“GENETIC DIVERSITY STUDIES IN RICE (*Oryza sativa* L.)”

by

Mr. Hake Pratap Appasaheb

(Reg. No. 019/041)

A thesis submitted to the
MAHATMA PHULE KRISHI VIDYAPEETH
RAHURI-413 722, DIST- AHMEDNAGAR
MAHARASHTRA, INDIA

In partial fulfilment of the requirements for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)
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APPROVED BY

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2021

CANDIDATE’S DECLARATION

I hereby declare that this thesis or part
thereof has not been submitted
by me or any other person to any
other University or Institution
for a Degree or
Diploma.

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This is to certify that the thesis entitled, **“GENETIC DIVERSITY STUDIES IN RICE (*Oryza sativa* L.)”** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar in partial fulfilment of the requirement for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)**, embodies the result of a piece of bonafide research work carried out by **MR. HAKE PRATAP APPASAHEB** under my guidance and supervision and that no part of the thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation have been duly acknowledged.

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Place: M.P.K.V., Rahuri. (Dr. P. N. Rasal)
Date: / /2021

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Place : M.P.K.V., Rahuri.
Date : / /2021 ***(Pratap Appasaheb Hake)***

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LIST OF ABBREVIATIONS

%	Per cent
-	minus
/	Per
∑	Summation of
b.s.	Broad sense
σ^2e	Environmental variance
σ^2g	Genotypic variance
σ^2p	Phenotypic variance
cm	Centimeters
C.D.	Critical difference
CMS	Cytoplasmic Male Sterile
Cov.	Covariance
C.V.	Coefficient of variation
DAC & FW	Department of Agricultural Cooperation and Farmers Welfare
D.F.	Degrees of freedom
et al.	*et allia* (And other)
Fig.	Figure
g	Grams
GA	Genetic advance
GAM	Genetic advance as per cent of mean
GCV	Genotypic Coefficient of Variation
GCOV	Genotypic covariance
ha^{-1}	Per hectare
h^2 (b.s.)	Heritability
i.e.	*id est* (that is)
kg	Kilogram (s)
L:B ratio	Length : Breadth ratio
MH	Million hectares
M.S.S.	Mean sum of squares
Mt	Million tonnes
mg	Milligrams
No.	Numbers
PCV	Phenotypic coefficient of variation
PCOV	Phenotypic covariance
R.B.D.	Randomized Block Design
r	Correlation coefficient
Via.	By way of, by means of
Viz.	Videlicet (Namely)

ABSTRACT

"GENETIC DIVERSITY STUDIES IN RICE (*Oryza sativa* L.)."
by

Mr. HAKE PRATAP APPASAHEB

A candidate for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

2021

Research Guide : **Dr. K. D. Bhoite**

Department : **Agricultural Botany**

Major discipline : **Genetics and Plant Breeding**

Genetic diversity was assessed in rice (*Oryza sativa* L.) germplasms with 50 genotypes of rice collected from various sources which were evaluated in RBD at ZARS, Igatpuri during kharif 2020. The experiment was carried out with objective to understand the variability parameters for grain yield and yield contributing characters in rice, to assess the genotypic and phenotypic correlation between yield and yield contributing characters, to estimate direct and indirect effect of different quantitative characters on seed yield and to identify suitable parents for future hybridization programme on the basis of genetic divergence.

The experimental material was sown in a Randomized Block Design with two replications and observations were recorded on randomly selected five plants for twelve characters *viz.* days to 50% flowering, days to physiological maturity, plant height (cm), panicle length (cm), number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, number of infertile spikelets panicle^{-1}, spikelet fertility (%), test weight (g), grain yield plant^{-1} (g) and grain type.

Genotypic coefficient of variation (GCV) was lower than the phenotypic coefficient of variation (PCV) for all the characters under investigation. The high GCV and PCV was observed for plant height, panicle length, number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, number of infertile spikelets panicle^{-1}, test weight and grain yield plant^{-1}indicating the presence of large variation among the genotypes for these characters. Seven characters exhibited high GCV and PCV, panicle length recorded moderate GCV and PCV, while three characters *viz;* days to 50% flowering, days to physiological maturity and spikelet fertility recorded low GCV and PCV.

All heritability values were more than 60% so all characters were classified under high heritability which indicates high transmission of characters from parents to their offspring which will be helpful for selection in future hybridization programme.

High heritability coupled with moderate genetic advance was observed in days to 50% flowering, days to physiological maturity, number of infertile spikelets plant^{-1}, spikelet fertility and grain yield plant^{-1} indicating that additive and non-additive both gene action were present. The

Continued……

characters such as plant height, number of spikelets panicle^{-1} and number of fertile spikelets panicle^{-1} exhibited high heritability coupled with high genetic advance indicating that most likely heritability is due to additive gene effect and selection may be effective for these characters.

Grain yield plant^{-1} was in highly significant positive relationship with test weight, number of panicles plant^{-1}, number of fertile spikelets panicle^{-1}, number of spikelets panicle^{-1}, spikelets fertility and panicle length indicating that selection for these characters would benefit in improvement of genotypes. Number of infertile spikelets showed highly significant negative relationship with grain yield plant^{-1}.

Data revealed that test weight exhibited highest positive direct effect on grain yield plant^{-1} and subsequently by spikelet fertility, number of panicles plant^{-1}, plant height, number of spikelets panicle^{-1}, panicle length and days to physiological maturity. Whereas, number of fertile spikelets panicle^{-1} recorded the highest negative direct effect on grain yield plant^{-1}. The characters *viz.*, number of panicles plant^{-1}, number of spikelets panicle^{-1}, spikelet fertility, test weight had exerted significant positive direct effect on grain yield plant^{-1} and correlation of these characters with grain yield plant^{-1} was positively significant. Thus, for yield improvement direct selection for these traits would be rewarding.

Fifty genotypes were grouped into eight clusters. Cluster II was biggest and consisted of 19 genotypes followed by cluster I with 11 genotypes. The cluster III and V both were consist of 8 genotypes. All remaining clusters *viz.*, cluster IV, VI, VII and VIII were solitary, with one genotype in each of these clusters. Intra cluster distance was ranged from zero (cluster IV, VI, VII and VIII) to 13.15 (cluster V). The highest intra cluster distance was observed in cluster V followed by cluster III, cluster II and cluster I. The high intra cluster distance values indicates the existence of variability within the cluster. Hence, there is a scope for exchange of genes among genotypes within these clusters. From the inter cluster D^2 values of the eight clusters, it can be seen that the highest divergence occurred between cluster VII and VIII followed by cluster I and VI, cluster VI and VII suggesting that the crosses involving varieties from these clusters would give wider and desirable recombination.

The character plant height had contributed highest for divergence, followed by number of spikelets panicle^{-1}, days to physiological maturity, days to 50% flowering, number of panicles plant^{-1}, panicle length, grain yield plant^{-1}, test weight, spikelet fertility and number of fertile spikelets panicle^{-1}. A trait, number of infertile spikelets panicle^{-1}, didn’t contribute at all towards total divergence. The plant height, number of spikelets panicle^{-1}, days to physiological maturity and days to 50% flowering together contributed 87.35% towards total divergence.

From the present study, on the basis of inter cluster distances and cluster mean values, the genotypes *viz.* Phule Samruddhi, IGP Local, Basmati 370, Vikram, Darna, IR 36, Pawana, IGP Local-3, IGP Local-8, Bhogawati, Kala Namak, Ratna, China 26 and LK-248 were concluded as diverse and could be classified as promising genotypes in crossing programme to achieve desired segregants in rice.

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1. INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important staple food crops for more than 60% of the world population and it has been the cheapest source of food, energy and protein. It belongs to family Poaceae (Gramineae) that includes other cereals such as wheat and corn. It provides 43% of calories of human diet in India; and contributes 20-25% of agricultural income due to its intensive cultivation. In Asia, majority of the population consumes rice in meal every day. In many countries, rice accounts for more than 70% of human calorific intake.

In India, rice is cultivated in an area of 43.79 MH with the production and productivity levels of 116.42 Mt and 2659 kg/ha, respectively (Anonymous, 2018), while in Maharashtra, rice is cultivated in an area of 1.54 MH with the production of 3.51 Mt (Anonymous, 2019). West Bengal has the highest rice production, while Punjab has the highest productivity of rice in India.

To fulfil the increasing food demands of the growing population and to achieve food and nutritional security in the country, the present food grain production levels need to be enhanced by 2 Mt every year. This would be achieved, when the productivity of the presently grown varieties is further increased by 20-25% by altering the genetic architecture. Any breeding programme to be successful it depends upon the degree of genetic variability available in the crop species, the efficiency of selection technique implemented by plant breeder. Grain yield is a complex phenotypic character which get influenced by several quantitative traits, these are governed by polygenes. An implementation of biometrical techniques in plant breeding has helped to better understand the genetics of quantitative characters and has proved useful to the plant breeder for systematic analysis at genetic level.

Genetic diversity within crop species is essential to maintain high level of productivity. The importance of information about the degree of genetic divergence in rice and its utilization for the selection of desirable parents either for exploitation of hybrid vigour or to get desirable segregants has been put forth by many workers (Anand and Murthy, 1968). Arunachalam (1981) reported that the greater probability of getting heterotic hybrids and improved variation in the segregating population of varietal improvement programmes mainly depended on genetic diversity. The variability and novel characters existing in the germplasm can be utilized during crossing programme to develop improved varieties and hybrids. Germplasm has to be characterized and the genetic diversity must be studied to use it effectively in the breeding programme.

A detail understanding of nature and degree of genetic variability and correlation of characters in a crop species is essential for a successful breeding programme. Information on direct and indirect effects exhibited by each yield contributing character towards yield will help in the selection process. In addition to the above estimates, analysis of degree of divergence in a given experimental material is of great value in identification of diverse genotypes for further use in hybridization programme to sustain variability. Mahalanobis D^2 statistic has proved to be a helpful tool for quantifying genetic divergence in a given population. Murthy and Arunachalam (1966) stated that multivariate analysis with Mahalanobis D^2 statistics is a tool to know the clustering pattern which helps to establish the relationship between genetic and divergence and to determine the contribution of different quantitative characters towards the divergence. Diverse genotypes could be obtained by collection from different eco-geographical regions or diversity could be induced by combination breeding.

Grain yield is result of integration of other component factors. Therefore, an analysis of the association between yields and other morphological components through correlation coefficient studies would be vital to understand the intricacy of the trait. Therefore, adequate knowledge about the degree and direction of association between yield and its contributing traits is of great significance for breeders when they have had to exercise selection for simultaneous improvement of more than one character for implementing productive breeding programme. However, simple correlation doesn’t take into consideration the complex relationship among various characters, which are related to dependent variable. In such a situation, path coefficient analysis which was proposed by Dewey and Lu (1959) proves helpful in partitioning the correlation coefficient into direct and indirect effects for set of independent variables on dependent variable.

Robinson *et al.* (1949) stated that heritability is the main concern to breeder, since it indicates that improvement can be achieved through selection. Heritability together with genetic advance would bring out the genetic gain expected from selection (Johnson *et al.,* 1955). The knowledge of the source of genetic diversity for the different characters is considered of great importance, since the target of the plant breeder is to improve the yield and the quality by evolving superior varieties. An investigation into the divergence is advantageous for understanding the course of evolution and classifying population into groups on the basis of diversity.

With this available background information, the present studies have been initiated with the following objectives:

1) To understand the variability for grain yield and yield contributing characters in rice.
2) To assess the genotypic and phenotypic correlation between yield and yield contributing characters.
3) Estimation of direct and indirect effect of different quantitative characters on seed yield.
4) To identify suitable parents for future hybridization programme on the basis of genetic divergence.

2. REVIEW OF LITERATURE

This study was aimed at evaluating the statistical characteristics of genetic variability, correlation coefficient and genetic diversity in 50 rice genotypes. As a result, in this chapter, the literatures on variability, heritability, genetic advance, correlation coefficients, path analysis and genetic diversity in rice (*Oryza sativa* L.) have been reviewed under following headings:

2.1 Genetic variability

2.2 Correlation and path analysis

2.3 Genetic divergence

2.1 Genetic Variability

All crop improvement programmes are generally founded on the nature and extent of variability. According to Allard (1960), yield is a complex quantitative character that is polygenically regulated and heavily influenced by the environment. To get a genuine estimate of the genetic coefficient of variability as a meaningful measure of the degree of genetic variation present in the population, partitioning observed variability into heritable and non-heritable components is critical.

Fisher (1930) was the first to provide a strategy for distinguishing genotypic and phenotypic effects caused by genotypic and environmental variables. He used an acceptable statistical approach to depict the degree of genotypic variability and that value was stated as a genotypic coefficient of variation.

Reddy *et al.* (1995) found considerable genotypic variation for all yield-related parameters such as number of tillers plant^{-1}, number of grains panicle^{-1}, 1000 grain weight and the yield plant^{-1}.

Pattanayak and Gupta (1999) assessed nine rice genotypes for yield components that were developed through F2 derived anther culture. For most traits, phenotypic coefficients of variation were larger than genotypic coefficients of variation, showing that the environment had an impact.

Yadav (2000) examined nine rice cultivars for performance in 1999 in Chhattisgarh, Madhya Pradesh, India (Annada, Aditya, Kalinga-3, Poorva, Sariya, Tulsi, Poornima, Gonda and Dani Gonda). Spikelets panicle^{-1} and grain yield had shown high genotypic and phenotypic coefficients of variation. Days to 50% flowering, days to maturity, plant height, number of panicles metre^{-1} row, panicle weight, test weight and grain length were all measured using the moderate PCV and GCV. The genotypic and phenotypic variance of the panicle length was reduced. With the exception of plant height and panicle length, all variables showed strong heritability and genetic progress.

Sinha *et al.* (2004) assessed variability in nineteen local midland landraces of rice of surguja district along with IR36 for yield and yield contributing characters. Grain yield was shown to have the highest genotypic coefficient of variation followed by test weight and panicle plant^{-1}.

Karim *et al.* (2007) examined variability and genetic parameter in forty-one aromatic rice genotypes. The phenotypic variance recorded was higher than the corresponding genotypic variance for all the characters. These variations were found in the number of panicles hill^{-1}, the number of filled grains panicle^{-1} and spikelet sterility (%) which indicate that the environment has a higher effect on the expression of these traits. The character test weight and days to maturity exhibited least difference between phenotypic and genotypic variance, which indicated additive gene action for expression of the characters.

Padmaja *et al.* (2008) recorded significant differences for all observed characters except leaf width and 100 seed weight among the genotypes. Except for days to 50% flowering and panicle length, all of the GCV and PCV estimates were high.

Rita *et al.* (2009) examined genetic parameters of yield and its contributing characters. A trial was conducted with four CMS lines, thirty-two hybrids and eight testers which were evaluated for thirteen characters related to yield. The GCV and PCV were found to be low, moderate and high. Total number of fertile spikelets panicle^{-1}, test weight and spikelet fertility (%) all had high GCV and PCV.

Sabesan *et al.* (2009) studied fifty-four rice varieties with diverse origin for genetic variability under costal low lands. PCV values were somewhat higher than that of GCV, indicating that environmental factors had little impact on character expression.

Ubarhande *et al.* (2009) assessed forty-four indica rice cultivars. Grain yield plant^{-1} had the highest PCV and GCV estimates of all characters, followed by filled grains panicle^{-1} and effective tillers plant^{-1}. Chlorophyll concentration had the highest broad sense heritability, followed by grain length and grain breadth.

Umadevi *et al.* (2009) studied genetic variability and correlation coefficients in seventy-four rice genotypes for morphological traits. Highest GCV and PCV were recorded for number of tillers plant^{-1}, leaf length and straw yield.

Atanu and Sabesan (2010) studied genetic variability in different traits in relation to lodging in 80 genotypes of rice. Preliminary results indicate highly significant differences for all traits studied thereby indicating the presence of genetic diversity.

Jayasudha and Deepak (2010) examined genetic variability in forty-seven rice genotypes including thirty-three hybrids and fourteen parents for grain yield and some physiological traits. For all of the traits, ANOVA revealed lot of variation between genotypes. Grain yield plant^{-1} and spikelet fertility showed high genotypic and phenotypic coefficients of variation (%).

Karthikeyan *et al.* (2010) assessed genetic parameters of variability and heritability of different characters in thirty-six genotypes of rice. The maximum GCV and PCV values were observed for grain yield plant^{-1} and number of branches panicle^{-1}.

Nandan *et al.* (2010) studied variability, degree of association between yield and it`s component characters and their direct and indirect effects on grain yield in rice (*Oryza sativa* L.). Thirty-three genotypes were undertaken research to see how efficient they were in terms of twenty yield and quality parameters.

Nandeshwar *et al.* (2010) examined twenty-five F_2 progenies derived from the crosses involving HYVs and quality rice. For assessing phenotypic variance, genotypic variance, GCV, PCV, genetic advance, heritability (broad sense), correlation coefficient and path coefficient, eleven biometrical characters were analysed. For all of the traits tested, analysis of variation indicated significant variability in genotypes.

Santosh *et al.* (2010) studied that traditional agro-ecosystem have been playing a key role in conserving agricultural diversity and assessment at genetic level is a prerequisite for understanding detrimental evolutionary patterns and devising appropriate plans for their conservation and sustainable use. The goal of this study was to better understand farmer management of rice landrace population structure in conventional farming systems, as well as inter and intra population molecular variations at microsatellite loci. The range was displayed for many characteristics such as panicle length (15.92 - 27.00 cm), days to maturity (122 - 179 days), grain yield plant^{-1} (4 - 17 g) and straw yield (45 - 95 g).

Sangam Kumar *et al.* (2011) concluded that the differences among eighty-one genotypes were significant for all characters except flag leaf width. Among all traits number of spikelets panicle^{-1} exhibited high estimates of GCV and PCV followed by harvest index, grain yield hill^{-1} and number of panicles hill^{-1}.

Abdul *et al.* (2011) carried out research work to study the response of rice genotypes and their quantitative traits under alkaline soil conditions to examine the variability, heritability and genetic advance. For the examined variables, variability analyses found considerable differences between genotypes. Total spikelet panicle^{-1}, test weight and total biomass all had high heritability and genetic advance. The traits that showed a significant positive relationship with grain yield were the number of productive tillers, total spikelets panicle^{-1}, days to 50%

flowering and plant height. As a result, these features that contribute to grain yield in alkaline soils could be used in future breeding programmes.

Keshava *et al.* (2011) recorded significant difference in the genotypes for the traits days to flowering, plant height, grain yield, panicle number, panicle length and test weight. Plant height and days to flowering had higher heritability coupled with high genetic advance.

Venkata *et al.* (2011) studied the extent of variability and its genetic parameters with 16 parents and 48 hybrids for nine yield and its components and twenty-five quality characters. The difference between PCV and GCV was relatively low for all the characters, indicating less environmental influence. High GCV and PCV were recorded for total number of productive tillers plant^{-1} and number of grains panicle^{-1}.

Parikh *et al.* (2012) reported highly significant differences in MSS for genotypes for all the characters indicating the existence of high variability among the varieties. Thus, there is a scope for selection of different quantitative characters for rice improvement. A perusal of GCV revealed that maximum value of variation was recorded for spikelet sterility percentage followed by hundred seed weight, fertile spikelet panicle^{-1}, spikelet density and grain yield plant^{-1}. The fertile spikelet panicle^{-1} exhibited maximum PCV followed by spikelet density and 100 seed weight.

Tuwar *et al.* (2013) concluded on twenty-nine genotypes of rice and revealed that GCV and PCV values of plant height were high, followed by number of tillers, effective tillers plant^{-1}, number of spikelets and grain weight panicle^{-1}. Heritability was higher for days to 50% flowering and subsequently for number of days to maturity, plant height and panicle length which implied that these traits would respond to selection due to their high genetic variability and transmissibility. High heritability with high GAM was recorded for number of spikelets, number of grains panicle^{-1} and grain weight panicle^{-1}. These characters indicated that predominance of additive gene effects in their expression and they would respond to selection effectively as they are less influenced by environment.

Lingaiah *et al.* (2014) revealed in the present study analysis of variance, the existence of significant differences in genotypes for all traits studied. All traits under study had higher PCV than GCV. The magnitude of PCV and GCV was moderate to high for the traits number of grains panicle^{-1}, test weight and yield. The high PCV observed for number of grains panicle^{-1}, test weight and yield. The high GCV obtained for number of grains panicle^{-1} indicating the improvement is possible through selection. GCV measures the extent of genetic variability (%) for a trait but does not assess the amount of genetic variation which is heritable. Heritability estimates were reported high for all characters except for number of productive tillers plant^{-1}. The traits number of grains panicle^{-1}, test weight, yield and plant height exhibited high magnitude of GAM. The traits numbers of grains panicle^{-1}, test weight, plant height and yield have high heritability along with GAM which indicate that these characters show predominance of additive gene effects which are fixable revealing that improvement in these characters will be possible through direct selection.

Fathelrahman *et al.* (2015) reported that GCV measures the range of variability in crop and also enables to compare the amount of variability present in different characters. The PCV estimates were higher than GCV for all the characters studied among the eighteen rice genotypes indicated the substantial effect of environment in the expression of these characters.

Sandeep *et al.* (2018) studied variability, heritability and genetic advance in rice (*Oryza sativa* L.) with two hundred genotypes of rice. Analysis of variance revealed highly significant differences among the genotypes for all the characters indicating sufficient variability existed in the present material selected for the study. Environmental influence was less on the expression of all the characters as there is a narrow difference between GCV and PCV. GCV and PCV values were high for single plant yield, number of grains panicle^{-1}, number of tillers hill^{-1} and spikelet fertility. The characters *viz.* spikelet fertility, plant height, single plant yield, number of grains panicle^{-1}, number of tillers hill^{-1}, number of productive tillers hill^{-1}, panicle length and test weight exhibited high heritability estimates along with high GAM which suggested that these traits were beneficial for further improvement by following simple selection methods.

Lingaiah *et al.* (2020) studied genetic variability and correlation in elite rice genotypes. The values of GCV and PCV were moderate for number of grain panicle^{-1}, test weight and yield and low for days to 50% flowering, number of effective tillers plant^{-1} and plant height. High heritability coupled with high GAM was found for number of grains panicle^{-1}, test weight and yield indicating the predominance of additive type of gene action and selection may be effective for improving these characters. Test weight exhibited positive and significant correlation with grain yield indicating the importance of this character for yield improvement. Selection for the characters no. of grains/panicle and test weight would be effective in improvement of yield in rice crop.

2.2 Correlation and Path Analysis

The knowledge of nature and extent of association between characters pair would give impulse to the selected programme aimed at the improvement in grain yield. As yield is a complex character and is governed by polygenic system, it is highly influenced by environmental fluctuations. Genotypic correlation coefficient measures the genotypic association between characters and indicates more useful characters. They provide useful information to the breeder in assessing nature of the species on which they work. It also helps in identifying characters that have little or no importance in the selection of programme. Correlation coefficient estimates give the amount of association between any pair of characters but direct and indirect effects of the contributing characters of yield are not revealed by this study. However, path coefficient analysis helps in partitioning the correlation coefficient into direct and indirect effects, thereby providing relative importance of each of causal factors. Dewey and Lu (1959) used this technique first time for plant selection in crested wheat grass. Many workers have studied the relationship between yield and other characters and carried out path analysis in rice. A brief review is given below.

Sawant *et al.* (1995) studied on character association indicated that test weight, panicle length and grains panicle^{-1} were significantly and positively correlated with grain yield. Grains panicle^{-1}, test weight and plant height were the components which influenced the grain yield.

Sarawgi *et al.* (1997) studied association analysis indicating that grain yield of rice had positive correlations with number of fertile spikelets panicle^{-1} and hundred grain weight. Path coefficient analysis revealed that direct selection for number of fertile spikelets panicle^{-1} would likely be effective for increasing grain yield. Direct selection of number of effective tillers plant^{-1}, grain yield plant^{-1} and hundred grain weight would increase harvest index. This study also revealed that there is no common causal factor that directly influenced both grain yield and harvest index, though, hundred grain weight could be augmented in selection criteria for the simultaneous improvement of both the traits.

Sangeeta *et al.* (2001) conducted a field trial during the kharif season of 1998 in Akola, Maharashtra, to investigate the correlation between the growth and yield contributing characters and crop yield of upland rice. Observations were recorded for growth attributes (plant height, number of tillers plant^{-1}, total dry matter plant^{-1}, leaf area plant^{-1} and leaf area index), yield attributes (number of effective tillers meter^{-1} row length, number of panicles plant^{-1}, length and weight of panicles, number of unfilled grains panicle^{-1}, test weight and grain yield plant^{-1}). A positive and significant correlation was observed between grain yield and total dry matter plant^{-1}, number of panicles plant^{-1}, panicle length, weight of panicle, unfilled grains plant^{-1} and test weight. Optimum sowing time and seed rate increases the growth and yield contributing characters, which results in the increase in yield.

Basavaraja *et al*. (2011) carried out an investigation in 100 local rice cultivars to understand the association among yield components and their direct and indirect influence on the grain yield. The correlation analysis indicated that grain yield was significantly associated with panicle length, test weight, number of tillers plant^{-1}. Path coefficient analysis revealed that, days to 50% flowering, plant height, panicle length, panicle number, number of productive tillers plant^{-1} had positive direct effect on grain yield. Even number of spikelet panicle^{-1} had positive significant correlation with grain yield but its direct effect on grain yield was negative. It is due to the maximum indirect effect of days to 50% flowering which is nullifying its negative direct effect on grain yield. The residual effect (0.0854) was very low which indicates that much of the variation in yield has been the result of characters studied and the choice of characters was appropriate. Hence, selection based on these traits could bring out simultaneous improvement of yield and yield attributes.

Dhakal *et al.* (2017) studied the correlation of thirteen yield contributing characters and nine grain quality characters with grain yield of aerobic rice genotypes on Vertisols. Correlation analysis of yield contributing characters shows that all the characters under study were significantly and positively correlated with grain yield plant^{-1} except days to 50% flowering and days to maturity at both genotypic and phenotypic levels. Path analysis studies of yield contributing characters indicated that number of effective tillers plant^{-1} had maximum positive direct effect followed by number of grains panicle^{-1} and test weight on grain yield plant^{-1}.

2.3 Genetic Divergence

Genetic improvement in any crop mainly depends on amount of genetic variability available in the population. This importance of genetic diversity in crop plants was first realized by Darwin and the term “morphism” employing genetic morphs which means the existence of distinct genetic forms in balance in a population.

This is conceivable using Mahalonobis's suggestion of a generalised distance between any two pairs of groups (1936). With many researchers realising that geographical isolation may not be the main cause of genetic divergence, Mahalanobis D^2 became a valuable statistical method for measuring it. Plant breeders have employed divergence analysis to help them classify their breeding material into useful categories.

Chaturvedi H. P. and Maurya D. M. (2005) studied genetic divergence analysis in 26 genotypes of rice for 20 characters. The genotypes were grouped in 8 clusters. Comparison of cluster means revealed that cluster VIII gave exceptionally high values for seven characters followed by cluster VII. The maximum inter cluster D^2 value was obtained between cluster III and VI. It is suggested that for developing better cultivar, the genotypes of cluster III could be utilized in hybridization programme with the genotypes of cluster VI and VIII.

Vaithiyalingan *et al.* (2005) collected twenty-nine strains of rice from different geographical regions of world and analysed the extent of genetic divergence. The genotypes were grouped into four clusters. The clustering pattern was independent of the geographical distribution, cluster II included 23 genotypes and these can be useful in hybridization to create a wide spectrum of variability. The highest inter cluster distance (97.34) was observed between clusters III and IV. Plant height, single plant yield and test weight were found to have significantly contributed to genetic divergence.

Gahalain *et al.* (2006) grouped 55 genotypes into 12 clusters based on D^2 values. High mean values for grain yield plant^{-1}, panicle length and weight, straw yield plant^{-1}, days to 50% flowering and days to maturity were observed in cluster VII. The maximum mean values for grain yield plant^{-1}, tillers plant^{-1} and test weight were obtained in clusters V, XII, X respectively. The highest contribution to divergence was recorded by total grains panicle^{-1} (22.6%), days to 50% flowering (7.6%) and shoot weight (7.2%).

Reddy *et al.* (2006) determined the genetic divergence in 64 early rice genotypes. Based on 10 yield contributing characters, these genotypes were grouped into 13 clusters. There was no relationship observed between geographical distribution and genetic diversity. Per cent contribution of characters *viz.* test weight, plant height, grain yield plant^{-1} and number of spikelets panicle^{-1} was highest into genetic divergence indicating that priority should be given to these characters while selecting parents from distant clusters for hybridization.

Chandra *et al.* (2007) assessed fifty-seven upland rice genotypes for genetic divergence based on 14 traits following Mahalanobis D^2 statistics and Anderson's canonical analysis. On the basis of D^2 values, the 57 genotypes were grouped into five clusters following Tocher's method. The most divergent clusters were III and IV (D^2 =3387.9) followed by III and V (D^2 = 2808.2) and clusters II and III (D^2 = 1908.7). Highest intra cluster distance was observed in cluster I followed by cluster II. Cluster I was largest one containing 50 genotypes from different origin. The clustering patterns of the genotypes indicated that the geographical origin and genetic diversity were not related. The characters contributing more towards the genetic divergence were grain L:B ratio, test weight, grain length, grain yield and biological yield.

Karthikeyan and Anubuselvam (2008) conducted divergence analysis with fifty-five cultivars of rice using Mahalanobis's D^2 statistic. The genotypes were grouped into five clusters. The association between genetic and geographic diversity cannot be generalized. Maximum intra cluster distance was observed within cluster III followed by cluster I. Plant height was the major contributor to the total divergence followed by boot leaf length.

Bupesh Kumar *et al.* (2014) reported 23 genotypes of rice were grouped into five clusters. Among the five clusters cluster III consisted of 7 genotypes (IARI 1460, PB-1, Basmati 564, Pusa 1121, SJR-129, Basmati 1509 and Pusa Sugandh) forming the largest cluster followed by cluster I and IV with 5 genotypes each (K-343, K-448, K-39, SJR-51, Gizza-14 and Saanwal Basmati, RR 600, Ranbir Basmati, Basmati 370, CSR 30) cluster II containing 4 genotypes (PC 19, Ratna, IET 1410, SJR 5) and cluster V including 2 genotypes (Jaya, RR 8585).

Nitesh Kumar *et al.* (2014) grouped 134 genotypes into five clusters based on Euclidean cluster analysis. The pattern of grouping of genotypes into various clusters was random and independent of geographical origin indicating geographical diversity and genetic diversity were not related.

Rai *et al.* (2014) studied genetic divergence as an efficient tool for the selection of parents used in hybridization programme. Forty rice genotypes were raised for identification of diverse genotypes using D^2 analysis. The forty genotypes were grouped into seven clusters based on Tocher cluster analysis with cluster III containing the maximum of 10 genotypes. The highest inter cluster distance was observed between cluster IV and VII followed by cluster III and VII, cluster III and VI these lines may be utilized in further breeding programme for the exploitation of hybrid vigour. The highest intra cluster distance was observed in cluster III indicates hybridization involving genotypes within the same cluster may result in good cross combinations. Among the thirteen traits studied, maximum contribution towards divergence was made by number of spikelets panicles^{-1} (38.08%) followed by grain yield (23.08%), plant height (13.59%) and flag leaf length (13.21%). Hence, these characters should be given importance during hybridization programme.

Tulasi Guru *et al.* (2017) grouped 58 genotypes into 13 clusters, of which clusters VII and XII (36.93) recorded maximum inter-cluster distance followed by clusters II and VI (33.48) and clusters XI and XIII (33.35). Hence, the genotypes in cluster VII *viz.* E-2940, E-3118, TJP-5, TJP-198, TJP-9, E-3138 and TJP-142 had wider diversity with RPHR-1005 in cluster XII and the genotypes in cluster II *viz.* TJP-2, TJP-221, TJP-81, TJP-138, TJP-186, TJP224, E-2875, TJP-229, TJP-60, TJP-58, TJP-99, TJP-6, TJP-191 and E-2710 had wider diversity with IBL-57 in cluster XIII and these lines may be utilized in further breeding programme for the exploitation of hybrid vigour.

Devi *et al.* (2020) assessed genetic divergence and variability among 33 elite germplasm lines which were evaluated in RBD with an objective to classify and understand the nature and magnitude of genetic diversity and variability with regard to grain yield, yield components and quality traits using Mahalanobis D^2 statistics. Genotypes were grouped into eight clusters and cluster I was the largest comprised of 23 genotypes. The maximum cluster distance was found between cluster II and cluster IV (2178.98). The minimum inter cluster distance was observed between cluster I and cluster III (540.96). The intra cluster distance was maximum for cluster II (354.1) indicating existence of variability within the cluster. A perusal of results on cluster means revealed that cluster VIII recorded highest cluster mean for yield plant^{-1}, panicle length, test weight, plant height. The most important trait contributing maximum towards divergence was plant height (31.8) which ranked 168 times first. PCV was slightly higher than GCV for all the traits. Moderate GCV and PCV estimates were observed for filled seeds panicle^{-1}, test weight, yield plant^{-1}. High heritability coupled with moderate GAM was observed for test weight, filled seeds panicle^{-1}, yield plant^{-1}.

Sujitha *et al.* (2020) studied genetic diversity and correlation in Rice. Understanding of genetic divergence and traits association among 108 rice genotypes, nine morphological traits were studied. Based on their D^{2} values the genotypes were grouped into 14 clusters and the maximum of 37 genotypes grouped under cluster 1. The highest intra and inter cluster distance was observed in cluster X and between cluster XII and XIV respectively. The trait grain length recorded maximum contribution to the divergence followed by plant height. Selection based on these traits would be more effective in creation of divergent population. Moderate PCV and GCV, high heritability and high GAM were observed for all the traits studied. The traits, number of productive tillers plant^{-1}, number of grains panicle^{-1} and thousand grain weight had shown significant positive correlation with yield and also recorded high direct effect on yield. Hence the selection based on these traits may helpful in planning efficient breeding programs.

3. MATERIAL AND METHODS

The present research work was carried out during *kharif*, 2020 at Zonal Agricultural Research Station, Igatpuri. The material used and methods followed are presented below.

3.1 Material

For the present study, 50 genotypes of rice originating from different geographic regions and showing phenotypic variability for different Agronomic yield characters were used from the germplasm maintained by Zonal Agricultural Research Station, Igatpuri.

3.2 Methods

3.2.1 Raising of Seedling

The 50 genotypes of rice were sown on 15th June, 2020 in a Randomized Block Design with two replications. Each entry was represented by a quadral row of 3 m length and 0.8 m breadth with a spacing of 25 cm between rows and 15 cm between plants within a row. Two border rows were sown on both the sides of plots to reduce the border effects. 3-4 grains were dibbled hill^{-1} to ensure better crop stand and a single seedling was kept hill^{-1} after thinning of seedlings.

Table 3.1 List of fifty rice genotypes

Sr. No.	Genotype	Source
1	Vikram	ARS, Shirgaon
2	Darna	ZARS, Igatpuri
3	Manibhog	ARS, Vadgaon Maval
4	Basmati370	ARS, Vadgaon Maval
5	PAU3079	PAU, Ludhiana
6	Jay Bangal	ARS, Vadgaon Maval
7	Nizamgod	ARS, Vadgaon Maval
8	W355	ARS, Vadgaon Maval
9	IGP Local	ZARS, Igatpuri
10	Varanasi	ARS, Varanasi
11	China-26	ARS, Vadgaon Maval
12	Krishna Sal	Farmer from Karad
13	Ratna	RARS, Karjat
14	IR 36	RARS, Karjat
15	RDN 185-2	ARS, Radhanagari
16	T-3	ARS, Radhanagari

17	Kala Namak	ARS, Radhanagari
18	Kala Girga	ARS, Radhanagari
19	Pawana	ARS, Vadgaon Maval
20	Adhaya	ARS, Vadgaon Maval
21	Pusa Basmati	Farmer from Karad
22	VDN-5-2-1-2	ARS, Vadgaon Maval
23	RTN-711	ARS, Shirgaon
24	IGP Local-3	ZARS, Igatpuri
25	VDN-1-6-1	ARS, Vadgaon Maval
26	Bhandardara Local	Farmer from Bhandardara
27	Ambemohor 157	ARS, Vadgaon Maval
28	P-6	ARS, Vadgaon Maval
29	IGP Local-8	ZARS, Igatpuri
30	RTN-24	ARS, Shirgaon
31	Almu Sathi	ARS, Shirgaon
32	IGP Local-10	ZARS, Igatpuri
33	Tilsha	Farmer from Bhandardara
34	P-1	Farmer from Bhandardara
35	NK-3325	Farmer from Bhandardara
36	Bhadas Bhog	Farmer from Bhandardara
37	KJT-3	RARS, Karjat
38	Phule Samruddhi	ARS, Vadgaon Maval
39	PKV HMT	ARS, Sindewahi
40	PKV Khamang	ARS, Sindewahi
41	Phule Radha	ARS, Radhanagari
42	KJT-4	RARS, Karjat
43	LK-248	ZARS, Igatpuri
44	Bhogawati	ARS, Radhanagari
45	Vasumati	Local collection from Nagpur
46	SKL-8	ARS, Sakoli
47	SYE-2001	ARS, Sindewahi
48	PKV-Kisan	ARS, Sindewahi
49	SYE-5	ARS, Sindewahi
50	PKV Makrand	ARS, Sindewahi

3.2.2 Cultural Practices

All prescribed agronomic techniques were implemented as needed. During crop period, the fertiliser dose was 100 kg N, 50 kg P_2O_5 and 50 kg K_2O ha^{-1}. Nitrogen is applied in three split dosages of 40, 30 and 30 kg N ha^{-1}, respectively, at field preparation, 35- 40 days after planting and panicle initiation. At the time of seeding, a full dose of P_2O_5 and K_2O was administered.

3.3 Observations Recorded

The following 11 quantitative and one qualitative character observations were made on five randomly selected plants from each plot in each replication. These plants were tagged before they bloomed. The characters studied and the techniques used to record observations are listed below.

3.3.1 Days to 50% Flowering (No.)

The number of days from sowing to the days when 50% of the plants' primary panicles were in heading was recorded.

3.3.2 Days to Maturity (No.)

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

3.3.3 Plant Height (cm)

Plant height is measured in centimetres from ground level to the tip of the tallest panicle in each plant at the time of harvest.

3.3.4 Panicle length (cm)

It was measured in centimetres at the time of plant maturity from the base of panicle to the tip of last spikelet prior to harvesting.

3.3.5 Number of Panicles Plant^{-1} (No.)

Number of panicles plant^{-1} was counted at the time of harvest.

3.3.6 Number of Spikelets Panicle^{-1} (No.)

The total spikelets of panicles plant^{-1} were counted and average of that was expressed as number of spikelets panicle^{-1}.

3.3.7 Number of Fertile Spikelets Panicle^{-1} (No.)

The total fertile spikelets of panicles plant^{-1} were counted and average of that was expressed as number of fertile spikelets panicle^{-1}.

3.3.8 Number of Infertile Spikelets Panicle^{-1} (No.)

The total infertile spikelets of panicles plant^{-1} were counted and average of that was expressed as number of infertile spikelets panicle^{-1}.

3.3.9 Spikelet Fertility (%)

The chaffy spikelets were separated out from filled and partially filled spikelets and were counted. Then the percentage of fertility was calculated as follows,

$$\text{Spikelet fertility (\%)} = \frac{\text{Number of filled spikelets}}{\text{Total number of spikelets}} \times 100$$

3.3.10 Test Weight (g)

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

3.3.11 Grain Yield Plant^{-1} (g)

Filled grains of all the three selected plants of each genotype were weighed and average yield plant^{-1} was recorded.

3.3.12 Grain Type

Harvested grains of each genotype were visually assessed and designated based on their size and length.

3.4 Statistical Analysis

The data collected for each character on individual plant basis for three randomly selected plants was analysed first by Randomized Block Design (Panse and Sukhatme, 1985) to test the significance of differences among the genotypes. The variability parameters were measured by the formula suggested by Johnson *et al.* (1955). The analysis for divergence was done by following Mahalanobis (1936) D^2 statistics. The path coefficient analysis was carried out by the procedure suggested by Dewey and Lu (1959).

3.4.1 Assessment of Variability

The analysis of variance was done as suggested by Panse and Sukhatme (1985) in the following form,

Source of variation	**D.F.**	**M.S.S.**	**Expected mean square**
Replication	(r-1)	MSr	σ2e + tσ2r
Treatment	(t-1)	MSt	σ2e + rσ2t
Error	(r-1) (t-1)	MSe	σ2e
Total	(rt-1)		

Where, r = number of replications

t = number of treatments

3.4.4.1 Variance:

The genotypic and phenotypic variance was calculated as per the formulae (Burton and Devane, 1953).

$$\text{Genotypic variance } (\sigma^2_g) = \frac{(MS_t - MS_e)}{r}$$

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

Error variance = (σ^2_e)

Where, Ms_t= Mean sum of square due to treatment,

Ms_e= Mean sum of square due to error,

3.4.4.2 Genotypic coefficient of variation (GCV)

Genotypic coefficient of variation (GCV) was estimated by formula suggested by Burton (1952).

$$GCV\ (\%) = \frac{\sqrt{\sigma^2_g}}{x} \text{ x } 100$$

Where, σ^2_g = Vg = Genotypic variance

X = General mean of the character

3.4.4.3 Phenotypic coefficient of variation (PCV)

Phenotypic coefficient of variation (PCV) was also estimated by the formula suggested by Burton (1952).

$$PCV\ (\%) = \frac{\sqrt{\sigma^2_P}}{x} \text{ x } 100$$

Where, $\sigma^2_p = V_p$ = Phenotypic variance

GCV and PCV were classified as follows (Robinson *et al.* 1949)

Low: 0 to 10%

Moderate:10-20%

High: > 20%

3.4.4.4 Heritability (h^2 b.s.)

Heritability estimates in broad sense (h^2) were computed by the formula suggested by Burton (1952).

$$h^2(\text{b.s.}) = \frac{V_g}{V_p} \text{ x } 100$$

Where, h^2 = Heritability (%) in broad sense.

V_g= Genotypic Variance and

V_p= Phenotypic Variance.

Heritability was classified as, (Robinson *et al.* 1949)

Low: 0 to 30%

Moderate: 30-60%

High: > 60%

3.4.4.5 Genetic advance

"Genetic advance can be defined as expected gain or improvement on the next generation by selecting superior individuals under certain amount of selection pressure."

From heritability estimates the genetic advance was estimated by the formula given by Burton (1952).

$$GA = K \times \frac{V_g}{V_p} \times \sigma_p$$

Where, V_g = Genotypic Variance and

V_p = Phenotypic Variance.

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

σ_p = Phenotypic standard deviation.

In order to estimate the relative utility of genetic advance among characters, genetic advance as per cent for mean is usually calculated.

$$\text{Genetic advance as per cent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

The range of genetic advance as per cent of mean was classified as per suggestion by Johnson *et al.* (1955).

Low: less than 10%

Moderate: 10-20%

High: more than 20%

3.4.1 Correlation

The correlation coefficients were calculated at both genotypic and phenotypic level to determine the degree of association of the characters with yield and yield attributes.

For that genotypic and phenotypic correlation coefficients were calculated by adopting method described by Singh and Chaudhary (1985).

Correlation coefficient at genotypic level were calculated as:

$$rg_{xy} = \frac{GCOV_{xy}}{\sqrt{\sigma^2 gx \times \sigma^2 gy}}$$

Where, rg_{xy} = Genotypic correlation between character X and Y,

$GCOV_{xy}$: Genotypic covariance between trait X and Y,

$\sigma^2 g_x$: Genotypic variance of trait X

$\sigma^2 g_y$: Genotypic variance of trait Y

Correlation coefficient at phenotypic level were calculated as:

$$rp_{xy} = \frac{PCOV_{xy}}{\sqrt{\sigma^2 Px \text{ x } \sigma^2 Py}}$$

Where, rp_{xy} = Phenotypic correlation between character X and Y,

$PCOV_{xy}$: Phenotypic covariance between trait X and Y,

$\sigma^2 P_x$: Phenotypic variance of trait X

$\sigma^2 P_y$: Phenotypic variance of trait Y

Significance of correlation coefficients was tested against “r” value at (n-2) degrees of freedom as given by Fisher and Yates (1938) both at 0.05 and 0.01 probability levels of significance.

3.4.2 Path Analysis

Correlation does not state relative importance of influence of the component characters. The path coefficient analysis, a cause-and-effect relationship provides knowledge of relative importance of each of the component character.

Path coefficient analysis was done according to the procedure suggested by Dewey and Lu (1959).

If y is the effect and X_1 is the cause, the path coefficient for the path from cause X_1 to the effect y is

$$\frac{\sigma x_1}{\sigma y}$$

Direct and indirect effects were worked out using genotypic correlation as below.

Direct effect of x_1 on y = Px_1y

Where, Px_1 – Path coefficient of x_1 on y.

Similarly, direct effects of other attributes on yield were worked out.

Indirect effect of x_1 via x_2 on y = $Px_2y.r\ x_1x_2$

Where, Px_2y – Path coefficient of the component character x_2 on y

$r\ x_1x_2$ – Genotypic correlation between x_1 and x_2.

Similarly, indirect effects in all possible combinations were calculated for 10 component characters.

The residual effect (R) was calculated as below:

$R = [1- (Px_1y.\ r\ x_1y) - (Px_2y.\ r\ x_2y)- \ldots\ldots. - (Pxqy.\ r\ xqy)]1/2$

Where, Px_1y, Px_2y, …., $Pxqy$ - Direct effects of respective characters on grain yield,

rx_1y, rx_2y, …., $rxqy$ - Correlation coefficients between respective characters and yield.

3.4.4 Genetic Divergence

The generalized distance between two population is defined by Mahalanobis (1936) as

$D^2 = \Sigma\Sigma\ \lambda ij.\ \delta i.\ \delta j.$

Where, λij = Reciprocal matrix to the common dispersion matrix

δi = difference between the mean values of two populations for i^{th} character

δj = difference between the mean values of two populations for j^{th} character

In the present study, estimating D^2 values from the aforementioned method would have been quite difficult. Because it necessitates the inversion of an eleventh order determinant and the evaluation of 11(11+1)/2 terms whose sum is D^2. It was discovered to be more practical to deal with a collection of uncorrelated characters derived from the original measurements. D^2 with such altered variables reduced to basic sum of squares evaluation. The crucial condensation approach was used for transformation (Singh and Chaudhary, 1985). The transformation coefficient was calculated by dividing the first row of the reduced matrix by the square root of the corresponding pivotal condensation elements.

3.4.4.1 Grouping of genotypes into various clusters

Tocher's method, as described by Rao (1952), was used to generate clusters. There are no systematic rules for locating clusters because the term "cluster" is not well defined. The only criterion appears to be that any two groups belonging to the same cluster should have a lower D^2 on average than those belonging to different clusters. K. D. Tocher suggests a simple device: start with the two closely related groups and identify the third group with the smallest D^2 of the two. Similarly, the fourth cluster was picked to have the least D^2 of the first three and so on. If the average D^2 of a group from those already listed appears to be high at any point, this group does not fit in the former groups and is thus removed from the former cluster. The first cluster's group is then omitted and the remainder are processed identically. It is also useful to determine the change in average D^2 within a cluster as a result of the addition of a new group. If the changes are significant, the newly added group must be considered outside the cluster.

3.4.4.2 Average intra and inter cluster D^2 and D values

Average intra cluster $D^2 = \Sigma\ Di^2 / n$

Where, $\Sigma\ Di^2$ is the sum of distances between all possible combinations (n) of the population included in the cluster.

Inter cluster D^2

$$D^2 = \frac{\Sigma \text{ of distances between the population of cluster i and j}}{Ni.Nj}$$

Where, Ni = Number of populations in cluster i

Nj = Number of populations in cluster j

3.4.4.3 Clusters means

Individual character cluster means were determined based on the mean performance of the genotypes contained in that cluster.

4. RESULTS AND DISCUSSION

The present research work was carried out to estimate the genetic diversity among 50 genotypes of Rice (*Oryza sativa* L.) for twelve characters at Zonal Agricultural Research Station, Igatpuri. The results obtained in the present investigation have been presented in brief under the following headings:

1. Mean performance of genotypes
2. Analysis of variance
3. Parameters of genetic variability
4. Correlation
5. Path analysis
6. Genetic divergence

4.1 Mean Performance of Genotypes

The mean performances of 50 genotypes for grain yield plant^{-1} and yield contributing characters have been presented in the Table 4.1.

4.1.1 Days to 50% Flowering

The average value for number of days to 50% flowering was 109 days. The genotype KJT-4 (94) recorded minimum number of days to 50% flowering and subsequently by SYE-2001 (95), SYE-5 (97), Basmati 370 (98), IR 36 (99), VDN-5-2-1-2 (99) whereas genotype Ambemohor 157 and Bhadas Bhog recorded maximum number of days i.e., 120 days to 50% flowering followed by IGP Local (119) and PKV Khamang (119).

4.1.2 Days to Physiological Maturity

Among 50 genotypes, the genotype KJT-4 took minimum number of days (128) to physiological maturity followed by Basmati 370 and SYE-5 (129), IR-36 (130), PKV-Kisan and PAU-3079 (131), KJT-3 (133). However, Ambemohor 157 recorded maximum number of days (157) to physiological maturity. The general mean for days to physiological maturity was 142 days.

4.1.3 Plant Height (cm)

The overall mean for plant height recorded was 83.55 cm. The genotype Ratna recorded lowest plant height (50.40 cm) among the genotypes. Twenty-four genotypes performed better over the general mean value.

4.1.4 Panicle Length (cm)

The panicle length ranged from 14.00 to 28.20 cm with a general mean of 21.53 cm. The genotype Bhogawati recorded longer panicle length (27.7cm) while genotype RTN 185-2 exhibited shorter panicle length (14.00 cm).

4.1.5 Number of Panicles Plant^{-1}

The mean value for panicles plant^{-1} was recorded 11.09. The genotype Phule Samruddhi was recorded with maximum number of panicles plant^{-1} (17.5), however, genotype RDN 185-2 depicted minimum number of panicles plant^{-1} (5.5). Twenty-three genotypes exhibited a greater number of panicles plant^{-1} as compared to general mean.

4.1.6 Number of Spikelets Panicle^{-1}

The genotype IGP Local recorded higher number of spikelets panicle^{-1} (288) followed by Phule Samruddhi (286), Nizamgod (282) and Pawana (281), whereas genotype Bhandardara Local recorded lower number of spikelets panicle^{-1} (92.5) followed by Pusa Basmati (96.5). The mean number of spikelets panicle^{-1} was 187.9.

4.1.7 Number of Fertile Spikelets Panicle^{-1}

The fertile spikelets panicle^{-1} was ranged from 82.5(Pusa Basmati) to 261.5 (IGP Local). Average value of fertile spikelets panicle^{-1} was 159.2. Twenty-one genotypes produced higher fertile spikelets panicle^{-1}, whereas twenty-eight genotypes recorded lower fertile spikelets panicle^{-1}.

4.1.8 Number of Infertile Spikelets Panicle^{-1} (No.)

The mean value for infertile spikelets panicle^{-1} was 28.73. The genotype IGP Local-10 recorded lowest number of infertile spikelets panicle^{-1} (11) followed by Darna (13), Pusa Basmati (14), PKV Makrand (16), Kala Namak (17), whereas genotype Jay Bangal recorded highest number of infertile spikelets panicle^{-1} (51.5) followed by Almu Sathi (48.5), P-6 (48), Vasumati (47.5), PAU-3079 (46).

4.1.9 Spikelet Fertility (%)

The average spikelet fertility was 83.26%. The spikelet fertility (%) ranged from 58.81 (P-6) to 94.22 (Darna). The highest spikelet fertility (94.22%) followed by the genotype Vikram (92.92%) and Phule Radha (92.34%), whereas genotype P-6 recorded lowest spikelet fertility (58.81%) followed by Manibhog (72.58%), Jay Bangal (72.68%).

4.1.10 Test Weight (g)

The general mean of 18.00 g of test weight was recorded. The highest test weight was recorded by genotype Phule Samruddhi (27.18 g) followed by IGP Local (26.80 g) and IGP Local-3 (25.77 g). However, lowest test weight was exhibited by genotype Bhandardara Local (11.19 g).

4.1.11 Grain Yield Plant^{-1} (g)

The genotype Phule Samruddhi recorded highest grain yield plant^{-1} (34.60 g) followed by IGP Local (33.35 g) and IGP Local-3 (33.28 g), whereas genotype genotype P-6 recorded lowest grain yield plant^{-1} (9.71 g) followed by RDN 185-2 (10.02 g) and Vasumati (11.35 g). The average of grain yield plant^{-1} for studied genotypes was 19.8 g. Out of 50 genotypes thirteen genotypes gave significantly higher yield than the general mean, whereas twenty-four genotypes gave lower yield than mean value.

4.1.12 Grain Type

The genotypes were grouped in five grain types on the basis of visual observation of size and shape of grain. The details of genotype and their grain type have been given in the Table 4.1.

Table 4.1: Grain type

Sr.No.	Genotypes	Grain Type	Sr.No.	Genotypes	Grain Type
1	Vikram	LS	26	Bhandardara Local	MB
2	Darna	LS	27	Ambemohor157	SB
3	Manibhog	LS	28	P-6	SB
4	Basmati370	LS	29	IGP Local-8	SS
5	PAU3079	MS	30	RTN-24	SS
6	Jay Bangal	MS	31	AlmuSathi	MS
7	Nizamgod	SB	32	IGP Local-10	SS
8	W355	SB	33	Tilsha	SB
9	IGP Local	SS	34	P-1	SS
10	Varanasi	SB	35	NK-3325	LS
11	China-26	LS	36	Bhadas Bhog	SB
12	Krishna Sal	MB	37	KJT-3	SB
13	Ratna	SB	38	Phule Samruddhi	MB
14	IR 36	SB	39	PKV HMT	MS
15	RDN 185-2	MB	40	PKV Khamang	SB
16	T-3	SS	41	Phule Radha	LS
17	Kala Namak	LS	42	KJT-4	SB
18	Kala Girga	MB	43	LK-248	SS
19	Pawana	SS	44	Bhogawati	MS
20	Adhaya	LS	45	Vasumati	SS
21	Pusa Basmati	SB	46	SKL-8	LS
22	VDN-5-2-1-2	SS	47	SYE-2001	SS
23	RTN-711	SS	48	PKV-Kisan	LS
24	IGP Local-3	SB	49	SYE-5	MS
25	VDN-1-6-1	SS	50	PKV Makrand	LS

Where,

LS- Long slender, MS - Medium slender,

SB - Short bold,

MB - Medium bold,

SS - Short slender.

Table 4.2: Mean performance of rice genotypes

Sr. No.	Genotypes	Days to 50% flowering	Days to physiological maturity	Plant height (cm)	Panicle length (cm)	No. of panicles plant^{-1}	No. of spikelets panicle^{-1}	No. of fertile spikelets panicle^{-1}	No. of infertile spikelets panicle^{-1}	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1}
1	**Vikram**	103.00	134.00	63.50	26.60	16.50	274.50	255.00	19.50	92.92	21.95	28.62
2	**Darna**	113.00	144.00	58.45	20.15	13.00	231.00	217.50	13.50	94.22	21.57	26.95
3	**Manibhog**	102.00	133.00	54.80	26.10	11.50	146.50	106.50	40.00	72.58	20.39	18.41
4	**Basmati370**	98.00	129.00	65.55	26.90	16.50	279.00	257.50	21.50	92.21	22.45	26.94
5	**PAU 3079**	100.00	131.00	66.40	16.50	11.00	237.50	191.50	46.00	80.57	16.05	17.21
6	**Jay Bangal**	103.00	145.00	109.60	19.70	9.50	187.50	136.00	51.50	72.68	14.40	17.57
7	**Nizamgod**	119.00	150.00	111.95	23.55	11.50	282.00	254.00	28.00	90.01	20.38	26.37
8	**W355**	114.00	152.00	108.50	20.85	10.50	218.00	181.50	36.50	83.34	18.16	18.99
9	**IGP Local**	119.00	151.00	114.95	22.50	16.50	288.00	261.50	26.50	90.85	26.80	33.35
10	**Varanasi**	118.00	152.00	56.60	22.15	9.50	179.00	141.00	38.00	78.65	15.12	18.03
11	**China-26**	100.00	137.00	51.65	24.75	13.50	220.50	195.00	25.50	88.50	20.10	22.49
12	**Krishna Sal**	111.00	141.00	109.75	21.05	9.50	136.50	106.50	30.00	78.24	14.32	21.66
13	**Ratna**	104.00	134.00	50.40	23.60	13.50	194.00	169.00	25.00	87.05	20.35	27.03
14	**IR 36**	99.00	130.00	53.80	26.15	12.50	232.50	209.00	23.50	89.83	22.37	28.19
15	**RDN 185-2**	108.00	137.00	103.55	14.00	5.50	114.00	88.00	26.00	77.42	13.53	10.02
16	**T-3**	109.00	138.00	93.05	23.50	10.50	126.50	97.50	29.00	77.05	13.63	12.70
17	**Kala Namak**	113.00	142.00	95.10	24.70	11.50	209.00	192.00	17.00	91.92	19.86	25.41
18	**Kala Girga**	112.00	143.00	108.50	20.55	9.00	133.50	105.50	28.00	78.74	13.42	11.81
19	**Pawana**	107.00	146.00	58.45	20.95	15.50	281.00	255.00	26.00	90.68	23.76	29.22
20	**Adhaya**	102.00	136.00	97.65	17.70	8.50	131.50	101.50	30.00	77.11	15.81	16.00
21	**Pusa Basmati**	102.00	140.00	85.05	16.55	7.00	96.50	82.50	14.00	85.28	12.31	11.72
22	**VDN-5-2-1-2**	99.00	142.00	76.15	16.85	7.00	132.50	103.50	29.00	77.94	14.48	14.85

Sr. No.	Genotypes	Days to 50% flowering	Days to physiological maturity	Plant height (cm)	Panicle Length (cm)	No. of Panicles plant^{-1}	No. of spikelets panicle^{-1}	No. of fertile spikelets panicle^{-1}	No. of infertile spikelets panicle^{-1}	Spikelet Fertility (%)	Test Weight (gm)	Grain yield plant^{-1}
23	**RTN-711**	104.00	135.00	57.10	15.15	8.50	148.50	135.00	13.50	90.70	14.02	14.16
24	**IGP Local-3**	117.00	157.00	111.70	24.15	16.50	269.00	247.00	22.00	91.79	25.77	33.28
25	**VDN-1-6-1**	113.00	146.00	95.20	16.95	9.50	128.50	98.50	30.00	76.81	15.24	14.40
26	**Bhandardara Local**	116.00	146.00	56.40	22.10	9.50	92.50	70.00	22.50	75.92	11.10	11.62
27	**Ambemohor 157**	120.00	157.00	115.15	21.65	11.50	183.50	147.00	36.50	80.00	17.14	13.54
28	**P-6**	114.00	145.00	73.50	20.25	7.50	116.50	68.50	48.00	58.81	14.20	9.71
29	**IGP Local-8**	106.00	147.00	134.10	24.05	14.50	228.50	208.50	20.00	91.19	24.43	27.09
30	**RTN-24**	118.00	150.00	93.50	22.05	7.50	141.00	120.00	21.00	85.24	13.39	14.47
31	**Almu Sathi**	114.00	145.00	95.45	15.85	9.50	194.50	146.00	48.50	74.98	18.84	12.99
32	**IGP Local-10**	117.00	154.00	101.40	18.20	7.50	119.50	108.50	11.00	90.71	20.82	23.36
33	**Tilsha**	113.00	143.00	99.25	22.05	13.50	200.50	165.50	35.00	82.70	20.84	23.90
34	**P-1**	109.00	143.00	100.95	16.95	10.50	135.00	92.50	42.50	68.43	14.28	11.45
35	**NK-3325**	116.00	145.00	65.65	28.20	13.50	254.50	220.50	34.00	86.56	20.98	22.30
36	**Bhadas Bhog**	120.00	153.00	100.50	20.50	11.50	161.50	125.00	36.50	77.26	19.10	18.99
37	**KJT-3**	103.00	133.00	65.10	24.00	13.50	180.00	152.50	27.50	84.61	17.70	22.22
38	**Phule Samruddhi**	106.00	136.00	105.65	27.60	17.50	286.00	252.00	34.00	88.03	27.18	34.60
39	**PKV HMT**	111.00	142.00	61.90	21.55	8.00	111.50	86.50	25.00	77.24	13.94	12.83
40	**PKV Khamang**	119.00	151.00	61.30	18.25	7.50	156.50	125.50	31.00	79.88	15.08	11.98
41	**Phule Radha**	117.00	148.00	89.45	25.35	12.50	238.50	220.50	18.00	92.34	21.89	20.13
42	**KJT-4**	94.00	128.00	63.05	21.75	11.50	153.50	124.50	29.00	81.10	17.28	23.08
43	**LK-248**	118.00	153.00	72.30	24.40	12.50	196.00	176.00	20.00	89.70	21.81	26.24
44	**Bhogawati**	110.00	139.00	79.35	27.70	13.50	269.50	247.00	22.50	91.60	24.43	27.96

Sr. No.	Genotypes	Days to 50% flowering	Days to physiological maturity	Plant height (cm)	Panicle Length (cm)	No. of Panicles plant^{-1}	No. of spikelets panicle^{-1}	No. of fertile spikelets panicle^{-1}	No. of infertile spikelets panicle^{-1}	Spikelet Fertility (%)	Test Weight (gm)	Grain yield plant^{-1}
45	**Vasumati**	119.00	151.00	106.00	17.45	7.50	201.00	153.50	47.50	76.15	12.38	11.35
46	**SKL-8**	111.00	142.00	80.30	21.20	11.50	211.00	174.50	36.50	82.73	15.54	15.18
47	**SYE-2001**	95.00	129.00	99.50	20.05	7.50	171.00	140.00	31.00	81.94	13.93	15.84
48	**PKV-Kisan**	101.00	131.00	86.40	23.05	12.00	252.00	220.50	31.50	87.42	20.92	21.13
49	**SYE-5**	97.00	129.00	77.65	19.60	8.50	138.50	116.50	22.00	84.07	11.87	14.51
50	**PKV Makrand**	109.00	150.00	56.30	21.55	10.50	125.50	109.50	16.00	87.11	14.47	17.39
	Mean	108.92	142.03	83.55	21.54	11.09	187.90	159.17	28.73	83.26	18.00	19.79
	C.V. (%)	1.56	1.53	2.97	5.44	6.99	8.23	9.94	18.53	3.71	5.90	11.33
	S.E.	1.20	1.53	1.75	0.83	0.55	10.93	11.18	3.76	2.19	0.75	1.59

4.2. Analysis of Variance

The analysis of variance for eleven characters has been presented in Table 4.3. It revealed that, the mean sum of square due to treatments for all characters studied is found to be significant. It indicated that appreciable amount of diversity is present in the material under study.

4.3. Parameters of Genetic Variability

The parameters range, GCV and PCV, heritability in broad sense and genetic advance as per cent of mean have been presented in the Table 4.4.

4.3.1. Coefficients of Variation

The table 4.4 revealed that estimates for genotypic coefficients of variation (GCV) were lower than the phenotypic coefficients of variation (PCV) for all characters under trial. The character days to physiological maturity exhibited the lowest GCV (5.58) as well as PCV (5.79), whereas number of fertile spikelets panicle^{-1} exhibited the highest GCV (36.22) and PCV (37.56). The highest difference between GCV and PCV values was observed for number of infertile spikelets panicle^{-1} followed by grain yield plant^{-1}. However, the lowest GCV and PCV difference was observed for days to 50% flowering. The high GCV and PCV was observed for plant height, panicle length, number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, number of infertile spikelets panicle^{-1}, test weight and grain yield plant^{-1}, indicating the presence of large variation among the genotypes for these characters. The character panicle length exhibited moderate GCV and PCV. Seven characters exhibited high GCV and PCV, one character recorded moderate GCV and PCV, while three characters recorded low GCV and PCV. Days to 50% flowering, days to physiological maturity and spikelet fertility recorded low GCV and PCV.

The characters *viz.* days to 50% flowering, days to physiological maturity and spikelet fertility registered low estimate of GCV and PCV which indicate that low degree of variation found in these characters in the present experimental material, thus gives little scope for future improvement of these characters. Similar types of findings were reported by Lingaiah *et al.* (2020) for days to 50% flowering.

4.3.2 Heritability (bs) and Genetic Advance

According to Robinson’s (1949) classification of heritability obtained in the present investigation for all the characters could be classified as very high heritability (> 61), medium heritability (31–60) and low heritability (< 30). Highest heritability was shown by plant height (98.65). All heritability figures were more than 60% so all characters have been classified under high heritability.

The character number of fertile spikelets panicle^{-1} showed highest genetic advance (114.53). The lowest genetic advance was observed for number of panicles plant^{-1} (5.78). According to Johnson *et al.* (1955) classification of GAM, days to 50% flowering, days to physiological maturity and spikelet fertility exhibited moderate GAM. Plant height, panicle length, number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, number of infertile spikelets panicle^{-1}, test weight and grain yield plant^{-1} exhibited high GAM.

Grain yield plant^{-1} (65.33) showed high genetic advance as per cent of mean, whereas days to physiological maturity (11.09%) showed lowest genetic advance as per cent of mean.

Heritability as well as genetic advance are regarded as an important selection parameter. Burton (1952) suggested that “genetic variation along with heritability estimate would give a better idea about the efficiency of selection.” From the present study, it can be concluded that high heritability values were recorded for all the characters, these estimates indicate the least effect of environment on these characters. These findings were in consonance with the report made by Tuwar *et al.* (2013) for days to 50% flowering, days to maturity, plant height and panicle length, Lingaiah *et al.* (2020) for test weight.

High heritability with moderate genetic advance was observed in days to 50% flowering, days to physiological maturity, number of infertile spikelets plant^{-1}, spikelet fertility and grain yield plant^{-1} which indicate that additive and non-additive both gene actions were present. Similar results were obtained by Devi *et al.* (2020) for test weight and grain yield plant^{-1}.

Plant height, number of spikelets panicle^{-1} and number of fertile spikelets panicle^{-1} exhibited high heritability with high genetic advance indicating that probably heritability is due to additive gene effect and selection could be effective for these characters. Similar results were observed by Abdul *et al.* (2011) for number of spikelets panicle^{-1}, Lingaiah *et al.* (2014) for plant height.

Recorded genetic advance as per cent of mean was high for plant height, panicle length, number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, number of infertile spikelets panicle^{-1}, test weight and grain yield plant^{-1} indicating that most likely the heritability due to additive gene effect and selection may be effective for these characters. Similar reports were identified by Abdul *et al.* (2011) for number of fertile spikelet panicle^{-1}, test weight and Parikh *et al.* (2012) for grain yield plant^{-1}.

Table 4.3: Analysis of variance for eleven characters of 50 rice genotypes

Sr. No.	Character	Replication	Genotypes	Error
	Degree of Freedom	1	49	49
1	Days to 50% flowering	0.64	111.82**	2.88
2	Days to physiological maturity	1.21	130.31**	4.70
3	Plant height (cm)	0.61	905.18**	6.14
4	Panicle length (cm)	2.82	24.85**	1.37
5	Number of panicles plant^{-1}	0.09	17.48**	0.60
6	Number of spikelets panicle^{-1}	1.44	6705.14**	238.97
7	Number of fertile spikelets panicle^{-1}	50.41	6897.87**	250.21
8	Number of infertile spikelets panicle^{-1}	68.89	192.21**	28.34
9	Spikelet fertility (%)	7.25	110.23**	9.57
10	Test weight (g)	0.19	36.50**	1.13
11	Grain yield plant^{-1}	6.46	92.81**	5.02

* Significant at 5% level

** Significant at 1% level

Table 4.4: Different parameters of variability in 50 rice genotypes

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	ECV (%)	Heritability h² (b.s.) (%)	Genetic Advance	Genetic Advance as per cent of Mean
1	**Days to 50% flowering**	108.92	94.00 – 120.00	6.78	6.95	1.56	94.97	14.82	13.60
2	**Days to physiological maturity**	142.03	128.00 – 157.00	5.58	5.79	1.53	93.04	15.75	11.09
3	**Plant height**	83.55	50.40 - 134.10	25.38	25.55	2.97	98.65	43.38	51.92
4	**Panicle length**	21.54	14.00 – 28.20	15.91	16.81	5.44	89.54	6.68	31.01
5	**No. of panicles plant^{-1}**	11.09	5.50 - 17.50	26.20	27.11	6.99	93.36	5.78	52.15
6	**No. of spikelet panicle^{-1}**	187.90	92.50 – 288.00	30.26	31.36	8.23	93.12	113.03	60.15
7	**No. of fertile spikelet panicle^{-1}**	159.17	70.00 - 261.50	36.22	37.56	9.94	93.00	114.53	71.96
8	**No. of infertile spikelet panicle^{-1}**	28.73	11.00 - 51.50	31.51	36.55	18.53	74.30	16.07	55.95
9	**Spikelet fertility**	83.26	58.81 - 94.22	8.52	9.30	3.72	84.03	13.40	16.09
10	**Test weight**	18.00	11.10 - 27.18	23.37	24.10	5.90	94.01	8.40	46.67
11	**Grain yield plant^{-1}**	19.79	9.71 - 34.60	33.48	35.35	11.33	89.73	12.93	65.33

4.4 Correlation

The phenotypic and genotypic correlation coefficients between grain yield plant^{-1} and its contributing characters in all possible combinations have been presented in Table 4.5.

Correlation estimates provide better understanding of yield components which helps the plant breeder during selection. The phenotype of a plant is result of interaction between many contributing factors, so the final yield is the sum total of the effects of several component characters. Yield is the complex phenotypic performance of the plant, which get influenced by many factors such as genetic, environment and their interactions. This complex quantitative character is under the control of polygene. Polygenes are highly sensitive to the environment. Hence, the selection of superior genotype based on yield alone may not be effective. For the rational approach towards the improvement of yield, selection should be operated through associated characters.

A study of association of yield contributing characters with yield assumes special importance and forms basis for selecting desired strains. Correlation coefficient indicates the magnitude and direction of association among the characters. The genotypic correlations between different characters within a plant often arise because of either genetic linkages or pleiotropy (Herald, 1939). It is important for breeders to establish and understand the existing correlation between the yield and yield contributing characters.

In the present study, various quantitative characters had been investigated and their relationship with yield and relationship among themselves was examined using correlation analysis. The character associations were studied in two parts *viz.* correlation of grain yield with its components and correlation of contributing traits within themselves.

The perusal of the Table 4.5 presented that grain yield plant^{-1} showed highly significant positive relationship with test weight (0.923) followed by number of panicles plant^{-1} (0.868), number of fertile spikelets panicle^{-1} (0.840), number of spikelets panicle^{-1} (0.794), spikelet fertility (0.760), panicle length (0.677), whereas number of infertile spikelets panicle^{-1} (-0.360) showed highly significant negative relationship with grain yield plant^{-1}. Days to 50% flowering, days to physiological maturity, plant height exhibited non-significant negative correlation with the grain yield plant^{-1}.

Days to 50% flowering had significant positive genotypic correlation with days to physiological maturity (0.887) followed by plant height (0.354). It has showed positive but non-significant correlation with number of infertile spikelets panicle^{-1} (0.079), test weight (0.073), number of spikelets panicle^{-1} (0.025), number of fertile spikelets panicle^{-1} (0.012). Days to 50% flowering exhibited non-significant negative correlation with panicle length (-0.005), number of panicles plant^{-1} (-0.041), spikelet fertility (-0.061), grain yield plant^{-1} (-0.061).

Days to physiological maturity showed positive significant genotypic correlation with plant height (0.391), whereas it showed non-significant positive genotypic correlation with number of infertile spikelets panicle^{-1} (0.053), test weight (0.050). It also showed negative but non-significant correlation with panicle length (-0.119), number of panicles plant^{-1} (-0.086), number of spikelets panicle^{-1} (-0.034), number of fertile spikelets panicle^{-1} (-0.042), spikelet fertility (-0.054) and grain yield plant^{-1} (-0.070). It exhibited significant positive phenotypic correlation with days to 50% flowering (0.889).

The plant height had positive but non-significant genotypic correlation with number of spikelets panicle^{-1} (0.048), number of fertile spikelets panicle^{-1} (0.009), number of infertile spikelets panicle^{-1} (0.240) and test weight (0.073). It also showed non-significant negative correlation with panicle length (-0.199), number of panicles plant^{-1} (-0.085), spikelet fertility (-0.103), grain yield plant^{-1} (-0.020). Also exhibited positive and significant phenotypic correlation with days to 50% flowering (0.355) and days to physiological maturity (0.389).

In case of panicle length, it registered positive and significant genotypic correlation with number of panicles plant^{-1} (0.751), number of spikelets panicle^{-1} (0.603), number of fertile spikelets panicle^{-1} (0.632), spikelet fertility (0.497), test weight (0.656) and grain yield plant^{-1} (0.677). It has also showed negative but non-significant genotypic correlation with number of infertile spikelets panicle^{-1} (-0.233). Also exhibited positive but non-significant phenotypic correlation with days to 50% flowering (0.012) and non-significant negative correlation with days to physiological maturity (-0.090) and plant height (-0.183).

The character number of panicles plant^{-1} had positive and significant genotypic correlation with number of spikelets panicle^{-1} (0.829), number of fertile spikelets panicle^{-1} (0.839), spikelet fertility (0.591), test weight (0.867) and grain yield plant^{-1} (0.868). It was also in negative but non-significant genotypic association with number of infertile spikelets panicle^{-1} (-0.134). It exhibited positive and significant phenotypic correlation with panicle length (0.709) and negative but non-significant phenotypic correlation with days to 50% flowering (-0.016), days to physiological maturity (-0.051) and plant height (-0.072).

A positive and highly significant genotypic correlation was shown by number of spikelets panicle^{-1} with number of fertile spikelets panicle^{-1} (0.988), spikelet fertility (0.652), test weight (0.824), grain yield plant^{-1} (0.794) and non-significant negative genotypic correlation with number of infertile spikelets panicle^{-1} (-0.009). It also exhibited positive and significant phenotypic correlation with panicle length (0.555), number of panicles plant^{-1} (0.800). It has exhibited positive but non-significant phenotypic correlation with days to 50% flowering (0.062), plant height (0.057) and days to physiological maturity (0.014).

The observations recorded for number of fertile spikelets panicle^{-1} exhibited positive and significant genotypic correlation with spikelet fertility (0.756), test weight (0.848), grain yield plant^{-1} (0.840) and negative but non-significant genotypic correlation with number of infertile spikelets panicle^{-1} (-0.165). It has exhibited positive and significant phenotypic correlation with panicle length (0.580), number of panicles plant^{-1} (0.816), number of spikelets panicle^{-1} (0.985) and non-significant positive phenotypic correlation with days to 50% flowering (0.051), days to physiological maturity (0.007) and plant height (0.020).

A character number of infertile spikelets panicle^{-1} exhibited negative and significant genotypic correlation with spikelet fertility (-0.721) and grain yield plant^{-1} (-0.360), whereas negative but non-significant correlation with test weight (-0.226). It has exhibited positive but non-significant phenotypic correlation with days to 50% flowering (0.061), days to physiological maturity (0.039), plant height (0.204), number of spikelets panicle^{-1} (0.007) and non- significant negative phenotypic correlation with panicle length (-0.188), number of panicles plant^{-1} (-0.158) and number of fertile spikelets panicle^{-1} (-0.169).

Spikelet fertility was in positive and significant genotypic correlation with test weight (0.662) and grain yield plant^{-1} (0.760). It also exhibited significant positive phenotypic correlation with panicle length (0.435), number of panicles plant^{-1} (0.573), number of spikelets panicle^{-1} (0.610), number of fertile spikelets panicle^{-1} (0.732) and significant negative phenotypic correlation with number of infertile spikelets panicle^{-1} (-0.739). It has exhibited negative but non-significant phenotypic correlation with days to 50% flowering (-0.020), days to physiological maturity (-0.010) and plant height (-0.100).

Test weight had been reported to show positive and significant genotypic correlation with grain yield plant^{-1} (0.923). It also recorded positive and significant phenotypic correlation with panicle length (0.617), number of panicles plant^{-1} (0.840), number of spikelets panicle^{-1} (0.807), number of fertile spikelets panicle^{-1} (0.831) and spikelet fertility (0.625). The character test weight also exhibited positive but non-significant phenotypic correlation with days to 50% flowering (0.099), days to physiological maturity (0.083), plant height (0.054) and negative but non- significant phenotypic correlation with number of infertile spikelets panicle^{-1} (-0.203).

4.4.1 Association of Grain Yield with its Components

The genotypic correlation among grain yield plant^{-1} and yield contributing traits revealed that grain yield plant^{-1} was positively and significantly correlated with panicle length, number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, spikelet fertility, test weight (Table 4.5). These results reveal that priority should be given to these traits while making selection of parents for future hybridization programme. Similar kind of associations were revealed by Sawant *et al.* (1995) for panicle length and test weight, Sarawgi *et* *al.* (1997) for number of fertile spikelets panicle^{-1}, Sangeeta *et al.* for panicle length and number of panicles plant^{-1} and Lingaiah *et al.* (2020) for test weight.

The observations of present study showed that the characters panicle length, number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, spikelet fertility and test weight were positively and significantly correlated with grain yield plant^{-1}. However, character number of infertile spikelets panicle^{-1} was significantly and negatively correlated with grain yield plant^{-1}. The characters days to 50% flowering, days to physiological maturity and plant height demonstrated negative association with grain yield plant^{-1} but it was non-significant.

4.4.2 Correlation of Quantitative Traits within them

Days to 50% flowering had displayed positive and significant association with days to physiological maturity, plant height. This result was in conformity with the findings of Satish *et al.* (2009)). Days to physiological maturity was significantly correlated with plant height. Sinha *et al.* (2004) reported similar type of positive association between days to physiological maturity and plant height.

Plant height had not exhibited significantly positive genotypic correlation with any other quantitative character. Similar results advocated by Jayasudha and Deepak (2010), Basavaraja *et al.* (2011).

Panicle length had positive and significant association with number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, spikelet fertility, test weight and grain yield plant^{-1}. Similar kind of association was also revealed by Abdul *et al.* (2011), Basavaraja *et al.* (2011).

Similarly, number of panicles plant^{-1} had highly significantly positive correlation with number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, spikelets fertility, test weight and grain yield plant^{-1}. This was in accord with the findings of Sarawgi *et al.* (1997) and Abdul *et al.* (2011).

The character number of spikelets panicle^{-1} had positive association with number of fertile spikelets panicle^{-1}, spikelets fertility, test weight and grain yield plant^{-1}. Similar kind of associations was also revealed by Abdul *et al.* (2011).

Similarly, number of fertile spikelets panicle^{-1} had highly significantly positive correlation with test weight, spikelet fertility and grain yield plant^{-1}. This is in conformity with the results of Sarawgi *et al.* (1997) and Abdul *et al.* (2011).

The trait spikelet fertility recorded positive and significant phenotypic association with panicle length, number of panicles plant^{-1}, number of spikelet panicle^{-1}, number of fertile spikelets panicle^{-1} and genotypic association with test weight and grain yield plant^{-1}. These were in consonance with the result of Abdul *et al.* (2011) and Basavaraja *et al.* (2011) for test weight and Jayasudha and Deepak (2010).

The character test weight had positive and significant correlation with panicle length, number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, spikelet fertility, test weight and grain yield plant^{-1}. This was in consonance with the results of Sarawgi *et al.* (1997).

Table 4.5: Estimates of genotypic (above diagonal) and phenotype correlation coefficients (below diagonal) among grain yield plant^{-1} and ten yield contributing characters in 50 rice genotypes

	Days to 50% flowering	**Days to physiological maturity**	**Plant height (cm)**	**Panicle length (cm)**	**No. of panicles plant^{-1}**	**No. of spikelets panicle^{-1}**	**No. of fertile spikelets panicle^{-1}**	**No. of infertile spikelets panicle^{-1}**	**Spikelet fertility (%)**	**Test weight (g)**	**Grain yield plant^{-1}**
Days to 50% flowering	**1.000**	0.887**	0.354**	-0.005	-0.041	0.025	0.012	0.079	-0.061	0.073	-0.061
Days to physiological maturity	0.890**	**1.000**	0.391**	-0.119	-0.086	-0.034	-0.042	0.053	-0.054	0.050	-0.070
Plant height (cm)	0.355**	0.389**	**1.000**	-0.199*	-0.085	0.048	0.009	0.240	-0.103	0.073	-0.020
Panicle length (cm)	0.012	-0.090	-0.183	**1.000**	0.751**	0.603**	0.632**	-0.233*	0.497**	0.656**	0.677**
No. of panicles plant^{-1}	-0.016	-0.051	-0.072	0.709**	**1.000**	0.829**	0.839**	-0.134	0.591**	0.867**	0.868**
No. of spikelets panicle^{-1}	0.062	0.014	0.057	0.555**	0.800**	**1.000**	0.988**	-0.009	0.652**	0.824**	0.794**
No. of fertile spikelets panicle^{-1}	0.051	0.007	0.020	0.580**	0.816**	0.985**	**1.000**	-0.165	-0.756**	0.848**	0.840**
No. of infertile spikelets panicle^{-1}	0.061	0.039	0.204	-0.188	-0.158	0.007	-0.169	**1.000**	0.721**	-0.226*	-0.360**
Spikelet fertility (%)	-0.020	-0.010	-0.100	0.435**	0.573**	0.610**	0.732**	-0.739**	**1.000**	0.662**	0.760**
Test weight (g)	0.099	0.083	0.054	0.617**	0.840**	0.807**	0.831**	-0.203	0.625**	**1.000**	0.923**
Grain yield plant^{-1}	-0.011	-0.006	-0.010	0.650**	0.841**	0.772**	0.817**	-0.319*	0.707**	0.889**	**1.000**

4.5 Path Analysis

Wright (1921) and Dewey and Lu (1959) developed a statistical device called path coefficient analysis which takes into account the cause-and-effect relations between the variables. It is unique in partitioning the association into direct and indirect effects through other independent variables. It calculates the direct and indirect contribution of independent variables on dependent variable which in turn helps breeder in identifying the yield components. It has three types *viz.* phenotypic, genotypic and environmental paths. The first two are in common use in breeding. The computation of path consists of three main steps *viz.* calculation of direct effects, indirect effects and residual effect. In the present research work, the path coefficient analysis was performed at genotypic level. The results of this analysis have been discussed below.

It was evident from Table 4.6 that grain yield plant^{-1} was the result of panicle length, number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, spikelet fertility, test weight as they were significantly correlated with it. These variables were interrelated, so that each factor influenced the grain yield by a direct contribution and indirect contributions through other variables with which it was correlated.

From the data, it can be concluded that the positive and highest direct effect on grain yield plant^{-1} was exhibited by test weight (0.581). This highest positive direct effect was followed by spikelet fertility (0.276), number of panicles plant^{-1} (0.263), plant height (0.051), number of spikelets panicle^{-1} (0.036), panicle length (0.035) and days to physiological maturity (0.002). The highest negative direct effect on grain yield plant^{-1} was exhibited by the number of fertile spikelets panicle^{-1} (-0.143) and subsequently by days to 50% flowering (-0.093) and number of infertile spikelets panicle^{-1} (-0.014).

The days to 50% flowering had direct phenotypic negative effect (-0.093) on grain yield and the correlation between days to 50% flowering and grain yield plant^{-1} was negative and non-significant. The correlation was negative and non-significant due to negative indirect effect on grain yield plant^{-1} via spikelet fertility (-0.017), number of panicles plant^{-1} (-0.011), number of fertile spikelets panicle^{-1} (-0.002), number of infertile spikelets panicle^{-1} (-0.001) and panicle length (-0.0002). However, it exhibited positive indirect effect on grain yield plant^{-1} might be due to test weight (0.042) followed by plant height (0.018), days to physiological maturity (0.002) and number of spikelets panicle^{-1} (0.001).

Data revealed that days to physiological maturity exhibited positive direct phenotypic effect on grain yield plant^{-1} while its correlation with grain yield plant^{-1} was negative and non-significant. The character recorded negative correlation with grain yield plant^{-1} due to its negative indirect effect on grain yield plant^{-1} via days to 50% flowering (-0.083), number of panicles plant^{-1} (-0.023), spikelet fertility (-0.015), panicle length (-0.004), number of spikelets panicle^{-1} (-0.001), number of infertile spikelets panicle^{-1} (-0.001).

Plant height had positive direct effect on grain yield plant^{-1} (0.051) while the correlation of plant height with grain yield plant^{-1} was negative and non-significant. The character plant height exhibited positive indirect effect on grain yield plant^{-1} via test weight (0.028), number of spikelets panicle^{-1} (0.002) and days to physiological maturity (0.001). However, its negative indirect correlation with grain yield plant^{-1} might be due to spikelet fertility (-0.034), days to 50% flowering (-0.033), number of panicles plant^{-1} (-0.022), panicle length (-0.007), number of infertile spikelets panicle^{-1} (-0.003) and number of fertile spikelets panicle^{-1} (-0.001).

Panicle length had direct positive effect on grain yield plant^{-1} (0.035) and the correlation was also positive and significant. The correlation was positive mainly due to positive indirect contribution through test weight (0.381), number of panicles plant^{-1} (0.361), number of panicles plant^{-1} (0.198), spikelet fertility (0.137), number of spikelets panicle^{-1} (0.022), number of infertile spikelets panicle^{-1} (0.003) and days to 50% flowering (0.001).

Number of panicles plant^{-1} exhibited direct positive effect on grain yield plant^{-1} (0.263) and correlation with grain yield plant^{-1} was positive and significant. This positive and significant correlation was also contributed by indirect effects through test weight (0.504), spikelet fertility (0.163), number of spikelets panicle^{-1} (0.030), panicle length (0.026), days to 50% flowering (0.004) and number of infertile spikelets panicle^{-1} (0.002).

Number of spikelets panicle^{-1} recorded direct positive effect on grain yield plant^{-1} (0.036) and correlation with grain yield plant^{-1} was also positive and significant. The correlation was positive with positive indirect effects via test weight (0.479), number of panicles plant^{-1} (0.219), spikelet fertility (0.180), panicle length (0.021), number of infertile spikelets panicle^{-1} (0.004), plant height (0.002) and number of infertile spikelets panicle^{-1} (0.0001).

Number of fertile spikelets panicle^{-1} had direct negative phenotypic effect on grain yield plant^{-1} (-0.143) while the correlation with grain yield plant^{-1} was positive and significant. The correlation was positive due to positive indirect effect on grain yield plant^{-1} via test weight (0.493) followed by number of panicles plant^{-1} (0.221), spikelet fertility (0.209), number of spikelets panicle^{-1} (0.036), panicle length (0.022), number of infertile spikelets (0.002) and plant height (0.001).

Number of infertile spikelets panicle^{-1} exhibited negative phenotypic effect on grain yield plant^{-1} (-0.014) and the correlation with grain yield plant^{-1} was also negative and significant. The correlation was negative with contribution of negative indirect effect via spikelet fertility (-0.199), test weight (-0.132), number of panicles plant^{-1} (-0.035), panicle length (-0.008), days to 50% flowering (-0.007) and number of spikelets panicle^{-1} (-0.0003).

Spikelet fertility had positive direct effect on grain yield plant^{-1} (0.276) and correlation with grain yield plant^{-1} was also positive and significant. The positive correlation was due to direct effect and indirect effect of spikelet fertility via test weight (0.385), number of panicles plant^{-1} (0.156), number of spikelet panicle^{-1} (0.024), panicle length (0.017), number of infertile spikelets panicle^{-1} (0.010) and days to 50% flowering (0.006).

Test weight had direct positive phenotypic effect on grain yield plant^{-1} and correlation with grain yield plant^{-1} was also positive and significant. The correlation was positive due to indirect effect test weight via number of panicles plant^{-1} (0.228), spikelet fertility (0.183), number of spikelets panicle^{-1} (0.030), panicle length (0.023), number of infertile spikelets panicle^{-1} (0.003), plant height (0.002) and days to physiological maturity (0.0001).

The direct and indirect contributions of different characters have been presented in Table 4.6. It revealed that grain yield plant^{-1} was mainly the result of panicle length, number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, spikelet fertility and test weight which was evident from their strong positive correlations with grain yield plant^{-1}.

The yield contributing characters *viz.* number of panicles plant^{-1}, number of spikelets panicle^{-1}, spikelet fertility, test weight had exerted significant positive direct effect on grain yield plant^{-1} (Table 4.6) and correlation of these characters with grain yield was positively significant. Thus, direct selection for these traits will be rewarding for yield improvement. These findings were in agreement with reports of Sawant *et al.* (1995) for test weight, panicle length, Sarawgi *et al.* (1997) for test weight, Sangeeta *et al.* (2001) for number of panicles plant^{-1} and Satish *et al.* for test weight.

Table 4.6: Estimates of genotypic direct (diagonal) and indirect effects (above and below diagonal) of contributing characters on grain yield in 50 rice genotypes

	Days to 50% flowering	Days to physiological maturity	Plant height (cm)	Panicle Length (cm)	No. of Panicles plant^{-1}	No. of spikelets panicle^{-1}	No. of fertile spikelets panicle^{-1}	No. of infertile spikelets panicle^{-1}	Spikelet Fertility (%)	Test Weight (g)	Grain Yield plant^{-1}
Days to 50% flowering	**-0.093**	0.002	0.018	-0.0002	-0.011	0.001	-0.002	-0.001	-0.017	0.042	-0.061
Days to physiological maturity	-0.083	**0.002**	0.020	-0.004	-0.023	-0.001	0.006	-0.001	-0.015	0.029	-0.070
Plant height (cm)	-0.033	0.001	**0.051**	-0.007	-0.022	0.002	-0.001	-0.003	-0.034	0.028	-0.020
Panicle Length (cm)	0.001	-0.0002	-0.010	**0.035**	0.198	0.022	-0.090	0.003	0.137	0.381	0.677**
No. of Panicles plant^{-1}	0.004	-0.0002	-0.004	0.026	**0.263**	0.030	-0.120	0.002	0.163	0.504	0.868**
No. of spikelets panicle^{-1}	-0.002	-0.0001	0.002	0.021	0.219	**0.036**	-0.141	0.0001	0.180	0.479	0.794**
No. of fertile spikelets panicle^{-1}	-0.001	-0.0001	0.001	0.022	0.221	0.036	**-0.143**	0.002	0.209	0.493	0.840**
No. of infertile spikelets panicle^{-1}	-0.007	0.0001	0.012	-0.008	-0.035	-0.0003	0.024	**-0.014**	-0.199	-0.132	-0.360**
Spikelet Fertility (%)	0.006	-0.0001	-0.006	0.017	0.156	0.024	-0.108	0.010	**0.276**	0.385	0.760**
Test Weight (g)	-0.007	0.0001	0.002	0.023	0.228	0.030	-0.121	0.003	0.183	**0.581**	0.923**

*, ** = significant at 5% and 1% levels, respectively

Residual effect (R): **0.2874** Bold figures indicate direct effect

4.6 Genetic Divergence

Genetic divergence in 50 genotypes of rice was measured by following Mahalanobis's D^2 statistic. The diversity available in the crop decides the success of any crop improvement programme with manifested objectives. Assessment of divergence in the germplasm is pre-requisite to know the spectrum of diversity. Clustering of genotypes following the Tocher's method as described by Rao (1952) led to formation of eight clusters. In the present investigation, 50 genotypes of rice were studied for their genetic diversity by multivariate analysis as per Mahalanobis D^2 statistic (1936) with respect to eleven important quantitative characters.

Table 4.7: Grouping of fifty rice genotypes based on D^2 values

Cluster No.	**No. of Genotype**	**Name of Genotype**
CL-I	11	Vikram, Basmati370, IR 36, KJT-3, Ratna, Manibhog, PAU-3079, KJT-4, China-26, Pawana, Darna
CL-II	19	VDN-1-6-1, Bhadas Bhog, P-1, Almu Sathi, Kala Girga, T-3, Vasumati, RTN-24, Ambemohor157, W355, RDN 185-2, Krishna Sal, Adhaya, Tilsha, Nizamgod, Kala Namak, Phule Radha, SKL-8, IGP Local-3
CL-III	8	Varanasi, PKV Khamang, PKV HMT, Bhandardara Local, LK-248, P-6, RTN-711, NK-3325
CL-IV	1	IGP Local
CL-V	8	Bhogawati, PKV-Kisan, SYE-5, SYE-2001, IGP Local-8, Pusa Basmati, Jay Bangal, VDN-5-5-1-2.
CL-VI	1	IGP Local-10
CL-VII	1	Phule Samruddhi
CL-VIII	1	PKV Makrand

4.6.1 Group Constellations

Tocher's method (Rao, 1952) was used for grouping of genotypes using the pairs of combinations of D^2 values. 50 genotypes were grouped in to eight clusters (Table 4.7). Cluster II was biggest and consisted of 19 genotypes. Cluster I was the second largest with 11 genotypes. The cluster III and V both were consisted of 8 genotypes. All remaining clusters *viz.* cluster IV, VI, VII and VIII were solitary, with one genotype in each of these clusters.

4.6.2 Intra and Inter Cluster Distances

Intra and inter cluster distance values have been presented in Table 4.8. Intra cluster distance was ranged from zero (cluster IV, VI, VII and VIII) to 13.15 (cluster V). The highest intra cluster distance was recorded in cluster V (13.15) followed by cluster III (10.05), cluster II (9.79) and cluster I (9.38). The high intra cluster distance values revealed the presence of genetic diversity between the genotypes grouped together in those clusters. Hence, there is a lot of scope for exchange of genes among genotypes within these clusters.

From the inter cluster distance values of the eight clusters, the highest divergence occurred between cluster VII and VIII (29.47) subsequently between cluster IV and cluster VIII (27.37), cluster III and VII (24.44) and cluster I and VI (21.74) suggesting that the crosses involving genotypes from these clusters would give desirable recombination. From the closest inter cluster distance it was concluded that these genotypes were not very distant but couldn’t be grouped together based on studied traits. Several authors have suggested that the crossing between the genotypes of clusters with high inter cluster would yield good segregants for selection. Devi *et al.* (2020) grouped genotypes into eight clusters and cluster I was the largest comprised of 23 genotypes. The maximum cluster distance was found between cluster II and cluster IV (2178.98). The minimum inter cluster distance was observed between cluster I and cluster III (540.96). The intra cluster distance was maximum for cluster II (354.10) indicating existence of variability within the cluster. A perusal of results on cluster means revealed that cluster VIII recorded highest cluster mean for yield plant^{-1}, panicle length, test weight and plant height.

Table 4.8: Average intra (bold) and inter cluster distance (D^2) values for eight clusters in fifty Rice genotypes

Clusters	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**
I	**9.38** **(87.98)**	18.98 (360.24)	15.61 (243.67)	20.32 (412.90)	16.48 (271.59)	21.74 (472.63)	18.70 (349.69)	16.59 (275.23)
II		**9.79** **(95.84)**	16.10 (259.21)	11.93 (142.32)	15.07 (227.10)	12.00 (144.00)	17.22 (296.53)	21.45 (460.10)
III			**10.05** **(101.00)**	20.95 (438.90)	19.23 (369.79)	17.69 (312.94)	24.44 (597.31)	14.21 (201.92)
IV				**0.00** **(0.00)**	17.11 (292.75)	15.44 (238.39)	9.79 (95.84)	27.37 (749.12)
V					**13.15** **(172.92)**	16.05 (257.60)	17.55 (308.00)	19.42 (377.14)
VI						**0.00** **(0.00)**	21.49 (461.82)	20.48 (419.43)
VII							**0.00** **(0.00)**	29.47 (868.48)
VIII								**0.00** **(0.00)**

Diagonal: Intra cluster and above diagonal: inter cluster D values

4.6.3 Cluster Mean

Table 4.9 contains cluster mean values for eleven characters under study. It revealed wide range of variability among the clusters for almost all characters under study.

Cluster mean values for days to 50% flowering were ranged between 101.31 days (cluster V) to 119.50 days (cluster IV). Mean performance of cluster I, II, III, VI, VII and VIII have 101.86, 113.32, 114.00, 116.50, 106.00, 108.50 days respectively for the trait under study.

In case of days to physiological maturity, range of cluster mean was observed between 134.18 (cluster I) to 153.50 (cluster VI). While, mean performance of clusters II, III, IV, V, VII and VIII were 145.68, 145.94. 151.00, 137.50, 135.50, 150.00 days respectively.

Plant height varied for their cluster means from 56.30 cm (cluster VIII) to 114.95 cm (cluster IV). Whereas, mean performance of clusters I, II, III, V, VI and VII were 59.20, 100.82, 63.09, 90.98, 101.40, 105.65 cm respectively.

Mean panicle length of clusters ranged between 18.20 (cluster VI) to 27.60 (cluster VII). Whereas, mean performance of clusters I, II, III, IV, V and VIII were 23.40, 20.53, 21.51, 22.50, 20.93, 21.55 cm respectively for character under investigation.

Number of panicles plant^{-1} showed the range of cluster means from 7.50 (cluster VI) to 17.50 (cluster VII). Mean performance of clusters I, II, III, IV, V and VIII were 13.50, 10.42, 9.56, 16.50, 9.94 and 10.50 respectively.

Number of Spikelets panicle^{-1} exhibited wide range of variation for cluster means between 119.50 (cluster VI) to 288.00 (cluster IV). While, mean performance of clusters I, II, III, V, VII and VIII were 220.91, 179.74, 156.88, 184.50, 286.00, 125.50 spikelets panicle^{-1} respectively.

Number of fertile Spikelets panicle^{-1} exhibited range of variation for cluster means between 108.50 (cluster VI) to 261.50 (cluster IV). While, mean performance of clusters I, II, III, V, VII and VIII were 193.91, 148.24, 127.88, 156.81, 252.00, 109.50 fertile spikelets panicle^{-1} respectively.

Number of infertile Spikelets panicle^{-1} exhibited range of variation for cluster means between 11.00 (cluster VI) to 34.00 (cluster VII). While, mean performance of clusters I, II, III, IV, V and VIII were 27.00, 31.50, 29.00, 26.50, 27.69, 16.00 infertile spikelets panicle^{-1} respectively.

Spikelet fertility varied for their cluster means between 79.69% (cluster III) to 90.85% (cluster IV). Whereas, mean performance of clusters I, II, V, VI, VII and VIII were 86.76, 81.17, 84.02, 90.71, 88.03, 87.12% respectively.

The character, test weight exhibited wide range of variation for cluster means between 14.48 g (cluster VIII) to 27.19 g (cluster VII). While, mean performance of clusters I, II, III, IV, V and VI were 20.36, 17.03, 15.79, 26.80, 17.10, 20.82 respectively.

Cluster mean for grain yield plant^{-1} ranged between 15.86 (cluster III) to 34.61 (cluster VII). Mean performance of cluster I, II, IV, V, VI and VIII were 24.58, 17.51, 33.36, 18.84, 23.37, 17.39 g respectively.

The data revealed that considerable differences existed among the clusters for most of the characters. The cluster VII showed the highest mean values for four characters *viz.* grain yield plant^{-1}, test weight, panicle length and number of panicles plant^{-1}. The cluster IV showed the highest values for characters like number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1} and spikelet fertility. The cluster VI exhibited lowest mean for number of panicles plant^{-1}.

From the results, it was noticed that cluster VII (Phule Samruddhi) performed better means in panicle length, number of panicles plant^{-1}, test weight and grain yield plant^{-1} but no cluster contained at least one genotype with all desirable characters, which eliminated the possibility of directly selecting one genotype for immediate use. Therefore, hybridization programme between the selected genotypes from diverse clusters is essential to combine all the targeted traits to improve phenotypic performance.

Table 4.9: Mean values of the eight clusters for eleven characters in fifty rice genotypes

Cluster No.	Days to 50% flowering	Days to physiological maturity	Plant height (cm)	Panicle length (cm)	No. of panicles plant^{-1}	No. of spikelets panicle^{-1}	No. of fertile spikelets panicle^{-1}	No. of infertile spikelets panicle^{-1}	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1}
CL-I	101.86	**134.18**	59.20	23.40	13.50	220.91	193.91	27.00	86.76	20.36	24.58
CL-II	113.32	145.68	100.82	20.53	10.42	179.74	148.24	31.50	81.17	17.03	17.51
CL-III	114.00	145.94	63.09	21.51	9.56	156.88	127.88	29.00	79.69	15.79	15.86
CL-IV	119.00	151.00	114.95	22.50	16.50	**288.00**	**261.50**	26.50	**90.85**	26.80	33.36
CL-V	**101.31**	137.50	90.98	20.93	9.94	184.50	156.81	27.69	84.02	17.10	18.84
CL-VI	116.50	153.50	101.40	18.20	7.50	119.50	108.50	**11.00**	90.71	20.82	23.37
CL-VII	106.00	135.50	105.65	**27.60**	**17.50**	286.00	252.00	34.00	88.03	**27.19**	**34.61**
CL-VIII	108.50	150.00	**56.30**	21.55	10.50	125.50	109.50	16.00	87.12	14.48	17.39

4.6.4 Per cent Contribution of Various Characters towards Divergence

The per cent contribution of eleven characters studied towards total divergence has been presented in Table 4.10. Data revealed that, plant height had contributed highest (44.65%) for genetic divergence and subsequently by number of spikelets panicle^{-1} (19.02%), days to physiological maturity (16.82%), days to 50% flowering (6.86%), number of panicles plant^{-1} (3.84%), panicle length (2.29%), grain yield plant^{-1} (2.20%), test weight (2.04%), spikelet fertility (1.47%) and number of fertile spikelets panicle^{-1} (0.82%). A trait, number of infertile spikelets panicle^{-1}, didn’t contribute at all towards total divergence.

Table 4.10: Per cent contribution towards divergence of eleven different characters of Rice genotypes

Sr. No.	Source	Times ranked first	Contribution (%)
1	Days to 50% flowering	84	6.86
2	Days to physiological maturity	206	**16.82**
3	Plant height (cm)	547	**44.65**
4	Panicle length (cm)	28	2.29
5	Number of panicles plant^{-1}	47	3.84
6	Number of spikelets panicle^{-1}	233	**19.02**
7	Number of fertile spikelets panicle^{-1}	10	0.82
8	Number of infertile spikelets panicle^{-1}	00	0.00
9	Spikelet fertility (%)	18	1.47
10	Test weight (g)	25	2.04
11	Grain yield plant^{-1} (g)	27	2.20

The per cent contribution of characters towards divergence was analysed and it was found that plant height, number of spikelets panicle^{-1} and days to physiological maturity contributed for maximum genetic diversity among the 50 genotypes (Table 4.10). The traits *viz.* days to 50% flowering, panicle length, number of panicles plant^{-1}, number of fertile spikelets panicle^{-1}, test weight, grain yield plant^{-1} and spikelet fertility having medium contribution towards the divergence in rice genotypes under study. Plant height, number of spikelets panicle^{-1} and days to physiological maturity had contributed highly towards genetic diversity which showed that the genotypes possessed unique features for most of the traits studied. The plant height, number of spikelets panicle^{-1} and days to physiological maturity and days to 50% flowering together contributed 87.35% towards total divergence. Therefore, these characters should be given priority during hybridization and selection in segregating populations. Similar results were reported by Devi *et al.* (2020), that most important trait contributing maximum towards divergence was plant height (31.8) which ranked 168 times first.

From the cluster analysis, conclusion could be drawn that in the studied population high variability was present between the genotypes in different clusters for different characters. Yield potential can be improved with recombination breeding between genotypes from cluster V having highest intra cluster distance. As maximum inter cluster distance was recorded between cluster VII and VIII, cluster I and VI, cluster VI and VII crosses involving genotypes belonging to these clusters would give desirable recombination.

4.6.5 Selection of Potent Parents

The utility of any crop improvement programme depends on the selection of the best parents having high potential for economically important characters. Among the different approaches of selecting parents, selection based on diversity has its own significance as diversity is the basic need of crop improvement. In the present study, studies on diversity among different genotypes yielded valuable information that could be useful in suggesting potent parents for crossing.

4.6.6 Promising Parents for Hybridization

From the present studies, on the basis of inter cluster distances and cluster mean values, the tentative hybridization programme was suggested (Table 4.11) which involves the genotypes, so recombinants may be obtained in the segregating generations. As some of the characters were showing the additive gene action, they are suggested for effective selection. The D^2 analysis thus proved to be a very useful technique in isolating diverse groups from the germplasm under study. On the basis of inter cluster distances and cluster mean values observed in the present study the fourteen genotypes *viz.* Phule Samruddhi, IGP Local, Basmati 370, Vikram, Darna, IR 36, Pawana, IGP Local-3, IGP Local-8, Bhogawati, Ratna, China-26, PLV Makrand, RTN 711 and LK-248 found superior and it would be beneficial to use them as a potent parent for improvement of rice.

Table 4.11 Promising parents for hybridization

Sr. No.	Characters	Cluster source	Superior genotype
1	Days to 50% flowering	I, V, VII	Vikram, Basmati370, IR 36, China-26, KJT4, SYE-5, Manibhog, SYE-2001, VDN-5-2- 1-2, Phule Samruddhi.
2	Days to physiological maturity	I, V, VII	Basmati370, IR 36, PKV-Kisan, KJT-3, KJT-4, PAU3079, SYE-5, Darna, SYE-2001.
3	Plant height (cm)	I, III, VIII	Varanasi, Bhandardara Local, China-26, Pawana, KJT-4, SYE-5, Manibhog, RTN 711.
4	Panicle length (cm)	I, IV, VII	NK-3325, IGP Local, Phule Samruddhi.
5	Number of panicles plant^{-1}	I, IV, VII	Vikram, Basmati 370, IGP Local, IGP Local-3, Phule Samruddhi.
6	Number of spikelets panicle^{-1}	I, IV, VII	Vikram, IGP Local, Pawana, Phule Samruddhi.
7	Number of fertile spikelets panicle^{-1}	I, IV, VII	Vikram, IGP Local, Pawana, Phule Samruddhi.
8	Number of infertile spikelets panicle^{-1}	VI, VIII	IGP Local-10, PKV Makrand.
9	Spikelet fertility (%)	IV, VI	IGP Local, IGP Local-10.
10	Test weight (g)	IV, VII	IGP Local, Phule Samruddhi.
11	Grain yield plant $^{-1}$ (g)	IV, VII	IGP Local, Phule Samruddhi.

5. SUMMARY AND CONCLUSION

Genetic diversity was assessed in rice (*Oryza sativa* L.) germplasms with 50 genotypes of rice collected from various sources which were evaluated in RBD at ZARS, Igatpuri during *kharif* 2020. The experiment was carried out with objective to understand the variability parameters for grain yield and yield contributing characters in rice, to assess the genotypic and phenotypic correlation between yield and yield contributing characters, to estimate direct and indirect effect of different quantitative characters on seed yield and to identify suitable parents for future hybridization programme on the basis of genetic divergence.

The experimental material was sown in a Randomized Block Design with two replications and observations were recorded on randomly selected five plants for twelve characters *viz.* days to 50% flowering, days to physiological maturity, plant height (cm), panicle length (cm), number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, number of infertile spikelets panicle^{-1}, spikelet fertility (%), test weight (g), grain yield plant^{-1} (g) and grain type.

5.1 Variability, Heritability and Genetic Advance

Genotypic coefficient of variation (GCV) was lower than the phenotypic coefficient of variation (PCV) for eleven characters under investigation. The high GCV and PCV was observed for plant height, panicle length, number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, number of infertile spikelets panicle^{-1}, test weight and grain yield plant^{-1}indicating the presence of large variation among the genotypes for these characters. Seven characters exhibited high GCV and PCV, panicle length recorded moderate GCV and PCV, while three characters *viz.* days to 50% flowering, days to physiological maturity and spikelet fertility recorded low GCV and PCV.

All heritability values were more than 60% so all characters were classified under high heritability which indicates high transmission of characters from parents to their offspring which will be helpful for selection in future hybridization programme.

According to Johnson *et al.* (1955) classification of genetic advance as per cent of mean, characters plant height, panicle length, number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, number of infertile spikelets panicle^{-1}, test weight and grain yield plant^{-1}exhibited high genetic advance as per cent of mean indicating additive gene action and selection would be effective for these characters.

High heritability coupled with moderate genetic advance was observed in days to 50% flowering, days to physiological maturity, number of infertile spikelets plant^{-1}, spikelet fertility and grain yield plant^{-1} indicating that additive and non-additive both gene action were present. The characters such as plant height, number of spikelets panicle^{-1} and number of fertile spikelets panicle^{-1} exhibited high heritability coupled with high genetic advance indicating that most likely heritability is due to additive gene effect and selection may be effective for these characters.

5.2 Correlation

Grain yield plant^{-1}was in highly significant positive relationship with test weight, number of panicles plant^{-1}, number of fertile spikelets panicle^{-1}, number of spikelets panicle^{-1}, spikelets fertility and panicle length indicating that selection for these characters would benefit in improvement of genetypes. Number of infertile spikelets showed highly significant negative relationship with grain yield plant^{-1}.

5.3 Path Analysis

Data revealed that test weight exhibited highest positive direct effect on grain yield plant^{-1} and subsequently by spikelet fertility, number of panicles plant^{-1}, plant height, number of spikelets panicle^{-1}, panicle length and days to physiological maturity. Whereas, number of fertile spikelets panicle^{-1} recorded the highest negative direct effect on grain yield plant^{-1}. The characters *viz.* number of panicles plant^{-1}, number of spikelets panicle^{-1}, spikelet fertility, test weight had exerted significant positive direct effect on grain yield plant^{-1} and correlation of these characters with grain yield plant^{-1} was positively significant. Thus, for yield improvement direct selection for these traits would be rewarding.

5.4 Genetic Divergence

Fifty genotypes were grouped into eight clusters. Cluster II was biggest and consisted of 19 genotypes followed by cluster I with 11 genotypes. The cluster III and V both were consist of 8 genotypes. All remaining clusters *viz.* cluster IV, VI, VII and VIII were solitary, with one genotype in each of these clusters.

Intra cluster distance was ranged from zero (cluster IV, VI, VII and VIII) to 13.15 (cluster V). The highest intra cluster distance was observed in cluster V followed by cluster III, cluster II and cluster I. The high intra cluster distance values indicates the existence of variability within the cluster. Hence, there is a scope for exchange of genes among genotypes within these clusters.

From the inter cluster D^2 values of the eight clusters, it can be seen that the highest divergence occurred between cluster VII and VIII followed by cluster I and VI, cluster VI and VII suggesting that the crosses involving varieties from these clusters would give wider and desirable recombination.

The character plant height had contributed highest for divergence, followed by number of spikelets panicle^{-1}, days to physiological maturity, days to 50% flowering, number of panicles plant^{-1}, panicle length, grain yield plant^{-1}, test weight, spikelet fertility and number of fertile spikelets panicle^{-1}. A trait, number of infertile spikelets panicle^{-1}, didn’t contribute at all towards total divergence. The plant height, number of spikelets panicle^{-1}, days to physiological maturity and days to 50% flowering together contributed 87.35% towards total divergence. Therefore, these characters should be given importance during hybridization and selection of segregating populations.

It can be concluded from cluster analysis that high variability was present between the genotypes from different clusters for different traits. Recombination breeding among genotypes belonging to cluster V having maximum intra cluster distance can improve the yield potential. As maximum inter-cluster distance was noticed between cluster VII and VIII and subsequently between cluster IV and VII, cluster III and VII crosses involving genotypes from these clusters would give wider and desirable recombinations.

From the present study, on the basis of inter cluster distances and cluster mean values, the genotypes *viz.* Phule Samruddhi, IGP Local, Basmati 370, Vikram, Darna, IR 36, Pawana, IGP Local-3, IGP Local-8, Bhogawati, Kala Namak, Ratna, China 26 and LK-248 were concluded as diverse and could be classified as promising genotypes in crossing programme to achieve desired segregants in rice.

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7. VITAE

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MASTER OF SCIENCE (AGRICULTURE)

IN

AGRICULTURAL BOTANY

2021

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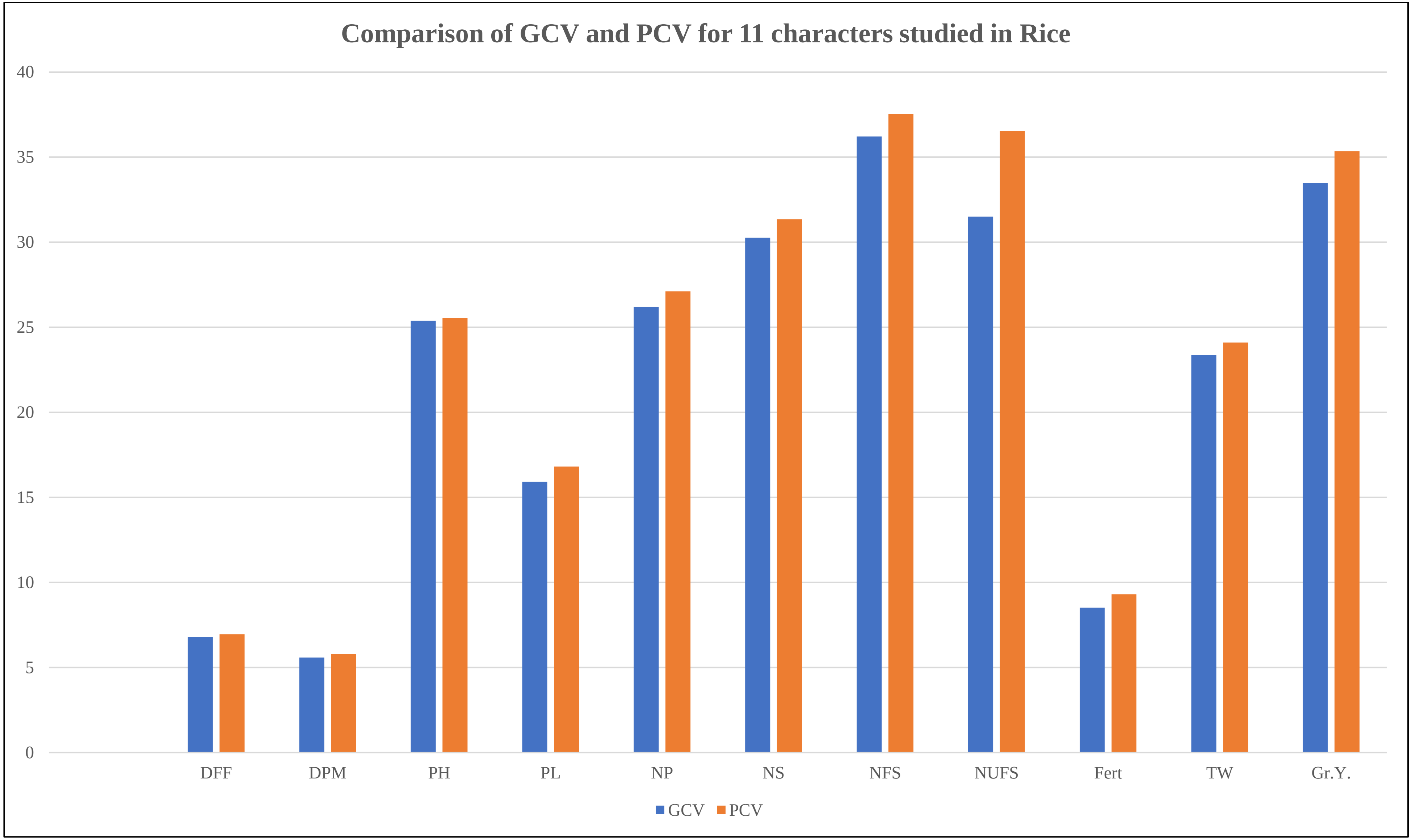

Fig. 4.1 Comparison of GCV and PCV for 11 characters studied in Rice

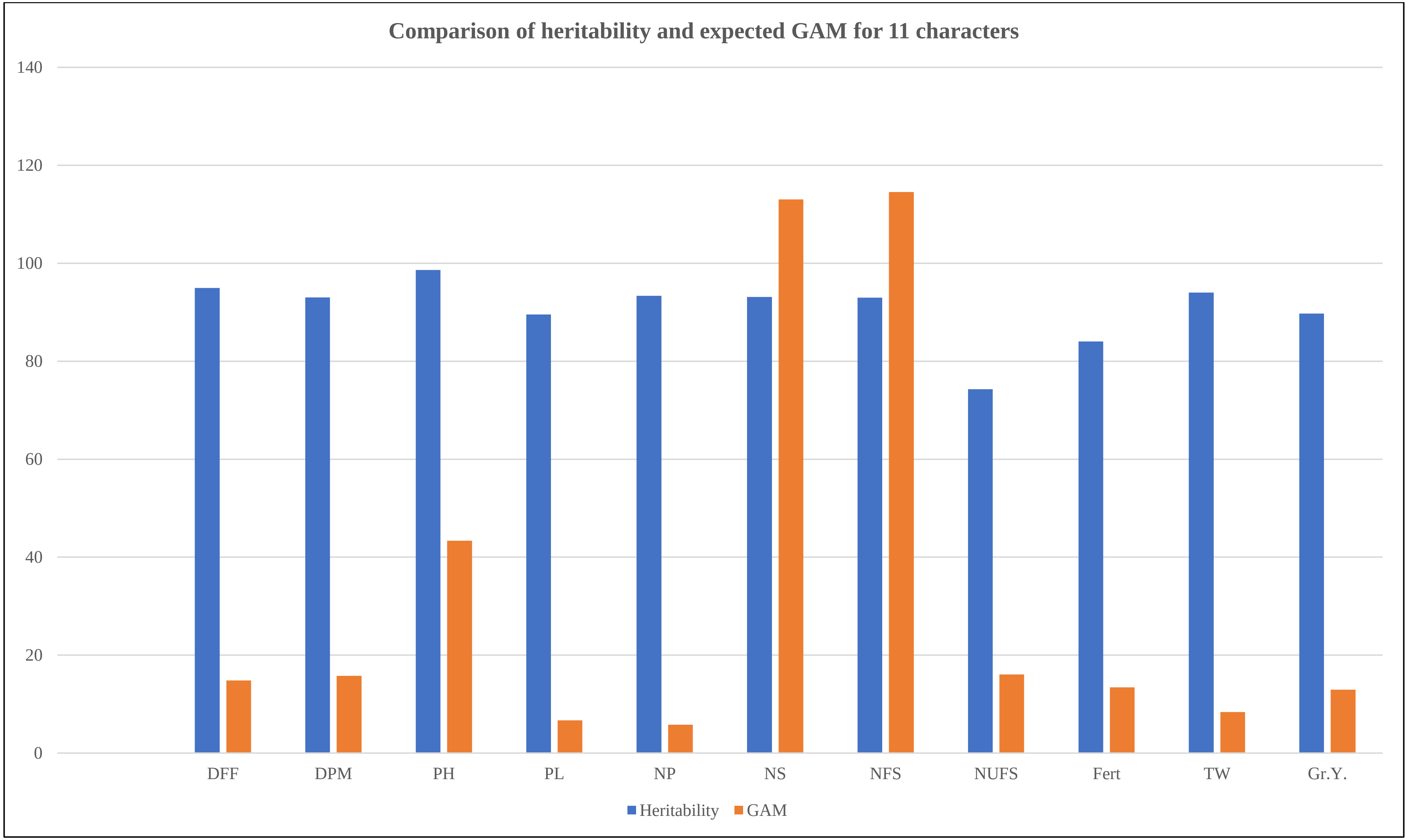

Fig. 4.2 Comparison of heritability and expected GAM for 11 characters

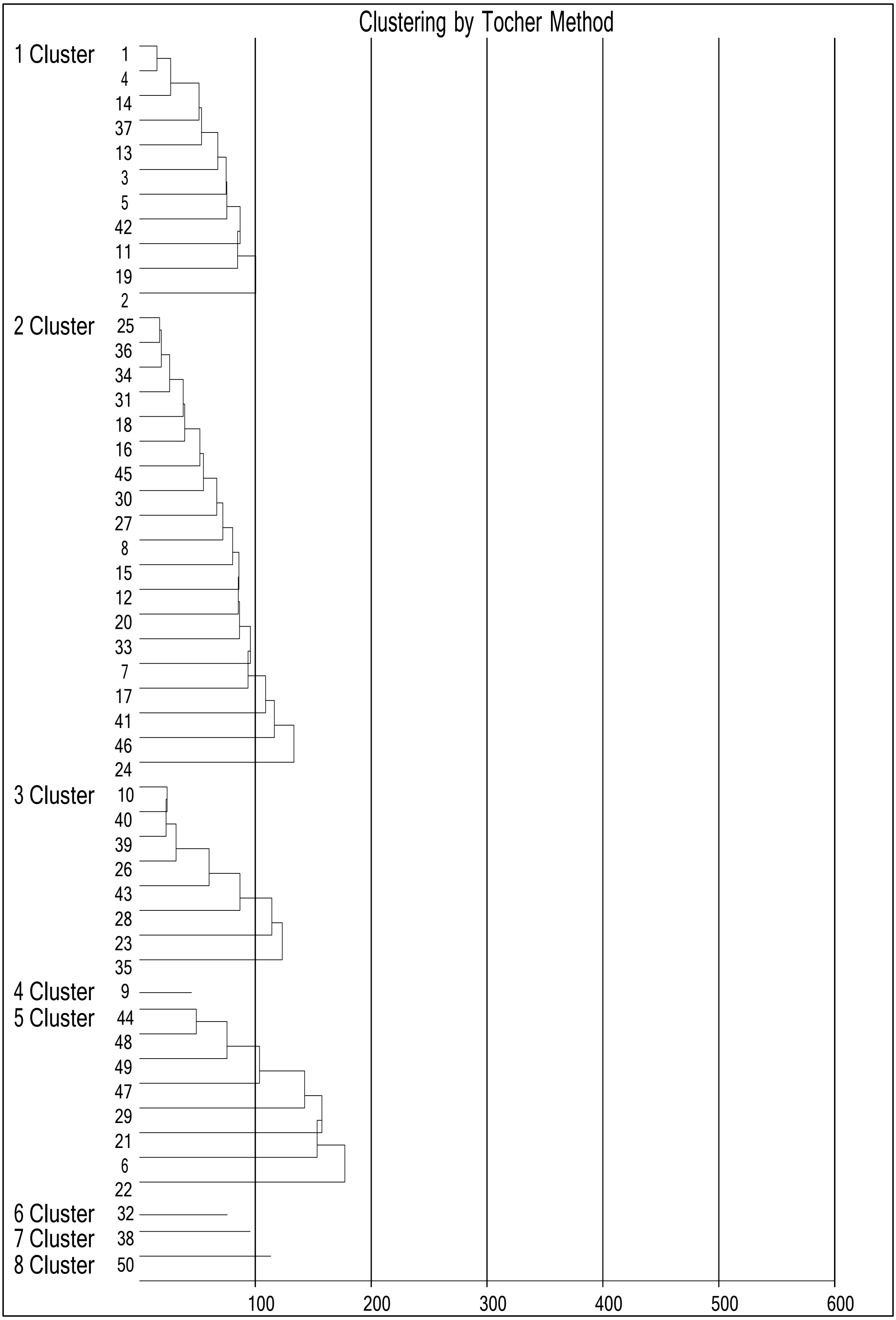

Fig. 4.4 Clustering pattern of fifty genotypes in rice by Tocher Method.

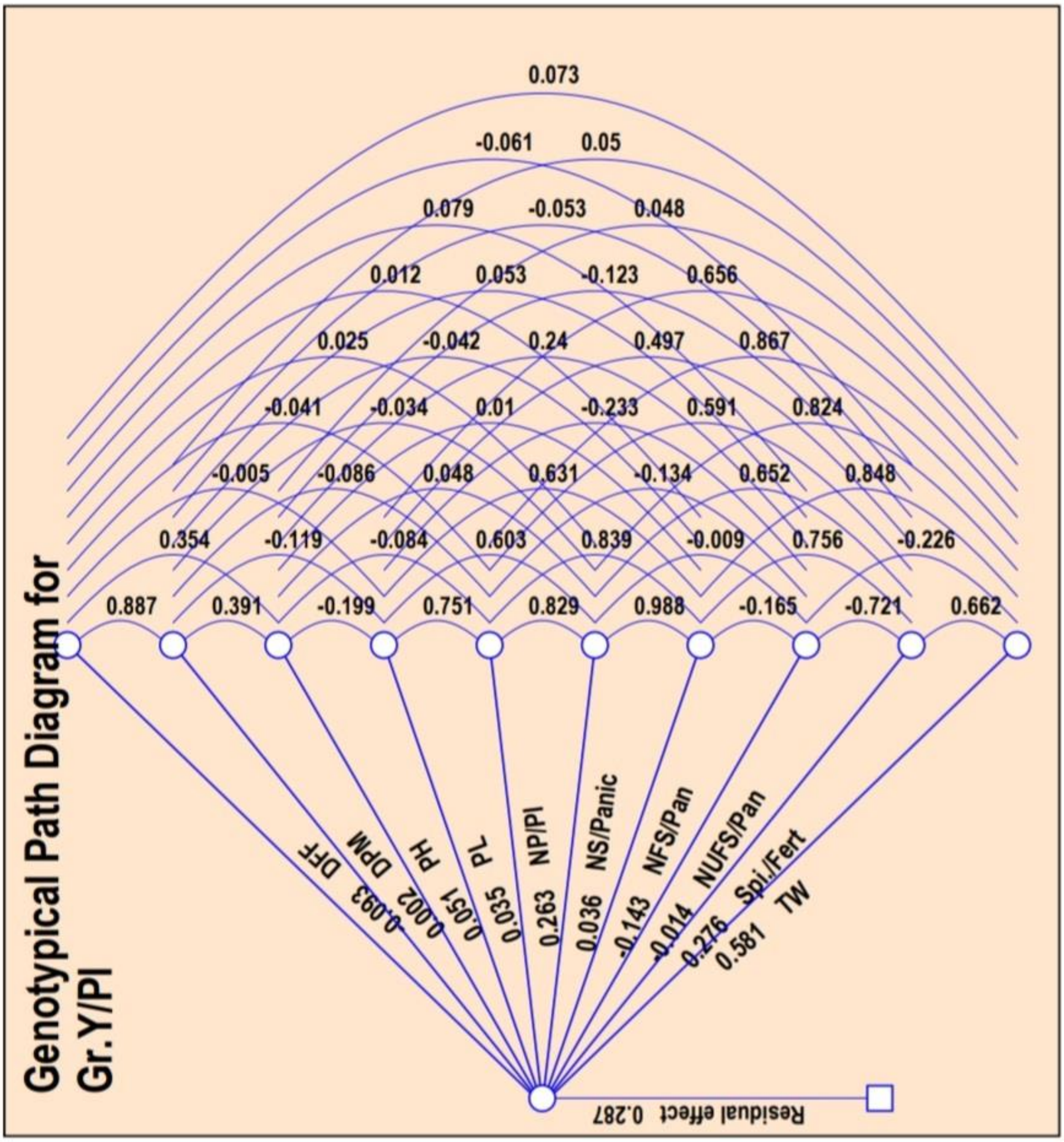

Fig. 4.3 Genotypic path diagram for grain yield plant^{-1}

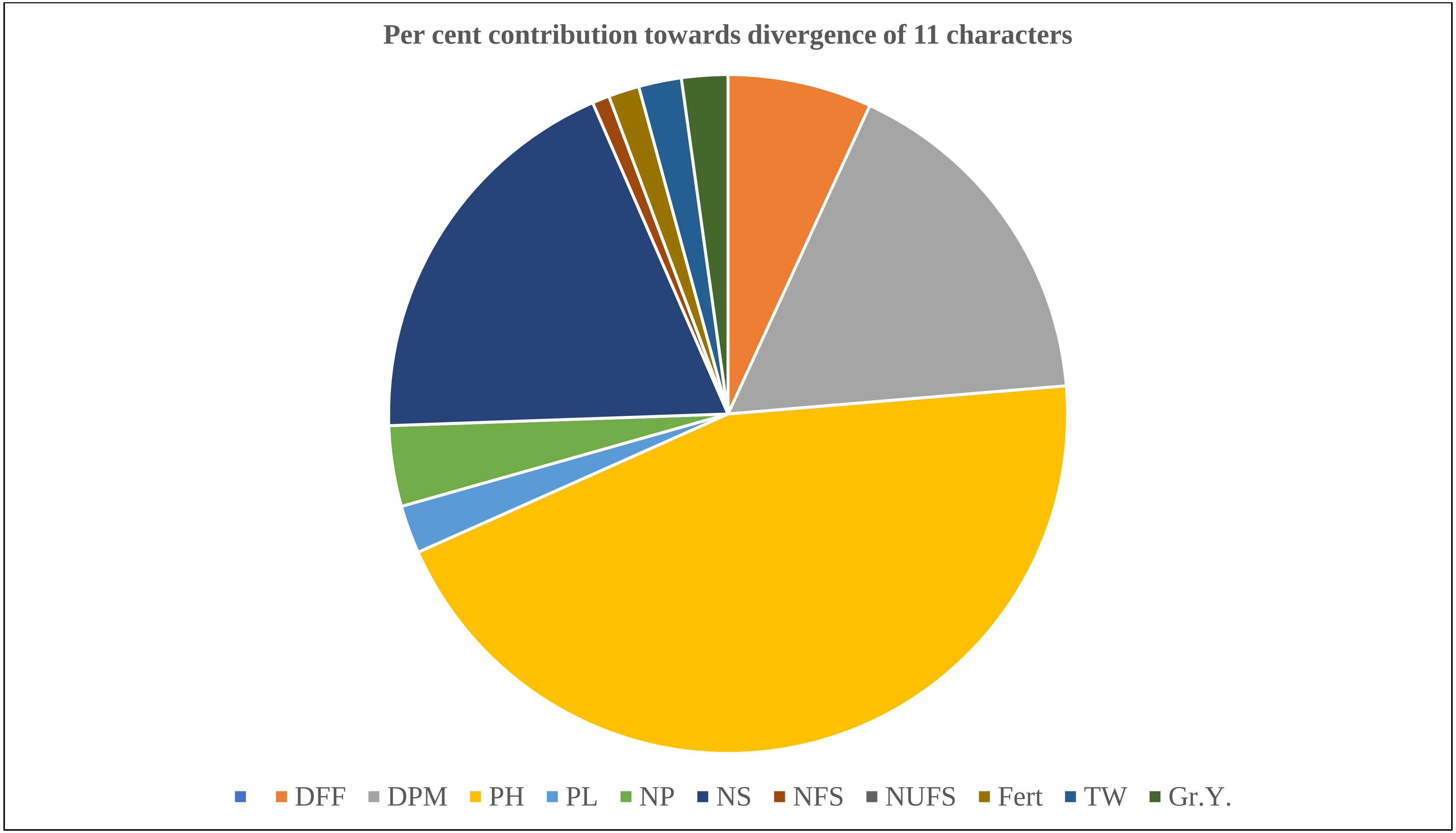

Fig. 4.5 Per cent contribution towards divergence of eleven characters in rice