), for harvest index by Elayaraja et al. (2004) and Girish et al. (2006) and for number of filled grains panicle^{-1} by Hasib et al. (2004). High genetic advance for characters *viz.,* biological yield plant^{-1}, dry weight plant^{-1}, spikelet sterility %, number of filled grains panicle^{-1} and spikelet density were reported by Madhavilatha et al. (2005), Panwar (2005) and Chandra et al. (2009).

High genetic advance observed for grain length was reported by Chand et al. (2004) and Hasib et al. (2004), for biological yield plant^{-1} and harvest index by Chaudhary et al. (2004) and Saleem et al. (2008).

Ananthi et al. (2006) reported moderate genetic advance for days to 50 % flowering, panicle length and 1000 grain weight.

Madhavilatha et al. (2005) and Chandra et al. (2009) reported high genetic advance for harvest index, grain yield panicle^{-1} and number of filled grains panicle^{-1}.

Narinder (2006) reported high genetic advance for grain yield per plant, biological yield per plant, panicle weight per plant, number of tillers per plant, number of productive tillers per plant, panicle length, number of spikelets per plant and filled grain per panicle. However, low genetic advance was also reported for plant height, L/B ratio of grain, days to maturity, 1000 grain weight and days to maturity.

Saleem et al. (2008) reported highest genetic advance for biological yield per plant followed by plant height, flag leaf area, yield plant^{-1}, harvest index and panicle density.

Jayasudha and Sharma, (2010) reported high heritability coupled with high genetic advance for spikelet fertility % followed by days to 50% flowering and grain yield per plant. High heritability associated with high genetic advance indicate considerable potential in the development of high yielding varieties through selection of desirable plants in succeeding generations.

Akinwale et al. (2011) reported high to medium genetic advance for the number of grains per panicle, grain yield, panicle weight and the number of panicles per plant.

Sharma (2013) observed high genetic advance for culm length, total spikelet, biological yield per plant, spikelet density, 1000 seed weight, number of productive tillers, number of tillers and plant height.

Soni et al. (2013) reported that the highest estimates of h^2 coupled with GA in percent of mean was recorded for spikelets/panicle, plant height , L:B ratio, grains/panicle, biological yield/ plant, flag leaf area, days to 50% flowering, plant height which might be due to the additive nature of gene action hence, these traits will be reliable for effective selection.

2.5 Correlation coefficients

Correlations coefficient is a statistical measure used to measure the degree and direction of relationship between two or more variables. The association between two variables that can be directly observed is termed as phenotypic correlation. It includes both genotypic and environmental effects. The inherent or heritable association between two variables is known as genotypic or genetic correlation. In general, phenotypic correlation coefficients are higher in magnitude than genotypic correlation coefficients (Lal et al. 1983). Correlation studies provides better pathway for yield improvement during selection Robinson et al. (1951) and Johnson et al. (1955).

Rao (2000) reported that grain yield plant^{-1} was positively associated with panicles plant^{-1}, panicle length and number of grains panicle^{-1}.

Grain yield plant^{-1} was found to be positively associated with number of grains panicle^{-1}, panicle weight plant^{-1} and number of primary rachis. Significant inter correlation was noticed between grains panicle^{-1} and single panicle weight, leaf area index and single panicle weight, flag leaf length and leaf area index and leaf area index and flag leaf width. Selection for these traits will lead to increased yield reported by Bastian et al. (2000). Whereas Thakur et al. (2000) reported that panicle weight plant^{-1} contributed significantly and positively to grain yield plant^{-1}.

Tomar et al. (2000), Nayak et al. (2001) and Sabu et al. (2009) reported that grain yield plant^{-1} was positively associated with plant height, number of effective tillers plant^{-1}, panicle length, number of grains panicle^{-1}, harvest index, biological yield plant^{-1} and days to 50 % flowering. While, Islam et al. (2002) found that grain yield plant^{-1} was positively correlated with plant height and grain weight plant^{-1} and negatively correlated with days to 50 % flowering.

Rasheed et al. (2002) reported the positive association of plant height with grain yield plant^{-1}. Correlation of plant height with number of tillers plant^{-1} was positive as reported by Rasheed et al. (2002). Samo et al. (2002) reported that grain yield plant^{-1} showed positive correlation with plant height, 1000 grain weight, number of panicles plant^{-1}, panicle length and number of

tillers plant^{-1}. Chaudhary and Motiramani (2003) reported that grain yield plant^{-1} indicated significant positive correlation with number of effective tillers plant^{-1} and biological yield plant^{-1}. While, Chand et al. (2004) observed significant positive correlations of grain yield plant^{-1} with grains panicle^{-1} and grain length.

Souroush et al. *(*2004) observed that results of genotypic and phenotypic correlations indicated that panicle plant^{-1}, filled grains panicle^{-1}, panicle weight, days to fifty per cent flowering and maturity had positive correlation with yield.

Tyagi et al. (2004) reported that the characters *viz.,* number of effective tillers plant^{-1}, panicle length, days to 50 % flowering and 100 seed weight showed significant and positive association with grain yield plant^{-1}. Therefore, selection for these characters may be useful for developing improved varieties.

A positive and significant correlation between grain length and grain yield per plant was reported by Chand et al. (2004) while, the same between grain breadth and grain yield was reported by Girish et al*.* (2006).

Grain yield plant^{-1} was observed to be positively associated with days to 50 % flowering, plant height, number of effective tillers plant^{-1}, panicle length, number of grains panicle^{-1}, harvest index and 1000 grain weight as reported by Madhavilatha et al. (2005). Grain yield plant^{-1} was observed to be positively associated with spikelet fertility, panicle length, number of grains panicle^{-1} and number of effective tillers plant^{-1} reported by Satyanarayana et al. (2005).

The characters *viz.,* plant height, number of effective tillers plant^{-1}, panicle length, number of grains panicle^{-1}, spikelet fertility and 1,000 grain weight had significant positive correlation with grain yield plant^{-1} reported by Vaithiyalingan and Nadarajan (2005) and Muthuswamy and Ananda Kumar (2006b).

Gazafrodi et al. (2006) reported significant and positive correlation between grain yield plant^{-1} and number of effective tillers plant^{-1} and number of tillers plant^{-1} and number of grains panicle^{-1}. Ramakrishna et

al. (2006) reported that panicle length and flag leaf area were significantly and positively correlated.

A significant and positive correlation was present between plant height and number of grains panicle^{-1}. A non-significant and negative association was observed between number of tillers plant^{-1} and grain yield plant^{-1} reported by Zahid et al. (2006).

Grain yield plant^{-1} was significantly correlated with days to 50 % flowering, number of tillers plant^{-1}, number of effective tillers plant^{-1}, number of grains panicle^{-1}, flag leaf length, flag leaf width and plant height as reported by Agahi et al. (2007).

Grain yield plant^{-1} was correlated significantly and positively with plant height, panicle length, flag leaf area, number of grains panicle^{-1}. Correlation of plant height with number of tillers plant^{-1} was positive. Number of grains panicle^{-1} showed positive correlation with grain yield plant^{-1} reported by Khan et al. (2009).

Correlation analysis revealed significant positive correlation of grain yield plant^{-1} with plant height, number of panicles plant^{-1}, panicle length, number of filled grains panicle^{-1} and harvest index as reported by Chakraborty et al. (2010).

Nandan et al. (2010) reported strong positive association of yield with days to 50 % flowering, plant height, number of grains per panicle, number of spikelets per panicle and spikelet fertility.

Kumar et al. (2010) studied grain quality components in thirty crosses of rice. In correlation studies, the following characters were found to be of importance in selection viz. , hulling percentage, paddy length, head rice recovery, milling percentage, brown rice length and it also exhibited a positive interrelation among themselves. Selection based on hulling percentage (HP) is suitable, since it brings simultaneous improvement in all other quality parameter traits.

Basavaraja et al. (2011) studied that the correlation analysis indicated that grain yield was significantly associated with panicle length, test

weight, number of tiller per plant, number of productive tiller per plant, number of spikelet per panicle and per cent spikelet fertility.

Nagaraju et.al., (2013) reported high significant and positive association of yield with number of grain per panicle, total number of productive tillers per plant, harvest index, L/B ratio, milling% and panicle length.

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

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

Madakemohekar et al. (2014) investigated genetic parameters for quality and nutritional characters in 60 recombinant inbred lines (RIL's) of rice. Analysis of variance revealed significant differences for all the traits. It was observed that grain yield per plant was positively significant associated with seed width, milling per cent, gelatinization temperature, amylose content and kernel breadth before cooking.

Rahman et al. (2014) reported that grain yield/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/panicle (0.110) and weight of 1000-grains (0.109), whereas significant negative association with panicle length (-0.609), number of unfilled spikelets/panicle (-0.542) and non significant negative association with plant height (-0.136) and number of ineffective tillers/hill (-0.304).

2.6 Path coefficient analysis

Path coefficient measures the direct and indirect contributions of independent variables on a dependent variable. Though the correlation coefficients depict the nature of association among the characters, it is the path analysis that splits the correlation coefficients into direct and indirect

effects thus specifying the relative contribution of each character. It further reveals the different ways in which a particular character influences a dependent variable. A brief reviews has been summarized below.

Low positive direct effect on grain yield plant^{-1} was contributed by number of panicles plant^{-1}, panicle length, culm length, 100 grain weight, days to 50 % flowering, plant height and harvest index reported by Padmavathi et al. (1996). Samonte et al. (1998) reported that traits *viz.,* panicle weight plant^{-1}, number of filled grains panicle^{-1}, spikelet density, maximum tiller density, number of grains panicle^{-1} and 1000 grain weight had positive path coefficients on grain yield. The nodes panicle^{-1} revealed negative direct effect on grain yield plant^{-1}.

Janardhanam et al. (2000) revealed that, plant height, spikelet panicle^{-1}, and grains panicle^{-1} had high direct effects on plant yield. The effects of these characters were further increased by positive indirect effect of plant height through spikelet and grains panicle^{-1}, productive tillers plant^{-1}, panicle length through plant height, spikelet panicle^{-1}, and grains panicle^{-1}, spikelet panicle^{-1} through plant height and grains panicle^{-1}, The major yield-contributing characters, based on indirect and direct effects, were plant height, spikelet panicle^{-1} and grains panicle^{-1}.

A high direct effect on grain yield plant^{-1} was due to number of effective tillers plant^{-1} reported by (Sinha and Banerjee, 2002).

Highest positive direct effect was contributed by panicle length on grain yield plant^{-1} reported by Mishra and Verma (2002). Number of panicles plant^{-1}, flag leaf width, days to 50 % flowering and flag leaf rolling contributed highest positive direct effect towards grain yield plant^{-1}.

Highest positive direct effect towards grain yield plant^{-1} was contributed by 100 grain weight elucidated by Tomar et al. (2000), Gazafrodi et al. (2006) and Agahi et al. (2007), for plant height reported by Babu et al. (2002), Babar et al. (2007), for number of effective tillers plant^{-1} reported by Tomar et al. (2000) and Gazafrodi et al. (2006). Harvest index, flag leaf length and number of grains panicle^{-1} had larger direct effects on grain yield plant^{-1} reported by Tomar et al. (2000) and Gazafrodi et al. (2006).

Positive indirect effects were contributed by panicle length, number of grains panicle^{-1} and spikelet fertility as advocated by Babu et al. (2002). Flag leaf width followed by flag leaf length, spikelet density, harvest index, biological yield plant^{-1} and plant height had the greatest positive effect on grain yield plant^{-1} as advocated by Mishra and Verma (2002).

Surek and Beser (2003) reported that biological yield plant^{-1} and harvest index had the highest positive direct effect on grain yield plant^{-1}. According to the magnitude as stated above, the order of yield components was number of filled grains panicle^{-1}> number of effective tillers square meter^{-1}> 1000 grain weight.

Khedikar et al. (2004) revealed that, 1,000 seed weight had the highest positive direct effect on grain yield followed by spikelet density, effective tillers plant^{-1}, panicle length and days to fifty per cent flowering and hence direct selection through these characters would be more effective. Whereas, Nayak et al. (2001) revealed that, panicle number plant^{-1}, grains panicle^{-1} and 1,000 seed weight contributed to the grain yield. However, (Vaithiyalingan and Nadarajan, 2005) reported that, grains panicle^{-1} had the highest positive direct effect on yield followed by productive tillers plant^{-1}.

Shanthala (2004) reported that spikelet density exhibited the highest direct effect on grain yield plant^{-1} followed by harvest index, 1000 grain weight and number of effective tillers plant^{-1}. However plant height, panicle weight plant^{-1}, panicle length and spikelet number recorded negative direct effect on grain yield plant^{-1}. Thus, a selection for spikelet density, harvest index, 1000 grain weight and number of effective tillers plant^{-1} is beneficial for direct enhancement of grain yield.

Vaithiyalingan and Nadarajan (2005) and Agahi et al. (2007) reported that number of grains panicle^{-1} and number of effective tillers plant^{-1} had the highest positive direct effect on grain yield plant^{-1}. Whereas, Agahi et al. (2007) advocated that 1000 grain weight contributed highest and maximum direct effect towards grain yield plant^{-1}.

Agahi et al. (2007) reported that, the productive tillers plant^{-1}had the highest positive direct effect on grain yield plant^{-1}, followed by the number of grains panicle^{-1} and 1,000 seed weight respectively.

Plant height and number of panicles plant^{-1} recorded the highest positive indirect effect on yield via harvest index whereas number of filled grains panicle^{-1} on grain yield plant^{-1} via harvest index and panicle length reported by Chakraborty et al. (2010).

Nandan et al. (2010) observed, path analysis 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.

Kumar et al. (2010) reported that path analysis of head rice recovery (HRR) showed that brown rice length (BRL), milling percentage (MP), hulling percentage (HP) and water uptake (WU) were most important contributing characters towards the head rice recovery (HRR) based on their high positive direct effects.

Basavaraja (2011) studied that Path coefficient analysis revealed that days to 50% flowering, plant height, panicle length, panicle number, number of productive tiller per plant, percent spikelet fertility and amylase percent had positively direct effect on grain yield. Hence, selection based on these traits could help to bring simultaneous improvement of yield and yield attributes.

Selvaraj et al. (2011) reported that path coefficient analysis for test weight exhibited maximum positive direct effect on grain yield per plant followed by filled grains per panicle, plant height, panicle length, number of tillers per plant and days to 50% flowering and they contributed primarily to yield and could be relied upon for selection of genotypes to improve genetic yield potential of rice.

Nagaraju et al. (2013) studied the path coefficient analysis in six parents and their 15 F_1 crosses for eleven component characters including grain yield and concluded number of grains per panicle and total number of

productive tillers per plant as the main yield components because these traits showed the highest positive direct effects towards increasing grain yield.

Dongre et al. (2014) reported that number of tiller/plant, culm height, plant height, biological yield/plant, panicle index and harvest index were positively correlated with grain yield and also had positive direct effect and therefore these traits should be given due importance while practicing selection, aimed for improvement of grain yield.

Madakemohekar et al. (2014) reported that kernel length after cooking, seed width, milling per cent amylose content and gelatinization temperature had positive direct effect on grain yield.

Rahman et al. (2014) studied newly developed advanced fine rice lines and check and reported that plant height had positive direct effect (0.154), number of effective tillers/hill had positive direct effect (0.065), number of ineffective tillers/hill had negative direct effect (-0.114), panicle length had positive direct effect (0.163), number of filled spikelets/panicle had positive direct effect (0.285), number of unfilled spikelets/panicle had negative direct effect (-0.154), weight of 1000-grains had positive direct effect (0.234) on grain yield/plant.

2.7 Principal component analysis

Principal component analysis, basically a well known data reduction technique, initially floated by Pearson (1901) and later developed by Hotelling (1933), offers solution to this complex problem by transforming the original set of variables into smaller set of linear combinations that account for most of the variability of the original data set. It is a standard tool in modern data analysis because it is a simple, non-parametric method for extracting relevant information from confusing data sets. With minimal effort PCA provides a roadmap for how to reduce a complex data set to a lower dimension to reveal the sometimes hidden, simplified structures that often underlie it. It reduces the dimensionality of the data while retaining most of the variation in the data set. PCA accomplishes this reduction by identifying directions, called principal components, along which the variation in the data is maximal. By using a few components, each sample can be represented by

relatively few numbers instead of by values for thousands of variables (Ringer, 2008). Thus, the primary benefit of PCA arises from quantifying the importance of each dimension for describing the variability of a data set. A brief reviews has been summarized below:

Zhang et al. (2004) studied coefficient of variance (CV), principal component and correlation analyses to test the quality characteristics of 89 japonica rice varieties. Chalkiness, head rice rate, gel consistency and amylose content showed fairly great CV, suggesting great potential for selection of these characters. Principal component analysis showed that brown rice rate, milled rice rate, length/width, chalky rice rate, chalkiness, gelatinisation temperature and gel consistency should be taken as the principal properties for estimating rice quality. In the same way, Liu et al. (2009) showed that grain length, length/width, milled rice rate and head milled rice rate were the main factors to influence rice quality.

Li et al. (2005) observed the agronomic characters (productive panicle, spikelets, filled grain, seed setting rate, 1000-seed weight, plant height, panicle length, spikelet density per panicle, flag leaf length, flag leaf width, 2nd top leaf length, 2nd top leaf width, 3rd top leaf length, 3rd top leaf width and yield) of core germplasm Luzhenzhan 8 and its pedigree grown in late-cropping season and quality indices were tested systematically.Principal component analysis indicated that panicle length factor had a very significant positive linear relationship with yield. Head rice factor had a very significant negative linear relationship with eating quality. Based on these studies an ideal plant type for breeding of South China late-cropping quality rice was constructed.

Zhang and Ma (2008) reported on the basis of mechanical indexes of cooked rice grain, the taste quality of brown rice was evaluated by principal component analysis. The main mechanical indexes of 7 varieties of cooked rice grain were determined from the specimen correlation matrix. According to more than 80.8% of the cumulative variance proportion, the 2 principal components were established for reflecting the taste quality of brown rice. Finally, the principal component values of varieties were obtained and

the taste quality was analysed. The results are similar to practical phenotypes and it is shown that the method of principal component analysis is more exact and feasible by the mechanical indexes of cooked rice grain was reported by In order to identify the major characters which account for variation among Basmati rice mutants, 11 mutants developed from Basmati-370 and 2 from Basmati-Pak along with parents and three standard checks were studied using Single Linkage Cluster Analysis (SLCA) and Principal Component Analysis (PCA). Seven characters were studied. The first three PCs with eigen-values > 1 contributed 78.7% of the variability among the genotypes. Four characters were positive to PC3 than PC2 and PC1. Productive tillers/plant and panicle fertility contributed maximum in PC3. Thus, this principal component is a weighted average of the characters (Rashid *et al.* 2008). However, Yang et al. (2009) classify 10 agronomic traits of 98 accessions of upland rice using PCA and showed that there was remarkable variance among traits of the accessions. Ten agronomic traits of the accessions could be classified into four principal components which with cumulative proportion of 77.03%. The first principal component was determined by spikelets per panicle, total grain per panicle. The second was determined by effective tillers per plant, 1000-grain weight and panicle length. The third mainly represented yield per plant, and the fourth reflected grain and growth period of the accessions.

Principal component analysis and clustering of 46 introduced black pericarp rice cultivars were carried out based on 8 agronomic traits of plant height, effective spikes, spikes length, number of grains per spike, seed setting ratio, 1000-grain weight, grain length/width, and initial heading difference. On the basis of principal components, these 46 black rice varieties were divided into 3 groups for 4.19 Euclidean distances. The characters of the first group were late maturity, high stalk, moderate spikes and many grains; and the second group had the characteristics of early maturity, medium stalk, long spike, and weighty grains; the third group was type of late maturity, high stalk, many spikes, many and light grains (Li et al*.,* 2010).

Anandan et al. (2011) assessed diversity of forty four salt tolerant rice genotypes from different geographic regions using Mahalanobis

D^2 and principal component analysis (PCA). The PCA revealed that axes 1 and 2 accounted for 82.88% and 11.14% of the variance, respectively. The highest contributing variable was the number of grains per panicle in PC1 and the plant height in PC2. Both D^2 and PCA revealed that the morphometric diversity was based on the pedigree and independent of geographical origin.

Ashfaq et al. (2012) performed PCA for twelve morphological traits (plant height, tillers per plant, panicle length, flag leaf area, primary branches, spikelets per panicle, seeds per panicle, seed weight per panicle, 1000 grain weight, plant yield, heading days and maturity days) of rice genotypes. They reported four principal components out of twelve which exhibited more than one eigen value and showed about 67.7% variability. The PC1 was more related to plant height, panicle length, flag leaf area, primary branches per panicle, number of spikelets per panicle, number of seed per panicle, seed weight per panicle, plant yield, heading days and maturity days so, it must be considered. In PC2 the primary branches, seeds per panicle, seed weight per panicle, 1000 grain weight and plant yield were more related traits. The PC3 exhibited positive effect for plant height, panicle length, flag leaf area, primary branches per panicle and 1000 grain weight. The PC4 was more related to number of spikelets per panicle, 1000 grain weight, heading days and maturity days. Based on first our PCs it was cleared that the 1000 grain weight, number of spikelets per panicle, primary branches per panicle, number of seeds per panicle and seed weight per panicle had high weight age value and number of tillers had lowest value.

Khan et al. (2012) evaluated forty rice genotypes on the basis of various morphological traits in a field experiment. There was a significant variation for all the traits studied among the genotypes. The results indicated that the highest genetic variability was observed in plant height, spikelets per panicle, panicle length, days to heading and days to maturity. All the traits were also studied through principal component analysis (PCA). The highest variability was observed in plant height, tillers per plant, panicle length and flag leaf area. The combined variation among these traits was 67.7%. The derived information would be very useful to select potentially breeding lines for future rice improvement programme.

Kumar et al. (2013) studied principal component analysis in RILs population derived from a cross between,JNPT 89 (Tropical *japonica*) and JR 75 (*indica*) and reported that only five principal components (PCs) exhibited more than 1.8 eigen value and showed about 68.34% variability. The PC1 showed 25.81%, while PC2, PC3, PC4 and PC5 exhibited 17.22%, 9.56%, 8.58% and 7.16% variability respectively. The PC1, PC2, PC3 and PC5 were mostly related to yield attributing traits, whereas PC4 was related to quality traits. Intensive selection procedures can be designed to bring about rapid improvement of dependent traits for yield by selecting the lines from PC1. Similarly, from quality aspect the lines from PC4 could be selected. Identified NPT derived RILs may be used as donor to improve the yield and quality traits in varietal development programme and some of the rice RILs may also be used directly for cultivation purposes.

Nachimuthu et al. (2014) studied a population panel of 192 rice genotypes comprising traditional landraces and exotic genotypes and reported that component 1 had the contribution from the traits such as days to 50% flowering, leaf length, plant height, panicle length, days to maturity and number of filled grains which accounted 28.46% of the total variability. Grain width and grain length width ratio has contributed 16.8% of total variability in component 2. The remaining variability of 14.4%, 11.7% and 9.3% was consolidated in component 3, component 4 and component 5 by various traits such as spikelet fertility, single plant yield, grain length and number of productive tillers. The cumulative variance of 80.56% of total variation among 12 characters was explained by the first five axes.

(B) Molecular level

The Indian subcontinent has a very rich diversity in rice germplasm which includes landraces, wild *Oryza* species, natural hybrids between the cultivars and wild relatives, and the germplasm resources generated in the breeding programmes (Rai, 1999 and Yadav et al., 2013). During the domestication process, individuals with desirable traits have been selected leaving most of the genetic diversity behind in the progenitors (Doebley et al., 2006).The protection against the loss of vast genetic diversity

found in rice varieties is crucial for maintaining future food security in the changing world (Chaudhary et al., 2013). Genetic diversity assessment of the contrasting rice lines is essential component for characterization and conservation to identify potential parents.

Molecular markers are potent tools to identify genetic relatedness effectively and efficiently Kresovich et al.1992. Unlike the morphological and biochemical markers, molecular markers are not stressed by environmental factors and growth practices (Ovesna et al., 2002). With the advent of DNA marker technology, several types of DNA markers like RAPD, SSR, RFLP, AFLP etc now available, but SSR markers are widely used in comparison to other types of markers because they are reproducible, co-dominant, species specific and highly polymorphic. Microsatellites (Litt and Luty, 1989) are tandemly arranged repeats of short DNA motifs (1-6 bp in length) that frequently exhibit variation in the number of repeats at a locus.

Microsatellite (or simple sequence repeats-SSR) (Akkaya et al*.* 1992) markers have been proposed for gene mapping in species. SSR markers have been effectively used in rice. Among PCR based markers, microsatellites are abundant and well distributed throughout the genome (Akagi et al*.,* 1996; McCouch et al., 1997; Wu and Tanksley., 1993). Many studies have also reported significantly greater allelic diversity of microsatellite markers than other molecular markers (McCouch et al., 2001).

SSR has much more polymorphism than any other DNA marker, therefore SSR marker have become an ideal molecular marker in identification of plant variety for diversity analysis among the genotypes or within the species (McCouch et al., 1997; Yang et al*.,*1994).

The use of these markers to investigate genotypic variations among different cultivars was previously reported by some researchers (Singh et al., 2004; Joshi and Behera, 2006). Various SSR markers have been reported to be gene based or linked to genes related to yield and yield component traits in rice (Zhang et al. 2010). Markers with the highest number of discernable alleles could be the best markers for molecular characterization and diversity analysis. Lu et al (2005); Wong et al (2009); Jain et al (2004)

and Hossain et al (2012) observed the level of polymorphism determined by the PIC, which is markedly higher than the result in our study.

SSR markers RM 219 (Xiao et al., 1998), RM228 (Mei et al., 2003; Jiang et al., 2004) and RM7 (Hittalmani et al., 2003) were found on chromosome 9, 10 and 3 in rice genome.

SSR's markers have been used to analyze diversity and to locate genes Temnykh et al. 2000 and Temnykh et al. 2001 and QTLs on rice chromosomes using both intra and inter specific crosses Bao et al. 2000 and Moncada et al. 2001. SSRs are increasingly useful for integrating the genetic, physical and sequence based maps of rice and they simultaneously provide information to link phenotypic and genotypic variation efficiently.

The number of bands produced across 24 rice lines by different SSR motifs is consistent with published reports on microsatellite frequency in their genome. Majority of SSR primers used in this study had dinucleotide repeats (GA and CT). The perfect dinucleotide repeat motif (GA) has been reported to display high level of variation among the rice genotypes (Temnykh et al. 2000).

Genetic diversity among 51 Sali rice accessions from Assam was characterized based on 72 RAPD markers Dakshina and Sarma(2004). 11 polymorphic primers showed a high degree of molecular variation with the range of polymorphic bands from 33 to 100%. The Jaccard's similarity coefficient (0.515) indicated high level of diversity. SSRs are among the most widely used DNA marker for many purposes such as diversity, genome mapping, varietal identification, etc. (Teixeira da Silva, 2005).

Tu et al. (2007) in China (0.706) and Thomson et al. (2007) in Indonesia (0.68) also detected the low genetic variation among rice varieties, whereas, detected overall gene diversity was higher.

Zeng et al. (2007) and Prathepha et al. (2012) reported an average of 7.7 and 11.85 alleles per locus using rice landraces from China and wild rice (*Oryza rufipogon)* from Northeastern Thailand and Laos respectively.

Studies were conducted to evaluate the genetic diversity of major commercial rice cultivars in China. A total of 63 conventional rice cultivars and parental lines of hybrid rice crosses were collected in China (Zhang et al. 2007) and assayed using a set of 24 micro-satellite markers (SSRs) distributed on the 12 rice chromosomes (2 markers in each chromosome). By using the 24 SSR markers, a total of 135 alleles were detected from all the tested cultivars (5.6 alleles per marker). Genetic diversity among the conventional *indica* cultivars was higher compared to the conventional *japonica* cultivars. Based on these results, the trends in the genetic relationship of the different rice cultivars in China constructed by the use of SSR markers were almost identical or more accurate than results based on pedigree analysis.

A study was conducted to differentiate Baro rice cultivars using SSRs markers well distributed on all 12 chromosomes to study rice diversity (Wong et al. 2009). A total of 31 alleles were generated by 12 polymorphic microsatellite loci among the cultivars with an average of 2.6 alleles per locus. Average PIC value obtained was 0.5204. An UPGMA dendrogram based on SSR polymorphism indicated high variation among the rice varieties with the coefficient ranging from 0.16 and 0.92.Genetic diversity determination using cluster analysis showed differentiation of rice cultivars into 2 major groups and several sub-groups. .

A study to evaluate the genetic divergence of 12 rice land races using five SSR markers was conducted . A total of 11 alleles were detected in 12 land races and the number of alleles per locus ranged from 2 to 3 with an average of 2.2 per locus. Among the primers used RM 481 indentified more number of alleles and average PIC was 0.43. The dendrogram based on SSR marker analysis grouped the 12 rice accession into six clusters, where cluster VI was the largest with three accessions. (Prabakaran., 2010)

Genetic diversity of 101 high quality conventional rice samples was analyzed with 16 pairs of SSR primers evenly distributed in 12 chromosomes of rice genome. All SSR primers showed polymorphism with 100% polymorphic locus rate. The 16 pairs of primers amplified polymorphic bands with 55 alleles, and the average alleles (Ap), effective alleles (Ae) and

polymorphism information content (PIC) were 3.4375, 2.0492, and 0.4760, respectively. Cluster analysis indicated that the genetic similarity coefficients among 101 high quality conventional rice varieties ranged from 0.6802 to 0.9798 (XiLan et al.2010).

A set of 29 accessions of Indian popular rice varieties was subjected to diversity study using simple sequence repeat (SSRs), a total of 87 alleles were produced that were 100% polymorphic. Twelve sets of SSR primers amplified specific alleles in 14 genotypes. The PIC value ranged from 0.57 (RM 313) to 0.98 (RM 442 and RM 163) with average of 0.78 and average genetic similarity of 0.38 was observed among the popular varieties. The maximum similarity of 0.82 was observed between Jayshree and Sarjoo52 and minimum similarity of 0.05, between Jaya and Pusa Basmati 1. Based on ecologies and duration groups showed a maximum similarity of 0.34 between IRM and RSL groups and a minimum similarity of 0.18 between IRE and RSL groups. Cluster analysis revealed PCA of rice microsatellite data from 20 primer pairs separated the four early varieties and land races from recently evolved varieties by the first and second principal component, which represent 15 and 12.2% of diversity in the sample. Out of 29 genotype, 14 genotypes produced specific alleles, which can be used as molecular tags for particular genotypes when utilized along with the non polymorphic markers in this set of genotypes it produces bar-coded molecular tags for the identification of the valuable new plant lines.(Upadhyay et al. 2011)

Etemad et al. (2012) detected 3.57 alleles per SSR locus among 26 rice (*Oryza sativa,* L.) accessions using SSR markers distributed across the rice genome. In another study, Hossain et al. (2012) found an average of 3.8 alleles per locus in rice using Bangladeshi ARLs. Variability in the number of alleles detected per locus might be due to the diverse lines used and selection of SSR primers with scorable alleles.

A total of 24 SSR markers were used across 12 elite aromatic rice genotypes for their characterization and discrimination. Among these 24 markers 9 microsatellite markers were showed polymorphism. The number of alleles per locus ranged from 2 alleles (RM510, RM244, and RM277) to 6 alleles (RM 163), with an average of 3.33 alleles across 9 loci obtained in the

study. The polymorphic information content values ranged from 0.14 (RM510) to 0.71 (RM163) in all 9 loci with an average of 0.48. RM163 was found the best marker for the identification of 12 genotypes as revealed by PIC values. The frequency of most common allele at each locus ranged from 41% (RM163, RM590, and RM413) to 91% (RM510). (Sajib et al., 2012)

To explore the genetic structure and diversity of rice varieties in NE India, 300 individuals of 24 indigenous rice varieties representing sali, boro, jum and glutinous types, 5 agronomically improved varieties, and one wild rice species (*O. rufipogon*) using seven SSR markers were genotyped . A total of 85 alleles and a very high level of gene diversity (0.776) were detected among the indigenous rice varieties of the region. (Chaudhary et al., 2013)

The study was carried out to decipher the pattern of genetic diversity in terms of both phenotypic and genotypic variability, and to assess the efficiency of random vis-à-vis QTL linked/gene based simple sequence repeat markers in diversity estimation. A set of 88 rice accessions that included landraces, farmer's varieties and popular Basmati lines were evaluated for agronomic traits and molecular diversity. The random set of SSR markers included 50 diversity panel markers developed under IRRI's Generation Challenge Programme (GCP) and the trait-linked/gene based markers comprised of 50 SSR markers reportedly linked to yield and related components. For agronomic traits, significant variability was observed, ranging between the maximum for grains/panicle and the minimum for panicle length. The molecular diversity based grouping indicated that varieties from a common centre were genetically similar, with few exceptions. (Yadav et al., 2013)

Chaudhari (2013) identified 25 QTLs to be associated with yield and yield attributing traits. Out of 40 SSR polymorphic markers 13 markers showed association for yield and its attributes. The number of QTLs was 1 to 11 and mapped chromosome 2,3,5,7,8,10 and 11. Phenotypic variance ranged from 18.48 to 69.87%.

Singh et al. (2013) evaluated that ample amount of genetic variability was observed for the characters, plant height, tillers/plant, kernel length, kernel breath and L/B ratio. The grain yield/plant showed positive correlation with productive tiller/plant and test weight. Path coefficient analysis showed that the productive tiller/plant and test weight contribute to grain yield/ plant through direct effect. A total of 54 randomly selected F5 plants were subjected to SSR marker analysis. SSR allelic profile based on two dimensional principal component analysis demonstrated high level of diversity among parents and F5 plants spread between them.

Duan et al. (2013) re-sequenced 781 lines from a segregating F2 population constructed by crossing the indica variety, “Giant Spike Rice"R1128 as trait donor with the japonica cultivar ‘Nipponbare” using high-throughout multiplexed shotgun genotyping (MSG) technology. High-density SNPs, QTL mapping and genetic effect analysis were performed for five yield factors (spikelet number/panicle, primary branches/panicle, secondary branches/panicle, plant height, and panicle length). 49 QTLs for 5 yield factors were distributed on 11 chromosomes. The super-hybrid line R1128 carries multiple major genes for good traits, including Sd1 for plant height, Hd1 and Ehd1 for heading date, Gn1a for spikelet number and IPA1 for ideal plant shape. These genes accounted for 44.3%, 21.9%, 6.2%, 12.9% and 10.6% of the phenotypic variation in the individual traits. Six novel QTLs, qph1-2, qph9-1, qpl12-1, qgn3-1, qgn11-1and qsbn11-1 were reported here for the first time.

Zhao et al. (2013) constructed genetic linkage map consisting 207 DNA markers, based on a RIL population derived from a cross between indica Luhui 99 and japonica Nipponbare. The markers in the linkage map were distributed on all the 12 rice chromosomes and covered 2397 cM of the genome with the average distance between the markers being 12.29 cM. QTL, QTL×QTL epstatic effects and QTL × environment (QE) interaction were detected for 7 traits, including number of panicles/plant, number of spikelet/panicle, number of filled grains/panicle, seed setting rate,1000-grain weight, grain yield /plant, plant height. A total of 22 QTLs with significant additive effects covering all chromosomes except chromosomes 6,11 and 12

and two QTL with significant QE interactions were detected. Seven pairs of QTLs showing significant additive ×additive epistatic effects were detected except for three traits including number of spikelet/ panicle, number of filled grains/ panicle, and seed setting rate. Genetic contributions were generally low for QTL showing epistatic effects. No significant interaction between epistatic QTL and environment was detected

Leng et al. (2014) studied a DH population derived from the cross between japonica CJ06 and indica TN1 to analyze the QTLs for amylose content, gel consistency (GC), gelatinization temperature (GT), protein content, and grain hardness under two different conditions. A total of 18 QTLs were detected on chromosomes 1, 2, 3, 6, 8, 10, and 12, with the additive heritability ranging from 10.4 to 66.3 %. Five-locus epistatic interactions were identified except for GC, and two QTLs for GT exhibited environmental interaction effects. The results facilitate further understanding of the genetic basis for eating and cooking quality, nutritive quality, and milling quality.

Singh et al. (2014) evaluated 16 highly diverse NPT lines derived from *indica* x *japonica* Sub-species crosses of rice (*Oryza sativa* L.) using SSR markers. In this study15 markers linked with different quantitative and qualitative traits were selected. Eight (RM16, RM223, RM234, RM256, RM259, RM276, RM42 and RM468) were polymorphic and rest seven loci (RM201, RM236, RM261, RM438, RM485, RM502 and RM529) produced monomorphic alleles.The total number of alleles amplified were 26 with a mean value of 1.733. Based on the genetic diversity and molecular analysis, it was found that the genotypes *viz*., NPT 40-01 x Pusa Basmati, NPT40-01 x H.M.T (a), NPT29 x Chhoti Luchai (a) and NPT(s)10 (d) could be utilized for crop improvement programmes especially for yield and quality attributing traits (Kernel length, Aroma, Grain protein, Panicle length, Grain length, Amylose content and Kernel width) in rice. On the basis of amplified unique alleles, SSR markers RM42, RM223, RM234, RM256, RM259 and RM276 may open new opportunity to search new alleles for different traits present in the rice lines/ germplasm**.**

MATERIAL AND METHODS

The present investigation entitled “Genetic analysis and Characterization of Inter-subspecific Cross Derived Genotypes for Yield and Quality Traits in Rice” was carried out during the *Kharif season* of 2014. The techniques followed and materials used during the course of investigation are presented in this chapter.

3.1 Experimental material and other details

The experiment will be conducted at two major levels:

(A) Field level

(B) Molecular level

(A) At Field level

3.1.1 Experimental site

The experiment was carried out at Seed Breeding Farm under Rice Improvement Project, Department of Genetics and Plant Breeding, College of Agriculture, J.N.K.V.V., Jabalpur (M.P.).The experimental area occupied was quite uniform in respect of topography and fertility.

3.1.2 Climate and weather

Jabalpur is situated at 23.90 N latitude and 79.58 E longitudes at an altitude of 411.87 m above the mean sea level. This region has subtropical, semi-arid climate with hot and dry summer and cold winter with occasional showers. The average rainfall is about 1258.4 mm, which is received mostly from July to September. Temperature vary from 6^0C being minimum in January to 45^0C being maximum in May and June. This area is under “Kymore Plateau and Satpura Hills Agro-Climatic Zone” as per norms of National Agricultural Research Programme.

This area as per National Bureau of Soil Science and Land Use Planning of ICAR comes under agro-ecological sub region number 10.1 named

as sub-humid dry eco-region. The data related to weekly maximum and minimum temperature, relative humidity, wind velocity, rainfall, number of rainy days, sunshine hours and evaporation of entire crop growing period of experiment has been presented in appendix-1.

3.1.3 Experimental material

The experimental material consists of 75 JNPT lines derived from *indica x japonica* subspecies crosses developed by JNKVV, Jabalpur and obtained from Seed Breeding Farm, JNKVV, Jabalpur. These lines were planted in Randomized Complete Block Design with three replications. A detail of these lines is given in table 1.

3.1.4 Experimental methods

Experiment consisted of 75 JNPT lines which were grown in Randomized Complete Block Design with three replications. Twenty one days old seedlings were transplanted in the experimental site with spacing of 15cm between plant to plant and 20 cm between the rows, keeping single seedling per hill. Gap filling was done within a week in order to maintain uniform plant population. Fertilizer dose of 100 kg N, 60 kg P_2O_5, and 40 kg K_2O was applied. Entire dose of P_2O_5 and K_2O along with half dose of N was applied as basal dose at the time of final field preparation, remaining amount of nitrogen was splitted in two equal splits and were applied at the time of active growth and grain filling stages. The standard agronomic practices were adopted for normal crop growth.

3.2 Observations recorded

Observations were recorded as per the DUS guidelines for rice. Observations were recorded on the basis of five random competitive plants selected from each line in every replication for the evaluation of yield and yield contributing traits. Mean of main, average and smallest panicle from each of the five randomly selected plants were used to record the observations of panicle traits. Observations on all the morphological characters were recorded on the net plot basis.

Table 1: Details of JNPT lines used in the study programme

1.	NPT(s) 4-1	2.	NPT(s) 5-1
3.	NPT(s) 6-1 (a)	4.	NPT(s) 6-1 (b)
5.	NPT(s) 6-1 (c)	6.	NPT(s) 6-1 (d)
7.	NPT(s) 6-1 (e)	8.	NPT(s) 6-1 (f)
9.	NPT(s) 6-1-1 (a)	10.	NPT(s) 6-1-1 (b)
11.	NPT(s) 6-1-1 (c)	12.	NPT(s) 6-3
13.	NPT(s) 6-4	14.	NPT(s) 6-5
15.	NPT(s) 6-7	16.	NPT(s) 6-11
17.	NPT(s) 6-12	18.	NPT(s) 6-13
19.	NPT(s) 8-1 (a)	20.	NPT(s) 8-1 (b)
21.	NPT(s) 8-2	22.	NPT(s) 10-1 (a)
23.	NPT(s) 10-1 (b)	24.	NPT(s) 10-1 (c)
25.	NPT(s) 10-1 (d)	26.	NPT(s) 10-1 (e)
27.	NPT(s) 10-8 (a)	28.	NPT(s) 10-8 (b)
29.	NPT(s) 23-1	30.	NPT(s) 23-2
31.	NPT(s) 23-3	32.	NPT 24 × IR 36 (a)
33.	NPT 24 × IR 36 (b)	34.	NPT 24 × IR 36 (c)
35.	NPT 24 × IR 36 (d)	36.	NPT 24 × IR 36 (e)
37.	NPT 24 × IR 36 (f)	38.	NPT 24 × IR 36 (g)
39.	25B × NPT 100 (a)	40.	25B × NPT 101 (d)
41.	25B × NPT 101 (e)	42.	25B × NPT 101 (f)
43.	NPT 32 × Pusa Bas (a)	44.	NPT 32 × Pusa Bas (b)
45.	NPT 32 × Pusa Bas (c)	46.	NPT 33 × Mahamaya (a)
47.	NPT 33 × Mahamaya (b)	48.	NPT 33 × Mahamaya (c)
49.	NPT 33 × Mahamaya (d)	50.	NPT 33 × Mahamaya (e)
51.	NPT 33 × Mahamaya (f)	52.	NPT 33 × Mahamaya (g)
53.	NPT 33 × Mahamaya (h)	54.	NPT 70 × Pusa Basmati (a)
55.	NPT 70 × Pusa Basmati (b)	56.	NPT 70 × Pusa Basmati (c)
57.	NPT 70 × Pusa Basmati (d)	58.	NPT 70 × OR1045 × R2964 (a)
59.	NPT 70 × OR1045 × R2964 (b)	60.	NPT 70 × OR1045 × R2964 (c)
61.	NPT 89 × IR 36 (a)	62.	NPT 89 × IR 36 (b)
63.	NPT 89 × IR 64 (a)	64.	NPT 89 × IR 64 (b)
65.	NPT 89 × IR 64 (c)	66.	NPT 100 × HMT (a)
67.	NPT 100 × HMT (b)	68.	NPT 100 × HMT (c)
69.	NPT 100 × HMT (d)	70.	NPT 100 × HMT (e)
71.	NPT 100 × HMT (f)	72.	NPT 121 × IR 64 (a)
73.	NPT 121 × IR 64 (b)	74.	25A × NPT 70-2-6-1
75.	25A × NPT 70-15		

3.2.1 Morphological characters

3.2.1.1 Basal Leaf sheath color

It was observed at initial stage and classified as green, purple lines, light purple and purple.

3.2.1.2 Leaf: Pubescence of blade surface

This character was recorded prior to boot stage and classified as glabrous, intermediate and pubescent.

3.2.1.3 Leaf Auricle

This trait was observed at boot stage and classified as absent and present.

3.2.1.4 Auricle colour

It was observed at boot stage and classified as colorless, light purple and purple.

3.2.1.5 Ligule shape

In present investigation, this trait was recorded at boot stage and categorized as truncate, acute and split.

3.2.1.6 Ligule colour

This character was recorded at boot stage and classified as white, light purple and purple.

3.2.1.7 Flag Leaf: Attitude of blade (early)

It was observed prior to boot stage and classified as erect, semi-erect, horizontal and drooping.

3.2.1.8 Spikelet: color of stigma

This trait was observed after panicle initiation and before milking stage and clasfied as white, light green, yellow, light purple, purple.

3.2.1.9 Stem: anthocyanin coloration of nodes

It was observed at milk stage and classified as present and absent.

3.2.1.10 Spikelet: density of pubescence

This character was observed during the ripening phase and classified as absent, weak, medium, strong and very strong.

3.2.1.11 Sterile lemma color

It was recorded during the ripening phase and classified as gold, straw, purple and red.

3.2.1.12 Spikelet: color of tip of lemma

This trait was recorded during the ripening phase and classified as white, yellowish, brown, red, purple and black.

3.2.1.13 Panicle: exsertion

This character was recorded during the ripening phase and classified as partially exserted, mostly exserted and well exserted.

3.2.1.14 Panicle - attitude of branches

It was recorded during the ripening phase and classified as erect, erect to semi-erect, semi-erect, semi-erect to spreading and spreading.

3.2.1.15 Panicle – awns

This trait was recorded during the ripening phase and classified as present and absent.

3.2.1.16 Panicle - distribution of awns

It was recorded during the ripening phase and classified as tip only, upper half only, whole length.

3.2.1.17 Panicle: color of awns

This character was observed during the ripening phase and classified as yellowish white, yellowish brown, brown, reddish brown, light red, red, light purple, purple and black.

3.2.1.18 Anthocyanin coloration on leaf sheath

The presence or absence of leaf sheath anthocyanin coloration was recorded at early boot stage by visual assessment of group of plant.

3.2.1.19 Presence of collar on leaves

The presence or absence of leaf collar that is the juncture between leaf blade and leaf sheath was recorded at early boot stage by visual assessment of individual plant.

3.2.1.20 Presence of ligule on leaf

Presence or absence of papery membrane at the inside juncture between the leaf sheath and blade called ligule was recorded at early boot stage by observation of individual plant or parts of plant.

3.2.1.21 Attitude of flag leaf blade (late)

The flag leaf attitude of blade was recorded at ripening stage (terminal spikelets ripened) and categorized in to erect, semi-erect, horizontal and deflexed types.

3.2.1.22 Culm attitude

This trait was recorded during booting stage and categorized into erect, semi-erect, open and spreading types.

3.2.1.23 Lemma anthocyanin colouration of area below apex

This trait was recorded after beginning of anthesis and before milking stage ie when anthesis is half way and classified as absent, weak, medium, strong and very strong.

3.2.1.24 Lemma anthocyanin colouration of apex

This trait was recorded after beginning of anthesis and before milking stage ie when anthesis is half way and classified as absent, weak, medium, strong and very strong.

3.2.1.25 Lemma and Palea colour

It was recorded between dough development and ripening stage and classified into straw, gold & gold furrows on straw background, brown spots

on straw, brown furrows on straw, brown, reddish to light purple, purple spots or furrows on straw, purple, black.

3.2.1.26 Panicle curvature of main axis

This character was recorded at ripening stage (terminal spikelets ripened) and categorized into straight, semi-straight, deflexed and drooping.

3.2.1.27 Panicle presence of secondary branching

it's absence and presence was observed at ripening stage (terminal spikelets ripened).

3.2.1.28 Panicle secondary branching

This trait was recorded at ripening stage (terminal spikelets ripened) and categorised into weak, strong, clustered.

3.2.2 Quantitative characters

3.2.2.1 Days to 50 per cent flowering

The number of days taken from sowing to heading in primary panicles in fifty percent plants was recorded.

3.2.2.2 Plant height (cm)

Plant height was measured in centimeters from ground level to the tip of the panicle of the main culm excluding awns if any at the time of maturity. It can also be calculated from the following formula.

Plant height (cm) = Stem length (cm) + Panicle length (cm)

3.2.2.3 Stem length (cm)

It was measured in centimeters from ground level to the base of the panicle of the main stem in cm.

3.2.2.4 Panicle length (cm)

Panicle length was measured in centimeters from neck node of the panicle to the tip of the uppermost spikelet, excluding awns if any.

3.2.2.5 Number of tillers per plant

Tillers were counted for each randomly selected five plants at the end of active tillering stage.

3.2.2.6 Number of productive tillers per plant

Out of the total number of tillers per plant, ear-bearing tillers were counted at maturity.

3.2.2.7 Number of panicles per plant

This observation was recorded after dough development and before ripening stage by counting the number of panicles in randomly selected plants.

3.2.2.8 Flag leaf length(cm)

The length of the leaf blade was measured in centimetres from randomly selected plants in each replication.

3.2.2.9 Flag leaf width (cm)

Width of middle portion of the erect flag leaf just below panicle was recorded in cm during booting stage from randomly selected plants in each replication.

3.2.2.10 Days to maturity

The days from nursery to maturity is calculated.

3.2.2.11 Stem thickness (mm)

It was measured by measuring the thickness of the base of the stem at milk development stage in mm.

3.2.2.12 Panicle weight per plant (g)

Total weight in grams of panicle was recorded after two days of sun drying

3.2.2.13 Number of spikelets per panicle

This was counted from main, average and smallest panicle for each of the plant selected.

3.2.2.14 Fertile spikelets per panicle

One panicle from each plant was selected randomly and the total numbers of fertile/healthy spikelets were counted in number.

3.2.2.15 Sterile spikelets per panicle

One panicle from each plant was selected randomly and the total numbers of sterile spikelets were counted in number.

3.2.2.16 Spikelet fertility per cent

The fertility percentage will be calculated as follows:

$$\text{Fertility \%} = \frac{\text{Total number of filled spikelets panicle}^{-1}}{\text{Total spikelets panicle}^{-1}} \times 100$$

3.2.2.17 1000-Grain weight (g)

One thousand sound filled grains were sun dried up to 12 % moisture level, were weighed in grams.

3.2.2.18 Spikelet density

It is calculated by using the following formula:

$$\text{Spikelet density} = \frac{\text{Total number of spikelets panicle}^{-1}}{\text{Length of panicle (cm)}}$$

3.2.2.19 Biological yield per plant (g)

Weight in grams of plants after harvesting from ground level (excluding roots) and sun drying was recorded in grams.

3.2.2.20 Grain yield per plant (g)

Individual plant was hand threshed, cleaned, dried up to 12 % moisture level and weighed in grams**.**

3.2.2.21 Harvest Index (%)

It was worked out by using the following formula:

$$\text{Harvest index} = \frac{\text{Seed yield plant}^{-1}\text{ (g)}}{\text{Biological yield plant}^{-1}\text{ (g)}} \times 100$$

3.2.2.22 Panicle Index

It was calculated by using the following formula:

$$\text{Panicle index} = \frac{\text{Grain yield plant}^{-1}\text{ (g)}}{\text{Panicle weight plant}^{-1}\text{ (g)}} \times 100$$

3.2.3 Quality traits

Observations on quality traits were recorded for all the 75 lines.

3.2.3.1 Grain length (mm)

The length of randomly selected ten filled grains was measured in mm and divided by ten to obtain the grain length.

3.2.3.2 Grain breadth (mm)

The breadths of randomly selected ten filled grains were measured in mm and divided by ten to obtain the grain breadth.

3.2.3.3 Decorticated Grain length (mm)

Ten randomly selected grains were arranged from tip to tip on a graph paper and the total length in millimeter was recorded. Total length was divided by number of grains to calculate mean length of individual grain.

3.2.3.4 Decorticated Grain breadth (mm)

Ten randomly selected grains were arranged side by side on a graph paper and grain width was recorded in millimeter. Total width was divided by number of grains to calculate mean width of individual grain in millimeter.

3.2.3.5 Length and breadth ratio (L:B)

It was calculated by the following formula

$$\text{LB Ratio} = \frac{\text{Length of milled grain}}{\text{Breadth of milled grain}}$$

3.2.3.6 Hulling percentage (%)

Properly cleaned 100 g paddy sample was dehusked using a huller and weight of hulled rice was recorded.

$$\text{Hulling percentage} = \frac{\text{Weight of hulled kernel}}{\text{Weight of paddy}} \times 100$$

3.2.3.7 Milling percentage (%)

Brown rice was put into standard miller for polishing and milled rice weight was recorded.

$$\text{Milling percentage} = \frac{\text{Weight of polished kernel}}{\text{Weight of paddy}} \times 100$$

3.2.3.8 Head rice recovery (%)

From milled rice the ¾ kernel was taken as whole grain. The sorting out of full and broken rice was done and its weight was recorded.

$$\text{Head Rice Recovery} = \frac{\text{Weight of whole polished kernel}}{\text{Weight of paddy}} \times 100$$

3.2.3.9 Alkali Spreading Value or Gelatinization Temperature

The alkali spreading value was measured in terms of alkali dis-integration using a '7' point numerical spreading scale as suggested by Little *et al.*, (1958). Six milled rice kernels were evenly placed in petridishes containing 1.7% KOH solution at 30^0C for 23 hours and the spreading scale was recorded.

Table 2. Alkali Spreading scale

Score	Spreading Value
1	Kernel not affected
2	Kernel swollen
3	Kernel swollen, collar complete and narrow
4	Kernel swollen, collar complete and wide
5	Kernel split or dis-integration, collar complete and wide
6	Kernel dispersed, merging with collar
7	Kernel completely dispersed and intermingled

Table 3: ASV and GT Score table

Classification	Alkali spreading value (ASV)	Gelatinization temperature (GT)
1-2	Low	High >74 ^{0}C
3	Low, medium	High, medium
4-5	medium	medium (70 ^{0}C – 74 ^{0}C)
6-7	High	Low (55 ^{0}C – 69 ^{0}C)

3.2.3.10 Determination of amylose content (%)

Weighing of 0.10 g of fine powdered rice grain sample in 100 ml volumetric flask was done and 1ml distilled ethanol was added and after that 10 ml of 1N NaOH was added and kept overnight. Next day 100 ml volume makeup was done with distilled water. From this,2. 5 ml sample in volumetric flask was taken and 20ml distilled water was added followed by 3 drops of phenopthelien. The solution was titrated with 0.1N HCl till pink colour disappears. Then 1ml of iodine reagent was added to the titrated sample and volume was made upto 50ml. The colour of the sample was read at 590nm wavelength in a spectrophotometer. Standard amylose solution of 0.2, 0.6, 0.8 and 1.0ml were made and the colour was developed as in the case of samples. 1ml of iodine reagent was diluted with 50ml distilled water to prepare the blank. For calculating amylose (per cent) standard graph was prepared.

Formula used is given as under

$$X = \frac{\text{Standard concentration}}{\text{ABS of standard X}} \text{ X ABS of the sample}$$

$$\text{Amylose \%} = \frac{X}{2.5} \text{ X } 100$$

3.3 Statistical analysis

The data in respect of various characters studied were subjected to the following analysis:

3.3.1 Characterization of each genotype based on morphological observation.

3.3.2 Analysis of variance

3.3.3 Estimation of mean, range, genotypic and phenotypic coefficient of variation, heritability, expected genetic advance and genetic advance as percentage of mean.

3.3.4 Estimation of phenotypic and genotypic correlations.

3.3.5 Path coefficient analysis.

3.3.6 Principal component analysis.

3.3.1 Characterization of each genotype based on morphological observation

All the qualitative characters showing discrete variation were analyzed by graphical representation and percentage frequency of different classes of characters were plotted, to know which particular trait was predominant amongst the lines studied. Genotypes were characterized as per DUS guidelines.

3.3.2 Analysis of variance

The data on quantitative characters were statistically analyzed on the basis of model described by Cochran and Cox (1950) for randomized complete block design. In order to test the significance of treatments critical difference was computed (Fisher and Yates, 1963).

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

Y_{ij} = Performance of j^{th} genotype in i^{th} block

M = General mean

b_i = True effect of i^{th} block

t_j = True effect of j^{th} treatment

e_{ij} = Random errors which are supposed to be identically and independently distributed with normal distribution having mean zero and variance σ^2_e

Table 4: ANOVA table for Randomized Block Design

Source of variation	d.f.	Sum of squares	Mean squares	Expected mean squares
Replication	(r-1)	S.S. due to replication	M_1	$\sigma^2_e + g\,\sigma^2_r$
Genotypes	(g-1)	S.S. due to genotypes	M_2	$\sigma^2_e + r\sigma^2_g$
Error	(r-1)(g-1)	S.S. due to error	M_3	σ^2_e
Total	(rg-1)			

1. Genotypic variance (σ^2_g) = $\frac{M2-M3}{r}$
2. Phenotypic variance (σ^2_p) = $\frac{M_2-M_3}{r}$ + M_3
3. Environmental variance(σ^2_e) = M_3

Where,

r = number of replications

g = number of genotypes

M_1 = mean square due to replication

M_2 = mean square due to genotypes

M_3 = mean square due to error

3.3.3 Parameters of genetic variability

3.3.3.1 Mean

Mean was calculated by the following formula:

$$\bar{X} = \frac{\sum Xi}{N}$$

Where,

$\sum Xi$ = Sum of all the observations of i^{th} traits

N = Total number of observations

3.3.3.2 Range

Range is the difference between the smallest and the greatest term of a series of observation and thus provides the information about the variability present in the genotypes.

3.3.3.3 Genotypic and phenotypic coefficient of variation

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the method suggested by Burton (1952).

Phenotypic coefficient of variation (PCV)

$\sigma^2_p = \sigma^2_g + \sigma^2_e$

$PCV = (\sigma_p / \bar{X}) \times 100$ where $\sigma_p = \sqrt{\sigma^2_p}$

Genotypic coefficient of variation (GCV)

$GCV = (\sigma_g / \bar{X}) \times 100$ where $\sigma_g = \sqrt{\sigma^2_g}$

Where,

σ^2_p = Phenotypic variance

σ_p = Phenotypic standard deviation

σ^2_g = Genotypic variance

σ_g = Genotypic standard deviation

σ^2_e = Environmental variance

$\bar{X}$ = General Mean

The estimates of PCV and GCV were classified as low, moderate and high according to Sivasubramanian and Madhavamenon (1973).

< 10 per cent	=	low
10-20 per cent	=	moderate
> 20 per cent	=	high

3.3.3.4 Heritability

It is the ratio of genotypic variance to the total phenotypic variance. Heritability for the present study was calculated in broad sense by adopting the formula as suggested by Hanson et al. (1956).

$$h^2 (bs)\ \% = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

$h^2(b)$ = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Heritability per cent in broad sense was classified into three groups:

High	More than 70%
Medium	50% to 70%
Low	Less than 50%

3.3.3.5 Expected genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. Expected genetic advance was calculated by the method suggested by Johnson et al. (1955).

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

Where,

GA = Genetic Advance

K = Constant (Standard selection differential) having the value of 2.06 at 5 per cent level of selection intensity

h^2 = Heritability of the character

σ_p = Phenotypic standard deviation

3.3.3.6 Genetic advance as percentage of mean

It was calculated by the following formula:

$$\text{GA as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

GA was categorized as:

< 10 per cent = low

10-20 per cent = moderate

>20 per cent = high

3.3.4 Correlation coefficient

Correlation coefficients were calculated for all quantitative characters combinations at phenotypic, genotypic and environmental level by the formula given by Miller et al. (1958).

$$r_{X_i X_j} = \frac{Cov X_i X_j}{\sqrt{(Var X_i)}.\sqrt{(Var X_j)}}$$

Where,

$r_{X_i X_j}$ = Coefficient of correlation between X_i^{th} and X_j^{th} traits

Cov X_iX_j = Covariance between X_i^{th} and X_j^{th} traits

Var X_i = Variance of X_i^{th} trait

VarX_j = Variance of X_j^{th} trait

Genotypic, phenotypic and environmental correlations were computed by substituting corresponding variance and covariance in the above formula. The estimation of covariance between two traits was derived in the same way as for corresponding variance components.

3.3.5 Path coefficient analysis

The direct and indirect contribution of various characters to yield were calculated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

The following set of simultaneous equations were formed and solved for estimating direct and indirect effects.

$$r_1Y = P_1Y + r_{12}P_2Y + r_{13}P_3Y + \ldots\ldots\ldots\ldots + r_{1k}P_kY$$

$$r_2Y = r_{21}P_1Y + P_2Y + r_{23}P_3Y + \ldots\ldots\ldots\ldots + r_{2k}P_kY$$

$$\vdots \qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad \vdots$$

$$r_kY = r_{k1}P_1Y + r_{k2}P_2Y + r_{k3}P_3Y + \ldots\ldots\ldots + P_kY$$

Where,

r_1Y to r_kY = Coefficients of correlation between causal factors 1 to 'k' and independent character Y

P_1Y to P_kY = Direct effects of characters 1 to 'k' on character Y

r_{12} to $r_{k-1,\,1}$ = Coefficient of correlation among causal factors

The above equations were written in a matrix form as under

$$\underset{A}{\begin{bmatrix} r_1Y \\ r_2Y \\ \vdots \\ r_kY \end{bmatrix}} = \underset{C}{\begin{bmatrix} 1 & r_{12} & r_{13} & \cdots & r_{1k} \\ r_{21} & 1 & r_{23} & \cdots & r_{2k} \\ \vdots & \vdots & \vdots & & \vdots \\ r_{k1} & r_{k2} & r_{k3} & \cdots & 1 \end{bmatrix}} \underset{B}{\begin{bmatrix} p_1Y \\ p_2Y \\ \vdots \\ p_kY \end{bmatrix}}$$

Then, $$B = [C]^{-1} \cdot A$$

Where,

$$[C]^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} & \cdots & C_{1k} \\ C_{21} & C_{22} & C_{23} & \cdots & C_{2k} \\ \vdots & \vdots & \vdots & & \vdots \\ C_{k1} & C_{k2} & C_{k3} & \cdots & C_{kk} \end{bmatrix}$$

Then direct effects were calculated as follows --

$$P_1 Y = \sum_{i=1}^{k} C_{1k} r_k Y$$

$$P_2 Y = \sum_{i=1}^{k} C_{2k} r_k Y$$

$$P_k Y = \sum_{i=1}^{k} C_{ki} r_k Y$$

Residual effect was obtained as per for formula given below –

$$R = \sqrt{1 - \sum d_i r_{ij}}$$

Where,

d_i = Direct effect of the i^{th} character

r_{ij} = correlation coefficient of the i^{th} character with j^{th} character

Later the path coefficients were rated based on the scales given below (Lenka and Mishra, 1973).

>1.00	=	Very high
0.3-0.99	=	High
0.2-0.29	=	Moderate
0.1-0.19	=	Low
0.0-0.09	=	Negligible

3.3.6 Principal Components Analysis

It is a multivariate statistical analysis to reduce the data with large number of correlated variables into a substantially smaller set of new variables through linear combination of the variables that accounts most of the variation present in the original variables. The objective of principal component analysis. is to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson, 1972 and Morrison, 1982) and also to rank genotypes on the basis of PC scores.

Principal components are generally estimated either from correlation matrix or covariance matrix. When the variables are measured in different units, scale effects can influence the composition of derived components. In such situations it becomes desirable to standardize the variables. In the present investigation correlation matrix was used to extract the principal components. PCA is a well-known method of dimension reduction (Massy, 1965; Jolliffe, 1986), which seeks linear combinations of the columns of X with maximal variance, or equivalently, high information. It is routinely applied in chemometrics with the goal of providing the most compact representation of the data. The original p variables X = [x1 . . . xp] aretransformed in a new predictor set T = [t1 . . . tk], with k ≤ min (n −1, p). The new variables tj, called scores, are a weighted average of the original X variables. The principal components are the eigenvectors, uj from the Eigen decomposition of X'X (and of the sample covariance matrix S, up to a constant). PCA sequentially maximizes the variance of a linear combination of the original predictor variables

Uj = arg max Var(Xu),

u=1

Subject to the constraint that u' i Suj = 0 for all 1 ≤ i < j. This ensures that tj = Xuj is uncorrelated with all the previous linear combinations ti = Xui. The principal components are ordered in terms of the amount of variation of the original data they account for. The first principal component direction has the property that t1 = Xu1 has the largest sample variance among all normalized

linear combinations of the columns of X. Each subsequent component gives combinations with the largest possible variance which is uncorrelated with those that have been taken earlier.

There are various standard approaches to find the principal components, e.g. taking the singular value decomposition of X. In chemometrics it is common to estimate the principal components using the nonlinear iterative partial least-squares (NIPALS) algorithm (Wold, 1966). This is because the number of required components is usually much less than the total possible number (*k* _ *p*). In fact, the NIPALS algorithm does not calculate all the principal components at once, but it first calculates t1 and u1 from the X matrix. Then the outer product t1u_1 is subtracted from X and the residual X2 is calculated. In turn, this residual can be used to calculate t2 and u2.

(B) Molecular level

3.4.1 Source of Biological Material

For the molecular analysis, 24 JNPT lines were selected on the basis of plant height, panicle length, stem thickness, number of panicles and 1000 grain weight. The source materials were obtained from Seed Breeding Farm, JNKVV, Jabalpur.

Table 5. Details of selected lines included for molecular analysis

S. No.	Genotypes	S. No.	Genotypes
1	NPT(s) 4-1	13	NPT 24 × IR 36 (d)
2	NPT(s) 6-1 (b)	14	NPT 24 × IR 36 (f)
3	NPT(s) 6-1 (c)	15	NPT 24 × IR 36 (g)
4	NPT(s) 6-1 (d)	16	25B × NPT 100 (a)
5	NPT(s) 6-1 (e)	17	NPT 32 × Pusa Basmati (a)
6	NPT(s) 6-1 (f)	18	NPT 32 × Pusa Basmati (b)
7	NPT(s) 6-1-1 (b)	19	NPT 32 × Pusa Basmati (c)
8	NPT(s) 6-4	20	NPT 33 × Mahamaya (c)
9	NPT(s) 6-7	21	NPT 89 × IR 64 (c)
10	NPT(s) 6-12	22	NPT 100 × HMT (b)
11	NPT(s) 8-2	23	NPT 100 × HMT (c)
12	NPT(s) 10-1 (e)	24	NPT 121 × IR 64 (a)

3.4.2 Germination of Seeds for DNA Extraction

Healthy seeds with identical dimensions were selected by visual observation and dipped in distilled water overnight. The floating, chaffy and non viable light grains were sorted out and discarded. The healthy seeds were kept in distilled sterilized water and after that seeds were placed in petri plates and then kept in germinator at 35°C for germination. Watering was done twice a week for proper emergence of radical and plumule. After two weeks, the etiolated leaves were harvested using a sharp sterilized blade. The leaves were surface sterilized with70% ethanol followed by distilled sterilized water.

3.4.3 Collection of samples

Green young and healthy leaves from ten plants of each line (Table5) were collected in the morning hours from the petri plates for extraction of DNA. The collected samples were placed on cooling pads and then stored at -80^0C.

3.4.4 Isolation of DNA

For genomic DNA extraction, the following chemicals were used with molecular biology grade or analytical grade (Promega Co. USA).

- Cetyl-trimethyl ammonium bromide (CTAB): C-TAB (2g) as detergent was used for 100ml DNA extraction buffer to break cell wall and remove impurities from leaf samples.
- 1M Trizma-base (pH 8.0):Trizma base 30.28g (MW = 121.1g) was dissolved in 200 ml of distilled water. The pH was adjusted to 8.0 with concentrated HCI. The final volume of the solution was made up to 250ml with distilled water before autoclaving. The solution was then stored at room temperature (25°C) after autoclaving. Trizma-base ensures the pH of the buffer solution.
- 0.5M EDTA (Disodium ethylenediaminetetraacetate) (pH 8.0):EDTA (46.53g, MW = 372.2g) was added to 200ml of distilled water. It was stirred vigorously with a magnetic stirrer and maintained at pH 8.0 using NaOH pallets and concentrated NaOH solution. The final volume of the solution was made up to 250ml with distilled water before autoclaving. The solution was stored at room temperature (25°C) before final adjustment of the pH after autoclaving. EDTA

performs as chelating agent that help to remove several kinds of divalent metal cations such as Mg^{2+} and Ca^{2+} that act as co-factor for the majority of DNases which degrade DNA.

- 5M NaCl:NaCl (73.05g,MW = 58.44g) was dissolved in 200ml and stirred vigorously with a magnetic stirrer. The final volume was adjusted to 250ml with distilled water before autoclaving. The solution was stored at room temperature (25°C) after autoclaving. NaCl is a salt that increases the solubility of DNA in the buffer solution and also increases the osmotic ability of the buffer and hence facilitates the process of cell lysis.
- Chloroform: isoamyl alcohol mixture: This is used in the proportion of 24:1 to remove proteins by denaturation and after this they aggregate in the intermittent phase along with cell debris.
- Isopropanol: It is used in equal volume to DNA extraction buffer for DNA precipitation.
- RNase (10mg/ml): RNase (~100mg) was dissolved in 10ml of sterile distilled water in a sterile 15ml centrifuge tube. It was dispensed into sterile 1.5ml micro-centrifuge tubes and stored at –20°C. The RNA is removed by RNase treatment at 37°C.
- 70% ethanol: The pellet is washed with 70% ethanol for removing any salts retained after precipitation.

DNA extraction buffer

The buffer was prepared as per specification (Table 4).

Table 6. Composition of DNA extraction buffer (100 ml)

Chemicals	Final Concentration	Working volume
Tris HCl (pH 8.0), 1M	100mM	10ml
EDTA (pH 8.0), 0.5M	20mM	4ml
β– Mercaptoethanol	0.1%	100µl
NaCl, 5M	1.4M	28ml
CTAB	2%	2g

- β-Mercaptoethanol(100µl) was added just prior to placement of DNA extraction buffer in water bath for incubation.

The technique of DNA isolation relied upon the fact that nucleic acid would form suitable complex with detergent cetyl trimethylammonium bromide (CTAB) under high salt concentration and when the concentration reaches 1.4M, NaCl forms CTAB-Na complex. Genomic DNA was isolated using Saghai-Maroof et al. (1984) method with some modifications. The method utilized and described below gives good quality and quantity of DNA.

1. Leaf sample (2g) was weighed and homogenized in 2ml CTAB buffer (preheated to 65^{o}C) using a pre-chilled pestle and a mortar.
2. The fine paste was transferred to a 2ml centrifuge tube and mixed thoroughly.
3. The samples were incubated in a water bath at 65^{o}C for 40 minutes. During incubation, the samples were gently shaked after every 10min.
4. After incubation the samples were taken out from the water bath and allowed to cool down at room temperature.
5. The sample tubes were then centrifuged for about 15min at 10,000rpm at room temperature.
6. Supernatant obtained was transferred to a 1.5ml fresh tube.
7. Then an equal (to supernatant) volume of chloroform: isoamyl alcohol (24:1 v/v) was added and mixed thoroughly but gently for not less than 5 min.
8. The mixture was then centrifuged for about 15 min at 10,000rpm at room temperature.
9. Supernatant was obtained again and then transferred to a 1.5ml fresh tube.
10. An equal (to supernatant) volume of pre-chilled isopropanol was added and mixed gently by inverting tubes and kept for 20 min undisturbed.
11. The DNA precipitate was then spooled out using 1ml cut tips and transferred to a 1.5ml micro-centrifuge tube.
12. DNA was again pelleted by centrifugation at 10,000rpm for 10min.
13. The supernatant was now discarded and pellet was washed twice with 70% ethanol.
14. The pellet was dried up at room temperature and dissolved in 200µl of M.Q (Milli Q) water for further use.

3.4.5 DNA purification

The purification of DNA was carried out in order to remove the impurities like RNA, proteins and polysaccharides. These are considered as inhibitors in DNA amplification during PCR.

1. 5µl of RNAase (5 mg ml^{-1}) was added to DNA extract, mixed well and incubated at 37°C for 40 min.
2. This was followed by the addition of equal volumes of chloroform: isoamyl alcohol (24:1 v/v) and mixed vigorously.
3. The above mixture was centrifuged at 10,000rpm for 15 min.
4. Supernatant was transferred to a 1.5ml fresh micro-centrifuge tube and 1/10 volume of 3M sodium acetate (pH 5.4) was added followed by further addition of two volumes of pre-chilled isopropanol that was mixed gently for DNA precipitation.
5. The precipitated DNA was pelleted by centrifugation at 10,000 rpm for 15 min.
6. The pellet was dried at room temperature to completely remove ethanol and was then dissolved in 100µl of water (M.Q.) and stored at -20°C for further use.

3.4.6 Quantification of DNA

Quality of DNA was determined by horizontal submarine gel electrophoresis on 0.8% agarose gel. Purity of DNA was checked by taking the ratio of optical density (OD) using spectrophotometer, at 260 nm to that of 280 nm. The samples with OD ratio (260nm/280nm) between 1.7-1.9 were used in subsequent experiments. DNA samples showing the values beyond this range were re-purified. Isolated DNA was quantified in UV spectrophotometer at 260 and 280nm. 50ng/ml concentrated solution of double stranded DNA showed absorbance of 1 at 260nm. DNA concentration of sample was calculated as:

OD 260 x 50 µg DNA/ ml x D.F. /1000

Table 7: List of sequences of thirteen SSR markers

S.№.	Marker	Forward sequence	Reverse sequence	Linked Character
1.	RM201	5'-CTCGTTTATTACCTACAGTACC-3'	5'-CTACCTCCTTTCTAGACCGATA-3'	Drought tolerance
2.	RM261	5'- CTACTTCTCCCCTTGTGTCG -3'	5'- TGTACCATCGCCAAATCTCC -3'	Grain yield
3.	RM16	5'- CGCTAGGGCAGCATCTAAA -3'	5'- AACACAGCAGGTACGCGC -3'	Kernel length
4.	RM236	5'-GCGCTGGTGGAAAATGAG-3'	5'-GGCATCCCTCTTTGATTCCTC-3'	Panicle number
5.	RM469	5'- AGCTGAACAAGCCCTGAAAG -3'	5'-GACTTGGGCAGTGTGACATG -3'	Plant height
6.	RM259	5'-CCCTCCCTTCTGTAAGCTCC-3'	5'-GAAGAACAATGGGGTTCTGG-3'	Grain length
7.	RM331	5'-GAACCAGAGGACAAAAATGC-3'	5'-CATCATACATTTGCAGCCAG-3'	Panicle number
8.	RM42	5'-ATCCTACCGCTGACCATGAG-3'	5'-TTTGGTCTACGTGGCGTACA-3'	Amylose content
9.	RM468	5'-CCCTTCCTTGTTGTGGCTAC-3'	5'-TGATTTCTGAGAGCCACCCC-3'	Kernel width
10.	RM228	5'-CTGGCCATTAGTCCTTGG -3'	5'-GCTTGCGGCTCTGCTTAC -3'	Panicle length
11.	RM341	5'-CAAGAAACCTCAATCCGAGC -3'	5'-CTCCTCCCGATCCCAATC -3'	Culm thickness
12.	RM7	5'-TTCGCCATGAAGTCTCTCG -3'	5'-CCTCCCATCATTTCGTTGTT -3'	1000 grain weight
13.	RM219	5'-CGTCGGATGATGTAAAGCCT -3'	5'-CATATCGGCATTCGCCTG -3'	Plant height

3.4.7 Stock buffers were prepared with following concentrations

Table 8. Reaction mixture for PCR to detect SSR markers

S.No.	Components	Concentration	Working volume
1	10X PCR buffer	2µl	2.0µl
2	$MgCl_2$	1.5mM	0.7µl
3	DNTPs	100µM	0.1µl
4	Primer	10pmol	1.0µl
5	Taq Polymerase	1unit	0.1µl
6	DD H_2O	-	5.1µl
7	DNA	50ng	1.0µl

Table 9.Temperature profile used in PCR Amplification for SSR

Steps	Temperature	Duration	Cycles	Activity
1.	94°C	4min	1	Initial Denaturation
2.	94°C	30sec	35	Denaturation
3.	55 °C	30sec		Annealing
4.	72°C	30sec		Elongation
5.	72°C	5min	1	Final elongation
6.	4ºC	1hrs		Storage

3.4.8 Dilution of DNA

The quantified DNA was diluted according to the DNA quantity in each sample for PCR amplification in sterile double distilled water. Dilutions were carried out according to the following formula:

$$\text{Dilution} = \frac{\text{Required concentration of DNA (ng/µl) X Total volume required (µl)}}{\text{Available concentration of DNA (ng/µl)}}$$

3.4.9 DNA analysis of simple sequence repeats

SSRs are co-dominant markers that target single loci in the genome and can easily and economically assayed by PCR. In the present study, polymorphism was analyzed among rice cultivars by using SSR markers.

3.4.10 Sources of SSR markers

The sequences of a total of thirteen SSR primer pairs (Table7) were synthesized from IDT USA (Promega).

3.4.11 PCR condition for (SSR) markers

PCR conditions were standardized considering different parameters *viz*. initial denaturation, denaturation, annealing, extension and final extension using Thermo Hybrid (*Px2*) PCR Machine. PCR profile was optimized for amplification by using primers of unique sequence with higher GC ratio at high stringency. The optimized conditions are presented in the Table 9.

3.4.12 Data analysis

The PCR products for SSR were resolved on agarose electrophoresis to generate microsatellite fingerprints. The products were stained by ethidium bromide and visualized under UV in Syngene Gel Documentation System. Band size was estimated using 100bp ladder.

PowerMarker version 3.25 was used to calculate the average number of alleles, gene diversity, and polymorphic information content (PIC) values. Phlylogenetic tree was generated on the basis of neighbor-joining method implemented in PowerMarker.

(http://statgen.ncsu.edu/powermarker/downloads.html)

RESULTS

The present investigation was carried out on 75 genotypes of JNPT lines of rice to select out the better lines, to know the genetics for morphological (twenty eight), biometrical (twenty two) and quality (ten) traits in randomized complete block design with three replications at Seed Breeding Farm, JNKVV, Jabalpur. To get a clear picture of variability in genotypes, the genetic parameters of variability were studied. Correlation analysis was performed to find out the degree of relationship between characters under study. However, simple correlation doesnot provide the adequate information about the contribution of each trait towards yield. Therefore, the tecnique of path coefficient analysis was utilised to have an idea of direct and indirect contribution of a trait towards yield which enables the breeder to rank genetic attributes according to their contribution (Dewey and Lu, 1959). In spite of these, principal component analysis (PCA) is used to quantify the importance of each dimension for describing the variability of a data set. In particular, the measurement of the variance along each principal component provides a means for comparing the relative importance of each dimension.

The JNPT lines were characterized based on the classical taxonomical approach; involving detailed observations on morphological description of seeds, flowers and inflorescence.

The experimental results of the present investigation have been given under the following heads:

4.1 Characterization

4.2 Analysis of variance

4.3 Parameters of genetic variability

4.2.1 Range and mean performance for different characters

4.2.2 Genotypic and phenotypic coefficient of variation

4.2.3 Heritability and Genetic advance

4.4 Correlation analysis

4.5 Path coefficient analysis

4.6 Principal component analysis

4.7 Molecular analysis

4.8 Classification of genotypes based on

4.8.1 Amylose content

4.8.2 Geletanization temperature

4.1 Characterization

The frequency distribution of seventeen morphological characters (discontinuous variables) is summarized in the present study (Table 10).

Basal leaf sheath color

Genotypes were categorized based on basal leaf sheath color at vegetative phase and classified as green, purple lines, light purple and purple. Green color was observed in 98.67% of the genotypes, followed by light purple in 1.33% of the genotypes.

Leaf sheath anthocyanin colouration

Anthocyanin coloration of leaf sheath was found absent in all the accessions.

Leaf: pubescence of blade surface

Genotypes were classified as weak, medium, strong and very strong on the basis of pubescence of blade surface. In the present investigation 76.67% genotypes had medium, 13.33% genotypes had weak, 9.33% genotypes had strong and 2.67% genotypes had very strong pubescence.

Leaf: auricles

Auriles were present in all the genotypes.

Leaf: anthocyanin coloration of auricles

All the genotypes expressed colorless auricles i.e., (100%).

Leaf ligule

This trait was expressed in all the genotypes i.e., (100%).

Table 10. Frequency Distribution of Morphological Characters in JNPT Lines

Character	Classes	Number of entry /Frequency	Percentage (%)
Basal leaf sheath color	**Green**	74	98.67
	Purple lines	00	00.00
	Light purple	01	1.33
	Purple	00	00.00
Leaf sheath anthocyanin colouration	**Present**	00	00.00
	Absent	75	100.00
Leaf: pubescence of blade surface	**Absent**	00	00.00
	Weak	10	13.33
	Medium	56	76.67
	Strong	07	9.33
	Very strong	02	2.67
Leaf: auricles	**Absent**	00	00.00
	Present	75	100.00
Leaf : anthocyanin colouration of auricles	**Colorless**	75	100.00
	Light purple	00	00.00
	Purple	00	00.00
Leaf ligule	**Present**	75	100.00
	Absent	00	00.00
Leaf: shape of ligules	**Truncate**	00	00.00
	Acute	00	00.00
	Split	75	100.00
Leaf ligule color	**White**	75	100.00
	Light purple	00	00.00
	Purple	00	00.00
Leaf collar	**Present**	75	100.00
	Absent	00	00.00
Flag leaf: attitude of blade (early)	**Erect**	29	38.67
	Semi-erect	40	53.33
	Horizontal	06	8.00
	Drooping	00	00.00

Culm attitude	**Semi erect**	34	45.33
	Erect	41	54.67
	Open	00	00.00
	Spreading	00	00.00
Stem:anthocyanin coloration of nodes	**Absent**	75	100.00
	Present	00	00.00
Flag leaf attitude of blade (late)	**Horizontal**	32	42.67
	Semi erect	28	37.33
	Erect	15	20.00
	Deflexed	00	00.00
Spikelet : color of stigma	**White**	75	100.00
	Light green	00	00.00
	Yellow	00	00.00
	Light purple	00	00.00
	Purple	00	00.00
Spikelet : density of pubescence	**Absent**	00	00.00
	Weak	18	24.00
	Medium	47	62.67
	Strong	10	13.33
	Very strong	00	00.00
Sterile lemma color	**Straw**	75	100.00
	Gold	00	00.00
	Red	00	00.00
	Purple	00	00.00
Spikelet: color of tip of lemma	**White**	00	00.00
	Yellowish	71	94.67
	Brown	04	5.33
	Red	00	00.00
	Purple	00	00.00
	Black	00	00.00
Panicle: exsertion	**Partly exserted**	33	44.00
	Mostly exserted	23	30.67
	Well exserted	19	25.33
Panicle: attitude of branches	**Erect**	00	00.00
	Erect to semi-erect	00	00.00
	Semi-erect	06	8.00
	Semi-erect to spreading	61	81.33
	Spreading	08	10.67
Panicle: awns	**Absent**	29	38.67
	Present	46	61.33
Panicle: distribution of awns	**Tip only**	08	10.67
	Upper half	17	22.67
	Whole length	21	28.00

Panicle: color of awns	**Yellowish white**	45	60.00
	Yellowish brown	01	1.33
	Brown	00	00.00
	Reddish brown	00	00.00
	Light red	00	00.00
	Red	00	00.00
	Light purple	00	00.00
	Purple	00	00.00
	Black	00	00.00
Lemma : anthocyanin Colouration of area below apex	**Absent**	75	100.00
	Weak	00	00.00
	Medium	00	00.00
	Strong	00	00.00
	Very strong	00	00.00
. Lemma:anthocyanin Colouration of apex	**Absent**	75	100.00
	Weak	00	00.00
	Medium	00	00.00
	Strong	00	00.00
	Very strong	00	00.00
Panicle curvature of main axis	**Straight**	08	10.67
	Semi Straight	65	86.67
	Deflexed	02	2.63
	Drooping	00	00.00
Panicle presence of Secondry branching	**Present**	75	100.00
	Absent	00	00.00
Panicle:secondry branching	**Weak**	15	20.00
	Strong	31	41.33
	Clustered	29	38.67
Lemma and palea colour	**Straw**	55	73.33
	Gold and gold Furrows on Straw background	05	6.67
	Brown spots On straw	00	00.00
	Brown furrows on straw	13	17.33
	Brown	02	2.67
	Reddish to Light purple	00	00.00
	Purple spots or Furrows on Straw	00	00.00
	Purple	00	00.00
	Black	00	00.00

Leaf : shape of ligules

In all the genotypes, the shape of ligule was split (100%).

Leaf ligule colour

White ligule was present in all the genotypes (100%).

Leaf collar

All the genotypes marked the presence of leaf collar.

Flag leaf: attitude of blade (early)

Semi-Erect leaf angle was exhibited by 53.33% of genotypes followed by erect (38.67%), horizontal (8%), however none of them had drooping attitude of blade.

Culm attitude

In the present investigation 54.67% genotypes had erect, whereas 45.33% genotypes had semi erect culm attitude. None of the genotypes had open or spreading culm attitude.

Stem: anthocyanin coloration of nodes

All the genotypes (100%) showed absence of nodes coloration .

Flag leaf: attitude of blade (late)

Most of the genotypes (42.67%) showed horizontal expression whereas 37.33% genotypes showed semi erect and 20% genotypes had erect attitude of blade.

Spikelet : colour of stigma:

All the genotypes (100%) had white colored stigma .

Spikelet : density of pubescence:

In the study 62.67% genotypes showed medium density of pubescence followed by weak (24%) and strong (13.33%), while none of the genotypes expressed very strong or absence of pubescence.

Sterile lemma colour

All the genotypes (100%) exhibited straw color.

Spikelet: colour of tip of lemma

Yellow color of tip of lemma was found in 94.67% of the genotypes, followed by brown in 5.33% of the genotypes.

Panicle: exsertion

Maximum number of the genotypes had partly exserted panicle (44%) followed by mostly exserted (30.67%) and well exserted (25.33%) types.

Panicle: attitude of branches:

Most of the genotypes (81.33%) showed semi-erect to spreading type branches followed by spreading type (10.67%) and semi- erect type (8%).

Panicle: awns:

In 61.33% of the genotypes awns were present, while rest of the genotypes 38.67% showed absence of the awns.

Panicle: distribution of awns:

The 28% of the genotypes had awns in the whole length, 22.67% showed awns in the upper half length and rest of genotypes (10.67%) showed awns in tip only.

Panicle: colour of awns:

Most of the genotypes (60%) exhibited yellowish white awns followed by yellowish brown (1.33%) awns.

Lemma: anthocyanin colouration of area below apex

Anthocyanin colouration was absent in all the genotypes.

Lemma: anthocyanin colouration of apex

This trait was not expressed in any of the genotypes.

Panicle: curvature of the main axis

Most of the panicles had semi straight curvature (86.67%), followed by straight (10.67%) and deflexed (2.67%) curvature of main axis.

Panicle : Presence of secondry branching

This trait was expressed in all the accessions.

Panicle: Secondry branching

Most of the genotypes had clustered secondry branches (41.33%), followed by strong (38.67%) and weak (20%).

Lemma and palea colour

The genotypes mostly had straw (73.33%) coloured lemma and palea followed by lemma and palea with brown furrows on straw (17.33) and gold and gold furrows on straw (6.67%). Tawny expression of lemma and palea was found only in 2.67% of the genotypes, while brown spots on straw, brown, reddish to light purple, purple spots or furrows on straw, purple and black expressions were not seen in any of the genotypes.

4.2 Analysis of variance:

Analysis of variance refers to the observable differences in individuals for a particular trait. To know the extent of variation in observed characters among the 75 JNPT lines, analysis of variance was performed and is presented in Table 11. Analysis of variance indicated that the mean sum of squares due to genotypes were significant for all the characters which revealed that there was considerable genetic variability amongst the material under study.

Considerable amount of variability was observed for all the yield and quality attributing traits. Maximum variability was observed for total number of spikelet per panicle and lowest for LB ratio.

The magnitude of variability in decreasing order for the traits i.e., number of spikelet per panicle, total filled spikelet per panicle, sterile spikelets per panicle, plant height, culm length, biological yield per plant, panicle index, panicle weight per plant, flag leaf length, days to maturity, days to 50% flowering, harvest index, spikelet fertility per cent, head rice recovery, grain yield per plant, 1000 grain weight, amylose percent, milling per cent, spikelet density, average panicle length, total tillers per plant, productive tillers per plant, no of panicles per plant, hulling per cent, decorticated grain length, grain length, decorticated grain width, grain width, stem thickness, flag leaf width, LB ratio.

4.3 Parameters of genetic variability

To predict genetic variability in the population, various parameters were estimated viz., range, mean, genotypic and phenotypic coefficient of variance, heritability, genetic advance for yield and quality attributing traits, and are presented in table 12.

4.3.1 Range and mean performance of different characters studied

The variation of different traits under study revealed the measure of free variability in the population of different genotypes which would reflect the unforeseen impact of potential variability on yield. The performance of the varieties was evaluated by the mean performance of the observed traits. It compares the varieties for the specific characters. Mean performances of all the observed traits are presented in table 12.

Days to 50% flowering- In the present study this character varied from 89.33days to 124.33 days with a mean value of 101.83 days.

Days to maturity- It varied from 123.67 days to 157.33 days with a mean value of 137.72 days.

Table 11: ANOVA for yield, yield and quality attributing traits in JNPT Lines

Source of variation	d.f.	Mean sum of squares									
		DFF	DTM	NOT	NOPT	NPa/pl	PH	SL	PL	FLL	FLW
Replication	2	2.06	9.72	1.28	2.06	2.06	1.39	1.61	0.05	1.35	0.02
Genotypes	74	144.90**	163.68**	6.72**	5.88**	5.88**	1156.49**	1029.68**	21.60**	197.28**	0.28**
Error	148	0.80	1.27	0.93	0.88	0.88	0.27	0.14	0.12	0.83	0.01

Source of variation	d.f.	Mean sum of squares									
		Stem thickness	No of SP/PA	NOFS	NOSS	SFP	SD	PaWT/PL	TGW	BY/Pl	Pl
Replication	2	0.00	48.28	65.62	57.29	7.22	0.04	0.38	3.17	5.31	210.81
Genotypes	74	0.289**	10775.82**	7654.34**	1793.45**	135.38**	22.01**	210.99**	78.36**	897.73**	595.88**
Error	148	0.01	6.82	5.87	3.14	0.36	0.03	0.64	0.71	0.53	32.48

Source of variation	d.f.	Mean sum of squares										
		HI	SL	SW	DSL	DSW	L/B	H%	M%	HRR	AMYL	GY/PL
Replication	2	35.44	0.01	0.09	0.03	0.10	0.17	10.33	3.87	17.38	2.18	6.32
Genotypes	74	142.44**	1.53**	0.29**	1.62**	0.29**	0.24**	4.16**	55.98**	100.37**	59.58**	91.62**
Error	148	2.63	0.02	0.01	0.04	0.02	0.09	0.36	0.61	13.22	0.61	0.45

*, ** Significant at 5% and 1% level of significance respectively.

Total number of tillers per plant- It varied from 3.67 to 10.00 with a mean value of 6.18.

Total number of productive tillers per plant- This character varied from 3.00 to 10.00 with a mean value of 5.98.

Number of panicles per plant- This character ranged from 3.00 to 10.00 with a mean value of 5.98.

Plant height- This trait varied from 85.2867 to 160.25 cm with a mean value of 97.51 cm.

Stem length- It varied from 63.73 cm to 133.43 cm with a mean value of 97.51 cm.

Panicle length- The panicle length varied from 20.66 cm to 33.62 cm with a mean value of 26.51 cm.

Flag leaf length- This character showed variation from 26.79 cm to 65.47 cm with a mean of 40.04 cm.

Flag leaf width- It varied from 1.30 cm to 2.80 cm with a mean of 1.98 cm.

Stem thickness- It ranged from 0.63 cm to 2.17 cm with a mean of 1.33 cm.

Total number of spikelets per panicle- It varied from 178 to 450.67 with a mean value of 289.06.

Fertile spikelets per panicle- This trait varied from 136 to 358.67 with a mean value of 239.68.

Sterile spikelets per panicle- It varied from 14.33 to 127.67 with a mean value of 49.40.

Spikelet fertility per cent- This trait varied from 61.04 % to 95.77 % with a mean value of 83.12%.

Spikelet density- It varied from 6.28 to 17.69 with a mean value of 11.05.

Panicle weight- This character varied from 7.20 g to 44.60 g with a mean value of 21.10 g.

1000 grain weight- This character varied from 13.17 g to 36.39 g with a mean value of 24.56 g.

Biological yield per plant- It varied from 25.10 g to 113.13 g with a mean value of 54.73 g.

Panicle index- Panicle index varied from 48.19% to 117.67% with a mean value of 83.08%.

Harvest index- It varied from 14.68 % to 46.77 % with a mean value of 31.42%.

Grain length- This trait varied from 7.70 mm to 10.37 mm with a mean value of 9.32 mm.

Grain breadth - It varied from 2.13 cm to 3.27 mm with a mean value of 2.80 mm.

Decorticated grain length- It varied from 6.33 mm to 9.13 mm with a mean value of 8.08 mm.

Decorticated grain breadth - This character varied from 1.90 mm to 3.00 mm with a mean value of 2.56 mm.

LB Ratio – This character varied from 2.64 to 4.01 with a mean value of 3.20.

Hulling per cent- This trait varied from 75.70% to 81.55% with a mean value of 78.54%.

Milling per cent- This character varied from 76.49% to 57.37% with a mean value of 68.15%.

Head rice recovery- This trait varied from 42.37% to 67.59% with a mean of 53.17%.

Amylose percent- It varied from 12.60% to 27.57% with a mean of 20.40%.

Grain yield per plant: It varied from 6.72 g to 32.74 g with a mean value of 16.88 g.

4.3.2 Genotypic and phenotypic coefficient of variation

The phenotypic coefficient of variation was higher in magnitude than that of genotypic coefficient of variation for all the characters studied. Phenotypic variance refers to the total or observable variation in a population. It is the sum of genotypic and environmental variance. Genotypic variance is the heritable portion of the total variance. It gives the variation between the genotypes. Environmental variance is the non-heritable portion of the total variance. It gives the variation within the genotypes.

To get a clear picture of variability among the lines under study coefficient of variation was calculated. The ratio of standard deviation of a sample to its mean and expressed in percentage is called as coefficient of variation. Phenotypic coefficient of variation is phenotypic standard deviation multiplied by 100 divided by its mean. Genotypic coefficient of variation is genotypic standard deviation multiplied by 100 divided by its mean. The phenotypic coefficient of variation was higher in magnitude than that of genotypic coefficient of variation for all the characters under study.

The genotypic and phenotypic coefficients of variation (%) for all the traits under study were analyzed and results were furnished in table 12.

Days to 50% flowering- In this study genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 6.81 and 6.86 respectively.

Days to maturity- Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 5.34 and 5.41 respectively.

Total number of tillers per plant- Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 22.48 and 27.36 respectively.

Total number of productive tillers per plant- This character showed genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates 21.58 and 26.69 respectively.

Total number of panicles per plant- Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 21.58 and 26.69 respectively.

Plant height- It exhibited genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates of 15.83 and 15.84 respectively.

Stem length- Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) observed for this trait were 18.99 and 19.002 respectively.

Panicle length- This character exhibited genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates of 10.09 and 10.18 respectively.

Flag leaf length- Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 20.21 and 20.34 respectively.

Flag leaf width - It exhibited genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates of 15.33 and 15.89 respectively.

Stem thickness- In this study genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed were 23.06 and 23.91 respectively.

Total number of spikelets per panicle- Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 20.73 and 20.75 respectively.

Fertile spikelets per panicle- It exhibited genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates 21.07 and 21.09 respectively.

Sterile spikelets per panicle- Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 49.45 and 49.58 respectively.

Spikelet fertility per cent- In this study genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed were 8.07 and 8.10 respectively.

Spikelet density- This character exhibited genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) of 24.50 and 24.56 respectively.

Panicle weight- Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 39.69 and 39.88 respectively.

1000 grain weight- This character showed genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) of 20.72 and 20.99 respectively.

Biological yield per plant- In this study genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed were 31.60 and 31.63 respectively.

Panicle index- Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 16.49 and 17.86 respectively.

Harvest index- This character exhibited genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates were 21.73 and 22.33 respectively.

Grain length- In this study genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 7.63 and 7.74 respectively.

Grain breadth- Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 10.83 and 11.68 respectively.

Decorticated grain length- Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 9.00 and 9.33 respectively.

Table 12. Genetic Parameters of Yield Attributing Characters of JNPT Lines

Traits	Mean	Range		Coefficient of variation		h^2(b) (%)	Genetic Advance	Genetic Advance as % of Mean
		Min	Max	GCV (%)	PCV (%)			
DFF	1.83	89.33	124.33	06.81	06.86	98.40	14.16	13.91
DTM	137.72	123.67	157.33	05.34	05.41	97.70	14.98	10.88
TT/P	06.18	03.67	10.00	22.48	27.36	67.50	02.35	38.06
PT/P	05.98	03.00	10.00	21.58	26.69	65.40	02.15	35.95
Pa/PL	05.98	03.00	10.00	21.58	26.69	65.40	02.15	35.95
PH	124.02	85.29	160.25	15.83	15.84	99.90	40.43	32.60
SL	97.51	63.73	133.43	18.99	19.00	100.00	38.15	39.13
PL	26.51	20.66	33.62	10.09	10.18	98.30	05.47	20.62
FLL	40.02	26.79	65.47	20.21	20.34	98.80	16.57	41.37
FLW	01.98	01.30	02.80	15.33	15.89	93.10	00.60	30.47
ST	01.33	00.63	02.17	23.06	23.91	93.00	00.61	45.82
No.sp/p	289.06	178.00	450.67	20.73	20.75	99.80	123.31	42.66
Fsp/pa	239.68	136.00	358.67	21.07	21.09	99.80	103.90	43.35
Ssp/pa	49.40	14.33	127.67	49.45	49.58	99.50	50.19	101.60
SF	83.12	61.04	95.78	08.07	08.10	99.20	13.77	16.56
SD	11.05	06.28	17.69	24.50	24.56	99.60	05.56	50.38
PaWt/Pl	21.09	07.19	44.60	39.69	39.88	99.10	17.17	81.39
TGW	24.56	13.17	36.39	20.72	20.99	97.30	10.34	42.10
BY/pl	54.73	25.10	113.13	31.60	31.63	99.80	35.59	65.04
PI	83.08	48.19	117.67	16.49	17.86	85.30	26.07	31.37
HI	31.42	14.68	46.77	21.73	22.33	94.70	13.68	43.55
GL	09.32	07.70	10.37	07.63	07.74	97.10	01.44	15.48
GW	02.79	02.13	03.27	10.83	11.68	86.10	00.58	20.71
DGL	08.08	06.33	09.13	09.00	09.33	93.00	01.44	17.89
DGW	02.55	01.90	03.00	11.89	13.07	82.80	00.57	22.29
LB	03.20	02.64	04.01	06.96	11.69	35.40	00.27	08.53
H%	78.54	75.69	81.55	01.43	01.622	78.10	02.05	02.61
M%	68.15	76.49	57.37	06.30	06.41	96.80	08.71	12.77
HRR	53.17	42.37	67.59	10.14	12.23	68.70	09.20	17.31
Amyl%	20.39	12.59	27.57	21.74	22.07	97.00	08.995	44.10
Gy/pl	16.88	06.72	32.74	32.66	32.91	98.50	11.27	66.79

Decorticated grain breadth- This character exhibited genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates of 11.89 and 13.07 respectively.

LB Ratio – Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 6.96 and 11.69 respectively.

Hulling per cent- It exhibited genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) of 1.43 and 1.62 respectively.

Milling per cent- Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates observed for this trait were 6.30 and 6.40 respectively.

Head rice recovery- This trait exhibited genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) of 10.13 and 12.22 respectively.

Amylose percent- In this study genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates were 21.74 and 22.07 respectively.

Grain yield per plant- In this study genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates were 32.66 and 32.91 respectively.

4.3.3 Heritability and Genetic Advance

Heritability measures the contribution of genetic variability to the phenotypic variability observed for quantitative traits and it is good index for the transmission of characters from parents to their offsprings. The estimate of heritability can be utilized for the prediction of genetic gain, which indicates the genetic improvement that would result from the selection of best individuals. Hence, estimate of heritability is an essential pre-requisite for formulation of an effective selection method for genetic improvement.

The estimates of heritability in broad sense were found highest for stem length (100%) followed by very high estimates for plant height (99.90%). Number of spikelets per panicle, fertile spikelets per panicle and biological yield per plant had equal heritability of 99.8%. These characters were followed by

spikelet density (99.6%), sterile spikelets per panicle (99.50%), spikelet fertility (99.2%), panicle weight per plant (99.10%), flag leaf length (98.8%), grain yield per plant (98.50%), days to 50% flowering (98.40%), panicle length (98.30%), days to maturity (97.70%), 1000 grain weight (97.30%), grain length (97.10%), amylose percent (97%), milling per cent (96.80%), harvest index (94.70%), flag leaf width (93.10%), stem thickness (93%), decorticated grain length (93%), grain breadth (86.10%), panicle index (85.30%), decorticated grain breadth (82.80%) and hulling percent (78.10%). (Table12).

The estimates of heritability were moderate for four characters i.e. head rice recovery (68.7%), total tillers per plant (67.5%), productive tillers per plant (65.4%) and total number of panicles per plant (65.4%). (Table12).

The estimate of heritability was low for LB ratio i.e. 35.40%. (Table12).

Table 13: Heritability estimates with Genetic Advance

	Characteristics
High Heritability with High Genetic Advance	Plant height, fertile spikelets per panicle, number of spikelets per panicle, stem length, harvest index, biological yield per plant, panicle index, spikelet density, sterile spikelets per panicle, panicle weight per plant, flag leaf length, flag leaf width, grain yield per plant, panicle length, 1000 grain weight, amylose percent, stem thickness, grain breadth, decorticated grain breadth
High Heritability with Moderate Genetic Advance	Spikelet fertility per cent, Days to 50% flowering, Days to maturity, Grain length, Milling percent , Decorticated grain length
High Heritability with Low Genetic Advance	Hulling percent
Moderate Heritability with High Genetic Advance	Total tillers per plant, Productive tillers per plant, total number of panicles per plant
Moderate Heritability with moderate Genetic Advance	Head rice recovery
Low Heritability with low Genetic Advance	LB Ratio

The estimates of genetic advance as percentage of mean at five per cent selection intensity is presented in table12. Genetic advance as percentage of mean recorded was highest for sterile spikelets per panicle (101.603) followed by panicle weight per plant (81.399), grain yield per plant (66.79), biological yield per plant (65.042), spikelet density (50.375), stem thickness (45.815), amylose percent (44.102), harvest index (43.549), fertile spikelets per panicle (43.348), number of spikelets per panicle (42.658), 1000 grain weight (42.108), flag leaf length (41.374), stem length (39.128), number of tillers per plant (38.058), productive tillers per plant (35.948), total number of panicles per plant (35.948), plant height (32.598), panicle index (31.374), flag leaf width (30.47), decorticated grain breadth (22.268), grain breadth (20.705 and panicle length (20.62).

Moderate estimates of genetic advance were observed for decorticated grain length (17.887), head rice recovery (17.31), spikelet fertility per cent (16.562), grain length (15.48), days to 50% flowering (13.95), milling per cent (12.774), days to maturity (10.879). Remaining only two traits LB ratio (8.533) and hulling per cent (2.609) denoted low genetic advance as percentage of mean. (Table12)

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance. The heritability estimates along with genetic advance, in present study, were categorized in table 13.

In this study high heritability with high genetic advance was observed for the characters plant height, fertile spikelets per panicle, number of spikelets per panicle, stem length, harvest index, biological yield per plant, panicle index, spikelet density, sterile spikelets per panicle, panicle weight per plant, flag leaf length, flag leaf width, grain yield per plant, panicle length, 1000 grain weight, amylose percent, stem thickness, grain breadth and decorticated grain breadth. High heritability with moderate genetic advance was also found for

spikelet fertility per cent, days to 50% flowering, days to maturity, grain length, milling per cent and decorticated grain length. While high heritability with low genetic advance was noticed for hulling per cent. Moderate heritability with high genetic advance was found for the characters total tillers per plant, productive tillers per plant and number of panicles per plant. Whereas moderate heritability with moderate genetic advance was observed for the character head rice recovery. Low heritability with low genetic advance was observed for LB ratio.

4.4 Correlation analysis

Phenotypic and genotypic correlations for various yield and quality attributing traits were estimated with grain yield per plant as dependent variable. The result revealed higher estimate of phenotypic correlation coefficient than genotypic correlation coefficient for almost all the characters studied. The findings of present investigation were furnished in table 12.

Days to 50% flowering

It had high significant positive association with days to maturity (0.8523), stem thickness (0.3723), sterile spikelets per panicle (0.3223) and panicle length (0.1803). High significant and negative association was recorded with spikelet fertility per cent (-0.3828), harvest index (-0.2535), 1000 grain weight (-0.2373) and flag leaf width (-0.2049). Significant and negative association was also observed with number of tillers per plant (-0.1390).

Days to maturity

This trait exhibited high significant and positive association with days to 50% flowering (0.8523), stem thickness (0.4409) and sterile spikelets per panicle (0.2840). Whereas high significant and negative association was observed with spikelet fertility percent (-0.3309), flag leaf width (-0.2423), 1000 grain weight (-0.2072) and stem length (-0.1834). It also showed significant and negative association with harvest index (-0.1694), plant height (-0.1568), milling percent (-0.1369) and hulling percent (-0.1333).

Total number of tillers per plant

This character had high significant and positive association with productive tillers per plant (0.9685), panicle number per plant (0.9685), grain yield per plant (0.44898), biological yield per plant (0.3844), panicle weight per plant (0.3836), spikelet fertility percent (0.3576) and fertile spikelets per panicle (0.2212), whereas, significant positive association was observed with harvest index (0.1589). The character showed highly significant and negative association with sterile spikelets per panicle (-0.2466), grain breath (-0.2286), decorticated grain breath (-0.2037), head rice recovery (-0.1914) and grain length (-0.1745). It also showed significant and negative association with decorticated grain length (-0.1654) and days to 50% flowering (-0.1390).

Total number of productive tillers per plant

It showed highly significant and positive association with number of panicles per plant (1.000), number of tillers per plant (0.9685), grain yield per plant (0.4596), panicle weight per plant (0.3711), biological yield per plant (0.3537), spikelet fertility percent (0.3281) and fertile spikelets per panicle (0.2305). However, it showed significant and negative association with grain breadth (-0.2333) and 1000 grain weight (-0.1464). Highly significant and negative association was observed with sterile spikelets per panicle (-0.2116), decorticated grain breath (-0.2096), grain length (-0.1761), head rice recovery (-0.1759) and decorticated grain length (-0.1662).

Panicle number per plant

It showed high significant and positive association with productive tillers per plant (1.000), total tillers per plant (0.9685), grain yield per plant (0.4596), panicle weight per plant (0.3711), biological yield per plant (0.3537), spikelet fertility percent (0.3281) and fertile spikelets per panicle (0.2305). However, it recorded significant and negative association with grain breath (-0.2333) and 1000 grain weight (-0.1464). Whereas highly significant and negative association was observed with sterile spikelets per panicle (-0.2116), decorticated grain width (-0.2096), grain length (-0.1761), head rice recovery (-0.1759) and decorticated grain length (-0.1662).

Plant height

The character recorded high significant and positive association with stem length (0.9917), 1000 grain weight (0.4801), panicle length (0.4683), biological yield per plant (0.4306), panicle weight per plant (0.4187), flag leaf width (0.3614), grain length (0.3064), decorticated grain length (0.3073), spikelet fertility percent (0.2400), flag leaf length (0.2087) and grain breadth (0.1851). Significant and positive association was observed with amylose percent (0.1630) and decorticated grain breadth (0.1574). High significant and negative association was observed with stem thickness (-0.4247), panicle index (-0.2200) and spikelet density (-0.1857). While it also showed significant and negative association with days to maturity (-0.1568) and sterile spikelets per panicle (-0.1523).

Stem length

Stem length had high significant and positive association with plant height (0.9917), 1000 grain weight (0.4916), biological yield per plant (0.4430), flag leaf width (0.4107), panicle length (0.3508), grain length (0.2934), decorticated grain length (0.2928), spikelet fertility percent (0.2832), flag leaf length (0.1952), and grain breadth (0.1749). Significant and positive association was observed with amylose percent (0.1630), decorticated grain breadth (0.1437) and fertile spikelets per panicle (0.1405). It also showed high significant and negative association with stem thickness (-0.4186), panicle index (-0.1995), sterile spikelets per panicle (-0.1837) and days to maturity (-0.1834).

Panicle length

The trait recorded high significant and positive association with plant height (0.4683), stem length (0.3508), decorticated grain length (0.2259), grain length (0.2154), days to 50 percent flowering (0.1803) and flag leaf length (0.1782). While significant and positive association was observed with decorticated grain breadth (0.1589), sterile spikelets per panicle (0.1529) and grain breadth (0.1464). However, it showed high significant and negative association with spikelet density (-0.5200), panicle index (-0.2311), stem

thickness (-0.2166), spikelet fertility percent (-0.1983) and flag leaf width (-0.1897). A significant and negative association was observed with fertile spikelets per panicle (-0.1651).

Flag leaf length

Highly significant and positive association was observed with flag leaf width (0.3642), panicle weight per plant (0.3214), biological yield per plant (0.3121), number of spikelets per panicle (0.3048), sterile spikelets per panicle (0.2992), fertile spikelets per panicle (0.2165), plant height (0.2087), stem length (0.1952), spikelet density (0.1854) and panicle length (0.1782). It had significant and positive association with grain length (0.1631), 1000 grain weight (0.1558), and decorticated grain length (0.1311). However, highly significant and negative association was observed with spikelet fertility percent (-0.1988), stem thickness (-0.1923) and panicle index (-0.1897).

Flag leaf width

Highly significant and positive association was observed with spikelet density (0.4299), fertile spikelets per panicle (0.4259), biological yield per plant (0.4190), stem length (0.4107), number of spikelets per panicle (0.3851), flag leaf length (0.3642), plant height (0.3614), panicle weight per plant (0.3509), 1000 grain weight (0.2595), grain length (0.2333) and decorticated grain length (0.2094). It also had significant and positive association with amylose percent (0.1643). However highly significant and negative association was recorded for days to maturity (-0.2423), days to 50% flowering (-0.2049) and panicle length (-0.1897). Significant and negative association was also observed with stem thickness (-0.1663).

Stem thickness

Highly significant and positive association was recorded for days to maturity (0.4409), days to 50 percent flowering (0.3723), grain yield per plant (3593), sterile spikelets per panicle (0.3352) and spikelet density (0.2364). Whereas positive and significant association was observed with number of spikelets per panicle (0.1655). Highly significant and negative association was

observed for plant height (-0.4247), stem length (-0.4186), spikelet fertility percent (-0.3220), amylose percent (-0.3152), 1000 grain weight (-0.2922) and LB ratio (-0.1865). While it also showed significant and negative association with grain length (-0.1693), harvest index (-0.1588) and decorticated grain length (-0.1425).

Total number of spikelets per panicle

Highly positive and significant association was observed with fertile spikelets per panicle (0.9156), spikelet density (0.8869), sterile spikelets per panicle (0.5582), panicle weight (0.4755), biological yield per plant (0.4310) and grain yield per plant (0.3952). Highly significant and negative association was observed with panicle index (-0.3010), decorticated grain breadth (-0.1781) and grain breadth (-0.1769). But significant and negative association was seen with spikelet fertility percent (-0.1451).

Fertile spikelets per panicle

In present investigation, this character was highly significantly and positively associated with number of spikelets per panicle (0.9156), spikelet density (0.8609), panicle weight per plant (0.5418), grain yield per plant (0.5167), biological yield per plant (0.4980), flag leaf width (0.4259), spikelet fertility percent (0.2588), productive tillers per plant (0.2305), panicle number per plant (0.2305), total tillers per plant (0.2212), flag leaf length (0.2165) and sterile spikelets per panicle (0.1774). However it had significant and positive association with stem length (0.1405). Highly significant and negative association was recorded for panicle index (-0.2426), decorticated grain breadth (-0.2105) and grain breadth (-0.2071), while it also showed significant and negative association with panicle length (-0.1651), grain length (-0.1460) and decorticated grain length (-0.1401).

Sterile spikelets per panicle

This character exhibited highly significant and positive association with number of spikelets per panicle (0.5582), spikelet density (0.3941), stem thickness (0.3352), days to 50 % flowering (0.3223), flag leaf length (0.2992),

days to maturity (0.2840) and fertile spikelets per panicle (0.1774). However, significant and positive association was observed with panicle length (0.1529). Highly significant and negative association was recorded for spikelet fertility percent (-0.8889), number of tillers per plant (-0.2466), number of productive tillers per plant (-0.2116), number of panicles per plant (-0.2116) and stem length (-0.1837), while, it also showed a significant and negative association with harvest index (-0.1667), plant height (-0.1523) and milling per cent (-0.1460).

Spikelet fertility per cent

In the present study, this trait showed highly significant positive association with number of tillers per plant (0.3576), grain yield per plant (0.3503), panicle number per plant (0.3281), productive tillers per plant (0.3281), stem length (0.2832), fertile spikelets per panicle (0.2588), plant height (0.2400), harvest index (0.2353), panicle weight per plant (0.2179) and biological yield per plant (0.2070). Significant and positive association was observed with panicle index (0.1342) and milling per cent (0.1565). Sterile spikelets per panicle (-0.8889), days to 50 % flowering (-0.3828), days to maturity (-0.3309), stem thickness (-0.3220), flag leaf length (-0.1988) and panicle length (-0.1983) showed highly significant and negative association. It also showed significant and negative association with number of spikelets per panicle (-0.1451).

Spikelet density

Spikelet density had highly significant and positive association with number of spikelets per panicle (0.8869), fertile spikelets per panicle (0.8609), flag leaf width (0.1854), sterile spikelets number per panicle (0.3941), panicle weight per plant (0.3932), grain yield per plant (0.3802), biological yield per plant (0.3332), stem thickness (0.2364) and flag leaf length (0.1854). Highly significant and negative association was noted for panicle length (-0.5200), decorticated seed breadth (-0.2111), seed breadth (-0.2004) and plant height (-0.1857). While, it also showed a significant and negative association with grain length (-0.1682), decorticated grain length (-0.1677), panicle index (-0.1431) and 1000 grain weight (-0.1420).

Panicle weight per plant

It exhibited highly significant and positive association with grain yield per plant (0.8850), biological yield per plant (0.8584), fertile spikelets per panicle (0.5418), number of spikelets per panicle (0.4755), stem length (0.4402), plant height (0.4187), spikelet density (0.3932), total tillers per plant (0.3836), number of productive tillers per plant (0.3711), panicle number per plant (0.3711), flag leaf width (0.3509), flag leaf length (0.3214), 1000 grain weight (0.2594) and spikelet fertility percent (0.2179). It also showed highly significant and negative association with panicle index (-0.5271).

1000 grain weight

This trait had highly significant and positive association with stem length (0.4916), plant height (0.4801), grain length (0.4697), decorticated grain length (0.4472), grain breadth (0.3321), grain yield per plant (0.3174), decorticated seed breadth (0.3082), flag leaf width (0.2595), panicle weight (0.2594), biological yield per plant (0.2523). Highly significant and negative association was observed for stem thickness (-0.2922), days to 50 percent flowering (-0.2373) and days to maturity (0.2072). It also showed significant and negative association with total tillers per plant (-0.1606), productive tillers per plant (-0.1464), panicle number per plant (-0.1464) and spikelet density (-0.1420).

Biological yield per plant

This character had high significant and positive association with panicle weight (0.8584), grain yield per plant (0.7762), fertile spikelets per panicle (0.4980), stem length (0.4430), number of spikelets per panicle (0.4310), plant height (0.4306), flag leaf width (0.3121), number of productive tillers per plant (-0.1464), panicle number per plant (-0.1464), flag leaf length (0.3121), 1000 grain weight (0.2523) and spikelet fertility percent (2070). However, it also showed highly significant and negative association with panicle index (-0.4220) and harvest index (-0.2639).

Panicle index

Highly significant and positive association was observed with harvest index (0.4149) and milling percent (0.2551), 1000 grain weight (0.1265). This character also had significant and positive association with spikelet fertility percent (0.1342). However significant and negative association was observed with grain length (-0.1477), spikelet density (-0.1431) and decorticated grain length (-0.1431). While, highly significant and negative association was observed with panicle weight per plant (-0.5271), biological yield per plant (-0.4220), number of spikelets per panicle (-0.3010), fertile spikelets per panicle (-0.2426), sterile spikelets per panicle (-0.2367), panicle length (-0.2311), plant height (-0.2200), stem length (-0.1995) and flag leaf length (-0.1897).

Harvest index

Highly significant and positive association was observed with panicle index (0.4149), grain yield per plant (0.3782), spikelet fertility percent (0.2353), number of productive tillers per plant (0.2215) and panicle number per plant (0.2215). It also had significant and positive association with number of tillers per plant (0.1589). Whereas highly significant and negative association was seen for biological yield per plant (-0.2639), days to 50 percent flowering (-0.2535) and panicle length (-0.2410). However significant and negative association with days to maturity (-0.1694), sterile spikelets per panicle (-0.1667) and stem thickness (-0.1588) was recorded.

Grain length

Highly significant and positive association was observed for decorticated grain length (0.9731), grain breadth (0.5705), decorticated grain breadth (0.5568), 1000 grain weight (0.4697), plant height (0.3064), stem length (0.2934), flag leaf width (0.2333) and panicle length (0.2154). But significant and positive association was recorded for flag leaf length (0.1631). Highly significant and negative association was observed for productive tillers per plant (-0.1761), number of panicles per plant (-0.1761), number of tillers per plant (-0.1745) and hulling percent (-0.2169). While, it showed significant and negative association with stem thickness (-0.1694), spikelet density (-0.1682), panicle index (-0.1477) and fertile spikelets panicle (-0.1460).

Grain breadth

Highly significant and positive association was observed with decorticated grain breadth (0.9803), grain length (0.5705), decorticated grain length (0.5561), 1000 grain weight (0.3321), plant height (0.1851) and stem length (0.1749). This character also had significant and positive association with panicle length (0.1464). However highly significant and negative association was observed for LB ratio (-0.4123), number of productive tillers per plant (-0.2333), panicle number per plant (-0.2333), number of tillers per plant (-0.2286), fertile spikelets per panicle (-0.2071), spikelet density (-0.2004) and number of spikelets per panicle (-0.1769).

Decorticated seed length

Highly significant and positive association was observed for grain length (0.9731), grain breadth (0.5561), decorticated grain breadth (0.5455), 1000 grain weight (0.4472), plant height (0.3073), stem length (0.2928), panicle length (0.2259) and flag leaf width (0.2094). It had significant and positive association with flag leaf length (0.1311). Highly significant and negative association was recorded for hulling percent (-0.2218). However, a significant and negative association was also observed with spikelet density (-0.1677), productive tillers per plant (-0.1662), panicle index (-0.1431), stem thickness (-0.1425) and fertile spikelets per panicle (-0.1401).

Decorticated seed width

In the present investigation, this trait showed highly significant and negative association for grain breadth (0.9803), grain length (0.5568), decorticated grain length (0.5455) and 1000 grain weight (0.3082). Significant and positive association was recorded for panicle length (0.1589), plant height (0.1574) and stem length (0.1437). While, it showed highly significant and negative association with LB ratio (-0.4201), spikelet density (-0.2111), fertile spikelets per panicle (-0.2105), number of productive tillers per plant (-0.2096), number of panicles per plant (-0.2096), total tillers per plant (-0.2037) and number of spikelets per panicle (-0.1781).

LB ratio

It showed significant and positive association with amylose percent (0.1532). While highly significant and negative association was observed with grain breadth (-0.4123), decorticated grain breadth (-0.4201) and stem thickness (-0.1865).

Hulling per cent

Highly significant and positive association was observed with milling percent (0.3471) and head rice recovery (0.2298). This character also had significant and positive association with stem thickness (0.1413). Significant and negative association was observed for days to maturity (-0.1333). However, it showed highly significant and negative association with decorticated grain length (-0.2218), grain length (-0.2169) and amylose percent (-0.2087).

Milling per cent

It had highly significant and positive association with head rice recovery (0.5106), hulling percent (0.3471), panicle index (0.2551), biological yield per plant (0.2551) and amylose percent (0.1972). Significant and positive association with spikelet fertility percent (0.1565) and grain yield per plant (0.1316) was recorded. While it also showed significant and negative association with sterile spikelets per panicle (-0.1460) and days to maturity (-0.1369).

Head rice recovery

Highly significant and positive association was observed with milling percent (0.5106), hulling percent (0.2298) and amylose percent (0.1972). It had significant and positive association with grain yield per plant (0.1316). Whereas highly significant and negative association was recorded for total tillers per plant (-0.1914), number of productive tillers per plant (-0.1759) and panicle number per plant (-0.1759).

Amylose percent

High positive and significant association was observed for milling percent (0.1972). This character was positively and significantly correlated with

stem length (0.1670), stem thickness (0.1643), plant height (0.1630), LB ratio (0.1532) and head rice recovery (0.1453). However high significant and negative association was recorded for number of spikelets per panicle (-0.3152) and hulling percent (-0.2078).

Grain yield per plant

In present investigation, the trait was highly significantly and positively associated with panicle weight per plant (0.8850), biological yield per plant (0.7762) fertile spikelets per panicle (0.5167), number of productive tillers per plant (0.4596), panicle number per plant (0.4596), total tillers per plant (0.4498), number of spikelets per panicle (0.3952), stem length (0.3938), spikelet density (0.3802), harvest index (0.3782), plant height (0.3602), flag leaf width (0.3593), spikelet fertility percent (0.3503), 1000 grain weight (0.3174) and flag leaf length (0.2673). Milling percent (0.1316) revealed significant positive association with grain yield per plant.

Table 14. Estimates of phenotypic correlation coefficient for various yield and quality attributing traits

	DFF	DTM	TT/P	PT/P	Pa/PL	PH	SL	PL	FLL	FLW	ST	NoSp/Pa
DFF	**1.0000**	0.8523**	-0.1390*	-0.1232	-0.1232	-0.0513	-0.0806	0.1803**	-0.0400	-0.2049**	0.3723**	0.0508
DTM		**1.0000**	-0.1184	-0.1000	-0.1000	-0.1568*	-0.1834**	0.1186	-0.0766	-0.2423**	0.4409**	0.0345
TT/P			**1.0000**	0.9685**	0.9685**	0.0204	0.0283	-0.0462	-0.0005	-0.0291	-0.0985	0.0859
PT/P				**1.0000**	1.000**	-0.0209	-0.0177	-0.0303	0.0143	-0.0499	-0.0921	0.1081
Pa/Pl					**1.0000**	-0.0209	-0.0177	-0.0303	0.0143	-0.0499	-0.0921	0.1081
PH						**1.0000**	0.9917**	0.4683**	0.2087**	0.3614**	-0.4247**	0.0302
SL							**1.0000**	0.3508**	0.1952**	0.4107**	-0.4186**	0.0432
PL								**1.0000**	0.1782**	-0.1897**	-0.2166**	-0.0768
FLL									**1.0000**	0.3642**	-0.1923**	0.3048**
FLW										**1.0000**	-0.1663*	0.3851**
ST											**1.0000**	0.1655*
NoSp/P												**1.0000**
FSp/Pa												
SSp/Pa												
SF												
SD												
PaWt/Pl												
TGW												
BY/Pl												
PI												
HI												
GL												
GW												
DSL												
DSW												
LBRatio												
H%												
M%												
HRR												
Amyl												
GYld/Pl	-0.0866	-0.0446	0.4498**	0.4596**	0.4596**	0.3602**	0.3938**	-0.0822	0.2673**	0.3593**	-0.0970	0.3952**

	FSp/Pa	SSp/Pa	SF	SD	PaWt/Pl	TGW	BY/Pl	Pl	HI	GL	GW
DFF	-0.0960	0.3223**	-0.3828**	-0.0405	-0.0122	-0.2373**	0.0642	-0.0622	-0.2535**	0.0135	-0.0348
DTM	-0.0965	0.2840**	-0.3309**	-0.0182	0.0039	-0.2072**	0.0478	-0.0394	-0.1694*	0.0302	0.0247
TT/P	0.2212**	-0.2466**	0.3576**	0.0902	0.3836**	-0.1606*	0.3844**	-0.0367	0.1589*	-0.1745**	-0.2286**
PT/P	0.2305**	-0.2116**	0.3281**	0.1042	0.3711**	-0.1464*	0.3537**	-0.0088	0.2215**	-0.1761**	-0.2333**
Pa/Pl	0.2305**	-0.2116**	0.3281**	0.1042	0.3711**	-0.1464*	0.3537**	-0.0088	0.2215**	-0.1761**	-0.2333**
PH	0.1099	-0.1523*	0.2400**	-0.1857**	0.4187**	0.4801**	0.4306**	-0.2200**	-0.0757	0.3064**	0.1851**
SL	0.1405*	-0.1837**	0.2832**	-0.1211	0.4402**	0.4916*	0.4430*	-0.1995**	-0.0451	0.2934**	0.1749**
PL	-0.1651*	0.1529*	-0.1983**	-0.5200**	0.0246	0.1179	0.0916	-0.2311**	-0.2410**	0.2154**	0.1464*
FLL	0.2165**	0.2992**	-0.1988**	0.1854	0.3214**	0.1558*	0.3121**	-0.1897**	-0.0348	0.1631*	0.0681
FLW	0.4259**	0.0636	0.1255	0.4299**	0.3509**	0.2595**	0.4190**	-0.0909	-0.0547	0.2333*	0.1155
ST	0.0338	0.3352**	-0.3220**	0.2364**	-0.0380	-0.2922**	-0.0177	-0.0930	-0.1588*	-0.1694*	0.0129
NoSp/P	0.9156**	0.5582**	-0.1451*	0.8869**	0.4755**	-0.1073	0.4310**	-0.3010**	0.0120	-0.0969	-0.1769**
FSp/Pa	**1.0000**	0.1774**	0.2588**	0.8609**	0.5418**	-0.0840	0.4980	-0.2426**	0.0947	-0.1460*	-0.2071**
SSp/Pa		**1.0000**	-0.8889**	0.3941**	0.0463	-0.0883	0.0277	-0.2367**	-0.1667*	0.0646	-0.0056
SF			**1.0000**	-0.0233	0.2179**	0.1088	0.2070**	0.1342*	0.2353**	-0.1289	-0.0806
SD				**1.0000**	0.3932**	-0.1420*	0.3332**	-0.1431*	0.1166	-0.1682*	-0.2004**
PaWt/Pl					**1.0000**	0.2594**	0.8584**	-0.5271**	0.1089	0.1182	-0.0305
TGW						**1.0000**	0.2523**	0.0045	0.1011	0.4697**	0.3321**
BY/Pl							**1.0000**	-0.4220**	-0.2639**	0.0895	-0.0559
Pl								**1.0000**	0.4149**	-0.1477*	0.0239
HI									**1.0000**	-0.1125	-0.0438
GL										**1.0000**	0.5705**
GW											**1.0000**
DSL											
DSW											
LB Ratio											
H%											
M%											
HRR											
Amyl											
GYld/Pl	0.5167**	-0.0987	0.3503**	0.3802**	0.8850**	0.3174**	0.7762**	-0.1187	0.3782**	0.0431	-0.0436

	FSp/Pa	SSp/Pa	SF	SD	PaWt/Pl	TGW	BY/Pl	Pl	Hl	GL	GW
DFF	-0.0960	0.3223**	-0.3828**	-0.0405	-0.0122	-0.2373**	0.0642	-0.0622	-0.2535**	0.0135	-0.0348
DTM	-0.0965	0.2840**	-0.3309**	-0.0182	0.0039	-0.2072**	0.0478	-0.0394	-0.1694*	0.0302	0.0247
TT/P	0.2212**	-0.2466**	0.3576**	0.0902	0.3836**	-0.1606*	0.3844**	-0.0367	0.1589*	-0.1745**	-0.2286**
PT/P	0.2305**	-0.2116**	0.3281**	0.1042	0.3711**	-0.1464*	0.3537**	-0.0088	0.2215**	-0.1761**	-0.2333**
Pa/Pl	0.2305**	-0.2116**	0.3281**	0.1042	0.3711**	-0.1464*	0.3537**	-0.0088	0.2215**	-0.1761**	-0.2333**
PH	0.1099	-0.1523*	0.2400**	-0.1857**	0.4187**	0.4801**	0.4306**	-0.2200**	-0.0757	0.3064**	0.1851**
SL	0.1405*	-0.1837**	0.2832**	-0.1211	0.4402**	0.4916*	0.4430*	-0.1995**	-0.0451	0.2934**	0.1749**
PL	-0.1651*	0.1529*	-0.1983**	-0.5200**	0.0246	0.1179	0.0916	-0.2311**	-0.2410**	0.2154**	0.1464*
FLL	0.2165**	0.2992**	-0.1988**	0.1854	0.3214**	0.1558*	0.3121**	-0.1897**	-0.0348	0.1631*	0.0681
FLW	0.4259**	0.0636	0.1255	0.4299**	0.3509**	0.2595**	0.4190**	-0.0909	-0.0547	0.2333*	0.1155
ST	0.0338	0.3352**	-0.3220**	0.2364**	-0.0380	-0.2922**	-0.0177	-0.0930	-0.1588*	-0.1694*	0.0129
NoSp/P	0.9156**	0.5582**	-0.1451*	0.8869**	0.4755**	-0.1073	0.4310**	-0.3010**	0.0120	-0.0969	-0.1769**
FSp/Pa	**1.0000**	0.1774**	0.2588**	0.8609**	0.5418**	-0.0840	0.4980	-0.2426**	0.0947	-0.1460*	-0.2071**
SSp/Pa		**1.0000**	-0.8889**	0.3941**	0.0463	-0.0883	0.0277	-0.2367**	-0.1667*	0.0646	-0.0056
SF			**1.0000**	-0.0233	0.2179**	0.1088	0.2070**	0.1342*	0.2353**	-0.1289	-0.0806
SD				**1.0000**	0.3932**	-0.1420*	0.3332**	-0.1431*	0.1166	-0.1682*	-0.2004**
PaWt/Pl					**1.0000**	0.2594**	0.8584**	-0.5271**	0.1089	0.1182	-0.0305
TGW						**1.0000**	0.2523**	0.0045	0.1011	0.4697**	0.3321**
BY/Pl							**1.0000**	-0.4220**	-0.2639**	0.0895	-0.0559
Pl								**1.0000**	0.4149**	-0.1477*	0.0239
Hl									**1.0000**	-0.1125	-0.0438
GL										**1.0000**	0.5705**
GW											**1.0000**
DSL											
DSW											
LB Ratio											
H%											
M%											
HRR											
Amyl											
GYld/Pl	0.5167**	-0.0987	0.3503**	0.3802**	0.8850**	0.3174**	0.7762**	-0.1187	0.3782**	0.0431	-0.0436

* Significant at 5% and ** Significant at 1% level

	DSL	DSW	LB Ratio	H%	M%	HRR	Amylose
DFF	-0.0359	-0.0300	0.0648	-0.1120	-0.0208	0.0767	0.0857
DTM	0.0437	0.0282	-0.0126	-0.1333*	-0.1369*	0.0327	0.0005
TT/P	-0.1654*	-0.2037**	0.0693	-0.0239	0.0762	-0.1914**	0.0001
PT/P	-0.1662*	-0.2096**	0.0747	-0.0267	0.0921	-0.1759**	0.0145
Pa/Pl	-0.1662*	-0.2096**	0.0747	-0.0267	0.0921	-0.1759**	0.0145
PH	0.3073**	0.1574*	0.0675	0.0083	0.0399	0.0144	0.1630*
SL	0.2928**	0.1437*	0.0738	0.0183	0.0522	0.0182	0.1670*
PL	0.2259**	0.1589*	-0.0153	-0.0657	-0.0678	-0.0203	0.0393
FLL	0.1311*	0.0626	0.0623	-0.0271	-0.0249	-0.0054	0.0880
FLW	0.2094**	0.0913	0.0676	0.0778	0.0225	-0.0669	0.1643*
ST	-0.1425*	0.0459	-0.1865**	0.1413*	-0.0295	-0.0299	-0.3152**
NoSp/P	-0.0916	-0.1781**	0.1133	0.0274	-0.0146	-0.0815	-0.0194
FSp/Pa	-0.1401*	-0.2105**	0.1097	0.0499	0.0529	-0.0822	-0.0387
SSp/Pa	-0.0656	-0.0016	0.0504	-0.0356	-0.1460*	-0.0307	0.0314
SF	-0.1260	-0.0847	-0.0064	0.0812	0.1565*	0.0019	-0.0760
SD	-0.1677*	-0.2111**	0.0947	0.0407	0.0104	-0.0650	-0.0449
PaWt/Pl	-0.1187	-0.0383	0.1194	-0.0084	0.0038	-0.0873	-0.0294
TGW	-0.4472**	0.3082**	0.0201	-0.0539	0.0740	0.0334	0.0607
BY/Pl	0.0930	-0.0637	0.1124	0.0604	0.0543	-0.0822	0.0775
PI	-0.1431*	0.0192	-0.0638	0.1111	0.2551**	0.1169	0.0854
HI	-0.1256	-0.0406	0.0070	-0.0375	0.0941	0.0199	-0.0546
GL	0.9731**	0.5568**	0.0940	0.2169**	-0.0055	-0.0813	0.0458
GW	0.5561**	0.9803**	-0.4123**	-0.0727	0.0875	0.0796	-0.0704
DSL	**1.0000**	0.5455**	0.0721	-0.2218**	0.0002	-0.0785	0.0381
DSW		**1.0000**	-0.4201**	-0.0720	0.0810	0.0731	-0.0958
LB Ratio			**1.0000**	-0.0480	0.0025	-0.0598	0.1532*
H%				**1.0000**	0.3471**	0.2298**	-0.2087
M%					**1.0000**	0.5106**	0.1972
HRR						**1.0000**	0.1453*
Amyl							**1.0000**
GYld/Pl	0.0380	-0.0535	0.1032	0.0074	0.1316*	-0.0750	0.0250

4.5 Path coefficient analysis

It is a standardized partial regression coefficient, which splits the correlation coefficients into the measures of direct and indirect effects. It measures the direct and indirect contribution of various independent characters on a dependent character. For a replicated data, it is of three types, phenotypic, genotypic and environmental path coefficient.

Phenotypic path coefficients are worked out from all possible phenotypic correlation coefficients among the various characters under study. Path coefficients that are worked out from all possible genotypic correlation coefficients of all the various characters under study constitute the genotypic path coefficients. Environmental path coefficients are worked out from all possible environmental correlation coefficients among various characters under study. Direct effect is the straightway effect of an independent character on a dependent one. Indirect effect is the effect of an independent character on the dependent one via other independent characters. Residual effect is the measure of the effect of the other possible independent characters, which were not included in the study of the dependent character.

In general, the genotypic direct as well as indirect effects were higher in magnitude as compared to the phenotypic direct and indirect effects. The estimates of path coefficients for yield and quality attributing traits on grain yield are furnished in table15. The result obtained from present investigation for direct and indirect effects are presented character wise as:

Direct effects

A. Positive direct effects

Amongst all the independent characters number of spikelets per panicle (3.4632) exhibited maximum positive effect followed by plant height (1.4783), biological yield per plant (0.5831), panicle weight per plant (0.4456), harvest index (0.3816), seed breadth (0.2387), panicle index (0.2151), seed length (0.1897), total number of productive tillers per plant (0.0732), stem

thickness (0.0703), milling per cent (0.0335), 1000 seed weight (0.0301), days to maturity (0.0203), flag leaf width (0.0079) and flag leaf length (0.0039).

B. Negative direct effects

Negative effect was manifested by fertile spikelets per panicle (-2.5334), sterile spikelets per panicle (-1.6651), stem length (-1.3713), spikelet fertility per cent (-0.3500), spikelet density (-0.3283), panicle length (-0.3199), decorticated seed breadth (-0.2589), decorticated seed length (-0.1832), hulling percent (-0.0627), total number of tillers per plant (-0.0527), days to 50 percent flowering (-0.0411), amylose percent (-0.0301), head rice recovery (-0.0174) and LB ratio (-0.0128).

Indirect effects

Days to 50% flowering

This character showed positive indirect effect via spikelet fertility percent (0.0160), harvest index (0.0107), flag leaf width (0.0089), total number of tillers per plant (0.0071), total number of productive tillers per plant (0.0062), number of panicles per plant (0.0062), hulling percent (0.0054), fertile spikelets per panicle (0.0041), stem length (0.0083) and panicle index (0.0026) on grain yield per plant.

Days to maturity

In present investigation, this character showed positive indirect effect via days to 50% flowering (0.0173), stem thickness (0.0093), sterile spikelets per panicle (0.0058) and panicle length (0.0024) on grain yield per plant

Total number of tillers per plant

This trait had positive indirect effect via grain width (0.0164), sterile spikelets per panicle (0.0160), decorticated grain width (0.0152), head rice recovery (0.0125), grain length (0.0112), decorticated grain length (0.0106), 1000 grain weight (0.0103), days to 50% flowering (0.0091), stem thickness (0.0083) and days to maturity (0.0082) on grain yield per plant.

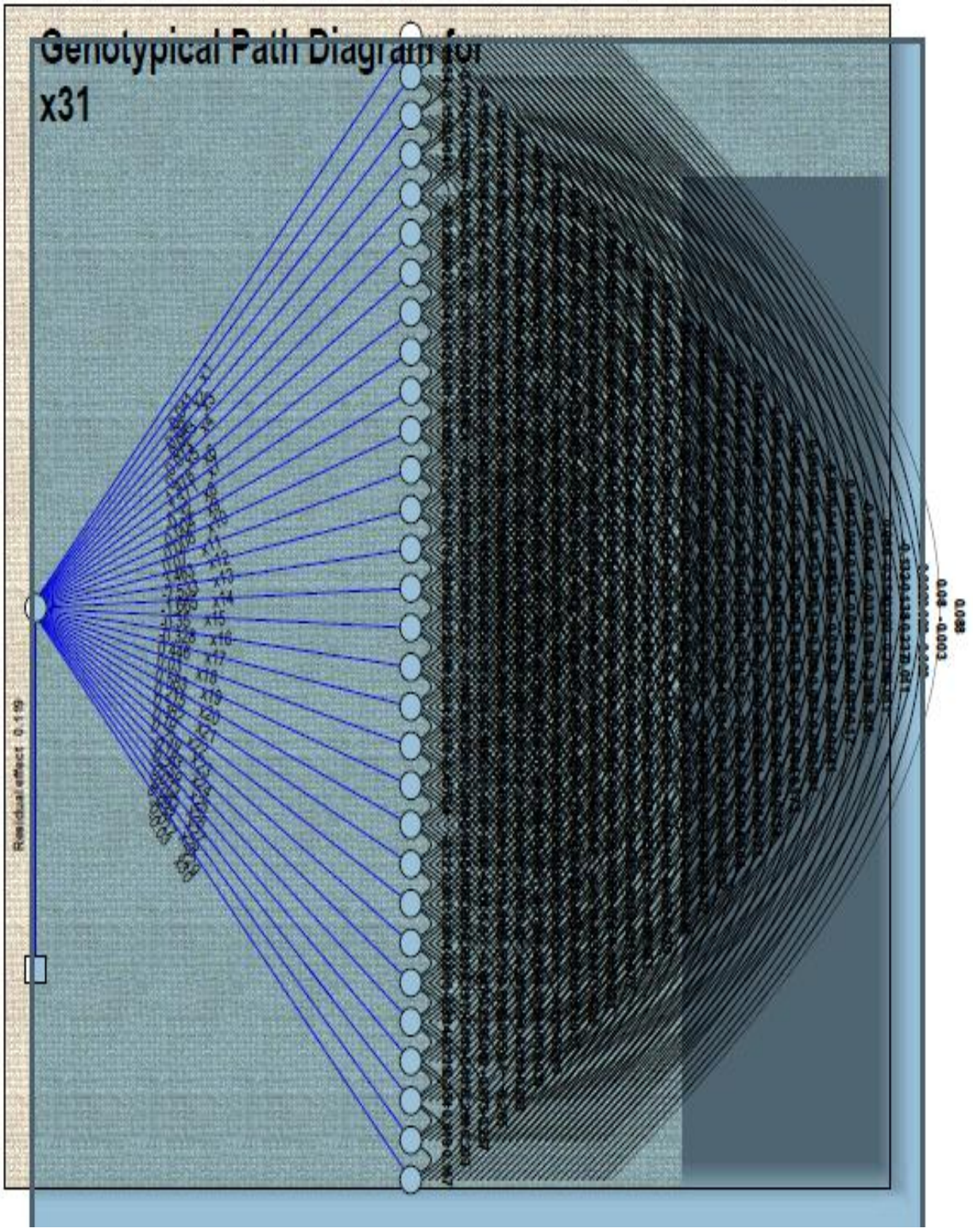

Fig. 1. Genotypical path diagram

Total number of productive tillers per plant

It had positive indirect effect via number of panicles per plant (0.0732), number of tillers per plant (0.0705), panicle weight per plant (0.0341), biological yield per plant (0.0319), spikelet fertility percent (0.0299), harvest index (0.0210), fertile spikelets per panicle (0.0207), spikelet density (0.0097), number of spikelets per panicle (0.0096) and LB ratio (0.0095) on grain yield per plant.

Panicle number per plant

This character had no positive or negative direct or indirect effect on grain yield per plant.

Plant height

This character showed positive indirect effect via stem length (1.4662), 1000 grain weight (0.7198), panicle length (0.6949), biological yield per plant (0.6373), panicle weight per plant (0.6218), flag leaf width (0.5548), decorticated grain length (0.4723), grain length (0.4601), spikelet fertility percentage (0.3564), flag leaf length (0.3110), grain breadth (0.2940), decorticated grain breadth (0.2553), LB ratio (0.1667), fertile spikelets per panicle (0.1626), milling percent (0.0593) and number of spikelets per panicle (0.0446) on grain yield per plant.

Stem length

This character, under study, had positive indirect effect via stem thickness (0.5939), panicle index (0.2967), days to maturity (0.2548), sterile spikelets per panicle (0.2528), spikelet density (0.1665), days to 50 percent flowering (0.1116), harvest index (0.0640), total number of productive tillers per plant (0.0281) and panicle number per plant (0.0281) on grain yield per plant.

Panicle length

Panicle length showed positive indirect effect via spikelet density (0.1660), panicle index (0.0809), harvest index (0.0806), stem thickness (0.0710), spikelet fertility percent (0.0643), flag leaf width (0.0615), fertile spikelets per panicle (0.0535), number of spikelets per panicle (0.0249), hulling percent (0.0242), total number of tillers per plant (0.0225), milling percent

(0.0224), total number of productive tillers per plant (0.0163), panicle number per plant (0.0163), head rice recovery (0.0116) and LB ratio (0.0101) on grain yield per plant.

Flag leaf length

Flag leaf length manifested positive indirect effect via flag leaf width (0.0015), panicle weight per plant (0.0013), biological yield per plant (0.0012), number of spikelets per panicle (0.0012) and sterile spikelets per panicle (0.0012) on grain yield per plant.

Flag leaf width

Flag leaf width had positive indirect effect via fertile spikelets per panicle (0.0035), spikelet density (0.0035), stem length (0.0034), biological yield per plant (0.0034), number of spikelets per panicle (0.0032), plant height (0.0030), flag leaf length (0.0030), panicle weight per plant (0.0029), 1000 grain weight (0.0022), grain length (0.0020), decorticated grain length (0.0018) and amylose percent (0.0014) on grain yield per plant .

Stem thickness

This character had positive indirect effect via days to 50 percent flowering (0.0271), sterile spikelets per panicle (0.0247), spikelet density (0.0172), number of spikelets per panicle (0.0121), hulling percent (0.0118), decorticated grain width (0.0037) and fertile spikelets per panicle (0.0024) on grain yield per plant .

Total number of spikelets per panicle

In the present investigation, this trait showed positive indirect effect via fertile spikelets per panicle (3.1720), spikelet density (3.0757), sterile spikelets per panicle (1.9352), panicle weight per plant (1.6565), biological yield per plant (1.4958), flag leaf width (1.3848), flag leaf length (1.0635), LB ratio (0.6483), total number of productive tillers per plant (0.4524), panicle number per plant (0.4524), total number of tillers per plant (0.3487), days to 50 percent flowering (0.1723), days to maturity (0.1143), stem length (0.1496), plant height (0.1044) and hulling percent (0.0418) on grain yield per plant.

Fertile spikelets per panicle

This character had positive indirect effect via panicle index (0.6703), decorticated grain breadth (0.5846), grain breadth (0.5636), panicle length (0.4233), grain length (0.3752), decorticated grain length (0.3715), days to maturity (0.2541), days to 50 percent flowering (0.2498), head rice recovery (0.2438), 1000 grain weight (0.2150) and amylose percent (0.1021) on grain yield per plant .

Sterile spikelets per panicle

It had positive indirect effect via spikelet fertility percentage (1.4800), total number of tillers per plant (0.1509), total number of productive tillers per plant (0.4401), panicle number per plant (0.4401), panicle index (0.4291), stem length (0.3069), harvest index (0.2871), plant height (0.2545), 1000 grain weight (0.1509), hulling percent (0.0731) and head rice recovery (0.0537) on grain yield per plant.

Spikelet fertility per cent

This character had positive indirect effect via sterile spikelets per panicle (0.3111), days to 50 percent flowering (0.1359), days to maturity (0.1183), stem thickness (0.1182), flag leaf length (0.0709), panicle length (0.0704), number of spikelets per panicle (0.0508), grain length (0.0462), decorticated grain length (0.0461), decorticated grain breadth (0.0326), grain breadth (0.0310) and amylose percent (0.0271) on grain yield per plant .

Spikelet density

The spikelet density showed positive indirect effect via panicle length (0.1704), decorticated grain width (0.0759), grain width (0.0704), plant height (0.0608), decorticated grain length (0.0576), grain length (0.0559), panicle index (0.0513), 1000 grain weight (0.0473), stem length (0.0399) and head rice recovery (0.0225) on grain yield per plant .

Panicle weight per plant

It had positive indirect effect via biological yield per plant (0.3845), fertile spikelets per panicle (0.2429), number of spikelets per panicle (0.2131), total tillers per plant (0.2114), productive tillers per plant (0.2079), panicle number per plant (0.2079), stem length (0.1971), plant height (0.1874), spikelet density (0.1765), flag leaf width (0.1646), flag leaf length (0.1449), 1000 grain weight (0.1178) and spikelet fertility percent (0.0982) on grain yield per plant .

1000 grain weight

This trait had positive indirect effect via stem length (0.0150), plant height (0.0147), grain length (0.0145), decorticated grain length (0.0140), grain breadth (0.0110) and decorticated grain breadth (0.0103) on grain yield per plant.

Biological yield per plant per plant

In this study, this trait had positive indirect effect via panicle weight per plant (0.5031), fertile spikelets per panicle (0.2910), total tillers per plant (0.2713), stem length (0.2586), productive tillers per plant (0.2538), number of panicles per plant (0.2538), flag leaf width (0.2528), number of spikelets per panicle (0.2518), plant height (0.2513), spikelet density (0.1949), flag leaf length (`0.1832), 1000 grain weight (0.1493), spikelet fertility percent (0.1212), LB ratio (0.1056), decorticated grain length (0.0568), panicle length (0.0540), grain length (0.0533), amylose percent (0.0449), hulling percent (0.0396), days to 50 percent flowering (0.0374), milling percent (0.0322), days to maturity (0.0275) and sterile spikelets per panicle (0.0163) on grain yield per plant.

Panicle index

It had positive indirect effect via harvest index (0.0862), milling percent (0.0615), head rice recovery (0.0329), spikelet fertility percent (0.0313), amylose percent (0.0195) and grain breadth (0.0089) on grain yield per plant.

Harvest index

Harvest index had positive indirect effect via panicle index (0.1528), productive tillers per plant (0.1096), panicle number per plant (0.1096), spikelet

fertility percent (0.093), total tillers per plant (0.0788), LB ratio (0.077), spikelet density (0.0460), panicle weight per plant (0.0428), 1000 grain weight (0.0425), milling percent (0.0381), fertile spikelets per panicle (0.0372), head rice recovery (0.0148) on grain yield per plant.

Seed length

Seed length showed positive indirect effect via decorticated grain length (0.1888), grain breadth (0.1141), decorticated grain breadth (0.1138), 1000 grain weight (0.0916), plant height (0.0590), stem length (0.0566), flag leaf width (0.0472), panicle length (0.0415), LB ratio (0.0329), flag leaf length (0.0319), panicle weight per plant (0.0227), sterile spikelets per panicle (0.0125) and biological yield per plant (0.0173) on grain yield per plant.

Seed width

It exhibited positive indirect effect via decorticated grain breadth (0.2371), decorticated grain length (0.1441), grain length (0.1435), 1000 grain weight (0.0868), plant height (0.0475), stem length (0.0449), panicle length (0.0374), flag leaf width (0.0308), stem thickness (0.0031), head rice recovery (0.0253), milling percent (0.0225) and flag leaf length (0.0165) on grain yield per plant.

Decorticated seed length

This trait had positive indirect effect via hulling percent (0.0467), number of productive tillers per plant (0.0374), panicle number per plant (0.0374), total tillers per plant (0.0368), spikelet density (0.0322), panicle index (0.0313), stem thickness (0.0282), fertile spikelets per panicle (0.0269), harvest index (0.0256), spikelet fertility percentage (0.0241), head rice recovery (0.0192) and number of spikelets per panicle (0.0176) on grain yield per plant.

Decorticated seed width

This trait exhibited positive indirect effect via LB ratio (0.2289), productive tillers per plant (0.0768), panicle number per plant (0.0768), total tillers per plant (0.0746), spikelet density (0.0599), fertile spikelets per panicle (0.0597), number of spikelets per panicle (0.0505), spikelet fertility percent (0.0241), amylose

percent (0.0241), biological yield per plant per plant (0.0180), hulling percent (0.0179), panicle weight per plant (0.0122) and harvest index (0.0110) on grain yield per plant .

LB Ratio

This character had positive indirect effect via decorticated grain width (0.0113), grain width (0.0108), stem thickness (0.0043) and panicle index (0.0018) on grain yield per plant.

Hulling per cent

This trait had positive indirect effect via amylose percent (0.0161), decorticated grain length (0.0160), grain length (0.0158), days to maturity (0.0096), LB ratio (0.0087) and days to 50 percent flowering (0.0083) on grain yield per plant.

Milling per cent

It had positive indirect effect via head rice recovery (0.0207), hulling percent (0.0118), panicle index (0.0096), amylose percent (0.0068), spikelet fertility percent (0.00545), productive tillers per plant (0.0039), panicle number per plant (0.0039), harvest index (0.0033), total tillers per plant (0.0031) and decorticated grain breadth (0.0031) on grain yield per plant .

Head rice recovery

This trait manifested positive indirect effect via total tillers per plant (0.0041), productive tillers per plant (0.0038), panicle number per plant (0.0038), panicle weight per plant (0.0019), biological yield per plant per plant (0.0018), grain length (0.0018), decorticated grain length (0.0018) and fertile spikelets per panicle (0.0017) on grain yield per plant.

Amylose percentage

This character had positive indirect effect via stem thickness (0.0101), hulling percent (0.0015), decorticated grain width (0.0028), spikelet fertility percent (0.0023), grain width (0.0019) and harvest index (0.0015) on grain yield per plant.

Table 15. Path Analysis of Yield Attributing and Quality Traits of JNPT Lines

	DFF	DTM	TT/P	PT/P	Pa/Pl	PH	SL	PL	FLL	FLW	ST	NoSp/Pa	FSp/Pa	SSp/Pa	SF
DFF	**-0.0411**	-0.0351	0.0071	0.0062	0.0062	0.0021	0.0033	-0.0075	0.0016	0.0089	-0.0158	-0.0020	0.0041	-0.0134	0.0160
DTM	0.0173	**0.0203**	-0.0031	- 0.0027	-0.0027	-0.0032	-0.0038	0.0024	-0.0015	-0.0051	0.0093	0.0007	-0.0020	0.0058	-0.0069
TT/P	0.0091	0.0082	**-0.0527**	-0.0508	-0.0508	-0.0013	-0.0019	0.0037	0.0009	0.0009	0.0083	-0.0053	-0.0140	0.0160	-0.0231
PT/P	-0.0111	-0.0096	0.0705	**0.0732**	0.0732	-0.0019	-0.0015	-0.0037	0.0002	-0.0035	-0.0111	0.0096	0.0207	-0.0193	0.0299
Pa/Pl	0.0000	0.0000	0.0000	0.0000	**0.0000**	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
PH	-0.0767	-0.2350	0.0359	-0.0388	-0.0388	**1.4783**	1.4662	0.6949	0.3110	0.5548	-0.6489	0.0446	0.1626	-0.2260	0.3564
SL	0.1116	0.2548	-0.0492	0.0281	0.0281	-1.3601	**-1.3713**	-0.4850	-0.2697	-0.5835	0.5939	-0.0592	-0.1930	0.2528	-0.3902
PL	-0.0585	-0.0384	0.0225	0.0163	0.0163	-0.1504	-0.1131	**-0.3199**	-0.0581	0.0615	0.0710	0.0249	0.0535	-0.0495	0.0643
FLL	-0.0002	-0.0003	-0.0001	0.0000	0.0000	0.0008	0.0008	0.0007	**0.0039**	0.0015	-0.0008	0.0012	0.0009	0.0012	-0.0008
FLW	-0.0017	-0.0020	-0.0001	-0.0004	-0.0004	0.0030	0.0034	-0.0015	0.0030	**0.0079**	-0.0014	0.0032	0.0035	0.0005	0.0010
ST	0.0271	0.0323	-0.0110	-0.0106	-0.0106	-0.0308	-0.0304	-0.0156	-0.0143	-0.0128	**0.0703**	0.0121	0.0024	0.0247	-0.0237
NoSp/p	0.1723	0.1143	0.3487	0.4524	0.4524	0.1044	0.1496	-0.2695	1.0635	1.3848	0.5957	**3.4632**	3.1720	1.9352	-0.5024
FSp/Pa	0.2498	0.2541	-0.6741	-0.7164	-0.7164	-0.2787	-0.3565	0.4233	-0.5510	-1.1192	-0.0871	-2.3204	**-2.5334**	-0.4534	-0.6538
SSp/Pa	-0.5421	-0.4803	0.5043	0.4401	0.4401	0.2545	0.3069	-0.2576	-0.5053	-0.1118	-0.5843	-0.9305	-0.2980	**-1.6651**	1.4800
SF	0.1359	0.1183	-0.1532	-0.1431	-0.1431	-0.0844	-0.0996	0.0704	0.0709	-0.0449	0.1182	0.0508	-0.0903	0.3111	**-0.3500**
SD	0.0137	0.0064	-0.0368	-0.0433	-0.0433	0.0608	0.0399	0.1704	-0.0613	-0.1459	-0.0802	-0.2916	-0.2832	-0.1296	0.0075
PaWt/P	-0.0060	0.0021	0.2114	0.2079	0.2079	0.1874	0.1971	0.0109	0.1449	0.1646	-0.0177	0.2131	0.2429	0.0207	0.0982
TGW	-0.0074	-0.0065	-0.0059	-0.0054	-0.0054	0.0147	0.0150	0.0037	0.0047	0.0082	-0.0091	-0.0033	-0.0026	-0.0027	0.0034
BY/Pl	0.0374	0.0275	0.2713	0.2538	0.2538	0.2513	0.2586	0.0540	0.1832	0.2528	-0.0116	0.2518	0.2910	0.0163	0.1212
PI	-0.0135	-0.0094	-0.0155	-0.0070	-0.0070	-0.0513	-0.0465	-0.0544	-0.0448	-0.0229	-0.0203	-0.0705	-0.0569	-0.0554	0.0313
HI	-0.0994	-0.0659	0.0788	0.1096	0.1096	-0.0299	-0.0178	-0.0962	-0.0131	-0.0226	-0.0602	0.0046	0.0372	-0.0658	0.0930
GL	0.0024	0.0056	-0.0402	-0.0412	-0.0412	0.0590	0.0566	0.0415	0.0319	0.0472	-0.0344	-0.0186	-0.0281	0.0125	-0.0250
GW	-0.0088	0.0068	-0.0740	-0.0763	-0.0763	0.0475	0.0449	0.0374	0.0165	0.0308	0.0031	-0.0452	-0.0531	-0.0010	-0.0212
DSL	-0.0078	-0.0086	0.0368	0.0374	0.0374	-0.0585	-0.0558	-0.0433	-0.0250	-0.0423	0.0282	0.0176	0.0269	-0.0124	0.0241
DSW	0.0085	-0.0088	0.0746	0.0768	0.0768	-0.0447	-0.0409	-0.0451	-0.0165	-0.0258	-0.0135	0.0505	0.0597	0.0002	0.0241
LB R	-0.0011	0.0005	-0.0013	-0.0017	-0.0017	-0.0014	-0.0016	0.0004	-0.0013	-0.0014	0.0043	-0.0024	-0.0023	-0.0011	0.0002
H%	0.0083	0.0096	0.0020	0.0022	0.0022	-0.0006	-0.0013	0.0048	0.0015	-0.0055	-0.0105	-0.0018	-0.0035	0.0028	-0.0060
M%	-0.0007	-0.0046	0.0031	0.0039	0.0039	0.0013	0.0018	-0.0023	-0.0008	0.0008	-0.0012	-0.0005	0.0018	-0.0050	0.0054
HRR	-0.0014	-0.0005	0.0041	0.0038	0.0038	-0.0003	-0.0004	0.0006	-0.0001	0.0011	0.0003	0.0016	0.0017	0.0006	0.0000
Amyl	-0.0026	0.0001	0.0002	-0.0003	-0.0003	-0.0050	-0.0051	-0.0012	-0.0027	-0.0052	0.0101	0.0006	0.0012	-0.0010	0.0023
GYld/Pl	-0.0865	-0.0441	0.5540	0.5739	0.5739	0.3627	0.3964	-0.0838	0.2722	0.3732	-0.0955	0.3987	0.5216	-0.1004	0.3552

	SD	PaWt/P	TGW	BY/Pl	Pl	HI	GL	GW	DSL	DSW	LB R	H%	M%	HRR	Amyl
DFF	0.0017	0.0006	0.0100	-0.0026	0.0026	0.0107	-0.0005	0.0015	-0.0018	0.0014	-0.0035	0.0054	0.0009	-0.0033	-0.0036
DTM	-0.0004	0.0001	-0.0044	0.0010	-0.0009	-0.0035	0.0006	0.0006	0.0010	0.0007	-0.0008	-0.0031	-0.0028	0.0006	-0.0001
TT/P	-0.0059	-0.0250	0.0103	-0.0245	0.0038	-0.0109	0.0112	0.0164	0.0106	0.0152	-0.0055	0.0017	-0.0049	0.0125	0.0004
PT/P	0.0097	0.0341	-0.0131	0.0319	-0.0024	0.0210	-0.0159	-0.0234	-0.0149	-0.0217	0.0095	-0.0026	0.0086	-0.0159	0.0008
Pa/Pl	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
PH	-0.2739	0.6218	0.7198	0.6373	-0.3528	-0.1159	0.4601	0.2940	0.4723	0.2553	0.1667	0.0138	0.0593	0.0245	0.2450
SL	0.1665	-0.6064	-0.6835	-0.6081	0.2967	0.0640	-0.4089	-0.2580	-0.4175	-0.2165	-0.1702	-0.0286	-0.0721	-0.0313	-0.2328
PL	0.1660	-0.0078	-0.0390	-0.0296	0.0809	0.0806	-0.0700	-0.0501	-0.0756	-0.0557	0.0101	0.0242	0.0224	0.0116	-0.0130
FLL	0.0007	0.0013	0.0006	0.0012	-0.0008	-0.0001	0.0007	0.0003	0.0005	0.0003	0.0004	-0.0001	-0.0001	0.0000	0.0004
FLW	0.0035	0.0029	0.0022	0.0034	-0.0008	-0.0005	0.0020	0.0010	0.0018	0.0008	0.0009	0.0007	0.0002	-0.0005	0.0014
ST	0.0172	-0.0028	-0.0213	-0.0014	-0.0066	-0.0111	-0.0127	0.0009	-0.0108	0.0037	-0.0235	0.0118	-0.0024	-0.0011	-0.0235
NoSp/	3.0757	1.6565	-0.3767	1.4958	-1.1354	0.0418	-0.3402	-0.6559	-0.3331	-0.6757	0.6483	0.1010	-0.0550	-0.3253	-0.0716
FSp/Pa	-2.1850	-1.3812	0.2150	-1.2645	0.6703	-0.2469	0.3752	0.5636	0.3715	0.5846	-0.4552	-0.1419	-0.1348	0.2438	0.1021
SSp/Pa	-0.6574	-0.0775	0.1509	-0.0467	0.4291	0.2871	-0.1096	0.0068	-0.1130	0.0012	-0.1459	0.0731	0.2498	0.0537	-0.0527
SF	0.0080	-0.0771	-0.0390	-0.0728	-0.0510	-0.0853	0.0462	0.0310	0.0461	0.0326	0.0052	-0.0332	-0.0562	0.0009	0.0271
SD	**-0.3283**	-0.1300	0.0473	-0.1098	0.0513	-0.0396	0.0559	0.0704	0.0576	0.0759	-0.0522	-0.0146	-0.0031	0.0225	0.0153
PaWt/P	0.1765	**0.4456**	0.1178	0.3845	-0.2445	0.0500	0.0533	-0.0162	0.0554	-0.0209	0.0892	-0.0033	0.0012	-0.0483	-0.0130
TGW	-0.0043	0.0080	**0.0301**	0.0077	0.0002	0.0034	0.0145	0.0110	0.0140	0.0103	0.0015	-0.0021	0.0022	0.0009	0.0018
BY/Pl	0.1949	0.5031	0.1493	**0.5831**	-0.2662	-0.1560	0.0533	-0.0351	0.0568	-0.0407	0.1056	0.0396	0.0322	-0.0600	0.0449
Pl	-0.0336	-0.1180	0.0015	-0.0982	**0.2151**	0.0862	-0.0349	0.0089	-0.0368	0.0071	-0.0298	0.0329	0.0615	0.0368	0.0195
HI	0.0460	0.0428	0.0425	-0.1021	0.1528	**0.3816**	-0.0456	-0.0162	-0.0533	-0.0162	0.0077	-0.0098	0.0381	0.0148	-0.0192
GL	-0.0323	0.0227	0.0916	0.0173	-0.0307	-0.0227	**0.1897**	0.1141	0.1888	0.1138	0.0329	-0.0477	-0.0009	-0.0199	0.0097
GW	-0.0512	-0.0087	0.0868	-0.0144	0.0098	-0.0101	0.1435	**0.2387**	0.1441	0.2371	-0.2021	-0.0182	0.0225	0.0253	-0.0154
DSL	0.0322	-0.0228	-0.0850	-0.0178	0.0313	0.0256	-0.1823	-0.1106	**-0.1832**	-0.1111	-0.0362	0.0467	-0.0009	0.0192	-0.0072
DSW	0.0599	0.0122	-0.0890	0.0180	-0.0085	0.0110	-0.1552	-0.2572	-0.1570	**-0.2589**	0.2289	0.0179	-0.0238	-0.0259	0.0241
LB R	-0.0020	-0.0026	-0.0006	-0.0023	0.0018	-0.0003	-0.0022	0.0108	-0.0025	0.0113	**-0.0128**	0.0018	0.0001	0.0009	-0.0034
H%	-0.0028	0.0005	0.0044	-0.0043	-0.0096	0.0016	0.0158	0.0048	0.0160	0.0043	0.0087	**-0.0627**	-0.0222	-0.0167	0.0161
M%	0.0003	0.0001	0.0025	0.0018	0.0096	0.0033	-0.0002	0.0032	0.0002	0.0031	-0.0002	0.0118	**0.0335**	0.0207	0.0068
HRR	0.0012	0.0019	-0.0005	0.0018	-0.0030	-0.0007	0.0018	-0.0018	0.0018	-0.0017	0.0013	-0.0046	-0.0108	**-0.0174**	-0.0029
Amyl	0.0014	0.0009	-0.0018	-0.0023	-0.0027	0.0015	-0.0015	0.0019	-0.0012	0.0028	-0.0080	0.0077	-0.0061	-0.0050	**-0.0301**

4.6 Principal Component Analysis

Principal Component Analysis (PCA) is a powerful tool in modern data analysis because this is a well-known multivariate statistical technique which is used to reduce the data with large number of correlated variables into a substantially smaller set of new variables through linear combination of the variables that accounts most of the variation present in the original variables. The objective of principal component analysis is to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson, 1972 and Morrison, 1978) and also to rank genotypes on the basis of PC scores. Principal components are generally estimated either from correlation matrix or covariance matrix. When the variables are measured in different units and scale effects, they can influence the composition of derived components. In such situations it becomes desirable to standardize the variables.

In present investigation, PCA was performed for yield, yield and quality contributing traits of JNPT rice lines and presented in Tables 16, 17, 18 and 19. Out of thirty one, only five principal components (PCs) exhibited more than 1.9 eigen value, and showed about 62.789% variability among the traits studied. So, these five PCs were given due importance for further explanation. The PC1 showed 19.214 % while, PC2, PC3, PC4 and PC5 exhibited 15.579 %, 12.520 %, 8.123 % and 7.353% variability respectively among the lines for the traits under study (Table 16).

Table 16. Eigen value and percentage of variation for corresponding 31 yield and quality traits in JNPT lines of rice

Traits	Principal component	Eigen value	Percentage of total variation	Cumulative percentage
DFF	PC1	5.956	19.214	19.214
DTM	PC2	4.830	15.579	34.794
TT/P	PC3	3.881	12.520	47.313
PT/P	PC4	2.518	8.123	55.436
Pa/PL	PC5	2.280	7.353	62.789
PH	PC6	1.901	6.134	68.923
SL	PC7	1.627	5.249	74.172
PL	PC8	1.324	4.270	78.442
FLL	PC9	1.134	3.659	82.101
FLW	PC10	1.073	3.461	85.562
ST	PC11	0.839	2.707	88.269
No.sp/p	PC12	0.785	2.531	90.800
Fsp/pa	PC13	0.672	2.167	92.967
Ssp/pa	PC14	0.475	1.533	94.500
SF	PC15	0.382	1.231	95.731
SD	PC16	0.341	1.100	96.831
PaWt/Pl	PC17	0.271	0.873	97.704
TGW	PC18	0.230	0.743	98.447
BY/pl	PC19	0.213	0.689	99.136
PI	PC20	0.109	0.350	99.486
HI	PC21	0.072	0.233	99.719
SL	PC22	0.034	0.109	99.828
SW	PC23	0.016	0.053	99.881
DSL	PC24	0.011	0.036	99.917
DSW	PC25	0.010	0.031	99.948
LB	PC26	0.008	0.027	99.975
H%	PC27	0.006	0.019	99.994
M%	PC28	0.002	0.006	100.000
HRR	PC29	1.452E-6	4.684E-6	100.000
Amyl%	PC30	1.901E-12	6.131E-12	100.000
Gy/pl	PC31	9.415E-19	3.037E-18	100.000

4.6.1 Extraction Method: Principal Component Analysis.

Scree plot explained the percentage of variance associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. PC1 showed 19.214% variability with eigen value 5.956 which then declined gradually. Elbow type line was obtained which after fifth PC tended to straight with little variance observed in each PC. From the graph, it is clear that the maximum variation was observed in PC1. So, selection of lines from this PC would be useful (Figure1).

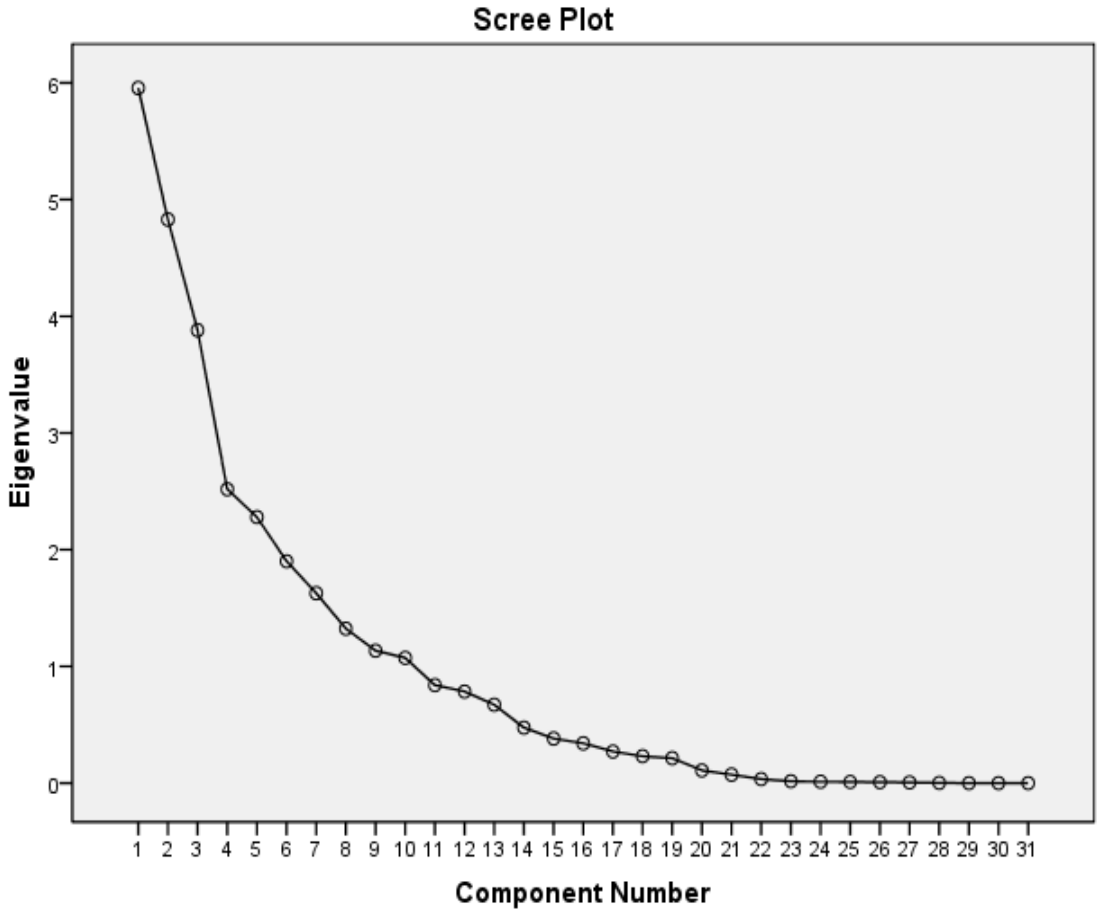

Fig. 2. Scree plot of principal component analysis of rice germplasm between eigen value and principal components

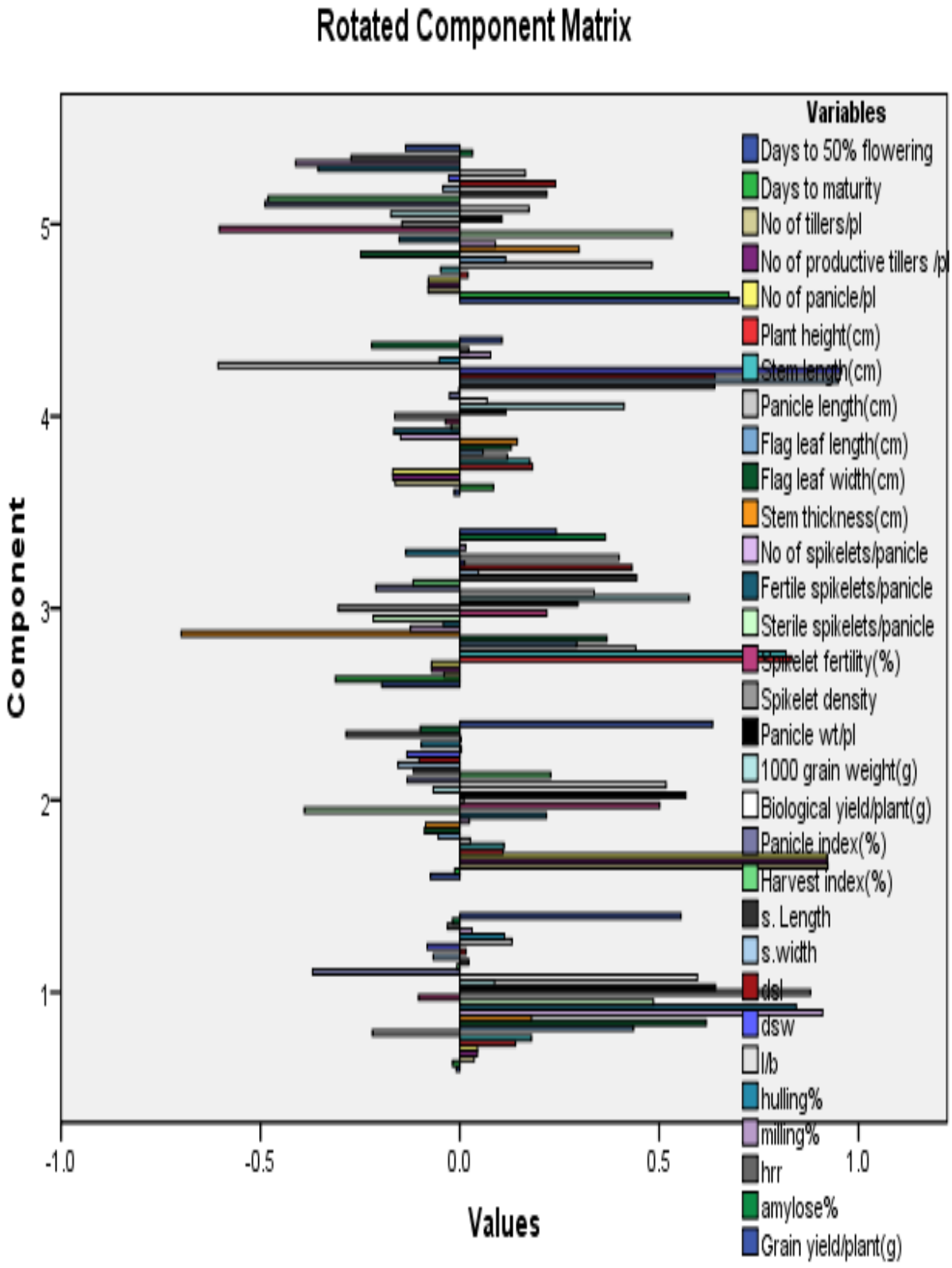

Fig. 3. Rotated Component Matrix

Table 17. Principal Components for 31 yield attributing and quality traits of JNPT lines

Rotated Component Matrix					
Traits	**Principle Component**				
	1	2	3	4	5
DFF	-0.009	-0.073	-0.196	-0.015	**0.700**
DTM	-0.018	-0.013	-0.312	0.085	**0.675**
TT/P	0.036	**0.923**	-0.040	-0.162	-0.079
PT/P	0.044	**0.922**	-0.071	-0.168	-0.079
Pa/PL	0.044	**0.922**	-0.071	-0.168	-0.079
PH	0.140	0.108	**0.832**	0.182	0.021
SL	0.180	0.111	**0.818**	0.176	-0.048
PL	-0.220	0.026	0.441	0.120	0.482
FLL	0.436	-0.054	0.293	0.058	0.115
FLW	**0.618**	-0.089	0.369	0.129	-0.248
ST	0.180	-0.086	-0.699	0.144	0.299
No.sp/p	**0.910**	0.024	-0.124	-0.149	0.089
Fsp/pa	**0.844**	0.217	-0.042	-0.166	-0.152
Ssp/pa	0.486	-0.390	-0.217	-0.022	0.533
SF	-0.104	**0.501**	0.218	-0.036	-0.603
SD	**0.880**	0.011	-0.305	-0.163	-0.145
PaWt/Pl	**0.642**	**0.567**	0.296	0.116	0.106
TGW	0.087	-0.067	**0.576**	0.412	-0.173
BY/pl	**0.596**	0.517	0.337	0.068	0.174
PI	-0.369	-0.132	-0.211	-0.026	-0.488
HI	-0.007	0.228	-0.117	-0.002	-0.481
GL	0.023	-0.117	0.444	**0.639**	0.218
GW	-0.067	-0.155	0.047	**0.949**	-0.042
DSL	0.016	-0.102	0.432	**0.640**	0.240
DSW	-0.082	-0.133	0.012	**0.958**	-0.028
LB	0.131	0.004	0.400	-0.606	0.164
H%	0.112	-0.097	-0.135	-0.052	-0.356
M%	0.031	0.003	0.015	0.077	-0.412
HRR	-0.031	-0.285	0.000	0.023	-0.273
Amyl%	-0.018	-0.099	0.365	-0.221	0.032
Gy/pl	0.555	**0.634**	0.242	0.106	-0.136

Extraction Method: Principal Component Analysis.
Rotation Method: Varimax with Kaiser Normalization.
a. Rotation converged in 9 iterations.

Rotated component matrix revealed that the PC1 which accounted for the highest variability (19.325%) was mostly related with traits such as panicle weight per plant, biological yield per plant, fertile spikelets per panicle, flag leaf width, number of spikelets per panicle and spikelet density. In second PC the traits *viz*., productive tillers per plant, panicle number per plant, total tillers per plant, spikelet fertility percent, and grain yield per plant were present. The PC3 was dominated by stem thickness, plant height, stem length and thousand grain weight. The fourth principal component was more related to grain length, decorticated grain length, grain breadth and decorticated grain breadth whereas PC5 was more related to days to 50 percent flowering, days to maturity and sterile spikelets per panicle (Table18). On the basis of PCA most of the important yield and yield and quality attributing traits were present in PC1, PC2 and PC3. Therefore a promising breeding programme could be initiated by selecting lines from these principal components. Similarly for quality improvement lines could be selected from PC4 since most of the quality traits were present in this principal component.

Table18: Interpretation of rotated component matrix for the traits having values >0.5 in each PCs.

	PC1	PC2	PC3	PC4	PC5
Traits	Number of spikelets per panicle	Number of tillers per plant	Plant height	Decorticated seed breadth	Days to fifty percent flowering
	Spikelet density	Productive tillers per plant	Stem length	Seed breadth	Days to maturity
	Fertile spikelets per panicle	Number of panicles per plant	Stem thickness	Decorticated seed length	Sterile spikelets per panicle
	Panicle weight per plant	Spikelet fertility percent	1000 grain weight	Seed length	---
	Flag leaf width	Grain yield per plant	---	---	---
	Biological yield per plant		---	---	---

In 75 JNPT lines, top principal component scores (PC scores) for all the lines were estimated in these five components and presented in Table19. These scores could be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of the principal component. High PC score for a particular line in a particular component denotes high values for the variables present in that principal component.

Table 19: Principle component scores of rice genotypes

Genotypes	PC1 score	PC2 score	PC3 score	PC4 score	PC5 score
NPT(s) 4-1	0.7094	**1.0881**	**1.2763**	**1.2899**	-0.5171
NPT(s) 5-1	0.2723	-1.0498	-0.5014	0.4590	-0.4762
NPT(s) 6-1 (a)	-0.44527	0.0858	0.6927	0.5901	-0.6653
NPT(s) 6-1 (b)	-1.14129	-0.1987	**1.0701**	0.1134	0.1448
NPT(s) 6-1 (c)	0.0129	-0.4518	0.9969	-1.537	-0.3177
NPT(s) 6-1 (d)	0.3725	-0.6866	0.8239	0.2427	-0.5830
NPT(s) 6-1 (e)	0.0180	0.0411	**1.0628**	0.3180	0.2697
NPT(s) 6-1 (f)	-0.0811	-0.1646	0.9994	0.4537	-0.4476
NPT(s) 6-1-1 (a)	0.8968	0.0829	**2.0753**	0.2312	-0.7929
NPT(s) 6-1-1 (b)	0.6965	-0.1739	**1.5330**	-1.0203	-1.0952
NPT(s) 6-1-1 (c)	-0.0475	-0.3070	**1.2489**	0.1807	-1.7053
NPT(s) 6-3	0.2503	-0.3571	0.6758	**1.1958**	-1.7771
NPT(s) 6-4	-1.1538	0.7769	**1.2782**	-1.6366	-0.3882
NPT(s) 6-5	-0.7911	-0.6081	**1.6369**	-0.0998	-1.5542
NPT(s) 6-7	-0.9218	-0.7192	0.6418	**1.1926**	-1.7123
NPT(s) 6-11	-0.8851	-0.0079	**1.6977**	-1.0604	-0.0388
NPT(s) 6-12	-0.5504	-0.5053	**1.3814**	0.6926	-1.4099
NPT(s) 6-13	-0.1597	-0.9581	**2.0391**	-1.6149	**1.0111**
NPT(s) 8-1 (a)	-0.1495	-0.8139	**1.4264**	-2.2903	0.6269
NPT(s) 8-1 (b)	-0.7374	-0.0882	0.4289	0.0673	-0.0654
NPT(s) 8-2	-1.5007	-1.0305	0.8752	-0.5771	0.5109
NPT(s) 10-1 (a)	-0.0143	0.3156	0.4968	0.6615	**2.1585**
NPT(s) 10-1 (b)	0.7095	0.3470	0.6146	0.4437	0.8439
NPT(s) 10-1 (c)	**1.0315**	-1.2661	0.6012	0.7624	**1.4711**
NPT(s) 10-1 (d)	**1.6498**	0.3131	0.9961	0.8179	**2.0719**
NPT(s) 10-1 (e)	**1.0899**	0.3024	0.5946	0.6791	**1.5117**
NPT(s) 10-8 (a)	**1.0583**	0.4727	0.6999	0.6290	-0.1793
NPT(s) 10-8 (b)	**2.4666**	-0.1838	0.9218	0.1223	0.9589
NPT(s) 23-1	**1.0118**	0.9538	-0.2827	0.0338	-0.4613
NPT(s) 23-2	0.8255	-1.4493	0.0463	-0.3301	**1.5841**
NPT(s) 23-3	**1.5446**	**2.4988**	0.8956	-1.5885	0.0216
NPT 24 × IR 36 (a)	0.9099	0.0562	-0.2621	-0.0392	-1.2233
NPT 24 × IR 36 (b)	0.9801	0.4687	-0.2192	-0.8473	-0.3621

NPT 24 × IR 36 (c)	**1.7349**	**1.3227**	-0.4150	0.5378	-0.4998
NPT 24 × IR 36 (d)	0.6371	0.4673	-0.3293	0.7133	-0.3195
NPT 24 × IR 36 (e)	**1.2942**	0.3503	-0.87925	0.82584	-0.8599
NPT 24 × IR 36 (f)	**1.2673**	0.1897	-0.9326	-0.1856	-1.2482
NPT 24 × IR 36 (g)	**2.2061**	0.2205	-1.1429	0.0139	0.3822
25B × NPT 100 (a)	**1.6314**	**1.8609**	-0.7472	-1.7161	0.9175
25B × NPT 101 (d)	-1.6104	0.0219	-0.5915	-0.7940	**1.9630**
25B × NPT 101 (e)	-0.2053	0.5295	-1.2249	-0.1455	0.8879
25B × NPT 101 (f)	0.2396	-0.1919	-0.8399	0.2102	**1.8425**
NPT 32 × Pusa Basmati (a)	0.2036	-0.4063	-1.4799	0.1742	-0.5688
NPT 32 × Pusa Basmati (b)	-0.5473	**1.01873**	0.1440	**1.3107**	**1.3649**
NPT 32 × Pusa Basmati (c)	**1.4869**	-1.5892	-0.4099	-1.63162	**1.2305**
NPT 33 × Mahamaya (a)	-0.4306	**1.1847**	0.1230	-0.2038	-0.0188
NPT 33 × Mahamaya (b)	-0.4324	-0.0492	-0.0302	-1.5552	-0.7352
NPT 33 × Mahamaya (c)	-0.9359	**1.7187**	0.0593	**1.0647**	-0.0098
NPT 33 × Mahamaya (d)	-0.7379	**2.3676**	-0.8270	0.6311	0.0427
NPT 33 × Mahamaya (e)	-0.5888	**1.3733**	-0.0577	0.2807	-0.7361
NPT 33 × Mahamaya (f)	-1.0739	0.6912	0.0905	**1.4121**	0.0285
NPT 33 × Mahamaya (g)	0.1433	-1.1991	-1.1203	0.4448	1.0639
NPT 33 × Mahamaya (h)	0.9986	-1.3505	-1.2776	0.1833	-1.7783
NPT 70 × Pusa Basmati (a)	0.2936	-0.6963	-1.2106	0.4443	-0.3568
NPT 70 × Pusa Basmati (b)	-1.5236	-0.3977	-0.0203	0.8652	0.6067
NPT 70 × Pusa Basmati (c)	-0.9647	0.1036	0.3347	0.8641	0.7456
NPT 70 × Pusa Basmati (d)	-1.0273	0.3533	-0.0349	**1.0572**	-0.1960
NPT 70 × OR1045 × R2964 (a)	-0.1938	-1.7966	-0.5776	0.0649	-0.5621
NPT 70 × OR1045 × R2964 (b)	-1.2495	-0.1139	-0.0476	-1.3421	-0.3272
NPT 70 × OR1045 × R2964 (c)	-0.0404	-0.4487	-0.6297	**1.2491**	**1.3797**
NPT 89 × IR 36 (a)	-1.6404	0.2503	-0.5789	**1.5468**	0.9994
NPT 89 × IR 36 (b)	-0.8354	-1.5315	-0.6082	**1.1532**	**1.6426**
NPT 89 × IR 64 (a)	-1.0156	-1.1522	0.0287	0.7297	0.5123
NPT 89 × IR 64 (b)	-1.0651	**2.5982**	-0.8217	0.6959	0.2642
NPT 89 × IR 64 (c)	-1.6012	0.0759	0.1143	-1.5226	-0.3979
NPT 100 × HMT (a)	-0.8181	-1.0059	-1.4701	0.1905	-0.2489
NPT 100 × HMT (b)	-0.8438	-0.9397	-2.3395	0.6272	-1.3653
NPT 100 × HMT (c)	0.2166	**1.3956**	-2.1881	-1.6795	-0.1919
NPT 100 × HMT (d)	-0.5489	-0.9838	-1.8476	-1.2742	-0.6966
NPT 100 × HMT (e)	-0.4929	**1.2224**	-1.4727	-1.9179	-1.2234
NPT 100 × HMT (f)	-0.3722	-0.7165	-0.9798	-1.6233	0.1265
NPT 121 × IR 64 (a)	-0.9477	-0.4515	-0.9114	-2.1626	**1.2365**
NPT 121 × IR 64 (b)	-1.0419	1.8250	-0.1982	0.4825	-0.3968
25A × NPT 70-2-6-1	**1.2409**	-1.4075	-0.2391	0.3859	-0.8669
25A × NPT 70-15	**1.2634**	-1.4966	-0.8754	**1.0597**	-1.0457

Study of Table19 revealed that NPT(s)10-8 (b) had highest PC score followed by NPT 24 × IR 36 (g), NPT 24 × IR 36 (c), NPT(s) 10-1 (d), 25B × NPT 100 (a), NPT(s) 23-3, NPT32 × Pusa Basmati (c), NPT 24 × IR 36 (e), NPT 24 × IR 36 (f), 25A × NPT 70-15, 25A × NPT 70-2-6-1, NPT(s) 23-1, NPT(s) 10-1 (e), NPT(s) 10-8 (a) and NPT(s) 10-1 (c) in PC1 indicating that they had high panicles weight per plant, biological yield per plant, fertile spikelets per panicle, flag leaf width, number of spikelets per panicle and spikelet density. Whereas in PC2 NPT 89 × IR 64 (b) had the highest value and succeded by NPT(s) 23-3, NPT 33 × Mahamaya (d), 25B × NPT 100 (a), NPT 33 × Mahamaya (c), NPT 100 × HMT(c), NPT 33 × Mahamaya (e), NPT 100 × HMT (e), NPT 33 × Mahamaya (a), NPT(s) 4-1 and NPT 32 × Pusa Basmati (b) and hence had high productive tillers per plant, panicle number per plant, total tillers per plant, spikelet fertility percent, and grain yield per plant. In PC3 NPT(s) 6-13 had the highest value that was followed by NPT(s) 6-1-1 (a), NPT(s) 6-11, NPT(s) 6-5, NPT(s) 6-1-1 (b), NPT(s) 8-1 (a), NPT(s) 6-12, NPT(s) 6-4, NPT(s) 4-1, NPT(s) 6-1-1 (c), NPT(s) 6-1 (b) and NPT(s) 6-1 (e). These genotypes had high value for stem thickness, plant height, stem length and thousand grain weight. The genotypes in PC4 were promising for quality traits as grain length, decorticated grain length, grain breadth and decorticated grain breadth. Here NPT 89 × IR 36 (a), secured highest value and then other genotypes in decreasing order were NPT 33 × Mahamaya (f), NPT 32 × Pusa Basmati (b), NPT(s) 4-1, NPT 70 × OR1045 × R2964 (c), NPT(s) 6-3, NPT(s) 6-7, NPT 89 × IR 36 (b), NPT 33 × Mahamaya (c), 25A × NPT 70-15 and NPT 70 × Pusa Basmati (d).

The genotypes NPT(s) 23-3, 25B × NPT 100 (a) and NPT 24 × IR 36 (c) were present in PC1 as well as PC2 and therefore these lines are superior for yield and yield attributing traits. While the lines NPT(s) 4-1, NPT 32 × Pusa Basmati (b), NPT 33 × Mahamaya (c) and 25A × NPT 70-15 fell in yield as well quality associated PCs hence these lines had high value for yield as well as quality traits. The top score genotypes are presented in the table.

Table 20. List of selected JNPT lines in each principal component

PC1	PC2	PC3	PC4	PC5
NPT(s)10-8 (b)	NPT 89 × IR 64 (b)	**NPT(s) 6-13**	NPT 89 × IR 36 (a)	NPT(s) 10-1 (a)
NPT 24 × IR 36 (g)	**NPT(s) 23-3**	NPT(s) 6-1-1 (a)	NPT 33 × Mahamaya (f)	**NPT(s) 10-1 (d)**
NPT 24 × IR 36 (c)	NPT 33 × Mahamaya (d)	NPT(s) 6-11	**NPT 32 × Pusa Basmati (b)**	25B × NPT 101 (d)
NPT(s) 10-1 (d)	**25B × NPT 100 (a)**	NPT(s) 6-5	**NPT(s) 4-1**	25B × NPT 101 (f)
25B × NPT 100 (a)	**NPT 33 × Mahamaya (c)**	NPT(s) 6-1-1 (b)	**NPT 70 × OR1045 × R2964 (c)**	NPT 89 × IR 36 (b)
NPT(s) 23-3	NPT 100 × HMT (c)	NPT(s) 8-1 (a)	NPT(s) 6-3	NPT(s) 23-2
NPT32 × Pusa Basmati (c)	**NPT 24 × IR 36 (c)**	NPT(s) 6-12	NPT(s) 6-7	**NPT(s)10-1 (e)**
NPT 24 × IR 36 (e)	NPT 33 × Mahamaya (e)	NPT(s) 6-4	NPT 89 × IR 36 (b)	**NPT(s) 10-1 (c)**
NPT 24 × IR 36 (f)	NPT 100 × HMT (e)	**NPT(s) 4-1**	**NPT 33 × Mahamaya (c)**	**NPT 70 × OR1045 × R2964 (c)**
25A × NPT 70-15	NPT 33 × Mahamaya (a)	NPT(s) 6-1-1 (c)	25A × NPT 70-15	**NPT 32 × Pusa Basmati (b)**
25A × NPT 70-2-6-1	**NPT(s) 4-1**	NPT(s) 6-1 (b)	NPT 70 × Pusa Basmati (d)	NPT 32 × Pusa Basmati (c)
NPT(s) 23-1	**NPT 32 × Pusa Basmati (b)**	NPT(s) 6-1 (e)	---	NPT 121 × IR 64 (a)
NPT(s) 10-1 (e)	---	---	---	**NPT(s) 6-13**
NPT(s) 10-8 (a)	---	---	---	---
NPT(s) 10-1 (c)	---	---	---	---

4.7 Molecular Analysis

Genetic diversity analysis is the first and foremost step in any crop improvement program. However, to have a reliable estimate of genetic relationship and genetic diversity generally a large number of polymorphic markers are required. DNA markers represent very effective tool for analyzing genetic diversity in any crop improvement programme**.** A total of 75 genotypes (Table 1) were included in the present study. Out of which 24 contrasting lines were selected on the basis of plant height, panicle length, stem thickness, number of panicles, stem thickness and 1000 grain weight for molecular analysis (Table 5)

4.7.1 Molecular analysis using SSR marker

During the present study, a total of 13 SSR markers were used for genetic diversity analysis in rice. The study revealed that the average percentage of major allele frequency ranged between 47.92% (RM468) to 100.00% (RM42, RM236, RM261, RM331, RM341 and RM469). The mean of major allele frequency was found to be 79.65% (Table 14). Genetic diversity varied from 0.0000 (RM42, RM236, RM261, RM331, RM341 and RM469). to 0.5859 (RM468) with an average of 0.2342 (Table 21).

The heterozygosity was found to be moderate with an average of 0.2212. Heterozygosity varied from 0.0000 to 1.0000 and highest heterozygosity was found for marker RM 16 (1.0000) (Table 21).

The genetic diversity for a specific locus/marker can be evaluated by the Polymorphic Information Content (PIC) value. The PIC value ranged between 0.0000 (RM42, RM236, RM261, RM331, RM341, RM469) to 0.4975 (RM468) with a mean value of 0.1873. The highest PIC value was observed for the marker RM468 (0.4975) (Table 21).

Table 21. Markers used along with the gene diversity, major allele frequency, heterozygosity and PIC values

Marker	Major Allele Frequency	Gene Diversity	Heterozygosity	PIC
RM331	1.0000	0.0000	0.0000	0.0000
RM259	0.5000	0.5382	0.9167	0.4316
RM468	0.4792	0.5859	0.9583	0.4975
RM16	0.5000	0.5000	1.0000	0.3750
RM201	0.8750	0.2188	0.0000	0.1948
RM341	1.0000	0.0000	0.0000	0.0000
RM219	0.5833	0.4861	0.0000	0.3680
RM228	0.8750	0.2188	0.0000	0.1948
RM236	1.0000	0.0000	0.0000	0.0000
RM261	1.0000	0.0000	0.0000	0.0000
RM7	0.5417	0.4965	0.0000	0.3733
RM42	1.0000	0.0000	0.0000	0.0000
RM469	1.0000	0.0000	0.0000	0.0000
Mean	0.7965	0.2342	0.2212	0.1873

It was found that all the six markers used were polymorphic. The markers namely, RM259, RM468, RM201, RM219, RM228 and RM7 (Table 22) were associated with important qualitative and quantitative traits i.e. grain length, kernel width, kernel length, drought tolerance, plant height, panicle length and thousand grain weight respectively. The total numbers of alleles amplified were 22 with a mean value of 1.69. The highest number of alleles were 3 amplified by marker RM259 and RM468 (Table 22) and unique alleles were amplified by four markers *viz.,* RM201, RM228, RM259 and RM468 (Table 23). Allele size was found to be highest in RM468 (280bp) whereas lowest in RM469 (100bp) (Table 22).

Table 22. Markers used with number of allele, polymorphic allele and allele size

Marker	Number of alleles	Polymorphic allele	Allele size range (bp)	Polymorphic /Monomorphic
RM331	1	0	260	**Monomorphic**
RM259	3	3	150, 190, 230	**Polymorphic**
RM468	3	3	170, 190,280	**Polymorphic**
RM16	2	0	200, 250	**Monomorphic**
RM201	2	2	220, 240	**Polymorphic**
RM341	1	0	170	**Monomorphic**
RM219	2	2	200, 250	**Polymorphic**
RM228	2	2	210, 290	**Polymorphic**
RM236	1	0	200	**Monomorphic**
RM261	1	0	200	**Monomorphic**
RM7	2	2	200, 220	**Polymorphic**
RM42	1	0	190	**Monomorphic**
RM469	1	0	100	**Monomorphic**
Total	22	14		
Mean	1.69	1.07		

Marker RM259 amplified a total of 3 alleles out of which two were unique alleles amplified in the genotypes NPT(s) 6-12, NPT(s) 8-2, NPT 32 × Pusa Basmati (b) with an allele size of 150bp and 230bp. Marker RM468 amplified a total of 3 alleles out of which two were unique allele in genotypes NPT(s) 4-1, NPT(s) 6-1 (b), NPT(s) 6-1 (c) and NPT(s) 6-1 (d) with an allele size of 170 and 280bp. RM228 amplified a total of 2 alleles, out of which one was unique allele in genotypes 25B × NPT 100 (a) and NPT 32 × Pusa Basmati (b) and another in NPT 100 × HMT (b) with size of 290bp and RM201 amplified total of two alleles out of which one was unique of size 220bp, which was found in genotypes NPT(s) 6-12, NPT(s) 8-2 and NPT 32 × Pusa Basmati (b).

Table 23: Markers with amplified unique alleles, their size and genotypes

Markers	Unique alleles	Allele size (bp)	Genotype
RM201	1	220	NPT(s) 6-12, NPT(s) 8-2 NPT 32 × Pusa Basmati (b)
RM228	1	290	25B × NPT 100(a) NPT 32 × Pusa Basmati (b) NPT 100 × HMT (b)
RM259	2	150	NPT(s) 6-1 (f)
		230	NPT 32 × Pusa Basmati (b)
RM468	2	170	NPT(s) 4-1, NPT(s) 6-1 (b)
		280	NPT(s) 6-1 (c), NPT(s) 6-1 (d)

4.7.2 Cluster analysis of SSR markers:

Based on the electrophoretic banding pattern of SSR primers, pair wise genetic similarity amongst twenty four genotypes of rice for genetic characterization were estimated and a dendogram (fig.3) was generated by neighbor-joining method implemented in PowerMarker version 3.25. The cluster analysis revealed that the total 24 genotypes were divided into two major cluster groups I and II. Group I consists of line NPT 32 × Pusa Basmati (b). The major group II was further subdivided into two major sub groups A and B. The subgroup A was further sub divided into two subgroups C and D. The subgroup C contained two genotypes i.e. 25B × NPT 100 (a) and NPT 100 × HMT (b), while subgroup D consisted of eight genotypes namely, NPT(s) 6-1-1 (b), NPT(s) 10-1 (e), NPT 24 × IR 36 (f), NPT 24 × IR 36 (g), NPT 33 × Mahamaya (c), NPT 89 × IR 64 (c), NPT 100 × HMT (c) and NPT 121 × IR 64 (a). The subgroup B was further sub divided into two subgroups E and F. The subgroup E consisted of seven genotypes, which were, NPT(s) 4-1, NPT(s) 6-1 (b), NPT(s) 6-1 (c), NPT(s) 6-1 (d), NPT(s) 6-1 (e), NPT 32 × Pusa Basmati (a) and NPT 32 × Pusa Basmati (c). Subgroup F contained six genotypes namely, NPT(s) 6-1 (f), NPT(s) 6-4, NPT(s) 6-7, NPT(s) 6-12 and NPT(s) 8-2.

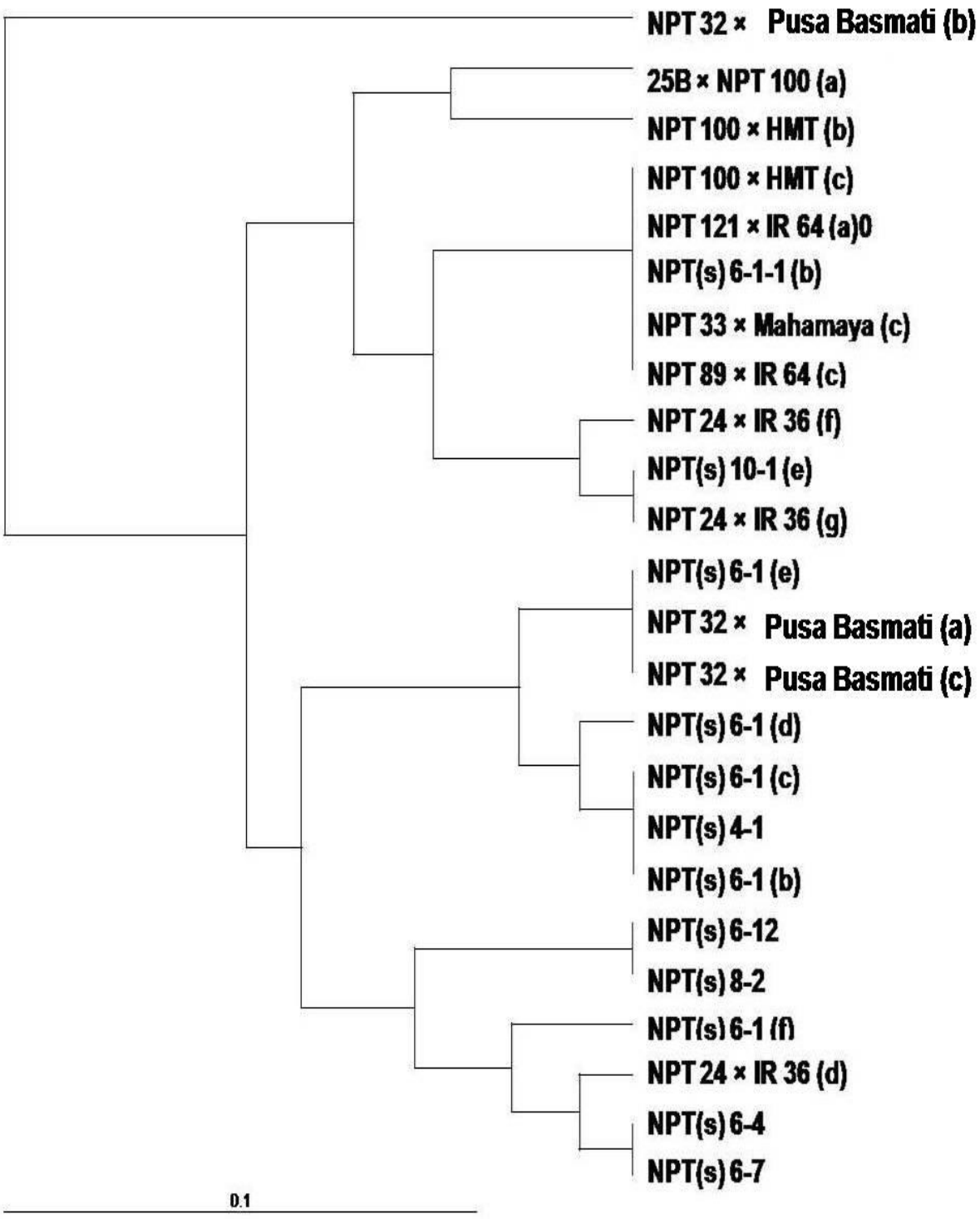

Fig 4 . Dendogram showing different clusters of JNPT lines

4.8 Classification of the genotypes on the basis of

4.8.1. Amylose percent

Table 24: Classification of the genotypes on the basis of Amylose percent

Amylose %	Classification	Frequency	Name of genotypes
>30%	Very high	0	None
26-30%	High	9	NPT(s) 8-1 (b), NPT(s) 10-1 (d), NPT(s) 23-3, 25A × NPT 70-15, NPT(s) 8-1 (a), NPT 100 × HMT (e), NPT(s) 6-1 (b), NPT 33 × Mahamaya (c), 25B × NPT 101 (d)
20-25%	Medium	32	NPT 70 × Pusa Basmati (b), NPT 89 × IR 64 (a), NPT 33 × Mahamaya (b), NPT(s) 6-1 (d), NPT 24 × IR 36 (b), NPT(s) 10-1 (a), NPT(s) 23-2, NPT 33 × Mahamaya (e), NPT(s) 6-13, NPT(s) 6-1 (c), NPT(s) 6-1-1 (c), NPT 70 × OR1045 × R2964 (a), NPT 121 × IR 64 (a), NPT 32 × Pusa Basmati (a), NPT(s) 8-2, NPT(s) 6-5, NPT(s) 6-1-1 (b), NPT 24 × IR 36 (d), NPT(s) 6-1 (a), NPT(s) 6-4, 25B × NPT 101 (f), 25A × NPT 70-2-6-1 , NPT 121 × IR 64 (b), NPT(s) 10-1 (b), NPT(s) 6-3, NPT(s) 6-12, NPT 24 × IR 36 (a), NPT(s) 6-1 (e), NPT 100 × HMT (d), NPT(s) 6-1 (f), NPT(s) 6-1-1 (a), NPT(s) 6-11.
10-19%	Low	34	NPT(s) 10-1 (c), NPT 24 × IR 36 (f), NPT(s) 10-8 (a), NPT 24 × IR 36 (g), NPT(s) 10-1 (e), NPT 89 × IR 36 (b), NPT 33 × Mahamaya (a), NPT 70 × OR1045 × R2964 (c), 25B × NPT 100 (a), NPT(s) 23-1, NPT 32 × Pusa Basmati (c), NPT(s) 6-7, NPT(s) 5-1, NPT 70 × Pusa Basmati (d), NPT 33 × Mahamaya (g), NPT 24 × IR 36 (e), NPT 33 × Mahamaya (h), NPT 100 × HMT (f), NPT 89 × IR 64 (b), NPT 24 × IR 36 (c), NPT 33 × Mahamaya (d), NPT 33 × Mahamaya (f), NPT 32 × Pusa Basmati (b), NPT 70 × OR1045 × R2964 (b), NPT 70 × Pusa Basmati (a), NPT 70 × Pusa Basmati (c), NPT(s) 10-8 (b), NPT 100 × HMT (c), 25B × NPT 101 (e), NPT(s) 4-1, NPT 89 × IR 36 (a), NPT 89 × IR 64 (c), NPT 100 × HMT (b), NPT 100 × HMT (a)
<10%	Very low	0	None

4.8.2. Alkali spreading value and gelatinization temperature

Table 25. Classification of the genotypes on the basis of alkali spreading value and gelatinization temperature

ASV	Classification	GT	Frequency	Genotypes
6-7	High	Low	00	None
4-5	Medium	Medium	30	NPT(s) 5-1, NPT(s) 6-1 (a), NPT(s) 6-1 (d), NPT(s) 6-1 (f), NPT(s) 6-1-1 (a), NPT(s) 6-1-1 (b), NPT(s) 6-4, NPT(s) 6-11, NPT(s) 10-1 (c), NPT(s) 10-1 (e), NPT(s) 10-8 (a), NPT(s) 23-3, NPT 24 × IR 36 (a), NPT 24 × IR 36 (c), NPT 24 × IR 36 (d), NPT 24 × IR 36 (e), NPT 24 × IR 36 (g), 25B × NPT 101 (d), 25B × NPT 101 (e), NPT 32 × Pusa Basmati (c), NPT 33 × Mahamaya (a), NPT 33 × Mahamaya (c), NPT 33 × Mahamaya (e), NPT 70 × OR1045 × R2964 (c), NPT 89 × IR 36 (a), NPT 89 × IR 64 (b), NPT 89 × IR 64 (c), NPT 100 × HMT (a), NPT 100 × HMT (c), NPT 100 × HMT (e)
3	Low, Medium	High, Medium	35	NPT(s) 6-1 (b), NPT(s) 6-1 (c), NPT(s) 6-1 (e), NPT(s) 6-1-1 (c), NPT(s) 6-3, NPT(s) 6-5, NPT(s) 6-12, NPT(s) 6-13, NPT(s) 8-1 (a), NPT(s) 10-1 (b), NPT(s) 10-1 (d), NPT(s) 10-8 (b), NPT(s) 23-1, NPT(s) 23-2, NPT 24 × IR 36 (b), NPT 24 × IR 36 (f), 25B × NPT 100 (a), 25B × NPT 101 (f), NPT 32 × Pusa Basmati (a), NPT 32 × Pusa Basmati (b), NPT 33 × Mahamaya (b), NPT 33 × Mahamaya (d), NPT 33 × Mahamaya (f), NPT 33 × Mahamaya (g), NPT 33 × Mahamaya (h), NPT 70 × Pusa Basmati (a), NPT 70 × Pusa Basmati (c), NPT 70 × OR1045 × R2964 (a), NPT 70 × OR1045 × R2964 (b), NPT 89 × IR 64 (a), NPT 100 × HMT (b), NPT 100 × HMT (d), NPT 100 × HMT (f), NPT 121 × IR 64 (a), 25A × NPT 70-2-6-1
1-2	Low	High	10	NPT(s) 4-1, NPT(s) 6-7, NPT(s) 8-1 (b), NPT(s) 8-2, NPT(s) 10-1 (a), NPT 70 × Pusa Basmati (b), NPT 70 × Pusa Basmati (d), NPT 89 × IR 36 (b), NPT 121 × IR 64 (b), 25A × NPT 70-15

DISCUSSION

Rice is the most important cereal crop that has been referred as Global grain because of its use as prime staple food in about 100 countries of the world. More than 90 percent of the world's rice is grown and consumed in Asia where 60 percent of the earth's people live. Rice accounts for 35 to 75 percent of the calories consumed by more than 3 billion Asians. It is planted to about 154 million hectares annually or on about 11percent of the world's cultivated land. The rising demand, saturation of cultivable field and climate change cause a supply shortage of a crop in the future. By the near 2025, about 785 million tonnes of paddy which is 70 percent more than the current production is needed to meet the growing demand. To achieve the target yield that is required to sustain the world population, rice varieties with a yield advantage of about 20 percent over currently grown varieties must be developed.

Although, hybrid rice technology appears to be a practically feasible option contributing 15-20 percent higher yield than normal varieties under same agronomical conditions. Despite this there is a need for genetical improvement of the existing varieties. The inter sub-specific rice hybrids have showed a higher heterosis *i.e., indica x japonica* crosses compared to *indica x indica* crosses. The high heterosis level for yield in *indica x* tropical *japonica* crosses seems to be promosing and prospects for large scale adoption of this technology in India appears to be bright. In view of this prospect, JNKVV has also developed new plant types *i.e*., Jawahar New Plant Type (JNPT) of rice by crossing *indica* and tropical *japonica*. In this present investigation, seventy five JNPT lines derived from *indica X japonica* sub-species crosses of rice had been used. The aim of investigation was to understand the behaviour of NPT lines, their morphological and molecular framework to enhance the yield potential of rice.

The biometrical techniques applied in the analysis of the data in the present investigation revealed conclusive findings. The merits of findings are discussed under the following heads.

5.1 Characterization

5.2 Genetic variability

5.3 Heritability and genetic advance analysis

5.4 Correlation coefficient analysis

5.5 Path coefficient analysis

5.6 Principal component analysis

5.7 Molecular analysis

5.1 Characterization

Morphological characterization refers to the characterization of rice on the basis of its morphological characters that is appearance, viz. leaf sheath color, stigma color, awns, height etc.

In the present investigation rice genotypes under study were characterized for twenty eight qualitative traits viz., basal leaf sheath color, leaf: pubescence of blade surface, leaf: auricles, leaf: anthocyanin coloration of auricles, Presence of ligule on leaf, leaf: shape of ligules, leaf ligule color, presence of collar on leaves, culm attiude, flag leaf: attitude of blade, stem: anthocyanin coloration of nodes, spikelet : color of stigma, spikelet : density of pubescence, sterile lemma color, spikelet: color of tip of lemma, panicle: exsertion, panicle: attitude of branches, panicle: awns, panicle: distribution of awns, panicle: color of awns, anthocyanin coloration on leaf sheath, lemma anthocyanin colouration of area below apex, lemma anthocyanin colouration of apex, lemma and palea colour, panicle curvature of main axis, panicle presence of secondry branching, panicle secondry branching and attitude of flag leaf blade (late). All the characters under study showed considerable genetic variability.

A majority of cultivars were found to possess green basal leaf sheath, green leaf blade, light green auricle, straw colored apiculus, white stigma, well to moderate panicle exertion and horizontal flag leaf. The results found in present investigation were in agreement with that reported by Motiramani et al. (2001) and Rao et al. (2001).

Most of the genotypes had medium culm length, greater stem thickness, more number of tillers and strong secondry branching in panicles.

These results were in accordance with findings reported by Sharma et al. (2013).

No variation was observed in ligule shape (all spilt), this was in confirmation with findings reported by Sajid et al. (2015).

5.2 Genetic variability

Variability refers to the presence of phenotypic differences among the individuals of plant population. Variability results due to differences either in the genetic constitution of the individuals of a population or in the environment in which they grown. Magnitude of genetic variability present in a population is of paramount importance to a plant breeder for starting a judicious breeding programme. Selection was only effective when there was a genetic variability among the genotypes in a population. The genotypic coefficient of variation (GCV) measures the extent of genetic variability present in a crop species and also enables to quantify the extent of variability present in different characters. The phenotypic coefficient of variation (PCV) of a character was the manifestation of genotypes, environment and interaction between the genotypes and environment. Therefore, the total variance needs to be partitioned into heritable and non-heritable components to assess the true breeding nature of that particular trait. The results obtained from present investigation are discussed here for yield and quality traits in all the lines and parents.

Results of analysis of variance indicated that the mean sums of squares due to genotypes were highly significant for all the traits, suggesting presence of sufficient variation among the genotypes for these traits. Maximum variability was observed for total number of spikelets per panicle and lowest for LB ratio.

The magnitude of variability in decreasing order for the traits i.e., number of spikelets per panicle, fertile spikelets per panicle, sterile spikelets per panicle, plant height, stem length, biological yield per plant, panicle index, panicle weight per plant, flag leaf length, days to maturity, days to 50 percent flowering, harvest index, spikelet fertility per cent, head rice recovery, grain yield per plant, 1000 grain weight, amylose percent, milling per cent, spikelet

density, average panicle length, total tillers per plant, productive tillers per plant, number of panicles per plant, hulling per cent, decorticated grain length, grain length, decorticated grain breadth, grain breadth, stem thickness, flag leaf width, LB ratio. These results of ANOVA were similar to the findings of Nadali (2009) and Selvaraj et al. (2011).

Coefficient of variation truly provides a relative measure of variance among the different traits. GCV was found to be highest for sterile spikelets per panicle followed by panicle weight per plant, grain yield per plant, biological yield per plant, spikelet density, stem thickness, number of tillers per plant, amylose percent, harvest index, number of productive tillers per plant, panicle number per plant, fertile spikelets per panicle, number of spikelets per panicle, 1000 grain weight, flag leaf length, stem length, panicle index, plant height, flag leaf width, decorticated grain breadth, grain breadth, head rice recovery, panicle length, decorticated grain length, spikelet fertility percent, grain length, LB ratio, days to 50 percent flowering, milling percent, days to maturity, and hulling percent. Similar trend was also observed for PCV.

Close relationship between GCV and PCV were found in all the traits except number of productive tillers per plant and panicle number per plant. This finding was similar to findings of Chakraborty et al. (2001).

PCV values were slightly greater than GCV, revealing very little influence of environment for their expression. This finding was in agreement with Mishra and Verma (2002).

The highest value of phenotypic and genotypic coefficient of variation was obtained for sterile spikelets per panicle. This was in agreement with the findings reported by Verma (2000) and Saxena et al. (2005).

Grain yield per plant manifested high values for GCV and PCV. It was similar to the findings of Verma (2000), Mishra

and Verma (2002), Nayak (2000), Chand et al. (2004), Hasib et al. (2004), Saxena et al. (2005), Tiwari et al. (2011), Singh et al. (2012), and Sharma (2013).

Higher magnitudes of phenotypic and genotypic coefficient of variation were obtained for, panicle weight per plant, grain yield per plant, biological yield per plant and spikelet density. This was in accordance with findings of Verma (2000), Mishra and Verma (2002), Saxena et al. (2005) and Sharma (2013).

Number of tillers per plant, number of productive tillers per plant, panicle number per plant, fertile spikelets per panicle, number of spikelets per panicle and 1000 grain weight showed high magnitude of GCV and PCV. This finding was in agreement with findings of Verma (2000), Nayak et al. (2002), Hasib et al. (2004), Chand et al., (2004), Saxena et al. (2005), Selvaraj et al. (2011), Tiwari et al. (2011) and Khan et al. (2012). This however was not in favour of the findings of Padmaja et al. (2008) and Sabu et al., (2009) who reported low GCV and PCV for 1000 grain weight.

The traits *viz*., stem length, panicle index, flag leaf width, decorticated grain breadth, grain breadth and panicle length showed moderate value of GCV and PCV. These results were not in agreement with the findings reported by Bhaskar (2006), who observed low magnitudes of PCV and GCV for panicle length and panicle index. While moderate value of GCV and PCV for flag leaf width was not in agreement with Padmaja et al. (2008). Sabu et al. (2009) and Selvaraj et al. (2011) reported low GCV and PCV for panicle length and hence had contradictory findings.

Plant height recorded a moderate value of genotypic and phenotypic coefficient of variation. This result was not in agreement with the findings reported by Tiwari (2011) and Khan et al. (2012). They reported high value of GCV and PCV for plant height. Bhaskar (2006) reported low value of GCV and PCV for plant height and so had dissimilar findings.

Decorticated grain length, grain length, LB ratio, days to 50 percent flowering and days to maturity, showed low value of GCV and PCV. This was in confirmation with the findings of Chakraborty et al. (2001) and Bhaskar (2006). Howerver this was not in agreement with findings of Chand et al. (2004), Saxena et al. (2005), and Singh et al. (2004). They reported high estimates of GCV and PCV for days to maturity, grain length and LB ratio.

5.3 Heritability and genetic advance

Heritability (h^2) is an estimate of the heritable portion of the phenotypic variation. It plays a vital role in deciding the suitability and strategy for selection of a particular character. A higher h^2 value in quantitative characters is useful as they provide the base of selection on the phenotypic performance. Although, the presence of high heritability values indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication to the amount of genetic progress for selecting the best individuals which is possible by using the estimates of genetic advance.

Genetic advance (GA) is the improvement in the mean genotypic value of selected individual over the parental population. It is the measure of genetic gain under selection. Thus, h^2 and GA are the important selection parameters. If high heritability is coupled with high GA, it indicates that the heritability is due to additive gene action and selection may be effective. High heritability in broad sense coupled with low genetic advance indicates predominance of non-additive gene action and selection for such characters may not be rewarding because h^2 is exhibited due to favourable influence of environment rather than genotype. The results obtained from present investigation are discussed here as below:

High heritability with high genetic advance was observed for plant height. This result was in agreement with the findings of Selvaraj et al. (2011), Singh et al. (2012) and Soni et al. (2013).

High heritability with high genetic advance was observed for the characters fertile spikelets per panicle, number of spikelets per panicle, harvest index, biological yield per plant, panicle index, spikelet density, sterile spikelets per panicle, flag leaf length, flag leaf width, grain yield per plant, 1000 grain weight, grain breadth and decorticated grain breadth. These results were in the favour of the findings of Jayasudha and Sharma (2010), Selvaraj et al. (2011), Tiwari et al. (2011), Singh et al. (2012), Soni et al. (2013) and Dongre et al. (2014).

High heritability with moderate genetic advance was found for spikelet fertility percent, days to 50 percent flowering but it was in disagreement with findings of Jayasudha and Sharma (2010) and Soni et al. (2013). They reported high heritability with high genetic advance for the same characters.

Moderate heritability with high genetic advance was found for total tillers per plant and productive tillers per plant. But these results were dissimilar to the findings reported by Selvaraj et al. (2011), Tiwari et al. (2011) and Dongre et al. (2014). They reported high heritability with high genetic advance for the mentioned characters.

Low heritability with low genetic advance was observed for LB ratio but Soni et al. (2013) reported heritability with high genetic advance for the LB ratio.

5.4 Correlation coefficient

Correlation analysis provides a good measure of the linear association between character(s) and helps to identify the most important character(s) to be considered for effective selection for increasing yield. In the present investigation correlations were worked out both at phenotypic and genotypic levels for all possible character combinations. In general, phenotypic correlation coefficients were higher in magnitude than genotypic correlation coefficients (Lal et al. 1983) in the same direction and magnitude

indicated that there is a strong inherent association between each pair of character(s) which might be due to masking or modifying effect of the environment.

The development of a high yielding genotype, through breeding rice, an autogamic species requires a thorough knowledge of the association of yield components. Grain yield per plant 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 rewarding unless yield components are taken into consideration. Very close values of genotypic and phenotypic correlation were also observed between some character combinations which might be due to reduction in error (environmental variance) to minor proportions as reported by Dewey and Lu (1959). A wide difference between genotypic and phenotypic correlations between two characters is due to dual nature of phenotypic correlations which is determined by genotypic and environmental correlations and heritability of the characters. When characters having direct bearing on yield are selected their associations with other characters are to be considered simultaneously as this will indirectly affect yield.

In the present investigation, an attempt has been made to estimate the phenotypic correlation in all character combinations with the objectives to get information about the nature, extent and direction of selection pressure to achieve practical and usable results.

Panicle weight per plant had positive and significant association with, grain yield per plant. This was in agreement with the findings of Bastian et al*.* (2000), Thakur et al. (2000), Souroush et al*.* (2004) and Soni et al*.* (2013).

Correlation was positive and significant between plant height and grain yield per plant per plant. These results were in favour of the findings of Tomar et al*.* (2000), Nayak et al*.* (2001) , Islam et al*.* (2002), Rasheed et al*.* (2002), Samo et al*.* (2002), Madhavilatha et al*.* (2005), Vaithiyalingan and Nadarajan (2005), Muthuswamy and Ananda Kumar (2006), Zahid et al*.* (2006), Khan et al*.* (2009), Sabu et al*.* (2009),

Chakraborty et al. (2010) and Nandan et al. (2010) and Dongre et al. (2014) . But it was in disagreement with the results of Rahman et al. (2014) where he reported non significant and negative association between the mentioned characters.

Biological yield per plant, fertile spikelets per panicle and number of spikelets per panicle recorded high positive and significant association with grain yield per plant. This was in confirmation with the findings of Rao (2000), Bastian et al. (2000), Tomar et al. (2000), Nayak et al. (2001), Souroush et al. (2004), Madhavilatha et al. (2005), Satyanarayana et al. (2005), Vaithiyalingan and Nadarajan (2005), Muthuswamy and Ananda Kumar (2006), Gazafrodi et al. (2006), Zahid et al. (2006), Agahi et al. (2007), Khan et al. (2009), Sabu et al. (2009), Nandan et al. (2010), Chakraborty et al. (2010), Basavaraja et al. (2011), Nagaraju et.al. (2013), Soni et al. (2013), Dongre et al. (2014) and Rahman et al. (2014).

Productive tillers per plant, panicle number per plant and total tillers per plant were significantly and positively correlated with grain yield per plant. These findings were similar to the results by Rao (2000), Tomar et al. (2000), Nayak et al. (2001), Samo et al. (2002), Souroush et al. (2004), Tyagi et al. (2004), Madhavilatha et al. (2005), Satyanarayana et al. (2005), Vaithiyalingan and Nadarajan (2005), Gazafrodi et al. (2006), Muthuswamy and Ananda Kumar (2006), Agahi et al. (2007), Khan et al. (2009), Chakraborty et al. (2010), Sabu et al. (2009), Basavaraja et al. (2011), Nagaraju et.al. (2013), Soni et al. (2013), Dongre et al. (2014) and Rahman et al. (2014). Zahid et al. (2006) reported different results by advocating non significant and negative association between number of tillers per plant and grain yield per plant.

A significant and positive association of harvest index, spikelet fertility and 1000 grain weight on grain yield per plant was found which were in confirmation with findings of Tomar et al. (2000), Nayak et al. (2001), Madhavilatha et al. (2005), Satyanarayana et al. (2005), Sabu et al. (2009), Vaithiyalingan and Nadarajan (2005), Muthuswamy and Ananda Kumar (2006), Chakraborty et al. (2010), Nandan et al. (2010), Basavaraja et al.

(2011), Nagaraju et.al. (2013), Soni et al. (2013), Dongre et al. (2014) and Rahman et al. (2014).

Flag leaf length and flag leaf width recorded significant and positive association with grain yield per plant. The results were similar to the findings of Agahi et al. (2007) and Soni et al. (2013).

Correlation studies revealed positive and highly significant association of panicle weight per plant, biological yield per plant, fertile spikelets per panicle, productive tillers per plant, panicle number per plant, total tillers per plant, number of spikelets per panicle, stem length, spikelet density, harvest index, plant height, flag leaf width, spikelet fertility percent, 1000 grain weight, flag leaf length and milling per cent with grain yield per plant per plant. Hence, these characters should be given due consideration in the formulation of selection criteria for the genetic improvement in present as well as future materials.

5.5 Path coefficient analysis

Path coefficient measures the direct and indirect contributions of independent variables on a dependent variable. Though the correlation coefficients depict the nature of association among the characters, it is the path analysis that splits the correlation coefficients into direct and indirect effects thus specifying the relative contribution of each character. It further reveals the different ways in which a particular character influences a dependent variable. The Path coefficient analysis has been discussed in the following paragraph.

Amongst all the independent characters the characters *viz*., number of spikelets per panicle exhibited maximum positive effect followed by plant height, biological yield per plant, panicle weight per plant, harvest index, seed breadth, panicle index, seed length, total number of productive tillers per plant, stem thickness, milling per cent, 1000 grain weight, days to maturity, flag leaf width and flag leaf length on grain yield per plant. Negative effect was manifested by fertile spikelets per panicle, sterile spikelets per panicle, stem length, spikelet fertility per cent, spikelet density, panicle length, decorticated seed breadth, decorticated grain length, hulling percent, total number of tillers

per plant, days to fifty percent flowering, amylose percent, head rice recovery and LB ratio.

Number of spikelets per panicle had positive direct effect on grain yield per plant per plant. This was in confirmation with the findings of Samonte et al. (1998), Janardhanam et al. (2000), Tomar et al. (2000), Nayak et al. (2001), Vaithiyalingan and Nadarajan (2005), Gazafrodi et al. (2006), Agahi et al. (2007) and Nandan et al. (2010). However this was in disagreement with the findings of Shanthala (2004), where spikelet number recorded negative direct effect on grain yield per plant.

High positive direct effect of plant height on grain yield per plant was in agreement with the results of Janardhanam et al. (2000), Agahi et al. (2007), Chakraborty et al. (2010), Nandan et al. (2010), Basavaraja (2011), Selvaraj et al. (2011), and Dongre et al. (2014). The result however was not in favour of findings of Padmavathi et al. (1996) where low positive direct effect and Shanthala (2004), where negative direct effect of plant height on grain yield per plant was reported respectively.

Biological yield per plant, panicle weight per plant and harvest index also exhibited positive direct effect on grain yield per plant. This was in the favour of the findings of Samonte et al. (1998), Mishra and Verma (2002), Surek and Beser (2003), Shanthala (2004) and Dongre et al. (2014).

Stem length had low positive direct effect on grain yield per plant, this was in agreement with the findings of Padmavathi et al. (1996) and Dongre et al. (2014).

Total number of productive tillers per plant had positive direct effect on grain yield per plant. This was in collaboration with the results of Tomar et al. (2000), Sinha and Banerjee (2002), Surek and Beser (2003), Shanthala (2004), Khedikar et al. (2004), Vaithiyalingan and Nadarajan (2005), and Gazafrodi et al. (2006), Agahi et al. (2007), Basavaraja (2011), Nagaraju et al. (2013) and Rahman et al. (2014).

1000 grain weight manifested positive direct effect on grain yield per plant and was in conformity with Samonte et al. (1998), Surek and Beser

(2003), Nayak et al. (2001), Khedikar et al. (2004), Shanthala (2004), Agahi et al. (2007), Selvaraj et al. (2011) and Rahman et al. (2014).

Flag leaf width and flag leaf length also recorded positive direct effect on grain yield per plant. The results were similar to advocated by Tomar et al. (2000), Mishra and Verma (2002) and Gazafrodi et al. (2006).

The negative direct effect of fertile spikelets per panicle was in disagreement with results of Samonte et al. (1998), Chakraborty et al. (2010), Selvaraj et al. (2011) and Rahman et al. (2014). They reported positive direct effect of fertile spikelets per panicle on grain yield per plant.

Spikelet density had negative direct effect on grain yield per plant. The results were dissimilar to the findings of Samonte et al. (1998), Mishra and Verma (2002), Khedikar et al. (2004) and Shanthala (2004). They reported positive direct effect on grain yield per plant.

Spikelet fertility per cent had negative direct effect on grain yield per plant but it was not in confirmation with positive direct effect on grain yield per plant advocated by Basavaraja (2011).

Total number of tillers per plant and days to 50 percent flowering showed negative direct effect on grain yield per plant but these results were not in agreement with results of Padmavathi et al. (1996), Mishra and Verma (2002), Khedikar et al. (2004), Nandan et al. (2010), Basavaraja (2011), Selvaraj et al. (2011) for days to 50 percent flowering and of Selvaraj et al. (2011) and Dongre et al. (2014) for total number of tillers per plant.

In this investigation, the characters *viz*., number of spikelets per panicle exhibited maximum positive effect followed by plant height, biological yield per plant, panicle weight per plant, harvest index, grain breadth, panicle index, grain length, total number of productive tillers per plant, stem thickness, milling per cent, 1000 grain weight, days to maturity, flag leaf width and flag leaf length had significant positive correlation with grain yield per plant. It indicates true relationship between them and direct selection for these traits will be rewarding for yield improvement.

5.6 Principal component analysis

Owing to lack of knowledge regarding relative importance and usefulness of variables, the investigator tries to include all the possible variables and makes the data matrix perceivably large, complicated and beyond comprehension. Therefore, the investigator requires a technique for systematic reduction and summarization of data sets. Principal component analysis, basically a well known data reduction technique, initially floated by Pearson (1901) and later developed by Hotelling (1933), offers solution to this complex problem by transforming the original set of variables into smaller set of linear combinations that accounts for most of the variability of the original data set. The objective of principal component analysis is to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson, 1972 and Morrison, 1982) and also to rank genotypes on the basis of PC scores.

The first principal component i.e. PC1 accounted for maximum proportion of total variability in the set of all variables and remaining components accounted for progressively less amount of variation. The first principal component accounted for maximum variability i.e., 19.21 percent. The first thirteen principal components with eigen values greater than 0.5 altogether explained 92.967 per cent of the total variation.

Rotated component matrix revealed that the PC1 which accounted for the highest variability (19.21 percent) was mostly related with traits such as number of spikelets per panicle, spikelet density, fertile spikelets per panicle, panicle weight per plant, flag leaf width and biological yield per plant. Number of spikelets per panicle hence was highest contributing variable. This was in agreement with Yang et al. (2009), Anandan et al. (2011), Khan et al. (2012) and Nachimuthu et al. (2014). But it was in disagreement with results of Ashfaq et al. (2012) where plant height was more related to PC1.

The PC2 was also dominated by yield related traits i.e. productive tillers per plant, panicle number per plant, total tillers per plant, spikelet fertility percent, and grain yield per plant. This was in favour of findings of Yang et al. (2009), but not in favour of Zhang and Ma (2008), where productive tillers per plant and panicle number per plant were

present in PC3 and Nachimuthu et al. (2014) where grain breadth and grain length dominated PC2.

The PC3 was dominated by stem thickness, plant height, stem length and 1000 grain weight and hence accounted for less variability than traits present in PC1 and PC2. This was in the favour of results of Ashfaq et al. (2012). But against Khan et al. (2012) who reported highest variability in to be in plant height among all the traits studied.

The PC4 was also dominated by quality traits i.e. grain length, decorticated grain length, grain breadth and decorticated grain breadth. This was in favour of Liu et al. (2009) who showed that grain length, LB ratio were the main factors to influence rice quality. But against the findings of Nachimuthu et al. (2014), where grain breadth and grain length dominated in PC2.

The PC5 was dominated by days to fifty percent flowering, days to maturity and sterile spikelets per panicle. But it was not in conformity with results of Ashfaq et al. (2012) where days to fifty percent flowering, days to maturity fell in PC1.

From this study it was clear that most of the important yield and yield and quality attributing traits were present in PC1, PC2, PC3 and PC5. Therefore a promising breeding programme could be initiated by selecting lines from these principal components. Similarly for quality improvement, lines could be selected from PC4 since most of the quality traits were present in this principal component. This was in agreement with the findings of Kumar et al. (2013).

The genotypes such as NPT(s) 4-1, NPT 32 × Pusa Basmati (b), NPT 33 × Mahamaya (c) and 25A × NPT 70-15 fell in yield as well quality associated PCs hence these lines had high value for yield as well as quality.On the basis of PC scores which is found to be common in yield as well quality associated PCs, maximum positive value recorded in NPT 33 × Mahamaya (c) (1.718). It can be concluded that PC analysis highlights the characters with maximum variability. So, intensive selection procedures can

be designed to bring about rapid improvement of yield and quality attributing traits.

On the basis of yield and quality traits the values in PC 1 were highest than PC 2, PC 3, PC 4 and PC 5. On the basis of PC score different lines like NPT(s) 23-3, 25B × NPT 100 (a), NPT 24 × IR 36 (c), NPT(s) 4-1, NPT 32 × Pusa Basmati (b), NPT 33 × Mahamaya (c) and 25A × NPT 70-15 can be utilized for trait improvement in breeding programs for the traits contributing for major variation.development of new varieties in breeding programmes.

5.7 Molecular analysis

The Indian subcontinent has a very rich diversity in rice germplasm which includes landraces, wild *Oryza* species, natural hybrids between the cultivars and wild relatives, and the germplasm resources generated in the breeding programmes (Rai, 1999 and Yadav et al., 2013).During the domestication process, individuals with desirable traits have been selected leaving most of the genetic diversity behind in the progenitors (Doebley et al., 2006).The protection against the loss of vast genetic diversity found in rice varieties is crucial for maintaining future food security in the changing world (Chaudhary et al., 2013). Genetic diversity assessment of the contrasting rice lines is essential component for characterization and conservation to identify potential parents. Morphological and seed traits have long been the means of studying taxonomy and variability among plant species (Sajib et al., 2012). SSRs are among the most widely used DNA marker for many purposes such as diversity, genome mapping, varietal identification, etc. (Teixeira da Silva, 2005). Unlike the morphological and biochemical markers, molecular markers are not stressed by environmental factors and growth practices (Ovesna et al., 2002). The use of these markers to investigate genotypic variations among different cultivars was previously reported by some researchers (Singh et al., 2004; Joshi and Behera, 2006). The primary objective of the investigation was to study the efficacy of markers in differentiating the rice germplasm from diverse source, by comparing clustering based on SSR markers vs the trait linked/gene based markers.

In this study, the molecular data generated using SSR markers which have been reported to be gene based or linked to genes related to yield and yield component traits in rice (Zhang et al. 2010). A total of 75 genotypes were included in the present study for morphological and biochemical characterization. Out of which 24 contrasting lines were selected on the basis of plant height, panicle length, stem thickness, no of panicles, stem thickness, 1000 grain weight and amylose content for molecular characterization. The present investigation addresses the utilization of SSR markers to reveal genetic polymorphism and ensures unambiguous identification of JNPT lines of rice. A total of 22 alleles were detected in 24 JNPT lines of rice and the number of alleles per locus ranged from 2 to 3 with an average of 1.69 per locus. This result indicates less magnitude of diversity with reference to the 13 markers among the plant materials similar to the investigation of Prabakaran et al. 2010. As compared to the present study, Etemad et al. (2012) detected 3.57 alleles per SSR locus among 26 rice (*Oryza sativa,* L.) accessions using SSR markers distributed across the rice genome. In another study, Hossain et al. (2012) found an average of 3.8 alleles per locus in rice using Bangladeshi ARLs. The number of alleles detected in the present study was lower than the average number of alleles reported by Zeng et al. (2007) and Prathepha et al. (2012) who reported an average of 7.7 and 11.85 alleles per locus using rice landraces from China and wild rice (*Oryza rufipogon)* from Northeastern Thailand and Laos respectively. Such variability in the number of alleles detected per locus might be due to the diverse lines used and selection of SSR primers with scorable alleles. Markers with the highest number of discernable alleles could be the best markers for molecular characterization and diversity analysis.

The number of bands produced across 24 rice lines by different SSR motifs is consistent with published reports on microsatellite frequency in their genome. From Table 7 it could be seen that there were no correlations between the number of allele detected and the number of SSR repeats present in a particular locus. Majority of SSR primers used in this study had dinucleotide repeats (GA and CT). The perfect dinucleotide repeat motif (GA)

has been reported to display high level of variation among the rice genotypes (Temnykh et al. 2000).

In the present study, the level of polymorphism determined by the PIC value ranged from 0.00 to 0.49 with mean value of 0.18, is consistent with the reported PIC value in previous works (Lu et al., 2005; Wong et al., 2009; Hossain et al., 2012). According to the early reports on the PIC values ranged from a low of 0.24 to a high of 0.92 and averaged 0.61 (Jain et al., 2004), 0.19 to 0.90 with an average of 0.75 (Borba et al., 2009), which is markedly higher than the result in our study. Thus, the PIC value indicates that all these primers were highly informative and capable of distinguishing between rice genotypes (Sajib et al., 2012).

It was found that out of the thirteen markers used six markers were found to be polymorphic. The markers namely, RM259, RM468, RM201, RM219, RM228 and RM7 are associated with important qualitative and quantitative traits i.e. grain length, kernel width, kernel length, plant height, panicle length, drought tolerance and thousand grain weight respectively. SSR markers used in this study were mapped and found QTLs for linked traits of RM 219 (Xiao et al., 1998), RM228 (Mei et al., 2003; Jiang et al., 2004) and RM7 (Hittalmani et al., 2003) on chromosome 9, 10 and 3 in rice genome. Several desirable alleles of the loci which showed significant trait-marker associations were identified. The research provided important information for further mining of these elite genes within rice landraces and using them for rice breeding.

The present study revealed low genetic variation with an average allelic richness of 0.796 and an overall Nei's gene diversity detected low (0.234) through 13 SSR markers among twenty four contrasting rice lines compared to individual gene diversity due to lack number of SSR markers used. Similarly, Tu et al. (2007) in China (0.706) and Thomson et al. (2007) in Indonesia (0.68) also detected the low genetic variation among rice varieties, whereas, detected overall gene diversity was higher.

The multivariate nature of SSR markers has the unambiguous advantage of discriminating rice lines more precisely. The UPGMA analysis

could reveal allelic richness of a lot of clusters for various sizes at a highest similarity coefficient level of 0.3462. Among them, rice line NPT 32 × Pusa Basmati (b) was found to be highly diverse, therefore it may be chosen as a parent for hybridization with any of the rice line from other divergent cluster. The use of more number of markers would be efficient to characterize the lines than used for the present study, which highlighted the presence of diversity at genomic level among the rice lines (Prabakaran et al., 2010). In this study, the larger range of similarity values for rice lines revealed by microsatellite markers provides greater confidence for the assessments of genetic diversity and relationships, which can be used in future breeding programs. With the aid of microsatellite makers and clustering data, different distantly related rice lines may be combined by intercrossing genotypes, for instance, aromatic rice genotypes with non-aromatic rice genotypes from different clusters to get hybrid varieties with highest heterosis. Many studies have also reported significantly greater allelic diversity of microsatellite markers than other molecular markers (McCouch et al., 2001). Marker-aided backcrossing (MAB), enabled by advances in genomics and molecular mapping in recent years, is more precise, time-saving, and cost-effective way to develop rice varieties that can withstand these abiotic stresses than conventional breeding.

Unique alleles provide new opportunity to search new alleles of different traits present in the material and in this investigation 4 markers viz., RM 201, RM 228, RM 259 and RM 468 amplified new alleles. Apart from the targeted alleles some new alleles proves the sufficient number of new genes (specific allele) are present in the materials studied. Allele mining is the suitable technique by which we can search and proves that what type of variability with targeted traits related to new alleles are present in the experimental material. This type of research will be possible when more number of markers will be applied to confirm the relevant traits. The findings of this study revealed that the identified markers with specific allele/alleles size may be used as a powerful tool in genotype identification and variety protection, seed-purity evaluation, germplasm characterization/diversity studies, gene and quantitative trait locus (QTL) analysis, pedigree analysis

and marker assisted breeding. These markers can also be used in conjunction with pedigrees and agronomic data to help document ownership and protect intellectual property rights. This is important especially for protection of proprietary germplasm.

In summary, the present study revealed a wide variation among the germplasms. The result indicated that the SSR markers are neutral and co-dominant and could be a powerful tool to assess the genetic variability of the cultivars. The information about the genetic diversity will be very useful for proper identification and selection of appropriate parents for breeding programs, including gene mapping, and ultimately for emphasizing the importance of marker-assisted selection (MAS) in rice improvement worldwide.

SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FURTHER WORK

6.1 Summary

The present investigation entitled “Genetic Analysis and Characterization of Inter-subspecific Cross Derived Genotypes for Yield and Quality traits in Rice” was conducted at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, J.N.K.V.V., Jabalpur, during *Kharif* 2014. This investigation was carried out with 75 JNPT lines of rice in randomized complete block design with three replications with the objectives to characterize JNPT lines based on morphological traits and to estimate genetic parameters of variability *viz.*, coefficient of variation, heritability, genetic advance as percentage of mean, correlation coefficient analysis, path analysis, principal component analysis and molecular diversity analysis using SSR markers.

In the present investigation rice genotypes under study were characterized for twenty eight qualitative traits viz., basal leaf sheath color, leaf: pubescence of blade surface, leaf: auricles, leaf: anthocyanin coloration of auricles, Presence of ligule on leaf, leaf: shape of ligules, leaf ligule color, presence of collar on leaves, culm attiude, flag leaf: attitude of blade, stem: anthocyanin coloration of nodes, spikelet : color of stigma, spikelet : density of pubescence, sterile lemma color, spikelet: color of tip of lemma, panicle: exsertion, panicle: attitude of branches, panicle: awns, panicle: distribution of awns, panicle: color of awns, anthocyanin coloration on leaf sheath, lemma anthocyanin colouration of area below apex, lemma anthocyanin colouration of apex, lemma and palea colour, panicle curvature of main axis, panicle presence of secondry branching, panicle secondry branching and attitude of flag leaf blade (late). All the characters under study showed considerable genetic variability.

Results of analysis of variance indicated that the mean sums of squares due to genotypes were highly significant for all the traits under study, suggesting presence of sufficient variation among the genotypes for these

traits. Maximum variability was observed for number of spikelet per panicle and minimum for LB ratio.

Coefficient of variation truly provides a relative measure of variance among the different traits. The values of PCV for all the traits under study were found to be more than GCV and slight difference between GCV and PCV were observed in all the traits, revealing very little influence of environment for their expression.

High Heritability accompanied with High Genetic Advance indicated the predominance of additive gene action for plant height, fertile spikelet per panicle, no of spikelets per panicle, stem length, harvest index, biological yield, panicle index, spikelet density, sterile spikelet per panicle, panicle weight per plant, flag leaf length, flag leaf width, grain yield per plant, panicle length, thousand grain weight, amylose percent, stem thickness, grain width, decorticated grain width. It indicates that the heritability is most likely due to additive gene effect and selection may be effective.

Characters having positive and significant correlation with grain yield per plant were number of spikelets per panicle, plant height, biological yield per plant, panicle weight per plant, harvest index , number of tillers per plant, productive tillers per plant, fertile spikelets per panicle, stem length, spikelet density, spikelet fertility percent, flag leaf length, flag leaf width and milling percentage.

The path coefficient analysis of different traits contributing towards grain yield revealed that number of spikelets per panicle exhibited maximum positive effect followed by plant height, biological yield per plant, panicle weight per plant, harvest index, seed breadth, panicle index, seed length, total number of productive tillers per plant, stem thickness, milling per cent, 1000 grain weight, days to maturity, flag leaf width and flag leaf length had positive direct effect on grain yield per plant .

The characters with positive and significant correlation along with positive direct effect on grain yield per plant were, spikelet number per panicle, plant height, biological yield per plant, panicle weight per plant,

harvest index, productive tillers per plant and milling percentage Hence, these characters are primary yield contributing characters and could be relied upon for selection to improve genetic yield potential of genotypes.

The principal component analysis revealed that out of thirty one, only five principal components (PCs) exhibited more than 1.9 eigen value, and showed about 62.789% variability among the traits studied. So, these five PCs were given due importance for further explanation. The PC1 showed 19.214 % while, PC2, PC3, PC4 and PC5 exhibited 15.579 %, 12.520 %, 8.123 % and 7.353% variability respectively among the lines for the traits under study. PCA also revealed that number of spikelets per panicle, spikelet density, fertile spikelets per panicle, panicle weight per plant, total tillers per plant, productive tillers per plant, grain yield per plant and biological yield per plant were the characters with maximum variability. On the basis of PCA most of the important yield as well as yield and quality attributing traits were present in PC1, PC2, PC3 and PC4. Therefore a promising breeding programme could be initiated by selecting lines from these principal components. Similarly for quality improvement lines could be selected from PC4 since most of the quality traits were present in this principal component. The genotypes NPT(s) 23-3, 25B × NPT 100 (a), NPT 24 × IR 36 (c) NPT(s) 4-1, NPT 32 × Pusa Basmati (b), NPT 33 × Mahamaya (c) and 25A × NPT 70-15 fell in yield and some in yield as well as quality associated PCs hence these lines had high value for yield and quality improvement.

On the basis of plant height, panicle length, stem thickness, no of panicles, stem thickness and 1000 grain weight performance twenty four diverse lines were selected for molecular characterization especially diversity analysis on the basis of polymorphic SSR markers reported for different qualitative and quantitative traits. A total of thirteen SSR markers having different linked traits were applied to analyze the genetic architecture of the present material utilized for this study. It was found that SSR markers namely RM259, RM468, RM201, RM219, RM228 and RM7 were polymorphic and associated with important qualitative and quantitative traits i.e. grain length, kernel width, kernel length, drought tolerance, plant height, panicle length and

thousand grain weight respectively. Unique alleles were amplified by four markers *viz.,* RM201, RM228, RM259 and RM468. The markers were linked to drought tolerance, panicle length, grain length and grain width respectively. RM 259 and RM 468 amplified 3 alleles each, which were maximum number of amplified alleles. It showed that sufficient amount of genetic diversity is present in genotypes included in this study. The lines NPT(s) 6-12, NPT(s) 8-2 and NPT 32 × Pusa Basmati (b), 25B × NPT 100(a), NPT 32 × Pusa Basmati (b) and NPT 100 × HMT (b), NPT(s) 6-1 (f) and NPT 32 × Pusa Basmati (b), NPT(s) 4-1, NPT(s) 6-1 (b), NPT(s) 6-1 (c) and NPT(s) 6-1 (d) showed the presence of unique alleles and hence are of importance in molecular breeding programme. From overall molecular analysis, it is summarized that that the polymorphic markers will be used for diversity analysis, mapping and tagging of targeted genes and also QTL analysis, candidate gene approach and other relevant fields of genetics and plant breeding.

6.2 Conclusions

- JNPT lines showed sufficient variation among the lines for the traits under study for morphological characterization as well as other traits under study. The values of PCV for all the traits were found to be more than GCV and very small difference was present in between GCV and PCV revealing very little influence of environment for their expression.
- Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability alone. Result showed that the characters *viz*., plant height, fertile spikelets per panicle, number of spikelets per panicle, stem length, harvest index, biological yield per plant, panicle index, spikelet density, sterile spikelets per panicle, panicle weight per plant, flag leaf length, flag leaf width, grain yield per plant, panicle length, 1000 grain weight, amylose percent, stem thickness, grain width, decorticated grain width had high heritability coupled with high genetic advance. It indicates that the heritability is most likely due to additive gene effect and selection may be effective.

- Based on the studies of correlation and path analysis, it may be concluded that number of spikelets per panicle, plant height, biological yield per plant, panicle weight per plant, harvest index, productive tillers per plant and milling percentage showed positive correlation with grain yield and at the same time exhibited positive direct effect towards yield. Therefore they seem to be primary yield contributing characters and could be relied upon for selection to improve genetic yield potential of rice.
- PCA also revealed that number of spikelets per panicle, spikelet density, fertile spikelets per panicle, panicle weight per plant, total tillers per plant, productive tillers per plant, grain yield per plant and biological yield per plant were the characters with maximum variability.
- On the basis of morphological characterization and quantitative analysis varieties NPT 24 × IR 36 (c), NPT(s) 23-3, 25B × NPT 100 (a), NPT 24 × IR 36 (f), NPT(s) 10-1 (b), NPT 24 × IR 36 (g), NPT 24 × IR 36 (f), NPT 24 × IR 36 (e) and NPT 100 × HMT (e) were found to be excellent for yield and yield attributing traits.
- The genotypes such as NPT(s) 23-3, 25B × NPT 100 (a), NPT 24 × IR 36 (c), NPT(s) 4-1, NPT 32 × Pusa Basmati (b), NPT 33 × Mahamaya (c) and 25A × NPT 70-15 fell in yield as well yield and quality associated PCs hence these lines had high value for yield as well as quality.s
- The genotypes with high amylose content (NPT(s) 8-1 (b), NPT(s) 10-1 (d), NPT(s) 23-3, 25A × NPT 70-15) and low amylose content [NPT(s) 10-1 (c), NPT 24 × IR 36 (f), NPT(s) 10-8 (a), NPT 24 × IR 36 (g)] were categorised.
- Unique alleles were amplified by four markers *viz.,* RM201, RM228, RM259 and RM468. Presence of specific bands reported earlier for drought tolerance, panicle length, grain length and grain breadth were found in genotype, NPT(s) 6-12, NPT(s) 8-2 and NPT 32 × Pusa Basmati (b), 25B × NPT 100(a), NPT 32 × Pusa Basmati (b) and NPT 100 × HMT (b), NPT(s) 6-1 (f) and NPT 32 × Pusa Basmati (b), NPT(s) 4-1, NPT(s) 6-1 (b), NPT(s) 6-1 (c) and NPT(s) 6-1 (d) for the respective markers. These genotypes could be directly used for identification of the QTLs linked with

these markers and cultivation purposes because each has unique alleles for specific yield contributing and quality character.

- The identified markers with specific allele/alleles size may be used as a powerful tool in genotype identification and variety protection, seed-purity evaluation, germplasm characterization/diversity studies, gene and quantitative trait locus (QTL) analysis, pedigree analysis and marker assisted breeding. These markers can also be used in conjunction with pedigrees and agronomic data to help document ownership and protect intellectual property rights. This is important especially for protection of proprietary germplasm.

6.3 Suggestions for further work

1. As evident from phenotypic and genotypic coefficients of variation, heritability and genetic advance, correlation coefficient, path analysis and PCA the characters viz., panicle weight per plant, biological yield per plant, harvest index, number of spikelets per panicle and productive tillers per plant may be utilized in designing high yielding plant ideotypes.
2. The genotypes NPT 24 × IR 36 (c), NPT(s) 23-3, 25B × NPT 100 (a), NPT 24 × IR 36 (f), NPT(s) 10-1 (b), NPT 24 × IR 36 (g), NPT 24 × IR 36 (f), NPT 24 × IR 36 (e) and NPT 100 × HMT (e) were found to be excellent on the basis of morphological characterization and quantitative analysis and could be utilized further in breeding programmes for improvement of lines or development of superior crosses.
3. The genotypes such as NPT(s) 23-3, 25B × NPT 100 (a), NPT 24 × IR 36 (c), NPT(s) 4-1, NPT(s) 4-1, NPT 32 × Pusa Basmati (b), NPT 33 × Mahamaya (c) and 25A × NPT 70-15 fell in yield and yield as well quality associated PCs hence these lines could be used in future for yield and quality improvement programmes.
4. The genotypes with high amylose content (NPT(s) 8-1 (b), NPT(s) 10-1 (d), NPT(s) 23-3, 25A × NPT 70-15) and low amylose content (NPT(s) 10-1 (c), NPT 24 × IR 36 (f), NPT(s) 10-8 (a), NPT 24 × IR 36 (g) could be used for specific quality improvement programme.

5. Unique alleles were amplified by four markers *viz.,* RM201, RM228, RM259 and RM468. Presence of specific band reported earlier for drought tolerance, panicle length, grain length and grain width were found in genotypes namely, NPT(s) 6-12, NPT(s) 8-2 and NPT 32 × Pusa Basmati (b), 25B × NPT 100(a), NPT 32 × Pusa Basmati (b) and NPT 100 × HMT (b), NPT(s) 6-1 (f) and NPT 32 × Pusa Basmati (b), NPT(s) 4-1, NPT(s) 6-1 (b), NPT(s) 6-1 (c) and NPT(s) 6-1 (d) for the respective markers. These genotypes could be directly used for identification of the QTLs linked with these markers. The identified markers with specific allele/alleles size may be used as in genotype identification and variety protection, seed-purity evaluation, germplasm characterization/diversity studies, gene and quantitative trait locus (QTL) analysis, pedigree analysis and marker assisted breeding.
6. In molecular work, Metaphor and polyacrylamide matrix can be used for better resolution of alleles

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Scientific interests

a. Molecular Breeding

b. Field Research and Development

For the partial fulfilment of the master's degree programme she was allotted a research problems on ***"*Genetic Analysis and Characterization of Inter-subspecific Cross Derived Genotypes for Yield and Quality Traits in Rice"** which was successfully conducted by her and being submitted in the form of the thesis .

ABSTRACT

1.	Title of the thesis	:	**"Genetic analysis and Characterization of Inter-subspecific Cross Derieved Genotypes for Yield and Quality traits in Rice"**
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ABSTRACT

The present investigation entitled “Genetic analysis and Characterization of Inter-subspecific Cross Derieved Genotypes for Yield and Quality traits in Rice” was conducted at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, J.N.K.V.V., Jabalpur, during *Kharif* 2014. This investigation was carried out with 75 JNPT lines of rice in randomized complete block design with three replications with the objectives to characterize JNPT lines based on morphological traits and to estimate genetic parameters of variability *viz.*, coefficient of variation, heritability, genetic advance as percentage of mean, correlation coefficient analysis, path analysis, principal component analysis and molecular diversity analysis using SSR markers.

In the present investigation rice genotypes under study were characterized for twenty eight qualitative traits viz., basal leaf sheath color, leaf: pubescence of blade surface, leaf: auricles, leaf: anthocyanin coloration of auricles, Presence of ligule on leaf, leaf: shape of ligules, leaf ligule color, presence of collar on leaves, culm attiude, flag leaf: attitude of blade, stem: anthocyanin coloration of nodes, spikelet : color of stigma, spikelet : density of pubescence, sterile lemma color, spikelet: color of tip of lemma, panicle: exsertion, panicle: attitude of branches, panicle: awns, panicle: distribution of awns, panicle: color of awns, anthocyanin coloration on leaf sheath, lemma anthocyanin colouration of area below apex, lemma anthocyanin colouration of apex, lemma and palea colour, panicle curvature of main axis, panicle presence of secondry branching, panicle secondry branching and attitude of flag leaf blade (late). All the characters under study showed considerable genetic variability.

Results of analysis of variance indicated that the mean sums of squares due to genotypes were highly significant for all the traits under study, suggesting presence of sufficient variation among the genotypes for these traits. Maximum variability was observed for number of spikelet per panicle and minimum for LB ratio.

Coefficient of variation truly provides a relative measure of variance among the different traits. The values of PCV for all the traits under study were found to be more than GCV and slight difference between GCV and PCV were observed in all the traits, revealing very little influence of environment for their expression.

High Heritability accompanied with High Genetic Advance indicated the predominance of additive gene action for plant height, fertile spikelet per panicle, no of spikelets per panicle, stem length, harvest index, biological yield, panicle index, spikelet density, sterile spikelet per panicle, panicle weight per plant, flag leaf length, flag leaf width, grain yield per plant, panicle length, thousand grain weight, amylose percent, stem thickness, grain width, decorticated grain width. It indicates that the heritability is most likely due to additive gene effect and selection may be effective.

Characters having positive and significant correlation with grain yield per plant were number of spikelets per panicle, plant height, biological yield per plant, panicle weight per plant, harvest index , number of tillers per plant, productive tillers per plant, fertile spikelets per panicle, stem length, spikelet density, spikelet fertility percent, flag leaf length, flag leaf width and milling percentage.

The path coefficient analysis of different traits contributing towards grain yield revealed that number of spikelets per panicle exhibited maximum positive effect followed by plant height, biological yield per plant, panicle weight per plant, harvest index, seed breadth, panicle index, seed length, total number of productive tillers per plant, stem thickness, milling per cent, 1000 grain weight, days to maturity, flag leaf width and flag leaf length had positive direct effect on grain yield per plant .

The characters with positive and significant correlation along with positive direct effect on grain yield per plant were, spikelet number per panicle, plant height, biological yield per plant, panicle weight per plant, harvest index , productive tillers per plant and milling percentage Hence, these characters are primary yield contributing characters and could be relied upon for selection to improve genetic yield potential of genotypes.

The principal component analysis revealed that out of thirty one, only five principal components (PCs) exhibited more than 1.9 eigen value, and showed about 62.789% variability among the traits studied. So, these five PCs were given due importance for further explanation. The PC1 showed 19.214 % while, PC2, PC3, PC4 and PC5 exhibited 15.579 %, 12.520 %, 8.123 % and 7.353% variability respectively among the lines for the traits under study. PCA also revealed that number of spikelets per panicle, spikelet density, fertile spikelets per panicle, panicle weight per plant, total tillers per plant, productive tillers per plant, grain yield per plant

and biological yield per plant were the characters with maximum variability. On the basis of PCA most of the important yield as well as yield and quality attributing traits were present in PC1, PC2, PC3 and PC4. Therefore a promising breeding programme could be initiated by selecting lines from these principal components. Similarly for quality improvement lines could be selected from PC4 since most of the quality traits were present in this principal component. The genotypes NPT(s) 23-3, 25B × NPT 100 (a), NPT 24 × IR 36 (c) NPT(s) 4-1, NPT 32 × Pusa Basmati (b), NPT 33 × Mahamaya (c) and 25A × NPT 70-15 fell in yield and some in yield as well as quality associated PCs hence these lines had high value for yield and quality improvement.

On the basis of plant height, panicle length, stem thickness, no of panicles, stem thickness and 1000 grain weight performance twenty four diverse lines were selected for molecular characterization especially diversity analysis on the basis of polymorphic SSR markers reported for different qualitative and quantitative traits. A total of thirteen SSR markers having different linked traits were applied to analyze the genetic architecture of the present material utilized for this study. It was found that SSR markers namely RM259, RM468, RM201, RM219, RM228 and RM7 were polymorphic and associated with important qualitative and quantitative traits i.e. grain length, kernel width, kernel length, drought tolerance, plant height, panicle length and thousand grain weight respectively. Unique alleles were amplified by four markers *viz.,* RM201, RM228, RM259 and RM468. The markers were linked to drought tolerance, panicle length, grain length and grain width respectively. RM 259 and RM 468 amplified 3 alleles each, which were maximum number of amplified alleles. It showed that sufficient amount of genetic diversity is present in genotypes included in this study. The lines NPT(s) 6-12, NPT(s) 8-2 and NPT 32 × Pusa Basmati (b), 25B × NPT 100(a), NPT 32 × Pusa Basmati (b) and NPT 100 × HMT (b), NPT(s) 6-1 (f) and NPT 32 × Pusa Basmati (b), NPT(s) 4-1, NPT(s) 6-1 (b), NPT(s) 6-1 (c) and NPT(s) 6-1 (d) showed the presence of unique alleles and hence are of importance in molecular breeding programme. From overall molecular analysis, it is summarized that that the polymorphic markers will be used for diversity analysis, mapping and tagging of targeted genes and also QTL analysis, candidate gene approach and other relevant fields of genetics and plant breeding.

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Genotypical Correlation Matrix

	x1	x2	x3	x4	x5	x6	x7	x8	x9	x10	x11	x12	x13	x14	x15
x1	**1.0000**	0.8544	-0.1724	-0.1518	-0.1518	-0.0519	-0.0814	0.1828	-0.0396	-0.2154	0.3856	0.0498	-0.0986	0.3256	-0.3883
x2	0.8544	**1.0000**	-0.1547	-0.1310	-0.1310	-0.1590	-0.1858	0.1199	-0.0759	-0.2530	0.4595	0.0330	-0.1003	0.2884	-0.3379
x3	-0.1724	-0.1547	**1.0000**	0.9637	0.9637	0.0243	0.0359	-0.0704	-0.0174	-0.0178	-0.1572	0.1007	0.2661	-0.3028	0.4376
x4	-0.1518	-0.1310	0.9637	**1.0000**	1.0000	-0.0263	-0.0205	-0.0509	0.0024	-0.0485	-0.1511	0.1306	0.2828	-0.2643	0.4087
x5	-0.1518	-0.1310	0.9637	1.0000	**1.0000**	-0.0263	-0.0205	-0.0509	0.0024	-0.0485	-0.1511	0.1306	0.2828	-0.2643	0.4087
x6	-0.0519	-0.1590	0.0243	-0.0263	-0.0263	**1.0000**	0.9918	0.4701	0.2103	0.3753	-0.4389	0.0302	0.1100	-0.1529	0.2411
x7	-0.0814	-0.1858	0.0359	-0.0205	-0.0205	0.9918	**1.0000**	0.3537	0.1967	0.4255	-0.4331	0.0432	0.1407	-0.1843	0.2846
x8	0.1828	0.1199	-0.0704	-0.0509	-0.0509	0.4701	0.3537	**1.0000**	0.1815	-0.1922	-0.2221	-0.0778	-0.1671	0.1547	-0.2011
x9	-0.0396	-0.0759	-0.0174	0.0024	0.0024	0.2103	0.1967	0.1815	**1.0000**	0.3810	-0.2040	0.3071	0.2175	0.3035	-0.2027
x10	-0.2154	-0.2530	-0.0178	-0.0485	-0.0485	0.3753	0.4255	-0.1922	0.3810	**1.0000**	-0.1822	0.3999	0.4418	0.0672	0.1283
x11	0.3856	0.4595	-0.1572	-0.1511	-0.1511	-0.4389	-0.4331	-0.2221	-0.2040	-0.1822	**1.0000**	0.1720	0.0344	0.3509	-0.3376
x12	0.0498	0.0330	0.1007	0.1306	0.1306	0.0302	0.0432	-0.0778	0.3071	0.3999	0.1720	**1.0000**	0.9159	0.5588	-0.1451
x13	-0.0986	-0.1003	0.2661	0.2828	0.2828	0.1100	0.1407	-0.1671	0.2175	0.4418	0.0344	0.9159	**1.0000**	0.1790	0.2581
x14	0.3256	0.2884	-0.3028	-0.2643	-0.2643	-0.1529	-0.1843	0.1547	0.3035	0.0672	0.3509	0.5588	0.1790	**1.0000**	-0.8888
x15	-0.3883	-0.3379	0.4376	0.4087	0.4087	0.2411	0.2846	-0.2011	-0.2027	0.1283	-0.3376	-0.1451	0.2581	-0.8888	**1.0000**
x16	-0.0418	-0.0195	0.1121	0.1319	0.1319	-0.1853	-0.1214	-0.5189	0.1866	0.4445	0.2442	0.8881	0.8625	0.3948	-0.0228
x17	-0.0134	0.0048	0.4744	0.4666	0.4666	0.4206	0.4422	0.0245	0.3251	0.3694	-0.0397	0.4783	0.5452	0.0465	0.2203
x18	-0.2442	-0.2149	-0.1954	-0.1794	-0.1794	0.4869	0.4984	0.1218	0.1564	0.2739	-0.3035	-0.1088	-0.0849	-0.0906	0.1113
x19	0.0642	0.0471	0.4654	0.4353	0.4353	0.4311	0.4435	0.0926	0.3143	0.4337	-0.0199	0.4319	0.4991	0.0280	0.2079
x20	-0.0627	-0.0437	-0.0722	-0.0327	-0.0327	-0.2386	-0.2163	-0.2530	-0.2082	-0.1066	-0.0944	-0.3279	-0.2646	-0.2577	0.1456
x21	-0.2606	-0.1726	0.2066	0.2873	0.2873	-0.0784	-0.0467	-0.2520	-0.0344	-0.0592	-0.1578	0.0121	0.0975	-0.1724	0.2436
x22	0.0129	0.0297	-0.2118	-0.2171	-0.2171	0.3112	0.2982	0.2189	0.1679	0.2489	-0.1814	-0.0982	-0.1481	0.0658	-0.1319
x23	-0.0369	0.0283	-0.3101	-0.3195	-0.3195	0.1989	0.1881	0.1565	0.0693	0.1289	0.0130	-0.1894	-0.2225	-0.0041	-0.0886
x24	0.0426	0.0471	-0.2006	-0.2041	-0.2041	0.3195	0.3044	0.2362	0.1364	0.2311	-0.1538	-0.0962	-0.1467	0.0678	-0.1318
x25	-0.0330	0.0341	-0.2881	-0.2968	-0.2968	0.1727	0.1579	0.1741	0.0638	0.0997	0.0520	-0.1951	-0.2308	-0.0007	-0.0932
x26	0.0855	-0.0403	0.1038	0.1295	0.1295	0.1128	0.1241	-0.0316	0.0999	0.1112	-0.3340	0.1872	0.1797	0.0876	-0.0150
x27	-0.1320	-0.1535	-0.0324	-0.0349	-0.0349	0.0093	0.0208	-0.0758	-0.0233	0.0884	0.1676	0.0292	0.0560	-0.0439	0.0949
x28	-0.0223	-0.1378	0.0931	0.1176	0.1176	0.0401	0.0526	-0.0701	-0.0242	0.0242	-0.0346	-0.0159	0.0532	-0.1500	0.1606
x29	0.0800	0.0277	-0.2369	-0.2179	-0.2179	0.0166	0.0228	-0.0363	0.0045	-0.0616	-0.0163	-0.0939	-0.0962	-0.0323	-0.0026
x30	0.0880	-0.0030	-0.0079	0.0107	0.0107	0.1657	0.1697	0.0407	0.0910	0.1728	-0.3344	-0.0207	-0.0403	0.0317	-0.0773
x31	-0.0865	-0.0441	0.5540	0.5739	0.5739	0.3627	0.3964	-0.0838	0.2722	0.3732	-0.0955	0.3987	0.5216	-0.1004	0.3552

	x16	x17	x18	x19	x20	x21	x22	x23	x24	x25	x26	x27	x28	x29	x30
x1	-0.0418	-0.0134	-0.2442	0.0642	-0.0627	-0.2606	0.0129	-0.0369	0.0426	-0.0330	0.0855	-0.1320	-0.0223	0.0800	0.0880
x2	-0.0195	0.0048	-0.2149	0.0471	-0.0437	-0.1726	0.0297	0.0283	0.0471	0.0341	-0.0403	-0.1535	-0.1378	0.0277	-0.0030
x3	0.1121	0.4744	-0.1954	0.4654	-0.0722	0.2066	-0.2118	-0.3101	-0.2006	-0.2881	0.1038	-0.0324	0.0931	-0.2369	-0.0079
x4	0.1319	0.4666	-0.1794	0.4353	-0.0327	0.2873	-0.2171	-0.3195	-0.2041	-0.2968	0.1295	-0.0349	0.1176	-0.2179	0.0107
x5	0.1319	0.4666	-0.1794	0.4353	-0.0327	0.2873	-0.2171	-0.3195	-0.2041	-0.2968	0.1295	-0.0349	0.1176	-0.2179	0.0107
x6	-0.1853	0.4206	0.4869	0.4311	-0.2386	-0.0784	0.3112	0.1989	0.3195	0.1727	0.1128	0.0093	0.0401	0.0166	0.1657
x7	-0.1214	0.4422	0.4984	0.4435	-0.2163	-0.0467	0.2982	0.1881	0.3044	0.1579	0.1241	0.0208	0.0526	0.0228	0.1697
x8	-0.5189	0.0245	0.1218	0.0926	-0.2530	-0.2520	0.2189	0.1565	0.2362	0.1741	-0.0316	-0.0758	-0.0701	-0.0363	0.0407
x9	0.1866	0.3251	0.1564	0.3143	-0.2082	-0.0344	0.1679	0.0693	0.1364	0.0638	0.0999	-0.0233	-0.0242	0.0045	0.0910
x10	0.4445	0.3694	0.2739	0.4337	-0.1066	-0.0592	0.2489	0.1289	0.2311	0.0997	0.1112	0.0884	0.0242	-0.0616	0.1728
x11	0.2442	-0.0397	-0.3035	-0.0199	-0.0944	-0.1578	-0.1814	0.0130	-0.1538	0.0520	-0.3340	0.1676	-0.0346	-0.0163	-0.3344
x12	0.8881	0.4783	-0.1088	0.4319	-0.3279	0.0121	-0.0982	-0.1894	-0.0962	-0.1951	0.1872	0.0292	-0.0159	-0.0939	-0.0207
x13	0.8625	0.5452	-0.0849	0.4991	-0.2646	0.0975	-0.1481	-0.2225	-0.1467	-0.2308	0.1797	0.0560	0.0532	-0.0962	-0.0403
x14	0.3948	0.0465	-0.0906	0.0280	-0.2577	-0.1724	0.0658	-0.0041	0.0678	-0.0007	0.0876	-0.0439	-0.1500	-0.0323	0.0317
x15	-0.0228	0.2203	0.1113	0.2079	0.1456	0.2436	-0.1319	-0.0886	-0.1318	-0.0932	-0.0150	0.0949	0.1606	-0.0026	-0.0773
x16	**1.0000**	0.3961	-0.1442	0.3343	-0.1564	0.1207	-0.1704	-0.2144	-0.1755	-0.2313	0.1590	0.0446	0.0095	-0.0684	-0.0465
x17	0.3961	**1.0000**	0.2643	0.8628	-0.5486	0.1121	0.1196	-0.0363	0.1244	-0.0470	0.2002	-0.0074	0.0028	-0.1083	-0.0291
x18	-0.1442	0.2643	**1.0000**	0.2561	0.0072	0.1113	0.4828	0.3638	0.4638	0.3437	0.0482	-0.0708	0.0745	0.0313	0.0612
x19	0.3343	0.8628	0.2561	**1.0000**	-0.4566	-0.2676	0.0914	-0.0603	0.0974	-0.0697	0.1812	0.0679	0.0553	-0.1029	0.0769
x20	-0.1564	-0.5486	0.0072	-0.4566	**1.0000**	0.4005	-0.1620	0.0411	-0.1710	0.0329	-0.1384	0.1530	0.2856	0.1711	0.0908

x21	0.1207	0.1121	0.1113	-0.2676	0.4005	**1.0000**	-0.1196	-0.0424	-0.1396	-0.0423	0.0203	-0.0257	0.0998	0.0389	-0.0503
x22	-0.1704	0.1196	0.4828	0.0914	-0.1620	-0.1196	**1.0000**	0.6013	0.9952	0.5996	0.1734	-0.2515	-0.0048	-0.1048	0.0513
x23	-0.2144	-0.0363	0.3638	-0.0603	0.0411	-0.0424	0.6013	**1.0000**	0.6037	0.9935	-0.8468	-0.0761	0.0943	0.1059	-0.0646
x24	-0.1755	0.1244	0.4638	0.0974	-0.1710	-0.1396	0.9952	0.6037	**1.0000**	0.6064	0.1974	-0.2549	0.0047	-0.1050	0.0391
x25	-0.2313	-0.0470	0.3437	-0.0697	0.0329	-0.0423	0.5996	0.9935	0.6064	**1.0000**	-0.8843	-0.0691	0.0918	0.1001	-0.0932
x26	0.1590	0.2002	0.0482	0.1812	-0.1384	0.0203	0.1734	-0.8468	0.1974	-0.8843	**1.0000**	-0.1389	-0.0071	-0.0731	0.2648
x27	0.0446	-0.0074	-0.0708	0.0679	0.1530	-0.0257	-0.2515	-0.0761	-0.2549	-0.0691	-0.1389	**1.0000**	0.3542	0.2663	-0.2566
x28	0.0095	0.0028	0.0745	0.0553	0.2856	0.0998	-0.0048	0.0943	0.0047	0.0918	-0.0071	0.3542	**1.0000**	0.6189	0.2029
x29	-0.0684	-0.1083	0.0313	-0.1029	0.1711	0.0389	-0.1048	0.1059	-0.1050	0.1001	-0.0731	0.2663	0.6189	**1.0000**	0.1672
x30	-0.0465	-0.0291	0.0612	0.0769	0.0908	-0.0503	0.0513	-0.0646	0.0391	-0.0932	0.2648	-0.2566	0.2029	0.1672	**1.0000**
x31	0.3840	0.8950	0.3288	0.7833	-0.1606	0.3658	0.0439	-0.0446	0.0380	-0.0576	0.1711	0.0177	0.1364	-0.0817	0.0269

PATH matrix of x31

	x1	**x2**	**x3**	**x4**	**x5**	**x6**	**x7**	**x8**	**x9**	**x10**	**x11**	**x12**	**x13**	**x14**	**x15**
x1	**-0.0411**	-0.0351	0.0071	0.0062	0.0062	0.0021	0.0033	-0.0075	0.0016	0.0089	-0.0158	-0.0020	0.0041	-0.0134	0.0160
x2	0.0173	**0.0203**	-0.0031	-0.0027	-0.0027	-0.0032	-0.0038	0.0024	-0.0015	-0.0051	0.0093	0.0007	-0.0020	0.0058	-0.0069
x3	0.0091	0.0082	**-0.0527**	-0.0508	-0.0508	-0.0013	-0.0019	0.0037	0.0009	0.0009	0.0083	-0.0053	-0.0140	0.0160	-0.0231
x4	-0.0111	-0.0096	0.0705	**0.0732**	0.0732	-0.0019	-0.0015	-0.0037	0.0002	-0.0035	-0.0111	0.0096	0.0207	-0.0193	0.0299
x5	0.0000	0.0000	0.0000	0.0000	**0.0000**	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
x6	-0.0767	-0.2350	0.0359	-0.0388	-0.0388	**1.4783**	1.4662	0.6949	0.3110	0.5548	-0.6489	0.0446	0.1626	-0.2260	0.3564
x7	0.1116	0.2548	-0.0492	0.0281	0.0281	-1.3601	**-1.3713**	-0.4850	-0.2697	-0.5835	0.5939	-0.0592	-0.1930	0.2528	-0.3902
x8	-0.0585	-0.0384	0.0225	0.0163	0.0163	-0.1504	-0.1131	**-0.3199**	-0.0581	0.0615	0.0710	0.0249	0.0535	-0.0495	0.0643
x9	-0.0002	-0.0003	-0.0001	0.0000	0.0000	0.0008	0.0008	0.0007	**0.0039**	0.0015	-0.0008	0.0012	0.0009	0.0012	-0.0008
x10	-0.0017	-0.0020	-0.0001	-0.0004	-0.0004	0.0030	0.0034	-0.0015	0.0030	**0.0079**	-0.0014	0.0032	0.0035	0.0005	0.0010
x11	0.0271	0.0323	-0.0110	-0.0106	-0.0106	-0.0308	-0.0304	-0.0156	-0.0143	-0.0128	**0.0703**	0.0121	0.0024	0.0247	-0.0237
x12	0.1723	0.1143	0.3487	0.4524	0.4524	0.1044	0.1496	-0.2695	1.0635	1.3848	0.5957	**3.4632**	3.1720	1.9352	-0.5024
x13	0.2498	0.2541	-0.6741	-0.7164	-0.7164	-0.2787	-0.3565	0.4233	-0.5510	-1.1192	-0.0871	-2.3204	**-2.5334**	-0.4534	-0.6538
x14	-0.5421	-0.4803	0.5043	0.4401	0.4401	0.2545	0.3069	-0.2576	-0.5053	-0.1118	-0.5843	-0.9305	-0.2980	**-1.6651**	1.4800
x15	0.1359	0.1183	-0.1532	-0.1431	-0.1431	-0.0844	-0.0996	0.0704	0.0709	-0.0449	0.1182	0.0508	-0.0903	0.3111	**-0.3500**
x16	0.0137	0.0064	-0.0368	-0.0433	-0.0433	0.0608	0.0399	0.1704	-0.0613	-0.1459	-0.0802	-0.2916	-0.2832	-0.1296	0.0075
x17	-0.0060	0.0021	0.2114	0.2079	0.2079	0.1874	0.1971	0.0109	0.1449	0.1646	-0.0177	0.2131	0.2429	0.0207	0.0982
x18	-0.0074	-0.0065	-0.0059	-0.0054	-0.0054	0.0147	0.0150	0.0037	0.0047	0.0082	-0.0091	-0.0033	-0.0026	-0.0027	0.0034
x19	0.0374	0.0275	0.2713	0.2538	0.2538	0.2513	0.2586	0.0540	0.1832	0.2528	-0.0116	0.2518	0.2910	0.0163	0.1212
x20	-0.0135	-0.0094	-0.0155	-0.0070	-0.0070	-0.0513	-0.0465	-0.0544	-0.0448	-0.0229	-0.0203	-0.0705	-0.0569	-0.0554	0.0313
x21	-0.0994	-0.0659	0.0788	0.1096	0.1096	-0.0299	-0.0178	-0.0962	-0.0131	-0.0226	-0.0602	0.0046	0.0372	-0.0658	0.0930
x22	0.0024	0.0056	-0.0402	-0.0412	-0.0412	0.0590	0.0566	0.0415	0.0319	0.0472	-0.0344	-0.0186	-0.0281	0.0125	-0.0250
x23	-0.0088	0.0068	-0.0740	-0.0763	-0.0763	0.0475	0.0449	0.0374	0.0165	0.0308	0.0031	-0.0452	-0.0531	-0.0010	-0.0212
x24	-0.0078	-0.0086	0.0368	0.0374	0.0374	-0.0585	-0.0558	-0.0433	-0.0250	-0.0423	0.0282	0.0176	0.0269	-0.0124	0.0241
x25	0.0085	-0.0088	0.0746	0.0768	0.0768	-0.0447	-0.0409	-0.0451	-0.0165	-0.0258	-0.0135	0.0505	0.0597	0.0002	0.0241
x26	-0.0011	0.0005	-0.0013	-0.0017	-0.0017	-0.0014	-0.0016	0.0004	-0.0013	-0.0014	0.0043	-0.0024	-0.0023	-0.0011	0.0002
x27	0.0083	0.0096	0.0020	0.0022	0.0022	-0.0006	-0.0013	0.0048	0.0015	-0.0055	-0.0105	-0.0018	-0.0035	0.0028	-0.0060
x28	-0.0007	-0.0046	0.0031	0.0039	0.0039	0.0013	0.0018	-0.0023	-0.0008	0.0008	-0.0012	-0.0005	0.0018	-0.0050	0.0054
x29	-0.0014	-0.0005	0.0041	0.0038	0.0038	-0.0003	-0.0004	0.0006	-0.0001	0.0011	0.0003	0.0016	0.0017	0.0006	0.0000
x30	-0.0026	0.0001	0.0002	-0.0003	-0.0003	-0.0050	-0.0051	-0.0012	-0.0027	-0.0052	0.0101	0.0006	0.0012	-0.0010	0.0023
x31	-0.0865	-0.0441	0.5540	0.5739	0.5739	0.3627	0.3964	-0.0838	0.2722	0.3732	-0.0955	0.3987	0.5216	-0.1004	0.3552
Partial R^2	0.0036	-0.0009	-0.0292	0.0420	0.0000	0.5361	-0.5436	0.0268	0.0011	0.0029	-0.0067	1.3807	-1.3215	0.1671	-0.1243

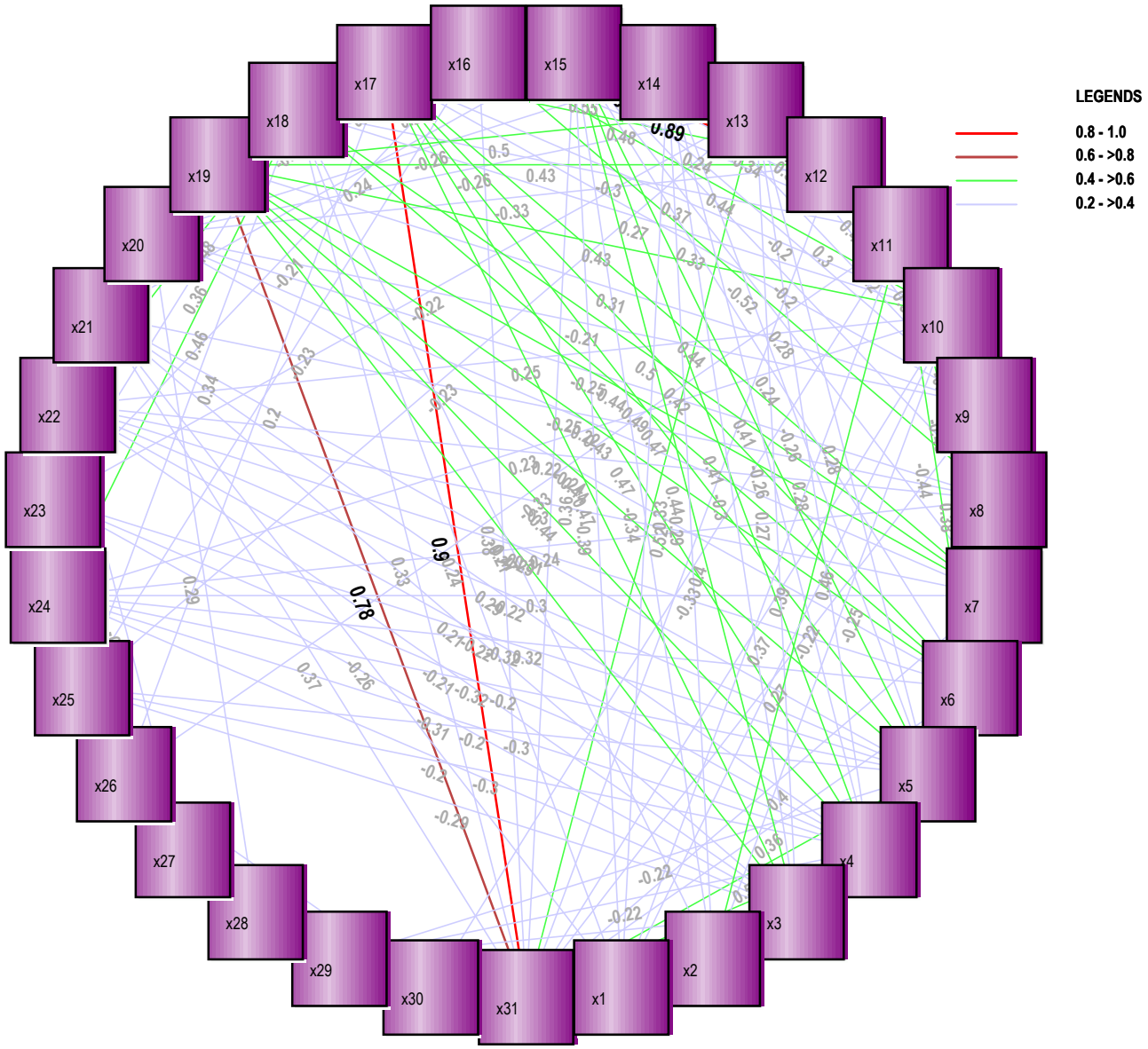
PATH matrix of x31

	x16	**x17**	**x18**	**x19**	**x20**	**x21**	**x22**	**x23**	**x24**	**x25**	**x26**	**x27**	**x28**	**x29**	**x30**
x1	0.0017	0.0006	0.0100	-0.0026	0.0026	0.0107	-0.0005	0.0015	-0.0018	0.0014	-0.0035	0.0054	0.0009	-0.0033	-0.0036
x2	-0.0004	0.0001	-0.0044	0.0010	-0.0009	-0.0035	0.0006	0.0006	0.0010	0.0007	-0.0008	-0.0031	-0.0028	0.0006	-0.0001

x3	-0.0059	-0.0250	0.0103	-0.0245	0.0038	-0.0109	0.0112	0.0164	0.0106	0.0152	-0.0055	0.0017	-0.0049	0.0125	0.0004
x4	0.0097	0.0341	-0.0131	0.0319	-0.0024	0.0210	-0.0159	-0.0234	-0.0149	-0.0217	0.0095	-0.0026	0.0086	-0.0159	0.0008
x5	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
x6	-0.2739	0.6218	0.7198	0.6373	-0.3528	-0.1159	0.4601	0.2940	0.4723	0.2553	0.1667	0.0138	0.0593	0.0245	0.2450
x7	0.1665	-0.6064	-0.6835	-0.6081	0.2967	0.0640	-0.4089	-0.2580	-0.4175	-0.2165	-0.1702	-0.0286	-0.0721	-0.0313	-0.2328
x8	0.1660	-0.0078	-0.0390	-0.0296	0.0809	0.0806	-0.0700	-0.0501	-0.0756	-0.0557	0.0101	0.0242	0.0224	0.0116	-0.0130
x9	0.0007	0.0013	0.0006	0.0012	-0.0008	-0.0001	0.0007	0.0003	0.0005	0.0003	0.0004	-0.0001	-0.0001	0.0000	0.0004
x10	0.0035	0.0029	0.0022	0.0034	-0.0008	-0.0005	0.0020	0.0010	0.0018	0.0008	0.0009	0.0007	0.0002	-0.0005	0.0014
x11	0.0172	-0.0028	-0.0213	-0.0014	-0.0066	-0.0111	-0.0127	0.0009	-0.0108	0.0037	-0.0235	0.0118	-0.0024	-0.0011	-0.0235
x12	3.0757	1.6565	-0.3767	1.4958	-1.1354	0.0418	-0.3402	-0.6559	-0.3331	-0.6757	0.6483	0.1010	-0.0550	-0.3253	-0.0716
x13	-2.1850	-1.3812	0.2150	-1.2645	0.6703	-0.2469	0.3752	0.5636	0.3715	0.5846	-0.4552	-0.1419	-0.1348	0.2438	0.1021
x14	-0.6574	-0.0775	0.1509	-0.0467	0.4291	0.2871	-0.1096	0.0068	-0.1130	0.0012	-0.1459	0.0731	0.2498	0.0537	-0.0527
x15	0.0080	-0.0771	-0.0390	-0.0728	-0.0510	-0.0853	0.0462	0.0310	0.0461	0.0326	0.0052	-0.0332	-0.0562	0.0009	0.0271
x16	**-0.3283**	-0.1300	0.0473	-0.1098	0.0513	-0.0396	0.0559	0.0704	0.0576	0.0759	-0.0522	-0.0146	-0.0031	0.0225	0.0153
x17	0.1765	**0.4456**	0.1178	0.3845	-0.2445	0.0500	0.0533	-0.0162	0.0554	-0.0209	0.0892	-0.0033	0.0012	-0.0483	-0.0130
x18	-0.0043	0.0080	**0.0301**	0.0077	0.0002	0.0034	0.0145	0.0110	0.0140	0.0103	0.0015	-0.0021	0.0022	0.0009	0.0018
x19	0.1949	0.5031	0.1493	**0.5831**	-0.2662	-0.1560	0.0533	-0.0351	0.0568	-0.0407	0.1056	0.0396	0.0322	-0.0600	0.0449
x20	-0.0336	-0.1180	0.0015	-0.0982	**0.2151**	0.0862	-0.0349	0.0089	-0.0368	0.0071	-0.0298	0.0329	0.0615	0.0368	0.0195
x21	0.0460	0.0428	0.0425	-0.1021	0.1528	**0.3816**	-0.0456	-0.0162	-0.0533	-0.0162	0.0077	-0.0098	0.0381	0.0148	-0.0192
x22	-0.0323	0.0227	0.0916	0.0173	-0.0307	-0.0227	**0.1897**	0.1141	0.1888	0.1138	0.0329	-0.0477	-0.0009	-0.0199	0.0097
x23	-0.0512	-0.0087	0.0868	-0.0144	0.0098	-0.0101	0.1435	**0.2387**	0.1441	0.2371	-0.2021	-0.0182	0.0225	0.0253	-0.0154
x24	0.0322	-0.0228	-0.0850	-0.0178	0.0313	0.0256	-0.1823	-0.1106	**-0.1832**	-0.1111	-0.0362	0.0467	-0.0009	0.0192	-0.0072
x25	0.0599	0.0122	-0.0890	0.0180	-0.0085	0.0110	-0.1552	-0.2572	-0.1570	**-0.2589**	0.2289	0.0179	-0.0238	-0.0259	0.0241
x26	-0.0020	-0.0026	-0.0006	-0.0023	0.0018	-0.0003	-0.0022	0.0108	-0.0025	0.0113	**-0.0128**	0.0018	0.0001	0.0009	-0.0034
x27	-0.0028	0.0005	0.0044	-0.0043	-0.0096	0.0016	0.0158	0.0048	0.0160	0.0043	0.0087	**-0.0627**	-0.0222	-0.0167	0.0161
x28	0.0003	0.0001	0.0025	0.0018	0.0096	0.0033	-0.0002	0.0032	0.0002	0.0031	-0.0002	0.0118	**0.0335**	0.0207	0.0068
x29	0.0012	0.0019	-0.0005	0.0018	-0.0030	-0.0007	0.0018	-0.0018	0.0018	-0.0017	0.0013	-0.0046	-0.0108	**-0.0174**	-0.0029
x30	0.0014	0.0009	-0.0018	-0.0023	-0.0027	0.0015	-0.0015	0.0019	-0.0012	0.0028	-0.0080	0.0077	-0.0061	-0.0050	**-0.0301**
x31	0.3840	0.8950	0.3288	0.7833	-0.1606	0.3658	0.0439	-0.0446	0.0380	-0.0576	0.1711	0.0177	0.1364	-0.0817	0.0269
Partial R^2	-0.1261	0.3988	0.0099	0.4567	-0.0346	0.1396	0.0083	-0.0107	-0.0070	0.0149	-0.0022	-0.0011	0.0046	0.0014	-0.0008

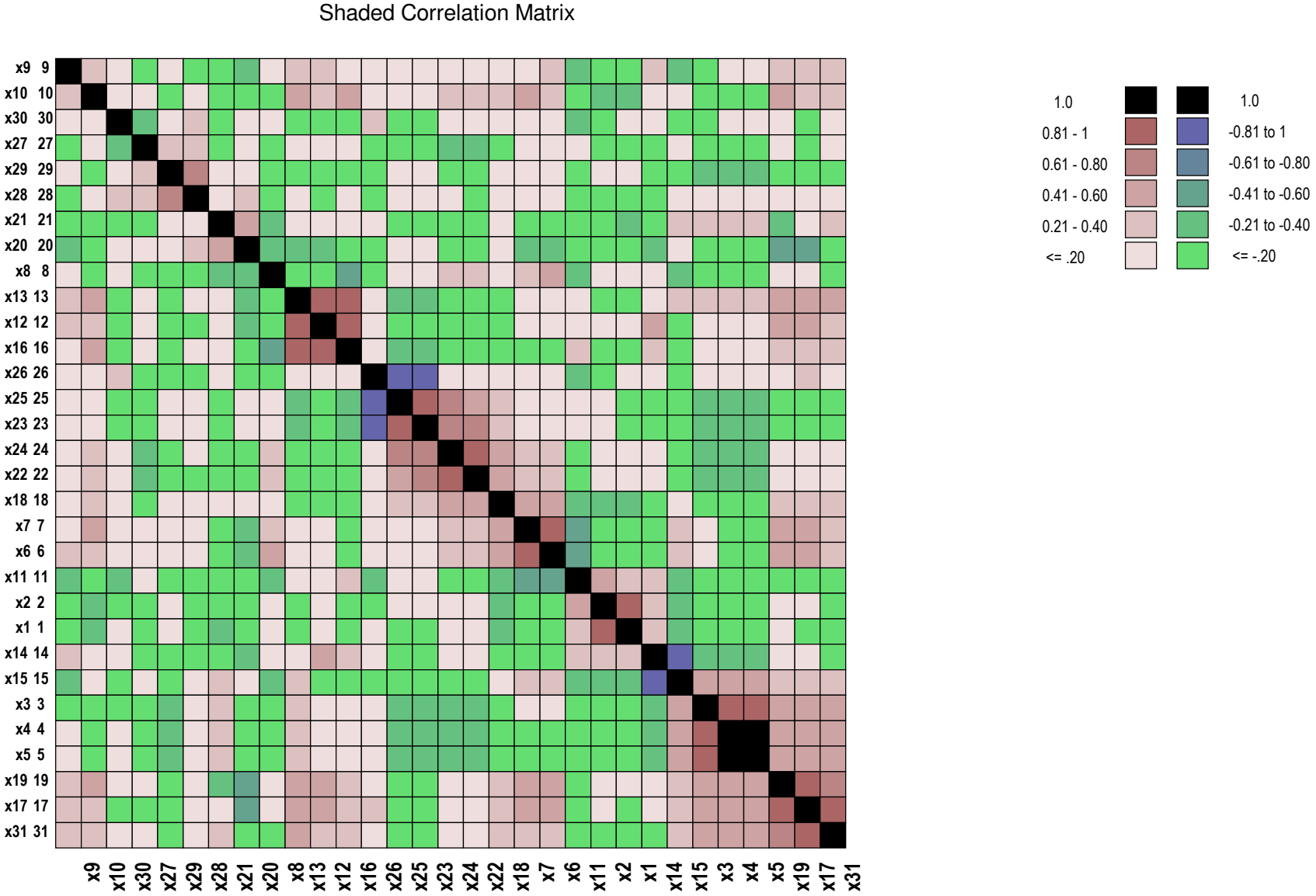
R SQUARE = 0.9859 RESIDUAL EFFECT = 0.1187

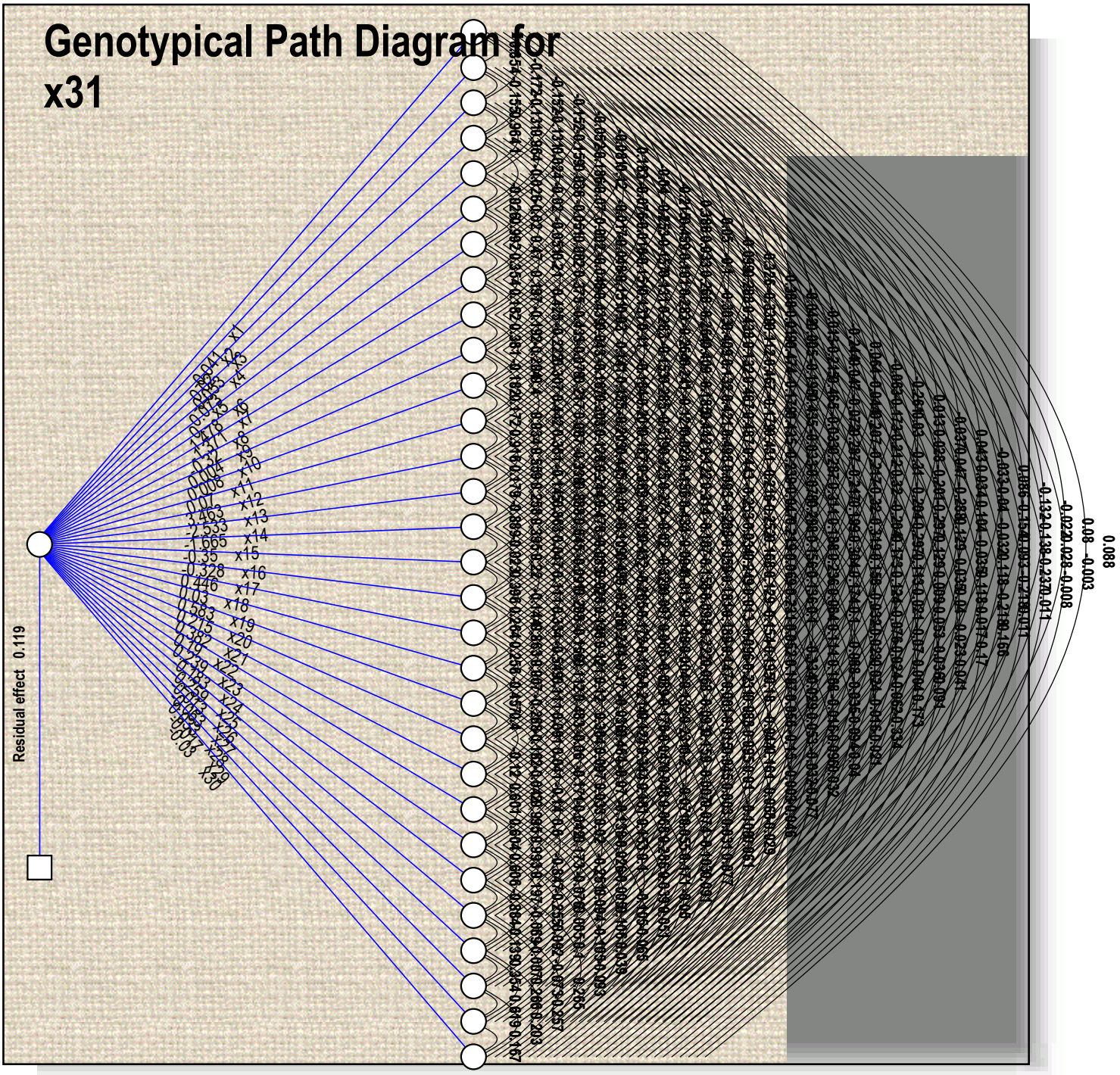
Genotypical Correlations



LEGENDS

- 0.8 - 1.0
- 0.6 - >0.8
- 0.4 - >0.6
- 0.2 - >0.4


Shaded Correlation Matrix
x9 9
x10 10
x30 30
x27 27
x29 29
x28 28
x21 21
x20 20
x8 8
x13 13
x12 12
x16 16
x26 26
x25 25
x23 23
x24 24
x22 22
x18 18
x7 7
x6 6
x11 11
x2 2
x1 1
x14 14
x15 15
x3 3
x4 4
x5 5
x19 19
x17 17
x31 31
x9 x10 x30 x27 x29 x28 x21 x20 x8 x13 x12 x16 x26 x25 x23 x24 x22 x18 x7 x6 x11 x2 x1 x14 x15 x3 x4 x5 x19 x17 x31
1.0
0.81 - 1
0.61 - 0.80
0.41 - 0.60
0.21 - 0.40
<= .20
1.0
-0.81 to 1
-0.61 to -0.80
-0.41 to -0.60
-0.21 to -0.40
<= -.20


Genotypical Path Diagram for x31
Residual effect 0.119
x1
x2
x3
x4
x5
x6
x7
x8
x9
x10
x11
x12
x13
x14
x15
x16
x17
x18
x19
x20
x21
x22
x23
x24
x25
x26
x27
x28
x29
x30