Studies on Genetic Variability, Characters Association and Genetic Divergence among Rice (*Oryza sativa* L.*)* Genotypes

[चावल (*ओराइजा सटाइवा* एल.) के जीन प्रारूपों में आनुवंशिक विभिन्नता, सह–सम्बन्ध और विविधता का अध्ययन]

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Thesis
Master of Science in Agriculture
(Genetics and Plant Breeding)

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Department of Genetics and Plant Breeding
College of Agriculture, Ummedganj, Kota
Agriculture University, Kota (Rajasthan)

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By

Deepak Meena
2020

College of Agriculture, Ummedganj, Kota
Agriculture University, Kota (Rajasthan)

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This is to certify that **Mr. Deepak Meena** student of **Master of Science** in **Agriculture** (**Genetics and Plant Breeding)** had successfully completed the comprehensive examination held on **11-05-2020** as required under the regulation for Post-Graduate Studies.

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Place : Ummedganj (Kota)
Date : **(DEEPAK MEENA)**

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Chapter-I

INTRODUCTION

Rice (*Oryza sativa* L.) is the world's most extensive staple cereal crop after wheat. It is an annual, self pollinated, C_3 crop plant with chromosome number 2n=2x=24. It belongs to the family Poaceae. The rice genus consists of 24 species, in which 22 are wild and two are cultivated *i.e. O. sativa* and *O. glaberrima*. It is originated from South-eastern Asia.

Rice is the primary source of food and calories for about half of the mankind (Khush, 2005) providing staple food for more than 60 per cent of the global population, about 75 per cent of the calories and 55 per cent of the protein intake in their average daily diet. Besides being the chief source of carbohydrate and protein, it provides minerals and dietary fibre also (Verma *et al*. 2006), and is a good source of vitamins like thiamine, riboflavin and niacin. Rice bran oil is used as medicine as well as cooking oil and its straw and bran are important animal feed in many countries. Unlike wheat and corn, rice is almost entirely consumed by humans.

Rice is a short day plant, needs a hot humid climate with average temperature 21^0 to 37^0C, throughout the life cycle of crop. It is grown under variable conditions and production systems. It is the only cereal crop that can grow for long periods of time in standing water to rainfed upland conditions with short span of time.

Asia is known as a 'rice bowl' of the world. Approximately 90 per cent of the world's rice is grown in the Asian continent. India ranks first in area 43.79 million hectare and second in the production 116.42 million tonnes with a productivity of 2650 kg/ ha. **(**Anonymous, 2018-19). Rice grown in almost all the states of India, but major rice producing states fall in the regions of middle and lower genetic plains, as well as the coastal lowlands of peninsular India. Major rice producing states are West Bengal, Utter Pradesh, Andhra Pradesh, Chhattisgarh, Telangana, Punjab, Tamil Nadu and Haryana. Rajasthan occupies an area of 0.199 million hectares with the production of 0.46 million tones and productivity of 2310 kg/ha. (Anonymous, 2018-2019). Rice growing tracts of the state can broadly be divided into four zones. The irrigated zone is humid south eastern plain which covers Kota, Bundi, Baran and Jhalawar districts and served by Chambal canal system. The second important zone is humid/sum-humid southern plain which is comprised of Banswara, Dungarpur, Udaipur, Pratapgarh, Rajasamand, Chittorgarh and Bhilwara. The area in this zone is mostly *rainfed*. The third zone is irrigated northern-western plain consisted of Sriganganagar and Hanumangarh districts. In these districts, rice is grown under irrigated condition in Ghaggar Nali Belt. Besides, the fourth zone is flood prone eastern plain comprised of Bharatpur, Alwar, Karauli and Sawaimadhopur districts where protected irrigation facilities are available during rainy season. Kota region (humid south eastern plain zone) occupies an area of 0.099 million hectare with a production of 0.35 million tones and productivity of 3530 kg/ha (Anonymous, 2018-2019).

Rice consuming population is increasing at an alarming rate, therefore there is need to enhance the yield to meet the rice demand of rapidly growing population. To overcome future food shortage it is direly requisite to develop new varieties which can break the yield ceiling. Among very few options for increasing yield potential of rice, improvement of the genetic potential of the crop cultivars is one of the best approaches.

The success of any crop improvement programme is highly dependent on the efficient manipulation of the genetic variability present in the germplasm and the selection of genotypes with all possible desirable yield and quality contributing traits. Genotypic and different components of variance, heritability and genetic advance are always considered as a parameter for identification of genotypes having broad genetic variability and characters with high heritability to execute effective selection.

Correlation estimates between yield and other characters are useful in selecting desired plant types in designing an effective breeding programme. When change in one variable causes the change on other variable, the variables are said to be correlated. It measures the degree of association, genetic or non-genetic between two or more characters which form the basis for selection**,** whereas path analysis splits the simple correlation between dependent and independent variables into direct and indirect effect. It helps in indirect selection for the traits that shows low heritability due to which direct selection is not fruitful. The knowledge of interrelationship of various components of yield is of paramount importance for a plant breeder for making the decisions regarding selection criteria.

To estimate the degree of divergence in populations at genotypic level and to assess the relative contribution of different characters to the total divergence, multivariate analysis D^2 statistic by Mahalanobis has been used as a powerful tool. It helps the plant breeder in choosing the right parents for breeding programmes. Also it provides a measurement of relative contribution of different components on diversity both in inter and intra-cluster levels and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generation.

Keeping this in view, present investigation was carried out with the following objectives:

1. To estimate genetic variability, heritability and genetic advance for yield and its attributing traits in rice.
2. To assess the character association among the genotypes for yield and its contributing traits in rice.
3. To measure genetic divergence among rice genotypes.

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Chapter-II

REVIEW OF LITERATURE

The present investigation designed to find out the statistical parameters *viz.*, genetic variability, correlation coefficient, path analysis and genetic diversity in 25 genotypes of rice. Hence, the literature pertaining to Genetic variability, character association and genetic divergence among rice (*Oryza sativa* L.) genotypes have been reviewed in this chapter under the following headings

2.1 Genetic variability parameters

2.2 Character association

2.3 Path coefficient analysis

2.4 Genetic divergence

2.1 Genetic variability parameters

The availability of variation in the crop germplasm is the foundation for any improvement programme. Higher the variation, greater is the chance for improvement over base population. Heritability is an index to transmissibility of a character from parents to their offspring. The concept of heritability is important in determining whether the phenotypic differences among the individual are genetically or the result of environmental factors. Genetic advance measures the expected gain from the selection applied in the population. Heritability along with genetic advance gives the best picture of the efficiency of selection.

Ahmadikhah (2012) studied genetic advance, heritability and selection in rice and observed high heritability for most of the traits, while plant height showed a considerable specific heritability and grain yield showed a relatively low specific heritability. The highest genetic advance was obtained for number of productive tillers per plant.

Vanisree *et al.* (2013) assessed rice genotypes and found significant differences for yield, its components and grain quality traits. Effective tillers per plant and filled grain per panicle exhibited highest variability, whereas panicle length, days to 50% flowering, kernel breadth and kernel elongation ratio having low estimates of variability**.**

Bhuvaneswari *et al.* (2015) evaluated F_2 segregating populations of two black rice crosses. Higher genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) recorded for number of productive tillers per plant, numbers of grains per panicle and grain yield per plant, moderate GCV and PCV observed for 1000-grain weight, plant height and days to first flowering and low of GCV and PCV reported for panicle length and days to first flowering in cross I.

Kahani and Hittalmani (2015) estimated coefficients of variability in F_2 segregating populations in rice. The result revealed that high GCV and PCV observed for grain yield per plant and 100-grain weight, whereas high PCV and moderate GCV for straw yield per plant and moderate GCV and PCV recorded for plant height, number of productive tillers per plant, panicle length while, low GCV and PCV for days to 50 per cent flowering and days to maturity.

Rahman *et al.* (2015) studied genetic variation among four parents and their 12 F_2 populations and found that Kashmir-Basmati/Kangni-27 F_2 population took minimum days to heading (100 days) while the Dilrosh/Kashmir-Basmati F_2 population displayed minimum days to maturity (135 days) The longest panicles (29.5cm) were observed for Kashmir-Basmati/Dilrosh while Dilrosh/Kashmir-Basmati population showed the highest number of primary (12.4) and secondary (35.9) branches per panicle.

Satyapal *et al.* (2015) observed high GCV and PCV for sterile spikelets per panicle, pollen fertility per cent, fertile spikelets per panicle, spikelet fertility per cent, grain yield per plant, harvest index and biological yield per plant in rice genotypes. High heritability coupled with high genetic advance was reported in fertile spikelet per panicle, sterile spikelets per panicle, pollen fertility %, grain yield per plant, productive tillers per plant, biological yield per plant, spikelet fertility %, 1000-grain weight, number of spikelet per panicle, and harvest index, suggesting that simple selection could be successful for improvement.

Savitha and Ushakumari (2015) carried out an investigation in F_3 population to estimate the genetic advance and heritability in rice genotypes. The results revealed that high heritability along with high genetic advance were observed for kernel length and kernel breadth while, high heritability with moderate genetic advance recorded for kernel L/B ratio.

Shrivasatava *et al.* (2015) observed the extent of variability and genetic parameters for yield and its components characters in rice. High GCV and PCV were recorded for seed yield per plant, whereas high heritability coupled with high genetic advance as percent of mean were observed for seed yield per plant and most of the other contributing characters indicating the additive gene effects in the genetic control of these traits and can be improved by simple selection in the present breeding material.

Tiwari (2015) evaluated ten diverse genotypes of rice for quantitative characters and reported that amount of variability GCV varied from 5.95 (Number of leaves per tiller) to 17.40 (grain yield per plant). High estimates of genetic advance were found for plant height, days to maturity, days to 50 per cent flowering and total biological yield per plant. However, high heritability estimates along with high predicted genetic advance recorded for plant height, days to maturity, days to 50 per cent flowering and numbers of spikelets per panicle.

Tuhina *et al*. (2015) observed highest phenotypic and genotypic coefficient of variation for the numbers of filled grains per panicle and yield per plant in rice genotypes. The high heritability estimates recorded for photosynthetic rate, transpiration rate, stomatal conductance, intercellular CO_2, and number of filled grains per panicle and yields per plant.

Anis *et al*. (2016) evaluated twenty promising lines of rice. The result revealed that high genotype coefficient of variation and phenotypic coefficient of variation was recorded for number of filled grains per panicle. The phenotypic variance was higher than the corresponding genotypic variance for all the traits. Estimation of heritability ranged from 49.16 to 99.52 per cent for number of panicle per plant, number of filled grain per panicle, grain yield, panicle length, plant height, hulling per cent and milling per cent. High heritability coupled with high genetic advance was observed for growing period and plant height.

Bagati *et al.* (2016) carried out study on 140 recombinant inbred lines of rice and reported that yield and associated traits *viz.*, tillering ability, spikelet fertility percentage, number of grains per panicle and 1000-grain weight showed high heritability (more than 80%) indicating that these traits would respond to selection.

Islam *et al.* (2016) investigated genetic variability among aromatic and fine local rice genotype. High heritability along with high genetic advance was observed for flag leaf area, secondary branches per panicle, filled grains per panicle, grain length breadth ratio and 1000-grains weight.

Konate *et al.* (2016) examined recombinant inbred lines of rice, their parents and check variety for genetic advance and heritability. Result showed high heritability estimates for days of 50 per cent flowering, plant height and grain yield per plant suggesting that the traits were primarily under genetic control. However, high heritability combined with moderate genetic advance recorded for day to 50 per cent flowering and grain yield per plant could be due to non-additive gene effect.

Kumar and Verma (2016) estimated heritability and genetic advance for yield and its contributing characters in rice and depicted that high estimate of heritability in broad sense was recorded for majority of the characters. High heritability coupled with high genetic advance were observed for characters *viz.,* 1000-grain weight, grain yield per plant, days to 50 per cent flowering, days to maturity and L/B ratio which indicates the involvement of additive gene action.

Mahantashivayogayya *et al*. (2016) conducted an experiment to assess the genetic variability for yield and yield component characters in mutant lines of rice. Genetic variability parameters showed that phenotypic coefficient of variation was higher than the respective genotypic coefficient of variation in days to 50% flowering, plant height, grain yield per plant, number of filled grains per panicle and all other characters.

Mallimar *et al.* (2016) evaluated F_3 generation of rice for heritability and genetic advance for yield and its attributing traits and revealed that high heritability coupled with high genetic advance as per cent of mean were found for plant height, number of grains per panicle, L/B ratio and grain yield per plant.

Rukminidevi *et al.* (2016) studied heritability and genetic advance in rice genotypes for all the yield component traits and recorded high magnitude of heritability values with high genetic advance as percent of mean for productive tillers per plant, plant height, number of grains per panicle, test weight, grain yield per plant and L/B ratio.

Sala and Shanthi (2016) assessed F_2 population of eight crosses of rice with 160 single plants to estimate the variability. The results showed that PCV value in general was higher than GCV for various characters studied. The high GCV and PCV values were recorded for grain yield per plant followed by number of productive tillers per plant.

Devi *et al.* (2017) investigated on 27 rice genotypes and found the higher magnitude of PCV and GCV for grain yield per plant and filled seeds per panicle indicate possibility of genetic improvement through direct selection.

Harsha *et al*. (2017) evaluated twenty-nine rice genotypes to determine genetic variability and the nature of association among different yield attributes and their direct and indirect contribution towards yield. Estimates of PCV and GCV were higher for the number of effective tillers per plant, flag leaf area, yields per plant and for test weight. Small differences between GCV and PCV were recorded for all the characters studied which indicated less influence of environment on these characters. The higher estimates of broad sense heritability observed for leaf length, test weight, days to 50 per cent flowering, leaf width, days to maturity and least for panicle length.

Prasad *et al*. (2017) evaluated fifty boro rice genotypes for variability, heritability and genetic advance for yield and yield contributing characters and observed high GCV and PCV values for number of filled grains per panicle, number of unfilled grains per panicle and grain yield per plant.

Rohit *et al.* (2017) assessed 35 diverse genotypes of rice with two checks for quantitative traits. The variability studies indicated that high PCV and GCV were observed for biological yield per plant. High heritability in broad sense was recorded for plant height followed by days to 50 per cent flowering, biological yield per plant, days to maturity, grain yield per plant test weight and spikelet per panicle whereas, flag leaf area per plant, spikelet fertility and harvest index showed moderate heritability.

Sahu *et al*. (2017) evaluated indigenous rice land races to estimate the components of genetic variability for grain quality traits. High heritability with high genetic advance as percent of mean were observed for all the grain quality traits expects hulling percent and milling percent. High PCV and GCV were observed for alkali spreading value.

Adhikari *et al.* (2018) estimated the genotypic and phenotypic variability, heritability, genetic advance for grain yield and yield associated traits using 26 genotypes of rice. Analysis of variance revealed the existence of significant difference for days to flowering, maturity, plant height, panicle length, test weight and grain yield. High heritability was estimated for days to flowering, maturity, 1000-grain weight and plant height.

Bagudam *et al.* (2018) investigated the extent of genetic variability in 46 genotypes of rice. The heritability and genetic advance estimates were moderate for panicle length and high for all the other traits *viz.*, days to 50 per cent 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, selection of these characters would likely be effective for improvement of these traits.

Iqbal *et al.* (2018) evaluated advanced lines of green super rice for genetic variability, heritability and genetic advance. Result revealed that phenotypic coefficient of variation was found slightly higher than genotypic coefficient of variation indicating negligible influence of environment on the yield and its components. Similarly, high heritability coupled with genetic advance was observed for all traits except for panicle length which indicates that selection can be used for improvement of these traits.

Ismaeel (2018) assessed fourteen parents and their ten F_1 hybrids of rice. Higher phenotypic and genotypic coefficients of variation were observed for grains per panicle and grain yield per plant. High heritability values were recorded for all the studied traits.

Kishor *et al.* (2018) studied seventy rice genotypes for genetic variability and heritability for yield and grain quality characters. High heritability combined with high genetic advance was shown by days to 50 per cent flowering and plant height.

Mamata *et al.* (2018) assessed F_2 populations of thirty-eight rice genotypes to estimate the variability, heritability, genetic advance and genetic advance as percentage of mean. High PCV and GCV values were recorded for grain yield per plant while low PCV and GCV were observed for 1000-grains weight and panicle length. Plant height, spikelet fertility, harvest index and grain yield per plant had high heritability coupled with high genetic advance as per cent of mean.

Meena *et al.* (2018) evaluated thirty-eight rice genotypes for yield and its contributing characters. Magnitude of PCV was found higher than GCV indicating more environmental fluctuations. Days to 50 per cent flowering followed by days to maturity showed highest heritability.

Monalisha and Das (2018) assessed seventeen elite rice hybrids to study genetic variability. The magnitude of genetic variance was high for most of traits except panicle length, panicle number, 1000-grain weight, harvest index and grain yield per plant. The higher magnitude of genetic variance for plant height, grain number, fertility per cent and plot yield, which have bearing on yield may be sorted out as important selection criteria for realization of higher productivity in hybrid rice.

Kumar *et al.* (2019) assessed twelve rice genotypes for evaluation of genetic variability and reported that analysis of variance revealed highly significant differences for all the six characters *viz.,* days to 50 per cent flowering, days to maturity, panicle length, plant height, number of panicle per meter square and grain yield. The magnitude of PCV was slightly higher than GCV for the traits *viz.*, days to 50 per cent flowering, days to maturity, plant height, number of panicles per meter square and grain yield indicating the considerable influence of the environment on the expression of the traits. The estimates of PCV and GCV were moderate for the traits *viz.,* number of panicles per meter square and grain yield indicating the influence of the environment rather than the genotype alone.

Kumari *et al*. (2019) investigated 240 mutant lines of rice for genetic variability. Higher magnitude of phenotypic coefficient of variation, genotypic coefficient of variation, 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 and Kumara (2019) assessed sixty-four rice genotypes for evaluation of genetic variability, heritability and genetic advance for grain yield. The analysis of variance revealed statistically significant differences ($p<0.05$) indicating the existence of genetic variability among the genotypes for all the traits studied. The highest heritability was recorded for days to 50 per cent flowering and plant height followed by yield kg/ha and panicles per meter square. High to medium heritability coupled with high GCV and high genetic advance as percentage of means were exhibited for plant height, panicles per square meter. High genetic advances as per cent of means were recorded by yield kg per hectare, panicles per square meter, plant height and days to 50 per cent flowering.

Tiwari *et al*. (2019) evaluated seven genotypes of rice for study of genetic variability. 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 rained environments.

2.2 Character association

Correlation coefficient is a statistical measure which is used to find out the degree and direction of relationship between two are more variable (Galton, 1888). This concept of correlation was later on elaborated and discussed by Fisher (1918) and Wright (1921) for plant breeding programmes. Some of the earlier reports of correlation coefficient analysis in rice have been reviewed as follows

Bhadru *et al.* (2011) studied that plant height, productivity per day, filled grains per panicle, days to 50 per cent flowering and panicle weight had a significant positive association with yield and also had a positive direct effect on yield at both phenotypic and genotypic levels.

Rajamadhan *et al*. (2011) evaluated on thirty-three genotypes of rice and observed that grain yield per plant exhibited positive and significant association with number of productive tillers, panicle length, number of grains per panicle, grain breadth and 1000-grains weight. The secondary trait panicle length showed significant positive association with number of grains per panicle, 1000-grain weight and grain yield, suggesting that selection based on this trait will be fruitful for enhancing grain yield.

Bhadru and Ramesha (2012) assessed sixty-eight hybrids, twenty-one parents and four checks of rice and found plant height, panicle length, productive tillers per plant, productivity per day and filled grains per panicle exhibited significant positive association with grain yield per plant and indirect association themselves at both genotypic and phenotypic levels.

Dhurai *et al*. (2016) estimated correlation coefficients for grain yield and its contributing traits in thirty-two rice genotypes. Results revealed significantly positive association of grain yield per plant with harvest index, days to maturity and number of grains per panicle.

Mishu *et al*. (2016) evaluated six aromatic varieties of rice and found that yield has positive significant correlation with days to maturity, spikelet length and 1000-seed weight and negative correlation with plant height.

Edukondalu *et al*. (2017) assessed 40 rice genotypes for 15 characters and reported that magnitudes of genotypic correlation were found to be higher than phenotypic correlations. The results indicated that grain yield per plant showed significant positive association with number of tillers per plant, panicle length and milling percentage.

Gour *et al.* (2017) assessed eighty-three genotypes of rice and reported that higher genotypic correlation coefficients than corresponding phenotypic correlation coefficients indicating a low influence of environmental factors and relative stability of the eighty-three rice genotypes. Panicle weight per plant followed by biological yield per plant, number of tillers per plant, filled spikelets per plant, harvest index and 1000-seed weight exhibited significant positive association with seed yield per plant indicating the importance of these traits as selection criteria in succeeding generations for yield improvement.

Jan *et al.* (2017) studied thirty-five rice genotypes and reported that harvest index showed significantly positive correlation with grain yield per hill followed by plant height, while days to 50 per cent flowering showed significant negative correlation with grain yield per hill.

Limbani *et al.* (2017) evaluated seventy-two genotypes of upland rice and found that grain yield per plot showed positive and highly significant association with harvest index, number of effective tiller per plant, milling percentage, number of filled grains per panicle and plant height while it showed highly significant but negative correlation with number of non-effective tillers per plot and days to 50 per cent flowering at genotypic as well as phenotypic levels.

Priya *et al.* (2017) evaluated 40 rice genotypes to find out characters association. The result indicated that traits like productive tillers per plant, number of grains per panicle, test weight, panicle length, days to maturity, kernel breadth, plant height, days to 50 per cent flowering and kernel length showed significant positive association with grain yield per plant at phenotypic level.

Sangare *et al.* (2017) estimated that plant height showed moderate to high significant positive phenotypic correlation with flowering time, number of grains per panicle and grain yield, which suggests that high yielding and late flowering rice varieties could be developed by indirectly selecting for taller plants. Plant height exhibited a negative correlation with number of tillers per plant and number of panicle in both phenotypic and genotypic level suggesting that selection for short genotypes would result in developing varieties with a higher number of tillers and panicles.

Kumar and Sonali (2018) conducted an experiment with ninety-four local landraces of rice and three popular standard checks of rice and found that grain yield per plant had positive significant correlation with total number of filled grains per panicle, total number of grains per panicle, plant height and number of effective tiller per plant, harvest index, test weight, flag leaf length and days to maturity.

Meena *et al.* (2018) studied correlation analysis in thirty-eight rice genotypes and concluded that days to 50 per cent flowering, number of effective tillers, panicle length, filled grain per panicle showed positive association with the grain yield.

Vengatesh and Govindarasu (2018) reported significant positive genotypic correlations of grain yield for root number at 15 cm spacing or depth. The characters *viz.*, root length, leaf area index, panicle number, panicle weight and grain weight would be the appropriate selection parameters for improvement of grain yield under aerobic rice system as these traits recorded strong positive correlation along with high magnitude of direct influence on grain yield.

Bhardwaj *et al.* (2019) found that amylose content in 140 recombinant inbred lines (RILs) of basmati rice showed a positive and significant correlation with grain length and grain breadth whereas it was found to be negatively correlated with grain length to grain breadth ratio.

2.3 Path coefficient analysis

Path coefficient is defined as the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect. It is simply a standardized partial regression coefficient analysis which may be useful in choosing the characters that have direct and indirect effect on yield.

The correlation coefficient provides information about the degree of association between two characters. However, it is now known that almost all characters are polygenic and almost all genes are pleiotropic in action such that each gene, apart from its direct contribution to a particular character contributes to several other characters also. Therefore, correlation coefficient alone would not provide a clear picture about the contribution of a particular character. Path coefficient analysis splits the correlation coefficient into the measures of direct and indirect effects. It measures the direct and indirect contribution of independent variables on dependent variable. In selection programme, when less variables are considered, correlation study can serve the purpose. However, when the number of variables increases the situation become complex, therefore, overcoming this complexity, path analysis is valuable in the sense that through this technique, it becomes possible to judge relative contribution of various characters towards grain yield in terms of direct and indirect effects. The analysis of correlation coefficient along with information on path coefficient helps considerably in identification of suitable characters for yield enhancement. Path analysis was initially suggested by Wright (1921) who gave the concept and methodology of path analysis but was applied for the first time in plant breeding by Dewey and Lu (1959).

Ghosal *et al.* (2010) evaluated 18 advanced breeding lines of rice for yield and yield contributing characters and observed that effective tillers/m², test weight (g) and growth duration (days) had higher direct effects on yield (t/ha).

Nandan and Sweta (2014) evaluated 33 rice genotypes for identifying their efficiency with respect to yield and quality traits. The result of path analysis indicated that the number of grains per panicle had maximum direct effect on grain yield per plant followed by kernel length after cooking, days to 50 per cent flowering, hulling percentage, plant height, harvest index and kernel breadth after cooking.

Khare *et al.* (2015) assessed sixty upland rice germplasm accessions and reported that the highest positive direct effect on grain yield by fertile spikelet per panicle, total number of grains per panicle, plant height and days to 50 per cent flowering in sixty upland rice germplasm.

Abdala *et al.* (2016) observed that paddy grain length has low direct and positive effect on brown grain length. The direct effect of brown rice width and brown grain shape on brown grain length was high and positive showing that these characters have a direct effect and influence on brown grain length thus indicating their importance in grain rice quality improvement.

Nayak *et al.* (2016) evaluated 25 rice germplasm accessions and found that panicle length, plant height, days to flowering and number of effective panicle bearing tillers per plant had direct positive effect on grain yield per plant.

Sameera *et al.* (2016) studied twenty-five rice varieties and recorded that number of tillers per plant, productive tillers per plant and number of filled grains per panicle showed high direct effect on grain yield per plant, whereas high indirect effects observed through productive tillers per plant.

Gunasekaran *et al.* (2017) evaluated nine rice genotypes for 11 agronomic and quality traits. The results revealed that number of productive tiller per plant and 1000-grain weight showed direct and indirect effect on grain yield per plant.

Hijam *et al.* (2017) carried out an experiment with fifty genotypes of rice and observed that day to 50 per cent flowering, number of effective tillers per plant, filled grains per panicle, grain breadth, grain, L/B ratio and harvest index had positive direct effect on yield.

Jan *et al.* (2017) studied the direct and indirect effect of 14 agro-morphological traits on yield among 35 rice genotypes. The result revealed that at genotypic level flag leaf length showed high direct positive effect with grain yield per hill followed by flag leaf width while at phenotypic level flag leaf area showed maximum positive direct effect with grain yield per hill followed by harvest index. Days to maturity and flag leaf width showed highest negative direct effect on grain yield per hill. Lowest negative direct effect was shown by flag leaf length, panicle length and number of filled grains.

Lakshmi *et al*. (2017) evaluated F_7 generation of aromatic rice genotype to study the direct and indirect effect of yield contributing characters on yield. The result revealed that kernel length exert the highest direct effect on grain yield followed by number of filled grains per panicle, 1000-grain weight, number of productive tillers per hill and plant height.

Priya *et al.* (2017) assessed forty genotypes to determine the magnitude of direct and indirect effect of yield component trait on grain yield of rice. The result revealed that kernel L/B ratio, productive tiller per plant, grain per panicle, test weight, days to maturity and days to 50 per cent flowering showed true relationship with grain yield per plant by establishing had highly significant positive direct effect in grain yield.

Rawte and Saxena (2017) evaluated forty-eight rice genotypes and reported that kernel length had the highest positive direct effect on grain yield followed by length breadth ratio after cooking, width of milled grain, elongation index and gel consistency and concluded that genetic improvement of grain quality in rice is admissible by selecting characters having high positive correlation and positive direct effect on grain yield.

Sowjanya *et al.* (2017) observed in F_3 segregating populations derived from MAS145 X MAS946-1 and IR64 × IM 192 crosses of rice and indicated harvest index, plant height at 30 days after transplanting, total numbers of tillers per plant, days to 50 per cent flowering exerted maximum positive direct effect on grain yield per plant, Therefore, during selection main attention need to be given for traits like plant height, productive tillers per plant, panicle weight, panicle length and harvest index.

Sowmiya and Venkatesan (2017) studied path coefficient analysis in 48 rice genotypes for nine characters. The result revealed that maximum direct effect on grain yield was exhibited by number of panicle per plant.

Gayathri (2018) studied path analysis in 25 rice varieties and observed that 1000-seed weight has maximum positive direct effect on yield followed by panicle length along with high positive association thus, concluded that selection of these traits could be useful in improving yield.

Yadav and Suresh (2018) evaluated in sixteen rice genotypes and found that yield components such as plant height, flag leaf width, flag leaf length, tillers per plant, panicles per plant, panicle length, number of spikelets per panicles, days to maturity, biological yield, harvest index, test weight had a direct effect on yield. An overall analysis of path coefficient suggested that panicles per plant, tillers per plant, number of spikelets per plant, biological yield and plan height should be given the maximum consideration for yield improvement and appropriate selection indices should be formulated using these traits.

2.4 Genetic divergence

The amount of diversity present in the crop decides the success of crop improvement programme with selected objectives. Composition and assessment of divergence in the germplasm is necessary to know the spectrum of diversity. Clustering of genotypes following the tocher's method as described by Rao (1952) laid to formation of six clusters in the present study. In the present study, 25 genotypes of rice for 10 important quantitative characters were studied for their genetic diversity by multivariate D^2 statistic as per given by Mahalanobis (1936).

Bose *et al*. (2011) studied genetic divergence in 22 aerobic rice varieties using Mahalanobis D^2 statistics. The cultivars were grouped into 6 clusters. Cluster IV and VI showed maximum inter-cluster distance, while cluster II exhibited maximum intra-cluster distance. The traits like days to 50 per cent flowering, 1000-grain weight, plant height, grain length and grain breadth were the major contributors to the genetic divergence.

Chaturvedi *et al.* (2011) assessed the nature and magnitude of genetic divergence in 35 rice genotypes by using Mahalanobis D^2 and grouped them into eight clusters. The panicle weight followed by effective tillers per plant and grain yield per plant contributed maximum towards divergence. The genotypes belonging to cluster VII, clusters II and VIII respectively could be utilized as diverse parent in hybridization program with the genotypes to achieve greater variability in the segregating generations.

Dutta *et al*. (2011) studied the genetic divergence in 62 aromatic rice genotypes by using Mahalanobis D^2 statistics and grouped them into eight clusters where, cluster I was largest containing 38 genotypes followed by cluster II with 9 genotypes.

Chouhan *et al.* (2014) evaluated 35 wild germplasm accessions and clustered them into six groups, the cluster III contained the highest 12 accession and cluster I and IV comprised 11 and seven accessions respectively; while cluster II and VI have two accessions each and cluster V was mono- genotypic. The maximum distance was observed between clusters V and VI followed by cluster II and V indicating wider genetic diversity between germplasm accessions.

Jha *et al.* (2014) assessed in forty-four rice genotypes and found that spikelets per panicle followed by fertile grains per panicle had the highest contributions towards the total genetic divergence. Plant height, 1000-grain weight and flag leaf area had more or less equal contributions toward divergence.

Kumar *et al*. (2014) estimated genetic divergence in 134 rice germplasm and observed higher order of divergence between cluster IV and V followed by cluster II and V. The highest intra-cluster distance were observed among the genotypes in cluster IV (12.19) followed by cluster III (11.03) and cluster V (10.90), indicating existence of wide genetic divergence among genotypes. Number of filled grains per panicle contributed highest towards divergence.

Ramanjaneyulu *et* al. (2014) evaluated 10 rice genotypes for genetic divergence under aerobic condition. The maximum intra-cluster distance was observed in cluster III. The trait test weight exhibit maximum contribution to total genetic divergence followed by grain yield, numbers of grains per spikelet, straw yield and spikelet length.

Sandhya *et al.* (2014) studied 32 elite rice genotypes to identify diversity among genotypes using Mahalanobis D^2 statistics and grouped all the genotypes into 6 clusters. Cluster I and VI was the largest cluster with 8 genotypes followed by cluster IV with 6 genotypes. The maximum inter-cluster distance was recorded between clusters V and VI and the maximum intra-cluster distance was found in cluster IV followed by I. The characters like number of spikelets per panicle, biological yield per plant, test weight, harvest index and days to 50 per cent flowering contributed maximum towards genetic divergence. Hence these characters could be given due importance for selection of genotypes for further crop improvement program.

Beevi and venkatsen (2015) studied genetic diversity among 60 rice genotypes which were grouped into six clusters. Cluster I was found to be largest with 50 genotypes followed by cluster II with four genotype and clusters IV and V with two genotypes each while cluster III and VI are mono-genotypic in nature.

Kumar (2015) carried out an investigation to assess the nature and magnitude of genetic diversity in 57 genotypes of rice using Mahalanobis D^2 statistics. Genotypes were grouped into 13 clusters. Clusters II and IV was the largest cluster containing 14 genotypes each followed by cluster III with 11 genotypes. The pattern of distribution of genotypes within different clusters was random and independent of geographical origin or region of adaptation. The characters like days to maturity (34.21%), days to flowering (27.44%), grain length (19.55%) and grain width (12.16%) contributing maximum towards diversity. Hence, these characters can be given consideration for selection of genotypes for future breeding programmes.

Kumar *et al.* (2015) performed genetic divergence analysis among 40 genotypes of rice for 12 quantitative characters and grouped them into eight clusters by using D^2 statistics. Cluster I was very large comprising 24 genotypes followed by clusters II with 10 genotypes, while clusters III to VIII were solitary clusters. The maximum inter cluster distance was observed between cluster VI and VII followed by cluster VII and VIII which served as potential source to select parents for hybridization.

Khare *et al.* (2015) evaluated sixty rice accessions for 10 quantitative traits and grouped them into seven clusters, the cluster III contained highest 14 accessions, followed by cluster I comprising 11 accessions and cluster VI, VII, V, IV and II have 9,8,7,6, and 5 accessions, respectively.

Bharathi *et al.* (2016) estimated genetic divergence among 32 rice genotypes using D^2 statistics for 10 characters and grouped into 9 clusters containing 1 to 12 genotypes. The random distribution of genotypes indicated the absence of parallelism between geographical diversity and genetic diversity.

Chandramohan *et al*. (2016) studied genetic divergence among 44 genotypes of rice using D^2 statistics and grouped them into 11 clusters. Maximum inter-cluster distance was observed in genotypes of cluster IV and V followed by V and IX. Parents of these clusters can be used further for hybridization programme.

Umesh *et al*. (2016) assessed the genetic divergence among 24 genotypes of basmati rice and grouped them into five different clusters based on the interaction in genetic distances. The maximum intra-cluster distance was found in cluster V followed by cluster I. The highest inter-cluster distance was found between clusters IV and V.

Ashok *et al.* (2017) evaluated 64 rice genotypes and grouped them into 9 clusters. Maximum numbers of genotypes (30) in cluster I.

Lahari *et al.* (2017) studied 49 genotypes of rice and grouped them into eight clusters. Cluster II had highest mean values for number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, grain yield per plant and straw yield per plant. The traits like days to 50 per cent flowering, days to maturity, plant height, number of filled grains per panicle and grain yield per plant had contributed 95.24 percent towards the total genetic divergence among the genotypes.

Sarawgi *et al*. (2017) grouped rice germplasm accessions into 8 clusters. Cluster VIII had highest mean value for 100 grain weight. Cluster II had highest mean value for panicle length, effective tillers per plant and L/B ratio. The cluster II showed highest grain yield per plant and effective tillers. These clusters can be utilized in the hybridization programme for obtaining desirable transgressive segregates.

Shaikh *et al.* (2017) grouped 40 rice genotypes into 6 clusters. The highest inter cluster distance was recorded between Clusters VI and IV hence, the genotypes from these clusters may be used in hybridization program. Maximum contribution towards genetic divergence was recorded for yield per plant.

Singh *et al.* (2017) evaluated 20 rice landraces and grouped them into five different clusters based on inter and intra-cluster genetic distances. Clustering pattern indicated that 13 out of 20 genotypes belong to the same cluster *i.e.* cluster I. On the other hand, four genotypes belong to cluster II, followed by cluster III, IV and V consists of one genotype each. Among all the characters, biomass contributed the maximum to the diversity by taking first rank, followed by grain yield per plant, harvest index, grain yield per plot and kernel breadth.

Graham-Acquaah *et al.* (2018) evaluated forty-five rice varieties and grouped them into five clusters, to know the extent of diversity. Paddy yield and chalkiness showing 68 per cent of total variation. Group I showed high head rice and low chalkiness for better breeding program varieties.

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Chapter-III

MATERIALS AND METHODS

The present investigation entitled "Studies on Genetic Variability, Characters Association and Genetic Divergence among Rice (*Oryza sativa* L.*)* Genotypes" was conducted during *Kharif* 2019. The techniques followed and materials used during the course of investigation are described under following sub heads:

3.1 Experimental site and location

The experiment was carried out at Agricultural Research Station, Ummedganj, Kota, Agriculture University Kota, Rajasthan. It is situated at the north western part of India and lies between 23°30' and 30°11' North latitude and 69°29' and 78°17' East longitude. It has an average elevation of 271 meter (889 ft).

3.2 Climate and weather condition

Kota region has a semi-arid climate (Koppen climate classification *BSh*) with high temperature remain throughout the year. The average temperature varies from 40 to 48 °C in May and June. The monsoon season follows with comparatively lower temperatures, but higher humidity and frequent, torrential downpours. The average rainfall is about 735-1005 mm which is most commonly received during July to September. The standard month-wise meteorological data for the period of this investigation recorded at the Meteorological Observatory, Agricultural Research Station, Ummedganj, Agriculture University, Kota are presented in Table. 3.1.

Table 3.1 Month-wise meteorological data recorded at Agricultural Research Station, Ummedganj, Kota during *Kharif* 2019

Month	**Rainfall (mm)**	**Temperature (^oC)**		**Relative Humidity (%)**	
		Maximum	**Minimum**	**Maximum**	**Minimum**
June	58.0	41.25	28.37	58.37	39.50
July	489.90	33.65	25.00	79.37	71.80
August	682.50	39.65	30.15	84.42	75.12
September	172.70	31.45	24.05	89.12	78.66
October	0.00	32.32	21.02	85.87	74.47
November	0.00	31.08	21.86	85.77	84.10

3.3 Experimental material

The experimental materials for the present study consisted of 25 rice genotypes which were collected from AICRP on rice and Agriculture Research Station, Ummedganj, Kota, Rajasthan. The details of genotypes used for study are presented in the table 3.2.

Table 3.2: List of twenty-five rice genotypes used in the study.

Sr. No.	Name of the genotypes	Source
1	RSK-1155-2-4-1	ARS, KOTA
2	RSK-1155-3-3-1	ARS, KOTA
3	RSK-1157-4-5-1	ARS, KOTA
4	RSK-1157-6-3-1	ARS, KOTA
5	RSK-1157-9-2-2	ARS, KOTA
6	RSK-1161-1-1	ARS, KOTA
7	RSK-1163-8-1	ARS, KOTA
8	RSK-1165-4-2	ARS, KOTA
9	RSK-1165-4-3	ARS, KOTA
10	RNSK-1167-11-1	ARS, KOTA
11	RNSK-1168-2-1	ARS, KOTA
12	RSK-1164-1-1	ARS, KOTA
13	RSK-1172-1-1	ARS, KOTA
14	RSK-1221-1-1	ARS, KOTA
15	RSK-1162-8-1	ARS, KOTA
16	RSK-1164-6-1	ARS, KOTA
17	RSK-1164-6-2	ARS, KOTA
18	RSK-1165-3-1	ARS, KOTA
19	RSK-1165-3-2	ARS, KOTA
20	RNSK-1167-5-1	ARS, KOTA
21	RSK-1155-6-1-2	ARS, KOTA
22	RSK-1155-6-3-1	ARS, KOTA
23	P-1121	IARI NEW DELHI
24	P-2511	IARI NEW DELHI
25	P-1460	IARI NEW DELHI

3.4 Date of sowing and transplanting

All the 25 genotypes were sown in nursery on 20 June, 2019 and healthy seedling of 24 days old were transplanted in Randomized Block Design with three replications on 14 July, 2019. Each genotype transplanted in plot of 10 m^2 having ten rows of five meter length. Row to row and plant to plant distance was maintained 20 cm. and 10 cm. respectively. The recommended agronomic practices and plant protection measures were followed to raise a healthy crop.

3.4.1 Observations recorded

Observations were recorded on ten randomly selected plants for 10 quantitative characters from each plot in each replication avoiding border plant. These plants were tagged before flowering. Detailed procedure adapted to record observations for each character is given below.

3.4.1. 1. Days to 50 per cent flowering

The numbers of days taken from the date of sowing to the date at which 50 per cent plants start flowering in whole plot were recorded.

3.4.1. 2. Days to maturity

The total number of days taken from sowing to maturity on plot basis were counted and recorded.

3.4.1. 3. Plant height (cm)

Plant height was measured from ground level to the top of the plant at the time of maturity.

3.4.1. 4. Numbers of productive tillers per plant

The numbers of panicle bearing tillers in each plant at maturity were counted.

3.4.1. 5. Panicle length (cm)

The length of the panicle from its base to the tip excluding awns if any was measured.

3.4.1. 6. 1000-grain weight (g)

Weight of one thousand randomly selected filled grains was recorded in gram for each genotype in each replication.

3.4.1. 7. Numbers of grains per panicle

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

3.4.1. 8. Amylose content % (Juliano 1971)

The Amylose content was estimated by using method described by Juliano, 1971.The detailed procedure is given in appendix-I.

3.4.1. 9. Protein content % (Lowry *et al.* 1951)

The protein content was estimated by using the method described by Lowry *et al.* 1951. The detailed procedure is given in appendix-II.

3.4.1. 10. Grain yield per plant (g)

Filled grains of all the ten selected plants in each plot were weighed and average yield per plant was recorded.

3.5. Statistical analysis

The data collected for each character on individual plant basis for ten randomly selected plants were analyzed. The variability parameters were measured by the formula suggested by Johnson *et al*. (1955). Correlation coefficient was calculated as per procedure given by Singh and Choudhary (1979) whereas path coefficient analysis was carried by the procedure suggested by Dewey and Lu (1959). The analysis for divergence was done by following Mahalanobis (1936) D^2 statistics.

3.5.1 Analysis of variance

The data were subjected to analysis of variance adopting standard statistical methods (Panse and Sukhatme, 1985). The analysis of variance including source of variations, their degree of freedom (D.F.) and expectations of mean squares are given below:

Source of variation	**df**	**Mean Sum of Squares**	**Expected Mean Sum of Squares**
Replication	(r-1)	MSr	$\sigma^2e + g\ \sigma^2r$
Genotypes	(g-1)	MSg	$\sigma^2e + r\ \sigma^2g$
Error	(r-1) (g-1)	MSe	σ^2e
Total	(r g – 1)		

Where,

r = Number of replications

g = Number of genotypes

MSr = Mean sum of squares due to replications

MSg = Mean sum of squares due to genotypes

MSe = Mean sum of squares due to error

$\sigma^2 g$ = Variance due to genotypes

$\sigma^2 r$ = Variance due to replications

$\sigma^2 e$ = Error variance

Analysis of variance components

The genotypic, phenotypic and error variance were calculated as follows.

3.5.1.1 Genotypic variance (σ^2_g)

The genotypic variance is due to the differences among genotypes included in the study. It was calculated as under

Genotypic variance (σ^2_g) = ($MS_g - MS_e$) / r

3.5.1.2 Phenotypic variance (σ^2_p)

It is the sum of variance contributed by genetic causes and environmental factors. It was calculated as under

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

3.5.1.3 Error variance ($\sigma^2 e$)

The mean square of error represented by the variation attributed to environmental causes.

Environmental variance (σ^2_e) = MS_e

3.5.2 Variability parameters

3.5.2.1 Range

It is the difference between the lowest and the highest value for each character.

Range = Highest value - Lowest value

3.5.2.2 Mean ($\bar{X}$)

It is computed by dividing the sum of all observations in a sample by their number.

$$(\bar{X}) = \Sigma X_i/n$$

Where, $(\bar{X})$ = General mean,

n = Number of observations,

ΣXi= Summation of all the observation

3.5.2.3 Standard error of mean (S.E$_m$)

The standard error of mean (S.E$_m$.) was calculated with the help of following formula.

$$S.E.m = \sqrt{\sigma_e^2/r}$$

Where, σ^2_e = Error variance

r = Replications

3.5.2.4 Coefficient of variation (C.V.)

The coefficient of phenotypic and genotypic variation was calculated by using the formula suggested by Burton (1952).

(a) Phenotypic coefficient of variation (PCV):

$$P.C.V.\ (\%) = \frac{\sqrt{\sigma_p^2}}{\overline{X}} \times 100$$

σ^2_p = Phenotypic variance

($\overline{X}$) = General mean

(b) Genotypic coefficient of variation (GCV):

$$G.C.V.\ (\%) = \frac{\sqrt{\sigma_g^2}}{\overline{X}} \times 100$$

σ^2_g = Genotypic variance

($\overline{X}$) = General mean

3.5.2.5 Heritability in broad sense

Heritability refers to the portion of variability which is heritable in nature out of the total variability. It is due to the genetic causes. Heritability in broad sense (H_{bs}) was calculated according to the following formula suggested by Burton and De Vane (1953).

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

3.5.2.6 Genetic advance (GA)

Genetic advance represents the shift in a population mean towards superior side under selection pressure after single generation of selection. This was estimated as per the formula suggested by Johnson *et al*. (1955).

$$GA = k \times H_{(b)} \times \sigma_p$$

Where,

GA = Genetic Advance

$H_{(bs)}$ = Heritability broad sense

k = Selection intensity, (k = 2.06 at 5 per cent selection intensity)

σ_p = Phenotypic standard deviation

3.5.2.7 Genetic advance as percentage of mean

The genetic advance (GA) as percentage of mean was calculated by using the formula suggested by Johnson *et al.* (1955).

$$\text{Genetic advance as per cent of mean} = \frac{G.A.}{\overline{X}} \times 100$$

Genetic advance as per cent mean was classified as follows. (Johanson *et al.,* 1955)

Low = 0 to 10 percent

Moderate = 10-20 percent

High = > 20 percent

3.6. Correlation coefficients analysis

The correlation coefficients were calculated to determine the degree of association of the characters with yield and its attributes. Genotypic and phenotypic correlation coefficients were worked out by a method described by Singh and Chaudhary (1979).

(a) The genotypic correlation = $r_{xy}(g) = \frac{Cov.\ xy(g)}{\sqrt{Vx(g).Vy(g)}}$

(b) The phenotypic correlation = $r_{xy}(p) = \frac{Cov.\ xy\ (p)}{\sqrt{Vx(p).Vy(p)}}$

Where,

r_{xy} (g) = Genotypic correlation coefficient between x and y traits

r_{xy} (p) = Phenotypic correlation coefficient between x and y traits

Cov. xy (g) = Genotypic covariance for x and y traits

Cov. xy (p) = Phenotypic covariance for x and y traits

V_x (g) = Genotypic variance for x trait

V_y (g) = Genotypic variance for y trait

V_x (p) = Phenotypic variance for x trait

V_y (p) = Phenotypic variance for y trait

Test of significance: The significance of correlation coefficient was tested using the following formula:

$$t = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}$$

Where,

n = Sample size

r = Correlation coefficient

3.7 Path coefficient analysis

The direct and indirect effects were estimated using path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). The following equations were solved for estimating the various direct and indirect effects.

$$r_{1y} = P_{1y} + r_{12}P_{2y} + \ldots\ldots\ldots\ldots + r_{1p}P_{py}$$

$$r_{2y} = r_{21}P_{1y} + P_{2y} + \ldots\ldots\ldots\ldots + r_{2p}P_{py}$$

$$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$$

$$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$$

$$R_{py} = r_{p1}P_{1y} + r_{p2}P_{2y} + \ldots\ldots\ldots\ldots + P_{py}$$

Where,

P_{1y}, P_{2y}……………P_{py} are direct effects of character 1,2, ………..p on y and

r_{1y}, r_{2y}…………r_{py} denotes correlation coefficient between independent characters 1,2……..p and dependent character ‘Y’.

Residual effect was calculated using the following formula:

$$1 = P^2Ry + \Sigma P_{iy}r_{iy}$$

$$P_{Ry} = \sqrt{1 - (P_{1y}r_{1y}) - (P_{2y}r_{2y})\ldots\ldots\ldots\ldots\ldots (P_{iy}r_{iy})}$$

Where,

P_{Ry} is the residual effect

3.8 Genetic divergence analysis

The Genetic divergence amongst different genotypes is assessed based on the estimated *inter-se* genetic distances amongst the genotypes. One of the potent techniques of assessing genetic divergence is the D^2 statistics proposed by Mahalanobis in 1936. D^2 statistics technique measures the forces of differentiation at two levels, namely, intra-cluster and inter-cluster levels, and thus helps in the selection of genetically divergent parents for exploitation in hybridization programmes.

3.8.1 Clustering of genotypes using the D^2 values

Tocher's method was used for clustering the genotypes into different groups (Rao, 1952). The basis of clustering by this method was that any two varieties belonging to the same cluster would show smaller D^2 values as compared to those belonging to two different clusters. This method started with two closely associated populations to find a third population which had the smallest average of D^2 values. In the same manner, fourth one was chosen having the smallest average of D^2 values from the first three and so on. This process was repeated until D^2 values of all the genotypes were exhausted, except those that were included in the former cluster.

3.8.2 Testing differences in the population

From the variance analyses, when the null hypothesis of no treatment differences fails with regards to individual characters, a dispersion table was prepared. Using V statistic, which intern utilize Wilk's criterion (Δ), a simultaneous test of differences between mean values of a number of correlated variables was done (Rao, 1952)

$$\text{Wilk's criterion } (\Delta) = \frac{\text{Determinants of error variance and covariance matrix (E)}}{\text{Determinants of genotypic + error variance and covariance metrix}}$$

$$\text{V statistic} = -m \text{ loge } \Lambda = -\left(n - \frac{p+q+1}{2}\right) \log \Lambda$$

Where,

$$m = \left(n - \frac{p+q+1}{2}\right)$$

p = Number of variables or characters

q = Degrees of freedom for population (i.e., number of genotypes-1)

n = Degrees of freedom for error + genotypes

$\log_e \Lambda$ = $2.3026 \log_{10} \Lambda$

'V' statistic is distributed as χ_2 with pq degrees of freedom. The test of significance of 'V' statistic showed that the differences between the means in respect of the pooled effect of p characters between different populations were significant. Hence further analyses were made to estimate D^2 values.

3.8.3 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 Y_i denotes the transformed variables (i = 1, 2, 3, 4, 5.........p) were calculated 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 considered.

3.8.4 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.

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Chapter IV

EXPERIMENTAL RESULTS

The results of the present investigation on "Studies on Genetic Variability, Characters Association and Genetic Divergence among Rice (*Oryza sativa* L.) Genotypes" are presented under following sub-heads:

4.1 Analysis of Variance

4.2 Genetic Variability Parameters

4.3 Correlation Coefficient Analysis

4.4 Path Coefficient Analysis

4.5 Genetic Divergence

4.1 Analysis of variance (ANOVA)

Twenty-five genotypes of rice were drawn from different sources were grown in Randomized Block Design with three replications. The mean square for all the characters are presented in Table 4.1. The analysis of variance showed highly significant differences among the 25 genotypes in respect of all the 10 characters under study indicating presence of good amount of variability in the materials used for present investigation.

Table 4.1 Analysis of variance for yield and its attributing traits in rice genotypes

Source of variation	Degree of freedom	Mean sum of square									
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers Per Plant	Panicle length (cm)	Number of grain per panicle	1000-grain weight (g)	Amylose content (%)	Protein content (%)	Grain yield per plant (g)
Replication	2	1.69	4.17	23.69	0.33	0.59	47.61	0.52	0.03	0.05	4.73
Genotypes	24	202.71**	227.04**	121.36**	9.91**	5.12**	930.51**	19.45**	4.89**	1.25**	38.56**
Error	48	1.25	2.02	15.62	0.49	0.21	214.89	0.19	0.20	0.05	1.59

***, ** = Significant at 5 and 1 per cent level, respectively.**

4.2 Mean performance and genetic variability parameters

Significant differences were found among the 25 genotypes for all the yield components. The mean performance, genetic variability, heritability and genetic advance as per cent of mean are presented in Table 4.2.

4.2.1. Days to 50 per cent flowering

The character days to 50 per cent flowering indicates appropriate duration of the variety, which is an important criterion in rice breeding programmes to develop rice varieties with early to long duration. The mean value for days to 50 per cent flowering was 94.09 days and ranged from 78.67-104.00 days. The genotype RSK-1165-3-1 recorded significantly less number of the days to 50 per cent flowering (78.67 days) followed by genotypes RSK-1165-4-3, RSK-1165-3-2 (79.00 days) and genotype RSK-1165-4-2 (79.67 days).

The genotypic and phenotypic coefficient of variation was low 8.71 % and 8.79 % respectively. The high heritability (98.17 %) along with moderate (17.78 %) genetic advance as per cent of mean was recorded for this trait.

4.2.2. Days to maturity

Genotypes with low number of days to maturity indicate the earliness of a variety, which is a desirable criterion for developing of rice varieties suitable for early *Kharif* season. The mean value for days to maturity was 129.25 days and ranged from 112.67-140.00 days. The genotype RSK-1165-4-3 and RSK-1165-3-2 recorded significantly less number of the day to maturity (112.67 days) followed by RSK-1165-3-1 (113.00 days), RSK-1165-4-2 (113.67 days), RNSK-1168-2-1 (116.00 days) and RNSK-1167-5-1 (123.33 days).

The genotypic and phenotypic coefficient of variation was low 6.70 % and 6.79 % respectively. High heritability (97.38 %) and moderate (13.62 %) genetic advance as per cent of mean was observed for it.

4.2.3. Plant height (cm)

Plant height ranged from 95.00 cm (RNSK-1168-2-1) to 117.33 cm (P-1121) with general mean value of 108.03 cm. The shortest genotype was RNSK-1168-2-1(95.00 cm) followed by RSK-1165-4-3 (99.00 cm), RSK-1165-3-1 & RSK-1165-4-2 (99.33 cm) and RSK-1165-3-2 (99.67 cm). Genotype P-1121 (117.33) was tallest among all genotypes followed by RSK-1163-8-1 (116.67 cm) and RSK-1161-1-1 (116.00 cm).

The genotypic and phenotypic coefficient of variation for this trait was low 5.50 % and 6.60 % respectively. The moderate heritability (69.29 %) with (9.42 %) genetic advance as per cent of mean was recorded for plant height.

4.2.4. Number of productive tillers per plant

The grain yield of any variety mainly depends upon the contribution of yield determining characters and among them productive tillers per plant is an important trait. The mean of productive tillers per plant was 8.03 and varied from 5.33 to 11.00. The highest number of effective tillers was recorded in the genotype RSK-1155-6-3-1(11.00) followed by genotypes RSK- 1157-9-2-2, RSK-1155-6-1-2 (10.67) and RNSK-1167-11-1(10.33). Minimum number of productive tillers per plant was observed in genotypes RSK-1165-3-1 and RSK-1165-4-2 (5.33).

Higher GCV and PCV were found 22.09 % and 23.73 % respectively. High heritability (86.60 %) and genetic advance as per cent of mean (42.35 %) were recorded for this character.

4.2.5. Panicle length (cm)

The panicle length is an important yield contributing trait and ranged from 25.23 cm to 29.83 cm with a mean of 27.59 cm. The longest length of panicle was observed in genotype RSK-1157-9-2-2 (29.83 cm) followed by genotypes RSK 1157-6-3-1 (29.40 cm), RSK-1157-4-5-1 (29.37 cm), while the shortest panicle length was recorded in genotype RSK-1162-8-1 (25.23 cm).

Low genotypic and phenotypic coefficient of variation were found 4.64 % and 4.93 % respectively. The high heritability (88.47 %) and low (8.98 %) genetic advance as per cent of mean was recorded.

4.2.6. Number of grains per panicle

The range for number of grains per panicle is not only an index of the photosynthetic efficiency but also an indicator for source sink relationship of the plant. Number of grains per panicle ranged from 133.67 to 199.00 with mean a of 164.25. The highest number of grains per panicle was observed in genotype P-2511

(199.00) followed by genotypes RSK-1163-8-1 (183.00) and RSK-1155-3-3-1 (180.67). The lowest value was exhibited by genotype RSK-1165-3-1 (133.67).

Low GCV (9.40 %) and moderate PCV (12.96 %) were found for this trait. The moderate heritability (52.61 %) and expected genetic advance (14.05 %) as per cent of mean were recorded.

4.2.7. 1000-grain weight (g)

The mean value for 1000-grain weight was 25.61g and ranged from 21.70 g to 30.33 g. The genotype RSK-1161-1-1 (30.33 g) having highest test weight followed by genotypes RSK-1157-4-5-1, RSK-1157-9-2-2 (28.87 g) and RSK-1157-6-3-1 (28.70 g) while the lowest was observed in RSK-1165-4-3 (21.70 g).

The genotypic and phenotypic coefficient of variation were low 9.89 % and moderate 10.04 % respectively. The high heritability (97.07 %) and genetic advance as per cent of mean (20.08 %) was recorded for this trait.

4.1.8. Amylose content (%)

The variation for amylose content in genotypes varied from 22.33 to 26.80 per cent with a mean of 23.90 per cent. Highest amylose content was recorded in RNSK-1167-5-1 (26.80 %) followed by genotypes RNSK-1167-11-1 (26.77 %) and RNSK-1168-2-1 (26.57%). Lowest amylose content was recorded in RSK-1155-3-3-1 (22.33 %).

The genotypic and phenotypic coefficient of variation were low 5.23 % and 5.55 % respectively. The heritability was high (88.85 %) and the genetic advance as per cent of mean was moderate (10.16 %).

4.1.9. Protein content (%)

The protein content varied from 6.86 % to 9.37 % with the mean of 8.06 per cent. The highest protein content was recorded in RNSK-1168-2-1 (9.37 %) followed by genotypes RNSK-1167-11-1 (9.09 %) and RNSK-1167-5-1 (9.05%). The lowest protein content was recorded in genotype P-2511 (6.86 %).

The genotypic and phenotypic coefficient of variation were low 7.82 % and 8.33 % respectively. High heritability (88.18 %) and moderate genetic advance (15.13 %) as per cent of mean was recorded for it.

4.1.10. Grain yield per plant (g)

Data for this important trait varied from 8.87 g to 19.03 g with a mean value of 13.73 g. The genotypes showing significantly higher mean values for grain yield per plant were RSK-1155-6-3-1 (19.03 g) Followed by RSK-1157-4-5-1 (18.87 g), RSK-1157-6-3-1 (18.70 g) and RSK-1157-9-2-2 (18.00 g). Lowest grain yield was recorded in RSK-1165-3-1 (8.87g).

Higher genotypic and phenotypic coefficient of variation were found 25.56 % and 27.16 % respectively. The heritability (88.58 %) and genetic advance as per cent of mean (49.55 %) were recorded higher for this trait.

Table 4.2: Genetic variability parameters for yield and its attributing traits in rice genotypes.

Sr. No.	Characters	Range	Mean	GCV(%)	PCV(%)	Heritability % (bs)	Genetic advance	Genetic Advance as % of mean
1.	Days to 50% flowering	78.67-104.00	94.09	8.71	8.79	98.17	16.73	17.78
2.	Days to maturity	112.67-140.00	129.25	6.70	6.79	97.38	17.60	13.62
3.	Plant height (cm)	95.00-117.33	108.03	5.50	6.60	69.29	10.18	9.42
4.	Number of productive tillers per plant	5.33-11.00	8.03	22.09	23.73	86.60	3.39	42.35
5.	Panicle length (cm)	25.23-29.83	27.59	4.64	4.93	88.47	2.48	8.98
6.	Number of grains per panicle	133.67-199.00	164.25	9.40	12.96	52.61	23.08	14.05
7.	1000-grain weight (g)	21.70-30.33	25.61	9.89	10.04	97.07	5.15	20.08
8.	Amylose content (%)	22.33-26.80	23.90	5.23	5.55	88.85	2.43	10.16
9.	Protein content (%)	6.86-9.37	8.06	7.82	8.33	88.18	1.22	15.13
10.	Grain yield per plant (g)	8.87-19.03	13.73	25.56	27.16	88.58	6.81	49.55

4.3 Correlation coefficient analysis

Correlation studies provide reliable information on nature, extent and the direction of selection, especially when the breeder needs to combine high yield potential with desirable agronomic traits. In the present study genotypic correlation coefficients were higher than their phenotypic correlation coefficients indicating elimination of environmental effects led to strengthen genetic association and these characters are positive governed by additive gene action and are useful in improvement.

The phenotypic and genotypic correlation coefficients were estimated using ten characters in twenty-five genotypes of rice to study the degree of mutual relationship between yield and its component characters. The estimates are presented in Table 4.3.

4.3.1. Days to 50 per cent flowering

This character was positively and significantly correlated with days to maturity (r_p 0.976** , r_g 0.999**), plant height (r_p 0.754** , r_g 0.926**), number of productive tillers per plant (r_p 0.302**, r_g 0.329**), panicle length (r_p 0.585** , r_g 0.631**), number of grains per panicle (r_p 0.694** , r_g 0.961**), 1000-grain weight (r_p 0.362** , r_g 0.372**) and grain yield per plant (r_p 0.294** , r_g 0.308**) at both phenotypic and genotypic level. Days to 50 per cent flowering had negative and significant correlation with amylose content at both phenotypic (r_p -0.446**) and genotypic (r_g -0.481**) level. This trait was negatively but non-significantly correlated with protein content at phenotypic (r_p -0.074) and genotypic (r_g -0.089) level.

4.3.2. Days to maturity

This trait shows positive and significant correlation with plant height (r_p 0.767**, r_g 0.941**), number of productive tillers per plant (r_p 0.323**, r_g 0.348**), panicle length (r_p 0.632**, r_g 0.668**), grains per panicle (r_p 0.677**, r_g 0.988**), 1000-grain weight (r_p 0.415**, r_g 0.430**) and grain yield per plant (r_p 0.293**, r_g 0.325**) at both phenotypic as well as genotypic levels. It was negatively and significantly correlated with amylose content at both phenotypic (r_p -0.418**) and genotypic level (r_g -0.446**) and negative but non- significantly correlation was observed with protein content at both the level. (r_p -0.040, r_g -0.036) level.

4.3.3. Plant height

In the present investigation plant height showed positive and significant correlation with following traits like number of productive tillers per plant (r_p 0.280*, r_g 0.383**), panicle length (r_p 0.567**, r_g 0.705**), number of grains per panicle (r_p 0.526**, r_g 0.859**), 1000-grain weight (r_p 0.411**, r_g 0.534**) and grain yield per plant at phenotypic (r_p 0.284*) and genotypic level (r_g 0.409**) levels. It had negatively significant correlation with amylose content at both phenotypic (r_p -0.331**) and genotypic (r_g -0.433**) level. It was negatively but non-significantly correlated with protein content at both phenotypic (r_p -0.101) and genotypic (r_g -0.133) level.

4.3.4. Number of productive tillers per plant

This trait having significant positive correlation with panicle length (r_p 0.396**, r_g 0.484**), 1000-grain weight (r_p 0.527**, r_g 0.577**) and grain yield per plant (r_p 0.881**, r_g 0.993**) at both the levels. It also shown same result with number of grains per panicle at genotypic level (r_g 0.233*). Positive and non-significant correlation of this trait was found with number of grains per panicle at phenotypic level (r_p 0.197), amylose content (r_p 0.117 , r_g 0.124) and protein content at phenotypic (r_p 0.214) as well genotypic level (r_g 0.210).

4.3.5. Panicle length

This character was positively and significantly correlated with number of grains per panicle at phenotypic (r_p 0.375**) and genotypic level (r_g 0.518**), 1000-grain weight at phenotypic (r_p 0.622**) and genotypic level (r_g 0.677**) and grain yield per plant at phenotypic (r_p 0.369**) and genotypic (r_g 0.459**) level. It also having positive and non-significantly correlation with amylose content (r_p 0.048, r_g 0.057) and protein content (r_p 0.031, r_g 0.058).

4.3.6. Number of grains per panicle

Positive and significant correlation of this traits was observed with 1000-grain weight at phenotypic (r_p 0.262*) and genotypic level (r_g 0.340**). This character was positively and non-significantly correlated with protein content (r_p 0.066, r_g 0.067) and grain yield per plant at both genotypic (r_g 0.204) and phenotypic level (r_p 0.146) and negatively significant with amylose content (r_p -0.334**, r_g -0.488**).

4.3.7. 1000-grain weight

1000-grain weight had positive and significant correlation with amylose content (r_p 0.284*, r_g 0.293**), protein content (r_p 0.420**, r_g 0.456**) and grain yield per plant (r_p 0.607**, r_g 0.645**) at both phenotypic as well as genotypic levels.

4.3.8. Amylose content

Amylose content was positively and significantly correlated with protein content at (r_p 0.384**, r_g 0.412**) at both the levels. It showed positive and non-significant correlation with grain yield per plant at both genotypic (r_g 0.157) and phenotypic (r_p 0.139) level.

4.3.9. Protein content

This character was positively and non-significantly correlated with grain yield per plant at phenotypic (r_p 0.178) and genotypic (r_g 0.185) level.

4.3.10. Grain yield per plant

This trait was positively and significantly correlated with days to 50 per cent flowering (r_p 0.294** , r_g 0.308**), days to maturity (r_p 0.293** , r_g 0.325**), plant height (r_p 0.284* , r_g 0.409**), number of productive tillers per plant (r_p 0.881** , r_g 0.993**), panicle length (r_p 0.369** , r_g 0.459**) and 1000-grain weight (r_p 0.607** , r_g 0.645**) at both phenotypic and genotypic level and positive and non-significant with number of grains per panicle (r_p 0.146, r_g 0.204), amylose content (r_p 0.139, r_g 0.157) and protein content at both phenotypic (0.178) and genotypic level (0.185).

Table 4.3: Phenotypic (P) and Genotypic (G) correlation coefficient among different Characters in rice genotypes.

Characters	r	Days to 50% flowering	Days to Maturity	Plant height	Number of productive tillers per plant	Panicle length	Number of grains per panicle	1000-grain weight	Amylose content	Protein content	Grain yield per plant
Days to 50% flowering	P	**1.000**	0.976**	0.754**	0.302**	0.585**	0.694**	0.362**	-0.446**	-0.074	0.294**
	G	**1.000**	0.999**	0.926**	0.329**	0.631**	0.961**	0.372**	-0.481**	-0.089	0.308**
Days to maturity	P		**1.000**	0.767**	0.323**	0.632**	0.677**	0.415**	-0.418**	-0.040	0.293**
	G		**1.000**	0.941**	0.348**	0.668**	0.988**	0.430**	-0.446**	-0.036	0.325**
Plant height	P			**1.000**	0.280*	0.567**	0.526**	0.411**	-0.331**	-0.101	0.284*
	G			**1.000**	0.383**	0.705**	0.859**	0.534**	-0.433**	-0.133	0.409**
Number of productive tillers per plant	P				**1.000**	0.396**	0.197	0.527**	0.117	0.214	0.881**
	G				**1.000**	0.484**	0.233*****	0.577**	0.124	0.210	0.993**
Panicle length	P					**1.000**	0.375**	0.622**	0.048	0.031	0.369**
	G					**1.000**	0.518**	0.677**	0.057	0.058	0.459**
Number of grains per panicle	P						**1.000**	0.262*	-0.334**	0.066	0.146
	G						**1.000**	0.340**	-0.488**	0.067	0.204
1000-grain weight	P							**1.000**	0.284*	0.420**	0.607**
	G							**1.000**	0.293**	0.456**	0.645**
Amylose content	P								**1.000**	0.384**	0.139
	G								**1.000**	0.412**	0.157
Protein content	P									**1.000**	0.178
	G									**1.000**	0.185
Grain yield per plant	P										**1.000**
	G										**1.000**

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

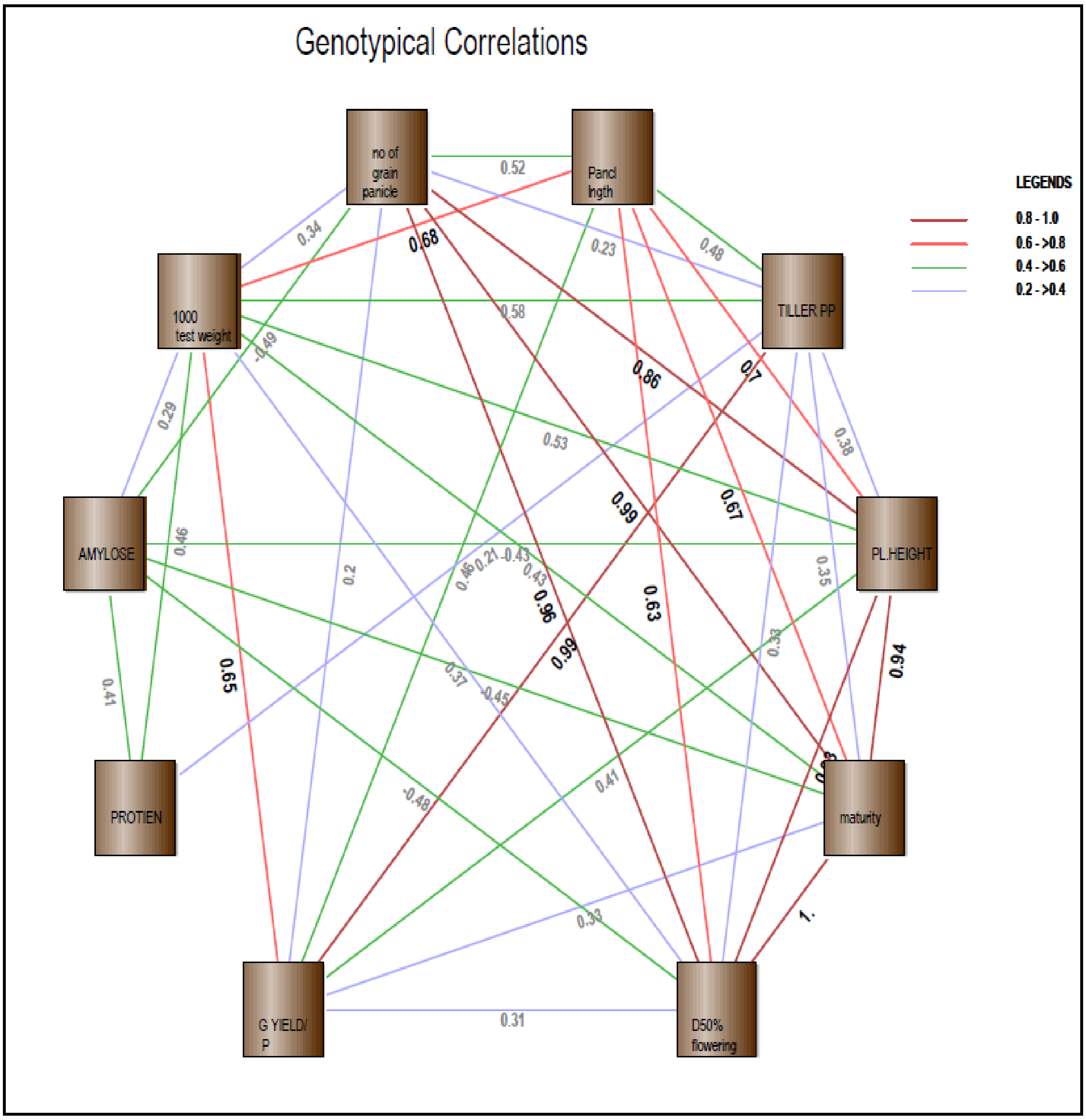

Fig 4.1 Genotypic correlation coefficient diagram for ten characters in rice genotypes.

4.4 Path coefficient analysis

The observed correlation between yield and its component characters is the net result of the direct and indirect effects of the component character through other yield attributes. The total correlation coefficient between yield and its component characters may sometimes be misleading, as it may be an over or under estimate of its association with other characters. In these cases, direct selection on the basis of correlated response may not be fruitful. For critical evaluation, the correlation coefficient need to be split into direct and indirect effects using path coefficient analysis since, many characters affect a given trait. Thus, the correlation and path coefficients in combination can give a better insight into cause and effect relationship between different pairs of character. The inter-relationship of the characters as revealed by the path coefficient analysis using genotypic and phenotypic correlation are presented in Table 4.4

At Genotypic level

The result revealed that at genotypic level number of productive tillers per plant (0.993) had highest significant and positive correlation on grain yield per plant followed by1000-grains weight (0.645), panicle length (0.459), plant height (0.409), days to maturity (0.325) and days to 50 per cent flowering (0.308). Each factor influenced the yield by a direct contribution and indirect contributions through other variables with which it was correlated. Among all the characters, number of productive tillers per plant (0.9336) had the maximum direct effect followed by plant height (0.2402), 1000-grain weight (0.1732), amylose content (0.0663), days to 50 per cent flowering (0.0607) and days to maturity (0.0199). On the other hand, negative direct effect were observed for panicle length (-0.2248), number of grains per panicle (-0.2051) and protein content (-0.0521).

Days to 50 per cent flowering

Days to 50 per cent flowering had positive and significant correlation with grain yield per plant (0.308). The result revealed that days to 50 per cent flowering had higher indirect positive effect through productive tillers per plant (0.3067), plant height (0.2224), 1000-grain weight (0.0645), days to maturity (0.0199) and protein content (0.0047) and on contrary, it exhibited negative indirect effect through number of grains per panicle (-0.1971), panicle length (-0.1418) and amylose content (-0.0319).

Days to maturity

Days to maturity had positive and significant correlation with grain yield per plant (0.325) due to positive indirect effect exhibited by number of productive tillers per plant (0.3248) followed plant height (0.2261), 1000-grain weight (0.0745), days to 50 per cent flowering (0.0606) and protein (0.0019). It had negative indirect effects through panicle length (-0.1503), number of grains per panicle (-0.2025) and amylose content (-0.0295).

Plant height

Plant height had positive and significant correlation with grain yield per plant (0.409). Highest positive indirect effect of plant height was exhibited through number of productive tillers per plant (0.3580) followed by 1000-grain weight (0.0925), days to 50 per cent flowering (0.0562), days to maturity (0.0187) and protein (0.0069). However panicle length (-0.1584), number of grains per panicle (-0.1763) and amylose content (-0.0287) having negative indirect effects on it.

Number of productive tillers per plant

It exhibited higher positive and significant correlation with grain yield per plant (0.993). Highest positive indirect effect of number of productive tillers per plant was exhibited through 1000-grain weight (0.1000), plant height (0.0921), days to 50 per cent flowering (0.0199), amylose content (0.0082) and days to maturity (0.0069). It had negative indirect effect through panicle length (-0.1087), number of grains per panicle (-0.0478) and protein content (-0.0109).

Panicle length

Panicle length had direct positive and significant correlation with grain yield per plant (0.459). Its highest positive indirect effect was exhibited through number of productive tillers per plant (0.4514), followed by plant height (0.1693), 1000-grain weight (0.1173), days to 50 per cent flowering (0.0383), days to maturity (0.0133) and amylose content (0.0038). It had indirect negative effect through number of grains per panicle (-0.1062) and protein content (-0.0030).

Number of grains per panicle

The number of grains per panicle exhibited positive and non-significant correlation with grain yield per plant (0.204). It had indirect positive effect through number of productive tillers per plant (0.2176), plant height (0.2065), 1000-grain weight (0.0590), days to 50 per cent flowering (0.0583) and days to maturity (0.0197). It showed negative indirect effects through panicle length (-0.1164), amylose content (-0.0324) and protein content (-0.0035).

1000-grain weight

It had high positive and significant correlation with grain yield per plant (0.645). The positive indirect effect on 1000-grain weight was observed through productive tillers per plant (0.5388) followed by plant height (0.1283), days to 50 per cent flowering (0.0226), amylose content (0.0195) and days to maturity (0.0086). It exhibited negative indirect effect *via* panicle length (-0.1523), number of grains per panicle (-0.0698) and protein content (-0.0238).

Amylose content

Amylose content per cent had a positive but non-significant correlation with grain yield per plant (0.157). Positive indirect effect on amylose content was exhibited through number of productive tillers per plant (0.1158), number of grains per panicle (0.1001) and 1000-grain weight (0.0508). Indirect negative effect on amylose content per cent exerted through 50 per cent flowering (-0.0292) followed by days to maturity (-0.0089), plant height (-0.1040), panicle length (-0.0128) and protein content (-0.0215).

Protein content

It had positive but non-significant correlation with grain yield per plant (0.185). Positive indirect effects on protein content was exhibited by number of productive tillers per plant (0.1956) followed by 1000-grain weight (0.0790) and amylose content (0.0273). It had negative indirect effects through days to 50 per cent flowering (-0.0054), days to maturity (-0.0007), plant height (-0.0320), panicle length (-0.0129) and number of grain per panicle (-0.0138).

Table 4.4: Phenotypic and genotypic path coefficient for grain yield per plant in rice.

Characters		Days to 50% flowering	Days to maturity	Plant height	Number of productive tillers per plant	Panicle length	Number of grains per panicle	1000-grain weight	Amylose content	Protein content	Correlation with grain yield per plant
Days to 50% flowering	P	**0.5771**	-0.5302	0.0029	0.2367	-0.0711	-0.0585	0.1273	0.0015	0.0078	0.294**
	G	**0.0607**	0.0199	0.2224	0.3067	-0.1418	-0.1971	0.0645	-0.0319	0.0047	0.308**
Days to maturity	P	0.5633	**-0.5431**	0.0030	0.2525	-0.0768	-0.0570	0.1457	0.0014	0.0041	0.293**
	G	0.0606	**0.0199**	0.2261	0.3248	-0.1503	-0.2025	0.0745	-0.0295	0.0019	0.325**
Plant height	P	0.4350	-0.4167	**0.0038**	0.2190	-0.0689	-0.0443	0.1443	0.0011	0.0106	0.284*
	G	0.0562	0.0187	**0.2402**	0.3580	-0.1584	-0.1763	0.0925	-0.0287	0.0069	0.409**
Number of productive tillers per plant	P	0.1745	-0.1752	0.0011	**0.7826**	-0.0481	-0.0166	0.1851	-0.0004	-0.0224	0.881**
	G	0.0199	0.0069	0.0921	**0.9336**	-0.1087	-0.0478	0.1000	0.0082	-0.0109	0.993**
Panicle length	P	0.3378	-0.3434	0.0022	0.3100	**-0.1214**	-0.0316	0.2183	-0.0002	-0.0033	0.369**
	G	0.0383	0.0133	0.1693	0.4514	**-0.2248**	-0.1062	0.1173	0.0038	-0.0030	0.459**
Number of grains per panicle	P	0.4005	-0.3675	0.0020	0.1540	-0.0455	**-0.0843**	0.0922	0.0011	-0.0069	0.146
	G	0.0583	0.0197	0.2065	0.2176	-0.1164	**-0.2051**	0.0590	-0.0324	-0.0035	0.204
1000-grain weight	P	0.2092	-0.2252	0.0016	0.4125	-0.0755	-0.0221	**0.3513**	-0.0009	-0.0438	0.607**
	G	0.0226	0.0086	0.1283	0.5388	-0.1523	-0.0698	**0.1732**	0.0195	-0.0238	0.645**
Amylose content	P	-0.2575	0.2272	-0.0013	0.0919	-0.0058	0.0282	0.0997	**-0.0033**	-0.0401	0.139
	G	-0.0292	-0.0089	-0.1040	0.1158	-0.0128	0.1001	0.0508	**0.0663**	-0.0215	0.157
Protein content	P	-0.0429	0.0215	-0.0004	0.1677	-0.0038	-0.0055	0.1474	-0.0013	**-0.1044**	0.178
	G	-0.0054	-0.0007	-0.0320	0.1956	-0.0129	-0.0138	0.0790	0.0273	**-0.0521**	0.185

Phenotypic residual effect = 0.16229, Genotypic residual effect = 0.1819

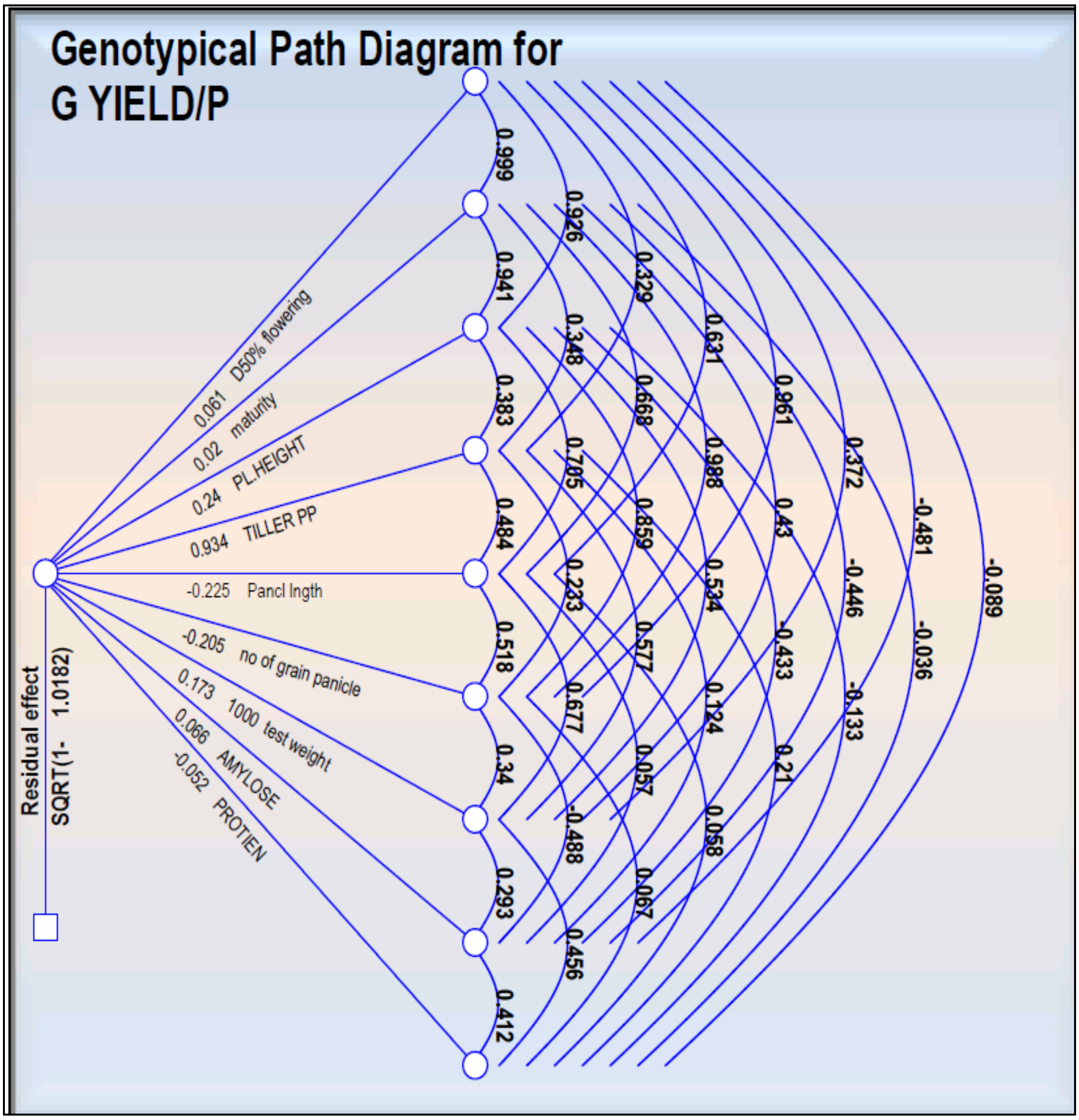

Fig 4.2 Genotypic path diagram for grain yield per plant for rice genotypes

At phenotypic level

In the present investigation number of productive tillers per plant (0.881) had highest significant and positive correlation with grain yield per plant followed by 1000-grain weight (0.607), panicle length (0.369), plant height (0.284), days to maturity (0.293) and days to 50 per cent flowering (0.294). Higher direct effect was observed for number of productive tillers per plant (0.7826) followed by days to 50 per cent flowering (0.5771), 1000-grain weight (0.3513) and plant height (0.038).

Days to 50 per cent flowering

Path analysis revealed that days to 50 per cent flowering had positive and significant correlation with grain yield per plant (0.294). It had positive indirect effect *via* productive tillers per plant (0.2367), 1000-grain weight (0.1273), protein content (0.0078), plant height (0.0029) and amylose content (0.0015). On contrary, it exhibited negative indirect effect through days to maturity (-0.5302), number of grains per panicle (-0.0585) and panicle length (-0.0711).

Days to maturity

Days to maturity exhibited positive and significant correlation with grain yield per plant (0.293). It had indirect positive effects through days to 50 per cent flowering (0.5633), number of productive tillers per plant (0.2525), 1000-grain weight (0.1457), protein content (0.0041), plant height (0.0030) and amylose content (0.0014). On the other hand it had negative indirect effects *via* panicle length (-0.0768) and number of grain per panicle (-0.0570).

Plant height

It had positive and significant correlation with grain yield per plant (0.284). The positive indirect effect of plant height was observed through days to 50 per cent flowering (0.4350), number of productive tillers per plant (0.2190), 1000-grain weight (0.1443), protein content (0.0106) and amylose content (0.0011). However negative indirect effects of this character were observed through days to maturity (-0.4167), panicle length (-0.0689) and number of grains per panicle (-0.0443).

Number of productive tillers per plant

It had higher positive and significant correlation with grain yield per plant (0.881). The positive indirect effect on number of productive tillers per plant was exhibited by 1000-grains weight (0.1851), days to 50 per cent flowering (0.1745) and plant height (0.0011). Negative indirect effect was exhibited *via* days to maturity (-0.1752), panicle length (-0.0481), number of grains per panicle (-0.0166), protein content (-0.0224) and amylose content (-0.0004).

Panicle length

Panicle length had positive and significant correlation with grain yield per plant (0.369). It had positive indirect effect through days to 50 per cent flowering (0.3378), number of productive tillers per plant (0.3100), 1000-grain weight (0.2183) and plant height (0.0022). The negative indirect effect on panicle length was observed through days to maturity (-0.3434), number of grain per panicle (-0.0316), protein content (-0.0033) and amylose content (-0.0002).

Number of grains per panicle

It had positive correlation with grain yield per plant (0.146). Positive indirect effect on number of grains per panicle was exhibited by days to 50 per cent flowering (0.4005), productive tillers per plant (0.1540), 1000-grain weight (0.0922) and plant height (0.0020). Days to maturity (-0.3675), panicle length (-0.0455) and protein content (-0.0069) exerted negative indirect effect on it.

1000-grain weight

This trait showed positive and significant correlation with grain yield per plant (0.607). Positive indirect effects on it were exhibited by productive tillers per plant (0.4125), days to 50 per cent flowering (0.2092) and plant height (0.0016). It had negative indirect effect *via* days to maturity (-0.2252), panicle length (-0.0755), number of grains per panicle (-0.0221), protein content (-0.0438) and amylose content (-0.0009).

Amylose content

Amylose content had positive correlation with grain yield per plant (0.139). Positive indirect effect on amylose content was exerted through days to maturity (0.2272), 1000-grain weight (0.0997), number of productive tillers per plant (0.0919) and number of grains per panicle (0.0282). It had negative indirect effect through days to 50 per cent flowering (-0.2575) followed by plant height (-0.0013), panicle length (-0.0058) and protein content (-0.0401).

Protein content

This character showed positive but non-significant correlation with grain yield per plant (0.178). Protein content had positive indirect effects *via* productive tillers per plant (0.1677), 1000-grain weight (0.1474) and days to maturity (0.0215). Negative indirect effects on it was observed through days to 50 per cent flowering (-0.0429), plant height (-0.0004), panicle length (-0.0038), number of grains per panicle (-0.0055) and amylose content (-0.0013).

Residual Effect

The residual effect determines how best the casual factors account for the variability of the dependent factor, the grain yield per plant in this case. In present study residual effect was 0.18 and 0.16 at genotypic and phenotypic level respectively. The residual effect 0.16 at phenotypic and 0.18 at genotypic level indicates that the nine traits explain 84 per cent and 86 per cent of variability in grain yield per plant. Beside, some other factors which have not been considered here need to be included in this analysis to account fully for the variation in yield.

4.5 Genetic divergence

D^2 analysis (Mahalanobis, 1936) was carried out to estimate genetic divergence among 25 genotypes of rice. Grouping of the genotypes was done by Tocher's method. The test of significance for multiple measurements using 'V' statistics (1143.78) which utilized Wilk's criterion confirmed significant differences among the genotypes for all the observed characters which indicated that the substantial amount of genetic variability was present in the genetic material. All the 25 genotypes were grouped in 6 clusters.

4.5.1. Genotypes grouping into clusters

The result of the genotypes grouping into clusters is presented in Table 4.5. As per the D^2 values, the 25 genotypes of rice were grouped into six clusters. Cluster II had maximum number of genotypes (8) followed by cluster I (7), cluster III (4) genotypes, Cluster IV had (3) and V had (2) genotypes in each cluster. Cluster VI is mono-genotypic.

Table 4.5: Grouping of twenty-five genotypes of rice into six clusters (by Tocher's method).

Cluster No.	Name of genotypes	Number of genotype
I	RSK-1155-2-4-1, RSK-1155-3-3-1, RSK-1157-4-5-1, RSK-1157-6-3-1, RSK-1157-9-2-2, RSK-1155-6-1-2, RSK-1155-6-3-1	7
II	RSK-1164-1-1, RSK-1172-1-1, RSK-1221-1-1, RSK-1162-8-1, RSK-1164-6-1, RSK-1164-6-2, RSK-1163-8-1,P-1460	8
III	RSK-1165-4-2, RSK-1165-4-3, RSK-1165-3-1, RSK-1165-3-2	4
IV	RNSK-1167-11-1, RNSK-1168-2-1, RNSK-1167-5-1	3
V	P-1121, P-2511	2
VI	RSK-1161-1-1	1

4.5.2 Average intra and inter cluster distance

Inter and intra-cluster distance among six clusters were presented in the Table 4.6. The intra cluster distance ranged from 0.00 (cluster VI) to 29.17 (cluster IV). Cluster IV had the highest intra-cluster distance (29.17) followed by cluster II (23.01), cluster I (16.16), cluster V (13.30) and cluster III (12.56).

The highest inter-cluster distance (495.10) was found between cluster III and VI followed by cluster I and III (391.90), cluster III and V (369.88), cluster IV and V (225.64) and cluster II and cluster III (211.67). The smallest inter-cluster distance (50.17) was observed between II and V followed by cluster I and VI (55.23) and cluster I and V (64.17).

Table 4.6: Average intra and inter-cluster distance based on corresponding D^2 values.

Clusters	**I**	**II**	**III**	**IV**	**V**	**VI**
I	**16.16**	94.62	391.90	145.98	64.17	55.23
II		**23.01**	211.67	133.36	50.17	130.44
III			**12.56**	149.75	369.88	495.10
IV				**29.17**	225.64	210.40
V					**13.30**	109.74
VI						**0.00**

4.5.3 Clusters mean for different quantitative characters by Tocher's method.

The cluster mean of different quantitative characters for different clusters have been presented in Table 4.7. The days to 50 per cent flowering was minimum in cluster III (79.08) followed by cluster IV (86.22), and cluster II (97.38) whereas, maximum values for days to 50 per cent flowering was observed in cluster V (102.67) followed by cluster VI (101.00) and cluster I (98.8 6).

Days to maturity was minimum in cluster III (113.00 days) followed by cluster IV (121.78 days), whereas it was recorded maximum in cluster V (137.83 days) followed by cluster VI (137.33 days). The cluster V (116.33) have the highest plant height (cm), followed by the cluster VI (116.00). Lowest plant height (99.33cm) was observed for cluster III. Maximum number of productive tillers per plant was observed in cluster I (10.00) followed by cluster IV (9.00) and cluster V (8.50), whereas, minimum number of productive tillers per plant was observed in cluster VI (5.67) followed by cluster III (6.42) and cluster II (6.92). The cluster VI (28.77) have the highest panicle length followed by cluster I (28.53) whereas, cluster III (25.47) have the shortest panicle length followed by cluster II (27.57). Maximum number of grains per panicle was observed in cluster V (189.67) followed by cluster VI (178.00) and cluster II (170.71) whereas the lowest number of grains per panicle was reported in cluster III (134.50). The highest 1000-grain weight (g) was recorded in cluster VI (30.33), followed by cluster I (28.20) and cluster IV (27.54) whereas, minimum 1000-grain weight (g) was reported in cluster III (22.52). The maximum value for grain yield per plant (g) was recorded in cluster I (17.97) followed by cluster IV (15.61) and cluster V (14.90), whereas minimum value was in cluster VI (9.47). The maximum per cent of amylose content estimated in cluster IV (26.71) followed by cluster III (23.95) and minimum value for amylose content recorded in cluster V (23.00). Maximum protein content (%) was recorded in cluster IV (9.17) and minimum protein content per cent found in cluster V (7.16). Cluster I had genotypes having higher mean values for characters like grain yield per plant, number of productive tillers per plant, whereas, clusters IV had high mean values for grain yield per plant, protein content, amylose content and also desirable for early flowering and maturity. Cluster VI for plant height, panicle length, number of grains per panicle, 1000-grain weight. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

Table 4.7: Mean values of different characters for twenty-five genotypes of rice grouped in different clusters.

Characters Cluster	Days to 50% flowering	Days to Maturity	Plant height (cm.)	Number of productive tillers per plant	Panicle length (cm.)	Number of grains per panicle	1000-grain weight (g)	Amylose content (%)	Protein content (%)	Grain yield per plant (g)
I	98.86	134.62	112.48	10.00	28.53	169.95	28.20	23.42	8.15	17.97
II	97.38	132.33	107.38	6.92	27.57	170.71	23.86	23.48	8.00	11.03
III	79.08	113.00	99.33	6.42	25.47	134.50	22.52	23.95	7.58	10.81
IV	86.22	121.78	102.78	9.00	27.81	151.89	27.54	26.71	9.17	15.61
V	102.67	137.83	116.33	8.50	27.73	189.67	24.43	23.00	7.16	14.90
VI	101.00	137.33	116.00	5.67	28.77	178.00	30.33	23.83	8.37	9.47

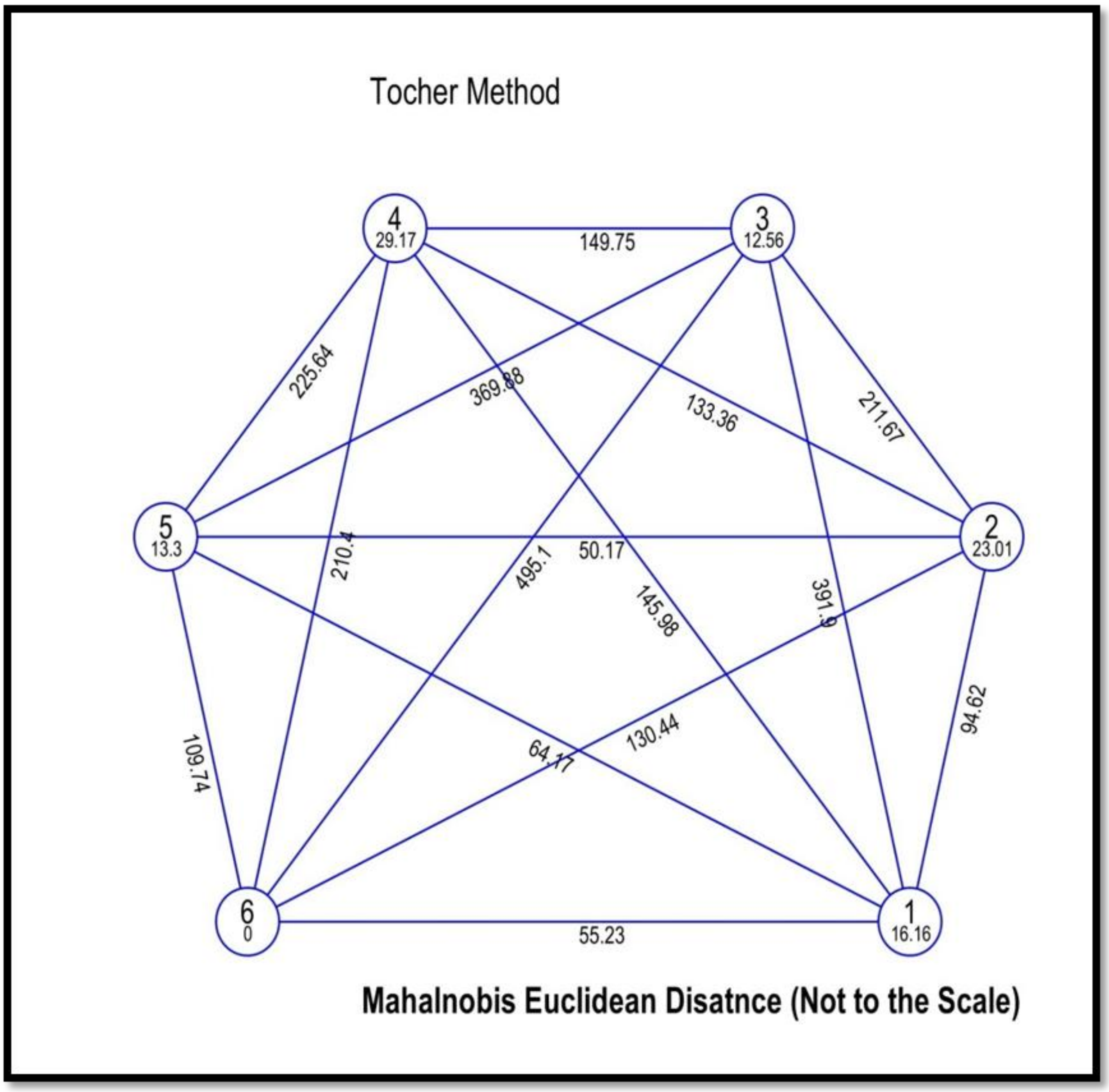

Fig 4.3 Relative disposition of clusters showing average intra and inter distance.

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Chapter-V

DISCUSSION

The success in plant breeding depends upon the genetic variability present within and between the available germplasm resources. For a crop improvement programme, it is prerequisite to maintain the wide genetic variability that allows identification of promising genotypes in the germplasm collection and the trait of interest to be incorporated in the breeding programme to develop promising cultivars. The germplasm could be identified based on the knowledge of extent of variability present in experimental material. The main objective in any plant breeding programme is to evolve promising and desirable varieties, possessing high yielding potential, sufficient success has been achieved by genetic manipulation in the improvement of cereals and it is now possible to augment the grain yield potential of Rice as well. Therefore, in the present study, an attempt has been made to elucidate the genetic information in crop material comprised of 25 genotypes of rice. The experiment was conducted at the Agricultural Research Station, Ummedganj, Agriculture University Kota.

The available information on various aspects of the investigation from 25 genotypes has been discussed under the following headlines-

5.1. Analysis of variance

5.2. Genetic variability parameters

5.3. Correlation coefficient analysis

5.4. Path coefficient analysis

5.5. Genetic divergence

5.1. Analysis of variance

The analysis of variance (ANOVA) indicated significant difference among 25 genotypes of rice for ten characters *viz.*, days to 50 per cent flowering, days to maturity, number of productive tillers per plant, panicle per plant, plant height, panicle length, number of grains per panicle, 1000-grain weight, amylose content and protein content which suggested that the materials selected for the study might be of diverse in origin or developed from diverse crosses. Yield and its attributing traits observed in the base population could be utilized to improve this crop by using simple breeding methods. A wide range of variability for various traits has been observed earlier by Paikhomba *et al.* (2014), Tiwari (2015), Anis *et al*. (2016), Gautam *et. al.* (2016), Sahu *et al*. (2017), Iqbal *et al.* (2018), Kishor *et al.* (2018), Mamata *et al.* (2018), Meena *et al.* (2018), Monalisha and Das (2018), Kumar *et al.* (2019), Kumari *et al*. (2019) and Manjunatha and Kumara (2019).

5.2 Genetic variability Parameters

The mean performance of different genotypes for the characters gave the first hand information for the variability present in the materials under study and gives an opportunity to the plant breeders to select the diverse parents as per objective of the breeding in any crop. Among 25 genotypes of rice RSK-1155-6-3-1 genotype had highest mean performance for grain yield per plant followed by RSK-1157-4-5-1 and RSK-1157-6-3-1 indicating that these genotypes can be used in hybridization programmes in order to achieve target environment in respect to yield. RSK-1165-3-1 was earliest in flowering and RSK-1165-3-2 in maturity. These genotypes can be used as a donor in hybridization programmes for evolving early maturity or short duration rice variety. Genotype RNSK-1168-2-1 was the shortest and P-1121 was the tallest among all 25 genotypes of rice. RSK-1157-9-2-2 genotype had highest mean performance for panicle length followed by RSK-1157-6-3-1 and RSK-1157-4-5-1.

The highest mean performance for number of productive tillers per plant was observed in genotype RSK-1155-6-3-1 followed by RSK-1155-6-1-2 and RSK-1157-9-2-2. Highest number of grains per panicle was observed in genotype P-2511 followed by P-1121 and RSK-1163-8-1. The genotype RNSK-1168-2-1 possessed the highest per cent protein content followed by RNSK-1167-11-1 and RNSK-1167-5-1 and the genotype RNSK-1167-5-1 had the higher amylose content followed by RNSK-1167-11-1 and RNSK-1168-2-1. Genotype RSK-1161-1-1 revealed highest mean performance for 1000- grain weight followed by genotype RSK-1157-4-5-1 and RSK-1157-6-3-1. Adequate number of fertile grains per panicle and heavy grains are important traits which should be considered in selection for high yield similar result were reported by Satyanarayana *et al*. (2005).

Genetic improvements through conventional breeding approaches depend mainly on the availability of the diverse germplasm and the amount of genetic variability present in the population for the desired characters. The genotypic coefficient of variation measures the range of variability available in the crop and also enables a breeder to compare the amount of variability present among different characters. The phenotypic expression of the character is the result of interaction between genotype and environment. Hence, the total variance should be partitioned into heritable and non-heritable components to assess the true breeding nature of the particular trait under study. The heritable portion of the variation can be ascertained by studying the components of variation such as GCV, PCV, heritability and predicted genetic advance.

In the present study, the estimates of PCV were higher than their corresponding GCV for all the traits studied which indicated effect of environment on the expression of characters. The characters like grain yield per plant, number of productive tillers per plant, number of grains per panicle and 1000-grain weigh showed higher estimates of GCV and PCV, indicating the presence of good amount of variation among the genotypes for these characters. Therefore, simple selection of these characters would be effective because the response of selection is directly proportional to variability present in the experimental material. These findings are in accordance with earlier findings of Tuhina *et al*. (2015), Anis *et al*. (2016), Sala and Shanthi (2016), Mahantashivayogayya *et al*. (2016), Meena *et al.* (2018) and Ismaeel (2018). The characters like panicle length, amylose content, plant height having low estimates of GCV and PCV indicating the low range of variation found in these characters in the present experimental material, thus offers little scope for further improvement of these characters. Similar kinds of findings were earlier reported by Abdul *et al.* (2011), Pathak *et al.* (2016), and Singh *et al.* (2017).

The coefficient of variation alone is not sufficient to determine the amount of heritable variability from one generation to the next generation. The heritable portion of variation is thus required to be estimated with the help of heritable estimates (Burton, 1952). In the present investigation, high heritability was recorded for most of the character except number of grains per panicle. Days to 50 per cent flowering exhibited highest heritability followed by days to maturity, 1000-grain weight, amylose content, grain yield per plant, panicle length, protein content, number of productive tillers per plant and protein content. This indicated that selection of these traits would be more effective as compared to others. Similar finding were reported earlier by Pathak *et al*. (2016), Singh *et al.* (2017), Bagudam *et al*. (2018), Mamata *et al.* (2018), Kumari *et al*. (2019) and Tiwari *et al*. (2019).

The heritability estimates alone do not provide authentic information about the gene governing the expression of a particular character and this do not provide the information of the amount of genetic progress that would result from the selection of best individuals. Johanson *et al.* (1955) had pointed about that the heritability estimates along with genetic advance as percent of mean were more useful than heritability estimates alone in predicting the response to selection. In the present investigation genetic advance as per cent of mean was highest for grain yield per plant and number of productive tillers per plant and 1000-grain weight, whereas it was moderate for days to 50 per cent flowering, protein content, number of grain per panicle, days to maturity, amylose content and it was low for plant height and panicle length. Similar finding were reported earlier by Ahmadikhah (2012), Bagudam *et al*. (2018), Kumari *et al*. (2019).

Heritability and genetic advance as per cent of mean are two complementary concepts. Thus, heritability values may be used to estimate the genetic advance through selection for predicting the utility and value of selection. In the present investigation, High heritability along with high genetic advance as per cent of mean was observed for grain yield per plant, number of productive tillers per plant and 1000-grain weight indicating the involvement of additive gene action in the inheritance of these traits hence simple selection would be rewarding. Similar finding were reported earlier by Mallimar *et al.* (2016), Mamata *et al.* (2018).

5.3 Correlation coefficient analysis

The potential productivity of any crop is basically valued in terms of the yield per unit area. Its improvement by direct selection is generally difficult because yield is a complex polygenic character largely influenced by its various component characters as well as by the environment. Hence, it becomes essential to estimate association of the yield with component characters and among themselves. The efficiency of selection thus can be increased, if it is simultaneously practiced for characters which are correlated with yield. In the quantitative traits, the genotypes are influenced by the environment, thereby, affecting the phenotypic expression as well as association and consequently direction of association between the characters. The knowledge of magnitude and direction of correlation is used for judging how improvement in one character will bring simultaneous change in the other characters. In general, the genotypic correlation coefficients were higher than the respective phenotypic correlation coefficients which might be from the modifying effect of environment on the association of characters at phenotypic level. Selection of yield as such may not be effective since there may be number of genes for yield *per se* and yield may be resultant of interaction among various components. Knowledge of relation between yield and its components is essential and selection for one component may bring about a simultaneous change in the other. Therefore, a rational approach to improve yield, is to collect information on character association. Hence, under the present investigation, the phenotypic and genotypic correlation coefficients were worked out for grain yield per plant and yield related characters. The correlations of grain yield per plant were positive and significant with characters *viz*., days to 50 per cent flowering, days to maturity, plant height, number of productive tillers per plant, panicle length and 1000-grain weight at phenotypic and genotypic levels. The association studies indicating grain yield of rice can be improved by selecting genotypes having higher values for these traits. These results were in accordance with the results of Rajamadhan *et al.* (2011), Limbani *et al.* (2017), Priya *et al.* (2017), Sangare *et al*. (2017), Edukondalu *et al*. (2017), Kumar and Sonali (2018).

5.4 Path coefficient analysis

The correlation analysis provide an information which is incomplete in the sense that it does not throw light on the underlying cause that are operative for the various interrelationship. The expression of a complex character such as grain yield per plant depends upon the interaction of a number of component attributes. A better picture of the contribution of each component building up the total genetic architecture of a complex character may be obtained through the analysis of causal schemes. Hence, in such a situation path coefficient analysis devised by Wright (1921) had been useful in partitioning direct and indirect causes of association which allow a detailed examination of specific forces acting to produce a given correlation and measures of the relative importance of each causal character. Such a study provides a realistic basis for allocation of weightage to each attributes in deciding a suitable criterion for genetic improvement. The aim of the analysis in the present investigation was to compare the results obtained from simple correlation and path coefficient analysis in determining the true nature of character association. In the present study, path coefficient analysis was computed at genotypic and phenotypic levels for all the characters. Path coefficient analysis was carried out by taking grain yield per plant as dependent variable to partition the correlation coefficient into direct and indirect effect in order to determine the contribution of different characters towards the grain yield per plant. Direct and indirect effect of various characters on grain yield per plant indicated that there is consent between direction and magnitude of direct effect of various characters and correlation with grain yield per plant. Thus a significant improvement in grain yield can be expected through selection in the component traits with high positive direct effect. At genotypic and phenotypic level, maximum direct positive effect on grain yield per plant were observed for number of productive tillers per plant, 1000-grains weight, panicle length, plant height, days to maturity and days to 50 per cent flowering. These results are in agreement to the earlier finding of Khare *et al.* (2015) Hijam *et al. (*2017), Sowjanya *et al.* (2017) and Monalisha and Das (2018). The high positive association of other characters with grain yield per plant was also due to high indirect effect through these characters.

5.5 Genetic divergence

For a successful breeding programme, the diversity of parents is of utmost importance, since the crosses made between the parents with maximum genetic divergence would more likely to yield desirable recombinants in the progenies. However, it is desirable to select suitable genetically divergent parents, based on information about the genetic variability and genetic diversity present in the available germplasm (Singh and Chaudhary 1977).

The variability among different genotypes of a species often reflects the genetic diversity of different characters considered in totality. One of potent techniques of measuring genetic diversity is the D^2 statistic proposed by Mahalanobis in 1936. This technique measures the forces of differentiation at two levels, namely intra cluster and inter cluster level, thus help in selection of genetically divergent parents for their exploitation in hybridization. D^2 statistic measures the degree of diversification and determines the relative importance of each character to total divergence.

On the basis of multivariate analysis as per Mahalanobis D^2 statistic 25 genotypes of rice for 10 important quantitative characters were grouped in six clusters following the Tocher's method as described by Rao (1952). This suggests the presence of diversity in the genotypes included in present investigation. The intra-cluster distance for clusters VI was observed to be zero since these contains only one genotype in cluster. Cluster IV had the highest intra-cluster distance followed by cluster II, cluster I, cluster V and cluster III. The highest inter-cluster distance was found between cluster III and VI followed by cluster I and III and cluster III and V. The greater the distance between two clusters, wider is the expected genetic diversity between them similar result were also reported by Kulsum *et al.* (2013), Khare *et al*. (2015), Kumar *et al.* (2015), Umesh *et al*. (2016), Rukmini *et al.* (2020), Sadia *et al*. (2020).

Cluster I had genotypes having higher mean values for characters like grain yield per plant, number of productive tillers per plant. whereas, clusters like IV had high values for grain yield per plant, protein content, amylose content per cent and also desirable for early flowering and maturity. Cluster VI for plant height, panicle length, number of grains per panicle, 1000-grain weight. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

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Chapter-VI

SUMMARY AND CONCLUSION

The present investigation was undertaken to assess the extent of genetic variability, character association and genetic divergence for yield and its contributing traits in 25 rice genotypes at Agriculture Research Station, Agriculture University Kota during *Kharif* 2019. The material was evaluated in Randomized Block Design with three replications following all recommended agronomic practices to raise a healthy crop.

1. Analysis of variance revealed highly significant differences among the genotypes for all the characters indicating presence of good amount of genetic variability in the genotypes.
2. The PCV values were higher than GCV values for all the characters studied indicating the effect of the environment on character’s expression. High GCV and PCV values were observed for grain yield per plant, number of productive tillers per plant, number of grains per panicle and 1000-grain weight indicating the presence of high amount of genetic variability for these characters, hence direct selection for these characters would be effective.
3. Heritability estimates were high for days to 50 per cent flowering, days to maturity, 1000-grain weight, amylose content, grain yield per plant, panicle length, number of productive tillers per plant and protein content indicating thereby important role of these characters in rice improvement.
4. Genetic advance as per cent of mean was high for grain yield per plant followed by number of productive tillers per plant and 1000-grain weight. It was medium for days to 50 per cent flowering, days to maturity, number of grains per panicle, protein content and amylose content.
5. High heritability along with high genetic advance was observed for grain yield per plant and number of productive tillers per plant indicating the involvement of additive gene action in the inheritance of these traits hence simple selection would be rewarding.

6. The correlation studies revealed that grain yield per plant was positively and significantly correlated with days to 50 per cent flowering, days to maturity, plant height, number of productive tillers per plant, panicle length and 1000-grain weight. The association studies indicating grain yield of rice can be improved by selecting genotypes at both genotypic and phenotypic level having higher values for these traits.

7. Path analysis revealed that maximum direct positive effect on grain yield per plant were observed for number of productive tillers per plant, 1000-grain weight, panicle length, plant height, days to maturity and days to 50 per cent flowering. These characters also showed prominent role as indirect effects on grain yield per plant through most of the component traits. Hence, these traits should be considered as important selection criteria for grain yield improvement.

8. Cluster IV had the highest intra cluster distance followed by cluster II, cluster I, cluster V and cluster III. The minimum intra-cluster distance was observed for cluster VI. The highest inter-cluster distance was found between cluster III and VI followed by cluster I and III and cluster III and V. The greater the distance between two clusters, wider is the expected genetic diversity.

9. Higher mean values were observed in cluster I for characters like grain yield per plant, number of productive tillers per plant, whereas clusters IV had high values for grain yield per plant, protein content, amylose content per cent and also desirable for earliness. Cluster VI had high values for plant height, panicle length, number of grains per panicle, 1000-grain weight. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

10. In the present investigation genotypes *viz*., RSK-1155-6-3-1, RSK-1157-4-5-1, RSK-1157-6-3-1, RSK-1157-9-2-2 and RSK-1155-3-3-1 were superior not only for grain yield per plant but also related traits like plant height, number of productive tillers per plant, days to 50 per cent flowering, days to maturity, panicle length, number of grains per panicle, 1000-grain weight, amylose and protein content. These diverse genotypes can be recommended for future breeding programmes in rice.

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Studies on Genetic Variability, Characters Association and Genetic Divergence among Rice (*Oryza sativa* L.) Genotypes

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Abstract

The present investigation was carried out to estimate "Studies on Genetic Variability, Characters Association and Genetic Divergence among 25 Rice Genotypes for 10 characters *viz.*, days to 50 per cent flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, number of grains per panicle, 1000-grain weight, amylose content, protein content and grain yield per plant. The experiment was laid out in a Randomized Block Design with three replications at Agricultural Research Station, Ummedganj, Kota during *Kharif* 2019.

The analysis of variance indicated the existence of significant differences among genotypes for all the characters studied. High GCV and PCV values were observed for grain yield per plant, number of productive tillers per plant, number of grains per panicle and 1000-grain indicating the presence of good amount of genetic variability for these characters so, direct selection for these characters would be effective. The characters *viz.*, number of productive tillers per plant and grain yield per plant exhibited high heritability coupled with high genetic advance indicating the involvement of additive gene action in the inheritance of these traits hence simple selection would be rewarding.

The result of character association indicated that grain yield per plant showed significant positive correlation with most of the traits except number of grains per panicle, amylose content and protein content at both the levels.

Genetic divergence studies by Mahalanobis D^2 analysis indicated the existence of significant diversity among rice genotypes which were grouped into six clusters. Greater genetic divergence was found between cluster III and VI. Cluster II was the largest comprising of eight genotypes and other clusters *viz.*, cluster I contain seven genotypes, cluster III comprising four genotypes, cluster IV include three genotypes, cluster V include two genotypes and cluster I was represented by single genotype indicating high degree of heterogeneity among the genotypes. The pattern of group constellations indicated significant diversity among the genotypes.

The cluster I having highest mean value for grain yield per plant and productive tillers per plant, cluster III for days to 50 per cent flowering, days to maturity and plant height, cluster IV for highest protein content and cluster V for number of grains per panicle and cluster VI having highest panicle length, 1000-grain weight and amylose content.

The genotype RSK-1155-6-3-1, RSK-1157-4-5-1, RSK-1157-6-3-1, RSK-1157-9-2-2 and RSK-1155-3-3-1 were superior not only for grain yield per plant but also related traits like plant height, number of productive tillers per plant, days to 50 per cent flowering, days to maturity, panicle length, number of grains per panicle, 1000-grain weight, amylose and protein content. These superior genotypes may be directly used in future breeding programmes in rice.

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चावल (*ओराइजा सटाइवा* एल.) के जीन प्रारूपों में आनुवंशिक विभिन्नता, सह–सम्बन्ध और विविधता का अध्ययन

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सारांश

वर्तमान अनुसंधान कार्य "चावल (*ओराइजा सटाइवा* एल.) के जीन प्रारूपों में आनुवंशिक विभिन्नता, सह–सम्बन्ध और विविधता का अध्ययन" शीर्षक के अन्तर्गत चावल के 25 जीन प्रारूपों को लेकर 10 लक्षणों के साथ *खरीफ* 2019 में तीन प्रतिकृति के साथ यादृच्छिक खंड अभिकल्पना में कृषि अनुसंधान केंद्र उम्मेदगंज कोटा के कृषि क्षेत्र में लगाया गया।

विचरण विश्लेषण से ज्ञात हुआ की जीन प्रारूपों के सभी 10 लक्षणों के लिए सार्थक अंतर था जो की इनके मध्य प्रयाप्त मात्रा में विभिन्नता को वयक्त करता है। अनुवांशिक विभिन्नता गुणांकों के मध्य कम अंतर को अध्यन के तहत सभी लक्षणों के लिए दर्ज किया गया था जो इन लक्षणों पर पर्यावरण के कम प्रभाव को इंगित करता है।

प्रति पौध उत्पादक कल्लो की संख्या, दाना प्रति पौध उपज की मात्रा उच्च अनुवांशिक विभिन्नता गुणांक और उच्च वंशानुगति दर्शाते हैं इसलिए इन लक्षणों का चयन भी प्रभावी हो सकता है।

साहचर्य अध्ययन से ज्ञात हुआ कि दाना प्रति पौध उपज का उत्पादक कल्लो की संख्या, 1000 दानों का वजन, मंजरी की लंबाई, पादप की ऊंचाई, परिपक्वता में लगे दिन और 50 प्रतिशत पुष्पन में लगे दिन के साथ लक्षण स्तर और जीन स्तर पर प्रबल धनात्मक साहचर्य था। पथ गुणांक विश्लेषण से ज्ञात हुआ है कि पादप की ऊंचाई और उत्पादक कल्लो की संख्या दाना प्रति पौध उपज पर प्रत्यक्ष एवं धनात्मक प्रभाव दर्शाते हैं।

आनुवंशिक विविधता से ज्ञात हुआ कि 25 जीन प्रारूपों को 6 समूहों में बांटा गया। एक ही समूह के बीच की दूरी समूह नंबर 4 में अधिकतम थी जबकि अनेक समूहों की दूरी समूह नंबर 3 व 6 में अधिकतम तथा समूह नंबर 2 व 5 मे कम पाई गई। समूह नंबर 2 सबसे बड़ा था जिसमें 8 जीन प्रारूपो को रखा गया। समूह नंबर 6 में केवल एक जीन प्रारूप पाया गया जो कि उच्च स्तर की अनुवांशिक विविधता को दर्शाता है।

जीन प्रारूप RSK–1155–6–3–1, RSK–1157–4–5–1, RSK–1157–6–3–1, RSK–1157–9–2–2 और RSK–1155–3–3–1 दाना प्रति पौध उपज के साथ साथ अन्य लक्षणों में भी सर्वश्रेष्ठ पाए गये, अतएव इनका उपयोग संकरण कार्यक्रम में भी किया जा सकता है।

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APPENDICES

APPENDIX – I

Estimation of amaylose content by Juliano method (1971).

A. Reagents

1. 95% ethanol

2. 1 N glacial acetic acid

3. Iodine solution (200 mg of iodine + 2.0 g of KI in 100 ml of distilled water)

B. Extraction

Weighed 100 mg of ground grain sample accurately in duplicate and 1 ml 95% ethanol and 9 ml 1 N NaOH was added. The sample was heated for 10 minutes in a boiling water bath to gelatinize the starch. Cool and transferred to 100 ml volumetric flask. The total volume was made upto 100 ml with distilled water and mixed well.

C. Estimation

The above solution (5 ml) was pipette into 100 ml volumetric flask. 1 ml of 1 N acetic acid and 2 ml of iodine solution was added and the final volume was made 100 ml with distilled water. The solution was shaken well and left undisturbed for 20 minutes. The colour developed was read at 620 nm against a reagent blank. The standard curve was prepared by using potato amylose in the range of 40-200 µg.

Based on the amylose per cent varieties can be grouped as follows

Category	**Amylose content (%)**
Waxy	1-2
Very low amylose	2-9
Low	10-20
Intermediate	20-25
High	25-30

APPENDIX – II

Estimation of protein content by Lowry method (Lowry *et al.*, 1951).

Extraction

Samples of grain flour (100-200 mg) were extracted twice with continuous stirring with 5 ml of 0.1 N NaOH for 30 min. Followed each time by centrifugation (14,000xg for 15 min). The supernatant were pooled diluted to a known volume. To the 2 ml aliquot of cold supernatant, added 2 ml chilled 20 per cent TCA and mixed thoroughly. After aging for 1h at 4 ºC, the contents were centrifuged (14,000xg for 15 min) and the precipitates were dissolved in 0.5 N NaOH for protein estimation.

Estimation

Reagents

1. **Reagent A** **:** 2 per cent sodium carbonate in 0.1 N sodium hydroxide
2. **Reagent B** **:** 0.5 per cent copper sulphate in 1 per cent solution of sodium potassium tartarate.
3. **Reagent C** **:** Mix reagent A and B in 50:1 ratio.
4. **Reagent D** **:** Folin- Ciocaltean phenol reagent (1 N)

Procedure

To 1 ml of appropriately diluted test solution, 5 ml of reagent C was added and the contents were mixed well. The mixture was allowed to stand for 10 minutes at room temperature. Then 0.5 ml of reagent D was added and shaken rapidly. The mixture was kept for 30 min and intensity of blue colour so developed was read at 520 nm. The concentration of total proteins was calculated from the BSA standards (20-100 μg) run simultaneously.

APPENDIX – III

Mean values of twenty-five genotypes for ten characters in rice.

Sr. No.	Genotype	Days to 50% flowering	Days to Maturity	Plant height (cm.)	Number of productive tillers per plant	Panicle length (cm)	Number of grains per panicle	1000-grain weight (g)	Amylose content (%)	Protein content (%)	Grain yield per plant (g)
1	RSK-1155-2-4-1	98.00	135.00	111.00	8.67	27.70	175.00	28.23	22.53	8.42	15.70
2	RSK-1155-3-3-1	98.67	133.67	111.67	9.33	27.77	180.67	27.87	22.33	8.64	17.57
3	RSK-1157-4-5-1	99.33	134.33	114.00	9.67	29.37	158.00	28.87	24.40	7.57	18.87
4	RSK-1157-6-3-1	98.33	135.00	115.00	10.00	29.40	160.33	28.70	24.50	7.50	18.70
5	RSK-1157-9-2-2	99.33	134.00	113.67	10.67	29.83	162.00	28.87	24.33	7.73	18.00
6	RSK-1161-1-1	101.00	137.33	116.00	5.67	28.77	178.00	30.33	23.83	8.37	9.47
7	RSK-1163-8-1	100.33	136.00	116.67	7.00	28.53	183.00	23.97	22.73	8.15	10.30
8	RSK-1165-4-2	79.67	113.67	99.33	5.33	25.40	134.00	22.17	23.50	7.45	9.15
9	RSK-1165-4-3	79.00	112.67	99.00	6.33	25.53	135.33	21.70	23.33	7.67	9.67
10	RNSK-1167-11-1	88.33	126.00	107.33	10.33	28.03	155.67	27.63	26.77	9.09	15.90
11	RNSK-1168-2-1	81.67	116.00	95.00	9.33	27.57	150.33	27.33	26.57	9.37	15.97
12	RSK-1164-1-1	97.00	132.00	106.67	6.33	28.52	154.67	23.50	23.40	7.28	10.30
13	RSK-1172-1-1	94.00	131.00	106.33	6.67	28.77	173.00	24.63	24.27	8.44	9.97

14	RSK-1221-1-1	98.67	133.33	102.33	8.67	27.83	167.33	23.47	23.63	7.22	13.67
15	RSK-1162-8-1	99.67	133.67	106.67	7.33	25.23	177.00	24.87	24.50	8.47	12.93
16	RSK-1164-6-1	95.00	129.33	105.67	6.00	27.23	175.00	24.37	23.53	8.07	9.60
17	RSK-1164-6-2	93.67	129.67	104.67	5.67	27.37	176.67	24.00	23.43	8.18	9.20
18	RSK-1165-3-1	78.67	113.00	99.33	5.33	25.30	133.67	23.27	24.40	7.52	8.87
19	RSK-1165-3-2	79.00	112.67	99.67	8.67	25.63	135.00	22.93	24.57	7.67	15.57
20	RNSK-1167-5-1	88.67	123.33	106.00	7.33	27.81	149.67	27.67	26.80	9.05	14.97
21	RSK-1155-6-1-2	98.67	135.00	111.33	10.67	27.70	174.00	27.47	22.87	8.60	17.90
22	RSK-1155-6-3-1	99.67	135.33	110.67	11.00	27.93	179.67	27.43	22.97	8.58	19.03
23	P-1121	104.00	140.00	117.33	8.33	27.33	180.33	24.13	22.43	7.45	14.50
24	P-2511	101.33	135.67	115.33	8.67	28.13	199.00	24.73	23.57	6.86	15.30
25	P-1460	100.67	133.67	110.00	7.67	27.03	159.00	22.10	22.37	8.20	12.27
26	Mean	94.09	129.25	108.03	8.03	27.59	164.25	25.61	23.90	8.06	13.73
27	S.E	0.645	0.821	2.282	0.403	0.267	8.464	0.254	0.256	0.133	0.728
28	C.D.5%	1.83	2.33	6.49	1.14	0.76	24.07	0.72	0.73	0.38	2.07
29	C.D.1%	2.45	3.11	8.66	1.53	1.01	32.10	0.96	0.97	0.51	2.76
30	C.V. (%)	1.19	1.10	3.66	8.69	1.67	8.92	1.72	1.85	2.86	9.18
31	Range	78.67-104.00	112.67-140.00	95.00-117.33	5.33-11.00	25.23-29.83	133.67-199.00	21.70-30.33	22.33-26.80	6.86-9.37	8.87-19.03