Genetic variability for morphological and quality characters in medium slender grain rice (*Oryza sativa* L.)

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Genetic variability for morphological and quality characters in medium slender grain rice (*Oryza sativa* L.)

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CERTIFICATE- I

This is to certify that the thesis entitled “**Genetic variability for morphological and quality characters in medium slender grain rice (*Oryza sativa* L.)**” submitted in partial fulfilment of the requirements for the award of the degree of **MASTER OF SCIENCE IN AGRICULTURE (PLANT BREEDING AND GENETICS)** to the Odisha University of Agriculture and Technology, Bhubaneswar is a faithful record of *bona fide* and original research work carried out by **Mr. PREETHAM K M, Adm. No. 191222113** under my guidance and supervision. No part of this thesis has been submitted for the award of any other degree or diploma.

It is further certified that the assistance and help availed by him from various sources during the course of investigation has been duly acknowledged.

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CERTIFICATE – II

This is to certify that the thesis entitled **“Genetic variability for morphological and quality characters in medium slender grain rice (*Oryza sativa* L.)”** submitted by **Mr. PREETHAM K M, Adm. No. 191222113** to the Odisha University of Agriculture and Technology, Bhubaneswar in partial fulfilment of the requirements for degree of **MASTER OF SCIENCE IN AGRICULTURE (PLANT BREEDING AND GENETICS)**, has been approved by the Student’s Advisory Committee and the External Examiner.

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ABBREVIATIONS

% : Percent
°C : Degree Celsius
cm : Centimeter
d.f. : Degree of freedom
et al. : and others
g : Gram
ha : Hectares
i.e. : that is
viz. : For example
m^2 : Meter square
cm : Centimeter
* : Significance at 5%
** : Significance at 1%
Approx. : Approximately
S.N. : Serial number
CV : Coefficient of variation
C.D. : Critical difference
GA : Genetic Advance
GCV : Genotypic Coefficient of Variation
PCV : Phenotypic Coefficient of Variation
SD : Standard deviation
h^2 (bs) : Heritability in broad sense
ANOVA : Analysis of Variance
RBD : Randomized Block Design
σ_p : Phenotypic standard deviation.
σ_g : Genotypic standard deviation
σ^2_p : Phenotypic variance
σ^2_g : Genotypic variance

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ABSTRACT

Rice is one of the major food grain crops in the world, particularly in Asian countries. Though population growth continues to boost the demand for rice, its production growth in all the ecosystems is attaining a plateau. Therefore, efforts to enhance rice productivity with keeping good grain quality must receive top priority. Quality rice is not only in big demand for home consumption, but also have great export potential and can earn a lot of foreign exchange. With an objective to assess the relative performance, study of variability, genetic advance, character association, genetic diversity and grain quality characters in 20 medium slender grain rice genotypes (including 6 checks). The experiment was laid out in RBD with 3 replications during kharif, 2020 at the Rice Research Station, O.U.A.T., Bhubaneswar. Observations were recorded for yield, various yield attributing characters and grain quality characters. The analysis of variance showed significant variation among the test genotypes for all the traits studied denoting the existence of wide genetic variation which was also supported by mean and range of variation. High GCV and PCV estimates were observed for traits like number of chaffy grains per panicle, grain yield per hectare, straw yield per plant and grain yield per plant. High heritability coupled with high genetic advance as percent of mean was observed for number of chaffy grains per panicle, grain yield per hectare, total number of grains per panicle, and number of filled grains per panicle indicating the presence of additive gene action in governing the inheritance of these traits. In the correlation study, grain yield was significantly correlated with days to 50% flowering, plant height, panicle length, 100-grain weight, grain yield per plant, straw yield per plant, number of filled grains per panicle, and grain fertility. Out of these traits, number of filled grains per panicle, straw yield per plant, grain fertility, harvest index, grain yield per plant and plant height had high direct contribution to yield. Following D^2 analysis, the 20 genotypes were classified into 8 clusters which contains 8, 4, 2, 2, 1, 1, 1, 1 genotypes in cluster I, II, III, IV, V, Ⅵ, Ⅶ, Ⅷ, respectively. The relative contribution to divergence was high for number of filled grains per panicle, days to 50% flowering and moderate for number of chaffy grains per panicle, grain yield per hectare, and grain fertility. All the genotypes had medium-slender grain type with kernel length 5.51mm to 6.60mm and L/B Ratio 2.1 to 3.0. The range of variability for Milling % and Hulling % varied from 64.1% - 71.4% and 70.6% - 81.4% respectively. Most of the genotypes had intermediate to high amylose content (range 20.7% - 26.9%, mean 24.99%), and intermediate to high alkali spreading value (range 4 - 7, mean 4.60) corresponding to intermediate to low gelatinization temperature. Length of rice after cooking ranges from 5.4mm to 6.3mm. On the basis of yield, the genotypes MTU 1320, RNR 28362, MTU 1321, AD 16168 and KPS-6262 were found promising and they also showed appreciable, if not best, grain quality characters.

Introduction

South East Asian countries mainly depend on the rice as staple food crop in the world. Over a hundred nations cultivate rice over an area of 158 million hectares, with an annual yield of nearly 700 million tonnes. Rice has the largest portion of around 38 million hectares among the major grain crops produced in India, with a production of about 121.46 million tonnes during 2020-2021 (www.indiastat.com). By the year 2050, the population is anticipated to reach about 1.63 billion. Hence, it is necessary to increase the production and productivity to feed the growing population. Rather, the availability of cultivated land decreases day by day because of the increased necessities for basic infrastructures like building construction, highways, industrial establishment etc., by introduction of high yielding semi dwarf rice varieties during the green revolution resulted in the higher production. But later on, these varieties reached plateau in yield in major productive regions. As a result, enhancing rice production to achieve expected demand is a difficult challenge.

Traditionally, rice plant breeders concentrated on breeding for high yield. In recent decades as living conditions are being steadily improved, human demand for highquality rice is continuously on increase. Quality rice is not only in big demand for home consumption, but also have great export potential and can earn a lot of foreign exchange. Hence, improving rice grain quality has been the most important objective next to enhancement in yield to meet the consumer preference and market demand. The desired quality characteristics in rice include the total head rice recovery in milling, the physical attributes of grain size, shape and appearance, the cooking and eating characteristics, gelatinization temperature, grain elongation, gel consistency and aroma.

Improvement in grain quality that does not lower the yield is the need of the hour to benefit all the rice growers and consumers. Like grain yield, quality is also not easily amenable to selection due to its complex nature. Therefore, efforts to enhance rice productivity with keeping grain quality must receive top priority.

In India only certain sections of population mainly in the northern parts prefer long slender grain while the remaining majority prefers short fine grain. But the cost of both these types of grains is high and the demand for these grains can only be met to a certain extent. As the median national income is very low, majority of the growing population cannot afford either the long slender grains or the short fine grains. For this reason emphasis needs to be given for the development of medium slender grains type varieties with high yielding potential and all the desirable grain quality parameters.

The degree of genetic variability present in plant species determines the efficiency of selection. Genetic variation has been a crucial component that man has used not just to meet his dietary requirements, but also to cultivate high quality varieties. The genotypic coefficient of variation and the phenotypic coefficient of variation are the fundamental genetic factors for determining the degree of variation present in the germplasm. Higher broad sense heritability coupled with high genetic advance may correctly determine the function of environmental parameters on the manifestation of any genotype and characteristic performance (Babu *et al*. 2012). A critical examination of genetic variability is a must for the successful execution of any crop improvement programme and the use of appropriate assessment methodologies.

Grain yield are complicated characteristics that are connected with a variety of component traits that are interdependent. Knowledge of character associations and how each feature contributes significantly to yield would be an added benefit in assisting with the selection process. Correlation defines the degree to which yield and its characteristics are connected, allowing for a clear understanding of their relationship with grain yield. Such a study may finally allow the breeder to design his preferred approach in order to improve grain yield (Babu *et al*. 2012).

The rate and extent of genetic improvement in a population are typically determined by the amount of genetic diversity present in a population. Genetic divergence influences a cross's intrinsic potential for hybrid vigour as well as the frequency of desirable recombinants in successive generations. As a result, by including the most divergent parents in the breeding programme, suitable segregants from segregating populations might be selected. Path analysis aids in dividing the correlation coefficient of a yield component with seed yield into direct and indirect effects, ensuring the real contribution of a characteristic as well as its influence through other characters.

In the current research, an effort was made to study the variability in twenty medium slender grain rice genotypes for different yield attributing traits as well as important quality characters, with the following objectives:

1. To study the comparative performance of medium slender grain rice cultures for yield and quality characters.
2. To estimate the genetic variability and find out the correlation among the different quantitative traits.
3. To find out the direct and indirect effect of the component characters on grain yield.
4. To study the genetic divergence among the test genotypes to select parent materials for future crossing programme.

REVIEW OF LITERATURE

Knowledge of the work done by previous researchers in the subject of study is necessary in order to have an idea of the relevance and prospects of the studies to be conducted. A brief review of literature of rice-related research pertinent to the current investigation was presented in the following aspects:

A. Medium slender grain rice
B. Genetic variability
C. Correlation analysis
D. Path coefficient analysis
E. Genetic divergence
F. Grain quality traits in rice

A. Medium slender grain rice

In terms of grain quality characteristics, rice has a wide spectrum of diversity. Rice genetic modification has resulted in a significant rise in fine grain rice yield. Despite the production and dissemination of a large number of high yielding cultivars, relatively few of them are widely grown. One of the most important elements influencing farmer selection for a rice variety is its marketability. Marketability is governed by the grain quality preferences of various stakeholders in the rice value chain, and ultimately by consumers (Laborte *et al*., 2015). Rice grain is considered as "medium slender" when the grain length is within the range of 5.51- 6.60 mm and L/B ratio of 2.5 to 3.0 (Cruz and Khush, 2000). Medium slender grain quality is one of the most preferred grain qualities among Indian rice consumers (Calingacion *et al*., 2014).

BPT5204, popularly called as "Samba Mahsuri" has evolued using three way cross GEB24/ TN1// Mahsuri. Mahsuri is one of the most popular medium slender grain rice variety. It is one of the mega rice varieties which is evident from its Breeder seed indent. Even to date, this variety is popular among the farmers due to its high yield, medium slender grains and outstanding cooking quality (Sundaram *et al*. 2008). It also has a high demand in Indian and International markets. It is exported to various American and Middle East countries and has a high export potential (Dev and Rao, 2004). Fine quality Samba Mahsuri grain type occupies a major share in the non-Basmati rice export from India.

Rajeswari *et al.* (2012) presented the results of the survey conducted in Tamil Nadu regarding the type of rice grain preferred by consumers, traders, and growers. The result reveals that most of the people of Tamil Nadu prefer medium slender rice grain with intermediate amylose content. Looking into consumer preferences they evolved the rice Variety CO(R) 49, which is medium slender rice grain with an amylose content of 23.25% (intermediate), medium gelatinization temperature, and excellent cooking quality and also have adequate resistance to disease and pests.

Kunkerkar *et al.* (2013) conducted the project for breeding for biofortified rice, red kernel rice, basmati rice, hybrid rice for medium slender grain type preferred by processing industries. They found that KJT-2-2-44-10 was a promising medium slender grain rice with a high yield and good cooking quality with an amylose content of 23.62%, excellent milling percent (71.69%), and head rice recovery (63.71%) which is highly suitable for processing industries as well as to consumers who preferred medium slender grain rice.

Kiani and Agahi (2016) explored the interrelationships between morphological features and rice grain shape using a collection of 25 rice genotypes. The findings revealed that first-order predictor variables such as grain breadth, grain length, and the number of grains per panicle had the most direct effect on grain shape and may be utilized as a selection criterion to improve rice grain form. Second-order predictor variables such as 100-grain weight, maturity date, number of tillers, and flag leaf width have an indirect effect on rice grain shape due to their effects on first-order predictor variables.

Waghmode *et al.* (2018) evolved the rice variety Ratnagiri-8, a medium slender high yielding variety from the parent material IR64, and Karjat 184 with the pedigree method of selection at Agricultural Research Station, Shirgaon, Ratnagiri. By looking into its consistent performance over the location, the variety was released for commercial cultivation in the zone IIIrd (Odisha and Uttar Pradesh), Vth (Chhattisgarh and Maharashtra), VIIth (Andhra Pradesh and Telangana).

B. Genetic variability

Genetic variability has an immense role in the success of any plant breeding program because the population going to increase at an alarming rate and the availability of cultivated land decreases day by day. To mitigate this problem and to meet food security the only way is to increase yield. But at the present condition, our improved varieties have reached a plateau in the yield. This plateau can be broken by identification of genetic variability found in the plant population and utilizing those variabilities in the crop improvement programs.

For any character to improve, there must be a vast genetic variability in that character. The extent and degree of genetic variability determine the scope and magnitude of character modification in crop improvement. Assessment and evaluating the magnitude of genetic variation present in various quantitative characters becomes the prime importance. A number of research have stressed the efficacy of estimation of Genotypic and phenotypic coefficient of variation (GCV and PCV), heritability, and genetic advance in the prediction of response to selection with respect to quantitative characters in rice. The details on the genetic variability of traits that influences grain yield in rice has been reviewed here.

Krishna *et al.* (2010) evaluated ninety-seven rice germplasm lines along with three check varieties and recorded a high magnitude of GCV for the number of unfilled spikelets per plant and maximum PCV for the total number of spikelets per plant. The highest estimate of heritability coupled with higher genetic advances was observed for total number of spikelets per plant and the number of filled spikelets per panicle, which signify that they might be significantly enhanced utilizing selection.

Banumathy and Manimaran (2010) found that grain yield was shown to have the greatest impact on variability, followed by days to fifty percent flowering, total grains per panicle, and plant height, as a result, overall divergence was 86.62 % due to grain yield, days to 50% flowering, total grains per panicle and plant height.

Tiwari *et al.* (2010) carried out experiment comprised with 3 CMS lines (viz IR58025A, NMS4A and PMS10A) and 20 diverse genotypes were crossed in a line x tester mating design to identify suitable parents for heterosis breeding. The study of variance shown that for treatments, parents, crosses and parents vs. crosses are highly significant for various characters under studied i.e. days to 50% flowering, effective tillers per plant, panicle length, number of spikelets per panicle, number of fertile spikelets, spikelet fertility percent, grain yield per plant, 100-grain weight, biological yield, harvest index except due to crosses for 100-grain weight. The higher magnitude of PCV and GCV was recorded for 100-grain weight, grain yield per plant, number of fertile spikelets, pollen fertility percent, effective tillers per plant, panicle length, number of spikelets per panicle and harvest index. All the characters showed high broad sense heritability, while narrow sense estimates were higher for biological yield, spikelet fertility percent and number of fertile spikelets and moderate for most of the traits except effective tillers per plant and panicle length. High heritability coupled with high genetic advance was recorded for number of fertile spikelets, spikelet fertility percent and pollen fertility percent indicating the major role of additive gene action in the inheritance of these characters. Thus, these characters may serve as an effective selection parameter during breeding programme.

Pal *et al.* (2010) observed that the genotypic and phenotypic coefficient of variation (PCV and GCV) for lodging percentage and days to maturity were found to be the highest and lowest, respectively. The phenotypic coefficient of variation was greater than the genotypic coefficient of variation, suggesting that the environment had an impact on character expression. All the characters under study showed maximum estimates of broad-sense heritability.

Jayasudha *et al.* (2010) studied fourty seven rice genotypes including 33 hybrids and 14 parents and analyzed the highest genotypic and phenotypic coefficient of variation for harvest index, grain yield, pollen fertility, and spikelet fertility percentage. Some traits like pollen fertility, spikelet fertility percentage, days to fifty percent flowering and grain yield per plant indicates a higher magnitude of heritability conjucted with the highest genetic advance.

Abdul *et al.*(2011) investigated the performance of rice genotypes and their quantitative characters in an alkaline soil environment. For the characters investigated, variability analyses indicated substantial variations between the genotypes. Total biomass and 1000-grain weight recorded high values of heritability and genetic advance under this study.

Akthar *et al.* (2011) find out that the characters like number of grains per panicle, number of productive tillers per hill, plant height and plot yield have PCV and GCV more than fifteen percent at phenotypic level and other characters like days to maturity, number of grains per panicle, number of tillers per plant and plant height estimates had high value of heritability suggesting that selection may be used to enhance plot yield in rice utilizing these characters.

Prajapati *et al.*(2011) found that harvest index had the highest heritability assessments as well as the most genetic advance, followed by number of spikelets per panicle, number of panicles per plant, and number of effective tillers per hill.

Immanuel *et al.* (2011) found that number of tillers per plant, number of productive tillers per plant, plant height, and grain weight per plant had high heritability along with strong genetic advance and genotypic coefficient of variation.

Singh *et al*. (2011) collected 81 rice genotypes for the 13 characteristics to investigate the presence and degree of heterogeneity, heritability (broad sense), and genetic advance during Kharif season 2010. Among all characteristics, the quantity of grains per panicle had the greatest genotypic coefficient of variation and phenotypic coefficient of variation followed by harvest index, grain yield per plant and number of panicles per plant.

Ashfaq *et al.* (2012) found that plant height, spikelets per panicle, panicle length, days to heading, and days to maturity were shown to have the largest genetic variability. Substantial correlation with yield was also observed for Panicle length, seeds per panicle and seed weight per panicle exhibited significant positive correlation with grain yield. All the traits were also calculated through principal component analysis (PCA). The maximum variability was witnessed in plant height, tillers per plant, panicle length and flag leaf area.

Kumar *et al.* (2012) detected in rice by considering 15 traits, highest GCV and PCV for effective tillers per plant, grain L/B ratio and grain yield/plant. All traits showed highest heritability except kernel breadth. High genetic advance was recorded for all characters except spikelet fertility.

Ratnakar *et al.* (2012) examined F_2 generation of aerobic rice which showed high PCV and GCV values for most of the characters except days to 50 % flowering and panicle length. However, all traits recorded high broad sense heritability complemented with high genetic advance.

Ghosh *et al*. (2012) investigated that the scale of difference between PCV and GCV was moderately low for all the characters viz., days to 50 % flowering, flag leaf length, flag leaf width, flag leaf area, plant height, pollen fertility, sterile spikelets per panicle, fertile spikelets per panicle, spikelets per panicle, spikelets fertility, panicle length, grain yield per plant, test weight and head rice recovery, representing less environmental impact. The high heritability along with high genetic advance were registered as percent of mean for grain yield per plant, pollen fertility (%), sterile spikelets per panicle, fertile spikelets per panicle, spikelet fertility (%), head rice recovery (%), 1000- seed weight and spikelets per panicle. High heritability coupled with high genetic advance specifies the preponderance of additive gene action and such characters could be improved through selection.

Srivastava and Jaiswal (2013) worked on native aromatic short grain cultivars of rice for grain characteristics and physico-chemical quality attributes. They recorded great variability for all the traits studied ranging from 9.1 - 25.2 g for one thousand grain weight, 3.33 - 8.02 mm for kernel length, 1.68 to 2.38mm for kernel breadth,5.25 - 14.68mm for kernel length after cooking, 2.17 - 3.67 mm for kernel breadth after cooking and 1.68 - 6.06 for L/B ratio after cooking.

Rakesh *et al.* (2013) observed that among the desirable quantitative traits, grain yield per plant and filled grains per panicle were found to have high GCV and PCV while alkali spreading value, gel consistency, water uptake showed high GCV and PCV among quality traits of rice. Almost all the characters showed a little variation between PCV and GCV revealing little influence of the environment in the expression of these traits. The characters showing high GCV and PCV were found to be highly heritable coupled with high genetic advance.

Patel *et al.* (2014) found that high assessment of heritability coupled with high estimated genetic advance as per cent of mean were observed for the characters like number of grains per panicle, grain yield per plant, straw yield per plant, harvest index, 1000-grain weight, grain L/B ratio and amylose content showed that selection may be operative for this character and concluded that for maximizing the grain yield per plant, emphasis should be given in selection of characters such as number of grains per panicle, straw yield per plant, harvest index and 1000- grain weight for further improvement of upland rice.

Hossain *et al*. (2015) observed high GCV and PCV for number of productive tiller, root weight, number of root hair and grain yield per hill indicating that selection of these traits would be effective. Correlation of Grain yield was found to be highly significant and positive for number of root hair, days to 50% flowering and plant height at both genotypic and phenotypic level and negatively significant for number of secondary branches per panicle at both level. Significant positive correlation of grain yield with number of root hair, days to 50% flowering and plant height implied that selection for these characters would lead to simultaneous improvement of grain yield in rice. Further, yield was observed to be positively associated with panicle bearing tillers and number of filled grains per panicle and these characters were noticed to exert high direct effects on grain yield per plant. High indirect effects of most of the traits were noticed mostly through panicle bearing tillers per hill indicating importance of the trait as selection criteria in crop yield improvement programs.

Venkatesan *et al*. (2017) studied variability for eleven characters both in submergence and normal conditions and found that the characters of major contributors in normal condition were number of panicles per plant, number of tillers per plant, intercellular CO2 Conc. and stomatal conductance. In case of submergence condition the major contributors were number of panicles per plant and 1000-grain weight. High heritability along with high genetic advance of mean was observed for number of panicles per plant, photosynthetic rate and grain yield per plant in normal and submergence conditions which indicate that these traits are governed by additive gene action. Low heritability along with high genetic advance of mean was observed for intercellular CO_2 Conc. in both normal and submergence conditions.

Umarani *et al*. (2017) found PCV to be slightly higher than GCV for all the traits, indicating less influence of environment. Total number of grains per panicle exhibited highest PCV and GCV whereas lowest PCV and GCV were recorded for spikelet fertility. All the characters under study except spikelet fertility and panicle length exhibited high heritability coupled with high genetic advance as a per cent of mean, which indicated the preponderance of additive gene action in controlling these traits. Hence direct selection of these characters would be effective in improving the seed yield.

Rashid *et al*. (2017) observed higher PCV compared to their corresponding GCV for all the traits but of small magnitude, indicating the little influence of environment. The higher estimates of PCV and GCV were observed for number of filled grains panicle and plant height indicating possibility of genetic improvement through direct selection for these traits, while days to 50% flowering, days to maturity, panicle length, number of effective tillers /plant, fertility (%), 1000 Seed weight and yield/ panicle showed low PCV and GCV values indicating the need for creation of variability by hybridization or mutation followed by selection. High heritability values (>60%) along with high genetic advance and genetic advance as percentage of mean were found for all the traits indicating prevalence of additive gene action, which provides good scope for further improvement by selection.

Devi *et al*. (2017) observed higher PCV and GCV for yield per plant and filled seeds per panicle indicating possibility of genetic improvement through direct selection. High heritability in broad sense coupled with high genetic advance as percent of mean exhibited by effective tillers, plant height, flag leaf length, filled grains per panicle, test weight, yield per plant, head rice recovery and length/breadth ratio indicating preponderance of additive gene action which provide good scope for further improvement by selection. Grain yield per plant had highest significant positive association with filled seeds per panicle, plant height, flag leaf length, effective tillers, flag leaf width and panicle length indicating importance of these characters for yield improvement, while head rice recovery was found to be significantly and positively correlated with milling percent and hulling percent. Test weight, effective tillers, and filled grains per panicle had positive direct effect on grain yield per plant. Among the quality traits kernel length followed by milling percent and kernel elongation ratio had direct effect on head rice recovery.

Sreedhar *et al.* (2017) observed ample variability for all the characters except the number of effective tillers/m^2 among the 36 genotypes, under this experiment PCV was in the highest magnitude compare to GCV for all the characters and thousand grain weight has a high degree of heritability and genetic advance too. In addition, moderate genetic advance conjunct with high heritability for days to 50% flowering, height of the plant, length of the panicle, and grain yield were observed.

Nanda *et al.* (2020) evaluated 29 rice genotypes including three check varieties intending to assess the extent and degree of genetic variability for grain yield and grain quality traits. The investigation reveals that there is a presence of a high degree of genetic variability among the test genotypes. The characters like the number of filled grains per panicle (23.99, 23.32) and flag leaf area(19.40, 18.21), grain yield (18.75, 17.82), plant height(11.68, 11.21) have a high and moderate phenotypic coefficient of variance, and genotypic coefficient of variation respectively, whereas flag leaf area, grain yield and 100-grain weight shows the high heritability along with high genetic advance percentage over mean.

Sathishkumar *et al.* (2020) recorded the highest genetic variability, heritability and genetic advance as percent mean for the six characters of F_2 population of two crosses that are MDU6 crossed with VGD1and improved samba mashuri with VGD1 and moderate PCV and GCV were recorded for the number of effective tillers per plant under this investigation.

Roy *et al.* (2020) measured a high degree of heritability and genetic advance in F_5 and F_3 lines of Tulaipanji, IR64, Badshabhog, and Swarna sub-1 which were developed through pre-breeding and hybridization, and also these lines were showed potential performance for agronomical and yield parameters. These lines were suggested to use in a future breeding programme to break the yield plateaus.

C. Character association

Examination of associations is an essential method to a crop improvement programme. It provides a concept of the interrelationship between the different traits and decides on the characteristics of the component on which selection may be dependent for genetic enhancement in yield and grain quality

Degree of association also influences the effectiveness of selection procedures.The coefficient of correlation ensures the degree of interaction, genetic or non-genetic relationship between two or more characters which constitutes the basis for selection.

Nandan *et al*. (2010) recorded a highly positive association of yield with days to 50 % flowering, plant height, number of grains per panicle and spikelet fertility percentage.

Yadav *et al*. (2010) studied that coefficient of correlation between seed yield per plant and other quantitative yield attributes showed that grain yield was significantly and positively correlated with harvest index, number of tillers per plant , number of panicles per plant , length of panicles, number of grains per panicle and 1000 seed weight at both phenotypic and genotypic levels.

Akinwale *et al*. (2011) evaluated the association study for yield and grain quality traits in rice. The analysis revealed that significant positive association of grain yield with number of tiller / hill, panicle weight and number of spikelet/panicle.

Basavaraja *et al*. (2011) studied in hundred local rice cultivars to recognize the correlation between the components of yield and their direct and indirect effect on the quality of grains and yield. Grain yield was associated positively with panicle length, 1000-seed weight, number of tiller per hill, number of productive tiller per hill, number of grains per panicle, spikelet fertility %, and amylose %.

Immanuel *et al*. (2011) reported characters like plant height, number of tillers per plant, panicle length, filled grain per panicle and test weight had significant and positive association with grain yield.

Ekka *et al*. (2011) studied the association analysis found positive correlation of grain yield per plant with leaf width, days to fifty percent flowering, plant height, panicle length , number of fertile spikelets per panicle, 1000 seed weight and paddy (crop) length. A positive and significant correlation of the percentage of head rice recovery was found with the length of the leaf, the width of the leaf, the days to 50 percent bloom, the number of filled spikete per panicle, the percentage of spikelet fertility and the percentage of milling.

Golam *et al*. (2011) studied fifty three rice genotypes including twelve globally popular aromatic rice cultivars and thirty nine advanced breeding lines were evaluated for yield and grain quality traits. Correlation analysis intended that the number of fertile tillers, total grain per panicle and fertile spikelets per panicle have the positive contribution to yield.

Babu *et al*. (2012) reported study of correlation of twenty one famous rice hybrids (Oryza sativa L.). The combination of yield attributing characteristics showed a substantially positive correlation of grain yield per plant with the number of panicle bearing tillers per plant. Selection for these characteristics can also increase yield.

Mohanty *et al*. (2012), revealed that strong positive association of kernel length,panicle length, plant height, number of productive tillers per plant ,1000-grain weight days to maturity and number of grains per panicle with grain yield. Path analysis revealed that kernel length, number of grains per panicle, plant height, number of productive tillers per plant and panicle length were the important characters contributing for grain yield.

Kumar *et al*. (2013) revealed that harvest-index followed by number of productive tillers per plant, Biological yield per plant, kernel length, LIB i'atio, fertility percentage and 100 grain weight emerged as the most important associate of grain yield in scented rice. Path analysis identified biological yield per plant and harvest index as major direct contributors and number of productive tillers per plant, days to 50 percentage flowering and days to maturity as main indirect contributors.

Veni *et al*. (2013) analyzed seventy rice genotypes (*Oryza sativa L.*) for genetic variability and association for yield and yield attributes as well as quality characteristics. Days to 50 percent flowering, productive tillers per plant, panicle length, percent head rice recovery (HRR) and volume expansion ratio found significant and positive association with grain yield, suggesting that all characters can be improved at the same time.

Lakshmi *et al*. (2014) studied during Kharif 2012, seventy rice genotypes (Oryza sativa L.) were assessed for the existence and strength of the association between yield and grain quality characteristics. The study showed that grain yield per plant was positively and significantly correlated to maturity days, number of productive tillers per plant, plant height and kernel length suggesting significance as selection criteria in yield improvement programmes.

Sinha *et.al.* (2015) studied Correlation for genetic response of seed yield traits at varying spacing in rice cultivars. Number of productive tillers per plant was found significantly correlated with grain yield per plot in positive direction at both spacing.

1000 grain weight and grain yield per plot showed significant positive association with seed yield.

Sathisha *et.al.* (2015) studied the correlation coefficient and path analysis using 130 traditional land races for quality and yield attributing traits and found highly significant and positive genotypic and phenotypic correlation between grain yield in 9 kg/ha with 50% days to flowering, days to maturity, panicle length, no of grains per panicle, plant height etc.

Kalyan *et al*. (2017) reported in Kharif 2014, seventy rice genotypes (*Oryza sativa L.*) were assessed to investigate the morphology and magnitude of the association between yield and grain quality characteristics. Studies of character association revealed that the grain yield per plant showed significant positive association with plant height, tillers per plant, panicle bearing tillers per plant, filled spikelet per panicle and test weight. This suggested that selection of all these characters at the same time was important for improvement in yield

Thippani *et al*. (2017) studied forty F1 crosses of rice were evaluated during Kharif 2015 to analyze the association among yield and yield attributing characters. The analysis showed that grain yield plant-1 was positively and significantly correlated with maturity days, effective tillers per plant, plant height and kernel length suggesting significance as selection criteria in yield improvement programs

Manjunatha *et al*. (2017) studied the correlation coefficients of thirteen growth characteristics with grain yield/ plant , for the characters chlorophyll content of flag leaf, chlorophyll content of third leaf, number of tillers/plant at 30DAT, the genotypic correlation coefficients were higher than phenotypic correlation coefficients, indicating the less influence of environment on these characters. Number of tillers/plant at 60DAT, number of tillers/plant at 90DAT and number of tillers/plant at harvest had higher phenotypic correlation coefficients than genotypic correlation coefficients, indicating the high influence of environment on these characters. Number of tillers at harvest and number of tillers at 60DAT possessed both positive association and direct effects and hence, selection for these characters could bring improvement in organic rice yield improvement programmes.

Pandey and Kar (2018) studied association for sixteen quantitative and twenty quality traits in ninty four popular landraces of rice. Correlation analysis showed a positive and highly significant association for grain 18 yield / plant with the total number of filled spikelet per panicle, total number of spikelet per panicle, plant height, number of productive tiller per hill, harvest index, 1000 grains weight, the length of the flag leaf and the days to maturity.

Kumar *et al*. (2018) reported biological yield / plant, harvest index, spikelet fertility percent, 1000 grain weight, L / B ratio, plant height and panicle length showed a positive and significant association with grain yield per plant to appear as the most relevant associates of grain yield in rice.

Sahu *et al*. (2019) studied hundred traditional rice accession for yield and quality parameters to study the nature and magnitude of genetic parameter and association analysis. Association analysis showed that grain yield per plant had a positive and significant association with grain length, panicle number, test weight, panicle length and flag leaf width.

Priyanka *et al*. (2020) studied the association of yield and yield components and grain quality traits. The weight of one hundred grains had a significant and negative association with grain yield per plant, grain elongation ratio showed significant and positive correlation with kernel breadth, kernel breadth before cooking, kernel length after cooking, and LB ratio after cooking and therefore selection of these traits will serve to improve LER.

Siddi (2020) studied eighteen rice (*Oryza sativa L*.) genotypes were used for yield and grain quality traits to study the association analysis. Grain yield had positively associated with days to fifty percent flowering, plant height and number of spikelets per panicle and negatively correlated with gall midge incidence at both genotypic and phenotypic levels suggesting that genotypes with longer duration, more plant height and good number of grains panicle with relatively very less silver shoots contribute for more grain yield.

D. Path analysis

Path analysis is an important method separates the correlation into two measures of direct and indirect effects and describes the relative importance of casual factors in producing the end product. Path analysis is used to study the cause and effect relationship, path coefficient worked out for different set of characters show remarkable differences in direct and indirect effects of the component characters on grain yield.

Kumar *et al*. (2013) studied on Correlation and path analyses for grain yield, its components and quality characters in a set of 65 genotypes of scented rice. A very strong positive correlation of grain yield per plant at genotypic, phenotypic and environmental levels was observed with harvest-index, while number of effective tillers per plant and biological yield per plant showed very strong positive association at both phenotypic and genotypic level.

Nagaraju *et al.* (2013) reported that number of grains per panicle and total number of productive tillers per plant should be considered as the main yield components because these traits showed the highest positive direct effects towards increasing grain yield .Number of grains per panicle and total number of productive

Naseem *et al.* (2014) studied of path analysis for yield related traits and concluded that number of productive tillers per plant, number of spikelets per panicle, number of grains per panicle and days to maturity had positive direct effect on grain yield per plant.

Sinha *et al*. (2015) studied on path co-efficient analysis for genetic response of seed yield traits at varying spacing in rice cultivars. Path analysis revealed that at space planting grain yield per plot showed maximum direct effect both at genotypic (0.993) and phenotypic level (1.640), its association with seed yield was also significantly positive

Sathisha *et al.* (2015) made an insight into the path analysis with 130 traditional land races for quality and yield attributing traits. The phenotypic and genotypic path coefficient analysis indicated highest positive effect on grain yield per ha was contributed by no of productive panicles per plant followed by panicle weight, L/B ratio etc.

Nayak *et al.* (2016) observed that panicle length, plant height, days to flowering and effective tiller per plant had high direct positive effect on grain yield per plant.

Madhukar *et al*. (2017) observed that number of filled grains per panicle played a key role for better yields under aerobic situation. A highly significant correlation was noticed between panicle length and plant height and also between panicle length and grains per panicle, indicating stature of plant to be very important under aerobic condition. Hence medium stature plant with long panicle, sturdy culms and more grains per panicle would be highly advantageous for aerobic situation. Spikelet fertility and 1000 seed weight could be simultaneously considered for yield enhancement.

Prasad *et al*. (2017) studied both correlation coefficients and path analysis together for grain yield and its components and indicated that, panicle weight, number of productive tillers per plant, numbers of filled grains per panicle and 1000 grain weight were more important in rice productivity. Panicle length, number of total tillers per plant could be considered for high grain yield, as there always existed a significant desirable association between this trait and number of grains per panicle. Spikelet fertility (%) and 1000-grain weight also exhibited positive direct effects on grain yield per plant.

Sowmiya *et al.* (2017) indicated that maximum direct effect on grain yield was exhibited by number of panicles per plant. Hence the trait should be taken into account during breeding programme to develop the maximum of threshold yield obtaining new rice varieties or hybrids.

Kumar *et al.* (2018) identified biological yield per plant followed by harvest-index as most important direct yield contributing traits and biological yield per plant followed by 1000-grain weight and panicle length exhibited high order of positive indirect effect as most important indirect components which merit due consideration at time of devising selection strategy aimed at developing high yielding varieties in rice.

Singh *et al.* (2019) studied and found that plant height, ear bearing tillers, panicle length, number of filled grains per panicle and test weight (g) exhibited positive direct effect on yield. Among these characters, ear bearing tillers and test weight possessed both positive association and high direct effects. Hence, selection for these character could bring improvement in yield and yield components.

Parimala *et al.* (2020) observed that number of filled grains per panicle and 1000- seed weight exhibited positive direct effects on grain yield at both genotypic and phenotypic level. The characters exhibiting high direct effects for grain yield also exhibited high degree of positive correlation with grain yield. The traits, number of filled grains per panicle and 1000 seed weight could be used as selection criteria for the improvement of grain yield.

E. Genetic Divergence

Multivariate analysis as a potent tool for assessment of diversity was first postulated by Mahalanobis (1928).Geographic diversity is often considered as an index of genetic diversity which implies that a positive relationship exists between the two parameters of variability. However, in comparing the various systems of selecting parents, Bhatt (1970) found that the application of multivariate analysis method of selecting parents and effecting crosses between parents from higher inter genotypic divergent clusters appeared to be more efficient than the method of selecting parents according to ecogeographic diversity. Murty and Arunachalam (1966) did not find parallelism between genetic diversity and geographic distribution and stated that genetic drift and selection in different environments could cause greater diversity than geographic distance. Mahalanobis generalized distance (D^2 - statistic) has been effectively used in assessing genetic divergence in rice by a number of workers.

Ahmed *et al*. (2010) examined that a number of characters viz. flag leaf area, harvest index, grain yield, 1000 grain weight show high genetic variability and moderate to high heritability coupled with moderate to high genetic advance. Mahalonabis's D^2 – statistics analysis revealed considerable amount of diversity in the material. Sixteen genotypes were grouped into six heterogeneous clusters.

Manohara and Singh (2013) revealed that among different traits, days to 50 % flowering (38.77%), 1000-grain weight (l9.93%), grain breadth (17.75) and plant height (14.86) had contribution towards the total divergence.

Nisar *et al*. (2017) studied 104 genotypes grown under sodic soil, and grouped them into eleven clusters. The lines belonging to diverse clusters and showing high mean performance in desirable direction for different traits, could be choosen as parents. The most promising genotypes for use as parents were recommended for exploitation in hybridization programme to enhance the production and productivity of sodic soil.

Maurya *et al*. (2017) studied 33 genotypes grown under sodic soil and grouped them into 6 different non-overlapping clusters. The discrimination of lines into so many discrete clusters suggested presence of high degree of genetic diversity in the materials evaluated. Presence of substantial genetic diversity among the lines indicated that the material could serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable segregates for developing high yielding varieties of rice suitable for sodic soil.

Sowmiya and Venkatesan (2017) studied the extent of divergence in 48 rice genotypes for nine characters and grouped them into nine clusters. The clustering pattern indicated that there was no parallelism between genetic diversity and geographical origin as the genotypes from different origins were included in same clusters and vice versa. Genetically distant parents from those clusters could be able to produce higher heterosis in progenies on hybridization. Grain yield per plant and thousand-grain weight were the major contributors towards the total genetic divergence among the genotypes studied. Selection could be made based on grain yield per plant and thousand-grain weight for the progenies identified.

Sarawgi *et al*. (2017) studied 10 quantitative traits in 208 core germplasm accessions (landraces) of rice and grouped them into 8 clusters. The paramount intercluster distance varied from 9.778 to 1.867. Maximum inter-cluster distance was observed between cluster VIII and IV (9.778) suggesting maximum diversity among them. Cluster VIII (3.84gm) had highest mean value for 100-grain weight. Cluster II had highest mean value for panicle length (28.55 cm.), effective tillers/plant (8.65) and L/B ratio (3.79). Better genotypes could be selected for most of the characters on the basis of mean performance from different clusters. The cluster II showed highest grain yield/plant and effective tillers (9 tillers/plant). These clusters can be utilized in the hybridization programme for obtaining desirable transgressive segregants. Grain yield had positive and significant correlation with days to 50% flowering, plant height and panicle length.

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

Subudhi *et al.* (2020) conducted the experiment to study the magnitude of genetic diversity among the genotypes and major traits contributing to variation. Based on Mahalanobis D^2 value, 100 genotypes are grouped in to 12 clusters. The single genotype having independent cluster are WITA-8, WGL32183, Konark, Purnendu, VLD-61, PusaSugandh-3 and Improved Lalat. Maximum 55 genotypes are in cluster 1. Maximum inter cluster divergence was observed between cluster 3 and 11(667.36) followed by cluster 8 and 11(615.50), cluster 7and 11(604.87). Lowest inter cluster distance was observed between cluster 2and 3(10.68).Intra cluster distance (D) ranged from 48.77(cluster 5) to 100.4(cluster 8). These are more diverse and can be used in hybridisation programme for development of effective hybrids. The inter cluster distance is higher than intra cluster distance indicating wide genetic diversity among the genotypes.

F. Grain quality traits in rice

Rathi *et al.* (2010) reported High heritability was showed high heritability with moderate genetic advance in total soluble sugar content while alkali spreading value and Paddy L/B ratio expressed high heritability with moderate genetic advance. This indicates that certain attributes are largely influenced by additives effects and may be based on further choice based on phenotypic quality.

Manonmani *et al.*(2010) reported genetic variation for fifteen yield and grain quality traits among the genotypes using twenty rice hybrids with checks. They estimate the cooking qualities such as ratio of elongation and ratio of volume expansion. They intended medium slender grain form reported by the hybrids viz., TNRH 160, TNRH 180, TNRH 174, TNRH 173, TNRH 179, high head rice recovery, high milling % , high LER and low BER and intermediate GT. Such hybrids don't have fragrance that south Indians like. Hence it will exploit these hybrids.

Fatema *et al*. (2011) studied that traits viz., grain breadth, grain length, grain L/B ratio, gelatinization temperature, gel consistency, amylose content (%), protein content (%), 1000 grain weight and grain yield plant-1were recorded significant variation for grain quality traits. High GCV, PCV, heritability and GA were recorded in amylose content, grain length average and L/B ratio revealed that those 3 traits were inherited by parent to offspring.

Kaur *et al*. (2011) found significant positive correlation between paddy length breadth ratio with kernel length breadth ratio, density, cooked kernel length and a negative correlation with bulk density. Amylose content showed a negative correlation with gel consistency, solid loss in gruel while it was positively correlated with cooked kernel length, elongation ratio and water uptake at 5% level of significance

Sarawgi *et al.* (2013) found that desirable quantitative traits like grain yield per plant, filled grains per panicle, to have high GCV and PCV while alkali spreading value, Gel consistency water uptake showed high GCV and PCV among quality traits of rice. The characters showing high GCV and PCV were found to be highly heritable coupled with high genetic advance. These characters are governed by additive gene action and one should go for direct selection for these traits.

Chukwuemeka *et al*. (2015) took four local rice varieties and one foreign rice variety (caprice gold) and found the cooking time to differ with variety ranging between 17-23 minutes. Volume expansion ratio varied from 1.67- 3.67cm . Gelatinization time varied with variety and ranged between 4-11 minutes. Grain elongation during cooking, amount of water evaporating during cooking and solid in cooking water ranged between 0.18-0.38m, 19-42%, 0.02-0.64(g) respectively. The values for the amylose ranged between 7.6-37.2% and amylopectin ranged between 69.8-79.8%. The range of physical properties from all the varieties were, length 0.595 to 0.753m, width 0.217 to 0.287m, length/ width ration 2.188 to 3.470mm.

Kumar (2015) observed high PCV, high heritability (broad sense) along with high genetic advance for grain L/B ratio and gelatinization temperature in land races, new plant types and japonicas, respectively. Grain length showed significant positive correlation with L/B ratio and grain elongation in land races and new plant types, while significant positive correlation with L/B ratio, 1000-grain weight and amylose content in japonica. Grain width showed significant positive correlations with 1000-grain weight and protein content in land races; with grain thickness and 1000-grain weight in new plant types and japonicas. This indicated that grain length; grain width and gelatinization temperature can be used for the improvement in grain quality in rice.

Gampala *et al*. (2015) observed highest to moderate range of GCV and PCV by L/B ratio, gel consistency, kernel breadth after cooking and kernel breadth before cooking. Gel consistency, L/B ratio and kernel length after cooking showed high heritability (broad sense) and high genetic advance. Therefore, these characters should be given priority during selection.

Nirmaladevi *et al*. (2015) observed high GCV and PCV for head rice recovery (%), water uptake, gel consistency and alkali spreading value. High broad sense heritability and genetic advance was obtained for head rice recovery, milling, water uptake, amylose content, and gel consistency which suggested that these traits would respond to selection. The significant positive correlation of KL AC with ER and L/B ratio, ASV with water uptake, hulling % with milling % and with HRR % indicated that these are the primary traits for improvement of rice grain quality.

Gangadharaiah *et al*. (2016) studied grain quality properties of high yielding slender grain rice varieties being cultivated in India and found highest milling yield and head rice recovery in CV in KRH-4 and MTU-1001 respectively. Thanu took least time for cooking compared to other varieties, whereas grain elongation was highest in KMP175. Majority of the rice varieties were of intermediate gelatinization temperatures. Protein content ranged from 10.12 to 14.63% with the mean of 12.84%. The Amylose content of the tested entries ranged from 9.21 to 14.0%. Most of the studied varieties possess >12.00% Amylose content and it was found to be highest in CV in KRH-4 and lowest in Gangavathi Sona and Mugaud Suganda. The zinc content was found highest in KRH-4 (27.61 ppm) and lowest in Mangala (17.11 ppm). Eight varieties possess >84 ppm iron content and highest was in IR-30864 (86.14 ppm).

Singh *et al*. (2017) found PCV to be higher than GCV for all the traits and also found high heritability for all the traits. High heritability with high genetic advance was found for kernel L/B ratio, cooked kernel length and alkali digestion value. Strong association was found between kernel length and kernel length/breadth ratio and hulling & milling recovery. Cooked kernel length was associated with most of the grain quality traits that could be given preference in selection criteria for improvement of multiple grain quality traits simultaneously.

Tamu *et al*. (2017) evaluated grain appearance, cooking and eating qualities of 87 rice varieties and found 64% with intermediate GT (70-74ºC), 20% with low GT (55-69 ºC), and 16% with high GT (above 74ºC). Hard gel consistency was observed in 71%, 22% recorded medium gel consistency, and 7% recorded soft gel consistency. Of the 87 test varieties, 34% were aromatic while 66% were not. Alkaline spread value had significant and positive correlation with water uptake, but gel consistency had negative correlation with volume expansion ratio. Based on the L/W ratio, 33 of the rice varieties had long slender grain type, 45 recorded medium slender grain and only 9 varieties recorded short bold grain.

Kumar *et al*. (2017) observed grain quality parameters such as the grain length, amylose content and alkali spreading value to record significantly higher values in SRI (System of Rice Intensification) method compared to Conventional Transplanting (CT). SRI method was found better over traditional method in respect of seed and grain quality attributes of rice.

Chetri *et al*. (2018) found the highest amylose content in the varietal treatment Dehradoon (V3) with the nutrient management T4 (100% recommended NPK as chemical fertilizer) while the other quality parameters viz. head rice recovery kernel length before and after cooking and the elongation ratio was highest under T5 nutrient management (100% recommended NPK as Vermicompost).

Chen *et al*. (2018) studied the effects of short-term high temperature (SHT) on grain quality and found that chalky rate and chalkiness increased while brown rice rate, milled rice rate, and head rice rate decreased with the increase of high temperature and prolonged duration. SHT stress reduced the accumulation of amylose as well as starch accumulation, starch granules arranged loosely and more single starch granules appeared after SHT treatment. The effects of SHT at anthesis stage were greater than that at grainfilling stage. High temperature causes negative effects on grain yield and quality of rice.

Nanda *et al.* (2020) studied twenty nine rice genotypes for their quality parameters, most of the genotypes exhibited long to medium slender grain type along with the kernel length of ≥ 6mm and kernel length to breadth ratio of ≥3mm. Genotypes having an moderate level of amylose content, gelatinization temperature and intermediate to soft gel consistency.

MATERIALS AND METHODS

The present investigation entitled "Genetic variability for morphological and quality characters in medium slender grain rice (*Oryza sativa* L.)" was conducted to assess the genetic variability, character association, genetic advance, genetic divergence, and grain quality characters among the test genotypes of medium slender grain rice. The present experimentation was laid out at EB-1 Rice Research Station, O.U.A.T. Bhubaneswar during 2020 Kharif season. This chapter mainly includes the materials used and the procedures followed for conducting the experiment.

3.1 General Details

The experimental materials consisted of twenty genotypes including high yielding varieties and hybrids having medium slender grains along with two national checks, two hybrid checks, one zonal check and one local check from the experimental materials of Advance Varietal Trail-1 (AVT-1 MS). The designation and grain type details of the entries are presented in the Table-3.1.

The experiment was laid out in a Randomized Block design with three replications. The experimental materials were planted on 31-07-2020 with the plot size measuring 5.7m^2 area each and made up of 10 rows with each row consisting of 19 plants maintaining the plant-to-plant and row-to-row spacing of 15cm x 20 cm. All the recommended crop management practices were followed including need-based irrigation and plant protection measures to raise a normal crop.

Observations were recorded for 13 metric traits. Five competitive plants were selected randomly from the middle rows of each plot for taking observations for eight metric traits, whereas the other two characters, grain yield and days to 50 % flowering were recorded on plot basis.

3.2 CHARACTERS STUDIED

Biometrical observations were recorded for each genotype on 10 characters as per the standard procedure as described below at perfect growth stages and after harvesting the samples.

Table 3.1. Details of 20 Medium slender grain rice genotypes used in the study

Entry no.	**Designation**	**Grain type**
1	MTU 1320	MS
2	RP 6346-36-16-24-2	MS
3	AD 16168	MS
4	KPS-6262	MS
5	RNR 28362	MS
6	MTU 1281	MS
7	MTU 1321	MS
8	CR 3511-1-1-1-4-1-1	MS
9	RNR 26121 (Hybrid)	MS
10	HRI-203 (Hybrid)	MS
11	TMRH-139 (Hybrid)	MS
12	US-308 (Hybrid)	MS
13	MEPH-155 (Hybrid)	MS
14	PHI-19101 (Hybrid)	MS
15	BPT 5204 (NC)	MS
16	WGL 14 (NC)	MS
17	Improved Samba Mahsuri (ZC)	MS
18	JKRH 3333 (H C)	MS
19	27 P 63 (H C)	MS
20	Manaswini (LC)	MS

NC-National check, ZC-Zonal check, HC-Hybrid check and LC-Local check

MS-Medium slender

3.2.1 Days to 50% flowering

The number of days taken from the beginning of the sowing date to the date when 50% of the plants flowered in a plot was recorded for each genotype in each replication (or) It was recorded when panicles were found to emerge out of the boot leaf in about 50% of tillers in the experimental plot.

3.2.2 Plant height (cm)

It was recorded as the height of the plant from the base to the top of the latest spikelet on the panicle excluding awn. It was measured in centimeters and averaged over five sample plants.

3.2.3 Number of Effective Tillers per plant

It was recorded as the number of productive tillers per plant at the maturity stage and averaged over five samples.

3.2.4 Panicle length (cm)

It was measured as the length of the panicle from ciliate base to the tip of the topmost panicle of the main culm. It was measured in centimeters and averaged over five sample panicles.

3.2.5 Number of grains per panicle

This parameter is again divided into two sub-parameters like chaffy seeds and filled seeds. By adding these two sub-parameters, a total number of grains per panicle was recorded and averaged over five sample panicles.

3.2.6 Fertility percentage (%)

It was calculated by computing the ratio of the number of filled grains to the total number of grains per panicle. It is expressed in percentage and this was averaged over five sample panicles.

3.2.7 100- grain weight (g)

From each replication for each genotype, 100 filled, fully developed grains were randomly selected at about 14% grain moisture level and weighed on a precision electronic balance. It is expressed in grams

3.2.8 Grain yield (q/ha)

It was recorded as the weight of grains from the entire plot area ($5.7m^2$) of each genotype and each replication at about 14% moisture level. Later on, Grain yield (kg/m^2) was converted to quintal per hectare for statistical analysis.

3.2.9 Straw weight (g)

Each tagged plant of each replication was harvested separately and allowed for drying to meet the optimum moisture level for threshing. The dried samples were threshed to separate grain and straw. Again the straw was sun-dried thoroughly and data recorded by weighed on a precision electronic balance and expressed in grams.

3.2.10 Harvest index (%)

The harvest index was calculated using the following equation

Harvest index (%) = (Economic yield / biological yield) × 100

Where,
conomic yield = grain yield per plant (g)
Biological yield = grain yield per plant + straw yield per plant (g)

3.3 Observations were recorded for the following Grain quality characters in the experiment

3.3.1 Physical properties

The physical property of the rice grain includes grain length, breadth, length-breadth ratio, hulling percentage, milling percentage, and grain chalkiness.

Grain length

The length of five randomly selected grains of each genotype from each replication was measured using digital vernier calipers and the average value was taken.

Grain breadth

The breadth of five randomly selected grain of each genotype from each replication was measured using a screw gauge and the average value was taken.

Grain shape

The grain length-breadth ratio determines the shape of the rice grain. The shape of the rice grain is classified into different categories based on the scale size used by IRRI as mentioned below.

Table 3.2. Grain type classification given by IRRI, Philippines

Grain type	Length(mm)
Extra long	>7.50
Long	6.61 to 7.50
Medium	5.51 to 6.60
Short	<5.50

Table 3.3. Grain shape classification given by IRRI, Philippines

Grain shape	L/B ratio
Slender	>3.0
Medium	2.1 to 3.0
Bold	1.1 to 2.0
Round	<1.0

Considering above mentioned table, the grain L/B ratio of genotypes used in the experiment which comes under 2.1 to 3.0 were recorded as medium slender grain rice.

Kernel length and breadth

Hulled rice grain is referred to as kernel. The length and breadth of the kernel were recorded with help of digital vernier calipers and screw gauge respectively from the five randomly selected grains of each genotype from each replication and the average value was taken.

Hulling percentage

Each rice genotype's 100 g seed sample was de-husked, and the weight of the de-husked kernel was recorded and the ratio of de-husked kernel weight and whole grain weight gives hulling percentage and expressed as a percentage.

$$\text{Hulling percentage} = \frac{\text{Weight of de-husked kernel}}{\text{Weight of grains}} \times 100$$

Milling percentage

De-husked rice grain is referred to as brown rice. The brown rice has to be subjected to a further process called milling to obtain white rice. Milling is the process of removing the bran layer of the rice kernel. It is expressed in percentage and calculated by using below mentioned equation.

$$\text{Milling \%} = \frac{\text{Total milled rice}}{\text{Total rough rice}} \times 100$$

3.3.2 Cooking Qualities

The following four cooking quality parameters were assessed for each genotype of each replication.

Amylose content

Rice's cooking and eating properties are heavily influenced by its amylose level. Rice with a high amylose level (25-30%) cooks firm and dry, whereas rice with a medium amylose content (20-25%) cooks softer and stickier, and rice with a low amylose content (<20%) cooks less soft and sticky. Waxy rice is sometimes known as sticky rice since it has no amylose.

Japonica rice has a low amylose content, while tropical japonica rice has intermediate or high amylose content and Indica rices comes under all type of amylose categories.

The starch granules in the grain expand during cooking, releasing amylose. The leached amylose chains line up, bind together, and form a gel as the cooked rice cools. The cooked grain of rice should be firmer if the amylose level of the rice is high. Amylose is also responsible for how rice hardens when it cools.

100mg finely ground rice seed powder was added with 1ml ethanol followed by adding 9ml 1N NaOH to the sample and shaked well for 30 min. to allow hydrolysis of starch granules and release of amylase. Sample was heated for 10min in boiling water bath and volume was made to 100ml by adding deionized water. To a 0.5ml aliquot, 0.1ml 1N acetic acid + 0.2ml iodine reagent (0.2g iodine + 2g Potassium iodide in 100ml water) were added and volume was made to 10ml by adding deionized water as per (Juliano, 1971). Absorbance of the sample was read at 720nm and plotted against the known percentage of amylose content using a standard curve (Ambardekar *et al.,* 2011).

Alkali spreading value

The temperature at which the molecular arrangement of starch granule disrupts during heating in excess water , they swell irreversibly & loose crystallinity and birefringence. It predicts the time and energy required for cooking rice, this is reffered as gelatinization temperature. Gelatinization temperature is estimated by the extent of alkali spreading value.

Randomly selected six milled rice kernels from each genotype of each replication were distributed evenly in petri dishes containing 10ml of 1.7% potassium hydroxide solution. The petri dishes were kept covered and undisturbed for 23 hours at room temperature. The samples were then rated visually for the degradation of kernel on a scale of one to seven as described by Little *et al.*(1958). Average score of the six kernels was taken as the alkali score of the sample.

The degree of spreading is measured using a seven-point scale as follows:

Table 3.4 Alkali digestion score

Score description	**Score**	**Alkali digestion**	**Score**	**Gelatinization temperature**
Kernel not affected	1	Low	7	High
Kernel swollen	2	Low	6	High
Kernel swollen, collar incomplete or narrow	3	Intermediate	5	Intermediate
Kernel swollen ,collar complete and wide	4	Intermediate	4	Intermediate
Kernel split or segmented, collar complete and wide	5	High	3	Low
Kernel dispersed, merging with collar	6	High	2	Low
Kernel completely dispersed and intermingled	7	High	1	Low

Table 3.5 Alkali spreading value corresponds to gelatinization temperature

Scale of alkali spreading value	Scoring of alkali spreading value	Gelatinization temperature
1-2	High	74.5^{o}C - 80^{0} C
3	High intermediate	74^{o}C
4-5	Intermediate	70^{o}C - 74^{o}C
6-7	low	<70^{0}C

Length of rice after cooking

Five randomly selected milled rice kernels of each genotype from each replication were cooked separately in a test tube on the water bath and after complete cooking, the elongated length was measured using digital vernier calipers and the average value was taken.

3.4 STATISTICAL ANALYSIS

The data collected as per the procedure described above were subjected to the following statistical analysis

1. Analysis of variance
2. Estimation of mean, range, and critical differences.
3. Estimation of genetic parameters i.e genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance.
4. Estimation of phenotypic and genotypic correlation
5. Path analysis
6. Estimation of genetic divergence using Mahalanobis's D^2 analysis.

3.4.1 Analysis of variance

The total variability present in each character among 20 genotypes was tested for significance by using analysis of variance. The skeleton of analysis of variance used was as follows

$Y_{ij} = M + g_i + r_j + e_{ij}$

Where,

Y_{ij} = Phenotypic observation of the ith genotype on jth replication.

M = general mean

g_i = effect of ith genotype

r_j = effect of jth replication

e_{ij}= random error associated with ith genotype and jth replication.

ANOVA

Source	**d.f**	**M.S**	**E(MS)**	**F**
Replication	(r-1)	M_r	$\sigma_e^2 + g\sigma_r^2$	M_r / M_e
Genotypes	(g-1)	M_g	$\sigma_e^2 + r\sigma_g^2$	M_g / M_e
Error	(r-1) (g-1)	M_e	σ_e^2	

Where,

r = number of replication,

g = number of genotypes.

Mr, Mg and Me stand for the mean sum of squares due to replication, genotype and error respectively

3.4.2 Estimation of mean, range, standard error and critical differences

Mean value of each character were worked out by dividing the total by the corresponding number of observations while the lowest and the highest values for each character were taken as the range.

Standard error of mean = $\sqrt{(EMS/r)}$

Critical difference = $\sqrt{(2EMS/r)}$ × t value at error degrees of freedom at 5% and 1% level of significance.

Where,

r = number of replications

EMS = error mean sum of square

3.4.3 Estimation of Genetic Parameters

Through the results obtained from the ANOVA the genetic parameters were estimated as follows

Variance: The genotypic and phenotypic variances were calculated according to the formulae proposed by Burton and Devane (1953)

Error variance $= \sigma_e^2$

Genotypic variance $= \sigma_g^2 = (M_g - M_e) / r$

Phenotypic variance $= \sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Genotypic and phenotypic coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed by the formulae given by Burton (1952).

$$\text{GCV} = \frac{\text{Genotypic standard deviation}}{\text{Grand mean}} \times 100$$

$$\text{PCV} = \frac{\text{Phenotypic standard deviation}}{\text{Grand mean}} \times 100$$

$$\text{CV} = \frac{\sqrt{\text{EMS}}}{\text{Grand mean}} \times 100$$

Categorization of range of variation was done as suggested by Sivasubramanian and Madhavamenon (1973)

Low: Less than 10%

Moderate: 10-20 %

High: More than 20%

3.4.4 Broad sense Heritability

Heritability in a broad sense was estimated by using the formula given by Lush (1940).

Heritability ($h^2_{(bs)}$) = $\frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$

As suggested by Johnson et al. (1955a), heritability estimates were categorized into

Low: 0-30%

Moderate: 30-60 %

High: More than 60%

3.4.5 Expected genetic advance

Genetic advance was calculated by the formula suggested by Johnson, Robinson and Comstock (1955).

$GA = K.h_b^2 .\sigma p$

Where,

GA = Genetic advance

σ_p = Phenotypic standard deviation

h_b^2= Broad sense Heritability

k = Selection differential at 5% selection intensity (2.06)

Genetic advance as percent of mean (GAM)

Genetic advance as percent of mean was calculated as per the formula.

Genetic advance as percent of mean = $\frac{Genetic\ advance\ (GA)}{Grand\ mean} \times 100$

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

Low: Less than 10%

Moderate: 10-20 %

High: More than 20%

3.4.6 Analysis of covariance:

The analysis of covariance between all possible pairs of characters was done on the mean values following the procedure of randomized design analysis. The structure of analysis of covariance is as follows.

ANCOVA

Source	D.f.	M.P.	Expected M.P
Replication	(r-1)	Mr_{xy}	$\sigma_{exy} + g\ \sigma_{rxy}$
Genotype	(g-1)	Mg_{xy}	$\sigma_{exy} + r\ \sigma_{rxy}$
Error	(r-1)(g-1)	Me_{xy}	σ_{exy}

Where, r = number of replications, g = number of genotypes

Mrxy, Mgxy, Mexy stand for mean sum of products between pairs of characters due to replication, genotype, error respectively. From the structure of the analysis of covariance the following statements are computed.

Error covariance = $\sigma_{exy} = Me_{xy}$

Genotypic covariance = $\sigma_{gxy} = (Mg_{xy} - Me_{xy}) / r$

Phenotypic covariance = $\sigma_{pxy} = \sigma_{gxy} + \sigma_{exy}$

3.4.7 Character Association Analysis

To determine the degree of association of the characters with yield and also among the yield components, genotypic and phenotypic correlation coefficients were calculated using the method given by Johnson *et al*. (1955).

Genotypic correlation coefficient (r_g)

$(r_g) = \sigma_{gxy} / (\sigma_{gxy} \times \sigma_{gy})$

Phenotypic correlation coefficient (rp)

$(r_P) = \sigma_{pxy} / (\sigma_{px} \times \sigma_{py})$

Where,

σ_{gxy} = Genotypic covariance between two traits X and Y

σ_{pxy} = Phenotypic covariance between two traits X and Y

σ_{gx} and σ_{gy} stands for genotypic standard deviation of X and Y, respectively

σ_{px} and σ_{py} stands for phenotypic standard deviation of X and Y, respectively

To test the significance of the phenotypic correlation coefficients, the estimated values were compared with the table values (Fisher and Yates, 1967) at (n-2) degrees of freedom at the 5% and 1% level of significance.

3.4.8 Path Coefficient Analysis

The path coefficient analysis is a type of cause and effect relationship among the various correlated characters. Path coefficients are standardized partial regression coefficients which individually provide a measure of the direct effect of a causal factor on the effect variable. These permit of the correlation between a causal factor and the effect variable into components of direct and indirect effects and thus give a better picture of the associations of the causal factors with the effect variables.

In the present investigation, grain yield per plot is taken as the ‘effect’ with other characters related to yield as the causal factors.

The path coefficients were obtained by solving the following simultaneous equations, which give the basic relationship between correlation and path coefficients in a system of correlated causes (Wright, 1921) Dewey and Lu, (1959).

$r_{1.10} = P_{1.10} + r_{1.2} P_{2.10} + r_{1.3} P_{3.10} + \ldots\ldots\ldots + r_{1.9} P_{9.10}$

$r_{2.10} = P_{2.10} r_{1.10} + P_{2.10} + r_{2.3} P_{3.10} + \ldots\ldots\ldots + r_{2.9} P_{9.10}$

$r_{3.10} = r_{3.10}\, P_{1.10} + r_{3.2}\, P_{2.10} + P_{3.10} + \ldots\ldots\ldots + r_{3.9}\, P_{9.10}$

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$r_{9.10} = r_{9.1}\, P_{1.10} + r_{9.2}\, P_{2.10} + r_{9.3}\, P_{3.10} \ldots\ldots\ldots\ldots + P_{9.10}$

Where, r_{ij} is the coefficient of correlation between i^{th} and j^{th} characters and pq is the path coefficient (direct effect) of the i^{th} character on yield.

The solutions for path coefficients, direct and indirect effects of the causal factors were calculated as per the values of right hand side of equation.

The coefficient of determination(R^2) and the residual effect (P_{11}.R) were calculated as follows

$1 = P^2_{11}.R_1. + P_{iy}.r_{iy}$

$R_2 = \Sigma P_{iy} r_{iy}$

$PR_{11} = \sqrt{1 - \Sigma P_{iy} r_{iy}}$

$$= \sqrt{1-(P_{1.11}r_{1.11} + P_{2.11}r_{2.11} + P_{3.11}r_{3.11} + \ldots.. + P_{10.11}r_{10.11})}$$

Hence, $PR_{11} = \sqrt{1 - R^2}$

The path analysis at the phenotypic level with the same cause and effect relationship was computed using the phenotypic correlation as stated earlier.

3.4.9 Studies on Genetic Diversity

Genetic diversity between genotypes was estimated using D^2 analysis as given by Mahalanobis (1928)

Test of significance

Variances were calculated for 10 characters and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values. After testing the difference between genotypes for each of the characters, a simultaneous test of significance for differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried out using "V" statistic, which in turn utilizes Wilk's criterion (Wilks, 1932). The sum of squares and sum of products of error and error plus variety, variance and covariance matrix were used for this purpose (Panse and Sukhantme, 1961).

The estimation of Wilk's criterion was done using the following formula

$$\text{“}\wedge\text{”} = \frac{(E)}{(E+V)}$$

Where,

"∧"= Wilk's criterion

(E) = Determinant of error matrix and

(E+V) = Determinant of error + variety matrix

The significance of "∧" was tested by

$X^2_{pq} = V = -m \log_e \wedge$

Where,

X^2_{pq} = Estimation of $\chi 2$ value at pq degree of freedom

m = n - (p + q + 1)/2 with pq degree of freedom

n = Degrees of freedom of error + varieties

p = Number of characters

q = Number of genotypes – 1

$\log_e \wedge = 2.3407 \log_{10} \wedge$

Transformation of correlated variables

In the present model, computation of D^2 value was reduced to simple summation of differences in mean values of various characters of two genotypes i.e.,$\sum d^2_{i.}$ Therefore, transformation of correlated variables into standardized uncorrelated ones was done before working out the D^2 values. Transformation was done using pivotal condensation method in computation of D^2 value.

Computation of D^2 values

For the combination of ith and jth genotype, the mean deviation i.e., Y_{it}-Y_{jt} for t = 1, 2,…p variables were computed and the D^2 values were calculated as:

$D^2_{ij} = p \sum t{=}1\ (Y_{it}^{-} - Y_{jt}^{-})^2$

Where,

$D_{ij}{}^{2}$ = D^2 value between ith and jth genotypes

Y_{it} = Uncorrelated mean value of ith genotype for ‘ t ’ character

Y_{jt}= Uncorrelated mean value of jth genotype for ‘ t ’ character

Testing the significance of D^2 values

The D^2 values obtained for a pair of genotypes was taken as the calculated value of $\chi 2$ and tested against the tabulated $\chi 2$ at “p” degrees of freedom where “p” is the number of characters considered.

Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using the Tocher’s method as described by Rao (1952). The criterion was that the two variables belonging to the same cluster at least on an average show a smaller D^2 value than those belonging to different clusters. The first step in grouping of the genotypes into different clusters was to arrange the genotypes in order to know their relative distance from each other. The combinations of each genotype were arranged in increasing (ascending) order of their magnitude in a tabular form as described by Singh and Chaudhary (1977).

To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2 , that population was not considered for including in that cluster. The genotypes of the first cluster were then omitted and the rest were treated in a similar way. This procedure was continued till all the genotypes were included into one or other cluster. After formation of the cluster, the average intra and inter cluster distances (divergence) were calculated.

Average intra-cluster distance

For the measurement of intra cluster distances, the formula used was $\sum D^2_i / n$

Where, $\sum D^2_i$ = the sum of distances between all possible combinations (n) of populations included in a cluster.

Average inter-cluster distance

Clusters were taken one by one and the distances from other clusters were calculated. The distance between two clusters was the sum of D^2 values between the members of one cluster to each of the members of the other clusters divided by the product of number of genotypes in both the clusters under consideration.

Average inter cluster distance = D^2/n_1*n_2

Where, n_1 and n_2 are number of genotypes of two clusters.

Cluster diagram

The various clusters and their mutual relationships were presented diagrammatically. The square root of average D^2, which was an approximate measure of divergence between groups, had been used to denote the distance.

Contribution of individual characters towards divergence

In all the combinations, each character was ranked on the basis of their contribution towards divergence between two entries (di = yit - yjt). Rank I was given to the highest mean difference and rank ‘P’ to the lowest mean difference, where ‘P’ is the total number of characters considered. The number of cases where a particular character ranked first was counted, the proportion of this to the total number of combinations is expressed in percentage was quantified as the contribution of character to the overall genetic divergence between the genotypes

$$X = \frac{N \times 100}{M}$$

Where, X = per cent contribution of character

N = Number of genotype combinations where the character ranked first

M = All possible combinations of the genotypes concerned.

RESULTS

The current investigation intended to evaluate 20 genotypes including high yielding varieties and hybrids along with six check varieties having medium slender grain type which were received as entries of AVT-1 (MS) experiment during 2020-21 with the objective of analyzing and understanding the genetic variability for morphological and quality characters among the genotypes. Various yield contributing characters and grain yield was evaluated to find out the variability. Along with this, the nature and degree of character association among yield and other yield attributing traits, direct and indirect contribution of each independent variable on the dependent variable measured using path analysis and genetic divergence using D^2 statistics were examined under this study.

Rice is the only cereal grain which is mostly cooked and consumed as whole grains, and quality issues are thus more prevalent (Hossain *et al*., 2009). Grain yield enhancement has been the primary goal of plant breeders for many decades, but the need for excellent quality rice has grown in the present decade as people's living standards progressively improve. As a result, improving rice grain quality attributes, in addition, to yield augmentation, has now become a major objective in rice breeding programmes in order to meet consumer and industrial requirements, hence the grain quality attributes and its variability range have also been investigated in this study.

The observed and recorded results from the present experiment were represented in topic wise under this chapter and are supported by tables at an appropriate place.

A. Study of variability parameters for different traits.
B. Analysis of variance
C. Character association
D. Path coefficient analysis
E. Genetic divergence analysis
F. Grain quality parameters

A) Study of variability

The presence of genetic variability is required for the establishment of an efficient breeding program. The genetic variability of a character is a direct measure of how far the character may be modified toward a particular norm or direction. Therefore, an analysis of variance for different characteristics is required in order to examine genetic variation. In this study, the variability of test genotypes was assessed using basic criteria such as range, mean, variance, heritability, and genetic advance.

B) Analysis of variance

Analyze of variance for 13 metric characters. The block, checks and error, mean sum of squares for all the characters are presented in Table 4.1. The results of the analysis of variance indicated that there is a significant difference among the genotypes for all the characters under investigation, which signifies the presence of ample variability. The degree of genetic variance for all the characters is high except for 100-grain weight, harvest index, number of effective tillers per plant and panicle length.

Estimation of mean performance of the genotypes

Twenty genotypes overall mean performance and range for 13 yield and yield attributing characters under study were presented in Table 4.2 and Table 4.3.

1) Days to 50 percent flowering

The observed range for days to 50 percent flowering was from 88 to 112 days. TMRH-139 showed early flowering whereas MTU 1320 late flowered late and over all mean was 99.03. Among twenty genotypes, ten genotypes showed early flowering when compared with mean.

2) Plant height (cm)

The mean values of genotypes for plant height ranged from 94.9cm to 127.9cm with a general mean height of 111.13 cm. Among all the genotypes Improved Samba Mahsuri was the shortest, whereas MTU 1281 was the tallest. Eight genotypes were taller in height compared to their general mean.

Table 4.1. Analysis of variance for various characters (Mean sum of squares) of 20 medium slender rice genotypes

S.N.	Characters	Mean sum of squares (df)		
		Replication (2)	**Genotype (19)**	**Error (38)**
1	Days to 50% flowering	2.72	119.82**	0.58
2	Plant height(cm)	71.90	193.37**	17.58
3	Panicle length(cm)	2.67	8.21**	0.61
4	Number of effective tillers per plant	6.36	2.31**	0.78
5	100-grain weight (g)	0.002	0.19**	0.002
6	Grain yield/ plant (g)	8.23	44.47**	4.26
7	Straw yield/plant (g)	26.90	52.56**	5.65
8	Harvest index	0.001	0.01**	0.002
9	No. of filled grains/panicle	18.26	3615.94**	11.67
10	No. of chaffy grains/panicle	8.42	1315.75**	5.96
11	Total number of grains/panicle	51.48	5253.39**	13.22
12	Grain fertility (%)	0.35	145.09**	0.94
13	Grain yield/hectare (q)	5.50	163.64**	1.73

** significant at 1% level

* significant at 5% level

3) Panicle length (cm)

The panicle length ranged from 23 cm to 28 cm with the mean panicle length of 25.59cm. The longest panicle was produced by the genotype MTU 1281, whereas the shortest panicle was recorded by the genotype 27 P 63. Eight genotypes had greater panicle length when compared to the mean panicle length of the genotypes.

4) Number of effective tillers per plant

The genotype Improved Samba Mahsuri recorded the highest number of effective tillers (11.00) and the genotype MTU 1321 recorded the lowest number of effective tillers (7.9) per plant. Twelve genotypes have recorded more number of effective tillers per plant when compared with the overall mean of the genotypes (9.33).

5) 100-grain weight (g)

100 grain weight value ranged from 2 g (MTU 1320 and MTU 1321) to 1.1 g (RNR26121) with a mean value of 1.62 g. Out of 20 genotypes, seven genotypes have the highest value for 100 grain weight when compared to the mean.

6) Grain yield per plant (g)

The range of variability for grain yield per plant among the test genotypes was recorded between 29.4 g (MTU 1320) to 16.1 g (RNR 26121) and the overall mean is 21.07 g, with the comparison of mean eight genotypes have the highest grain weight per plant.

7) Straw yield per plant (g)

The mean of the genotypes for straw yield per plant ranged from 28.9 g (MTU 1320) to 13.2 g (TMRH-139) with a mean of 21.14 g. Ten genotypes showed high values for straw weight when compared with the mean.

8) Harvest index

The range of harvest index varies from 0.3 (AD 16168) to 0.6(TMRH-139) with a mean 0.44. Seven genotypes recorded the highest values for harvest index when compared to mean.

9) Number of filled grains per panicle

The range for the number of filled grains per panicle varies from 131.6 to 249.6 with a mean performance of 188.33. The maximum filled grains per panicle was recorded in MTU 1320 and the minimum in BPT 5204. Ten genotypes have recorded more number of grains per panicle when compared to a general mean of this character

10) Number of chaffy grains per panicle

The chaffy grains per panicle ranges from 23.5 to 100.3 with an overall mean performance of 47.84, ten genotypes exhibit the lowest number of chaffy seeds per panicle when compared with the mean of the character.

11) Total number of grains per panicle

The range of 165.7 (BPT 5204) to 321.2 (RNR 26121) total grains (including filled and chaffy grains) per panicles were observed with a general mean of 236.17, ten genotypes showed highest number of grains per panicle.

12) Grain fertility %

The grain fertility ranges from 63.5% to 91.00%. The highest grain fertility was observed by the genotype MTU 1320, whereas the lowest grain fertility was observed by the genotypes JKRH 3333. The overall mean of the genotypes recorded was 79.93%

13) Grain yield per hectare (q)

The grain yield per hectare ranges from 24.6 q/ha to 54.6 q/ha, with an overall mean of 36.06 q/ha. Among all the genotypes, the best promising genotypes with respect to the yield of the best check genotypes is presented in table 4.4 and these genotypes could be used in the crop improvement programme. The most promising genotype is MTU 1320 having high grain weight, filled grains per panicle, high grain fertility percentage and grain yield.

Table 4.2. Mean and range for various characters of 20 medium slender grain rice genotypes

S.N.	Characters	Mean	Range	
			minimum	maximum
1	Days to 50% flowering	99.03	87.7	112
2	Plant height(cm)	111.13	94.9	127.9
3	Panicle length(cm)	25.59	23.0	28.0
4	Number of effective tillers per plant	9.33	7.9	11.0
5	100-grain weight (g)	1.62	1.1	2.0
6	Grain yield/ plant (g)	21.07	16.1	29.4
7	Straw yield/plant (g)	21.14	13.2	28.9
8	Harvest index	0.44	0.3	0.6
9	No. of filled grains/panicle	188.33	131.6	249.6
10	No. of chaffy grains/panicle	47.84	23.5	100.3
11	Total number of grains/panicle	236.17	165.7	321.2
12	Grain fertility (%)	79.93	63.5	91.0
13	Grain yield/hectare (q)	36.06	24.6	54.6

Table 4.3. Mean performance of 20 medium slender grain rice genotypes with respect to various characters

S. N.	Genotypes designation	DTF (no.)	PH (cm)	PL (cm)	ETP	100-GW (g)	GYP (g)	SYP (g)	HI	FGP	CGP	TGP	GF (%)	GY/ ha (q)
1	MTU 1320	112.0	116.4	27.1	8.1	2.0	29.4	28.9	0.4	249.6	24.7	274.3	91.0	54.6
2	RP 6346-36-16-24-2	90.0	97.7	23.9	9.5	1.6	17.0	15.4	0.4	141.7	62.7	204.4	69.3	24.6
3	AD 16168	104.0	118.8	27.3	9.5	1.4	16.8	25.0	0.3	199.4	24.6	224.0	89.0	43.1
4	KPS-6262	101.0	105.9	25.8	9.6	1.5	29.2	19.8	0.5	240.0	36.2	276.2	86.9	39.3
5	RNR 28362	95.0	120.4	27.8	9.2	1.4	24.2	23.0	0.4	203.2	50.3	253.5	80.2	49.1
6	MTU 1281	106.0	127.9	28.0	8.3	1.9	22.5	28.3	0.4	198.3	41.8	240.1	82.6	34.4
7	MTU 1321	105.0	114.1	25.5	7.9	2.0	22.9	22.2	0.5	218.3	32.2	250.5	87.1	44.3
8	CR 3511-1-1-1-4-1-1	105.0	119.6	24.1	9.5	1.9	19.3	24.0	0.4	153.6	23.5	177.1	86.8	35.4
9	RNR 26121 (Hybrid)	95.7	117.4	26.3	9.7	1.1	16.1	22.5	0.4	231.0	90.2	321.2	71.9	27.5
10	HRI-203 (Hybrid)	94.0	110.4	25.2	9.2	1.4	17.2	20.0	0.4	212.6	61.4	274.0	77.6	34.0
11	TMRH-139 (Hybrid)	87.7	106.9	27.9	10.1	1.9	23.6	13.2	0.6	160.4	51.8	212.3	75.6	33.6

12	US-308 (Hybrid)	99.0	110.9	25.0	9.1	1.6	19.7	17.7	0.5	226.4	67.3	293.7	77.1	33.1
13	MEPH-155 (Hybrid)	96.3	116.1	24.6	10.1	1.5	19.0	18.9	0.4	178.9	48.8	227.7	78.6	37.3
14	PHI-19101 (Hybrid)	95.0	106.5	23.5	9.9	1.5	25.7	17.1	0.5	191.5	52.7	244.2	78.5	34.5
15	BPT 5204 (NC)	95.3	100.9	23.1	9.8	1.8	18.0	22.4	0.4	131.6	34.1	165.7	79.4	32.7
16	WGL 14 (NC)	106.0	108.7	25.0	10.0	1.5	22.3	22.8	0.5	182.4	32.3	214.7	85.0	39.3
17	Improved Samba Mahsuri(ZC)	104.3	94.9	23.3	11.3	1.4	20.8	25.8	0.4	165.0	28.3	193.3	85.4	31.9
18	JKRH 3333 (HC)	94.7	110.4	24.5	7.6	1.6	17.5	20.1	0.4	174.2	100.3	274.5	63.5	32.7
19	27 P 63 (HC)	99.0	108.7	23.0	8.7	1.5	18.8	17.9	0.5	172.9	52.0	224.9	76.9	34.3
20	Manaswini (LC)	94.0	105.2	24.8	9.6	1.9	21.3	17.9	0.5	135.6	41.5	177.1	76.6	25.6
	Grand mean	99	111.13	25.59	9.33	1.62	21.07	21.14	0.4	188.33	47.84	236.17	79.9	36.06
	CD	1.24	6.85	1.28	1.44	0.07	3.49	3.8	0.07	5.58	3.99	5.94	1.58	2.15

DTF = Days to 50% flowering, PH= Plant height(cm), PL= Panicle length(cm), ETP= Number of effective tillers per plant, 100GW=100 grain weight (g), GYP=Grain yield/ plant (g), SYP=Straw yield/plant (g), HI= Harvest index, FGP=Number of filled grains/panicle, CGP=Number of chaffy grains/panicle, TGP=Total number of grains/panicle, GF=Grain fertility (%), GY/ha=Grain yield/hectare (q). NC= National check, ZC=Zonal check, HC=Hybrid check, and LC=Local check.

Table 4.4. Promising rice genotypes on the basis of grain yield

S.N.	Name of the genotypes	DTF	PH (cm)	PL (cm)	ETP	100-GW	GYP (g)	SYP (g)	HI	FGP	CGP	TGP	GF (%)	GY/ha (q)
1	MTU 1320	112.0	116.4	27.1	8.1	2.0	28.8	29.6	0.4	249.6	24.7	274.3	91.0	54.6
2	RNR28362	95.0	120.4	27.8	9.2	1.4	22.5	22.0	0.4	203.2	50.3	253.5	80.2	49.1
3	MTU 1321	105.0	114.1	25.5	7.9	2.0	22.9	22.2	0.5	218.3	32.2	250.5	87.1	44.3
4	AD 16168	104.0	118.8	27.3	9.5	1.4	18.7	25.0	0.3	199.4	24.6	224.0	89.0	43.1
5	KPS-6262	101.0	105.9	25.8	9.6	1.5	26.4	23.1	0.5	240.0	36.2	276.2	86.9	39.3
6	WGL 14 (NC)	106.0	108.7	25.0	10.0	1.5	20.2	21.0	0.5	182.4	32.3	214.7	85.0	39.3
7	MEPH-155 (Hybrid)	96.3	116.1	24.6	10.1	1.5	19.0	18.9	0.4	178.9	48.8	227.7	78.6	37.3
8	CR 3511-1-1-1-4-1-1	105.0	119.6	24.1	9.5	1.9	25.0	24.7	0.4	153.6	23.5	177.1	86.8	35.4
9	PHI-19101 (Hybrid)	95.0	106.5	23.5	9.9	1.5	21.5	18.1	0.5	191.5	52.7	244.2	78.5	34.5
10	US-308 (Hybrid)	99.0	110.9	25.0	9.1	1.6	19.7	17.7	0.5	226.4	67.3	293.7	77.1	34.4

DTF = Days to 50% flowering, PH= Plant height(cm), PL= Panicle length(cm), ETP= Number of effective tillers per plant, 100GW=100 grain weight (g), GYP=Grain yield/ plant (g), SYP=Straw yield/plant (g), HI= Harvest index, FGP=Number of filled grains/panicle, CGP=Number of chaffy grains/panicle, TGP=Total number of grains/panicle, GF=Grain fertility (%), GY/ha=Grain yield/hectare (q).

Estimation of genotypic and phenotypic coefficients of variation

The degree of genetic variability contained in a crop variety is assessed by the genotypic coefficient of variation, which allows for the enumeration of the level of variability in the different traits. The GCV computes the amplitude of genetic variation in the crop and expresses the heritable portion of the variability. As a result, it is thought to be more helpful than the phenotypic coefficient of variance. Furthermore, the discrepancy between PCV and GCV implies that environmental variables play a role. As a result, in order to analyse the real breeding essence with these particular characteristics, the entire variation has to be divided into heritable and non-heritable parts.

Table 4.5 show estimates of phenotypic and genotypic coefficients of variation for all the parameters.

The GCV and PCV were found to have a significant connection for all characters. As a result, their PCV was greater than their eventual GCV. In the present research, the estimated of phenotypic coefficients of variation for all traits were greater than the estimates of genotypic coefficients of variation, which might be attributed to the interaction of genotypes with environment (Table 4.5) and was also revealed by Sameera *et al*. (2016), Rashmi *et al*. (2017) and Mamata *et al*. (2018). Large variations in GCV and PCV values indicate a significant environmental effect on trait performance (Number of effective tillers per plant). Minor differences in this study for most of the characters showed a limited environmental effect and, as a result, a substantial involvement of genetic variables in trait expression.

A wide range of PCV was recorded for quantitative characters ranged from 6.412 for days to 50% flowering to 43.975 for number of chaffy grains per panicle. Highest magnitude of PCV was recorded for number of chaffy grains per panicle (43.975), followed by straw yield (21.792), grain yield per hectare (20.699) and grain yield per plant (20.125). While moderate estimates for number of effective tillers per plant (12.179), 100-grain weight (15.5), harvest index (15.968), number of filled grains/panicle (18.494), total number of grains/panicle (17.763). Lowest estimates of pcv were recorded for days to 50% flowering (6.412), plant height (7.854), panicle length (7.013), grain fertility (8.753).

The calculated GCV for all the quantitative characters ranged from 6.366 to 43.678. The highest degree of genotypic coefficient of variation was recorded for the number of chaffy grains per panicle (43.678), followed by grain yield per hectare (20.373), and straw yield per plant (18.679). Moderate estimates for number of filled grains per panicle (18.405), total number of grains per panicle (17.697), grain yield per plant (17.325), 100 grain weight (15.296), and harvest index (12.255). Lowest estimates of GCV were recorded for grain fertility (8.67), number of effective tillers per plant (7.655), plant height (6.888), days to 50% flowering (6.366) and panicle length (6.291).

Heritability (broad sense) %

Heritability is used to examine the participation of genotypic and phenotypic variability seen for quantitative characters, and it is vital to transfer ancestral traits to their offspring. Heritability assessment may be used to assess genetic advance, which leads to the selection of the best individuals for genetic advancement. Heritability assessment is thus a critical requirement for developing an effective selection mechanism for yield and quality improvement.

Heritability indicates how much emphasis should be placed on the selection of a certain attribute. However, because heredity is impacted by environment, heritability in general cannot be used to guide phenotypic selection. Therefore, assessing heritability in conjunction with genetic advance is more efficient in analyzing the gain under selection than heritability alone. In the current experiment the heritability and genetic advance of all thirteen quantitative characters are presented in Table 4.5

The estimate of greater heritability (above 60%) was detected for all eleven quantitative traits under investigation, which ranged from (73.47%) for straw yield per plant to (99.249%) for total number of grains per panicle. Only two characters namely number of effective tillers per plant (39.512) and harvest index (58.907) had low heritability. High heritability is a significant component of the heritable fraction of variation that breeders may use to choose superior genotypes based on phenotypic output.

Genetic advance as per cent of mean

Genetic advance as percent mean was highest for number of chaffy grains per panicle (89.369), followed by grain yield per hectare (41.309), number of filled grains per panicle (37.731), total number of grains per panicle (36.318), straw yield per plant (32.981), 100 grain weight (31.095) and grain yield (30.725). Moderate estimates of genetic advance as percent of mean were exhibited by grain fertility (17.69), days to 50% flowering (13.02), plant height (12.445), and panicle length (11.623). However, low genetic advance as percent of mean was shown by number of effective tillers per plant (9.913).

Table 4.5. Estimates of PCV, GCV, $h^2_{(bs)}$ and genetic advance for various characters of 20 medium slender grain rice genotypes

S.N.	**Characters**	**PCV**	**GCV**	**$h^2_{(bs)}$**	**GA**	**GA% over mean**
1	Days to 50% flowering	6.412	6.366	98.571	12.894	13.02
2	Plant height(cm)	7.854	6.888	76.919	13.83	12.445
3	Panicle length(cm)	7.013	6.291	80.45	2.939	11.623
4	Number of effective tillers per plant	12.179	7.655	39.512	0.925	9.913
5	100 grain weight (g)	15.523	15.296	97.388	0.503	31.095
6	Grain yield/ plant (g)	20.125	17.325	74.114	6.462	30.725
7	Straw yield/plant (g)	21.792	18.679	73.467	6.982	32.981
8	Harvest index	15.968	12.255	58.907	0.086	19.376
9	No. of filled grains/panicle	18.494	18.405	99.038	71.058	37.731
10	No. of chaffy grains/panicle	43.975	43.678	98.652	42.752	89.369
11	Total number of grains/panicle	17.763	17.697	99.249	85.771	36.318
12	Grain fertility (%)	8.753	8.67	98.108	14.14	17.69
13	Grain yield/hectare (q)	20.699	20.373	96.879	14.897	41.309

C) Character association

Correlation study is an essential technique for all breeding method. It offers an overview of the relationship among the diverse characters and decides the component characteristics on which greater importance may be applied when selecting for genetic enhancement in grain yield. In general, genotypic correlation estimates were greater than phenotypic correlation estimates, showing that environmental sources of correlation have influenced the genetic cause, decreasing the dependability of phenotypic correlation for use in crop development programmes. However, both phenotypic and genotypic associations revealed comparable patterns. Thus in the present investigation, the nature and magnitude of correlation of character pairs were estimated at genotypic and phenotypic levels which are presented in Table-4.6

Correlation between grain yield and other component characters

Grain yield showed positive correlation with all the characters except number of effective tillers per plant, harvest index and number of chaffy grains per panicle. The highest correlation of grain yield is with grain fertility in both phenotypic (r_p=0.651) and genotypic level (r_g=0.675) and followed by days to 50% flowering (r_p=0.566) (r_g=0.579), number of filled grains per panicle (r_p =0.562) (r_g =0.577), grain yield per plan (r_p =0.503) (r_g =0.611), straw yield (r_p =0.462) (r_g =0.576), panicle length (r_p 0.443) (r_g =0.500) and plant height (r_p =0.381) (r_g =0.463). Total number of grains per panicle and 100-grain weight showed a positive correlation but non significance with grain yield. The rest of the traits showed a negative correlation with the grain yield.

Correlation among other component characters

Plant height had significant positive correlation with days to 50% flowering (r_p=0.295) (r_g=0.351).

Panicle length had significant positive correlation with plant height (r_p=0.600) (r_g=0.679)

Grain yield per plant showed significant positive correlation with days to 50% flowering (r_p=0.322) (r_g=0.352), panicle length (r_p=0.286) (r_g=0.356) and 100 grain weight (r_p=0.299) (r_g=0.345).

Straw yield per plant had significant positive correlation with days to 50% flowering (r_p=0.766) (r_g=0.872), plant height (r_p=0.435) (r_g=0.482), and panicle length (r_p=0.269) (r_g=0.329).

Harvest index showed significant positive correlation with 100 grain weight (r_p=0.325) (r_g=0.418) and grain yield per plant (r_p=0.365) (r_g=0.448).

Filled grains per panicle had significant positive correlation with days to 50% flowering (r_p=0.418) (r_g=0.421), plant height (r_p=0.397) (r_g=0.442), panicle length (r_p=0.465) (r_g=0.507), grain yield per plant (r_p=0.385) (r_g=0.437) and straw yield per plant (r_p=0.324) (r_g=0.367).

Total grains per panicle showed significant positive correlation with plant height (r_p=0.316) (r_g=0.350), panicle length (r_p=0.355) (r_g=0.389), filled grain per panicle (r_p=0.866) (r_g=0.867) and chaffy grains per panicle (r_p=0.561) (r_g=0.562).

Grain fertility showed significant positive correlation with days to 50% flowering (r_p=0.787) (r_g=0.794), 100 grain weight (r_p=0.256) (r_g=0.260), grain yield per plant (r_p=0.481) (r_g=0.535), straw yield per plant (r_p=0.575) (r_g=0.645) and filled grains per panicle (r_p=0.349) (r_g=0.346).

Days to 50% flowering showed significant positive correlation with plant height (r_p =0.295) (r_g=0.351), grain yield per plant (r_p=0.322) (r_g=0.352), straw yield per plant (r_p=0.766) (r_g=0.872), filled grains per panicle (r_p=0.418) (r_g=0.421), grain fertility (r_p=0.787) (r_g =0.794) and grain yield per hectare (r_p=0.566) (r_g =0.579).

Table 4.6. Estimates of phenotypic and genotypic correlation coefficient among various characters for 20 medium slender grain rice genotypes

Characters		**DTF**	**PH (cm)**	**PL (cm)**	**ETP**	**100 GW (g)**	**GYP (g)**	**SYP (g)**	**HI**	**FGP**	**CGP**	**TGP**	**GF (%)**
PH (cm)	r_p	**0.295***											
	r_g	**0.351****											
PL(cm)	r_p	0.110	**0.600****										
	r_g	0.135	**0.679****										
ETP	r_p	-0.147	-0.342**	-0.133									
	r_g	-0.257*	-0.663**	-0.378**									
100GW(g)	r_p	0.203	0.113	0.087	-0.281*								
	r_g	0.205	0.121	0.103	-0.424**								
GYP(g)	r_p	**0.322***	0.067	**0.286***	0.091	**0.299***							
	r_g	**0.352****	0.052	**0.356****	-0.222	**0.345****							
SYP(g)	r_p	**0.766****	**0.435****	**0.269***	-0.041	0.093	0.220						
	r_g	**0.872****	**0.482****	**0.329***	-0.379**	0.096	0.125						
HI	r_p	-0.290*	-0.194	0.021	0.241	**0.325***	**0.365****	-0.495**					
	r_g	-0.368**	-0.241	-0.027	-0.113	**0.418****	**0.448****	-0.74**					
FGP	r_p	**0.418****	**0.397****	**0.465****	-0.269*	-0.265*	**0.385****	**0.324***	-0.148				
	r_g	**0.421****	**0.442****	**0.507****	-0.457**	-0.270*	**0.437****	**0.367****	-0.209				
CGP	r_p	-0.607**	-0.026	-0.062	-0.217^{NS}	-0.442**	-0.400**	-0.413**	-0.021	0.071			
	r_g	-0.611**	-0.033	-0.064	-0.293*	-0.449**	-0.442**	-0.459**	0.004	0.075			

TGP	r_p	0.042	**0.316***	**0.355****	-0.332**	-0.442**	0.119	0.062	-0.134	**0.866****	**0.561****		
	r_g	0.044	**0.350****	**0.389****	-0.525**	-0.449**	0.142	0.075	-0.171	**0.867****	**0.562****		
GF(%)	r_p	**0.787****	0.224	0.236	0.109	**0.256***	**0.481****	**0.575****	-0.093	**0.349****	-0.898**	-0.161	
	r_g	**0.794****	0.256*	0.258*	0.110	**0.260***	**0.535****	**0.645****	-0.157	**0.346****	-0.898**	-0.162	
GY/ha(q)	r_p	**0.566****	**0.381****	**0.443****	-0.270*	0.170	**0.503****	**0.462****	-0.139	**0.562****	-0.458**	0.237	0.651**
	r_g	**0.579****	**0.463****	**0.500****	-0.406**	0.171	**0.611****	**0.576****	-0.185	**0.577****	-0.472**	0.242	0.675**

* and ** significant at 5% and 1% level of significance respectively

DTF = Days to 50% flowering, PH= Plant height(cm), PL= Panicle length(cm), ETP= Number of effective tillers per plant, 100GW=100 grain weight (g), GYP=Grain yield/ plant (g), SYP=Straw yield/plant (g), HI= Harvest index, FGP=Number of filled grains/panicle, CGP=Number of chaffy grains/panicle, TGP=Total number of grains/panicle, GF=Grain fertility (%), GY/ha=Grain yield/hectare (q).

D) Path coefficient analysis

Path coefficient analysis helps in partitioning of correlation coefficients into direct and indirect effects of various characters on grain yield. It provides an effective means of finding out direct and indirect causes of association and presents a critical examination of the specific forces acting to produce a given correlation and measures the relative importance of each causal factor.

The association of different component characters among themselves and with yield is quite important for devising an efficient selection criterion for yield. Such interdependence often affects the relationship of component characters with yield, thereby making correlation coefficient to be ineffective. So there is a need to partition the correlation into direct and indirect effects to get the information on actual contribution of each character to yield. Thus, correlation in conjunction with path analysis could give a better insight into cause and effect relationship between different pairs of characters along with grain yield in breeding programme.

In the present study the path analysis was carried out at genotypic level and the results found are presented in Table-4.7

It was shown that the highest direct positive effect on grain yield was exhibited by number of filled grains per panicle (1.205) followed by straw yield per plant (1.071), grain fertility (0.437), harvest index (0.292), grain yield per plant (0.291), plant height (0.106) and the number of chaffy grains per panicle (0.099). The rest of the characters like days to 50% flowering (-1.134), panicle length (-0.283), number of effective tillers per plant (-0.384), 100 grain weight (-0.291), and the total number of grains per panicle (-1.066) showed a negative direct effect on grain yield.

Total number of grains per panicle showed highest indirect effect on grain yield via number of filled grains per panicle followed by days to 50% flowering via straw yield per plant, number of chaffy grains per panicle via days to 50% flowering and grain fertility via straw yield per plant.

The residual effect estimated at genotypic level was 0.214 which is low indicating that the characters included in the study contributed for yield.

Table 4.7. Direct and indirect effects of component traits on yield at genotypic level for 20 medium slender grain rice genotypes

Characters	**Days to 50% flowering**	**Plant height(cm)**	**Panicle length(cm)**	**Number of effective tillers per plant**	**100 grain weight(g)**	**Grain yield/ plant(g)**	**Straw yield/plant(g)**
Days to 50% flowering	**-1.134**	0.037	-0.038	0.099	-0.060	0.103	0.934
Plant height(cm)	-0.398	**0.106**	-0.193	0.255	-0.035	0.015	0.516
Panicle length(cm)	-0.153	0.072	**-0.284**	0.145	-0.030	0.104	0.352
Number of effective tillers per plant	0.291	-0.070	0.107	**-0.385**	0.124	-0.065	-0.406
100 grain weight(g)	-0.232	0.013	-0.029	0.163	**-0.292**	0.101	0.103
Grain yield/ plant(g)	-0.399	0.006	-0.101	0.085	-0.101	**0.292**	0.134
Straw yield/plant(g)	-0.989	0.051	-0.093	0.146	-0.028	0.036	**1.071**
Harvest index	0.418	-0.026	0.008	0.044	-0.122	0.131	-0.793
Number of filled grains/panicle	-0.477	0.047	-0.144	0.176	0.079	0.128	0.393
No. of chaffy grains/panicle	0.693	-0.004	0.018	0.113	0.131	-0.129	-0.492
Total number of grains/panicle	-0.049	0.037	-0.110	0.202	0.131	0.041	0.080
Grain fertility (%)	-0.900	0.027	-0.073	-0.042	-0.076	0.156	0.691

Characters	Harvest index	Number of filled grains/panicle	No. of chaffy grains/panicle	Total number of grains/panicle	Grain fertility (%)	Grain yield/hectare (q)
Days to 50% flowering	-0.108	0.507	-0.061	-0.046	0.348	0.579
Plant height(cm)	-0.070	0.532	-0.003	-0.373	0.112	0.463
Panicle length(cm)	-0.008	0.611	-0.006	-0.414	0.113	0.500
Number of effective tillers per plant	-0.033	-0.550	-0.029	0.560	0.048	-0.406
100 grain weight(g)	0.122	-0.326	-0.045	0.479	0.114	0.171
Grain yield/ plant(g)	0.131	0.527	-0.044	-0.151	0.234	0.611
Straw yield/plant(g)	-0.216	0.442	-0.046	-0.080	0.282	0.576
Harvest index	**0.292**	-0.252	0.000	0.182	-0.069	-0.185
Number of filled grains/panicle	-0.061	**1.205**	0.007	-0.924	0.152	0.577
No. of chaffy grains/panicle	0.001	0.090	**0.099**	-0.599	-0.393	-0.472
Total number of grains/panicle	-0.050	1.045	0.056	**-1.066**	-0.071	0.242
Grain fertility (%)	-0.046	0.418	-0.089	0.172	**0.438**	**0.675**

Residual effect = 0.214

E) Genetic divergence analysis

The assessment of genetic divergence for 20 genotypes under study was done by using Mahalanobis D^2 statistic for 13 characters. The outcomes were discussed as follow

Clustering of genotypes by tocher method

Twenty genotypes were categorized into eight clusters, based on cluster analysis under the present study as presented in Table 4.8. The highest number of genotypes *i.e.* eight were found in cluster I, cluster II includes four genotypes, cluster III and cluster IV include two genotypes each and the remaining cluster V, VII, VI, and VIII each includes one genotype.

Table 4.8. Clustering of 20 medium slender grain rice genotypes

Cluster	Number of genotypes	Genotypes designation
I	8	MEPH-155, PHI-19101, 27 P 63, HRI-203, RNR 28362, WGL 14, Improved Samba Mahsuri, AD 16168
II	4	BPT 5204, Manaswini, TMRH-139, RP 6346-36-16-24-2
III	2	US-308, KPS-6262
IV	2	MTU 1281, MTU 1321
V	1	CR 3511-1-1-1-4-1-1
VI	1	MTU 1320
VII	1	RNR 26121
VIII	1	JKRH 3333

Inter and intra cluster distance

The average intra and inter cluster distance among the genotypes were presented in the Table 4.9. The inter cluster distance varied from 514.42 to 3296.03 and the range of intra cluster distance varied from 0.00 to 451.02. The highest inter cluster distance was recorded between cluster IV and cluster VIII (3296.03), followed by VI and VII (2847.28), cluster II and VII (2535.30), cluster II and IV (2506.20), cluster V and VII (2486.76), genotypes comes under these cluster indicates that they were highly divergent from each other.

The lowest inter cluster distance was recorded between cluster VII and VIII (514.42), followed by cluster I and IV (516.20), cluster III and IV (545.49), cluster I and III (553.74) and cluster IV and VI (601.71) genotypes under this category indicates that less divergent from each other. The highest intra cluster distance was shown by cluster III (451.02) followed by cluster I (357.25), cluster II (278.21) and cluster IV (252.95). The clusters V, VI, VII, and VIII were monogenotypic and hence recorded zero intra cluster distance.

Table 4.9. Average intra-inter cluster distances (D^2) (Intra cluster distance in diagonal) in 20 medium slender grain rice genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	357.26	904.76	553.75	516.21	750.60	1268.84	1289.68	1308.93
II		278.22	1437.18	1088.09	862.84	2506.20	2535.31	1778.68
III			451.02	545.50	1539.07	868.88	1015.48	1488.91
IV				252.96	656.02	601.72	1781.67	1724.81
V					0	1907.79	2486.76	1787.03
VI						0	2847.28	3296.03
VII							0	514.43
VIII								0

Cluster means for various characters

Cluster mean recorded for twenty characters under study were presented in table 4.10. Among the eight clusters, cluster I recorded moderate values for days to 50% flowering, plant height, panicle length, number of filled grains per panicle, total number of grains per panicle, grain fertility and grain yield per hectare. The lowest value was for 100-grain weight and harvest index.

Cluster II indicated lower values for days to 50% flowering, plant height, panicle length, straw yield per plant and number of filled grains per panicle. The highest value recorded for the number of effective tillers per plant and harvest index, while remaining traits showed moderate values.

Cluster III recorded highest value for the harvest index and remaining traits were showed moderate values.

Cluster IV showed highest value for plant height, lowest value for the number of chaffy grains per panicle and rest of the characters in the cluster recorded moderate values.

Cluster V showed highest value for plant height, lowest value recorded for the number of chaffy grains per panicle and total number of grains per panicle. Remaining traits wereshowed moderate values

Cluster VI recorded highest values for days to 50% flowering, panicle length, 100 grain weight, grain yield per plant, straw yield per plant, number of filled grains per, grain fertility and grain yield per hectare. Moderate values were recorded for remaining characters.

Cluster VII showed highest values for number of chaffy grains per panicle and total number of grains per panicle and lowest value recorded for harvest index, 100 grain weight and grain yield per hectare, while other characters showed moderate values.

Cluster VIII recorded highest value for number of chaffy grains per panicle, while number of effective tillers per plant and grain fertility exhibited lowest values and other characters showed moderate values.

Table 4.10. Mean performance of different clusters

Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**
Days to 50% flowering	99.42	91.75	100.00	105.50	105.00	112.00	95.67	94.67
Plant height(cm)	110.56	103.86	108.43	120.98	119.60	116.43	117.37	110.43
Panicle length(cm)	24.96	24.93	25.38	26.77	24.13	27.10	26.27	26.27
Number of effective tillers per plant	9.73	9.77	9.33	8.10	9.47	8.13	9.67	7.60
100 grain weight (g)	1.45	1.82	1.52	1.92	1.90	2.00	1.10	1.57
Grain yield/ plant (g)	20.13	19.14	23.05	22.72	24.97	28.77	16.07	17.20
Straw yield/plant (g)	20.95	17.20	20.38	25.25	24.73	29.57	21.87	20.13
Harvest index	0.43	0.48	0.48	0.45	0.43	0.40	0.37	0.40
No. of filled grains/panicle	188.23	142.33	233.20	208.30	153.60	249.63	230.97	174.23
No. of chaffy grains/panicle	43.80	47.53	51.75	37.02	23.47	24.70	90.23	100.30
Total number of grains/panicle	232.03	189.86	284.95	245.32	177.07	274.33	321.20	274.53
Grain fertility (%)	81.38	75.22	81.98	84.87	86.73	90.97	71.90	63.47
Grain yield/hectare (q)	37.95	29.11	36.20	39.35	35.37	54.57	27.50	32.73

Relative contribution of each character towards genetic divergence

The number of time each of the 13 characters appeared first and their respective percentage of relative contribution towards genetic divergence under study were presented in Table 4.11

Number of filled grains per panicle (31.05%) has the maximum contribution for genetic divergence, followed by Days to 50% flowering (24.21%), number of chaffy grains per panicle (17.36%), grain yield per hectare (14.21%), grain fertility (8.42%), 100 grain weight (4.21%) and harvest index (0.52%). The characters like plant height, panicle length, number of effective tillers per plant, grain yield/ plant, straw yield/plant, and total number of grains/panicle showed no contribution towards genetic divergence.

Table 4.11. Relative contribution of different characters to genetic divergence

Characters	**Rank total**	**Contribution percent of total D^2**
Days to 50% flowering	46	24.21
Plant height(cm)	0	0
Panicle length(cm)	0	0
Number of effective tillers per plant	0	0
100-grain weight (g)	8	4.21
Grain yield/ plant (g)	0	0
Straw yield/plant (g)	0	0
Harvest index	1	0.52
No. of filled grains/panicle	59	31.05
No. of chaffy grains/panicle	33	17.36
Total number of grains/panicle	0	0
Grain fertility (%)	16	8.42
Grain yield/hectare (q)	27	14.21

F) Grain quality analysis.

Analysis of the grain quality characters revealed that there exists significant difference among the test genotypes. The mean and range of different grain quality characters are given in Table 4.12

1) Grain length

Grain length of 20 medium slender grain rice genotypes ranged from 8.3mm (MEPH-155) to 9.8mm (MTU 1281) with the over all mean of 8.91mm.

2) Grain breadth

The overall mean for grain breadth of 20 genotypes were 2.73mm and it is ranged from 2.5mm (MEPH-155) to 2.9mm (MTU 1320) and (MTU 1321).

3) Grain L/B ratio

The overall mean for grain L/B ratio of 20 genotypes were 3.18 and it is ranged from 2.9(MTU 1320) to 3.4 (MTU 1281) and (TMRH139).

But the grain type classification given by IRRI, Philippines was based on the dehusked brown rice *i.e* kernel length, kernel breadth, and kernel L/B ratio. Hence kernel length and breadth was measured and the values were recorded as below.

4) Kernel length

Kernel length of 20 genotypes ranged from 4.9mm to 5.6mm in (MTU 1320 and Improved Samba Mahsuri) and (MTU 1321 and TMRH139) respectively. The overall mean was 5.13mm.

5) Kernel breadth

Kernel breadth of 20 genotypes ranged from 1.6mm to 2.0mm in (RNR28362 and RNR26121) and (MTU 1320 and CR 3511-1-1-1-4-1-1) respectively. The overall mean was 1.80mm.

6) Kernel L/B ratio

The overall mean for L/B ratio of 20 genotypes were 2.65 and the range was from 2.3 to 2.9 in MTU 1320 and MTU 1281 respectively.

According to IRRI, Philippines grain shape classification, the grain L/B ratio of 2.1 to 3.0 were considered as medium slender grain rice. In the present study L/B ratio of all the genotypes was 2.65, which indicated that the genotypes under study belong to medium slender grain type.

Table 4.12. According to L/B ratio the genotypes were classified as follow

Entry no.	Genotypes	Grain type
1	MTU 1320	Medium slender
2	RP 6346-36-16-24-2	Medium slender
3	AD 16168	Medium slender
4	KPS-6262	Medium slender
5	RNR 28362	Medium slender
6	MTU 1281	Medium slender
7	MTU 1321	Medium slender
8	CR 3511-1-1-1-4-1-1	Medium slender
9	RNR 26121 (Hybrid)	Medium slender
10	HRI-203 (Hybrid)	Medium slender
11	TMRH-139 (Hybrid)	Medium slender
12	US-308 (Hybrid)	Medium slender
13	MEPH-155 (Hybrid)	Medium slender
14	PHI-19101 (Hybrid)	Medium slender
15	BPT 5204 (NC)	Medium slender
16	WGL 14 (NC)	Medium slender
17	Improved Samba Mahsuri (ZC)	Medium slender
18	JKRH 3333 (H C)	Medium slender
19	27 P 63 (H C)	Medium slender
20	Manaswini (LC)	Medium slender

7) Hulling %

The overall mean for hulling % of 20 genotypes were 78.97% and ranging from 70.6% (AD 16168) to 81.4%(KPS-6262). High hulling percentage resulted in higher head rice yield.

8) Milling %

The observed range for milling % among the 20 genotypes was 64.1% (MEPH-155) to 71.4% (MTU 1281 and BPT 5204). The overall mean was 68.42%. High milling %

indicates the higher head rice recovery .The genotypes showed moderate milling quality.

9) Alkali spreading value

The observed range for alkali spreading value of 20 genotyupes was from 4 to 7 and the overall mean was 4.60. Most of the genotypes had intermediate alkali spreading value ranging from 3 to 4 with very few of them having high alkali spreading value of 5 to 7. It indicated that rice would cook at a moderate space and would take less to moderate time to cook. The genotype named Manaswini was showed high alkali spreading value of 7 and low gelatinization temperature.

10) Amylose content

The overall mean for amylose content of the 20 test genotypes was 24.99%. Most of the genotypes had intermediate to high amylose content ranging from 20.7% to 26.9% . This indicated that most of the genotypes would cook dry and fluffy and will have moderate to high volume expansion upon cooking. The genotype recording highest amylose content was CR 3511-1-1-1-4-1-1 and lowest was US-308. This indicated that most of the genotypes would cook dry and fluffy and will have moderate to high volume expansion upon cooking.

11) Length of rice after cooking

The observed kernel length increases of the 20 rice genotypes after cooking were ranging from 5.4mm to 6.3mm in Improved Samba Mahsuri and MTU 1321 respectively. The overall mean was 5.84mm.

Table 4.13. Mean & Range of Grain quality characters in 20 medium slender grain rice genotypes.

S.N.	Genotypes designation	Grain length (mm)	Grain Breadth (mm)	Grain L/B ratio	Kernel length (mm)	Kernel Breadth (mm)	Kernel (L/B) ratio	Hulling %	Milling %	Alkali spreading value	Amylose content (%)	Length of rice after cooking
1	MTU 1320	8.7	2.9	2.9	4.9	2.0	2.3	80.0	69.7	5	26.8	5.6
2	RP 6346-36-16-24-2	8.9	2.7	3.2	5.0	1.8	2.6	78.7	70.2	5	24.4	5.8
3	AD 16168	8.7	2.7	3.2	5.1	1.7	2.7	70.6	65.5	4	24.5	5.7
4	KPS-6262	9.0	2.7	3.2	5.0	1.7	2.6	81.4	68.9	5	25.4	5.8
5	RNR28362	8.7	2.8	3.1	5.0	1.6	2.8	79.9	69.8	4	24.1	5.8
6	MTU 1281	9.8	2.8	3.4	5.5	1.8	2.9	81.1	71.4	4	25.5	6.2
7	MTU 1321	9.6	2.9	3.3	5.6	1.9	2.7	79.1	70.4	5	25.8	6.3
8	CR 3511-1 -1-1-4-1-1	9.2	2.8	3.2	5.1	2.0	2.5	78.0	64.4	5	26.9	5.8
9	RNR26121 (Hybrid)	8.6	2.6	3.2	5.1	1.6	2.8	78.1	67.9	5	26.5	5.9
10	HRI-203 (Hybrid)	8.6	2.7	3.1	5.1	1.8	2.8	79.6	67.2	4	26.7	5.7
11	TMRH139 (Hybrid)	9.7	2.8	3.4	5.6	2.0	2.7	80.2	66.8	5	25.6	6.3
12	US-308 (Hybrid)	9.4	2.8	3.3	5.0	1.7	2.7	80.6	70.2	4	20.7	5.7
13	MEPH-155 (Hybrid)	8.3	2.5	3.3	5.1	1.9	2.6	77.2	64.1	4	24.9	5.8

14	PHI-19101 (Hybrid)	8.9	2.8	3.1	5.2	1.9	2.6	80.0	69.6	4	26.5	5.9
15	BPT 5204 (NC)	8.6	2.7	3.0	5.0	1.7	2.8	81.1	71.4	5	24.6	5.8
16	WGL 14 (NC)	8.9	2.7	3.2	5.1	1.8	2.7	78.3	66.9	5	23.3	5.8
17	Improved Samba Mahsuri(ZC)	8.7	2.7	3.1	4.9	1.8	2.6	76.7	68.7	4	22.2	5.4
18	JKRH 3333 (HC)	8.8	2.8	3.1	5.1	1.8	2.6	79.5	68.0	4	26.4	5.8
19	27 P 63 (H C)	8.4	2.6	3.1	5.2	1.8	2.7	79.9	69.4	4	23.9	5.9
20	Manaswini (LC)	8.8	2.7	3.2	5.2	1.7	2.8	79.6	68.1	7	25.6	5.9
Statistics												
	Range maximum	9.8	2.9	3.4	5.6	2.0	2.9	81.4	71.4	7	26.9	6.3
	Range minimum	8.3	2.5	2.9	4.9	1.6	2.3	70.6	64.1	4	20.7	5.4
	Mean	8.91	2.73	3.18	5.13	1.80	2.65	78.97	68.42	4.93	24.99	5.84
	CV	5.93	4.64	7.06	5.0	4.66	5.27	4.65	4.66	3.00	4.91	4.75
	CD	0.86	0.21	0.37	0.42	0.14	0.23	6.00	5.21	0.24	2.01	0.45

Discussion

South East Asian countries mainly depend on the rice as staple food crop in the world. The requirement for increased productivity among medium slender rice varieties of diverse group by utilizing available variability in the rice germplasm has been long left. Therefore, crucial analysis of genetic variability is a pre-requisite for initiating rice crop improvement programme and for adopting of appropriate selection techniques (Sreedhar *et al.*,2017). Once the genetic variability is established for yield and yield contributing characters in the population, implementation of new crop improvement programme is possible with the aid of suitable selection procedure for the development of these germplasm as varieties in rice.

Grain yield enhancement has been the primary goal of plant breeders for many decades, but the need for excellent quality rice has grown in the present decade as people's living standards progressively improve. As a result, improving rice grain quality attributes, in addition, to yield augmentation, has now become a major problem in rice breeding programmes in order to meet consumer and industrial requirements, hence, improving rice grain quality has been a major concern in rice breeding programs to meet the consumer preference and market demand.

In the current study, an effort has been made for assessment of twenty medium slender grain rice varieties received in the national trail AVT-1(M.S.) including six promising check varieties and assess their yield potential along with grain quality characteristics and genetic diversity among medium slender grain rice genotypes. Study on genetic parameter has also been made on various features as presented below.

5.1 Study of variability

The presence of genetic variability is required for the establishment of an efficient breeding program. The genetic variability of a character is a direct measure of how far the character may be modified toward a particular norm or direction. Therefore, an analysis of variance for different characteristics is required in order to examine genetic variation. In this study, the variability of test genotypes was assessed using basic criteria such as range, mean, variance, heritability, and genetic advance with appropriate formulae.

5.1.1 Analysis of variance

Thirteen characters including grain yield were subjected to analysis of variance. There is a significant variation among the test genotypes for all the characters as the results obtained from the analysis of variance. The characters that exhibited greater degree of genetic variance were filled grains/panicle, chaffy grains/panicle, total number of grains/panicle, grain fertility, grain yield/hectare, days to 50% flowering, plant height, grain yield/ plant, straw yield/plant and the remaining characters like panicle length, effective tillers per plant, harvest index and 100-grain weight showed lower magnitude of variance. Therefore the characters with higher amount of genetic variance which have a direct impact on yield can be considered as significant selection method for achieving greater rice productivity as showed from the analysis of variance (Table 4.1). Similar results have also been recorded by Nanda *et al.* (2020) and Vageeshvari *et al.*(2020)

5.1.2 Mean performance of the genotypes

The range for days to 50% flowering varied from 87.7 to 112 days with overall mean of 99.03 days. It showed that the test genotypes comes under mid-early to late duration groups and the similar difference among the genotypes have also been showed by Patel *et al.* (2001), Krishna *et al.* (2010), and Gosh *et al.* (2012).

The maximum value of plant height recorded was 127.9cm, whereas lowest value recorded was 94.9cm, with the mean of 111.13cm. Plant vigour and genetic potential was indicated by the plant height and also genotypes showed intermediate to long type for plant height. The similar types of results were reported by Devi *et al.*(2017).

The panicle length of the genotypes ranged from 23cm to 28cm with the mean panicle length of 25.59cm. The genotypes are medium to long type panicle bearer. This is a stable yield attribute character that is least impacted by the environment. It has been discovered that longer panicle types predominate over short panicle types. Hence, selecting genotypes bearing longer panicle types may be advantageous for achieving high yield .

The number of effective tillers per plant showed the range of variability among the genotypes from 8 to 11 tillers with an overall mean of 9 effective tillers per plant. As per the results obtained, the genotypes were categorized as moderate tillering type. Prolific tillering type generally showed higher biomass production. Higher biomass output cannot be used productively unless it is accompanied by a big sink size that accumulates a greater part of dry matter during the grain filling phase for increased productivity. It is emphasized that the need of a low to intermediate number of effective tillers per plant with a large panicle and a high grain number for good yield in rice.

The varieties with more filled grains per panicle are preferred, since they contribute directly to increased grain yield. The range for number of filled grains per panicle varies from 131.6 to 249.6 with mean performance 188.33 and a less number of chaffy grains were determined to be more beneficial for increasing grain production. The range for chaffy grains per panicle varies from 23.5 to 100.3 with the mean performance of 47.84. Highest total number of grains per panicle, including filled and unfilled, is a desired feature for boosting grain production. The total number of grains per panicle ranges from 177.1 to 321.2 with the overall mean of 236.17. Similar results were recorded by Nanda *et al*. (2020).

It has also been noted that when selection for greater grain number is performed, there is a proportional drop in grain size, which decreases grain weight. As a result, it is advised that, in order to sustain higher production, a balance between grain number and grain weight be achieved. In case of ideal rice crop the 100-grain weight is around 2.02 to 2.50gm. In the present experiment, 100-grain weight ranged from 1.1gm to 2.0gm. As a result, the genotypes with acceptable grain size may be chosen from the range of variability in the current set of material for enhancing production potentiality in rice.

The grain fertility percentage ranged from 63.5% to 90.1% with an overall mean of 79.93%. As per the results of range and mean for grain fertility percentage, the test genotypes could be categorized as partly sterile to fertile type, suggesting that the character is extremely changeable and may vary as a result of changes in environmental factors. Low light intensity throughout the reproductive and ripening phases is one of the primary environmental factors that cause spikelet sterility. High wind also inhibits pollination and causes chaffiness during the course of flowering period. Nayak *et al.* (1998) showed that the total dry matter production, spikelets per unit area and grain size was mainly affected by the low light intensity. Genotypes based on grain fertility may be chosen to achieve high production in rice.

The degree of variability for harvest index ranged from 0.3 to 0.6 with an overall mean of 0.44. The greater the harvest index, the higher the output and productivity. The harvest index indicates a genotype's physiological efficacy. It is a high heritability trait that may be utilised for genotype selection, similar results was recorded by Hossain *et al.* (2015).

The grain yield per hectare ranged from 24.6q/ha to 54.6q/ha with an overall mean of 36.06q/ha. On the basis of range of variability, the test genotypes could be classified as moderate to high yielding genotypes. Genotypes with desired grain yields might be chosen for future breeding programmes aimed at achieving high and steady yields in rice.

5.1.3 Coefficient of variation, heritability and genetic advance

The coefficient of variation values varied from 0.77 in days to 50% flowering to 11.23 in straw yield per plant. The coefficient of variation for all the characters is less than 15% which signified that the sampling techniques and assessment of the characteristics under research were linked with a low degree of experimental error. The genotypic coefficient of variation is less than the phenotypic coefficient of variation for all the characters under investigation, which may due to the environmental interactions in the inheritance of these characters. Characters like number of chaffy grains per panicle, grain yield per hectare, straw yield per plant and grain yield per plant showed high to moderate PCV and GCV estimates, which indicated the presence of high magnitude of variation for these characters among the genotypes which could be improved through selection in desirable direction. Similar results were noted by Jayasudha *et al.*(2010), Krishna *et al.*(2010), Tiwari *et al.*(2010), Kumar *et al.*(2012), Babu *et al.*(2012), Rakesh *et al.*(2013), Hossain *et al.*(2015), and Rashmi *et al.*(2017).

The heritable part of a character inherited from parents to their children is referred as heritability. Estimates of heritability assist plant breeders in providing information on the amount of variation that is transmissible to progenies in successive generations and in selecting superior genotypes from the population. Furthermore, heritability estimates in combination with genetic advance are more helpful in realizing the gain under selection. In the current study, high heritability was recorded for eleven characters, which ranged from 73.47% for straw yield per plant to 99.24% for total number of grains per panicle. Only two characters namely number of effective tillers per plant (39.51%) and harvest index (58.90%) had low heritability. High heritability values indicated that the characters might be enhanced by phenotypic based selection. Low heritability values indicated that the selection for these traits could be difficult due to environmental masking effect on the expression of the characters. The similar findings were noted by Jayasudha *et al.* (2010) for days to 50% flowering and grain fertility, Immanuel *et al.* (2011) and Akthar *et al.* (2011) for effective tillers per plant, Tiwari *et al.* (2010), Krishna *et al.* (2010) for number of filled grains per panicle, Gosh *et al.* (2012) and Venkatesan *et al.* (2017), for grain yield and number of grains per panicle, and Sreedhar *et al.*(2017) for 100-grain weight, plant height and panicle length.

High heritability may not always signify a large genetic benefit. Characters with a high heritability and a high genetic advance as a percentage of the mean might be utilized as a strong tool in the selection process since they are controlled by additive genes and are less impacted by the environment. In the current study, high heritability coupled with genetic advance values were recorded for grain yield, total number of grains per panicle, filled grains per panicle and 100-grain weight. Similar observations were also recorded by Krishna *et al.* (2010) for number of filled grains per panicle, Tiwari *et al.* (2010) for 100-grain weight and grain fertility and Jayasudha *et al.* (2010) for grain yield.

Prajapathi *et al* (2011), Singh *et al*.(2011), Umarani *et al.*(2017) and Roy *et al*.(2020) also recorded similar results.

5.2 Nature of character association

Correlation analysis is an important tool in any breeding system. It offers an overview of the relationships between the various features and determines which component characteristics should be prioritized when selecting for genetic improvement in grain yield. As a result, research on character association not only aid in understanding physical linkage, but also provides information on the type and direction of selection. Hence, in the current investigation, an effort has been made to assess the nature and extent of correlation of character pairs, which would enable selection of genotypes where a stable combination of characters is associated with increased productivity.

In the current study, genotypic correlations (r_g) were of higher degree than phenotypic correlations (r_p), which showed that environmental cause of correlation has not affected the genetic cause (Prajapati *et al*., 2011).

The assessment of correlation revealed that the characters like days to 50% flowering, plant height, panicle length, 100-grain weight, grain yield per plant, straw yield per plant, filled grains per panicle, and grain fertility showed significant positive association with grain yield. This signified that the selection based on these characters could be useful for genetic enhancement in grain yield. Similar observation have been noted by Nandan *et al*. (2010), Ekka *et al*. (2011), Mohanty *et al*. (2012), Veni *et al*. (2013), Sathisha *et al*. (2015), Kalyan *et al*. (2017), and Kumar *et al*. (2018).

5.3 **Path analysis of yield components**

The association of different component characters among themselves and with yield is quite important for devising an efficient selection criterion for yield. Such interdependence often affects the relationship of component characters with yield, thereby making correlation coefficient to be ineffective. So there is a need to partition the correlation into direct and indirect effects to get the information on actual contribution of each character to yield. Thus, correlation in conjunction with path analysis could give a better insight into cause and effect relationship between different pairs of characters along with grain yield in breeding programme.

In the present study, it was shown that the highest direct positive effect on grain yield was exhibited by number of filled grains per panicle followed by straw yield per plant, grain fertility, harvest index, grain yield per plant and plant height. Whereas total number of grains per panicle showed highest indirect effect on grain yield through days to 50% flowering and number of chaffy grains per panicle. Therefore from the observations of direct and indirect effects of different characters on yield it revealed that the traits like number of filled grains per panicle, straw yield per plant, grain fertility, harvest index, grain yield per plant and plant height could be used as significant criteria for enhancement of grain yield and yield components. Similar observations were reported by Kumar *et al.* (2013), Sinha *et al.* (2015), Behera *et al.* (2017), Madhukar *et al.* (2017), Kumar *et al.* (2018), and Parimala *et al.* (2020).

5.4 Genetic divergence

The rate and extent of genetic improvement in a population are typically determined by the amount of genetic diversity present in a population. Genetic divergence influences a cross's intrinsic potential for hybrid vigour as well as the frequency of desirable recombinants in successive generations. As a result, by include the most divergent parents in the breeding programme, suitable segregants from segregating populations might be selected. Mostly D^2 statistic is used for the assessment of genetic diversity in the population. As a result, understanding the genetic diversity inherent in germplasm for various yield parameters is critical for any breeder commencing on a breeding programme for crop improvement (Sreedhar 2017)

Twenty genotypes were categorized into eight clusters, based on cluster analysis. The highest number of genotypes *i.e.* eight were found in cluster I, cluster II includes four genotypes, cluster III and cluster IV include two genotypes each and the remaining cluster V, VII, VI, and VIII each includes one genotype.

Intra cluster distance is less when compared to inter cluster distance which signifies that the genotypes comprised within the cluster exhibited less divergence from each other. The highest inter cluster distance was recorded between cluster IV and cluster VIII (3296.03), followed by VI and VII (2847.28). Genotypes coming under these cluster indicates that they were having high magnitude of divergence and would produce more desirable segregants to achieve greater genetic divergence. Therefore, crossing between genotypes belonging to these clusters may result in high heterosis, which could be exploited in crop improvement.

The characters like filled grains per panicle followed by days to 50% flowering and grain yield show the highest relative contribution to the divergence.

The similar findings were observed by Manohar and Singh (2013) for days to 50% flowering, Sowmiya and Venkatesan (2017) for grain yield and Ranjith *et al*. (2018) for number of filled grains per panicle.

5.5 Grain quality analysis

5.5.1 Grain length and breadth

Grain length and breadth are an important parameter because it is a grain appearance character, on which marketable quality and industrial demands depended. Grain length of 20 medium slender grain rice genotypes ranged from 8.3mm to 9.8mm, with the overall mean of 8.91mm. The overall mean for grain breadth was 2.73mm and it is ranged from 2.5mm to 2.9mm. Similar findings were recorded by Vageeshvari *et al*. (2020).

5.5.2 Grain L/B ratio

Grain L/B ratio determines the grain shape. Overall mean for grain L/B ratio of 3.18 and it is ranged from 2.9 to 3.4.

But the grain type classification given by IRRI, Philippines was based on the dehusked brown rice *i.e* kernel length, kernel breadth, and kernel L/B ratio. Hence kernel length and breadth were measured and the values ranged from 4.9mm to 5.6mm for kernel length and 1.6mm to 2.0mm for kernel breadth and with overall mean of 5.13mm and 1.8mm for kernel length and breadth respectively. Kernel L/B ratio ranged from 2.3 to 2.9, with the overall mean performance of 2.65.

According to IRRI, Philippines grain shape classification, the grain L/B ratio of 2.1 to 3.0 were considered as medium slender grain rice. In the present study the mean L/B ratio of all the genotypes was 2.65, which indicated that the genotypes under study belong to medium slender grain type. Similar results were recorded by Nirmaladevi *et al*. (2015)

5.5.3 Hulling %

The overall mean for hulling % of 20 genotypes were 78.97% and ranging from 70.6% to 81.4%. High hulling percentage resulted in higher head rice yield of 93.3% in parboiled rice with the higher process steam pressure (Igbeka *et al*., 2008).

Rita and Sarawgi (2008) reported that the more than 80 value of hulling percentage is preferred and if the hulling percentage increases the head rice recovery also increased.

5.5.4 Milling %

The observed range for milling % among the 20 genotypes was 64.1% to 71.4%. The overall mean was 68.42%. High milling % indicates the higher head rice recovery .The genotypes showed moderate milling quality. Similar observations were recorded by Nirmaladevi *et al*. (2015), Singh *et al*. (2017), Chetri *et al*. (2018).

5.5.5 Amylose content

The overall mean for amylose content of the 20 test genotypes was 24.99%. Most of the genotypes had intermediate to high amylose content ranging from 20.7% to 26.9%. This indicated that most of the genotypes would cook dry and fluffy and will have moderate to high volume expansion upon cooking. Similar findings were recorded by Nirmaladevi *et al.* (2015) and Nanda *et al*. (2020).

5.5.6 Alkali spreading value

The observed range for alkali spreading value of 20 genotyupes was from 4 to 7 and the overall mean was 4.60. Most of the genotypes had intermediate alkali spreading value ranging from 3 to 4. It indicated that rice would cook at a moderate space and would take less to moderate time to cook. Similar observation were recorded by Nanda *et al*. (2020)

5.5.7 Length of rice after cooking

The observed kernel length increases of the 20 rice genotypes after cooking ranged from 5.4mm to 6.3mm. The overall mean was 5.84mm. Longer grain length genotypes showed longer elongation under the investigation. Similar results were found by Singh (2012).

SUMMARY AND CONCLUSION

The present investigation entitled “Genetic variability for morphological and quality characters in medium slender grain rice (*Oryza sativa* L.)” was conducted to assess the genetic variability, character association, genetic advance, genetic divergence, and grain quality characters among the test genotypes of medium slender grain rice. The present experimentation was laid out at EB-1 Rice Research Station, O.U.A.T. Bhubaneswar during 2020 Kharif season. The experimental materials consisted of twenty genotypes including high yielding varieties and hybrids having medium slender grains from the experimental materials of Advance Varietal Trail-1 (AVT-1 MS). The experiment was laid out in a Randomized Block design and replicated thrice.

Observations were recorded for thirteen metric traits. Five competitive plants were selected randomly from the middle rows of each plot for taking observations for eleven metric traits, whereas the other two characters, grain yield and days to 50 % flowering were recorded on a plot basis. The characters studied under this experiment were days to 50% flowering, plant height(cm), panicle length(cm), number of effective tillers per plant, 100-grain weight(g), grain yield/ plant(g), straw yield/plant(g), harvest index, number of filled grains/panicle, number of chaffy grains/panicle, total number of grains/panicle, grain fertility(%), grain yield/hectare(q) and grain quality characters *viz*., grain length(mm), grain breadth(mm), grain l/b ratio, kernel length(mm), kernel breadth(mm), kernel l/b ratio, hulling %, milling %, alkali spreading value, amylose content(%), length of rice after cooking(mm) were also studied under the present investigation.

The key investigation findings are given here under.

The analysis of variance indicated that the mean sum of squares due to treatment was highly significant for all quantitative and qualitative characteristics at the 1% and 5% level of significance. The finding suggests that there had been wide opportunity for the choice of good potential lines for yield and grain appearance quality, milling and eating quality attributes from existing lines of germplasm. The result implies that there is a large possibility for selecting promising genotypes for yield and grain quality parameters, milling and eating quality parameters from current germplasm lines. Highest mean value for total number of grains per panicle showed for quantitative character was 236.17. Consequently, the highest mean value of 78.97 was recorded for the grain quality character namely hulling percent. A higher genetic variation is a fundamental need in any breeding material since it provides not only a preference basis but also some important information on the selection of different parents to be utilized for crop improvement.

The GCV and PCV were found to have a significant connection for all characters. As a result, their PCV was greater than their eventual GCV. In the present research, the estimated phenotypic coefficients of variation for all traits were greater than the estimates of genotypic coefficients of variation, which might be attributed to the interaction of genotypes with environment. Large variations in GCV and PCV values indicate a significant environmental effect on trait performance. Number of effective tillers per plant showed larger variation for GCV and PCV. Minor differences in this study for most of the characters showed a limited environmental effect and, as a result, a substantial involvement of genetic variables in trait expression. Both PCV and GCV are high for grain yield. As a result, making a selection based on grain yield would be effective.

Magnitude of heritability was high for total number of grains per panicle, number of filled grains per panicle and days to 50% flowering. Lowest heritability was observed for harvest index and number of effective tillers per plant where as remaining characters showed moderate heritability. Genetic advance as percent of mean was high for number of chaffy grains per panicle, grain yield per hectare, and total number of grains per panicle. Higher degree of heritability coupled with high genetic advance was noted for grain yield per hectare and number of filled grains per panicle, and signifies the significance of additive gene action in inheritance of these characters. As a result, direct phenotypic selection is beneficial for these characteristics.

Grain fertility in both phenotypic and genetic level was estimated high having significant positive correlation with grain yield, followed by days to 50% flowering, number of filled grains per panicle and grain yield per plant. These traits showed strong relation with the grain yield. This signified that the selection based on these characters could be useful for genetic enhancement in grain yield.

Path coefficient analysis in the present study showed that the highest direct positive effect on grain yield was exhibited by number of filled grains per panicle followed by straw yield per plant, grain fertility, harvest index, grain yield per plant and plant height. Whereas total number of grains per panicle showed highest indirect effect on grain yield followed by days to 50% flowering and number of chaffy grains per panicle. Therefore from the observations of direct and indirect effects of different characters on yield it revealed that the traits like number of filled grains per panicle, straw yield per plant, grain fertility, harvest index, grain yield per plant and plant height could be used as significant criteria for enhancement of grain yield and yield components.

Twenty genotypes were categorized into eight clusters, based on cluster analysis. Eight genotypes were found in cluster I. Cluster II includes four genotypes, cluster III and cluster IV include two genotypes each and the remaining cluster V, VI, VII and VIII each includes one genotype. Intra cluster distance is less when compared to inter cluster distance which signifies that the genotypes comprised within the cluster exhibited less divergence from each other. The highest inter cluster distance was recorded between cluster IV and cluster VIII, followed by VI and VII, genotypes coming under these cluster indicates that they were having high magnitude of genetic divergence. This signifies that the selection of genotypes as parents from these diverse groups could be useful in hybridization and crop improvement programme.

Conclusion

Based on grain yield per hectare, genotypes namely, MTU 1320 (54.6 q/ha) recorded highest grain yield per hectare followed by RNR 28362 (49.1 q/ha), MTU 1321(44.3 q/ha), AD 16168 (43.1 q/ha) and KPS-6262(39.3 q/ha).

Among the twenty rice genotypes under study, the entry MTU 1320 had a superiority from others by exhibiting greater proficiency in quantitative characters with days to 50% flowering, 100-grain weight, grain yield per plant, straw yield per plant, filled grains per panicle, grain fertility and grain yield followed by MTU 1321 and RNR 28362.

The characters like grain yield, total number of grains per panicle, number of filled grains per panicle and 100-grain weight having highest estimates of PCV, GCV, and heritability coupled genetic advance as percentage of mean.

Grain fertility in both phenotypic and genetic level was having significant positive correlation with grain yield, followed by days to 50% flowering, number of filled grains per panicle and grain yield per plant.

The highest direct positive effect on grain yield was exhibited by number of filled grains per panicle followed by straw yield per plant, grain fertility, harvest index, grain yield per plant and plant height.

From the Mahalanobis D^2 analysis, cluster VI and cluster VII were most divergent, *i.e.* MTU 1320 and RNR 26121 were the most divergent genotypes as they belong to these two clusters, respectively.

Based on the grain shape twenty genotypes were classified as medium slender grain rice based on kernel length and kernel breadth ratio. High kernel length was recorded by MTU 1321 and TMRH 139 (5.6mm). High kernel breadth was recorded by MTU 1320 and CR 3511-1-1-1-4-1-1 (2.0mm).

The highest hulling and milling percent were recorded by the genotypes namely KPS-6262 (81.4%) and MTU 1281 (71.4%), respectively.

Most of the genotypes had intermediate to high amylose content ranging from 20.7% to 26.9%. This indicated that most of the genotypes would cook dry and fluffy and will have moderate to high volume expansion upon cooking. High amylose content of 26.9% was recorded in the genotype CR 3511-1-1-1-4-1-1.

Most of the genotypes had intermediate alkali spreading value ranging from 4 to 5. It indicated that rice would cook at a moderate space and would take less to moderate time to cook. The genotype named Manaswini showed high alkali spreading value of 7 and low gelatinization temperature.

The genotype TMRH 139 recorded high value for length of rice after cooking (6.3mm).

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