GENETIC VARIABILITY AND DIVERSITY ANALYSIS FOR YIELD AND YIELD ATTRIBUTING TRAITS OF WILD GERMPLASM IN RICE

THESIS SUBMITTED IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE OF

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in

Genetics and Plant Breeding

Submitted by

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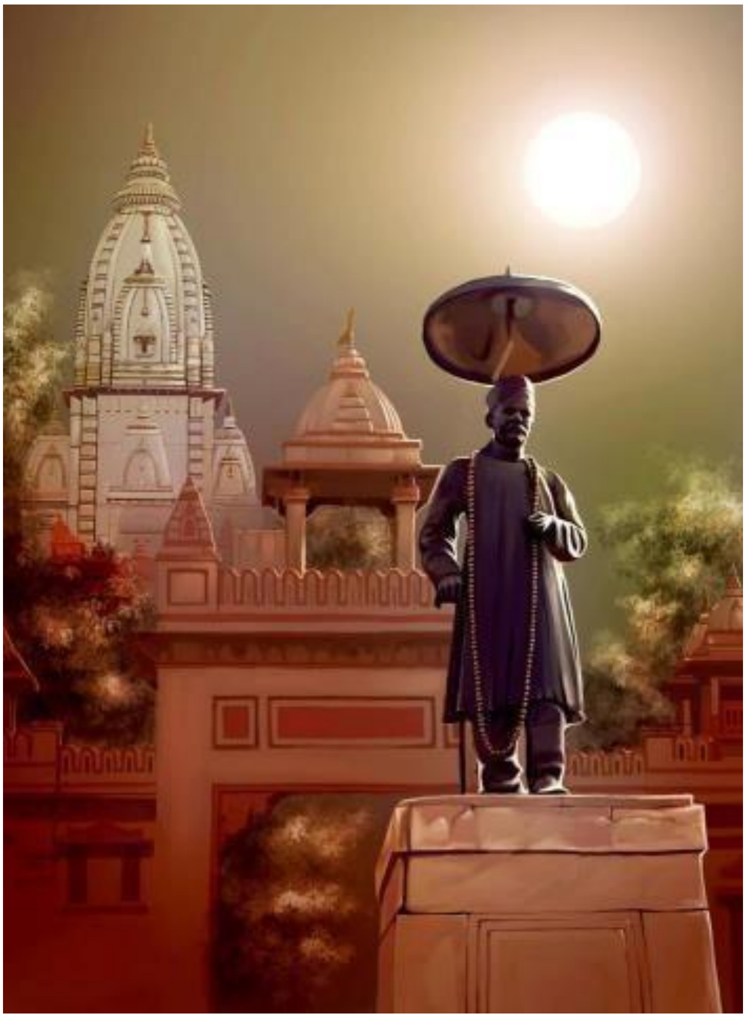

Dedicated to
My
Parents
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Ms. Bhagwati Devi

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CERTIFICATE

To,
The Registrar (Academic)
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Through: The Head, Department of Genetics and plant Breeding, Institute of Agricultural Sciences, B.H.U, Varanasi.

Dear Sir,

We have great pleasure in forwarding the thesis entitled **"GENETIC VARIABILITY AND DIVERSITY ANALYSIS FOR YIELD AND YIELD ATTRIBUTING TRAITS OF WILD GERMPLASM IN RICE"** submitted by **Mr. Ganesh Kumar Koli**, **I.D. No. 17412GPB005**, in partial fulfillment of the requirements for the degree of **Master of Science (Agriculture)** in the Department of Genetics and plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (U.P).

We certify that the entire work reported herein, was planned and carried out by the candidate under our guidance and supervision and to the best of our knowledge and belief, the data presented in the thesis are genuine and original.

Thanking you.

Forwarded by: yours faithfully,

Prof. R. P. SINGH
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Date: *, June, 2019*
Place: *Varanasi.* *(Ganesh Kumar Koli)*

LIST OF ABBREVIATIONS

ANOVA	Analysis of Variance
%	Percentage
^{O}C	Degree Celsius
Cm	Centimeter
CV	Coefficient of variation
DAC&FW	Department of Agriculture Cooperation and Farmers welfare
et al.	And co worker
etc	Et cetera
GA	genetic advance
GCV	Genotypic coefficient of variation
GM	geometric mean
gm	Gram
h^2	Heritability
i.e.	In otherwords
Mha	MillionHectare
MT	MillionTonnes
PCV	Phenotypic coefficient of variation
RBD	Randomized Block Design
r_g	Genotypic Correlation
r_p	Phenotypic Correlation
USDA	United States Department Of Agriculture

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Chapter-I

INTRODUCTION

Rice is a monocotyledonous angiosperm belongs to the Family Poaceae, Sub family Oryzoideae, The rice (*Oryza sativa* L.) commonly divided into three sub-species i.e. *Indica*, *Japonica* and *Javanica*. Genus Oryza has 24 recognized species out of which two species are cultivated and twenty two are wild species. The two cultivated species are *Oryza sativa and Oryza glaberrima.* Asian rice, *Oryza sativa* grown worldwide where *Oryza glaberrima* the African rice is cultivated in West Africa. The Asian rice is believed to have origin from Asia in the region encompassing North-Eastern India, the triangle adjoining Burma, Northern Bangladesh, Thailand, Laos, Vietnam and Southern China while *Oryza glaberrima* is believed to have origin from Africa.

Rice is possibly the oldest domesticated grain ~10,000 years (Kovach *et al*., 2007). Rice is the staple food for 2.7 billion people and to mark its importance year 2004 is celebrated as international year of rice. It covering 9% of the earth's arable land. 21% of global human per capita energy provided by rice and 15% of per capital protein (IRRI, Rice Almanac, 4th Edition). Calories from rice are particularly important in Asia countries, where it accounts for 50-80% of daily caloric intake (FAO Rice Market Monitor, Volume XXI, Issue No. 1, 2018). As expected, Asia accounts for over 90% of the world's production of rice, with China, India and Indonesia producing the most (IRRI, Rice Web). 85% of the rice that is produced in the world is used for direct human consumption (IRRI, Rice Almanac, 4th Edition) and also for ready to eat products e.g. popped and puffed rice, instant or rice flakes, canned rice and fermented products are produced etc. Inflorescence of rice is known as Panicle. Rice need hot and humid climatic conditions (RH 60%) and the average temperature required throughout the life period of the rice ranges from 21 °C to 37 °C. Rice is a short day and self-pollinated plant which grown under different conditions and production system. In India rice grown as low land and upland rice.

Cultivated area utilizes by rice is approximately 9-10 % of all available crop land worldwide 167mha (FAO Rice Market Monitor, Volume XXI, Issue No. 1, 2018). In India it is cultivated in an area of 43.19 million hectares with a production of 112.76 million tonnes and productivity 2.55 tonnes/hectare during year 2017-18 (Directorate of Economics & Statistics, DAC&FW). Rice is the staple food crop of India, providing 43% of caloric requirement for more than 70% Indian population. In India, West Bengal, Uttar Pradesh, Andhra Pradesh, Telangana Punjab, Bihar and Orissa are the major states in rice production. Chhattisgarh state is known as 'rice bowl' of India. The International Rice Research Institute (IRRI 2000) studied the food problem in relation to world population, and they predict that 800 million tons of rice will be required in 2025. Most of the increase in demand will occur in Asia and Africa, where the population lives on rice. High yielding varieties is essential in order to meet the food requirement of growing population.

The selection of parents for hybridization is very important for success of any breeding programme. The parents involved in the development in varieties should be divergent. The germplasm provides immense scope for wide variability. Crop improvement programme depends on nature and magnitude of genetic variability, heritability, genetic advance, characters association, direct and indirect effects on yield and its attributes and considerable genetic diversity present among the genotypes. The development of high yielding improved varieties, has led to monoculture or restricted the use of eminent genotypes, thus leading to genetic erosion. Hence, efforts are taken to conserve such eminent genotypes and now this object assumed global importance. The efficiency of selection depends upon the magnitude of genetic variability present in the plant population. Thus, the success of genetic improvement in any character depends on the nature of variability present in the gene pool for that character, to start a successful plant breeding programme. Characters like yield and its components being polygenic in nature, the breeder has to isolate desired genotypes from the knowledge of components of variations. The partitioning of total variation into phenotypic, genotypic and environmental components helps in determining the magnitude of these components for various traits, which finally helps in deciding a breeding procedure for the genetic improvement of a trait.

information of diversity at cluster level and crossing between germplasm of diverse cluster may give heterotic progeny.

Realizing the importance of the variability, correlation and genetic diversity based on quantitative traits, the present investigation was carried out with the following objectives:

1. To estimate genetic variability, heritability and genetic advance for yield.
2. To study character association among yield and yield attributing traits.
3. To estimate direct and indirect effects of traits under study on grain yield.
4. To study genetic divergence in rice germplasm for yield and quality.

Chapter -II

REVIEW OF LITERATURE

The main aim of any breeding programme is improvement of both quantitative and qualitative characters of a crop. The information on genetic architecture of various quantitative and qualitative traits is useful in planning the breeding programmes. This information can be used for developing more sophisticated and efficient approach to select the parents. A brief review of literature related to the objectives of the present study with respect to genetic diversity in wild germplasm rice employing yield related traits are presented under the following heads.

2.1 Variability, heritability and genetic advance.

2.2 Character association.

2.3 Path-coefficient analysis.

2.4 Genetic divergence.

2.1 Variability, heritability and genetic advance:

Rahim *et al*. (2004) studied the genetic diversity of quantitative and qualitative traits of thirty six lines and cultivars of rice. Analysis of variance showed significant differences among genotypes for all traits and revealed the existence of genetic variation among genotypes. The phenotypic coefficients of variability were greater than the genotypic ones for all the traits although differences for most of them were small.

Borkakati *et al.* (2005) conducted study to determine the extent of genetic variability, heritability, genetic advance as percent of mean and correlation for yield and yield attributing characters including spikelet fertility in sixteen rice hybrids. The estimates of genetic parameters revealed moderate to high estimates of genotypic coefficient of variation and phenotypic coefficient of variation for the number of fertile spikelets per panicle, number of spikelets per panicle and grain yield.

Shankar *et al.* (2006) studied on variability, correlation and path-coefficients were made on single plant yield and its components in thirty four rice genotypes. CSR 23, TRY1, CO 43, IR 71910-3R-2-1, IR 72048-B-R-l 1-1-1 and AD 01004 were identified as promising genotypes for multiple desirable traits. High hertability and genetic advance were obtained for the traits days to 50 per cent flowering, plant height, productive tillers/plant, panicle length, grains/panicle, 100 seed weight and single plant yield.

Jadhav (2008) estimated genetic variability and genetic advance for 23 traits in 49 genotypes of indigenous and exotic rice. These genotypes were studied for genetic seedling growth and yield attributing traits. The highest magnitude of genotypic coefficient of variation was observed for plant height followed by seedling length. High estimates of heritability coupled with high genetic advance were recorded for plant height, seedling length, speed of germination, seedling moisture weight, number of spikelet per panicle, fertile spikelet per panicle, 100 seed weight and germination percentage.

Veerabadhiran (2009) studied the extent of variability and genetic parameters in 15 rice hybrids and five checks for seventeen qualitative traits along with grain yield. The magnitude of difference between PCV and GCV was relatively low for all the traits, indicating less environmental influence. High (>20%) GCV and PCV were recorded for gelatinization temperature and gel consistency.

Anjaneyulu *et al.* (2010) studied Genetic variability studies using 50 germplasm lines of rice revealed that maximum phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for number of grains per panicle, fertility percentage and grain yield per plant. Number of grains per panicle, plant height and fertility percentage recorded high heritability coupled with high genetic advance indicating the reliability of these characters for selection.

Singh *et al*. (2011) studied Eighty one rice (*Oryza sativa* L.) genotypes for thirteen quantitative traits to examine the nature and magnitude of variability, heritability (broad sense) and genetic advance. Analysis of variance revealed that the differences among eighty one genotypes were significant for all the characters except flagleaf width. Among the all traits number of spikelets per panicle exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV)followed by harvest index, grain yield per hill and number of panicles per hill.

Bhadru *et al.* (2012) evaluated 21 rice genotypes (resistant to gall midge biotype 3 and BPH were evaluated for their variability and genetic divergence. The highest genotypic and phenotypic coefficient of variation, heritability and genetic advance % of mean corresponded to grains per panicle, seed yield, 1000 grain weight and plant height and direct selection for these traits would be useful for yield improvement in rice. The D^2 values were significant among the 21 genotypes, which were grouped into 6 clusters.

Sathya & Jebaraj (2013) estimated heritability, coefficients of variability and genetic advance computed for 19 characters including drought and yield contributing traits. The traits *viz*., productive tillers per plant, panicles per plant, filled grains per panicle, harvest index, proline content, SPAD chlorophyll meter reading, chlorophyll stability index, biomass yield, dry root weight, dry shoot weight, root: shoot ratio and root length had high heritability accompanied with high genetic advance indicating lesser environmental influence and were under the control of additive gene effect.

Dhurai *et al*. (2014) the analyzed variance revealed significant differences among the genotypes for the all the 9 quantitative and 5 quality traits in rice indicating that enough variability is present in the studied material. The magnitude of difference between PCV and GCV were relatively low for all the traits revealing little influence of the environment in the expression of these traits. All the characters showed high broad sense heritability.

Nirmaladevi *et al*. (2015) ninety-two rice (*Oryza sativa* L.) genotypes were evaluated to estimate the genetic variability, heritability and correlation coefficients for 14 physicochemical and cooking quality traits. Highest broad sense heritability and genetic advance was obtained for head rice recovery (89% and 29%), milling (84% and 21%), water uptake (90% and 24%), amylose content (93% and 29%) and gel consistency (90% and 31%) which suggested that these traits would respond to selection owing to their high genetic variability and transmissibility.

Namita *et. al.* (2016) conducted experiment with 110 genotypes of rice during *Kharif* 2012 in RBD. The data were recorded for 19 quantitative characters and 5 qualitative character to study genetic variability, broad sense heritability, genetic advance, correlation coefficient and path coefficient. Analysis of variance revealed significant difference among 110 rice genotypes for all characters indicating the existence of variability.

Nayak *et al.* (2016) twenty-five rice germplasm accessions were evaluated to assess their genetic variability, heritability, genetic advance, character association and path coefficient analysis for grain yield and yield traits. The high estimate of genotypic and phenotypic coefficient of variation, heritability and genetic advance were observed for effective tillers per plant, filled grains per panicle, total grains per panicle and grain yield per plant.

Ajmera *et. al*. (2017) thirty seven rice genotypes were evaluated for their variability, heritability and genetic advance with regards to yield and yield components. All the characters under study except days to 50% percent flowering exhibited high heritability coupled with high genetic advance as per cent of mean, which indicated that these traits were controlled by additive type of gene action in the inheritance of these characters. These characters can be improved by simple selection procedure. The high estimates of heritability coupled with low genetic advance as percent of mean for days to 50% percent flowering indicated the presence of non-additive gene effects, in addition to influence of environment to some extent, hence its response to selection would be poor.

Edukondalu *et al*. (2017) carried out to study the heritability for 15 characters in 40 genotypes of rice during *Kharif*, 2016. Analysis of variance revealed that mean sum of squares due to genotypes showed significant differences for all 15 characters studied. The magnitude of PCV and GCV was high for number of grains per panicle. High heritability coupled with high genetic advance as per cent of mean was observed for number of grains per panicle, number of tillers per plant, 1000-grain weight, L/B ratio, plant height, kernel length, grain yield per plant, kernel breadth and days to flowering

Srujana *et al*. (2017) conducted investigation consists of 29 rice genotypes including one check to study genetic variability, heritability and Genetic advance. Analysis of variance revealed that there is considerable variability among the genotypes. High estimates of heritability were observed for spikelets per panicle, days to maturity, biological yield, grain yield per hill, panicles per hill and tillers per hill.

Sumanth *et al.* (2017) investigated of 23 rice genotypes for 13 quantitative characters to study genetic variability, heritability, genetic advance, correlation coefficient analysis and path analysis. Analysis of variance among 23 genotypes showed significant difference for all characters studied. High estimates of heritability were observed for plant height, flag leaf length, biological yield per plant, spikelets per panicle, panicles per plant. High genetic advance were observed for number of spikelets per panicle and plant height, indicating predominance of additive gene effects and possibilities of effective selection for the improvement of these characters.

Adhikari *et al.* (2018) estimated the genotypic and phenotypic variability, heritability, genetic advance and correlation on grain yield and yield associated traits using 26 advance genotypes of lowland irrigated rice in Nepal. Analysis of variance revealed the existence of significant difference for days to flowering, maturity, plant height, panicle length, thousand grain weight and grain yield.

Bagudam *et al.* (2018) investigated the extent of genetic variability present in forty six genotypes of rice during *Kharif* 2017. Analysis of variance revealed highly significant differences for all the 12 characters, indicating the presence of genetic variability among the genotypes. The heritability and genetic advance estimates were moderate for panicle length and high for all the other traits *viz*., days to 50% flowering, plant height, number of tillers per plant, number of panicles, panicle length, panicle weight, grain number, test weight, single plant yield, plot yield, biomass and harvest index, indicating the influence of additive gene action, as such selection would likely be effective for improvement of these traits.

Bhat *et al.* (2018) studied genetic variability components i.e. GCV & PCV, heritability (broad sense) and genetic advance of various agronomical traits using F_2 segregating population. Analysis of variance (ANOVA) revealed statistically significant differences ($p<0.05$) indicating the existence of genetic variability amongst the population. Heritability coupled with genetic advance was also recorded for all the given traits in the population. The estimation of these parameters helps the breeder in achieving the required crop improvement by selection.

Monalisha *et al.* (2018) studied genetic variability, correlation & path analysis for 10 characters on 17 elite rice hybrids along with 7 different checks. The magnitude of genetic variance was high for majority of traits except for panicle length, panicle number, 100-grain weight, harvest index and grain yield per plant. The higher magnitude of genetic variance for plant height, grain number, fertility % and plot yield, which have bearing on yield may be sorted out as important selection criteria for realization of higher productivity in hybrid rice.

Ismaeel *et al*. (2019) estimated genetic variability and heterosis in rice genotypes using fourteen parents and their ten F_1 hybrids. Significant differences among the parents and F_1 hybrids were observed for all the studied traits. High phenotypic and genotypic coefficient of variation (PCV and GCV) values were observed for grains per panicle and grain yield per plant. High heritability values were recorded for all the studied traits.

Kumari *et al.* (2019) investigated 240 mutant lines for genetic variability. Analysis of variance revealed highly significant differences among the mutant lines for all morpho-physiological characters under study. Higher magnitude of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance as percentage of mean were observed for number of tillers per plant, number of fertile tillers per plant, relative shoot elongation and survival percentage, indicating that these traits could be used as selection indices for yield improvement and submergence tolerance.

Manjunatha *et al.* (2019) conducted study of sixty four rice genotypes at Karnataka for evaluation of genetic variability, heritability and genetic advance for grain yield along with four yield-associated traits. The analysis of variance revealed statistically significant differences ($p<0.05$) indicating the existence of genetic variability among the sixty four genotypes for all the traits studied.

Tiwari *et al*. (2019) conducted experiment for genetic variability in seven genotypes of rice including Hardinath-1 as standard check variety. Various quantitative traits were measured to investigate the variability. All the genotypes showed significant variations for all the traits considered. The results indicated that days to heading, days to maturity, grain yield, 1000-grain weight demonstrating higher heritability and remarkable genetic advance could be considered the most appropriate traits for improvement and selection of trait to achieve stable and high yielding early rice genotypes under rainfed environments.

2.2 Character association:

Qamar *et al.* (2005) studied association analysis for yield and yield components in rice, involving nine genotypes of aromatic group and eight genotypes of non-aromatic group were conducted separately. In the non-aromatic group, productive tillers per hill showed highly significant positive association with grain yield per plant. Whereas in the aromatic group days-to-50% flowering and days-to-maturity exhibited highly significant negative genetic association with grain yield per plant.

Shankar *et al*. (2006) studied correlation on plant yield and its components in 34 rice genotypes. CSR 23, TRY1, CO 43, IR 71910-3R-2-1, IR 72048-B-R-l 1-1-1 and AD 01004 were identified as promising genotypes for multiple desirable traits. Single plant yield was positively and significantly correlated with days to 50 per cent flowering, productive tillers/plant, panicle length and grains/panicle and hence can be taken as indices for improving yield in rice. The correlated traits except panicle length exhibited high positive direct effects towards single plant yield.

Sharma *et al.* (2007) studied correlation of 12 quantitative traits in forty four extra early and early maturing rice genotypes. Grain yield per palnt exhibited highly significant and positive correlation with fertile grains per panicle, grains per panicle, test weight, panicle length, flag leaf area and spikelets per panicle.

Reddy *et al.* (2008) performed correlation and component analysis for 12 characters in 20 genotypes of rice to find out the character association and their effects on seed yield. A positive and significant correlation was found for the characters, panicle length, number of spikelets per panicle, flag leaf length, flag leaf width, biological yield and harvest index with grain yield per plant at genotypic level. Highly significant and positive correlation was observed between number of tillers and number of panicles per plant.

Subudhi *et al.* (2009) studied forty-two released lowland rice varieties including check to obtain information on interrelationship of grain yield and its components. Highly significant differences were observed among the genotypes in all the characters. Plant height had significant positive correlation with panicle weight, grains/panicle, test weight and negative correlation with single plant yield

Nandan *et al.* (2010) studied degree of association between yield and its component characters in rice (*Oryza sativa* L.). Thirty three genotypes were evaluated for identifying their efficiency with respect to 20 yield and quality traits. The correlation studies revealed 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.

Hasan *et al*. (2011) studied genetic association of yield and its component characters in twenty four hybrid rice varieties of diverse origin. Grain yield showed positive significant association with number of effective tillers/hill, panicle/m^2, spikelet fertility and thousand grain weight at both genotypic and phenotypic levels. Same traits had highest significant positive effect on yield.

Saravan *et al*. (2012) studied interrelationship of grain yield and its component traits in upland direct seeded rice using thirty six exotic breeding lines. Grain yield per plant had significant positive correlation with biological yield per plant, harvest index, panicles per plant, plant height, spikelets per panicle, panicle length, test weight, spikelet fertility and flag leaf length.

Veni *et al.* (2013) studied seventy rice (*Oryza sativa* L.) genotypes for estimate correlations between yield and yield components and quality parameters. Days to 50 per cent flowering, productive tillers per plant, panicle length, Head Rice Recovery (HRR) and volume expansion ratio manifested significant positive association with grain yield indicating that simultaneous improvement of all the characters is possible.

Lakshmi *et al.* (2014) evaluated seventy genotypes of rice (*Oryza sativa* L.) to study the nature and extent of correlation among yield and yield attributing characters, days to 50 per cent flowering, days to maturity, number of effective tillers per plant, plant height, panicle length, number of grains per panicle, 1000-grain weight, grain yield per plant, kernel length, kernel breadth and L/B ratio. The results revealed that grain yield per plant to be positively and significantly associated with days to maturity, number of productive tillers per plant, plant height and kernel length indicating importance of these traits as selection criteria in yield improvement programmes.

Allam *et al*. (2015) carried out an investigation to study the correlation in twenty five genotypes of basmati rice (*Oryza sativa* L.). Character association of the yield attributing traits revealed significantly positive association of grain yield per plant with number of effective tillers per plant and spikelets per panicle. Hence, selection for these traits can improve yield.

Naseer *et al*. (2015) studied about yield and its contributing components on 8 morphological traits, which were studied in 24 Asian accessions of rice (*Oryza sativa* L.). Plant yield was positively and significantly correlated with filled grains weight per panicle, number of grains per panicle, 1000-grain weight and spikelet fertility percentage at genotypic and phenotypic levels. Thus, these traits could play pivotal role in the development of high yielding rice genotypes.

Sravan *et al*. (2016) evaluated sixty rice genotypes sixteen quantitative and quality traits to examine the nature of correlation. Grain yield per plant had significant and positive correlation with days to 50% flowering, days to maturity, plant height, effective tillers per plant, panicle length, seeds per panicle and kernel breadth after cooking.

Dhurai *et al.* (2016) conducted field experiment using thirty two rice genotypes to estimate correlation coefficients for grain yield and yield contributing traits in rice. Character association analysis revealed significantly positive association of grain yield per plant with harvest index, days to maturity and number of grains per panicle. Correlations among yield components were positive, encouraging rapid improvement of yield. Path analysis revealed that kernel elongation ratio, kernel length, harvest index and days to maturity have shown high positive direct effects on grain yield.

Premkumar *et al*. (2016) studied character association and path-coefficient analysis on forty three rice genotypes including thirty hybrids and thirteen parents for grain quality traits on grain yield. The correlation analysis indicated that grain yield was significantly associated with kernel breadth, breadth wise expansion ratio and water uptake at genotypic level.

Biswaji *et al*. (2017) fifty diverse paddy genotypes were evaluated under low land submerged field condition at two different locations for the study of association between yield and yield components under submerged condition where the water depth was more than 50 cm at least for two weeks at the vegetative stage of crop. Fertile grains per panicle, panicle length and test weight (1000 seed weight) are consistently highly positively correlated with the seed yield. These yield attributes were the major contributing traits for seed yield in rice under submergence in the set of genotypes under study.

Jan *et al.* (2017) studied character association and path-coefficient using fourteen agro-morphological traits among 35 rice *(Oryza sativa* L.) genotypes. Analysis of variance (ANOVA) revealed a substantial level of variability among the tested genotypes for all the traits. Correlation studies revealed that harvest index (0.47) and (0.43) showed significant positive correlation with grain yield per hill at both genotypic and phenotypic level. While days to 50% flowering (−0.31) showed significant negative correlation with grain yield per hill.

Pachauri *et al.* (2017) estimated character association in identified 225 core rice germplasm accessions. The correlation coefficient of grain yield had positive and significant correlation with leaf length, days to 50% flowering, plant height, panicle length, number of effective tillers/plant, plant height and panicle length, had positive and significant correlation with leaf width, leaf length, days to 50% flowering and plant height, while leaf width had positive correlation with plant height.

Manjunatha *et al.* (2017) carried out an investigation to study the character association and path analysis in sixty-five genotypes of rice *(Oryza sativa* L.) under organic management. Among the correlation coefficients of thirteen growth characteristics with grain yield per plant, for the characteristics chlorophyll content of flag leaf, chlorophyll content of third leaf, number of tillers per plant at 30DAT, the genotypic correlation coefficients were higher than phenotypic correlation coefficients, indicating the less influence of environment on these characters.

Sudeepthi *et al*. (2017) measured the character association and direct and indirect effects of component characters on yield using 33 genotypes of rice. The association studies revealed that the genotypic correlations were, in general higher than the phenotypic correlations and thus suggested that the observed relationships among the characters were due to genetic factors. Grain yield per plant exhibited significant positive association with days to 50% flowering, days to maturity, plant height, number of productive tillers per plant and number of filled grains per panicle and non-significant positive association with panicle length and test weight.

Ali *et al.* (2018) studied character association in the F_2 population of rice cross CB 08504 × Prasanna. The traits days to first flowering, number of productive tillers per plant, panicle length, number of filled grains per panicle, spikelet fertility percentage and harvest index were showing significant and positive correlation with single plant yield. The F_2 population of CB 08504 × Prasanna performed better for earliness, yield and yield associated traits and could be utilised in future breeding programs to meet the increasing demand of rice.

Banumathy *et al.* (2018) studied correlation for yield and its components in 32 Saltol introgressed backcross inbred lines (BIL) of rice along with a tolerant parent FL 478, susceptible check IR 29 and two recurrent parents under normal and saline environments. Grain yield per plant showed positive significant association with all traits except 100 grain weight under normal environment and it showed positive significant association with all traits except panicle length, spikelet fertility and 100 grain weight under saline condition.

Lilly *et al.* (2018) carried out an experiment to explore correlation and path coefficient analysis in two F_2 populations of rice derived from the cross AD 16019 x ADT43 and AD16019 x WGL 14377. In both the crosses single plant yield shows positive association with 1000 grain weight, plant height, number of productive tillers, panicle length. In the cross AD 16019 x ADT43 1000 grain weight and number of productive tillers per plant showed high direct positive effect on single plant yield and in the cross AD16019 x WGL 14377 only 1000 grain weight had high positive direct effect on single plant yield. Hence, selection of positively associated characters could bring improvement in yield and component characters.

Panigrahi *et al.* (2018) studied character association among the lines homozygous dominant for gall midge resistance genes Gm1 and Gm4 in the genetic background of ADT 38 variety of rice in advanced backcrossed (BC_1F_5) generation of rice. The highly significant positive correlation with single plant yield was exhibited by traits like number of tillers, number of productive tillers and number of filled grain per panicle. Positive direct effect was exhibited by number of tillers, number of filled grains per panicle and hundred grain weight towards single plant yield. These characters will be useful for further breeding.

Shivakumar *et al*. (2018) carried out an investigation to study the correlation in 42 rice varieties and 18 rice genotypes. The correlation analysis revealed that the seed yield/plant showed significant positive correlation with total number of tillers/plant, number of productive tillers/plant, number of grains/panicle, number of filled grains/panicle, spikelet fertility (%) and 100-seed weight and negative correlation with days to 50% flowering. Hence, selection for these traits can improve yield.

Kumari *et al*. (2019) carried out an investigation with 240 mutant lines for association study of characters. Association study revealed that number of tillers per plant and survival percentage had significant positive high to moderate direct association with grain yield per plant under submergence condition. Thus, these traits may be used as selection criteria in further crop improvement programmes for submergence tolerance.

2.3 Path-coefficient analysis:

Path coefficient analysis measures the direct and indirect contributions of independent variables on 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 character influence the dependent variable. A brief reviews has been summarized below:

Zahid *et al.* (2006) conducted path coefficient analysis for yield, yield components and grain quality characteristics in 14 genotypes of Basmati rice. Number of tillers per plant, No. of grains per panicle and 1000 grain weight contributed maximum direct effect on yield indicating these traits should be given emphasis while selecting high yielding Basmati rice cultivars for Kallar Tract.

Babar *et al.* (2007) studied path coefficient analysis for some leaf and panicle traits affecting grain yield was in 93 doubled haploid lines of rice (*Oryza sativa* L.). Path coefficient analysis indicated that plant height followed by number of panicles, flag leaf width, days to heading and flag leaf rolling had higher direct effect on grain yield.

Rokonuzzaman *et al*. (2008) evaluated twenty modern Boro rice varieties with a view to find variability and genetic association for grain yield and yield components characters. Path coefficient showed that number of effective tiller per plant and plant height are the characters that contribute largely to grain yield.

Chandra *et al*. (2009) studied path analysis in rice . Path analysis revealed that number of grains per panicle, days to 50 per cent flowering, 1000-grain weight and number of productive tillers per plant have shown high positive direct effects on grain yield.

Abarshahr *et al*. (2011) studied 30 varieties of rice under two irrigation regimes for path analysis. There were significant differences among the varieties for all traits. Path analysis for paddy yield indicated that the number of spikelet per panicle and flag leaf length had positive direct effects and days to complete maturity and plant height had negative direct effects on paddy yield under optimum irrigation condition, while flag leaf width and number of filled grains per panicle had positive direct effects and days to 50% flowering had negative direct effect on paddy yield under drought stress condition.

Babu *et al.* (2012) studied the path analysis in twenty one popular hybrids of rice (*Oryza sativa* L.). Path coefficient analysis revealed that panicle length and number of productive tillers per plant exhibited positive direct effect on yield. Among these characters, number of productive tillers per plant possessed both positive association and high direct effects.

G**opikannan *et al*. (2013)** investigated the path analysis in 10 parents and their F_1 hybrids of rice (*Oryza sativa* L.) under sodic environment. Investigation on path coefficient analysis showed that number of productive tillers per plant and number of filled grains per panicle expressed high and positive direct effect on grain yield. The study also inferred that productive tillers per plant and filled grains per panicle contributed equally through direct and indirect effects for yield improvement.

Lingaiah *et al.* (2014) studied path analysis studies for yield and yield contributing characters in sixty four mid early group genotypes of rice. Path analysis indicated that panicle length, effective tillers per plant and test weight exhibited direct positive effect on yield indicating the importance of these traits during selections for improvement of yield in rice.

Sarker *et. al*. (2014) analyzed correlation and path coefficient for thirty two (32) exotic early maturing rice (*Oryza sativa* L.) lines were evaluated through their yield and yield contributing characters. Almost all the lines exhibited significance difference for different characters. Results suggest days to maturity, total number of tillers hill-1, and effective number of tillers per hill may be used as reliable criteria for improving yield of early maturing rice.

Allam *et al.* (2015) studied the path analysis in twenty five genotypes of basmati rice (*Oryza sativa* L.). Path coefficient analysis revealed that effective tillers per plant, spikelets per panicle, test weight and kernel length exhibited positive direct effect on yield. Among these characters, number of effective tillers per plant and spikelets per plant possessed both positive association and high direct effects. Hence, selection for these characters could bring improvement in yield.

Kishore *et al*. (2015) studied seventy three rice varieties for the character associations and path coefficients with regards to yield and yield components. Yield was observed to be positively associated with panicle bearing tillers and number of filled grains per panicle and these characters were noticed to exert high direct effects on grain yield per plant. High indirect effects of most of the traits were noticed mostly through panicle bearing tillers per hill indicating importance of the trait as selection criteria in crop yield improvement programmes.

Ratna *et al.* (2015) path coefficients analyzed among fourteen morphological characters were studied in six advanced lines of Basmati rice and one commercial check namely BRRI Dhan 29. Path coefficient analysis revealed highest positive direct effect of number of filled spikelets/panicle on grain yield but plant height and number of unfilled spikelets/panicle had negative direct effect on grain.

Dhurai *et al.* (2016) conducted a field experiment using thirty two rice genotypes to estimate correlation coefficients and path analysis for grain yield and yield contributing traits in rice. Highly significant ($p<0.01$) variation was obtained for almost all the characters studied. Path analysis revealed that kernel elongation ratio, kernel length, harvest index and days to maturity have shown high positive direct effects on grain yield.

Nayak *et al.* (2016) evaluated twenty-five rice germplasm accessions to assess path coefficient analysis for grain yield and yield traits. Path coefficient analysis showed that panicle length, plant height, days to flowering and effective tiller per plant had high direct positive effect on grain yield per plant.

Devi *et al*. (2017) studied variability, correlation and path analysis for yield and quality traits on 27 rice genotypes. Path analysis reveals that test weight (3.48), effective tillers (1.57), and filled grains per panicle (1.41) had positive direct effect on grain yield per plant. Among the quality traits kernel length followed by milling percent and kernel elongation ratio had direct effect on head rice recovery.

Jan *et al.* (2017) studied path-coefficient using fourteen agro-morphological traits among 35 rice (*Oryza sativa* L.) genotypes. Path coefficient studies revealed that at genotypic level flag leaf length (0.62) showed high direct positive effect with grain yield per hill followed by flag leaf width (0.61)-while as at phenotypic level flag leaf area (0.49) showed maximum positive direct effect with grain yield per hill followed by harvest index (0.36).

Priya *et al*. (2017) carried out an investigation to assess the character association and the magnitude of direct and indirect effects of yield component traits on grain yield of rice for 11 characters. Path analysis studies revealed that kernel breadth, L/B ratio, productive tillers per plant, grains per panicle, test weight, days to maturity, days to 50% flowering and plant showed true relationship with grain yield per plant by establishing significant positive association and high positive direct effect.

Sowmiya *et al*. (2017) carried out experiment to explore correlation and path coefficient analysis in 48 rice genotypes for nine characters *viz*., days to first flower, plant height, number of tillers per plant, number of panicles per plant, number of grains per panicle, panicle length, thousand grain weight, grain L/B ratio and grain yield per plant. Path analysis indicated that maximum direct effect on grain yield was exhibited by number of panicles per plant. Hence the trait should be taken in account of breeding programme to develop the maximum of threshold yield obtaining new rice varieties or hybrids.

Bhujel *et al*. (2018) carried out in an experiment for path analysis using six genotypes of irrigated rice. The number of fertile spikelets, number of panicles per square meter, panicle mass and mass of one thousand grains influenced grain yield, both through phenotypic correlation and direct effects. In addition, there was a high direct linear tendency of these variables towards yield. Panicle length and number of sterile spikelets showed a potential of use in the indirect selection for grain yield.

Kumar *et. al*. (2018) studied correlation and path coefficient analysis in rice for characters like biological yield per plant, harvest index, spikelet fertility, 1000-grain weight, L/B ratio, plant height and panicle length. Path analysis identified biological yield per plant followed by harvest-index as most important direct yield contributing traits and biological yield per plant followed by 1000-grain weight and panicle length exhibited high order of positive indirect effect as most important indirect components which merit due consideration at time of devising selection strategy aimed at developing high yielding varieties in rice.

Francis *et al.* (2018) conducted study among the thirty two rice varieties of the Breeders Seed Production chain of Tamil Nadu during *Kharif* 2016-17. Correlation study showed significant positive correlation on single plant yield by leaf length, leaf width, number of panicles per plant, number of grains per panicle, 1000 grain weight and time to maturity. Path analysis for direct and indirect effects on yield revealed significant high direct effects for number of panicles per plant, number of grains per panicle, 1000 grain weight, days to 50 percent flowering and time to maturity.

Shobhana *et al*. (2018) studied Line x Tester mating of nine new plant type lines that are developed in the International Rice Research Institute, Philippines and four high yielding indica rice varieties (*Oryza sativa* L.) of Tamil Nadu.. Partitioning the correlation coefficient with direct and indirect effects revealed that number of productive tillers per plant, number of grains per panicle and 100 grain weight are the major yield contributing characters on which selection pressure has to be applied for improving grain yield.

Vengatesh *et. al*. (2018) studied the correlation and path analysis in twenty five rice (*Oryza sativa* L.) genotypes and the observations were recorded for eight root, six physiological and nine yield related traits. Correlation studies revealed that among the traits studied, six root traits, four physiological traits and six yield related traits observed significant positive genotypic correlations with grain yield.

2.4 Genetic divergence:

Hegde *et al.* (2000) studied genetic divergence in 40 genotypes of rainfed rice using Mahalanobis's D^2 statistic. The cultivars fell into 7 clusters. Cluster I, II, III and IV comprised 18, 14, 3 and 2 genotypes, respectively, while Cluster V, VI and VII were solitary clusters. The average intercluster D value was highest (51.88) between the Clusters V and VII, indicating high genetic divergence between the cultivars of these 2 clusters. The highest contributing characters to D^2 values were spikelet number per panicle, photosynthetic rate and 1000-grain weight.

Patil *et al.* (2005) evaluated genetic diversity among 100 genotypes of rice germplasm using Mahalanobis' D_2 staticss. Based on genetic distance, these genotypes were grouped into 8 different clusters. Based on cluster analysis, the genotypes selected for grain yield per plant were Chepti Gurmatia and Bangla Gurmatia; for early maturity were Jal Keshar and Rani Kajar; for achieving long panicle length were Man Keshari and Rani Kajar; and for maximum number of tillers per plant were Cross Luchai and Luchai Nag Keshar. Among the characters studied, days to 50% flowering, flag leaf length, flag leaf width, plant height and panicle length were the major components contributing to the total genetic diversity. The rest of the characteristics showed low contribution towards the total divergence.

Singh *et al.* (2006) investigated genetic divergence of 52 traditional lowland rice (*Oryza sativa* L.) using Mahalanobis D^2 statistic. Based on 15 agro-morphological characters, these genotypes were grouped into six clusters. Clusters II, III, and IV exhibited high values for most of the characters. Plant height, followed by leaf angle and leaf area, highly contributed (32.43%) to the formation of clusters. Clusters II, IV, and V, which had maximum inter-cluster distances and high values of plant height, days to 50% flowering, panicle length, grain yield/plant, and milling percent, may be used for initiating a hybridization programme.

Chandra *et al.* (2007) evaluated genetic divergence in 49 genotypes of non-scented rice including three checks by using Mahalanobis D^2-statistics for eight quality and seven quantitative characters. The genotypes were grouped into clusters based on the D^2-values. Based on the mean performance genetic divergence and clustering pattern, the worker suggested that the genotypes MAUB-13, NLR-34450, RDR-916, MTU-1078 and NWGR-99014 from these clusters may be used as potential donors for future hybridization programme in order to get the desirable recombinants in segregating generation with higher yield potential.

Singh *et al.* (2008) studied forty five genotypes of Basmati rice (*Oryza sativa* L.) for genetic diversity on the basis of quality characteristics utilizing Mahalanobis D^2 analysis. Based on the genetic distance (D^2 values), the rice genotypes were grouped into eight clusters. The highest genetic divergence was observed between cluster V and VI exhibiting wide diversity between the groups.

Banumathy *et al*. (2010) studied fifty three rice genotypes to identify diverse genotypes. They were evaluated for eight yield and yield attributing characters using D^2analysis, to study the diversity pattern among the genotypes. Based on the analysis, the genotypes were grouped into 11 clusters. Maximum inter cluster D^2 value was observed between cluster I and X (32.96) followed by cluster I and IV (32.90). The greater the distance between the two clusters indicates wider the genetic diversity between genotypes. The intra cluster distance was maximum in cluster VII (24.62) followed by cluster XI (22.15) indicates hybridization involving genotypes within the same clusters may result in good cross combinations.

Garg *et al*. (2011) carried out an investigation with the forty eight genotypes of rice to study the nature and magnitude of genetic divergence using D^2 statistics. The forty eight genotypes were grouped into five clusters based on Euclidean cluster. Maximum intra-cluster distance was observed in cluster I indicating greater genetic divergence between the genotypes belonging to this cluster. Days to maturity, gel consistency and days to 50 per cent flowering contributed 74.55 per cent of total divergence. Maximum inter-cluster distance was recorded between clusters II and III followed by clusters III and IV indicating wide genetic diversity and it may be used in rice hybridization programme for improving grain yield.

Bhadru *et al.* (2012) studied 21 rice genotypes were evaluated for their variability and genetic divergence. The D^2 values were significant among the 21 genotypes, which were grouped into 6 clusters. For getting desirable transgressive segregants for the development of early duration (Genotypes from the clusters II and Cluster VI) and medium duration (from the clusters I and IV), coarse and medium slender high yielding gall midge and BPH resistant varieties genotypes could be utilized in the hybridization programme.

Kar *et al*. (2013) studied 65 indigenous aromatic rice genotypes collected from different parts of Odisha were evaluated for divergence analysis. The genotypes were grouped into thirteen clusters. Based on clustering pattern, the maximum genetic distance among genotypes existed between cluster IV, V and XI. The clusters V and X were ascertained outstanding on the basis of higher cluster means for most of the component characters. The most divergent clusters have been isolated as V containing Acharmati, Kanikabhog and Bashuabhog and Cluster X having Nalidhan.

Ahamed *et al.* (2014) studied to assess the the genetic diversity in exotic and indigenous germplasm of rice for twelve quantitative characters. Fifty test genotypes along with three checks were evaluated. Members of cluster II and III were highly diverse from each other as these clusters showed maximum inter-cluster distance. Hence, genotypes belonging to the cluster II and III can be used as parents for hybridization programme for the development of high yielding rice genotypes.

Sarawagi *et al.* (2015) studied 188 rice germplasm accessions (landraces) to understand the genetic diversity. The accessions grouped in to XVI cluster, the cluster VII has largest no of accessions (20 accessions). The maximum inter cluster distance between cluster VI and I (10.1) and minimum inter cluster distance is observed between cluster II and cluster XV (2.02).

Chandramohan *et al.* (2016) studied 44 genotypes of rice for all the traits except for number of effective bearing tillers per plant to evaluated genetic diversity. Based on D^2 analysis the genotypes were grouped into 11clusters. On the basis of inter cluster distance genotypes from clusters IV and V followed by V and IX could be used as parents for future hybridization programme. Cluster mean analysis revealed the genotypes, JGL 21820 and JGL 21849 could be used in breeding programme for obtaining high yielding super fine grain segregants. Days to 50% flowering and 1000 grain weight manifested highest contribution towards total divergence, thus, these traits could be given due importance for further crop improvement.

Pachauri *et al.* (2017) estimated magnitude of genetic divergence and character association in identified 225 core rice germplasm accessions (landraces). A total of 11 quantitative traits were measured at suitable stage of rice germplasm. Core rice germplasm accessions were grouped into 15 clusters. The highest inter-cluster distance was observed between clusters XIII and VIII suggesting maximum variability among them. The cluster XV showed highest grain yield/plant and effective tillers/plant (9 tillers/plant). This indicated that these clusters could be utilized in the hybridization programme for obtaining desirable transgressive segregants.

Sathish *et al*. (2017) studied forty-nine rice genotypes consisting of high yielding rice genotypes to evaluate and identify diverse genotypes for twenty yield and yield attributing characters using the D^2 statistic. Highest inter cluster generalized distance (1957.68) was between cluster- IV and cluster-V. The intra cluster distance was maximum in cluster-III (684.04) followed by Cluster-II (646.28) and cluster-I (630.83) indicates hybridization of genotypes within this cluster may result in good cross combinations.

Tripathi *et al.* (2017) studied on variability and diversity of 32 genotypes of rice (*Oryza sativa* L.) under direct seeded condition. Genetic divergence analysis using D^2 statistic grouped the genotypes into 7 clusters. Cluster II had maximum number (16) of genotypes. Maximum inter cluster distance was found between cluster IV and VII (984.82). However, intra cluster distance was maximum in cluster III (363.58). Genotypes from diverse clusters viz.NR 89, PAU 3284, ARIZE SWIFT, RY 248, Varadhan, RYC489, MTU 1010 and RYC 674 could be recommended for inclusion in hybridization programme for breeding under aerobic rice condition.

Iqbal *et al.* (2018) conducted study to generate scientific information on nature and magnitude of genetic variability and relationship of yield and related attributes and to classify genotypes into distinct clusters on the basis of quantitative traits. Fourteen elite rice genotypes were evaluated and grouped 14 rice genotypes into four clusters. Cluster IV incorporated the highest number of genotypes, which also had highest cluster mean for paddy yield, followed by cluster I. Therefore, prominence should be given to genotypes aggregated in cluster I and IV that having high yield potentiality. Based on mean performance, Irrigated-04, E-93, E-94 and E-107 showed superiority in respect of paddy yield and some other traits, hence these lines could be recommended for varietal development.

Ranjith *et al.* (2018) estimated magnitude of genetic divergence in 30 rice genotypes in six environments using Mahalanobis D^2 – statistics by considering 12 quantitative characters. The genotypes were grouped into six clusters. Cluster I constituted maximum number of genotypes (19). The genotypes falling in cluster II had the maximum divergence. The inter cluster distance was maximum between cluster II and V (228.14) followed by cluster III and V (214.44), suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme. Traits like; plant height, fertile grains, panicle length and plot yield were the major contributors to genetic divergence.

Chapter-III

MATERIALS AND METHODS

The present experiment on genetic variability and diversity analysis for yield and yield attributing traits of wild germplasm in rice was carried out during the *Kharif* 2018. This field experiments were conducted at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (UP). This research work consisted of forty different rice genotypes.

3.1. Experimental material and site:

In this field experiment forty different rice genotypes were evaluated for genetic variability, correlation, path coefficient analysis and genetic divergence. The present field experiment was conducted at Agricultural Research Farm, Banaras Hindu University, Varanasi (UP), which is located in North-eastern zone of Uttar Pradesh at 25.28°N latitude and 83.08°E longitude. This eastern Indo - Gangetic Plains is very fertile due to annual low level floods in the Ganges. The experiment was carried out in randomized block design (RBD) with three replications. The nursery was sown on 25th June, 2018 and twenty one days old seedlings were transplanted in the main field. Normal spacing of (15 × 20) cm with recommended cultural practices were followed for raising a good and healthy crop. The details of rice genotypes are given in the table 3.1.

3.2. Experimental material used in the present study:

The experimental material used in present study comprised of forty late maturing wild rice germplasm lines (*Oryza nivara* and *Oryza rufipogon*). These lines were received from **Dr. N. K. Singh**, National Research Center on Plant Biotechnology, New Delhi. These experimental materials were evaluated for its heritability, variability, characters association, path analysis and genetic divergence. The details of rice germplasm are listed sources in the Table 3.1.

Table 3.1 List of forty wild germplasm of rice:

S. No.	Name of germplasm
1	WRG(NKS)-401
2	WRG(NKS)-402
3	WRG(NKS)-403
4	WRG(NKS)-404
5	WRG(NKS)-405
6	WRG(NKS)-406
7	WRG(NKS)-407
8	WRG(NKS)-408
9	WRG(NKS)-409
10	WRG(NKS)-410
11	WRG(NKS)-411
12	WRG(NKS)-412
13	WRG(NKS)-413
14	WRG(NKS)-414
15	WRG(NKS)-415
16	WRG(NKS)-416
17	WRG(NKS)-417
18	WRG(NKS)-418
19	WRG(NKS)-419
20	WRG(NKS)-420
21	WRG(NKS)-421
22	WRG(NKS)-422
23	WRG(NKS)-423
24	WRG(NKS)-424
25	WRG(NKS)-425
26	WRG(NKS)-426
27	WRG(NKS)-427
28	WRG(NKS)-428
29	WRG(NKS)-429
30	WRG(NKS)-430
31	WRG(NKS)-431
32	WRG(NKS)-432
33	WRG(NKS)-433
34	WRG(NKS)-434
35	WRG(NKS)-435
36	WRG(NKS)-436
37	WRG(NKS)-437
38	WRG(NKS)-438
39	WRG(NKS)-439
40	WRG(NKS)-440

3.3. Observations recorded on quantitative characters:

Five plants were randomly selected from each entry in each replication and their mean were used for the statistical analyses. The plants were selected from the middle rows to minimize the border effect. Observations were recorded on twelve yield and yield contributing quantitative traits as below:

3.3.1. Days to 50 % flowering:

This was counted from date of seedling sowing in nursery to the date of emergence of first panicle in 50 per cent of the plants.

3.3.2. Days to maturity:

Number of days from seedling to grain ripening (80 per cent of the grain in a panicle mature) was recorded.

3.3.3. Effective tillers per plant:

Number of panicle bearing tillers in a plant excluding late tillers.

3.3.4. Plant height (cm):

Height of plant from the ground to the tip of the tallest panicle (awn excluded) was recorded.

3.3.5. Panicle length (cm):

Length measured from panicle base (neck) to tip at maturity (excluding awn) was recorded.

3.3.6. Filled grains per panicle:

Number of filled grains per panicles was estimated by recording data of filled grains on five randomly selected panicles per plant, and average was used for calculations.

3.3.7 Unfilled grains per panicle:

Number of unfilled grains per panicles was estimated by recording data of unfilled grains on five randomly selected panicles per plant, and average was used for calculations.

3.3.8. Total grains per panicle:

Total number of grains per panicles was estimated by recording data on five randomly selected panicles per plant in each replication, and average was used for computation.

3.3.9. Spikelet Fertility %:

Estimated by dividing number of filled grains per panicle to the total number of grains per panicle and multiplied by 100.

3.3.10. Test weight (g):

Weight of 1000 well-developed grains at 12-14 per cent moisture content was recorded using an electronic balance.

3.3.11. Panicle weight (g):

Measure by weight of single panicle randomly selected from plant.

3.3.12. Grain yield per plant (g): Weight of paddy (rough rice) per plant at 12-14 per cent moisture content was recorded using electronic balance.

3.4. Statistical Analysis:

The experimental data were compiled by taking mean value over randomly selected plants for all the three replications and subjected to the following statistical analysis:

3.4.1. Analysis of variance for the design of experiment.

3.4.2. Selection parameters:

A. Mean and range.
B. Phenotypic and genotypic coefficient of variability.
C. Heritability and genetic advance.

3.4.3 Correlation coefficient analysis.
3.4.4 Path coefficient analysis.

3.4.5 Genetic divergence.

3.4.1 Analysis of variance:

Analysis of variance is used for testing whether there is significant difference between the treatment or not. It was carried out by following the procedure of randomized block design (RBD) analysis (Panse and Sukhatme, 1967) for each of the thirty two genotypes. The variance was partitioned in to three sources of variance, *viz*. replications, treatments and error.

The model of ANOVA is given bellow:-

Model: $Y_{ij} = \mu + g_i + r_j + e_{ij}$

Where, Y_{ij} = Phenotypic observation in the i^{th} Genotype in the j^{th} Block

μ = Grand Mean

g_i = Effect of i^{th} Genotype

r_j = Effect of j^{th} Replication

e_{ij} = Random Error

Here, i = 1, 2, 3, ... 32.

J = 1, 2, 3.

Table 3.2 Analysis of variance (ANOVA):

Source	**df**	**SS**	**MSS**	**F value** (Calculated)
Replication	**r-1**	**SSr**	$\frac{SSr}{(r-1)}$ = **MSR**	
Treatment	**t-1**	**SSt**	$\frac{SSt}{(t-1)}$ = **MST**	$\frac{MST}{MSE}$
Error	**(r-1) (t-1)**	**SSe**	$\frac{SSe}{(r-1)(t-1)}$ = **MSE**	
Total	**(rt-1)**	**TSS**		

Where,

r = Number of replications

t = Number of treatments

df = Degree of freedom

SSr = Replication sum of square

SSt = Treatment sum of square

SSe = Error sum of square

TSS = Total sum of square

MST = Treatment mean sum of square

MSR = Replication mean sum of square

MSE = Error mean sum of square

The significance of difference among the treatments was tested by comparing the calculated ‘F’ value with table value of ‘F’ at 5 and 1 per cent level of significance at (t-1) and (r-1) (t-1) degrees of freedoms, respectively.

3.4.2 Selection parameters:

A. Mean and range:

Mean:

The mean value of each character was determined by summing up all the observations and dividing them by corresponding number of observations.

$$\overline{X} = \frac{\sum_{i=1}^{N} X_i}{N}$$

Where,

$\overline{X}$ = mean,

$\sum_{i=1}^{N} X_i$ = Sum of all observations

N = Number of observations

Range:

The lowest and highest values for each character were taken as the range.

B. Phenotypic and genotypic variances:

These estimates were obtained as below-

Error variance, $\sigma^2_E = M_E$

Genotypic variance, $\sigma^2_g = \frac{M_T - M_E}{r}$

Phenotypic variance, $\sigma^2_p = \sigma^2_g + \sigma^2_e$

Standard error of difference between two means [S.E.d.(M)] :

S.E.d. (M) was calculated with the help of error mean square from ANOVA table.

$$S.E.d.(M) = \sqrt{\frac{2M.S.E.}{r}}$$

Where,

r = Number of replications

MSE = Mean sum of square due to error

B. Coefficient of variation (CV) :

Phenotypic and genotypic coefficient of variation was calculated by the method suggested by Burton and Devane (1953):

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\text{Phenotypic standard deviation}}{\text{General mean}} \times 100$$

$$= \frac{\sigma_p}{\bar{\bar{X}}} \text{ x } 100$$

$$\text{Genotypic coefficient of variation (PCV)} = \frac{\text{Genotypic standard deviation}}{\text{General mean}} \times 100$$

$$= \frac{\sigma_g}{\bar{\bar{X}}} \text{ x } 100$$

C. Heritability and genetic advance:

Heritability:

Heritability is the proportion of genetic variance to the phenotypic variance an expressed in percentage. It was calculated by the formula given by Allard (1960) which is given below:

$$H = \frac{\sigma_g^2}{\sigma_p^2}$$

Where,

H = Heritability in broad sense

$\sigma 2g$ = Genotypic variance = $\frac{MST - MSE}{r}$

$\sigma 2p$ = Phenotypic variance= $\sigma 2g + \sigma 2e$

Genetic Advance (Expected):

The improvement in the performance of selected lines over the original population is called genetic advance. The genetic advance i.e. expected genetic gain resulting from selecting five per cent superior plants was estimated by the following formula suggested by Allard (1960):

Genetic advance (Expected) = $H \times \sqrt{\sigma_p^2} \times k$

Where,

H = Heritability coefficient

$\sqrt{\sigma_p^2}$ = Phenotypic standard deviation

K = Selection differential in standard units which is 2.06 at 5% selection intensity.

Genetic advance as percentage of mean was calculated by the following formula:

Genetic advance as percentage of mean = $\left(\frac{GA}{\overline{X}}\right) \times 100$

Where,

GA = Expected genetic advance

$\bar{X}$ = General mean of the character in the population

3.4.3 Correlation and Path coefficient analysis:

3.4.3.1 Correlation coefficient:

The simple phenotypic correlation coefficients among pairs of characters were calculated according to the formula suggested by Searle (1961).

$$r(X_1X_2) = \frac{Cov\ (X_1X_2)}{\sqrt{V(X_1) \cdot V(X_2)}}$$

Where,

X_1 = Character 1

X_2 = Character 2

r (X_1X_2) =Correlation between characters X_1 and X_2

Cov X_1X_2 = Covariance between X_1 and X_2

$V(X_1)$ = Variance of X_1

$V(X_2)$ = Variance of X_2

In the estimation of phenotypic correlation coefficients, phenotypic covariance and variance are considered for calculation.

To test the significance of correlation coefficients, the estimated values were compared with the table value (statistical table by Fisher and Yates, 1963) at n-2 degrees of freedom (where n denotes the number of genotypes tested) at 5% and 1% levels of significance.

3.4.3.2 Path-coefficient analysis:

Path-coefficient analysis was done to partition the total correlation into direct and indirect effects due to the dependent variable. Wright (1934) suggested this analysis and it was further elaborated by Dewey and Lu (1959).

Path-coefficient is the ratio of standard deviation of the effect due to a given cause to the total standard deviation of the effect i.e. if grain yield per plant (Y) is the function of the causal factor X_1, then path co-efficient for the path from causal factor X_1 to the effect Y is $\sigma X_1 / \sigma Y$.

In other words, it is a standardized partial regression coefficient, which individually provides a measure of direct effect of the causal factor or independent variables on the dependent variable. These permit partitioning of the correlation between the causal factor and the effect of variable into components of direct and indirect effects and this makes the association of causal factor with the effect of variable more clear.

Here, grain yield per plant (Y) was taken as effect of the other characters like days to maturity, effective tillers per plant, plant height and 1000-grain weight.

The path-coefficients were obtained by solving a set of simultaneous equations of the form:

$$r_{X_1Y} = P_{X_1Y} + r_{X_1X_2} P_{X_2Y} + r_{X_1X_3} P_{X_3Y} + ... + r_{X_1X_6} P_{X_5Y}$$

$$r_{X_2Y} = r_{X_2X_1} P_{X_1Y} + P_{X_2Y} + r_{X_2X_3} P_{X_3Y} + ... + r_{X_2X_6} P_{X_5Y}$$

$$r_{X_5Y} = r_{X_5X_1} P_{X_1Y} + r_{X_5X_2} P_{X_2Y} + r_{X_5X_3} P_{X_3Y} + ... + r_{X_5Y}$$

Where,

r_{X_1Y} to r_{X_5Y} denotes coefficient of correlation between independent characters X_1 to X_5 and dependent character Y.

$r_{X_1X_2}$ to $r_{X_4X_5}$ denotes coefficient of correlation between all possible combinations of independent characters.

P_{X_1Y} to P_{X_5Y} denotes direct effects of character X_1 to X_5 on Y.

The solutions for path-coefficients, direct and indirect effects of the causal factor were calculated as per the mentioned above.

Indirect effect = $r_{ij}.P_{ij}$

i = 1……n

j = 1…..n

and P_{ij} = P_{1Y}, P_{2Y}, P_{3Y} ….. P_{ny}.

The residual factor (P_{RY}) i.e. the variation in yield unaccounted for causal effects under consideration or the path values for residual effect was calculated as follows:

Residual factor (P_{RY}) = $\sqrt{1 - R^2}$

Where, $$(R^2) = \sum_{i=1}^{5} P_{X_1Y} r_{X_5Y}, \quad = \sqrt{1 - (P_{1Y} r_{1Y} + P_{2Y} r_{2Y} + ... + P_{iY} r_{iY})}$$

Where,

P_{RY} = Residual effect

P_{iY} = Direct effect of X_i on Y

r_{iY} = Correlation coefficient of X_i and Y.

R^2 is the coefficient of determination, and is the amount of variation in yield that can be accounted for the yield component trait. Path-coefficient at phenotypic level was calculated using phenotypic correlation coefficient.

3.4.4 Genetic divergence by Mahalanobis' D^2 statistics:

Genetic divergence amongst different genotypes is assessed based on the estimated *inter-se* genetic distances amongst the genotypes. D^2 statistics of Mahalanobis (1928) is one of the most effective tools to measure the genetic distance between genotypes as measured by allelic frequencies at a sample of loci. Genetic similarity is defined as the converse of the genetic divergence i.e. the extent of gene similarity among the genotypes.

3.4.4.1 Mahalanobis' D^2-statistics:

In the present investigation, genetic divergence was estimated based on Mahalanobis' generalized distance as described by Rao (1952). Original variable means were transformed to un-correlated variables by the pivotal condensation method of inversion matrix.

The D^2-values between the genotypes were obtained as the sum of squares of differences of the values of the corresponding transformed variables.

For each pair of combinations the mean deviation *i.e.* $di = Y_i^1 - Y_i^2$,

where Yi denotes the transformed variables (i = 1, 2, 3, 4, 5 ……….p) and the D^2 was then calculated as sum of the squares of those deviations, *i e.* $D^2 = \Sigma (Y_i^1 - Y_i^2)^2$

Where, p = Number of characters.

The significance of D^2-values was tested by treating them as chi-square (χ^2) at p degrees of freedom where p is the number of characters.

3.4.4.3 Grouping of genotypes by Tocher's method:

After arranging the D^2 values of all combinations of one genotype with the others in ascending order of magnitudes, the genotypes were grouped into a number of clusters by Tocher's method described by Rao (1952). The criterion used in this method was that any two varieties belonging to the same cluster, at least on an average, show a smaller D^2 value than those belonging to two different clusters. Then inter and intra-cluster distances were calculated and their relationships were diagrammatically represented.

3.4.4.4 Contribution of individual characters towards divergence:

In all the combinations of genotypes, each character was ranked on the basis of

$di = Y_i^j - Y_i^k$ values. Rank 1 was given to the highest mean difference and rank p to the lowest mean difference, where, p represented the total number of characters. The per cent contribution was calculated by considering total number of combinations as 100 per cent.

Chapter-IV

EXPERIMENTAL RESULTS

The present experiment comprising of forty genotypes of rice was carried out in a Randomized Block Design with three replications at the Agricultural Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during *Kharif* season 2018 to study the extent of variability in twelve quantitative characters *viz*., days to 50% flowering, days to maturity, effective tillers per plant, plant height, panicle length, filled grains per panicle, unfilled grains per panicle, total grains number per panicle, per panicle weight, spikelet fertility %, test weight and grain yield per plant.

The results obtained in this experimental finding during *Kharif* 2018 are presented in this chapter as following heads:

4.1 Analysis of variance.

4.2 Mean performance and range.

4.3 Variability, heritability and genetic advance parameters.

4.4 Character association.

4.5 Path-coefficient analysis.

4.6 Genetic divergence.

4.1Analysis of variance (ANOVA):

The Analysis of variance was based on the mean values of twelve quantitative traits in forty rice germplasms to partition the total variation into genotypic variation and variation due to other sources. Table 4.1 presenting the results of analysis of variance and showing significance differences for all the characters under study. Analysis of variance showed that the treatment differences were highly significant for all the traits. This indicates that genetic difference among the genotypes is inheritable in nature.

4.2 Analysis of Mean performance and Range:

Mean of a replication is calculated by taking the average of five randomly selected plants of each genotype. Similarly mean of the other two replications were also generated by taking the average of five randomly selected plants of each genotype and a final mean was calculated from these three replication mean data. The mean performance and range of all the characters under study among forty genotypes are presented in Table 4.2 and the mean performance of grain yield per plant is presented in fig 4.1.

4.2.1 Days to 50% flowering:

Days to 50% flowering ranged from 77 to 118.67 days. The mean values for this trait was 96.81 days. The earliest flowering was observed in genotype WRG(NKS)-432 while genotype WRG(NKS)-426 showed late days to 50% flowering.

4.2.2 Days to maturity:

Days to maturity varied from 109.00 to 148.67 days with a mean value of 129.00. Among the forty rice genotypes the highest days to maturity was observed in genotype WRG(NKS)-426 while lowest was exhibited by WRG(NKS)-401.

4.2.3 Number of tillers per plant:

The mean values of genotypes ranged from 9.43 to 23.35 with a general mean of 15.56. The highest number of effective tillers was recorded by the genotype WRG(NKS)-432 whereas lowest value was registered by WRG(NKS)-402.

4.2.4 Plant height (cm):

Plant height ranged from 46.60 cm to 151.97 cm with mean value of 123.70 cm. Among all genotypes WRG(NKS)-406 was the shortest whereas, WRG(NKS)418 was the tallest.

4.2.5 Panicle length (cm):

Panicle length ranged from 9.96 cm to 29.33 cm with mean value of 23.16 cm. The longest panicle length was recorded in WRG(NKS)-430 while the shortest panicle was recorded in genotype WRG(NKS)-406.

4.2.6 Panicle weight (g):

Panicle weight varied from 0.37 g to 3.45 g with a mean value of 1.27 g. The genotype WRG(NKS)-440 exhibited highest panicle weight while the lowest value for this trait was observed in genotype WRG(NKS)-410.

4.2.7 Filled grains per panicle:

The filled grains per panicle ranged from 14.16 to 107.96 with a mean of 50.33. The lowest number of filled grains per panicle was observed in genotype WRG(NKS)-426 while, the highest value was exhibited by genotype WRG(NKS)-420.

4.2.8 Unfilled grain per panicle:

The unfilled grains per panicle ranged from 9.75 to 36.87 with a mean of 18.82. The lowest number of unfilled grains per panicle was observed in genotype WRG(NKS)-417 and the highest number of unfilled grains observed in WRG(NKS)-429.

4.2.9 Total grains per panicle:

Total grains per panicle showed a range of 37.23 to 134.15 with a mean value of 69.157. Genotype with maximum number of total grains per panicle was found in WRG(NKS)-420 whereas the genotype with minimum total grains per panicle was exhibited by WRG(NKS)-426.

4.2.10 Spikelet fertility per cent:

The trait spikelet fertility percent ranged from 42.00 to 84.07 with a general mean of 70.79.The highest spikelet fertility percent was recorded in WRG(NKS)-421, whereas the lowest was recorded in WRG(NKS)-426.

4.2.11 Test weight (g):

Test weight ranged from 12.42g to 28.37g with a mean value of 21.14g. The genotype with highest test weight was recorded in WRG(NKS)-422 while the lowest was observed in WRG(NKS)-439.

4.2.12 Grain yield per plant (g):

Data for this important trait varied from 5.75 g to 53.40 g with a mean value of 16.814 g. Highest grain yield was observed in genotype WRG(NKS)-440 whereas lowest grain yield was observed in genotype WRG(NKS)-413.

4.3 Genetic Variability and Heritability and Genetic advance parameters:

The results pertaining to genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance expressed as percent of mean for all the characters under study are presented in Table 4.3 and fig. 4.2.

4.3.1 Phenotypic and Genotypic coefficient of variation:

A scrutiny of Table 4.3 revealed considerable variation present among the traits under study they exhibit a wide range of phenotypic as well as genotypic coefficient of variation. Generally the values of genotypic coefficient of variance were smaller than those of phenotypic coefficient of variance. The relative magnitudes of the genotypic as well as phenotypic variances between the traits were compared based on the phenotypic and genotypic coefficient of variation.

PCV was recorded highest for total grain yield per plant (57.92) followed by per panicle weight (56.11), filled grain per panicle (44.598), total grains number per panicle (36.43) and unfilled grain per panicle (34.70). Low magnitude of PCV was exhibited by days to maturity (7.30) followed by days to 50% flowering (11.527) and spikelet fertility % (13.06). Rest of the traits exhibited medium values of PCV like effective tiller (21.67), panicle length (21.21), plant height (23.80) and test weight (17.71) with moderate PCV values.

Similarly, GCV was also highest for total grain yield per plant (57.23) followed by per panicle weight (54.62), filled grain per panicle (43.58), total grains number per panicle (35.70) and unfilled grain per panicle (33.07). Low magnitude of GCV was exhibited by days to maturity (5.20) followed by days to 50% flowering (10.27) and spikelet fertility % (10.89). Remaining other traits exhibited medium values of GCV like effective tiller (20.12), panicle length (18.37), plant height (22.30) and test weight (16.96) with moderate GCV value. Here differences between the values of PCV and

GCV were small for almost all the twelve traits, indicating less influence of environment in expression of these traits.

4.3.2. Heritability:

In the present study, heritability (broad sense) ranged from 50.8% to 97.60%. The highest heritability was found in total grain yield per plant (97.60%) followed by total grains number per panicle (96.00%) filled grain (95.50%), per panicle weight (94.80%), test weight (91.70%), unfilled grain (90.80%), plant height (87.80%) and effective tillers per plant (86.20%). Lowest heritability observed in days of maturity followed by spikelet fertility. All the characters showed high heritability.

4.3.3. Genetic advance as percent of mean:

Genetic advance as percent of mean (5%) was realized highest for plant height (53.24) followed by grain number per plant (49.84) and filled grain (44.17). Lowest value was observed in per panicle weight (1.39) followed by effective tiller number (5.99). All the characters studied had high to moderate genetic advance as percent of mean.

4.4 Character association:

Character association or correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. The phenotypic correlation coefficient between yield and its component traits were computed for all possible combinations and presented in Table 4.4 and fig 4.3.

4.4.1 Correlation between grain yield and other yield factors:

In the present investigation, character viz. panicle weight (0.7606), filled grain (0.7254), total grains per panicle (0.6970) and spikelet fertility (0.3806), found highly significant and positive correlation with yield which indicated strong association of these traits with the yield. Positive and significant correlation was also observed between effective tiller (0.2327), panicle length (0.2104), plant height (2076) and unfilled grain (0.195). Whereas negative correlation was observed in days of 50% flowering (-0.065) and days of maturity (-0.054). At genotypic level, panicle weight

(0.7864), filled grain (0.7523) and grain number per panicle (0.7199) showing high positive significant correlation.

4.4.2 Mutual association between different yield components:

4.4.2.1 Days to 50% flowering:

Days to maturity (0.8443), plant height (0.3944) and panicle length (0.3475), exhibited positive and highly significant correlation and, filled grain (0.0566), grain number per panicle (0.0413) and test weight (0.0129) exhibited positive but non-significant correlation while negative correlation exhibited by with test weight(-0.1966), effective tiller (-0.0240), spikelet fertility (-0.0466), and unfilled grain (-0.0351).

4.4.2.2 Days to maturity:

Positive and highly significant association exhibited by day to 50% flowering (0.8443), plant height (0.3559) and panicle length (0.3078), other positive but non-significant characters are effective tillers (0.0015) and filled grains (0.0037) while negative correlation with unfilled grain (-0.0845), grain number per panicle (-0.0186), panicle weight (-0.0301)), spikelet fertility (-0.0603) total grain yield per plant (-0.0541) and test weight (-0.0290).

4.4.2.3 Plant height:

Days of 50% flowering exhibited (0.3944), test weight (0.4605), panicle length (0.8587), days of maturity (0.3559) highly positive and highly significant association with plant height than other positive and significant association *viz*. filled grain (0.2712) panicle weight (0.2774) grain number per panicle (0.2650) and total grain yield per plant (0.2076). While showed positive and non-significant correlation with unfilled grain (0.0902), and spikelet fertility (0.0943). Negatively associated with effective tiller (-0.0480).

4.4.2.4 Panicle weight:

Panicle weight was positively and highly significantly correlated with filled grains per panicle (0.8776), number of grains per panicle (0.8562), test weight (0.4046), spikelet fertility (0.4439) and total grain yield per panicle (0.7606). Unfilled grain (0.2866), panicle length (0.2778) and plant height (0.2774) also exhibited positive and significant correlation. Positive and non-significant correlation was exhibited by effective tiller (0.0652) and negative and non-significant association with days of 50% flowering (-0.0078) and days of maturity (-0.0301).

4.4.2.5 Panicle length:

Panicle length exhibited highly positive significant association days of 50% flowering (0.3475), number of grains per panicle (0.3021), panicle weight (0.2778), plant height (0.8587), test weight (0.4745), filled grains per panicle (0.3018), days to maturity (0.3078) whereas positive and non-significant association with unfilled grain per panicle (0.1284), spikelet fertility % (0.0992) and negative correlation with effective tiller (-0.0454).

4.4.2.6 Filled grains per panicle:

Filled grain per panicle showed positive and significant association with total grains per panicle (0.9508), plant height (0.2214), Days to 50% flowering (0.5286), panicle weight (0.5957) and Days to maturity (0.4907) whereas positive and significant association with spikelet fertility % (0.1965) while negative and significant association with test weight (-0.6109) and effective tillers per plant (-0.193).

4.4.2.7 Unfilled grins per panicle:

Unfilled grain exhibited high positive and significant association with grain number per panicle (0.5275), filled grain (0.3010), and panicle weight (0.2866) while positively non-significant association with plant height (0.0902) and panicle length (0.1284). Negative significant association with spikelet fertility (-0.4249).

4.4.2.8 Number of effective tiller:

Number of effective tiller tillers showed positive and significant association with total grain yield (0.2327). Number of effective tiller not exhibited any high positive and high significant correlation with any characters. Positive non-significant correlation observed with grain number per panicle (0.0611), panicle weight (0.0652), filled grain (0.0966), test weight (0.0583), days of maturity (0.0015), and spikelet fertility (0.0647). Negative and non-significant correlation with days of 50% flowering (-0.0240), unfilled grain per panicle (-0.0963) panicle length (-0.0454) and plant height (-0.0480).

4.4.2.9 Total grain number per panicle:

Total grain per panicle showed positive and highly significant association with Filled grain per panicle (0.9689), unfilled grain per panicle (0.5275), Panicle weight (0.8562), plant height (0.2650), test weight (0.2862), panicle length (0.3021), spikelet fertility % (0.3741), and total grain yield (0.6970). Negative and non-significant association with days of maturity (-0.0186).

4.4.2.10 Spikelet fertility:

Spikelet fertility % exhibited positive and significant correlation with plant height (0.213) filled grain per panicle (0.5436), unfilled grain per panicle (0.3741), panicle weight (0.4439), test weight (0.3647) and total grain yield (0.3806) while positive and non-significant association with plant height (0.0943), effective tiller (0.0647), and panicle length (0.0992) but negative and significant correlation with unfilled grain per panicle (0.42249)

4.4.2.11 Test weight:

Test weight showed positive and highly significant association with panicle length (0.4645), panicle weight (0.4046), plant height (0.4605), test weight (0.3497), spikelet fertility (0.3647) and total grain per panicle (0.2862) whereas positive and non-significant association with days to 50% flowering (0.0129), and effective tillers per plant (0.0583) while negative and non-significant correlation with unfilled grain per panicle (-0.0976) and days to maturity (-0.0290).

4.5 Path coefficient analysis:

Path analysis is a Biometrical tool and it is a standardized partial regression coefficient. Path analysis used to splits the correlation coefficient into the measures of direct and indirect effects on dependent variables by a set of independent variables. If the correlation between yield and character is due to the direct effects of character or indirect effect of character. Direct effect reflects true relationship between dependent and independent character and selection can be practiced for such a character in order to improve yield. Indirect effect reflects that independent character indirectly correlated to the dependent character through another component trait. Phenotypic Path coefficient showing direct and indirect effect of characters are presented in Table 4.5 and fig. 4.4.

4.5.1 Days to 50% flowering:

Direct effect of days of 50% flowering on the grain yield per plant was negative (-0.1497)). Its highest positive indirect effect was exhibited by effective tillers (3.0975) while highest negative indirect effect exhibited by grain number per panicle (-2.5243). Other positive and negligible indirect effects are plant height (0.0269), panicle length (0.0032), days to maturity (0.0425), spikelet fertility per cent (0.0014). The resulting phenotypic correlation with grain yield per plant was negative (-0.0654) and non-significant.

4.5.2 Days to maturity:

Days to maturity had positive direct effect (0.0503) with grain yield per plant. Its highest positive indirect effect was exhibited by grain per panicle (1.1374) followed by filled grain per panicle (0.2028) while highest negative indirect effect exhibited by unfilled grain number per panicle (-1.335). Other positive and negligible indirect effects by plant height (0.0243), test weight (0.0025), effective tillers (0.0002) and panicle length (0.0028). The resulting phenotypic correlation with grain yield per plant was negative (-0.0541) and non-significant.

4.5.3 Effective tillers per plant:

Effective tillers per plant exhibited positive and direct effect (0.1701) with the grain yield per plant. Its highest positive indirect effect was exhibited by filled grain per panicle (5.2852) followed by total grain yield (0.2327) while highest negative indirect effect exhibited by grain number per panicle (-3.7314). Other characters with positive effects was panicle weight (0.0358) and panicle length (0.0001). The resulting phenotypic correlation with grain yield per plant was positive (0.2327) and significant.

4.5.4 Plant height:

The direct effect of plant height on the grain yield per plant was positive and negligible (0.0682) while highest positive indirect effect was exhibited by filled grain (14.8320) followed by grain yield per panicle (0.2076). Highest negative indirect effect exhibited by grain number per panicle (-16.1845). Panicle weight (0.1521) and panicle length (0.0079) also exhibited positive indirect but negligible. The resulting phenotypic correlation with grain yield per plant (0.2076) was positive and significant.

4.5.5 Panicle length:

The direct effect of panicle length on the grain yield per plant was positive (0.0092). Highest positive indirect effect was exhibited by filled grain (16.5068) followed by unfilled grain yield per panicle (2.0264). Highest negative indirect effect exhibited by grain number per panicle (-18.4556). Panicle weight (0.1524), plant height (0.0586), days maturity (0.0155) also exhibited positive indirect effect. The resulting phenotypic correlation with grain yield per plant was positive (0.2104) and significant.

4.5.6 Panicle weight:

The direct effect of panicle weight on the grain yield per plant was positive (0.5484). Highest positive indirect effect was exhibited by filled grain (48.006) followed by unfilled grain yield per panicle (4.5234) while days to 50% flowering (0.0012), plant height (0.0189), effective tiller (0.0111), and panicle length (0.0026) showed positive but negligible indirect effect. Highest negative indirect effect exhibited by grain number per panicle (-52.2953). The resulting phenotypic correlation with the grain yield per plant was positive (0.7606) and highly significant.

4.5.7 Filled grain:

The direct effect of filled grains per panicle on the grain yield per plant was highly positive (54.6447) and highest among all the characters. Highest indirect positive effect exhibited by unfilled grain per panicle (4.7509) and highest negative indirect effect exhibited by grain per panicle (-59.1839). Positive but negligible indirect exhibited by panicle weight (0.4813), plant height (0.0185), effective tiller (0.0164), panicle length (0.0028) and days of maturity (0.0002). The resulting phenotypic correlation with grain yield per plant was positive (0.7254) and highly significant.

4.5.8 Unfilled grain:

The direct effect of unfilled grains per panicle on the grain yield per plant was highly positive (15.7816). Highest indirect positive effect exhibited by filled grain number per panicle (16.4653) and highest negative indirect effect exhibited by grain number per panicle (-32.2219). Other characters exhibited positive but negligible indirect was panicle weight (0.1572), plant height (0.0062), test weight (0.0084), panicle length (0.0012) and spikelet fertility (0.132). The resulting phenotypic correlation with grain yield per plant was positive (0.1957) and significant.

4.5.9 Test weight:

Test weight exhibited negative and low direct effect (-0.0862) with grain yield per plant. Highest positive indirect effect was exhibited by filled grain (19.1272) and highest negative indirect effect exhibited by grain number per panicle (-17.4835). Positive but negligible indirect exhibited by panicle weight (0.2219), plant height (0.0314), effective tiller (0.0099) and panicle length (0.0043). The resulting phenotypic correlation with the grain yield per plant was positive (0.2700) and significant.

4.5.10 Grain number per panicle:

The direct effect of grain number per panicle on the grain yield per plant was highly negative (-61.0813). Highest positive indirect effect was exhibited by filled grain number (52.9957) followed by unfilled grain (8.3252). Positive but negligible indirect exhibited by panicle weight (0.4695), plant height (0.0181), effective tiller (0.0104) and panicle length (0.0028). The resulting phenotypic correlation with the grain yield per plant was positive (0.6970) and significant.

4.5.11 Spikelet fertility:

The direct effect of spikelet fertility on the grain yield per plant was negative and negligible (-0.0310). Highest indirect positive effect exhibited by filled grain number per panicle (29.7322) and highest negative indirect effect exhibited by grain number per panicle (-22.8493). Positive but negligible indirect exhibited by panicle weight (0.2434), plant height (0.0064), effective tiller (0.0110) and panicle length (0.0009). The resulting phenotypic correlation with the grain yield per plant was positive (0.3806) and significant.

4.6 Genetic Divergence:

D^2 statistics is a numerical approach for measuring genetic divergence in the germplasm collections. The composition of different clusters obtained from the D^2 analysis has been presented in the Table 4.6 and illustrated in fig 4.5. Forty rice germplasms were grouped into seven different clusters by using Tocher's method.

This indicated presence of considerably diverse groups of rice germplasm in the material under study. Detail insight into the diversity present in material under study is important in order to select the desirable genotypes to be utilized in the breeding programs.

The germplasms under study were grouped into seven clusters. Clustering pattern indicated that thirty two out of forty germplasms belong to the same cluster *i.e*. cluster I. On the other hand, three belong to cluster IV and cluster II, III, V, VI, and VII, contain 1 germplasm. Intra and inter-cluster distances among the genotype i.e. D^2 values have been presented in the Table 4.7. The highest intra-cluster distance was observed in the cluster I (44.67) which comprised of thirty two germplasms followed by cluster IV (40.31). Cluster II, III, V, VI and VII showing 0.00 intra cluster distance. The highest inter- cluster distance (588.21) was found between cluster II and VII followed by cluster I and VII (354.02) and cluster V and VII (332.73). The smallest inter-cluster distance (72.91) was observed between III and VI followed by cluster III and VI (72.98) and cluster V and VI (81.27). Representation of clusters with intra and inter cluster D values has been represented diagrammatic in figure 4.6.

Mean values for different quantitative traits for different clusters have been presented in Table 4.8. The extreme mean values of the traits under study were observed to fall in different clusters. The highest mean values for filled grains per panicle (103.20), total grain number per panicle (124.73), effective tiller (17.86) and spikelet fertility (81.33) were observed in cluster IV. Highest mean values for days of 50% flowering (118.67) and days of maturity (148.67) were observed in cluster II. Highest mean value for unfilled grain (36.88), plant height (147.84), and panicle length (27.93) were exhibited in cluster III. Cluster VII exhibited highest mean values for total grain yield (53.41), panicle weight (3.45), and test weight (24.62). Thus, the germplasms in cluster II, III, IV, and VII seems to be quiet promising for many of the traits under study.

4.6.1 Contribution of individual characters towards genetic divergence:

All the characters contributed to genetic divergence except days of maturity and spikelet fertility. The percentage of contribution towards genetic divergence by all the characters is presented in table 4.9 and figure 4.7. The character grain yield per plant contributed maximum to genetic divergence (32.18%) followed by filled grain number per plant (15.00%), test weight (14.36%). Contribution of other characters were plant height (12.69%), unfilled grain (11.54%), effective tiller (7.18%), panicle weight (3.85%), days of 50% flowering (2.82%), panicle length (00.26%) and grain number per panicle (00.13%).

Chapter -V

DISCUSSION

The ultimate objective of every plant breeding programme is to develop promising cultivars with improved features. Goal of crop improvement can only achieved by carefully planned selection and hybridization programme. The hereditary variations are the prerequisite for any crop improvement programme. The plant breeder work to sort out these heritable variations which will be useful for the improvement of crop plants and use these variations for crop improvement programme. Partition of the genotypic and environmental components of total variation is very important in order to estimate reliable conclusion about the exploitable (genetic) variability in a set of genotypes. Information about genetic advance, character association, path-coefficient and genetic divergence are very important for utilization of rice germplasm in different breeding programme. Path-coefficient analysis gives the information about direct/indirect effect of independent variable on dependent variable. Characters association gives an information about the genotypic and phenotypic correlation coefficient between yield and its component traits. Genetic divergence study gives information about the divergence between the genotype and suitable genotype as parent in breeding. All the genetic parameter listed above are important for breeder for successful breeding programme.

In the present experiment estimation of variability, heritability, genetic advance, character association, path-coefficient analysis and genetic divergence in forty genotypes of rice was conducted. The experiment was conducted at the Agriculture Research Farm, Institute of Agricultural Sciences, BHU, Varanasi. The results obtained in the present investigation are discussed in this chapter.

The results obtained from the present experiment with respect to twelve characters, including grain yield obtain per plant in a set of forty rice germplasm have been discussed here in the reference of observations made by earlier rice workers in related aspects under the following heads.

5.1 Analysis of variance:

The studies of genetic variance among forty genotypes for twelve characters revealed that the genotypes differed significantly for all the characters which suggested that the materials selected for the studies might be of diverse origin and can be used for breeding programme. Earlier several workers, who worked on rice, have reported the presence of variability amongst the genotypes of rice for different quantitative traits and qualitative traits. These findings are in accordance with the findings of Rahim *et al*. (2004), Singh *et al*. (2011), Dhurai *et al*. (2014) and Namita *et. al*. (2016)

5.2 Mean performance:

The highest mean performance for grain yield per plant was observed for germplasm WRG(NKS)-440 followed by WRG(NKS)-421 and WRG(NKS)-424 indicating that these germplasm can be used in hybridization programme to achieve higher yield. Earliest flowering exhibited by genotype WRG(NKS)-432 followed by WRG(NKS)-401 and WRG(NKS)-436. The highest mean performance filled grain observed in WRG(NKS)-420 followed by WRG(NKS)-421 and WRG(NKS)-440. Lowest unfilled grain observed in WRG(NKS)-417 followed by WRG(NKS)-413 and WRG(NKS)-436. Highest mean performance for grain number per panicle observed in WRG(NKS)-434 followed by WRG(NKS)-440 and WRG(NKS)-421. Highest mean performance for panicle weight observed in WRG(NKS)-440 followed by WRG(NKS)-420 and WRG(NKS)-421. Short plant height observed in WRG(NKS)-406 followed by WRG(NKS)-408 and WRG(NKS)-401. Highest mean performance for test weight observed in WRG(NKS)-422 followed by WRG(NKS)-412 and WRG(NKS)-421. WRG(NKS)-416 showed highest mean performance for effective tiller followed by WRG(NKS)-420 and WRG(NKS)-405. Highest mean performance for panicle length observed in WRG(NKS)-430 followed by WRG(NKS)405 and WRG(NKS)-429. Early maturing genotype was WRG(NKS)-401 followed by WRG(NKS)- 431 and WRG(NKS)-406. Spikelet fertility mean performance highest in WRG(NKS)-421 followed by WRG(NKS)-436 and WRG(NKS)-440. Information about mean performance helpful in selection of high performance genotype. Adequate number of fertile grains per panicle and heavy grains are important traits which should be considered in selection for high yield **(**Adhikari *et al*. 2018).

5.3 Character Association:

Complete knowledge on relationship between of plant characters like grain yield with other quantitative characters is importance for the breeder for making improvement in performance of any variety for which direct selection is not much effective. Hence, association analysis was undertaken to determine the direction of association and number of characters to be considered in improving grain yield of genotype. Complex trait such as yield, and much influenced by its component traits. In this case it is important to know the correlation between the different component traits of yield, among themselves and with the grain yield to ease the selection for improvement in yield. Values of correlation are based on the variance and covariance for all possible combination of the characters studied.

In the present experiment, study has been made to estimate the phenotypic correlation among all the character combinations with the objectives to get information about the nature, extent and direction of selection pressure to achieve practical and desirable results.

The results on correlation analysis showed that grain yield has positive and highly significant association with panicle weight, followed by filled grain, grain number per panicle, spikelet fertility, test weight, effective tiller, panicle length, plant height and unfilled grain. Similar results were also reported by Reddy *et al*. (2008) for plant height and total grains per panicle. Days of 50% flowering and days of maturity are negatively associated with grain yield simmeler result also observed by Qamar *et al*. (2005).

The study of character association revealed that the genotypic correlation coefficient were found to be higher than the phenotypic correlation coefficient and thus suggested that the observed relationship among the different characters was due to genetic factors or due to modified effect of environment.

5.4 Heritability and genetic advance:

Heritability and genetic advance both are important selection parameters for selection. Selection based only on heritability is not such much effective as heritability with genetic advance because it not sure that the characters showing high heritability will also show high genetic advance. The breeder should be more careful in making selection based on heritability as it can imply both additive and non-additive gene action. Thus, selection based on heritability values coupled with genetic advance would be more reliable and useful in formulating selection procedure as it indicates that most likely the heritability is due to additive gene effects.

In present experiment, high heritability coupled with high genetic advance was recorded for total grains yield followed by grain number per panicle, filled grains per panicle, panicle weight, test weight, unfilled grain, plant height, effective tiller, days of 50% flowering, panicle length, spikelet fertility and days of maturity. Similar observation was obtained by Bhadru *et al*. (2012) for highest heritability and genetic advance % of mean corresponded to grains per panicle, seed yield, 1000 grain weight and plant height and direct selection for these traits would be useful for yield improvement in rice. Sathya & Jebaraj (2013) also reported similar observation for heritability and genetic advance for nineteen characters including drought and yield contributing traits.

5.5 Path Analysis:

Path analysis used to splitting the total correlation into direct and indirect effects of various causes as devised by Wright (1934). Path analysis gives information about direct and indirect effects of independent traits on dependent traits like grain yield. It is an advance statistical technique that helps in indirect selection of yield contributing characters.

The correlation coefficients among the yield and its component characters may sometimes be misleading because it does not provide the magnitude of associations**.** Therefore, for effective interpretation, splitting the total correlation into direct and indirect effect is necessary. Highest positive direct effect observed in filled grain followed by unfilled grain and panicle weight. Other positive but nonsignificant effect observed in plant height, effective tiller, panicle length and days of maturity. The direct negative significant effect observed in grain number per panicle while negative nonsignificant effect observed in days of 50% flowering and spikelet fertility.

Filled grain also give indirect positive and significant effect through unfilled grain, panicle weight and negative indirect effect exhibited by grain number per panicle, days of 50% flowering and spikelet fertility. Grain number per panicle exhibited indirect positive significant through filled grain followed by unfilled grain but direct negative is more than indirect positive effect hence selection is not effective. These finding were in accordance with Rokonuzzaman *et al.* (2008) for number of effective tiller per plant and plant height; Devi *et al*. (2017) for test weight, effective tillers, and filled grains per panicle. Similar observation also recorded by Sowmiya *et al*. (2017), Neethu-Francis *et al.* (2018) and Katiyar *et al*. (2019).

Considering the magnitude of character association and nature of their direct and indirect effects, in present experiment it can be concluded that simultaneous improvement of grain yield per plant is possible through manifestation of filled grain, unfilled grain, and panicle weight.

5.6 Genetic Divergence:

Estimation of genetic diversity among the set of experimental material is the first step of every breeding programme. There are different methods for assessment of genetic diversity but Mahanobis' D^2-statistics most suitable for this study. Estimation of genetic diversity helps in selection of diverse genotypes for breeding programmme. Progeny obtain from such diverse parents gives more hybrid vigour.

In the present experiment, D^2 analysis revealed the presence of considerable genetic diversity in the set of forty germplasm. Maximum numbers of germplasm observed under cluster I and least number of germplasm (only one) observed in cluster II, III, V, VI and VII. The germplasm were observed to be distributed in seven different clusters. The intra-cluster distance in clusters II, III, V, VI, and VII was observed to be zero since these contains only one genotype in each cluster. Maximum intra-cluster distance observed in Cluster I with thirty two genotypes followed by cluster IV which included three genotypes. Genotypes from same cluster indicated their close relationship among genotypes as compared to genotypes in other clusters. Due to close relationship the genotypes from same cluster are less divergent than those which are placed in different cluster. Cluster II and VI showed maximum inter-cluster distance followed by cluster I and VII. High distance between these clusters indicating that the hybridization between these genetically diverse genotypes would yield desirable segregates with the accumulation of favorable genes in the segregating generations. Other diverse clusters were cluster V and VII and cluster II and IV. The clustering divides germplasm on the bases of their diversity systematic and easy way. The clusters with greater the distance will wider in the expected genetic advance between them. Therefore, indication of the genetic diversity analysis of genotypes would help in selecting parents for hybridizing programme.

Highest mean value for days of 50% flowering and days of maturity fallen in cluster II, highest mean value for unfilled grain, plant height and panicle observed in cluster III, highest mean value for filled grain, grain number per panicle, effective tiller and spikelet fertility observed in cluster IV and cluster VII showed highest mean value for grain yield, panicle weight and test weight. Highest percent contribution toward total genetic diversity observed in total grain yield followed by filled grain, test weight, plant height, unfilled grain, effective tiller, panicle weight, days of 50% flowering, but there is no contribution of days of maturity and spikelet fertility for total genetic divergence. Similar results were observed by Hegde *et al.* (2000), Singh *et al.* (2006) and Bhadru *et al.* (2012)

In the present experiment, based on inter-cluster distances and cluster mean, suitable germplasm may be selected as a parent for hybridization programme. Germplasm from different cluster with high inter cluster distance is more desirable. Genetically diverse germplasm is expected to be effective in accumulation of favorable genes for bringing together different desirable traits into the common background. Thus by utilizing diverse germplasm an improved germplasm can be developed.

Chapter-VI

SUMMARY AND CONCLUSION

The present investigation entitled **"GENETIC VARIABILITY AND DIVERSITY ANALYSIS FOR YIELD AND YIELD ATTRIBUTING TRAITS OF WILD GERMPLASM IN RICE"** was carried out with forty diverse rice genotypes for its twelve quantitative character with the aim to study magnitude and nature of genetic variation found within them and portioning this variation in different component to study its effect. In this study, degree of association between grain yield and its component traits, genetic diversity present among the genotypes and the direct and indirect effect of independent traits on dependent trait like grain yield was estimated.

The present experiment was carried out at Agriculture Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi in a randomized block design with three replication to evaluate the experimental material during *kharif* 2018. Observations were based on five randomly selected plants of each genotype from each replication. The twelve characters studied under this experiment were days to 50% flowering, effective tillers per plant, plant height, days to maturity, panicle length, test weight of grain, grain yield per plant, total grains per panicle, unfilled grain per panicle, filled grain per panicle, panicle weight, spikelet fertility % and grain yield per plant.

Analysis of variance revealed that the difference among the genotypes for all the twelve characters under study were highly significant. The genotypes exhibited a wide range of variability for most of the traits. This indicated that there is great scope for selection of promising genotypes from present set of genotypes for yield improvement. On the basis of *per se* performance, genotypes *viz*., WRG(NKS)-440, WRG(NKS)-434 and WRG(NKS)-421 were found to be the best for yield and yield contributing traits. Therefore, these can be successfully utilized as parent in future

Breeding programme for improvement of yield performance. Genotype WRG(NKS)-401 and WRG(NKS)-432 were earliest in flowering and maturity hence these genotypes can be used as a donor in hybridization programme for evolving early maturing rice variety.

From the study of variability parameters, the high estimates of variation were observed for grain yield per plant, it indicates that for improvement of rice yield this trait is very important. Other characters showed high variability were panicle weight, filled grains per panicle, and grain number per panicle indicating the importance in selection for improving the rice yield. Almost all the characters under the present investigation showed high heritability with high genetic advance indicating the less influence of environmental variance in the inheritance of these traits, this traits can be further improved by means of simple selection.

The character association study under this experiment revealed that grain yield per plant exhibited high positive and significant association with panicle weight followed by filled grain per panicle, grain number per panicle and spikelet fertility percentage. This association studied under present experiment indicates that grain yield of rice can be improved by selecting genotypes having higher performances for panicle weight, filled grain per panicle, grain number per panicle and spikelet fertility percentage. In present experiment the path coefficient analysis of direct and indirect effect of yield related traits on the yield of rice indicates that filled grain per panicle and unfilled grain per panicle exhibited maximum direct positive effects on grain yield per plant. Other traits like Panicle weight, plant height, effective tiller, panicle length, days of maturity also exhibited positive direct effect on the grain yield. From both correlation and path coefficient analysis it can be predict that the filled grain per panicle and panicle weight are most important traits, the genotypes showing high performance for this traits should be selected for the improvement of grain yield in rice.

Genetic diversity analysis was carried out through D^2 analysis in order to assess the genetic divergence among genotype under study. Based on D^2 analysis forty rice genotypes were grouped in seven clusters. The maximum numbers of genotypes (32) belong to cluster I and due to maximum numbers of member genotypes this cluster showing highest intra cluster distance followed by cluster IV which is second largest cluster with 3 genotypes while cluster II, III, V, VI and VII showed zero intra cluster distance because of single member in these clusters. The highest inter cluster distance observed between cluster II and Cluster VII, indicates high genetic divergence found between these two clusters and more suitability for breeding programme than other clusters. The highest contribution towards the total genetic divergence observed in total grain yield per plant followed by filled grain.

The present study provided valuable information about various parameters in forty rice genotypes and on the basis of this study it can be concluded that genotypes WRG(NKS)-440, WRG(NKS)-434 and WRG(NKS)-421 were found to be the promising genotypes for yield and yield contributing traits. Hence these three genotypes can be utilized as parents in hybridization programme to obtain improved grain yield in rice.

Table 4.1 Analysis of variance (ANOVA) for twelve quantitative traits in forty rice genotypes

Source of variation	df	Mean Sum of Squares											
		DM	ET	PH	PL	PPW	FG	UFG	GNPP	SF%	TW	TGY	DF
Replication	2	35.32	4.410	510.46	5.79	0.079	35.75	11.74	73.47	45.16	2.66	32.68	62.55
Treatment	39	178.78	30.99	2389.17	60.41	1.473	1466.54	120.24	1854.16	204.59	39.75	280.10	322.47
Error	78	43.62	1.59	105.94	6.020	0.025	22.54	3.91	25.27	26.00	1.169	2.23	25.59

*and ** depict significant values at 5% and 1% level of significance, respectively.

Where, (DF)= Days of 50% flowering, (DM)= Days of maturity, (ET)= Effective tillers, (PH)= Plant height, (PL)= Panicle length, (PPW)= per panicle weight, (FG)= Filled grain, (NFG)= Unfilled grain, (GNPP)= Grain Number per panicle, (SF%)= Spikelet fertility, (TW)= Test weight, (TGY)= Total grain yield

Table 4.2: Mean performance of 40 Rice genotypes for yield and yield attributing traits

Genotype	DF	UFG	FG	GNPP	TGY	PPW	PH	TWT	ET	PL	DM	SF
WRG(NKS)-401	79.33	22.26	41.59	63.85	16.31	1.16	60.74	17.53	16.71	17.83	109	65.10
WRG(NKS)-402	105.00	24.72	76.71	101.43	12.50	2.03	148.55	22.54	9.43	27.23	135	73.97
WRG(NKS)-403	108.66	21.94	48.43	70.37	15.57	1.75	127.44	19.43	13.46	25	140	65.06
WRG(NKS)-404	104.33	25.50	30	55.50	6.70	0.71	134.01	20.53	16.62	27.1	133.66	53.83
WRG(NKS)-405	103.00	13.41	35.37	48.79	13.70	0.74	138.74	22.73	20.80	28.66	130.66	69.12
WRG(NKS)-406	84.00	26.44	49.79	76.23	13.24	1.13	46.6	19.24	17.93	9.96	120	63.42
WRG(NKS)-407	102.33	22.43	47.52	69.96	13.84	1.17	132.37	21.66	13.88	23.43	132.66	67.89
WRG(NKS)-408	92.66	14.43	34.21	48.64	10.18	0.89	47.83	16.87	17.03	11.35	124.66	72.89
WRG(NKS)-409	104.66	16.41	56.91	73.32	11.21	0.98	83.43	18.68	13.49	21.46	134.66	75.80
WRG(NKS)-410	103.00	12.99	24.35	37.35	6.03	0.37	134.25	17.63	15.5	20.4	133	65.04
WRG(NKS)-411	92.66	11.78	41.95	53.73	11.32	1.32	93.72	23.66	19.77	18.3	128.33	78.11
WRG(NKS)-412	91.00	16.68	30.20	46.89	9.06	0.97	140.36	26.04	13.37	23.53	127.33	64.42
WRG(NKS)-413	89.33	10.09	34.53	44.623	5.75	0.63	119.72	28.36	13.85	23.35	121	77.54
WRG(NKS)-414	85.33	17.27	37.32	54.6	7.15	0.72	79.63	14.84	13.9	16.13	123	70.47
WRG(NKS)-415	107.00	19.91	39.19	59.10	9.33	0.75	124.84	19.27	12.96	25.2	137	66.24
WRG(NKS)-416	104.00	15.84	52.14	67.98	28.94	1.23	143.65	22.10	22.03	25.63	134	71.34
WRG(NKS)-417	112.00	9.75	33.49	43.22	14.11	0.91	135.98	21.22	19.11	24.36	139.66	77.21
WRG(NKS)-418	107.33	15.12	52.89	68.02	24.87	1.39	151.97	21.75	18.33	24.4	135.66	77.78
WRG(NKS)-419	106.66	18.67	61.28	79.95	16.41	1.11	135.04	21.77	17.49	25.83	136.66	72.37
WRG(NKS)-420	103.33	26.19	107.96	134.15	32.82	2.28	140.55	23.6	21.31	25.25	133.33	80.42
WRG(NKS)-421	109.00	13.53	104.97	118.51	34.64	2.80	150.57	25.67	15.92	25.6	137.33	84.07
WRG(NKS)-422	107.66	12.58	45.39	57.973	14.80	1.41	146.11	28.37	10.48	25.66	134.33	79.49
WRG(NKS)-423	109.66	11.16	42.9	54.06	11.32	0.55	118.05	16.87	15.19	20.56	139.66	79.39
WRG(NKS)-424	89.66	22.31	39.59	61.90	34.31	0.99	88.54	16.22	11.60	16.76	127.33	66.57
WRG(NKS)-425	81.66	17.02	33.84	50.87	13.97	1.03	88.87	18.44	15.63	15.99	121	61.86
WRG(NKS)-426	118.66	22.61	14.61	37.22	6.15	0.45	142.81	14.46	15.98	25.56	148.66	42.00
WRG(NKS)-427	88.66	13.24	34.49	47.74	9.22	0.78	117.56	17.44	11.89	19.46	119.66	72.33
WRG(NKS)-428	94.66	14.64	40.88	55.52	17.09	1.03	148.30	24.49	14.98	27.66	126.33	73.68

WRG(NKS)-429	89.33	36.87	76.91	113.79	21.50	1.82	147.84	24.56	13.34	27.93	119.33	69.15
WRG(NKS)-430	98.66	29.42	41.47	70.89	13.81	1.21	149.70	23.61	11.15	29.33	128.66	60.83
WRG(NKS)-431	93.00	12.44	33.61	46.05	6.57	0.54	117.35	20.67	11.92	22.3	127.33	71.88
WRG(NKS)-432	77.00	23.75	32.44	56.19	15.47	0.82	134.28	21.32	23.35	23.24	119.00	63.58
WRG(NKS)-433	90.66	20.46	38.84	59.31	18.28	1.26	131.54	23.5	14.82	21.72	120.66	64.16
WRG(NKS)-434	94.00	24.86	96.65	121.52	24.67	3.32	146.47	22.71	16.35	25.03	124	79.50
WRG(NKS)-435	80.33	11.02	46.52	57.55	16.59	1.06	126.20	22.19	13.68	25.93	122.66	76.26
WRG(NKS)-436	80.33	10.74	62.92	73.67	21.06	1.62	140.46	21.57	16.69	27.33	122.66	82.44
WRG(NKS)-437	98.00	20.71	66.08	86.80	20.36	1.42	121.71	22.4	18.88	25.07	130	73.42
WRG(NKS)-438	98.66	24.38	65.33	89.71	23.83	1.76	147.46	24.76	14.08	25.7	128.66	72.75
WRG(NKS)-439	99.00	28.80	60.17	88.97	16.34	1.14	135.02	12.42	12.8	24.41	129	69.32
WRG(NKS)-440	88.33	20.50	99.72	120.23	53.40	3.45	129.95	24.61	16.77	26.92	124.33	81.08
Mean	**96.81**	**18.82**	**50.33**	**69.15**	**16.81**	**1.27**	**123.70**	**21.14**	**15.56**	**23.16**	**129**	**70.79**
C.V.	5.22	10.51	9.43	7.26	8.88	12.85	8.32	5.11	8.03	10.59	5.12	7.20
S.E.	2.92	1.14	2.74	2.90	0.86	0.094	5.94	0.62	0.72	1.41	3.81	2.94
C.D. 5%	8.22	3.21	7.71	8.17	2.42	0.26	16.73	1.75	2.03	3.98	10.73	8.28
C.D. 1%	10.90	4.26	10.23	10.83	3.21	0.35	22.18	2.33	2.69	5.28	14.2	10.99
Range Lowest	77.00	9.75	14.61	37.22	5.75	0.37	46.6	12.42	9.43	9.96	109	42.00
Range Highest	118.66	36.87	107.96	134.15	53.40	3.45	151.97	28.37	23.35	29.33	148.66	84.07

Where, (DF)= Days of 50% flowering, (DM)= Days of maturity, (ET)= Effective tillers, (PH)= Plant height, (PL)= Panicle length, (PPW)= per panicle weight, (FG)= Filled grain, (NFG)= Unfilled grain, (GNPP)= Grain Number per panicle, (SF%)= Spikelet fertility, (TW)= Test weight, (TGY)= Total grain yield

Table 4.3 Variability parameters for 12 quantitative characters in 40 rice genotypes

Trait		DF	UFG	FG	GNPP	TGY	PPW	PH	TWT	ET	PL	DM	DF
Range	Min.	77	9.75	14.61	37.22	5.75	0.37	46.6	12.42	9.43	9.96	109	42.00
	Max.	118.6	36.87	107.96	134.15	53.40	3.45	151.9	28.37	23.35	29.34	148.6	84.07
GCV		10.27	33.07	43.58	35.70	57.23	54.62	22.30	16.96	20.12	18.37	5.20	10.89
PCV		11.52	34.70	44.59	36.43	57.92	56.11	23.80	17.71	21.66	21.21	7.30	13.06
h^2 (Broad Sense)		0.79	0.90	0.95	0.96	0.97	0.94	0.87	0.91	0.86	0.75	0.50	0.69
G.A. as % of Mean 5%		18.86	64.94	87.76	72.06	116.51	109.52	43.04	33.45	38.49	32.80	7.64	18.72
G..A. as % of Mean 1%		24.17	83.22	112.47	92.35	149.32	140.36	55.15	42.86	49.33	42.04	9.79	24.00
General Mean		96.81	18.82	50.33	69.15	16.81	1.27	123.70	21.14	15.56	23.16	129.0	70.79

Where, (DF)= Days of 50% flowering, (DM)= Days of maturity, (ET)= Effective tillers, (PH)= Plant height, (PL)= Panicle length, (PPW)= per panicle weight, (FG)= Filled grain, (NFG)= Unfilled grain, (GNPP)= Grain Number per panicle, (SF%)= Spikelet fertility, (TW)= Test weight, (TGY)= Total grain yield

Table 4.4 Estimate of Phenotypic correlation between yield and its related characters from 40 genotypes of rice germplasms

Trait	**DF**	**UFG**	**FG**	**GNPP**	**PPW**	**PH**	**TWT**	**ET**	**PL**	**DM**	**SF**
DF	1.000										
UFG	-0.0351	1.000									
FG	0.0566	0.3010***	1.000								
GNPP	0.0413	0.5275***	0.9689***	1.000							
PPW	-0.0078	0.2866***	0.8776***	0.8562***	1.000						
PH	0.3944***	0.0902	0.2712***	0.2650**	0.2774**	1.000					
TWT	0.0129	-00976	0.3497***	0.2862**	0.4046***	0.4605***	1.000				
ET	-0.0240	-0.0963	0.0966	0.0611	0.0652	-0.0480	0.0583	1.000			
PL	0.3475***	0.1284	0.3018***	0.3021***	0.2778**	0.8587***	0.4645***	-0.0454	1.000		
DM	0.08443***	-0.0845	0.0037	-0.0186	-0.0301	0.3559***	-0.0290	0.0015	0.3078***	1.000	
SF	-0.0466	-0.4249***	0.5436***	0.3741***	0.4439***	0.0943	0.3647***	0.0647	0.0992	-0.063	1.000
TGY	-0.0654	0.1957*	0.7254***	0.6970***	0.7606***	0.2076*	0.2700**	0.2327*	0.2104*	-0.054	0.3806***

*, ** and *** depict significant values at 5%, 1% and 0.1% level of significance, respectively.

Where, (DF)= Days of 50% flowering, (DM)= Days of maturity, (ET)= Effective tillers, (PH)= Plant height, (PL)= Panicle length, (PPW)= per panicle weight, (FG)= Filled grain, (NFG)= Unfilled grain, (GNPP)= Grain Number per panicle, (SF%)= Spikelet fertility, (TW)= Test weight, (TGY)= Total grain yield

Table 4.5 Phenotypic Path coefficient analysis showing direct and indirect effects of different characters on yield of Rice

Traits	DF	UFG	FG	GNPP	PPW	PH	TWT	ET	PL	DM	SF
DF	**-0.1497**	0.0053	-0.0085	-0.0062	0.0012	-0.0591	-0.0019	0.0036	-0.0520	-0.1264	0.0070
UFG	-0.5535	**15.7816**	4.7509	8.3252	4.5234	1.4238	-1.5403	-1.5199	2.0264	-1.3335	-6.7054
FG	3.0975	16.4653	**54.6947**	52.9957	48.0006	14.8320	19.1272	5.2852	16.5068	0.2028	29.732
GNPP	-2.5243	-32.2219	-59.183	**-61.081**	-52.295	-16.184	-17.4835	-3.7314	-18.4556	1.1374	-22.843
PPW	-0.0043	0.1572	0.4813	0.4695	**0.5484**	0.1521	0.2219	0.0358	0.1524	-0.0165	0.2434
PH	0.0269	0.0062	0.0185	0.0181	0.0189	**0.0682**	0.0314	-0.0033	0.0586	0.0243	0.0064
TWT	-0.0011	0.0084	-0.0302	-0.0247	-0.0349	-0.0397	**-0.0862**	-0.0050	-0.0401	0.0025	-0.0314
ET	-0.0041	-0.0164	0.0164	0.0104	0.0111	-0.0082	0.0099	**0.1701**	-0.0077	0.0002	0.0110
PL	0.0032	0.0012	0.0028	0.0028	0.0026	0.0079	0.0043	-0.0004	**0.0092**	0.0028	0.0009
DM	0.0425	-0.0043	0.0002	-0.0009	-0.0015	0.0179	-0.0015	0.0001	0.0155	**0.0503**	-0.0032
SF	0.0014	0.0132	-0.0169	-0.0116	-0.0138	-0.0029	-0.0113	-0.0020	-0.0031	0.0020	**-0.0310**
TGY	-0.0654	0.1957	0.7254	0.6970	0.7606	0.2076	0.2700	0.2327	0.2104	-0.0541	0.3806
Partial R^2	0.0098	3.0882	39.6768	-42.573	0.4172	0.0142	-0.0233	0.0396	0.0019	-0.0027	-0.0118

R SQUARE = 0.6364 RESIDUAL EFFECT = 0.6030

Where, (DF)= Days of 50% flowering, (DM)= Days of maturity, (ET)= Effective tillers, (PH)= Plant height, (PL)= Panicle length, (PPW)= per panicle weight, (FG)= Filled grain, (NFG)= Unfilled grain, (GNPP)= Grain Number per panicle, (SF%)= Spikelet fertility, (TW)= Test weight, (TGY)= Total grain yield

Table 4.6 Grouping of 40 rice germplasm into seven clusters (by Tocher method)

Cluster	Germplasm	Number
I	WRG(NKS)-427, WRG(NKS)-431, WRG(NKS)-415, WRG(NKS)-423, WRG(NKS)-410, WRG(NKS)-414, WRG(NKS)-425, WRG(NKS)-408, WRG(NKS)-407, WRG(NKS)-404, WRG(NKS)-419, WRG(NKS)-403, WRG(NKS)-411, WRG(NKS)-405, WRG(NKS)-435, WRG(NKS)-428, WRG(NKS)-433, WRG(NKS)-417, WRG(NKS)-412, WRG(NKS)-437, WRG(NKS)-401, WRG(NKS)-430, WRG(NKS)-432, WRG(NKS)-436, WRG(NKS)-418, WRG(NKS)-406, WRG(NKS)-422, WRG(NKS)-413, WRG(NKS)-438, WRG(NKS)-402, WRG(NKS)-416	32
II	WRG(NKS)-426	1
III	WRG(NKS)-429	1
IV	WRG(NKS)-420, WRG(NKS)-421, WRG(NKS)-434	3
V	WRG(NKS)-39	1
VI	WRG(NKS)-424	1
VII	WRG(NKS)-440	1

Table 4.7 Average Intra and inter-cluster D^2 value among 7 Clusters (by Tocher method)

Cluster	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	**44.67**	86.41	98.30	153.56	73.83	101.23	354.02
Cluster 2		**0.00**	214.15	305.92	86.81	184.40	588.21
Cluster 3			**0.00**	72.91	72.98	101.57	215.30
Cluster 4				**40.31**	132.21	116.14	104.04
Cluster 5					**0.00**	81.27	332.73
Cluster 6						**0.00**	173.73
Cluster 7							**0.00**

Table 4.8 Mean values of different characters of 40 rice germplasms grouped in seven clusters

S.NO.	DF	UFG	FG	GNPP	TGY	PPW	PH	TWT	ET	PL	DM	SF
Cluster 1	96.29	17.42	44.15	61.56	14.02	1.08	120.83	21.30	15.58	22.79	128.65	70.62
Cluster 2	**118.67**	22.62	14.61	37.23	6.16	0.46	142.81	14.46	15.98	25.57	**148.67**	42.01
Cluster 3	89.33	**36.88**	76.91	113.79	21.51	1.82	**147.84**	24.56	13.35	**27.93**	119.33	69.16
Cluster 4	102.11	21.53	**103.20**	**124.73**	30.71	2.80	145.87	24.00	**17.86**	25.30	131.56	**81.33**
Cluster 5	99.00	28.81	60.17	88.98	16.34	1.15	135.02	12.43	12.80	24.42	129.00	69.32
Cluster 6	89.67	22.31	39.60	61.91	34.31	0.99	88.54	16.22	11.60	16.77	127.33	66.57
Cluster 7	88.33	20.51	99.72	120.23	**53.41**	**3.45**	129.95	**24.62**	16.77	26.92	124.33	81.09

(Numerical in bold indicates higher values for concerned characters)

Where, (DF)= Days of 50% flowering, (DM)= Days of maturity, (ET)= Effective tillers, (PH)= Plant height, (PL)= Panicle length, (PPW)= per panicle weight, (FG)= Filled grain, (NFG)= Unfilled grain, (GNPP)= Grain Number per panicle, (SF%)= Spikelet fertility, (TW)= Test weight, (TGY)= Total grain yield

Table 4.9 Percent contribution of each character towards total genetic divergence in 40 Germplasms

Source	Times Ranked 1st	Contribution%
DF	22	2.82%
UFG	90	11.54%
FG	117	15.00%
GNPP	1	00.13%
TGY	251	32.18%
PPW	30	3.85%
PH	99	12.69%
TWT	112	14.36%
ET	56	7.18%
PL	2	00.26%
DM		00.00%
SF		00.00%

Where, (DF)= Days of 50% flowering, (DM)= Days of maturity, (ET)= Effective tillers, (PH)= Plant height, (PL)= Panicle length, (PPW)= per panicle weight, (FG)= Filled grain, (NFG)= Unfilled grain, (GNPP)= Grain Number per panicle, (SF%)= Spikelet fertility, (TW)= Test weight, (TGY)= Total grain yield

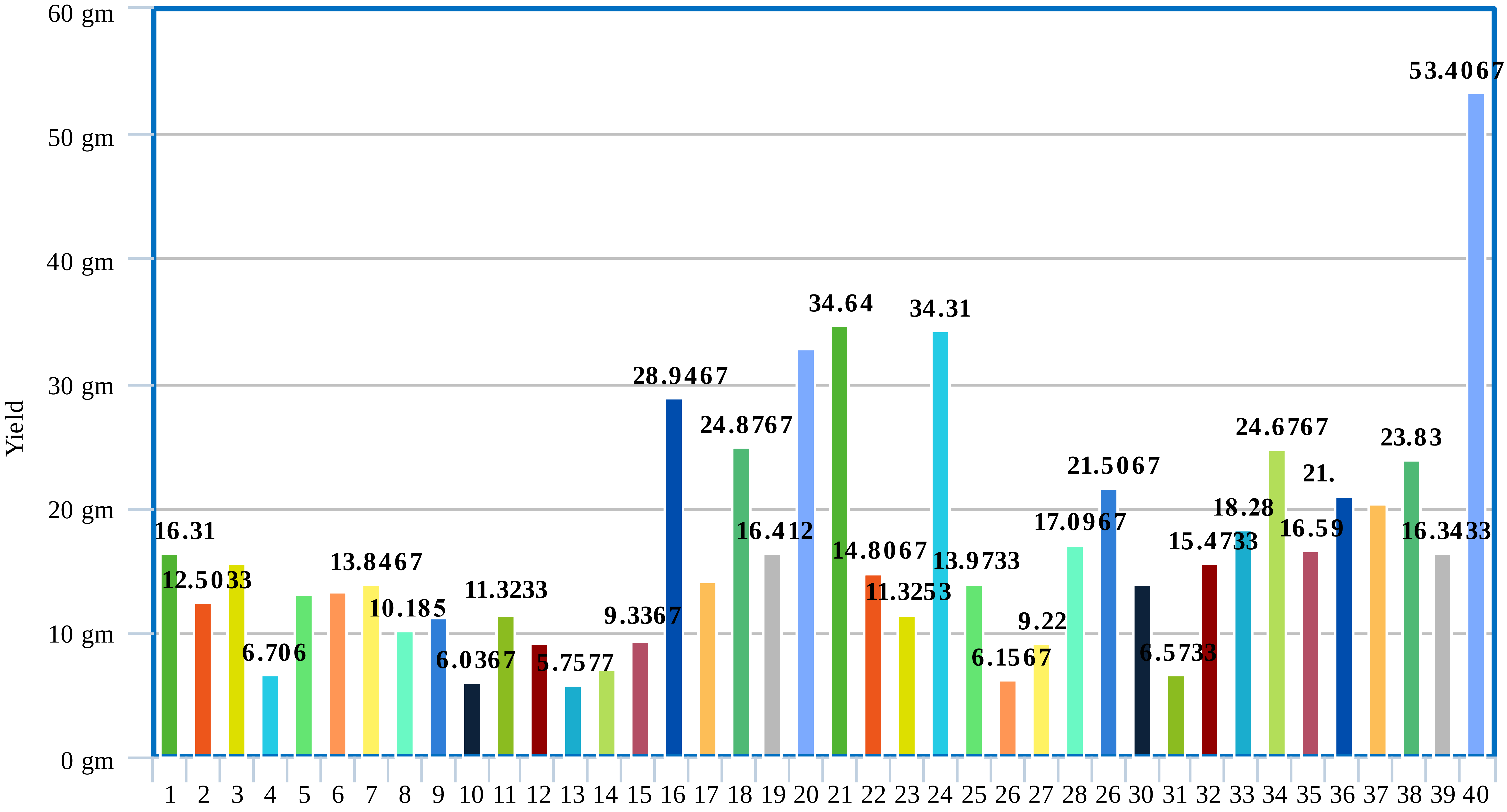

Figure: 4.1 Mean performance of forty rice genotypes for yield

Where 1 to 40 numbering on X axis representing the genotype WRG(NKS)-401 to WRG(NKS)-440

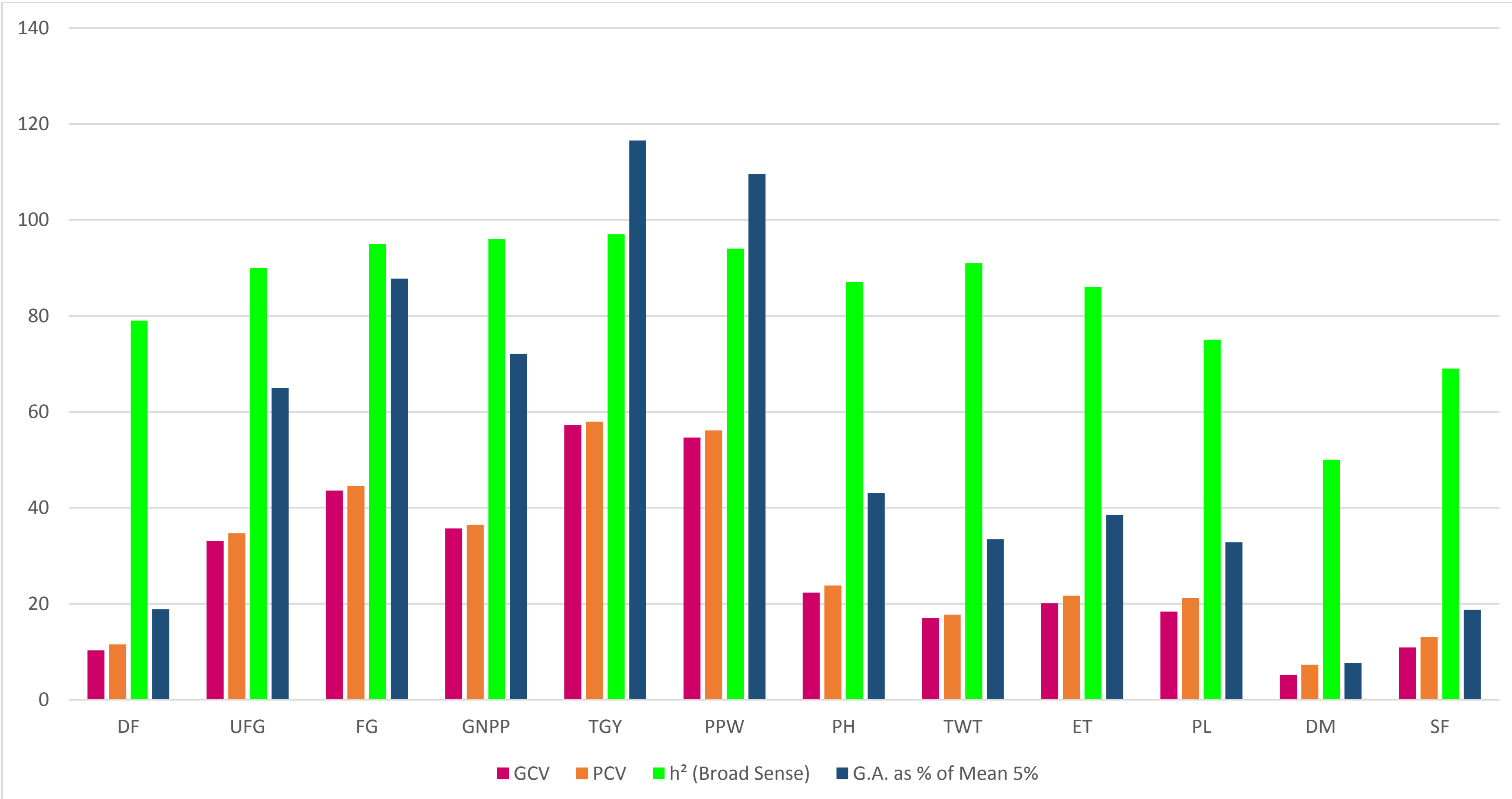

Figure:4.2 Histogram depicting estimates of phenotypic and genotypic coefficient of variation, genetic advance and heritability of yield component in forty rice germplasm.

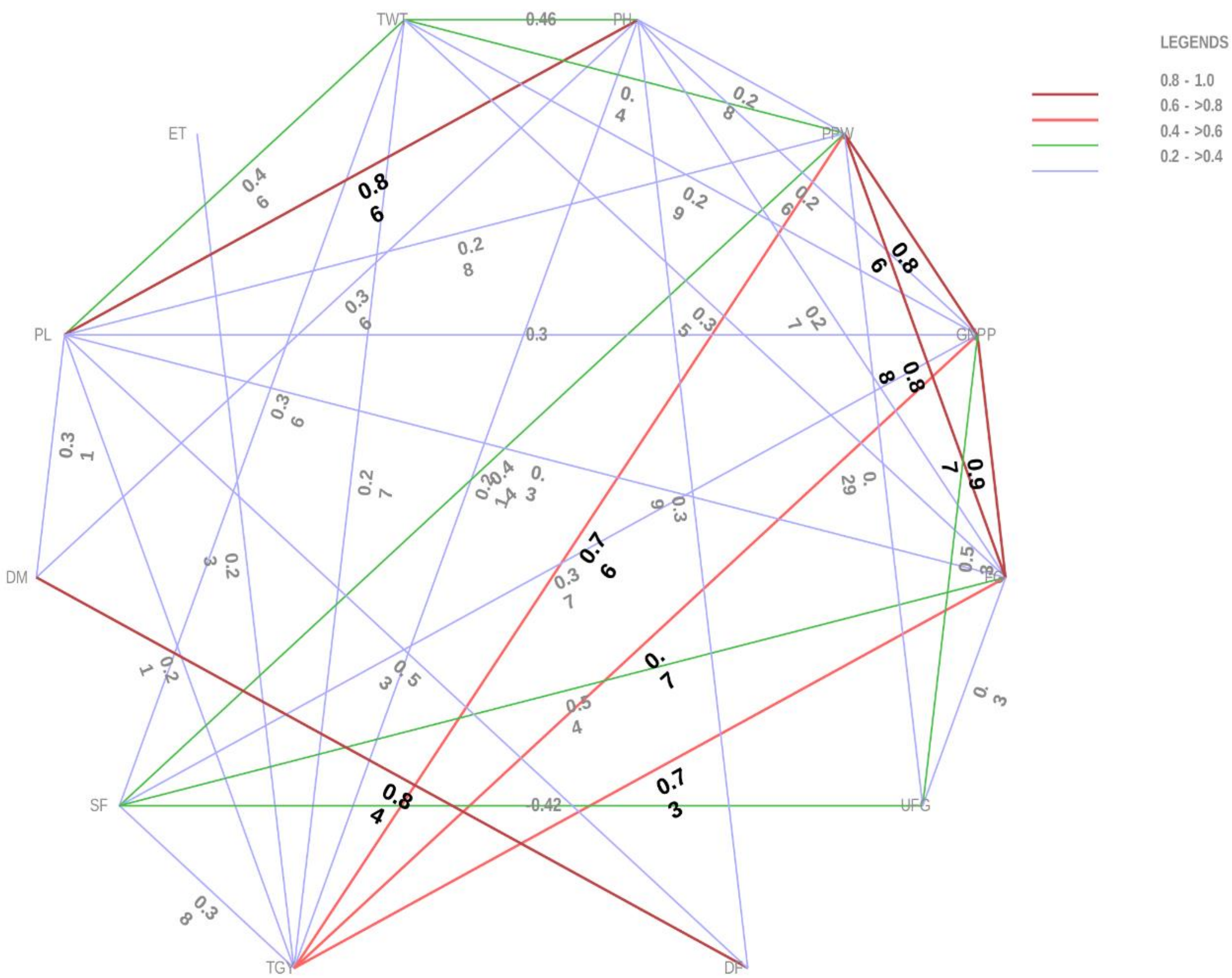

Fig: 4.3 Phenotypic correlation between twelve traits of rice germplasm

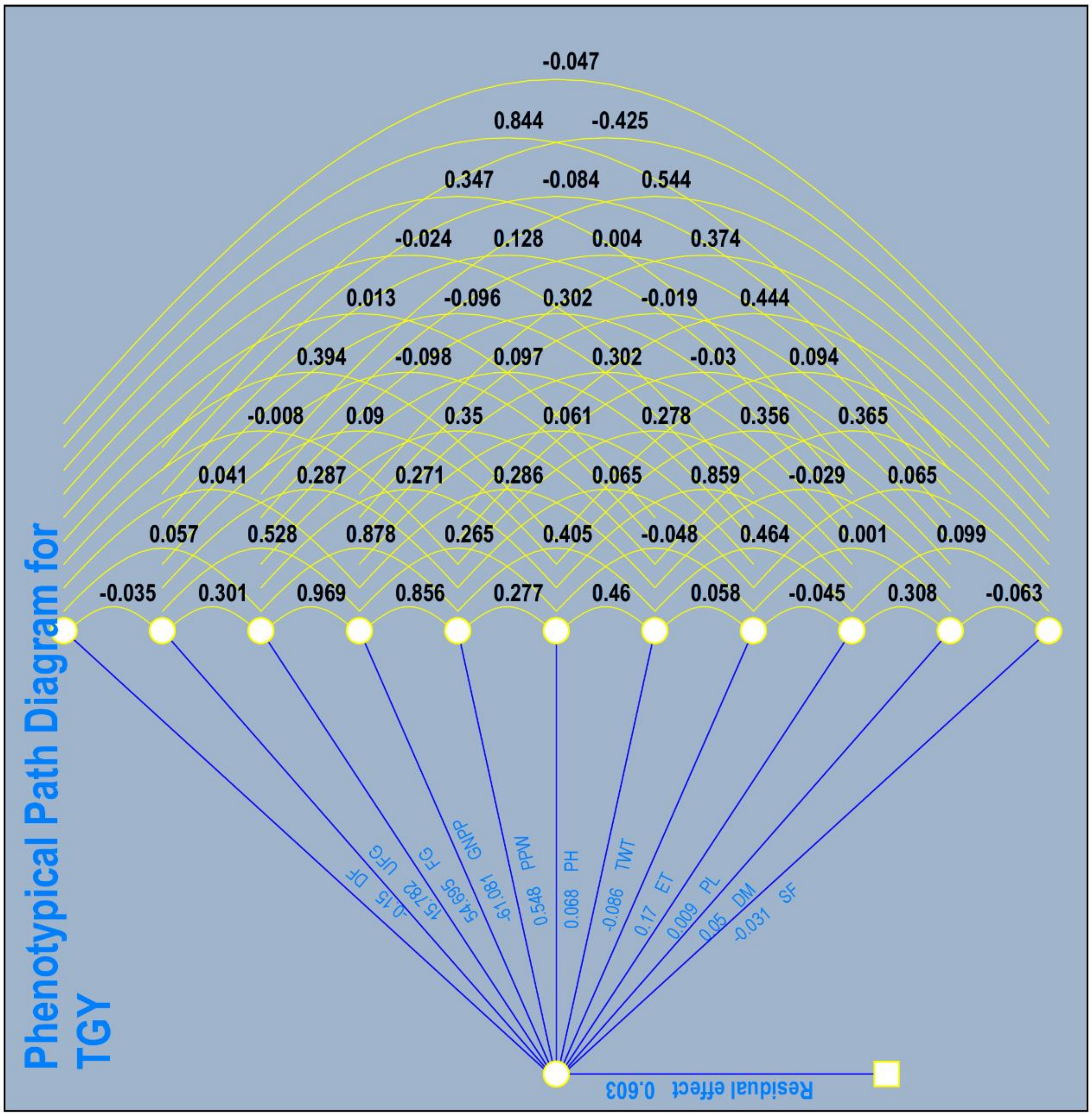

Figure: 4.4 Path diagram for grain yields as a dependent character

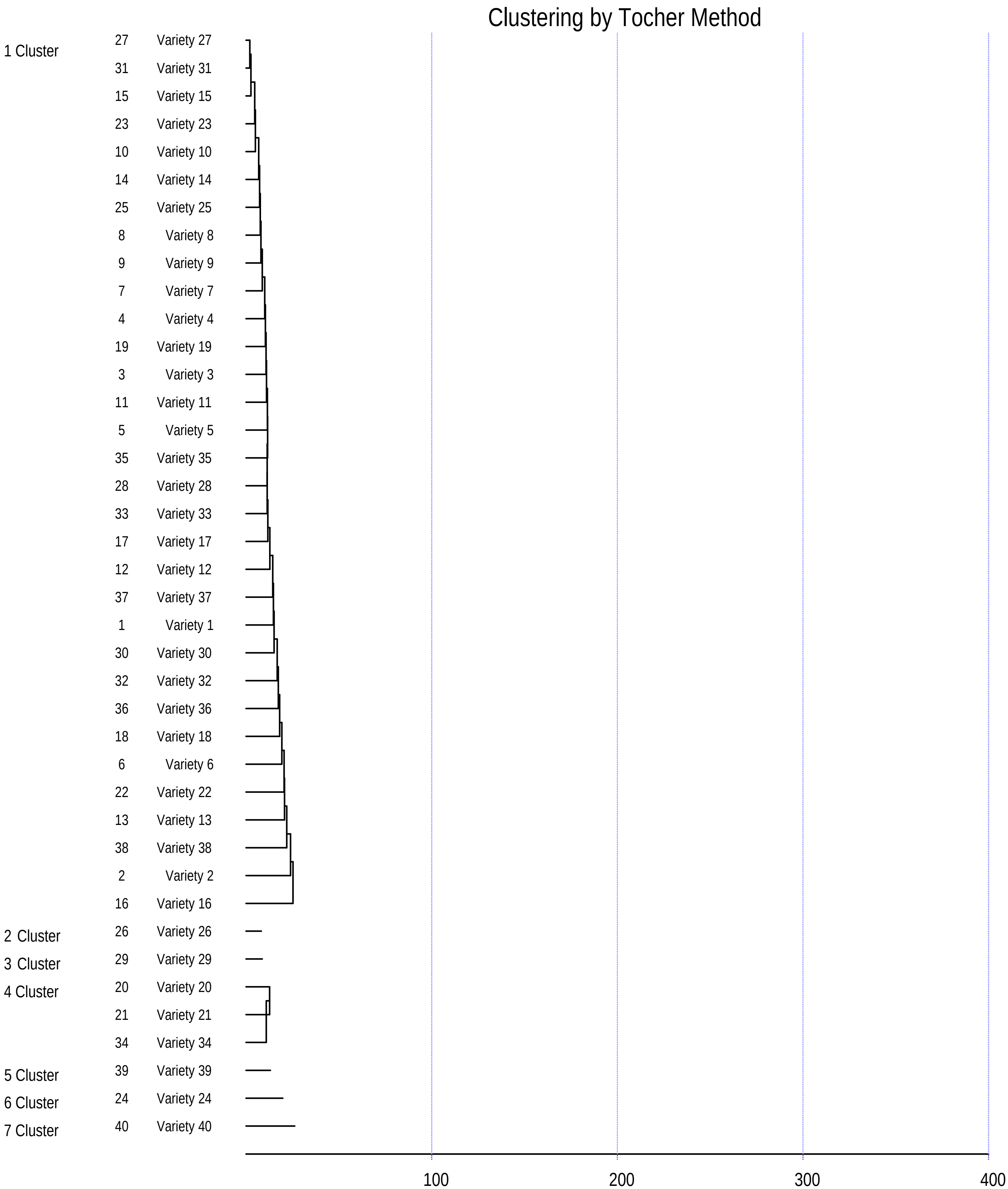

Figure: 4.5 The dendrogram clustering of forty genotypes of rice by Tocher method

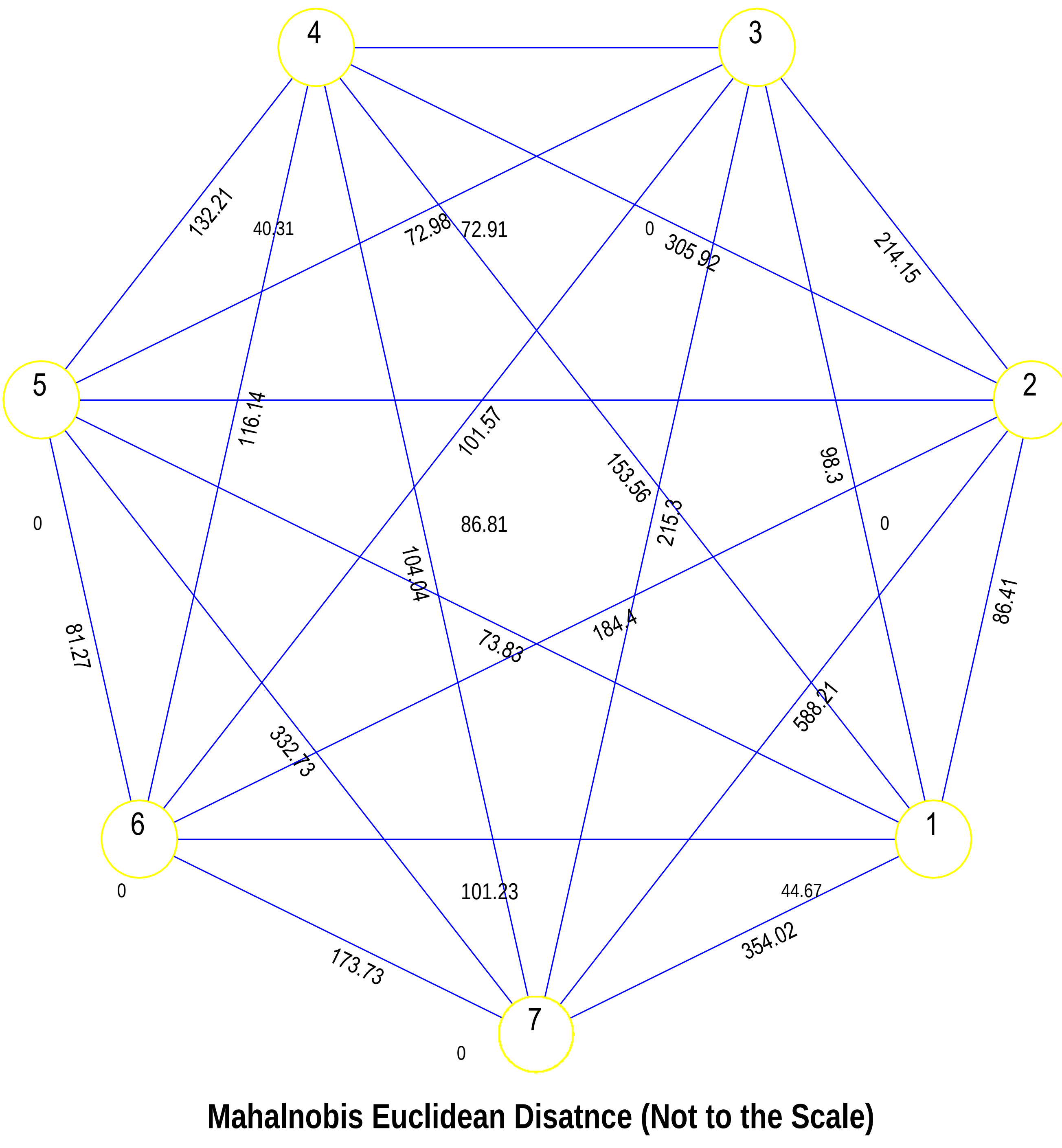

Figure: 4.6 Relative disposition of clusters showing average genetic distance (D^2) between and within them by Tocher methods

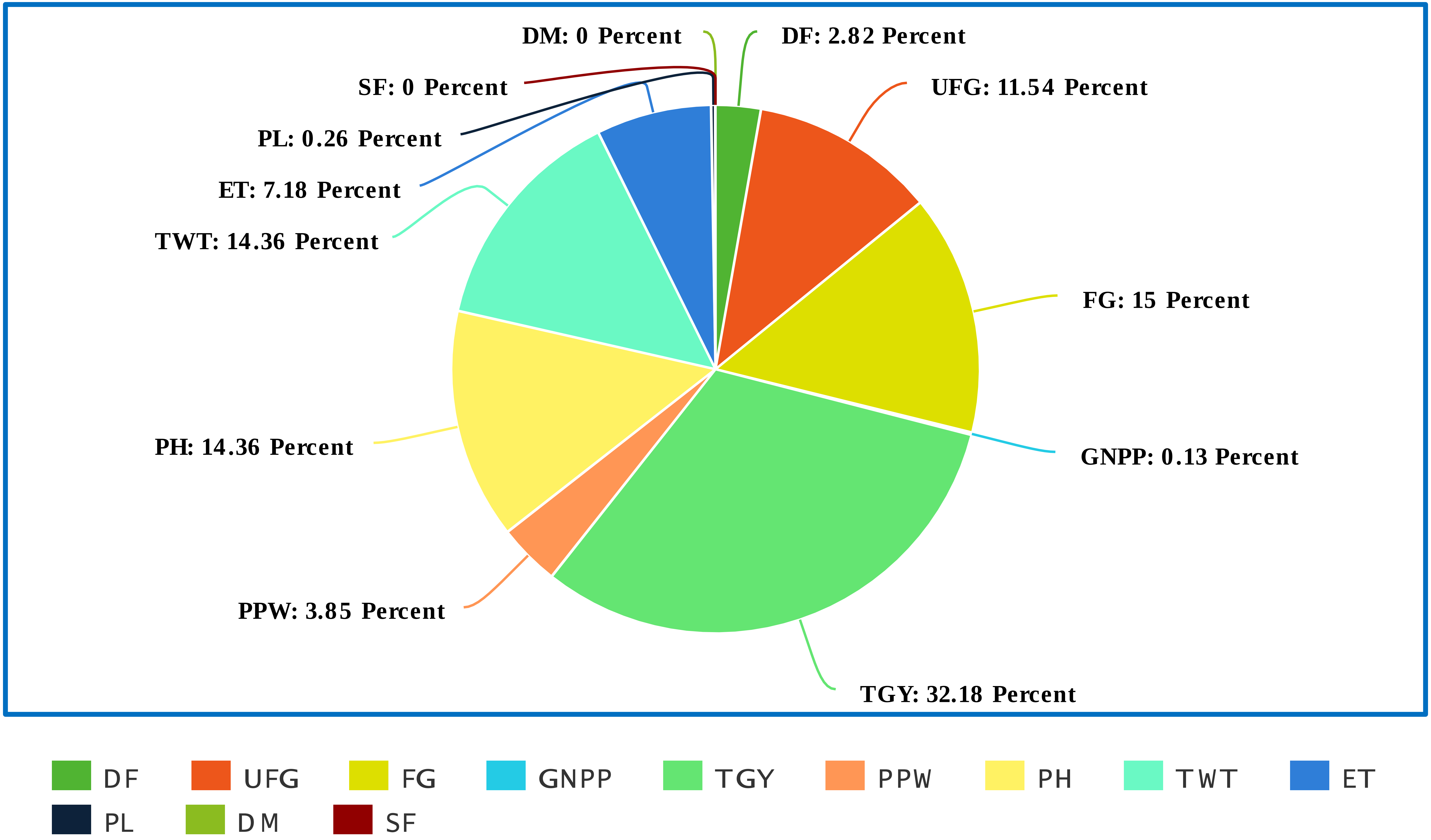

Figure: 4.7 Pie chart for relative contribution of characters toward total diversity

WEEKLY METEOROLOGICAL DATA: VARANASI, YEAR- 2018
DEPARTMENT OF AGRONOMY

Week No.	Month & Date	Rainfall mm	Temperature ^{0}C		R.H. %		Wind Speed km/hr	Sunshine (hours)	Evaporation (mm)
			MAX	MIN	Mor.	Eve.			
1	Jan 1-7	0.0	16.1	6.2	93	69	0.8	0.8	0.7
2	8-14	0.0	19.4	5.9	96	57	1.6	5.7	1.0
3	15-21	0.0	23.1	6.4	94	49	1.3	8.0	1.2
4	22-28	0.0	2.1	7.7	94	60	1.7	7.3	2.1
5	29-04	0.0	24.9	9.1	86	47	2.5	8.8	2.3
6	Feb 05-11	0.0	24.4	9.5	80	38	2.2	7.0	2.5
7	12-18	0.0	24.6	11.8	87	55	2.3	6.7	2.4
8	19-25	0.0	29.6	13.2	90	42	1.0	8.6	2.6
9	26-04	0.0	30.0	14.9	88	43	2.6	9.3	3.5
10	March 05-11	0.0	30.4	13.8	82	36	2.4	7.9	3.9
11	12-18	0.0	33.1	15.7	72	28	2.2	8.5	4.5
12	19-25	0.0	34.1	15.6	73	27	1.8	8.8	4.8
13	26-01	0.0	35.4	16.8	69	24	3.7	9.0	6.6
14	April 02-08	9.4	33.8	20.0	70	42	3.2	7.9	6.4
15	09-15	0.0	34.8	20.2	72	35	2.6	8.8	5.8
16	16-22	0.0	39.0	21.9	55	25	2.2	9.6	7.9
17	23-29	0.0	36.6	20.8	57	31	3.7	9.8	8.2
18	30-06	15.4	34.3	21.9	78	49	5.4	8.8	6.6
19	May 07-13	0.0	36.9	24.0	69	62	3.3	10.1	8.0
20	14-20	0.0	35.2	25.1	73	43	4.4	8.6	7.2
21	21-27	0.0	41.0	27.1	72	29	3.0	9.7	8.2
22	28-03	0.0	36.1	26.3	69	50	4.9	8.4	7.0
23	June 04-10	0.0	36.1	27.5	71	52	3.6		7.4
24	11-17	2.4	41.0	27.3	60	36	6.9	7.1	9.1
25	18-24	0.0	40.4	28.3	63	36	3.6	9.1	8.8
26	25-01	33.3	33.9	26.7	80	61	4.1	4.0	6.1

Week No.	Month & Date	Rainfall mm	Temperature ^{0}C		R.H. %		Wind Spee d km/hr	Sunshine hours	Evaporatio mm
			MAX	MIN	Mor.	Eve.			
27	July 02-08	8.0	35.5	27.9	77	57	3.6	6.4	4.4
28	09-15	11.6	35.5	26.0	83	58	4.4	7.8	5.8
29	16-22	78.4	33.3	25.4	86	66	4.5	4.9	4.4
30	23-29	91.4	28.4	23.6	88	87	2.5	0.3	1.7
31	30-05	86.8	28.1	22.8	93	88	4.2	0.1	1.4
32	Aug 06-12	26.6	31.8	24.7	92	77	2.0	4.8	2.7
33	13-19	20.4	33.3	25.3	88	70	2.4	5.9	2.8
34	20-26	154.8	31.1	24.0	91	81	2.4		2.6
35	27-02	118.4	32.0	24.3	93	77	1.7		2.6
36	Sep 03-09	94.6	30.6	23.6	91	79	2.3		2.4
37	10-16	0.0	32.4	23.6	88	68	2.7		3.8
38	17-23	53.4	32.5	22.8	88	65	3.7		3.1
39	24-30	0.0	33.4	25.9	88	63	1.1		3.5
40	Oct 01-7	0.0	34.2	20.8	83	51	0.8		3.7
41	08-14	0.0	31.0	20.0	89	61			2.9
42	15-21	0.0	33.4	16.5	84	40			2.8
43	22-28	0.0	31.5	14.4	89	41			2.6
44	29-04	0.0	31.1	16.7	91	48			2.3
45	Nov 05-11	0.0	28.2	12.2	87	44			2.0
46	12-18	0.0	29.0	11.7	89	45			1.8
47	19-25	0.0	27.9	10.1	88	44			2.0
48	26-02	0.0	26.4	10.1	93	48			1.5
49	Dec 03-09	0.0	24.8	7.1	94	46			1.5
50	10-16	0.0	24.3	7.9	92	48			1.4
51	17-23	0.0	22.0	5.9	91	47			1.2
52	24-31	0.0	21.9	3.9	87	38			1.7

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