

**Characterization for yield and quality traits
under aerobic and transplanted condition
in Rice (*Oryza sativa* L.)**

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(HARYANA)**

2021

CERTIFICATE-I

This is to certify that this thesis entitled, “**Characterization for yield and quality traits under aerobic and transplanted condition in rice (*Oryza sativa* L.)**” submitted for the degree of **Master of Science** in the subject of **Genetics and Plant Breeding** to the **Chaudhary Charan Singh Haryana Agricultural University, Hisar** is a bonafide research work carried out by **Bhawana**, Admission. No. **2019A85M** under my supervision and that no part of this thesis has been submitted for any other degree.

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

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CERTIFICATE-II

This is to certify that this thesis entitled, “**Characterization for yield and quality traits under aerobic and transplanted condition in rice (*Oryza sativa* L.)**” submitted by **Bhawana**, Admission. No. **2019A85M** to the **Chaudhary Charan Singh Haryana Agricultural University, Hisar** in partial fulfillment of the requirement for the degree of **Master of Science** in the subject of **Genetics and Plant Breeding**, has been approved by the Student's Advisory Committee after an oral examination on the same, in collaboration with an external examiner.

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ABBREVIATIONS

%	:	Percentage	DM	:	Days to maturity
PCV	:	Phenotypic co-efficient of variation	PH	:	Plant height
GCV	:	Genotypic co-efficient of variability	PL	:	Panicle length
GA	:	Genetic advance	NT/P	:	Number of tillers per plant
GAM%	:	Genetic advance as percent of mean	GN/PL	:	Number of grains per panicle
q/ha	:	Quintal per hectare	TW	:	Test weight
Cm	:	Centimeters	BY/P	:	Biological yield per plant
g/p	:	Gram per plant	HI	:	Harvest index
RBD	:	Randomized block design	HULL	:	Hulling %
DSR	:	Direct seeded rice	MILL	:	Milling %
TPR	:	Transplanted rice	HRR	:	Head rice recovery %
d.f.	:	Degree of freedom	KL	:	Kernel length
ml	:	Milliliter	KB	:	Kernel breadth
mm	:	Millimeter	GY	:	Grains yield per plant
viz.	:	Videlicet (namely)	RL	:	Root length
i.e.	:	That is	RFW	:	Root fresh weight
No.	:	Number	RV	:	Root volume
et. al.	:	And others	RDW	:	Root dry weight
KLBR	:	Kernel length breadth ratio	RFW/ RDW	:	Root fresh weight and dry weight ratio
DTF	:	Days to 50% flowering	h ²	:	Heritability

CHAPTER-I

INTRODUCTION

Rice (*Oryza sativa* L.) is most important crop of the world. It provides food and economic security to many Asian countries including India. It ranks second after wheat and is main source of staple food for more than half of the world's population accounting for 20% of calorie and 15 % of protein consumption (Tabl, 2021) besides being a good source of vitamin-B complex such as thiamin, riboflavin and niacin (Fresco, 2005) and minerals (Ca, Mg & P) with traces of iron, copper, zinc and manganese (Oko *et al.* 2012). It belongs to the family Poaceae and genus *Oryza* which consists of 2 cultivated species (*Oryza sativa* and *Oryza glaberrima*) along with 22 wild species. Rice is a self-pollinated, diploid ($2n = 2x = 24$), short day C_3 plant. Though, it prefers flooding, yet it is grown under diversified edaphic conditions like aerobic to anaerobic (amphibian in nature) and in areas ranging from hills to coasts. "Rice is life" for citizenry especially in Asian subcontinent, where 90 per cent of world's rice is grown (China and India alone contribute nearly half the worldwide output) and consumed especially where about two-thirds of world's poor live (Khush and Virk 2000).

India has the largest area under cultivation and is the second largest producer (accounts 22% of total global production) and the largest exporter of rice in world. India alone exported 65 % of world basmati rice market (APEDA 2020) and Haryana contributed 50 % share of total export of basmati rice from the country. Being a crop of hot and humid season, it is cultivated round the year in one or other part of the country. In India, it is cultivated over 43.79 million ha area with the production of 116.42 million tons and productivity 2.65 t/ha. Rice in Haryana occupied 1.56 million ha with a production of 5.19 million tones and productivity 3.33 t/ha (Anonymous 2019). The state contributes substantially to the central pool and is well known for production and export of top quality scented (basmati) and superfine quality non-scented rice. Traditional basmati rice possesses some fewer desirable traits such as tall stature, photoperiod sensitivity and poor response to fertilizer application leading to low yield. Basmati genotypes are distinguished from non-basmati ones by their superfine grain, pleasant aroma, soft texture and higher grain elongation with lesser breadth-wise swelling on cooking.

Conventionally transplanted rice consumes about two to three times more water than by any other cereals. It uses 3000 to 5000 liters of water for producing one kg of rice. Global grain production is expected to increase by 50 % till 2030 to meet the food demands of continuously increasing population (Avnery *et al.*, 2013). Climatic change and scarcity of water and labour becomes serious and wide spread problems which will limit the future rice

production. To cope up with this challenge, alternate cultivation technologies must be developed to reduce labour and water requirement while maintaining yield potential (Yuans *et al.*, 2017). Thus, there is strong need to reduce the water use in rice through the use of sustainable water saving technologies to sustain the rice production and to feed the increasing global population (Joshi *et al.*, 2018).

Among different water saving technologies like alternate wetting and drying, system of rice intensification and direct seeded rice (aerobic rice), the latter is emerging as an efficient and economically viable planting method. The aerobic rice can be an alternative to puddled transplanted rice and has the potential to effectively address water shortage while ensuring sustainable rice production (Liu *et al.*, 2015). In aerobic condition, rice crop is established by sowing the seed (dry or water-soaked seed) in dry soils (direct seeding) and growing the crop under non-puddled and non-flooded conditions, thus saving the labour for transplanting and reducing water consumption for maintenance of flooding in conventionally transplanted rice besides reducing greenhouse gas (methane) emission from flooded soil surfaces. Aerobic rice system uses less water than conventional flooded rice through the use of rice varieties capable of responding well to reduced water inputs in non-puddled and non-saturated soils (Peng *et al.*, 2006). Currently, the varieties bred for transplanted puddled rice are being used in the aerobic systems which are not able to achieve their potential yield under direct seeded system (Mahajan *et al.*, 2018). The development of aerobic rice varieties by combining the traits of upland varieties (tolerance of water deficit, early vigour and weed competitiveness) and lowland varieties (high yield potential, efficient nutrient uptake and good grain quality), could be a sustainable strategy to tackle the problem of water–labour scarcity and climate change. Few aerobic rice varieties viz., CR Dhan 200, CR Dhan 201 and CR Dhan 202 have been developed for cultivation. But still, there is lack of suitable rice genotypes for aerobic cultivation.

Genetic variability is very important for crop improvement because proper management of diversity can affect permanent gain in the yield of plant and provide buffer against seasonal fluctuations in yield (Perween *et al.*, 2020). The success of any crop breeding program depends upon the magnitude and direction of genetic association of the traits within the base population. The generation of suitable varieties largely depends on the availability of desirable genetic variability for important traits (Partap *et al.*, 2012). A critical appraisal of the genetic variability is a pre requisite for plant breeder to work on crop improvement programs.

Heritability used to assess the amount of genetic improvement to be transferred from parents to offspring. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population. Genetic advance refers to the upgradation in the genotypic value of the new population over the original one. The estimates of genetic advance, as per cent of mean, provide more authentic information regarding the effectiveness

of plant selection in improving the traits. Heritability coupled with genetic advance is more potent in predicting genetic gain than heritability alone (Nirmala *et al.*, 2015).

Grain yield is a complex trait which is regulated by genes (QTL) and influenced by environment (Zhang *et al.*, 2017). Therefore, selection only on the basis of yield is not reliable. Correlation is a very important factor for any selection program. The genotypic association is important in determining the degree to which various yield attributing traits are associated with grain yield (Kishore *et al.*, 2015). Further, partitioning of the correlation coefficients through path analysis is very significant to understand the cause-effect relationship and helps in understanding the relative importance of component traits for improvement in grain yield of a crop. Selection of grain yield by considering morphological and physiological traits as indirect selection criteria is an alternative breeding approach. Path coefficient analysis also provides useful information regarding the association of traits with themselves and grain yield which is important for direct and indirect selection of traits contributing to yield (Girma *et al.*, 2018). It also enables the breeder to rank the attributes according to their contribution to yield.

Genetic diversity within and between groups of germplasm is useful in selecting parents for obtaining useful recombinants. Mahalanobis D^2 statistics offer a powerful tool for quantifying the degree of divergence (clustering pattern) in germplasm to establish relationships between genetic and geographical divergence as well as investigating the roles of different quantitative characters towards maximum divergence (Murty *et al.*, 1966). Identification and proper characterization of the germplasm is, therefore, needed.

In recent past, Rice production in India is facing unprecedented challenge of environmental degradation and climate change affecting the grain yield. Now there has been enormous pressure on the breeders to develop suitable genotypes both for irrigated (transplanted) and aerobic (direct seeded) conditions to mitigate the effect of water stress while maintaining sustainable rice production.

Keeping the above facts in view, the present experiment entitled “**Characterization for yield and quality traits under aerobic and transplanted conditions in rice (*Oryza sativa* L.)**” is undertaken with the subsequent objectives:

1. To estimate genetic variability parameters among the rice genotypes under aerobic and transplanted conditions for yield and quality traits
2. To review character association and path analysis for yield and quality traits under aerobic and transplanted conditions
3. To assess genetic divergence among the rice genotypes

CHAPTER-II

REVIEW OF LITERATURE

The literature concerning to present investigation has been briefly reviewed and presented under the following headings:

2.1. Genetic variability, heritability and genetic advance

2.2. Correlation coefficient and path coefficient analysis

2.3. Genetic divergence

2.1 Genetic variability, heritability and genetic advance

The improvement in any crop depends upon the extent, nature and magnitude of genetic variability present in the base material and the degree to which it is heritable. Yield is complex and polygenic trait and is highly influenced by fluctuating environments. Therefore, it is very important to know the role of environment for expression of traits. The variability among base population is the potential of a genotype to change or deviate when these are exposed to environment or genetic factors. An assessment of genetic variability with the assistance of parameters such as genotypic coefficient of variance, phenotypic coefficient of variance, heritability approximation and genetic advance are essential for any successful crop improvement strategies. Estimated heritability (broad sense) itself alone is not very useful because it includes the effect of both additive and non-additive gene. The genetic advance is therefore a useful indicator to achieve expected result on the trait of interest of a population after selection. A thorough understanding of the inheritance of traits and relationship with other component traits is foundation for the choice of breeding and selection methods for crop improvement. The opinions concerning genetic variability, heritability and genetic advance are detailed below.

Nath and Kole (2021) evaluated 26 rice genotypes to study genetic variation of different quantitative characters and reported significant variation for all the characters. High genotypic and phenotypic coefficients of variation was recorded for the flag leaf area, spikelet number, grain number, test weight and grain yield. High heritability coupled with high genetic advance were observed for plant height, grain number and test weight indicated the expression of these characters is under the control of preponderant additive genetic effects.

Parimala *et al.* (2020) conducted an experiment to obtain information about the amount of genetic variability in 77 rice genotypes. The degree of PCV was observed more than GCV which reflected the effect of environment on these characters. High heritability along with high genetic advance was observed for test weight, showed the role of additive gene action in controlling the trait.

Toppo *et al.* (2020) screened 30 genotypes of rice to know about variability present in the gene pool. ANOVA showed significant differences for all the characters reflecting presence of substantial amount of variability among the genotypes. High GCV and PCV were noticed for grain yield per hill followed by harvest index. High estimates of heritability coupled with high genetic advance were observed for spikelet/panicle and biological yield/hill.

Bhattacharya and Chakraborty (2019) evaluated 28 diverse genotypes of aromatic non-basmati rice to study variability for yield and yield attributing traits. Harvest index showed high coefficient of variability succeeded by number of productive tillers/plant. GCV and PCV values for number of panicles, harvest index, spikelet density showed higher differences indicated the greater role of external or environmental factors. High to moderate estimation of heritability and genetic advance were observed for number filled grain, days to 50% flowering, grain yield/plant.

Akter *et al.* (2018) assessed the nature and extent of genetic variability among 26 rice genotypes and reported vast and significant variations for 13 morphological traits. GCV & PCV were maximum for number of filled grains/panicle and test weight. High heritability coupled with high genetic advance were observed for number of filled grains/panicle and 1000 grain weight.

Behera *et al.* (2018) evaluated 22 aerobic genotypes to assess variability, heritability and genetic advance. High PCV and GCV were recorded for effective tiller/panicle, flag leaf area, fertile grain/panicle, fertility percentage, grain yield. High heritability estimates coupled with high genetic advance (%) over mean were recorded for flag leaf area, number of fertile grains/panicle and plot yield indicating that selection based on phenotypic performance would be effective for these traits.

Girma *et al.* (2018) assessed 64 rice genotypes to study genetic variability. Phenotypic coefficient of variance was observed slightly higher than genotypic coefficient of variance which showed the effect of external factors except for panicle length. High heritability and genetic advance were recorded for most of the traits, indicating the presence of additive gene action.

Tripathi *et al.* (2017) evaluated 32 rice genotypes under aerobic conditions to assess genetic variability. Adequate variability was observed among the genotypes for all the characters under study. Greater extent of broad sense heritability was noticed for days to 50% flowering, filled grains and test weight indicated the scope for improvement in grain yield and its attributing traits.

Manjunatha *et al.* (2017) carried out an experiment with 64 elite rice genotypes and revealed significant differences for all the traits under study. Higher phenotypic co-efficient of variation with respect to genotypic coefficient of variation were observed for all the

characters under study. Plant height, days to 50% flowering, panicles/m² and grain yield showed high heritability along with genetic advance as percent of mean.

Kumar *et al.* (2017) examined 40 rice genotypes to study genetic variability and reported significant differences among the genotypes for all the 13 traits. High GCV & PCV were noticed for tillers/hill, panicle/hill, spikelets/panicle, biological yield, test weight and grain yield reflecting that these characters are under the genetic control. High heritability coupled with high genetic advance was noticed for plant height, flag leaf length, panicle/hill, tillers/hill, days to maturity, spikelets/panicle, biological yield, harvest index, test weight and yield indicating that selection will be 100 % effective for these characters.

Bagati *et al.* (2016) carried out an experiment with 140 F₇ recombinant inbred lines (RILs) to obtain information on genetic variability and heritability for yield along with its 5 components. The outcomes corresponding to analysis of variance revealed accountable differences for yield and its attributes. Slightly higher phenotypic coefficient of variation than genotypic coefficient of variation indicated the negligible influence of environment on the expression of traits. High heritability was recorded for yield and associated traits and hence can be used as selection indices for improving grain yield.

Kishore *et al.* (2015) screened 73 rice varieties to study variability along with heritability and genetic advance for yield and its components. The results revealed that grain yield showed high variability, heritability and genetic advance while panicle bearing tillers and 1000 grain weight had recorded high heritability coupled with low genetic advance as percent of mean.

Naseer *et al.* (2015) carried out experiment to study genetic variability among 24 basmati and non-basmati genotypes. High magnitude of phenotypic variance was observed for most of the traits indicating the effect of environment on expression of these traits. Moreover, number of grains/panicle, plant height and number of spikelets/panicle showed high GCV, PCV, heritability and genetic advance. These results suggested the importance of these traits in crop improvement programs.

Lingaiah *et al.*, (2014) evaluated 33 rice cultures to estimate the variability parameters for quantitative traits. The genotypic and phenotypic coefficients of variations were moderate to high for number of grains/panicle, test weight and yield. High heritability coupled with high genetic advance as percent of mean was observed for number of grains/panicle, test weight and yield indicating the role of additive gene in controlling these characters and improvement in these characters would be possible through direct selection.

Gangashetty *et al.* (2013) studied variability among 42 diverse rice genotypes and observed the existence of significant genetic variability for all the 13 quantitative traits. High heritability with high genetic advance was observed for most of the traits indicating the

presence of considerable variation and improvement of these traits could be effective through phenotypic selection.

Kumar *et al.* (2012) assessed 30 popular rice genotypes collected from the different geographical areas to study genetic variability and reported higher contribution of number of unfilled grains per panicle, seed yield (q/h) and harvest index towards genetic variability. Results also revealed that the traits with high heritability and high genetic advance perhaps subjected to mass/progeny/family selection, anticipated to make use of additive genetic variance so that a widely adapted genotype having higher productivity with lower water requirement may be developed.

Seyoum *et al.* (2012) conducted an experiment on 14 rice genotypes to estimate the genetic variability for yield and its component traits. Significant variation was observed for days to 50 per cent flowering, 85 per cent maturity, plant height, panicle length, spikelet/panicle. High heritability was observed for plant height, 50 per cent flowering, test weight, days to 85 per cent maturity, panicle length and spikelets per panicle.

Prasad *et al.* (2011) investigated 52 rice genotypes to know the extent of genetic variability. Analysis of variance showed accountable differences for all the characters except spikelet sterility, early seedling vigour and coleoptiles length. Variation studies disclosed that PCV is minutely higher than GCV regarding panicle length, spikelet sterility, seed yield per plant and coleoptile length indicating that the characters were less influenced by the environment.

Abarshahr *et al.*, (2011) evaluated 30 rice varieties for genetic variability under two irrigation regimes. ANOVA revealed significant differences among the varieties for all the traits. Estimation of co-efficient of variation showed that the minimum and maximum PCV were noticed for panicle fertility% and paddy yield whereas, GCV showed positive association with brown grain width and plant height under optimum irrigation system. Days to 50% flowering showed minimum PCV & GCV while paddy yield and plant height exhibited maximum GCV under drought stress condition.

2.2. Correlation coefficient and path coefficient analysis

Kushwaha *et al.* (2020) studied path coefficient analysis using 22 rice genotypes to study the relation between 15 yield and its contributing characters. The correlation coefficient analysis had that grain length, root volume, panicle length of main axis, number of panicles/hill indicated positive accountable correlation with grain yield/plant. Grain length, root volume, panicle length of main axis and leaf length reflected high direct effect on grain yield/plant.

Khatriyar *et al.* (2019) evaluated 27 rice genotypes to study trait association and path analysis. Harvest index showed highly significant and positive phenotypic correlation with economic yield components. Path coefficient analysis revealed that harvest index showed highest positive direct effect on economic yield succeeded by biological yield and root length.

Bhattachraya and Chakraborty (2019) assessed direct and indirect effects of different yield contributing traits in 28 diverse genotypes of aromatic non-basmati rice. Grain yield/plant observed significant positive association with agronomical traits at both genotypic and phenotypic levels reflecting the importance of these characters for yield improvement. Results revealed that more attention during selection of characters should be given on number of panicle/plant, primary branch, number of filled grain/panicle and test weight for improvement of grain yield.

Khokhar and Sarial (2018) evaluated 25 rice varieties belonging to different maturity groups and genetic background (basmati, non-basmati and hybrids) under aerobic and transplanted conditions for 12 yield and quality traits. The analysis of variance revealed significant differences among the genotypes for all the characters in both the production systems. Grain yield was significantly correlated with percent filled spikelets, days to maturity, 1000 grains weight and biological yield per plant under both the production systems. Harvest index and biological yield under aerobic condition whereas, tillers/plant and 1000 grain weight were found to be prominent yield contributing variables under transplanted production system.

Reddy *et al.* (2018) screened 24 different near isogenic lines of rice and their parents to study character association for yield and lodging parameters. Correlation analysis reflected that grain yield/plant had considerable positive genotypic association with number of grains/panicle, days to 50% flowering and panicle length. Indirect selection for wider, thicker culms, intermediate height of 125-130 cm might result in non-lodging genotypes with higher yield.

Priya *et al.* (2017) evaluated 40 genotypes to assess the character association and the magnitude of direct and indirect effects for 11 characters. Assessment of character association showed that productive tillers/plant, grains/panicle, test weight, panicle length, days to maturity, kernel breadth, plant height, days to 50% flowering and kernel length had significant positive association with grain yield/plant at phenotypic level. Path analysis revealed that kernel breadth, L/B ratio, effective tillers/plant, grains/panicle, test weight, days to maturity, days to 50% flowering showed significant positive association and high positive direct effect on grain yield.

Rashid *et al.* (2017) screened 10 rice genotypes to study character association and path coefficient analysis for yield and its component traits. Results indicated that traits viz., days to 50% flowering, days to maturity, plant height and number of filled grains per panicle could be used as an important selection index for the improvement of yield.

Priyanka *et al.* (2016) conducted an experiment with 11 parents and their 24 F₁ crosses to study correlation and direct and indirect effects of different yield component on grain yield. The correlation studies revealed that grain yield per plant exhibited a significant positive correlation with plant height, number of productive tillers per plant, panicle length,

grain per panicle and harvest index while days to 50% blooming showed non-significant negative association with the grain yield.

Allam *et al.*, (2015) conducted an experiment with 23 genotypes of basmati rice to study correlation and path analysis. Results indicated that yield per plant expressed highly significant positive genotypic and phenotypic correlation with days to maturity, spikelets per panicle and amylose content. Kernel length breadth ratio showed positive and significant correlation with kernel length after cooking. Effective panicles per plant imparted the highest positive direct contribution towards yield followed by test weight, spikelets per panicle, kernel length and spikelet fertility.

Chandra *et al.* (2015) examined 25 rice genotypes under aerobic and normal conditions to study correlation and path coefficient analysis on 15 morpho-physiological traits. Grain yield per plot showed significant positive correlation with plant height, panicle length, number of tillers per plant, number of spikelets per panicle, relative water content, maximum root length, flag leaf area, harvest index, chlorophyll content and test weight. Path analysis revealed that traits viz., days to 50 % flowering, number of spikelets per panicle, number of tillers per plant, relative water content and maximum root length expressed highest positive direct effect on yield.

Roy *et al.* (2015) investigated 7 elite rice genotypes to study correlation and path coefficient analysis for yield and its component traits and reported that flag leaf area, productive tillers per plant, 1000-grain weight, growth duration and harvest index exhibited direct effect on grain yield and are important characters to be considered for yield improvement.

Lingaiah *et al.* (2014) studied correlation and path analysis in 64 mid-early group genotypes of rice for yield and its attributes. Grain yield exhibited positive association with effective tillers per plant, panicle length and test weight and negative association with days to 50% flowering and plant height. Path analysis indicated that panicle length, effective tillers per plant and test weight observed significant positive direct effect on yield.

Lakshmi *et al.* (2014) evaluated 70 rice accessions to obtain information about type and degree of correlation between 11 yield and its attributing characters. Results revealed that phenotypic and genotypic correlation to be of similar direction and significance. Days to maturity, number of productive tillers/plant, plant height and kernel length were significantly and positively correlated with grain yield/plant.

Suma *et al.* (2014) assessed 98 double haploid lines to study morphological characters of root and shoot for improving grain yield of rice under aerobic and transplanted conditions. Grain yield was positively correlated with maximum root length, volume, dry weight and root number under aerobic condition. Shoot characters such as plant height, panicle length, number of productive tillers and straw yield/plant were positively correlated

with grain yield/plant. Path analysis reflected that root characters (highest root length, root dry weight and root number), shoot characters (plant height, panicle length, number of productive tillers, test weight and straw yield/plant) showed positive direct effect on grain yield. Results demonstrated the effectiveness of root traits for improving grain yield under aerobic conditions on root traits for improving grain yield.

Osman *et al.* (2012) evaluated 13 rice genotypes for maturity, morphological and yield associated traits. Correlation studies revealed that grain yield had significant positive correlation with panicle length, number of tillers per plant, no. of filled grains per panicle and test weight. Path analysis showed that number of tillers per plant, test weight, panicle length and number of filled grains per panicle had direct positive effect on grain yield.

Abharshahr *et al.* (2011) estimated inter relationships among 30 rice varieties under two irrigation systems. Path analysis revealed that under the optimum irrigation condition, number of spikelet/panicle and length of flag leaf possessed positive direct effects while days to complete maturity and plant height had negative direct effects on paddy yield. Under drought condition, flag leaf width and number of filled grains/panicle showed positive direct effects whereas, days to 50% flowering had negative direct effect on paddy yield.

Bagheri *et al.* (2011) conducted field experiment to study path analysis in 26 rice genotypes and reported that panicle length exerted the highest positive direct effect on grain yield. Grain yield observed strong association with panicle length, the number of panicles per plant, and the number of filled grains per panicle. Results demonstrated that a plant type for increasing grain yield should have high panicle length with total numbers of spikelet per panicle, high number of filled grains per panicle and the number of panicles per plant.

Kaur *et al.* (2011) studied correlation between different physical, chemical and cooking properties of 80 rice varieties of basmati and non-basmati genotypes and reported significant variations within different quality attributes. Evolved basmati varieties were better in some parameters like more kernel length breadth ratio, size of kernel after cooking, more amylose content and higher water uptake during cooking as comparison of traditional basmati varieties. Non-basmati varieties showed similar set of properties and can be clearly differentiated from basmati varieties. Amylose content exhibited positive correlation with cooked kernel length, elongation ratio and water uptake, which may serve as good donors for further improvement in quality parameters.

Allah *et al.*, (2010) studied correlation and path analysis in 33 local and exotic genotypes under normal and drought conditions to identify traits that may confer drought resistance. Among the traits studied viz. number of tillers per plant, number of panicles per plant, 100 grain weight and panicle weight observed significant genotypic association with grain yield. Number of filled grains per panicle depicted the highest direct contribution towards grain yield. Path coefficient analysis demonstrated that number of panicles per plant,

100 grain weight, number of filled grains per panicle, panicle weight should be improved in order to increase grain yield under both normal and drought conditions.

Kanbar *et al.* (2009) evaluated recombinant inbred lines to understand the relationship between root characters and yield traits. The interrelationships clearly identified the importance of root to shoot length weight ratio and root dry weight under well-watered condition, whereas, maximum root length and root number are a better combination under low moisture stress condition. Results indicated the importance of root characters on grain yield under stress condition than well-watered condition.

2.3 Genetic divergence

Existing genetic diversity within and between groups of germplasm is important and particularly useful in proper choice of parents for obtaining useful segregants. Physio-morphological traits have been successfully used for estimation of genetic diversity and cultivar development as they provide a simple way of quantify the genetic variation. Mahalanobis (1936) defined a statistical method, D^2 statistic; for estimating the genetic divergence in a selected population. This concept is based on the technique of utilizing measurements in respect of cluster of characters. Multivariate analysis based on Mahalanobis D^2 statistic has been considered in different crops (Rao, 1952). In rice D^2 statistic has been extensively used to find out genetic divergence by various workers.

Devi *et al.* (2020) assessed genetic divergence among 33 rice genotypes for yield and quality parameters using D^2 statistics. Genotypes were grouped into eight clusters and cluster I was the largest consisted of 23 genotypes. The intra cluster distance was maximum for cluster II indicating the existence of variability within the cluster. Plant height, alkali spreading value, days to 50% flowering and test weight were observed most important trait and contributed maximum towards genetic divergence.

Sabarinathan *et al.* (2020) evaluated 26 genotypes of rice to confirm the presence of genetic diversity using multivariate analysis and concluded that there is no relationship between genetic and geographical diversity in the material under investigation. The grouping pattern was not consistent across seasons, indicating genotype $\times$ season interaction affects genetic diversity. The traits viz., DPPH antioxidant activity and seed yield per plant contributed maximum towards absolute genetic divergence.

Perween *et al.* (2020) screened 48 rice genotypes in two different production system *i.e.*, irrigated and drought stress to know the magnitude of diversity present among the genotypes. According to D^2 statistics, genotypes were grouped into 19 & 11 clusters respectively under irrigated and drought stress production system respectively. Highest inter-cluster distance was observed between clusters XVIII and XIX in irrigated condition and in drought condition it was noticed between cluster IX & X reflecting wider genetic diversity among the genotypes of these clusters.

Mishra *et al.* (2019) studied divergence among 35 rice accessions from different agro climatic zones and reported significant diversity for spikelet per panicle and branches per panicle. All traditional Basmati rice varieties were grouped into same cluster demonstrating the importance of regional genetic studies for understanding the diversification.

Soe *et al.* (2019) conducted an experiment to determine genetic diversity among 87 rice accessions from six countries for 17 quantitative traits and observed significant divergence among them. Genotypes were grouped into seven clusters. The results demonstrated the importance genetic diversity revealed by the morpho-agronomic traits in selecting appropriate genotypes for rice improvement.

Tripathi *et al.* (2017) estimated divergence among 32 rice genotypes under direct seeded condition using Mahalanobis D^2 statistics. Genotypes were grouped into seven clusters and Cluster II was observed largest with 16 genotypes. Highest and lowest inter cluster distances were observed between cluster IV and VII (984.82) and cluster III (363.58) respectively. Results indicated that genotypes from different clusters could be used as donors in hybridization programme for aerobic cultivar development.

Pachauri *et al.*, (2017) carried out to an experiment to characterize 124 rice germplasm accessions on the basis of 19 morphological and 11 agronomical traits. Results demonstrated that identified germplasm for different agronomical characters in phenotypically divergent sources would help in pre-breeding and breeding programs.

Chandra and Nilanjaya (2016) assessed 25 rice genotypes to study the nature and magnitude of genetic diversity under aerobic and normal transplanted condition and reported that there was no formal relationship between geographical diversity and genetic diversity. The genotypes were grouped into six clusters on the basis of D^2 statistics. The genotypes in cluster III and cluster VI exhibited maximum inter cluster distance. Peroxidase activity in leaves, relative water content and grain yield per plot were observed as the major contributors to the genetic diversity under aerobic as well as normal conditions.

Kumari *et al.* (2016) studied genetic divergence among 24 rice genotypes with 13 yield attributing traits and grouped them into 5 clusters primarily based on similarities in performances. Result demonstrated that harvest index and number of spikelets per panicle contributed maximum towards the total divergence, indicating that these traits might be given priority during selection of parents as well as segregating generations.

Khokhar and Sarial (2016) studied nature and magnitude of genetic diversity among 25 rice genotypes under aerobic and transplanted conditions for 12 quantitative traits. The range of D^2 values and the maximum divergence showed that clustering pattern was different under both the two production systems. Genotypes were grouped into 6 clusters each under aerobic and transplanted conditions respectively, yet their members were different. Plant

height and days to flowering was observed as highest contributor towards divergence under aerobic and transplanted condition respectively.

Pandey and Anurag (2015) assessed nature and magnitude of genetic divergence among 40 rice genotypes. On the basis of D^2 values genotypes were grouped into seven clusters. The composition of clusters indicated nonexistence of correspondence between genetic diversity and geographical distribution. Plant height biological yield and 1000 seed weight contributed considerably toward total divergence. Maximum inter-cluster distance was noticed between cluster II and VII.

Kumar *et al.*, (2014) studied genetic diversity among 23 rice genotypes with 10 quantitative traits using Mahalanobis D^2 statistics and grouped them into five clusters. Inter cluster distances were found to be higher than intra cluster distances which depicted wide genetic diversity among the genotypes. Clustering pattern did not show any association between the morphological characters and the origin of the cultivars. 1000 grain weight exerted maximum contribution towards total genetic diversity.

Nikhil and Rangare (2012) screened 40 rice genotypes to estimate genetic divergence using Mahalanobis D^2 statistics for 13 agro-morphological traits. Genotypes were grouped into seven clusters and cluster I was the largest with 12 genotypes. There was no relationship observed between clustering pattern and geographic distribution. Results demonstrated that traits like biological yield/hill, days to maturity and spikelet/panicle contributed maximum in the formation of clusters.

Pratap *et al.* (2012) evaluated 104 rice accessions to determine genetic divergence and grouped them into eleven distinct clusters. Cluster IV was observed the largest with 21 genotypes. Clustering pattern showed lack of any relationship between geographic origin and genetic diversity. Maximum inter cluster distances were observed between cluster VI and cluster X. The crossing between superior genotypes of these clusters may provide desirable segregants for developing high yielding rice varieties.

Thayumanavan *et al.* (2009) assessed 26 rice genotypes to obtain information regarding genetic diversity using Mahalanobis D^2 statistics. The genotypes were grouped into 13 clusters on the basis of D^2 values. Geographical origin was not found to be a good parameter of genetic divergence. The intra cluster distance in cluster I and inter cluster distances between cluster II and III was recorded maximum. Multivariate analysis showed that number of grains per panicle and days to first flower had contributed maximum towards total genetic divergence.

CHAPTER-III

MATERIALS AND METHODS

The experiment was conducted during *kharif* 2020 at research farm of Rice Research Station, Kaul, a regional research station of Chaudhary Charan Singh Haryana Agricultural University, Hisar. The experimental site is situated at latitude 29°51' N, longitude 76° 39' E and altitude 230.87 m above mean sea level. It comes under sub-tropical region of North West India and is located in North Eastern part of Haryana state in Kaithal district, which is the heart of the rice-growing region, called 'Rice Bowl of Haryana'. The soil was clay loam in texture.

3.1 Experimental Materials:

The experimental materials consisted of forty-eight (48) rice genotypes (24 basmati and 24 non-basmati genotypes) comprising traditional basmati (12 genotypes), evolved basmati (12 genotypes) and non- basmati genotypes of early and mid-early group (12 genotypes each) collected from CCS HAU Rice Research Station, Kaul. The detail of genotypes is given in Table 3.1.

Table 3.1: List of genotypes used in the present investigation

Basmati Genotypes				Non-Basmati Genotypes			
Traditional Basmati		Evolved Basmati		Early Duration		Mid Early Duration	
1.	Basmati 370	13.	HB-1	25.	IR 14L521	37.	HKR 16-35
2.	Taraori Basmati	14.	HB-2	26.	CR Dhan 201	38.	HKR 16-58
3.	CSR-30	15.	PB-1	27.	PAU 7551-1-1-1	39.	HKR 14-30
4.	Type - 3	16.	PB-1121	28.	RP 5591-123-16-2	40.	PR-126
5.	HKR 15-482	17.	PUSA 1557-06-08-126-162-156	29.	IR 99784-255-91-1-5	41.	HKR 16-29
6.	Super Basmati	18.	Pusa 1718-14-2-150	30.	IR 95780-43-1-1-1	42.	HKR 17-33
7.	HKR 03-408	19.	Pusa 1656-10-705	31.	IR 98976-20-1-2-2	43.	HKR 17-34
8.	HKR 15-483	20.	HKR 15-455	32.	IR 99784-11-8-1-2	44.	HKR 17-35
9.	HKR 15- 488	21.	HKR 14-410	33.	HKR 17-44	45.	RDR-1158
10.	HKR 15-487	22.	HKR 06-443-66	34.	NVSR-2107	46.	NVSR-474
11.	HKR 08-408	23.	HKR 16-459	35.	HKR-48	47.	IR-64
12.	HKR 06-434	24.	HKR 16-464	36.	GOVIND	48.	HKR-47

3.2 Layout of experiment:

Genotypes were sown under two production systems viz; aerobic (direct seeded) and irrigated (transplanted) conditions (fig. 1) in three replications using randomized block design (RBD). Plot size consisted of single row (5m long) of each genotype with plant to plant spacing of 15 cm in each row. A spacing of 20 cm was kept between rows. Under aerobic condition, the seeds were sown by dibbling on 20 June, 2020 in the well-prepared seed bed in dry field. The field was irrigated lightly just after sowing to ensure proper germination and subsequent irrigation at an interval of 5-7 days were applied in experimental plot to maintain

sufficient moisture in the soil. For irrigated (transplanted) condition, nursery was sown on raised nursery bed, the same day (20 June, 2020) as for direct seeding. Thirty days old seedlings were transplanted in the puddled field and the crop was irrigated frequently (3-5 cm) to maintain submerged condition throughout the season. Recommended cultural practices each for direct seeded and transplanted crop were followed to raise a healthy crop.

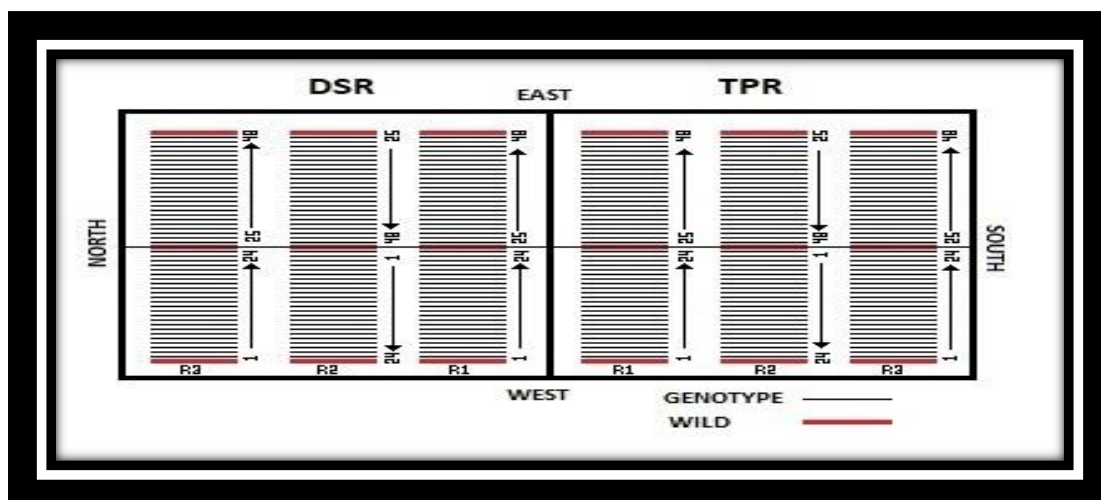


Fig. 1: Layout of the field

3.3 Observations:

The observations from five randomly selected plants were recorded for each genotype under aerobic and transplanted conditions and replicated data for each genotype were recorded and analysed for following characters:

Morpho-physiological and yield traits

1. Days to 50 % flowering:

Dates were recorded when 50 per cent of plants of a genotype showed flowering i.e. panicle emergence. Days were then counted from the day of sowing to the day when 50% flowering occurred.

2. Days to maturity:

Date on which 75 % plants matured in each replication of a genotype was recorded. Then numbers of days to maturity were determined from day of sowing to the day of maturity

3. Plant height (cm):

Height of main culm from base to tip of panicle including awns was measured in centimetres.

4. Number of tillers/plant:

Tillers bearing fully developed panicle of selected five plants from each row of a genotype were counted at the time of harvest.

5. Panicle length (cm):

The length of five main panicles (in cm) from each row of a genotype was measured from base/node of panicle to its tip at time of harvest.

6. Number of grains/panicle:

The total number of filled grains in each of five randomly selected panicles from each row were counted and averaged.

7. 1000 seed weight (g):

Thousand grains from each row of a genotype were taken and their weight was recorded in grams.

8. Biological yield (g)/plant:

Dry weight of above ground part of the selected plants after drying, was recorded in grams and averaged.

9. Grain yield (g)/plant:

The grain yield of selected plants in each row was recorded after threshing and was determined at 14 % moisture level and averaged.

10. Harvest Index:

After recording the grain yield as well as the biological yield/plant, the harvest index was calculated as:

$$HI(\%) = \frac{\text{Grain yield}}{\text{Biological yield}} \times 100$$

11. Root length (cm):

Root length of five selected plants from each row of a genotype was measured in centimetres from coleoptilar node to the longest terminal root tip and averaged.



Fig. 2: Roots of rice plant



Fig. 3: Root length

12. Root volume (ml³):

Volume of the root was measured by water displacement method. Freshly uprooted roots of five selected plants from each row were dipped into water filled measuring cylinder. Water level rise up from the initial to final level was the volume of the roots.

13. Root fresh weight (g)/plant:

Roots of the five randomly selected plants from each row were uprooted; adhered soil particles were removed by washing and fresh weight was taken in grams.

14. Root dry weight (g)/plant:

Roots of the selected plants from each row were oven dried till a constant weight was obtained and then their weight was recorded.

15. Ratio of root fresh weight and dry weight:

It was calculated by a ratio of root fresh weight to dry weight and expressed in percentage.

Quality Traits:

1. Hulling %:

A sample (25g) of rough rice (paddy or grains with husk) obtained from threshing of five selected plants was dehusked (removal of husk or hull) with the help of a dehusker. The weight of dehusked or hulled grains (called kernels or brown rice) was recorded. Hulling % was determined using following formula and expressed in % as:

$$\text{Hulling(\%)} = \frac{\text{Weight of hulled or brown rice (g)}}{\text{Weight of paddy (g)}} \times 100$$

2. Milling %:

Brown rice sample obtained after dehushing was subjected to milling (removal of brown layer or rice bran from kernel) with the help of a miller (Satake polisher) and weight after milling was recorded. Milling percentage was computed as:

$$\text{Milling(\%)} = \frac{\text{Weight of milled rice (g)}}{\text{Weight of paddy}} \times 100$$



Fig. 4: Brown rice (dehusked rice)



Fig. 5: Milled rice

3. Kernel length (mm) :

Length of milled grains or kernel was measured in mm with the help of Vernier Calliper.



Fig. 6: Kernel length



Fig. 7 Kernel breadth

4. Kernel breadth (mm):

Breadth of milled grains or kernels was also measured in mm by Vernier Calliper.

5. Ratio of kernel length and breadth:

Kernel length breadth ratio (KLBR) was calculated using following formula

$$KLBR = \frac{\text{Mean length of kernel}}{\text{Mean breadth of kernel}}$$

6. Head rice recovery (HRR)%:

After milling, the whole rice kernels (kernels having 75 to 100% of its original length) were separated from the milled sample and their weight was recorded.

$$HRR \% = \frac{\text{weight of full rice (g)} + \frac{3}{4} \text{ broken rice}}{\text{weight of paddy(g)}} \times 100$$

3.4 Statistical analysis:

Statistical analysis was done by software OPSTAT and INDOSTAT. The data of all the parameters of each genotype from each replication was subjected to statistical analysis using following methods.

3.4.1 Analysis of variance:

The analysis of variance (ANOVA) was carried out to test the significance of difference among genotypes by F-test. ANOVA helps in separating the total variance into three components viz., replication, treatment and error. Analysis of variance was carried out according to Fisher (1925) under the fixed effective model given below:

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

Where,

μ = Overall mean

Y_{ij} = phenotypic observation of the i_{th} treatment and in j_{th} replication

g_i = effect of i_{th} treatment ($i = 1, 2, 3, 4, \dots, 48$)

r_j = effect of j_{th} replication ($j = 1, 2, 3, 4, 5, 6$)

e_{ij} = Random error associated with i_{th} treatment and j_{th} replication

Here,

$i = 1, 2, 3, 4, \dots, 48$

$j = 1, 2, \dots, 6$

Null hypothesis,

$H_0: g_1 = g_2, \dots, 48$

The sum of squares was arranged in following manner to test the significance between treatments.

Source of variation	d.f.	S.S.	M.S.S.	Variance ratio/F- value (calculated)
Replication	(r-1)	SSr	SSr/(r-1) = MSr	
Treatment	(t-1)	SSt	SSt/(t-1) = MSt	MSt/EMS
Error	(r-1) (t-1)	SSe	SSe/(r-1) (t-1) = EMS	
Total	(rt-1)	SST		

Where,

r = Number of replications

t = Number of treatments

SSr = Sum of squares due to replications

SSt = Sum of squares due to treatments

SSe = Sum of squares due to error

SST = Total sum of squares

ESS = Error sum of squares

MSr = Mean sum of squares due to replications

MSt = Mean sum of squares due to treatments

EMS = Error mean sum of squares

Test of significance:

If the variance ratio (calculated F) was larger than the F value at 5 % and 1 % level of significance, the difference among the different genotypes in terms of various characters was considered to be significant and highly significant, respectively and if it was lesser than the F-value, it was considered non-significant.

3.4.2 Variability parameters:

1) Mean:

The mean value of each character was computed by dividing the sum of all the observations in a replication by the corresponding number of observations.

$$\text{Mean} = \frac{\sum X}{N}$$

Where;

$\sum X$ = Sum of all the observations for each character in a replication

N = Total number of observations

2) Range:

It was calculated as the difference between the highest and lowest mean value for each character.

$$\text{Range} = X_n - X_t$$

Where;

X_n = highest mean value of the character

X_t = lowest mean value of the character

3) Standard error:

Standard error of mean was calculated from analysis of variance as

$$SE(m) = \sqrt{\frac{2EMS}{r}}$$

Where,

$SE(m)$ = Standard error of mean

r = Number of replications

4) Critical difference:

Critical difference was calculated by using following formula:

$$CD = \sqrt{2EMS \div r} \times t\text{-value at 5\%}$$

Where,

$t\text{-value}$ = table value of error difference at 5% of level of significance

r = number of replications

EMS = error mean sum of squares

Component of variance:

a) Genotypic variance (V_g or σ^2_g):

The genotypic variance is the variation in phenotype due to differences genotype. The formulae used for calculating the extent of genotypic variance was as follows:

$$\sigma^2_g = \frac{Mst - EMS}{\text{number of replications (r)}}$$

b) Environmental or error variance (VE or σ^2_e):

The error variance is the variation due to environmental factors.

$$\sigma^2_e = \text{EMS}$$

c) Phenotypic variance (VP or σ^2_p):

Phenotypic variance denotes the sum total of the variance available in a population for particular character and calculated by following formula

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

Where;

σ^2_g = genotypic variance

σ^2_e = error variance

3.4.3 Co-efficient of variability:

The co-efficient of phenotypic and genotypic variability was calculated according to the formula given by Burton and De vane (1953).

Genotypic co-efficient of variability (GCV):

$$\text{GCV}\% = \frac{\sigma_g}{\bar{X}} \times 100$$

Phenotypic co-efficient of variability (PCV):

$$\text{PCV}\% = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = general mean

σ_g = genotypic variance

σ_p = phenotypic variance

Categorization of co-efficient of variation according to Burton and De vane (1953):

Range	Classification
0 to 10 %	Low
10 to 20 %	Moderate
More than 20 %	High

3.4.4 Heritability in broad sense (h^2):

Heritability measures fraction of the phenotypic variability that can be attributed to genetic variation. It was calculated according to the formula suggested by Lush (1949) as:

$$h^2 = \frac{V_g}{V_p} \times 100$$

Where,

h^2 = heritability in broad sense

V_g = genotypic variance

V_p = phenotypic variance

The heritability was grouped as low, moderate and high as proposed by Robinson *et al.* (1949).

Range	Classification
0 - 30 %	Low
30 - 60 %	Moderate
60 % and above	High

3.4.5 Genetic advance:

Genetic advance is the enhancement in mean genotypic value of selected plants over the parental population. The estimates of genetic advance were calculated by the formula given by Johnson *et al.* (1955).

$$GA = h^2 \times \sigma_p \times K$$

$$\text{Variance} = K \times \sigma_p \frac{\sigma^2_g}{\sigma^2_p}$$

Where,

h^2 = Heritability in broad sense

σ^2_p = Phenotypic standard deviation

K = Selection differential at 5 per cent intensity i.e., 2.06 which is a constant

Further the genetic advance as per cent of the mean (GA %) was calculated by using the following formula:

$$\text{Genetic advance as percent of mean(\%)} = \frac{GA}{\bar{X}} \times 100$$

The range of genetic advance is categorized as proposed by Johnson *et al.* (1955)

Range	Classification
0 to 10 %	Low
10 to 20 %	Moderate
More than 20 %	High

3.4.5 Correlation co-efficient analysis:

Correlation co-efficient is a statistical measure of the strength of relationship between the relative movements of two variables. It was computed according to the formula given by Al jibouri *et al.* (1958) which is as follows:

$$\text{Phenotypic correlation co-efficient (r}_{pxy}) = \frac{\sigma_{pxy}}{\sqrt{\sigma^2_{px} \cdot \sigma^2_{py}}}$$

Where,

r_{pxy} = Phenotypic correlation coefficient between X & Y variables

σ_{px} = Phenotypic co-efficient of variance of X variable

σ_{py} = Phenotypic co-efficient of variance of Y variable

σ_{pxy} = Phenotypic co-efficient of co-variance of X & Y variables

$$\text{Genotypic correlation co-efficient}(r_{gxy}) = \frac{\sigma_{gxy}}{\sqrt{\sigma_{gx}^2 \cdot \sigma_{gy}^2}}$$

Where,

r_{gxy} = Genotypic correlation coefficient between X & Y variables

σ_{gx} = Genotypic co-efficient of variance of X variable

σ_{gy} = Genotypic co-efficient of variance of Y variable

σ_{gxy} = Genotypic co-efficient of co-variance of X & Y variables

To check the significance of correlation coefficient, the calculated values were compared with table value of correlation coefficient at (n-2) degree of freedom at 5% and 1% level of significance. If the calculated value of correlation coefficient is more than tabulated value, it is considered as significant

Scales for correlation coefficients [Searle, 1965]:

1. > 0.65 : Very strong
2. 0.50 to 0.64 : Moderately strong
3. 0.30 to 0.49 : Moderately weak
4. < 0.30 : Very weak

3.4.6 Path co-efficient analysis:

Path coefficient analysis has been widely used in crop breeding programs to determine the nature of relationships between grain yield and its contributing components and to identify the components with significant effects on yield to be used as selection criteria. Genotypic correlation coefficients were used to find out path co-efficient analysis. Path coefficients were calculated according to Dewey and Lu (1959).

$$r_{ny} = P_{ny} + r_{n2}P_{2y} + r_{n3}P_{3y} + \dots + r_{nx}P_{xy}$$

Where,

r_{ny} = Correlation coefficient between the character and yield

P_{ny} = Path coefficient between the character and yield

$r_{n2}, r_{n3}, \dots, r_{nx}$ = Represent correlation coefficient between that character and yield component in turn

The following correlation matrix was formed:

$$\begin{matrix} \text{Matrix A} & & \text{Matrix B} & & \text{Matrix C} \\ \begin{bmatrix} r_{1y} \\ r_{2y} \\ \vdots \\ r_{ny} \end{bmatrix} & = & \begin{bmatrix} r_{11} & r_{12} & r_{13} & \dots & r_{1n} \\ r_{21} & r_{22} & r_{23} & \dots & r_{2n} \\ \vdots & \vdots & \vdots & \dots & \vdots \\ \vdots & \vdots & \vdots & \dots & \vdots \\ r_{n1} & r_{n2} & r_{n3} & \dots & r_{nn} \end{bmatrix} & \times & \begin{bmatrix} P_{1y} \\ P_{2y} \\ \vdots \\ P_{ny} \end{bmatrix} \end{matrix}$$

Where,

r_{12} = r_{21} or so on

r_{1y} = Correlation between first component character and yield and so on

Path coefficients (P_{jy}) were obtained as follows:

$$P_{jy} = (B)^{-1} \times (A)$$

The indirect effects for a particular character through other characters were obtained by multiplication of direct Path and particular correlation coefficient between those two characters, respectively.

$$\text{Indirect effects} = r_{ij} \times P_{jy}$$

Where,

$$i = 1 \dots \dots \dots n$$

$$j = 1 \dots \dots \dots n$$

$$P_{jy} = P_{1y} P_{2y} P_{3y} \dots \dots \dots P_{ny}$$

$$r_{ij} = \text{Correlation between two independent characters}$$

The residual factors i.e., the variation in yield unaccounted for those associated was calculated from the following formulae.

$$\text{Residual factor (x)} = \sqrt{(1 - R^2)}$$

Where,

$$R^2 = P_{1y}r_{1y} + P_{2y}r_{2y} + \dots \dots \dots + P_{ny}r_{ny}$$

R^2 , is squared multiple correlation coefficients and is the amount of variation in yield that can be accounted for by the yield component characters.

Scales for Path Coefficients [Lenka and Mishra, 1973]

1. 0.00-0.09 : Negligible
2. 0.10-0.19 : Low
3. 0.20-0.29 : Moderate
4. 0.30-1.00 : High
5. More than 1.00 : Very high

3.4.7 D^2 statistic (Mahalanobis, 1936):

Mahalanobis D^2 statistic was used for evaluating the genotypic divergence among the forty-eight genotypes. The D^2 statistics between the genotypes as estimated from the sample on the basis of 'P' character is,

$$D^2P = \sum_{i=1}^p \sum_{j=1}^p (\lambda_{ij}) \sqrt{j} \sqrt{i}$$

Where,

$$ij = \text{Reciprocal of the common dispersion matrix}$$

$$i = \text{Difference in mean values for the } i^{\text{th}} \text{ character of the two populations}$$

$$j = \text{Difference in the mean values for the } j^{\text{th}} \text{ character of the two populations}$$

Similarly, error variance, covariance matrix was calculated. The correlated variables were changed into uncorrelated variables by pivot condensation method as given by Rao

(1952). The actual values of D^2 between any two variables were obtained by squaring and adding differences corresponding to the transformed mean values of the two genotypes.

Clustering pattern:

There is no specific standard for making the clusters because cluster is not a precisely defined term. Two genotypes belonging to the different cluster should show higher D^2 value than those belonging to similar clusters. D^2 values of all possible combinations in the matrix form were organized in ascending order of magnitude and clustering was done according to the method suggested by Toucher's (Rao, 1952). Initially, the most closely related genotypes were taken and further third genotype was located on the basis of smaller average D^2 values with the first two genotypes. Thereafter, the fourth genotype was taken having the smallest average D^2 value from the first three genotypes. Due to addition of another genotype, a relative change in D^2 values within a cluster was observed and computed. The new genotypes were added continuously till a D^2 value becomes promptly high; thereafter this genotype was not included in formation of group. Then, first cluster genotypes were excluded and remaining genotypes were considered for group constellations.

Intra and inter cluster distances:

The intra cluster D^2 value was calculated as the sum of $n(n-1)/2$. Zero intra cluster D^2 values were observed by single genotype. All possible D^2 values of two clusters were added and then divided by $n_1 \times n_2$ for computing inter-cluster D^2 values where n_1 represent number of genotypes in first cluster and n_2 represent number of genotypes in second clusters. The square roots of respective D^2 values between genotypes of a cluster and between genotypes of two different clusters were used for estimation of intra and inter cluster distances.

Cluster mean value:

For a particular character cluster mean is the summation of genotypes mean values in a cluster divided by total number of genotypes in that particular cluster.

CHAPTER-IV

EXPERIMENTAL RESULTS

The results of the present experiment entitled “**Characterization for yield and quality traits under aerobic and transplanted conditions in Rice (*Oryza sativa* L.)**” conducted to evaluate 48 genotypes (basmati and non-basmati) to assess genetic variability, heritability, genetic advance, character association, direct and indirect effects of different yield attributing traits on yield and genetic divergence are presented under following heads:

4.1 Analysis of variance

4.2 Genetic variability, heritability and genetic advance

4.3 Correlation co-efficient analysis

4.4 Path co-efficient analysis

4.5 Genetic divergence analysis (D^2 statistics)

4.1 Analysis of variance

Analysis of variance (ANOVA) is a collection of statistical models and their associated estimation procedures (such as the variation among and between the groups) used to analyse the differences among the means. The analysis of variance for 21 yield and quality traits showed that mean sum of squares due to genotypes were highly significant for all the traits under aerobic and transplanted conditions, indicated the presence of considerable genetic variability among the genotypes which can be further exploited in future breeding programmes. Results are given in table 4.1 and 4.2 for basmati and non-basmati genotypes respectively.

4.2 Genetic Variability, heritability and genetic advance

The extent to which the observed variations were due to genetic factors, the mean, range, genotypic co-efficient of variability (GCV), phenotypic co-efficient of variability (PCV), heritability (broad sense) and genetic advance as percent of mean were analysed under aerobic and transplanted conditions for all the traits (Table 4.3 and 4.4) and represented graphically in Fig 8 to 15. Results indicated the presence of variability among the genotypes for all the traits under study. Traits wise description was given under the following subheads:

4.2.1 Grain yield per plant (g)

Under aerobic condition in basmati genotypes, genotype yielded as low as 11.87 g/plant and as high as 19.83 g/plant with general mean 15.47 g/plant whereas in transplanted condition, it varied from 12.3 g/plant to 21.89 g/plant with grand mean 16.60 g/plant for basmati genotypes. Grain yield/plant had moderate GCV (13.09%, 12.59 %), PCV (15.47%, 14.12%) and high heritability (71.66 %, 79.48 %) coupled with high genetic advance as percent of mean (22.83 %, 23.12 %) under both the production system (aerobic and transplanted).

Table 4.1 Analysis of variance for yield and quality traits in Basmati Genotypes

Sr. No.	Characters	Mean sum of squares			Mean sum of squares		
		Aerobic condition			Transplanted condition		
		Replication (df: 2)	Treatment (df: 23)	Error (df: 46)	Replication (df: 2)	Treatment (df: 23)	Error (df: 46)
1	Grain yield/plant (g)	2.441	13.902**	1.619	5.733	12.222**	0.968
2	Days to 50% Flowering	1.097	111.028**	1.199	0.931	96.144**	1.423
3	Days to maturity	1.514	82.889**	1.412	0.500	82.986**	1.572
4	Plant height (cm)	30.262	800.946**	7.170	115.790	875.661**	51.445
5	Panicle length (cm)	0.134	2.857**	0.964	1.864	2.425**	0.633
6	Number of tillers/plant	1.321	5.669**	0.586	4.360	3.332**	0.682
7	Number of grains/panicle	60.177	663.639**	22.640	22.446	594.043**	18.546
8	Test weight (g)	3.222	18.834**	1.612	0.193	29.375**	0.090
9	Biological yield/plant (g)	1.806	65.556**	15.309	262.954	61.844**	28.964
10	Harvest index %	0.293	56.105**	3.616	89.149	32.179**	13.805
11	Hulling %	9.973	3.398**	1.713	3.591	1.685**	0.694
12	Milling %	17.144	8.030**	2.564	0.331	2.585**	0.843
13	Head rice recovery %	11.522	52.663**	19.446	2.791	44.777**	11.105
14	Kernel length (mm)	0.004	0.463**	0.005	0.012	0.471**	0.004
15	Kernel breadth (mm)	0.001	0.031**	0.001	0.001	0.032**	0.001
16	Kernel length breadth ratio	0.006	0.155**	0.006	0.016	0.310**	0.009
17	Root length (cm)	27.886	5.347**	0.838	27.886	5.347**	0.838
18	Root fresh weight (g)	50.972	26.862**	6.397	75.648	51.090**	5.159
19	Root volume (ml)	30.832	26.553**	10.699	63.681	33.616**	5.829
20	Root dry weight (g)	1.217	2.229**	0.200	1.217	2.229**	0.200
21	Root fresh and dry weight ratio	0.560	3.835**	0.672	1.304	1.366**	0.370

** Significant at 1 % level

Table 4.2 Analysis of variance for yield and quality traits in Non-basmati Genotypes

Sr. No.	Characters	Mean sum of squares			Mean sum of squares		
		Aerobic condition			Transplanted condition		
		Replication (df: 2)	Treatment (df: 23)	Error (df: 46)	Replication (df: 2)	Treatment (df : 23)	Error (df: 46)
1	Grain yield/plant (g)	4.916	30.662**	1.771	26.727	20.528**	1.689
2	Days to 50% Flowering	3.722	64.941**	1.171	1.722	85.389**	0.824
3	Days to maturity	1.500	57.835**	1.036	2.764	76.681**	1.619
4	Plant height (cm)	914.493	292.011**	57.719	11.536	144.111**	12.19
5	Panicle length (cm)	8.599	6.795**	1.001	1.451	6.009**	0.726
6	Number of tillers/plant	3.433	3.101**	1.204	13.065	2.317**	0.848
7	Number of grains/panicle	8.863	283.342**	24.507	199.503	395.320**	14.445
8	Test weight (g)	0.424	7.501**	1.016	5.295	7.563**	0.626
9	Biological yield/plant (g)	11.742	63.614**	5.831	93.356	109.136**	8.123
10	Harvest index %	1.710	34.408**	2.652	5.452	54.754**	3.752
11	Hulling %	11.556	3.956**	1.545	94.424	12.793**	3.66
12	Milling %	41.707	23.125**	10.123	64.505	13.386**	6.68
13	Head rice recovery %	12.001	50.005**	11.545	79.668	82.410**	6.903
14	Kernel length (mm)	0.009	0.296**	0.009	0.073	0.305**	0.008
15	Kernel breadth (mm)	0.001	0.010**	0.001	0.001	0.015**	0.002
16	Kernel length breadth ratio	0.001	0.091**	0.005	0.021	0.103**	0.006
17	Root length (cm)	20.082	5.456**	1.160	0.921	6.925**	2.794
18	Root fresh weight (g)	60.866	43.001**	4.551	23.878	25.029**	5.302
19	Root volume (ml)	76.925	38.854**	3.617	22.075	23.957**	5.285
20	Root dry weight (g)	1.966	3.816**	0.224	0.893	0.908**	0.217
21	Root fresh and dry weight ratio	0.356	5.541**	0.310	0.169	0.936**	0.446

** Significant at 1 % level

In non-basmati genotypes, grain yield per plant ranged from 19.33 g/plant to 33.87 g/plant with overall mean 24.14 g/plant under aerobic condition while in transplanted condition it was observed between 23.36 g/plant to 33.30 g/plant with grand mean 27.61 g/plant. Moderate GCV (12.85 %, 10.08), PCV (13.98 %, 11.23) and high heritability (84.45 %, 78.80%) were observed while value of genetic advance as percent of mean was noticed high (24.32 %) in aerobic condition and moderate in transplanted condition (16.60 %).

4.2.2 Days to 50 % flowering

Under aerobic condition days to 50% flowering varied from 82.67 days to 108.33 days with general mean 100.01 days while in transplanted condition, it ranged from 84.67 days to 109.67 days with grand mean 101.18 days for basmati genotypes. Low value of GCV (6.05 %, 5.55%), PCV (6.15 %, 5.68 %) and high heritability (96.83 %, 95.69 %) coupled with moderate genetic advance as percent of mean (12.26 %, 11.19 %) were recorded for days to 50 % flowering under both the production system (aerobic and transplanted).

In non-basmati genotypes, maximum and minimum days taken for 50% flowering recorded were 77 days to 95 days under aerobic condition with general mean 85.99 days whereas it varied between 77 days to 99 days with general mean 89.31 days in transplanted condition. Similar trend as low value of GCV (5.36 %, 5.95 %), PCV (5.51 %, 6.03 %) and high heritability (97.78 %, 97.16 %) coupled with moderate genetic advance as percent of mean (10.75 %, 12.07 %) were observed for days to 50 % flowering under both the production system (aerobic and transplanted).

4.2.3 Days to maturity

In basmati group, genotypes matured earliest and late took 122.33 days to 145 days under aerobic condition with general mean 138.78 days while in transplanted condition it was recorded between 122.67 days to 145.33 days with grand mean 139.83 days. Results indicated the presence of relative low value of GCV (3.76 %, 3.73%), PCV (3.85 %, 3.83 %) but high heritability (95.06 %, 94.52 %) along with low genetic advance (7.54 %, 7.46 %) under both the production system.

Under non-basmati genotypes, days to maturity varied from 111.33 days to 128.33 days under aerobic condition with general mean 118.29 days while in transplanted condition it ranged from 110.33 days to 128.33 days with overall mean 121.68 days. Similar results as basmati genotypes were observed having low value of GCV (3.67 %, 4.11%), PCV (3.78 %, 4.24 %) with high heritability (94.81 %, 93.92 %) coupled with low genetic advance (7.38 %, 8.21 %) under both the production system.

4.2.4 Plant height (cm)

In basmati genotypes, mean plant height varied between 93.56 cm to 151.99 cm with general mean 138.93 cm under aerobic condition whereas in transplanted condition it ranged from 98.37 cm to 163.92 cm with grand mean 138.93 cm. Plant height showed moderate

value of GCV (12.8 %, 11.99 %), PCV (12.97 %, 13.07 %) and high heritability (97.36 %, 84.23 %) coupled with high genetic advance as percent of mean (26.02 %, 22.67 %) in aerobic and transplanted condition respectively.

In non-basmati genotypes, plant height varied from 86.61 to 123.3 cm with general mean 108.60 cm under aerobic condition while in transplanted condition it ranged from 105.59 cm to 130.57 cm with overall mean 121.28 cm. Under aerobic condition plant height observed low GCV (8.17 %), moderate PCV (10.77 %), heritability (57.50 %) and genetic advance as percent of mean (12.76%), whereas in transplanted condition low GCV (5.78 %), PCV (9.57 %) high heritability (78.30 %) with low genetic advance as percent of mean (9.97 %) were recorded for non-basmati genotypes.

4.2.5 Panicle length (cm)

Under basmati genotypes, minimum to maximum panicle length recorded in between 25.13 cm to 28.94 cm under aerobic condition with grand mean 27.09 cm while in transplanted condition, it was observed between 26.21 cm to 29.15 cm with general mean 27.66 cm. Panicle length had low value of GCV (2.93 %, 2.79 %), PCV (4.66 %, 4.01 %), moderate heritability (39.55 %, 48.52 %) along with low genetic advance as percent of mean (3.80 %, 4.01 %) in aerobic and transplanted condition respectively,

In non-basmati genotypes, shortest and longest panicle was observed between 22.84 cm and 27.49 cm with general mean 25.28 cm in aerobic condition while in transplanted it ranged from 23.17 cm to 28.55 cm with general mean 26.42 cm. Panicle length showed low value of GCV (5.49, 5.02 %), PCV (6.77 %, 5.97 %) as well as genetic advance as percent of mean (9.18 %, 8.71 %) with high heritability (65.87%, 70.80 %) for panicle length in both the production system.

4.2.6 Number of tillers/plant

In basmati genotypes, number of tillers/plant varied from 9.16 to 14.31 with grand mean 12.55 in aerobic condition, while in transplanted condition it ranged from 10.71 to 13.80 with grand mean 12.47. Number of tillers/plant exhibited moderate GCV (10.37 %), PCV (12.04 %), high heritability (74.30 %) coupled with moderate genetic advance as percent of mean (18.42 %) under aerobic condition, whereas, low value of GCV (7.41 %), PCV (9.87 %) with moderate heritability (56.46 %) and genetic advance as percent of mean (11.47 %) were recorded in transplanted condition.

In non-basmati genotypes, number of tillers per plant ranged from 10.07 to 13.91 with general mean 12.56 under aerobic condition whereas in transplanted it varied from 10.2 to 13.93 with general mean 12.15.

Table 4.3 Mean, Range, Co-efficient of variation, Heritability and genetic advance as percent of mean for yield and quality traits in Basmati Genotypes

	Characters	MEAN		Range				Coefficient of variation %				Heritability %		GAM %	
	BASMATI			Max.	Min.	Max.	Min.	GCV		PCV					
		DSR	TPR	DSR		TPR		DSR	TPR	DSR	TPR	DSR	TPR	DSR	TPR
1	Grain yield/plant (g)	15.47	16.60	19.12	11.27	21.86	12.30	13.09	12.59	15.47	14.12	71.66	79.48	22.83	23.12
2	Days to 50% Flowering	100.01	101.18	108.33	82.67	109.67	84.67	6.05	5.55	6.15	5.68	96.83	95.69	12.26	11.19
3	Days to maturity	138.78	139.83	145.00	122.33	145.33	122.67	3.76	3.73	3.85	3.83	95.06	94.52	7.54	7.46
4	Plant height (cm)	129.56	138.93	151.99	93.56	163.92	98.37	12.80	11.99	12.97	13.07	97.36	84.23	26.02	22.67
5	Panicle length (cm)	27.09	27.66	28.94	25.13	29.15	25.96	2.93	2.79	4.66	4.01	39.55	48.52	3.80	4.01
6	Number of tillers/plant	12.55	12.68	14.31	9.16	14.59	10.71	10.37	7.41	12.04	9.87	74.30	56.46	18.42	11.47
7	Number of grains/panicle	82.51	82.93	111.35	66.61	115.33	64.77	17.72	16.87	18.63	17.67	90.42	91.18	34.70	33.19
8	Test weight (g)	24.78	25.14	29.13	21.13	32.67	21.07	9.67	12.42	10.94	12.48	78.08	99.09	17.60	25.46
9	Biological yield/plant (g)	42.08	44.25	54.15	32.83	54.65	40.77	9.63	7.16	13.32	13.66	52.25	27.45	14.34	7.73
10	Harvest index %	36.61	35.82	45.19	29.58	42.41	29.68	11.66	7.36	12.81	13.28	82.87	30.73	21.87	8.41
11	Hulling %	76.43	76.29	79.19	74.73	78.00	75.07	0.98	0.75	1.97	1.32	24.69	31.80	1.00	0.87
12	Milling %	65.15	69.38	68.71	61.42	71.21	68.00	2.05	1.09	3.19	1.71	41.55	40.78	2.73	1.44
13	Head rice recovery %	59.75	61.01	59.61	44.30	59.61	44.30	6.07	6.07	10.08	8.56	36.28	50.27	7.53	8.86
14	Kernel length (mm)	7.33	7.36	8.07	6.54	8.13	6.57	5.36	5.39	5.45	5.47	96.77	97.40	10.87	10.97
15	Kernel breadth (mm)	1.80	1.81	1.92	1.50	1.94	1.51	5.51	5.60	5.78	5.92	91.03	89.49	10.83	10.92
16	Kernel length breadth ratio	4.06	4.06	4.76	3.80	4.95	3.58	5.52	7.84	5.83	8.18	89.59	92.00	10.76	15.49
17	Root length (cm)	14.75	17.25	18.11	13.20	20.61	15.70	8.31	7.11	10.37	8.87	64.21	64.21	13.72	11.73
18	Root fresh weight (g)	24.79	22.00	29.86	20.11	29.73	14.59	10.35	17.79	14.40	20.57	51.61	74.80	15.31	31.69
19	Root volume (ml)	18.78	19.79	25.67	14.93	26.10	13.44	12.24	15.22	21.29	19.50	33.06	60.86	14.50	24.45
20	Root dry weight (g)	4.55	4.57	6.59	3.25	6.46	3.16	17.48	18.09	19.90	20.59	77.13	77.18	31.62	32.74
21	Root fresh and dry weight ratio	5.62	4.86	8.00	3.83	5.96	3.67	17.88	11.77	22.88	17.13	61.09	47.27	28.79	16.67

Table 4.4: Mean, Range, Co-efficient of variation, Heritability and genetic advance as percent of mean for yield and quality traits in Non-Basmati Genotypes

NO.	Characters	MEAN		Range				Coefficient of variation %				Heritability %		GAM %	
	NON-BASMATI			Max.	Min.	Max.	Min.	GCV		PCV					
		DSR	TPR	DSR		TPR		DSR	TPR	DSR	TPR	DSR	TPR	DSR	TPR
1	Grain yield/plant (g)	24.14	27.61	33.87	19.33	33.30	23.37	12.85	10.08	13.98	11.23	84.45	78.80	24.32	16.60
2	Days to 50% Flowering	85.99	89.31	95.00	77.00	99.00	77.00	5.36	5.95	5.51	6.03	94.78	97.16	10.75	12.07
3	Days to maturity	118.29	121.68	128.33	111.33	130.67	110.33	3.68	4.11	3.78	4.24	94.81	93.92	7.38	8.21
4	Plant height (cm)	108.60	121.28	129.22	86.61	131.99	105.59	8.17	5.47	10.77	6.18	57.50	78.30	12.76	9.97
5	Panicle length (cm)	25.28	26.42	28.81	22.84	28.81	23.17	5.49	5.02	6.77	5.97	65.87	70.80	9.18	8.71
6	Number of tillers/plant	12.56	12.15	14.00	10.07	13.93	10.20	6.29	5.78	10.72	9.56	34.45	36.60	7.61	7.20
7	Number of grains/panicle	113.44	131.66	125.00	96.73	153.73	102.13	8.37	8.64	9.49	9.12	77.88	89.78	15.22	16.87
8	Test weight (g)	26.42	26.46	30.13	22.47	30.13	22.47	5.57	5.76	6.75	6.49	68.04	78.69	9.46	10.52
9	Biological yield/plant (g)	52.94	54.95	63.67	45.46	66.82	42.57	8.29	10.56	9.46	11.77	76.76	80.56	14.96	19.53
10	Harvest index %	45.53	50.28	53.19	39.22	59.05	41.88	7.15	8.16	7.99	9.02	79.97	81.92	13.17	15.21
11	Hulling %	76.26	75.61	78.73	73.40	79.53	71.32	1.18	2.30	2.01	3.42	34.21	45.41	1.42	3.20
12	Milling %	64.36	64.67	69.08	60.38	68.72	61.43	3.22	2.31	5.89	4.61	29.98	25.08	3.64	2.38
13	Head rice recovery %	54.32	53.75	61.75	45.27	61.72	42.96	6.57	9.30	9.05	10.50	52.62	78.48	9.81	16.97
14	Kernel length (mm)	6.29	6.42	6.76	5.53	6.90	5.57	4.92	4.90	5.15	5.10	91.12	92.41	9.67	9.71
15	Kernel breadth (mm)	2.07	2.09	2.27	2.00	2.32	2.00	2.62	3.15	3.13	3.86	69.70	66.50	4.50	5.29
16	Kernel length breadth ratio	3.05	3.07	3.30	2.44	3.33	2.40	5.55	5.86	6.05	6.40	84.12	83.82	10.49	11.05
17	Root length (cm)	15.26	17.58	18.97	13.63	20.03	11.67	7.84	6.68	10.55	11.62	55.24	33.02	12.00	7.90
18	Root fresh weight (g)	22.84	24.74	35.57	18.30	30.48	16.08	15.45	11.35	17.99	15.42	73.80	54.14	27.35	17.20
19	Root volume (ml)	20.71	22.03	32.57	16.90	28.05	14.47	16.31	11.50	18.69	15.63	76.13	54.08	29.31	17.42
20	Root dry weight (g)	4.95	4.12	7.15	3.59	5.30	2.83	18.78	11.76	21.07	16.40	79.44	51.46	34.48	17.38
21	Root fresh and dry weight ratio	4.88	6.04	9.36	3.02	6.96	4.34	22.06	6.69	25.07	12.93	84.93	26.80	37.41	7.14

Under aerobic condition, number of tillers per plant showed low GCV (6.29 %) with moderate PCV (10.71 %) and heritability (34.45 %) along with low genetic advance as percent of mean (7.61%) whereas low GCV (5.78 %), PCV (9.56 %) with moderate heritability (36.96 %) and low genetic advance as percent of mean (7.2 %) were observed in transplanted condition.

4.2.7 Number of grains per panicle

In basmati genotypes, number of grains/panicle varied from 66.61 to 124.62 with general mean 82.51 under aerobic condition while in transplanted condition, it was found in between 64.77 to 127.27 with general mean 82.93. It had moderate GCV (17.72%, 16.87 %), PCV (18.63%, 17.67%) and high heritability (90.42 %, 91.18 %) coupled with high genetic advance as percent of mean (34.70 %, 33.19 %) under both the production system.

Whereas in non-basmati genotypes, number of grains per panicle varied from 96.73 to 152.73 with general mean 113.44 under aerobic condition while in transplanted condition it was observed in between 102.13 to 155.2 with grand mean 131.66. Number of grains/panicle showed low GCV (8.37 %, 8.64 %), PCV (9.49 %, 9.12 %) and high heritability (77.88 %, 89.78 %) coupled with moderate genetic advance as percent of mean (15.22 %, 16.87 %) for both the production system.

4.2.8 Test weight (g)

In basmati genotypes, test weight varied from 21.57 g to 29.13 g with general mean 24.78 g in aerobic condition while it was observed in between 21.06 g to 32.66 g with general mean 25.14 g under transplanted condition. Low GCV (9.67 %), moderate PCV (10.94 %), high heritability (78.08 %) with moderate genetic advance as percent of mean (17.60 %) were observed for test weight under aerobic condition, while moderate GCV (12.42 %), PCV (12.48 %), high heritability (99.09 %) coupled with high genetic advance as percent of mean (25.46 %) were observed in transplanted condition.

In non-basmati genotypes test weight ranged from 22.47 g to 30.13 g under aerobic as well as transplanted condition with general mean 26.42 g and 26.46 g for aerobic and transplanted condition respectively. Test weight showed low GCV (5.57 %, 5.73 %), PCV (6.75 %, 6.49%) and high heritability (68.04 %, 78.69 %) coupled with low (9.46 %) to moderate (10.52) genetic advance as percent of mean in aerobic and transplanted conditions respectively.

4.2.9 Biological yield/plant (g)

In basmati genotypes, biological yield per plant varied from 36.51 g to 54.15 g with general mean 42.08 g under aerobic condition while in transplanted it ranged from 40.77 g to 51.27g with overall mean 44.25 g. It exhibited low GCV (9.63 %), moderate PCV (13.32 %) and heritability (52.25 %) along with genetic advance as percent of mean (14.34 %) under aerobic condition, while low value of GCV (7.16 %), moderate PCV (13.66 %) and low

heritability (27.45 %) and genetic advance as percent of mean (7.73 %) were recorded in transplanted condition.

Moreover, in non-basmati genotypes it varied from 47.71 g to 63.37g with general mean 52.94 g in aerobic condition while under transplanted condition it was ranged in between 42.56 g to 66.82 g with general mean 54.95 g. Biological yield per plant showed low GCV (8.29 %), PCV (9.46 %), high heritability (76.76 %) with moderate genetic advance as percent of mean (14.96%) in aerobic condition, whereas moderate GCV (10.56 %), PCV (11.77 %), high heritability (80.56 %) and moderate genetic advance as percent of mean (19.53 %) were recorded in transplanted conditions.

4.2.10 Harvest Index %

Harvest index % was recorded in between 29.58 % to 45.19 % with general mean 36.61% under aerobic condition while it varied from 29.68% to 50.33% in transplanted condition with grand mean 35.82% for basmati genotypes. Moderate GCV (11.66%), PCV (12.81%) and high heritability (82.87 %) coupled with high genetic advance as percent of mean (21.87 %) was observed in aerobic condition while low GCV (7.36 %), moderate PCV (13.28 %) and heritability (30.73 %) with low genetic advance as percent of mean (8.41 %) were observed under transplanted conditions.

In non-basmati genotypes, harvest index % varied from 39.22 % to 53.19% under aerobic condition while 41.88 % to 59.15% under transplanted condition with general mean 45.53 % and 50.28 % in aerobic and transplanted conditions respectively. Harvest index % showed low GCV (7.15 %, 8.16 %), PCV (7.99%, 9.02 %) and high heritability (79.97 %, 81.2 %) coupled with moderate genetic advance as percent of mean (13.17 %, 15.21 %) was recorded under both the production system.

4.2.11 Hulling %

In basmati genotype, lowest and highest hulling % was recorded in between 74.73% to 79.17% under aerobic condition with general mean 76.43 % while it varied from 75.06% to 78% with general mean 76.29% under transplanted condition. Low GCV (0.98%), PCV (1.97 %), heritability (24.69 %) and genetic advance as percent of mean (1.00 %) as well as low GCV (0.75 %), PCV (1.32 %), moderate heritability (31.80 %) with low genetic advance as percent of mean (0.87 %) were observed in aerobic and transplanted condition respectively.

In non-basmati genotypes hulling % varied from 73.40% to 77.51% with general mean 76.26 % in aerobic condition and 72.2% to 78.4% in transplanted condition with over all mean 75.61 %. Hulling % showed low GCV (1.18 %, 2.30 %), PCV (2.01 %, 3.42 %) and moderate heritability (34.21 %, 45.41 %) coupled with low genetic advance as percent of mean (1.42 %, 3.2 %) in both production system.

4.2.12 Milling %

In basmati genotypes, milling % varied in between 61.42 % to 68.71% with general mean 65.15 % under aerobic condition whereas in transplanted condition it ranged from 68 % to 71.21% with general mean 69.38%. Low GCV (2.05 %, 1.09 %), PCV (3.19 %, 1.71 %) and moderate heritability (41.55 %, 40.78 %) with low genetic advance as percent of mean (2.73 %, 1.44 %) were observed under both the production system.

In non-basmati genotypes, milling % ranged from 60.74 % to 68.95% with general mean 64.36 % under aerobic condition while it varied from 61.42% to 68.72% under transplanted condition with general mean 64.67 %. Low GCV (3.22 %, 2.30), PCV (5.89 %, 4.61), heritability (29.97%, 25.08%) and low genetic advance as percent of mean (3.64 %, 2.38 %) were observed under both aerobic and transplanted conditions.

4.2.13 Head rice recovery %

In basmati genotypes, head rice recovery % varied from 44.30 % to 59.61% under both production systems with general mean 59.75 % and 61.01 % in aerobic and transplanted conditions respectively. Head rice recovery % in aerobic condition exhibited low GCV (6.07 %), moderate PCV (10.08 %) and heritability (36.28 %) with low genetic advance as percent of mean (7.53 %), while in transplanted condition it showed low GCV (6.07 %), PCV (8.56 %) and moderate heritability (50.27 %) with low genetic advance as percent of mean (8.86 %).

In non-basmati genotypes, head rice recovery % varied from 50.30 % to 61.75 % in aerobic condition while it ranged in between 42.95% to 61.71% under transplanted condition with general mean 54.32 % and 53.75 % under aerobic and transplanted conditions respectively. Low GCV (6.57 %), PCV (9.05%) and moderate heritability (52.62 %) coupled with low genetic advance (9.81 %) while low GCV (9.30%), moderate PCV (10.50 %) and high heritability (78.48 %) along with moderate genetic advance (16.97 %) was observed in aerobic and transplanted conditions.

4.2.14 Kernel length

In basmati genotypes, kernel length varied in between 6.54 mm to 8.23 mm in aerobic condition and 6.57 mm to 8.21 mm in transplanted condition with general mean 7.33 mm and 7.36 mm under aerobic and transplanted conditions respectively, while in non-basmati genotypes it varied from 5.53 mm to 6.76 mm in aerobic condition and 5.56 mm to 6.83 mm in transplanted condition with general mean 6.29 mm and 6.42 mm under aerobic and transplanted conditions respectively.

Low value of GCV (5.36 %, 5.39 %), (4.92 %, 4.90 %) and PCV (5.45%, 5.47 %), (5.15 %, 5.1 %) were observed under both production systems respectively for basmati and non-basmati genotypes. High heritability (96.77 %, 97.40 %), (91.12%, 92.41 coupled with moderate to low genetic advance as percent of mean (10.87 %, 10.97 %), (9.67 %, 9.71 %) were noticed for basmati and non-basmati genotypes under both the production system.

4.2.15 Kernel breadth

In basmati genotypes, kernels breadth varied from 1.71 mm to 1.92 mm under aerobic condition with general mean 1.80 mm while in transplanted condition it ranged from 1.5 mm to 1.91 mm with general mean 1.81 mm. Kernel breadth observed low value of GCV (5.51 %, 5.60 %), PCV (5.78%, 5.92 %) and high heritability (91.03 %, 89.49 %) coupled with moderate genetic advance as percent of mean (10.83 %, 10.92 %) in aerobic and transplanted condition respectively for basmati genotypes,

In non-basmati, kernel breadth varied from 2 mm to 2.27 mm with overall mean 2.07 mm in aerobic condition while in transplanted condition it was ranged in between 2 mm to 2.32 mm with general mean 2.09 mm. It showed low value of GCV (2.62 %, 3.15 %), PCV (3.13 %, 3.86 %) and low genetic advance as percent of mean (4.50 %, 5.29 %) but heritability (69.7%, 66.45 %) was observed high in both the production system.

4.2.16 Kernel length breadth ratio

In basmati genotypes, kernel length breadth ratio varied from 3.8 to 4.76 in aerobic condition and 3.64 to 4.95 in transplanted condition with grand mean 4.06 under both the production systems. Minimum and maximum kernel length breadth ratio recorded was 2.44 and 3.33 with general mean 3.05 and 3.07 under aerobic and transplanted condition respectively in non-basmati genotypes.

Under aerobic and transplanted production system for basmati and non-basmati genotypes respectively low value of GCV (5.52 %, 7.84 %), (5.55 %, 5.86 %), PCV (5.83%, 8.18 %) (6.05%, 6.40 %) and high heritability (89.59 %, 92.00 %), (84.12 %, 83.19 %) coupled with moderate genetic advance as percent of mean (10.76 %, 15.49 %), (10.49%, 11.05 %) were recorded.

4.2.17 Root length

Root length in basmati genotypes varied from 13.2 cm to 18.11 cm with grand mean 14.75 cm in aerobic condition whereas it ranged in between 15.7 cm to 20.61 cm under transplanted condition with over all mean 17.25 cm. It had low GCV (8.31 %), moderate PCV (10.37%) and high heritability (64.21 %) coupled with moderate genetic advance (13.72 %) under aerobic condition, whereas it showed low GCV (7.11 %), PCV (8.87%) and high heritability (64.21 %) along with moderate genetic advance as percent of mean (11.73 %) in transplanted condition.

Root length in non-basmati genotypes ranged from 13.63 cm to 18.97 cm with general mean 15.26 cm under aerobic condition while it lies in between 11.67 cm to 20.23 cm with grand mean 17.58 cm in transplanted condition. It exhibited low GCV (7.83 %, 6.68 %), moderate PCV (10.55 %, 11.62 %) and heritability (55.24 %, 33.02 %) in both the production

system but genetic advance as percent of mean was recorded moderate in aerobic and low in transplanted condition.

4.2.18 Root Fresh Weight

In basmati genotypes, root fresh weight varied between 20.11 g to 29.86 g and 14.59 g to 29.73 g with general mean 24.79 g and 22 g under aerobic and transplanted condition respectively. Moderate GCV (10.35 %), PCV (14.40 %) and heritability (51.61 %) coupled with genetic advance as percent of mean (15.31 %) were observed under aerobic condition while it had moderate GCV (17.79 %), high PCV (20.57 %) and high heritability (74.80 %) coupled with high genetic advance as percent of mean (31.69 %) under transplanted condition.

In non-basmati genotypes, root fresh weight ranged from 18.30 g to 35.57 g, 16.77 g to 30.48 g with grand mean 22.84 g and 24.74 g under aerobic and transplanted condition respectively. It had moderate GCV (15.45 %, 11.35 %) and PCV (17.99 %, 15.42 %) in both production environment whereas, high heritability (73.80 %) coupled with high genetic advance as percent of mean (27.35 %) was observed under aerobic condition while moderate heritability (54.14 %) along with moderate genetic advance as percent of mean (17.20 %) were recorded in transplanted condition.

4.2.19 Root Volume

Root volume varied from 14.93 ml³ to 23.6 ml³ with general mean 18.78 ml³ under aerobic condition while it ranged in between 13.44 ml³ to 26.1 ml³ with overall mean 19.79 ml³ in transplanted condition for basmati genotypes. It exhibited moderate GCV (12.24 %), high PCV (21.29 %) and moderate heritability (33.06 %) with genetic advance as percent of mean (14.50 %) under aerobic condition while it showed moderate GCV (15.22 %), PCV (19.50 %) and high heritability (60.86 %) coupled with high genetic advance as percent of mean (24.45 %) under transplanted condition.

In non-basmati genotypes, root volume varied from 16.9 ml³ to 32.57 ml³ with general mean 20.71 ml³ under aerobic condition while it ranged from 15.23 ml³ to 30.48 ml³ with general mean 22.03 ml³ in transplanted condition. It had moderate GCV (16.31 %, 11.50 %), PCV (18.69 %, 15.63 %) in both the production system whereas, it had high heritability (76.13 %) coupled with high genetic advance as percent of mean (29.31 %) in aerobic condition and moderate heritability (54.08 %) and genetic advance as percent of mean (17.42 %) in transplanted conditions for non-basmati genotypes.

4.2.20 Root Dry Weight

In basmati genotypes, root dry weight varied from 3.16 g to 6.46 g with over all mean 4.55 g under aerobic condition while it ranged in between 3.19 g to 6.49 g under transplanted condition with general mean 4.57g. It expressed moderate GCV (17.48 %), PCV (19.9 %) and high heritability (77.13 %) coupled with high genetic advance as percent of mean (31.62 %)

in aerobic condition while moderate GCV (18.09 %), high PCV (20.59 %) and high heritability (77.13 %) together with high genetic advance as percent of mean were noticed under transplanted condition.

Root dry weight ranged from 3.59 g to 7.15 g with general mean 4.95 in aerobic condition while 3.52 g to 5.3 g in transplanted condition with grand mean 4.12 g for non basmati genotypes. Moderate GCV (18.78 %), high PCV (21.07 %) and high heritability (79.44 %) along with high genetic advance as percent of mean (34.48 %) were observed under aerobic condition while it had moderate GCV (11.76 %), PCV (16.40 %), heritability (51.46 %) coupled with genetic advance as percent of mean (17.38 %) under transplanted condition for non basmati genotypes.

4.2.21 Root fresh weight and dry weight ratio

In basmati genotypes, root fresh and dry weight ratio varied from 3.83 to 8.0 in aerobic condition with general mean 5.62 while in transplanted condition it ranged from 3.64 to 5.88 with over all mean 4.86. Root fresh and dry weight ratio recorded moderate GCV (17.88 %), high PCV (22.88 %) and high heritability (61.09 %) coupled with high genetic advance as percent of mean (28.79 %) in aerobic condition while in transplanted condition, moderate GCV (11.77 %), PCV (17.13 %), heritability (47.27 %) and genetic advance as percent of mean (16.67 %) were observed.

In non-basmati genotypes, root fresh and dry weight ratio varied from 3.48 to 9.36 with grand mean 4.88 under aerobic condition whereas, it varied in between 4.34 to 6.96 with general mean 6.09 under transplanted condition. High value of GCV (22.06 %), PCV (25.07 %) and high heritability (84.93 %) along with high genetic advance as percent of mean (37.11%) were observed in aerobic condition while it had low GCV (6.69 %), moderate PCV (12.93 %) and low heritability and genetic advance as percent of mean under transplanted condition for non-basmati genotypes.

4.3 Character association analysis of basmati and non-basmati genotypes

Association studies reveals behaviour of one variable with respect to another and determine the component traits on which selection can be based for crop improvement. It reveals how a character responds to the change in another character. A positive value of correlation shows the changes of two variables are in the same direction i.e., the high value of one variable is associated with high value of other variable and vice- versa. Nature and extent of association studies of contributing traits would be helpful in developing suitable plant type, in addition to the improvement of yield a complex trait for which direct selection is not effective. In this study 21 characters including yield, morphological and quality traits had been investigated for their association. Results are presented in table 4.5, 4.6, 4.7 and 4.8 for both the production systems.

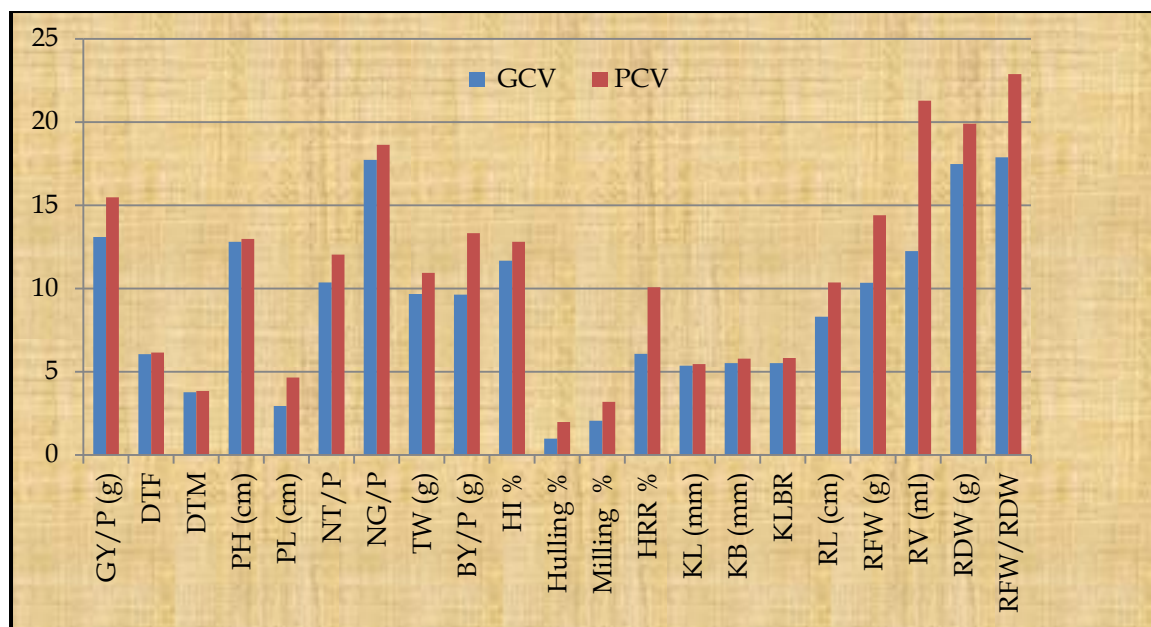


Fig. 8: GCV and PCV for morphological and quality traits of basmati genotypes under aerobic condition

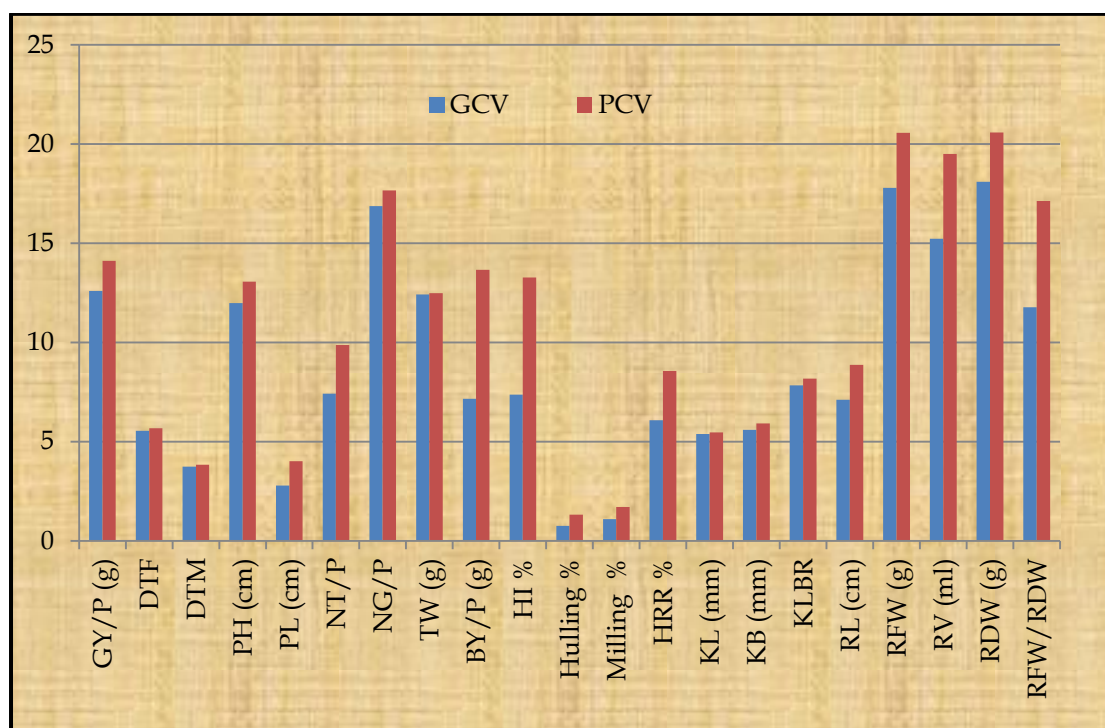


Fig. 9: GCV and PCV for morphological and quality traits of basmati genotypes under transplanted condition

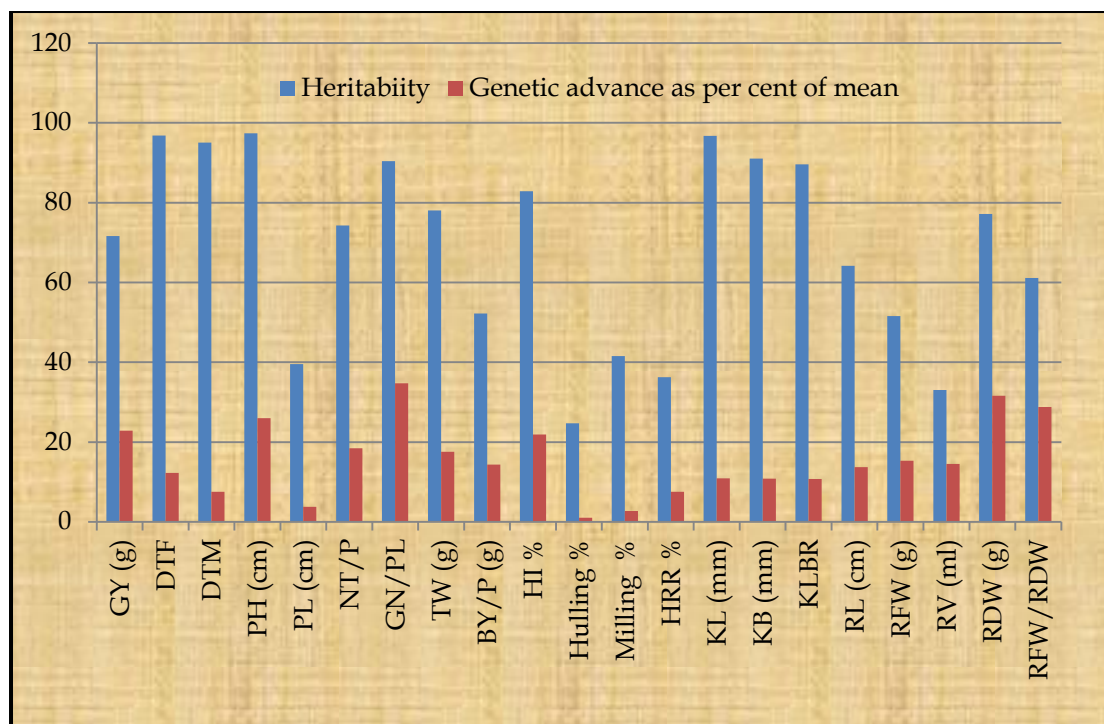


Fig. 10: Heritability and Genetic advance as per cent of mean for morphological and quality traits of basmati genotypes under aerobic condition

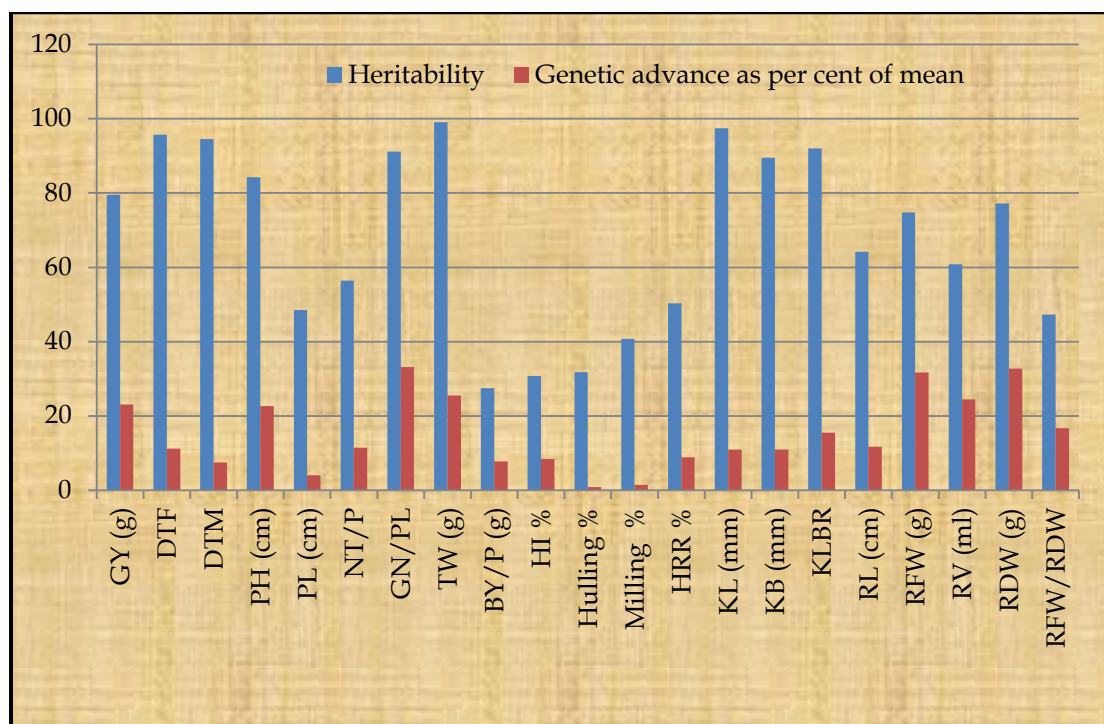


Fig. 11: Heritability and Genetic advance as per cent of mean for morphological and quality traits of basmati genotypes under transplanted condition.

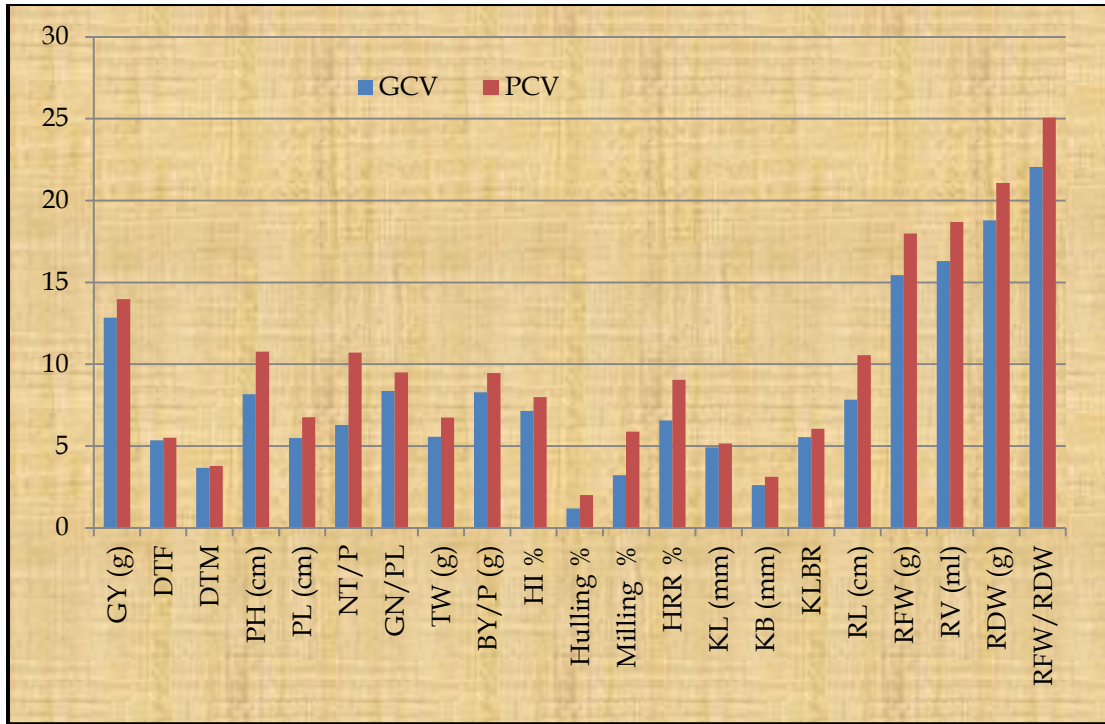


Fig. 12: GCV and PCV for morphological and quality traits of non-basmati genotypes under aerobic condition.

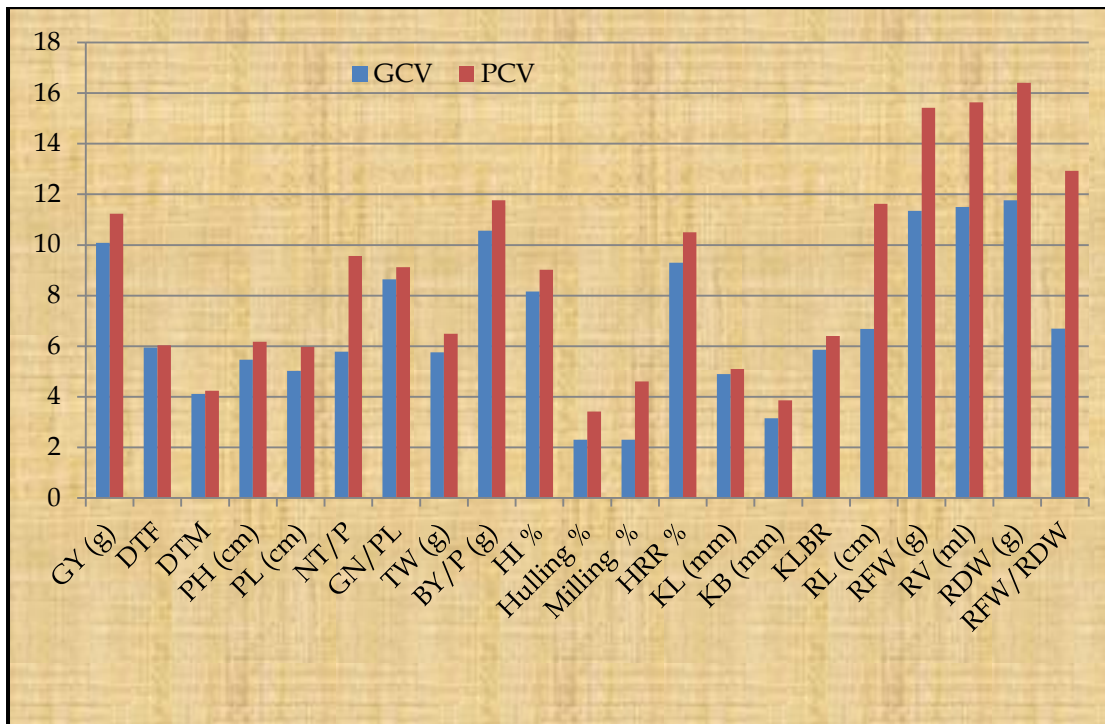


Fig. 13: GCV and PCV for morphological and quality traits of non-basmati genotypes under transplanted condition

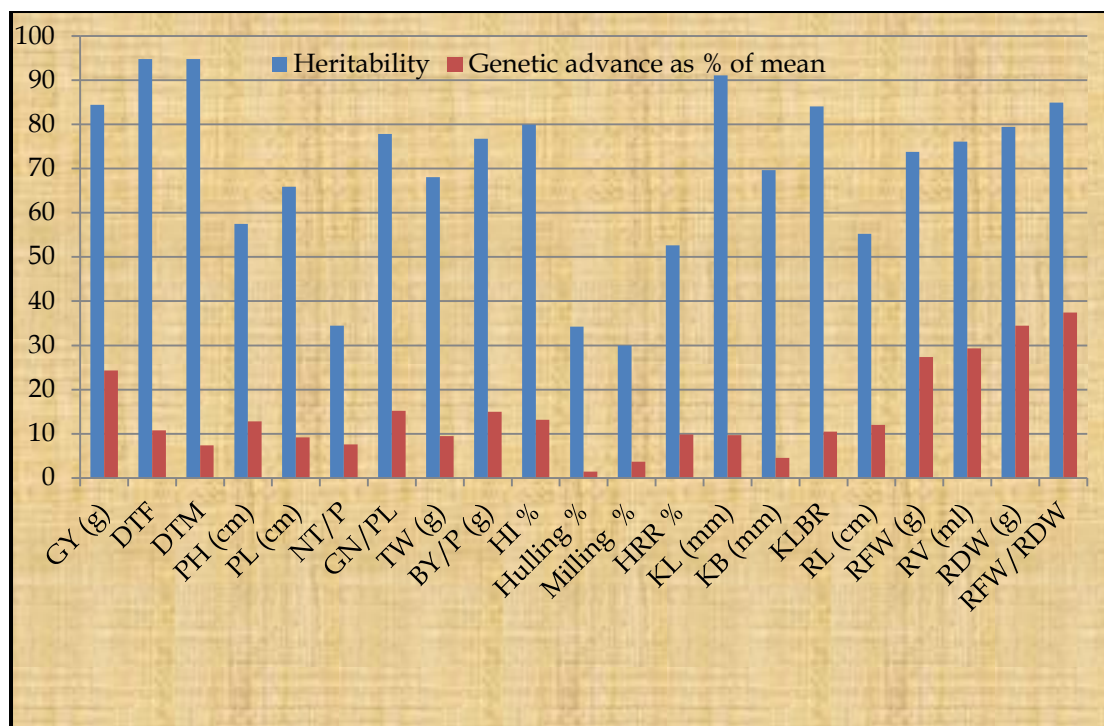


Fig. 14: Heritability and Genetic advance as per cent of mean for morphological and quality traits of non-basmati genotypes under aerobic condition

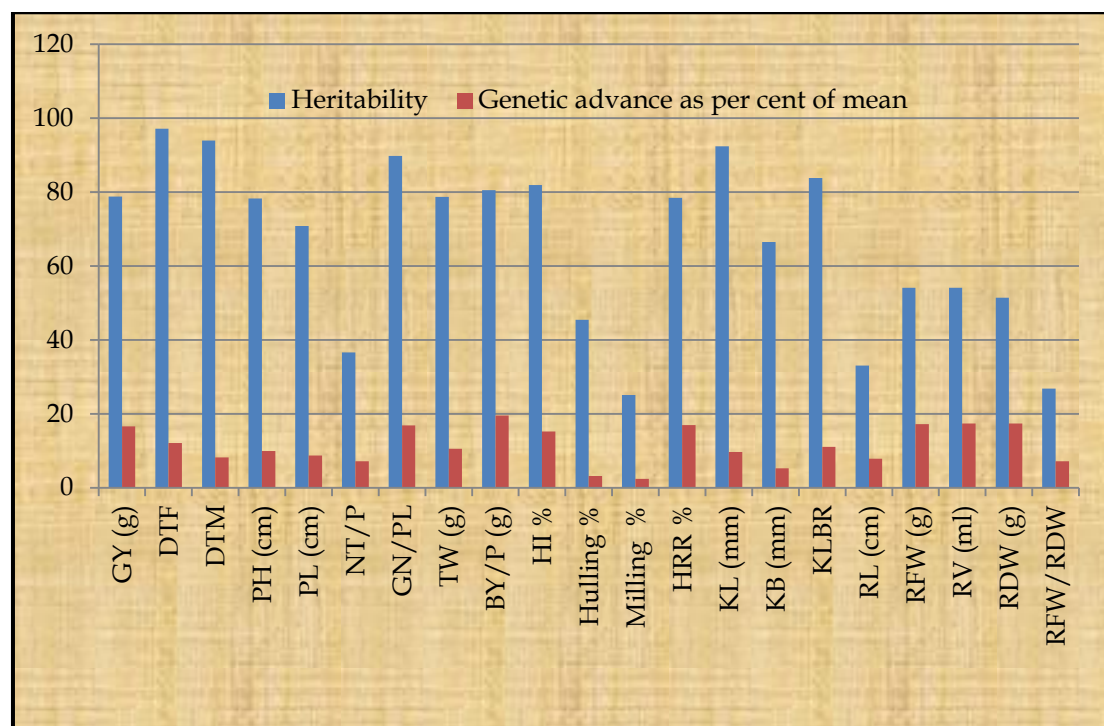


Fig. 15: Heritability and Genetic advance as per cent of mean for morphological and quality traits of non-basmati genotypes under transplanted condition.

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

4.3.1 Grain yield per plant (g)

Grain yield per plant in basmati genotypes exhibited highly significant positive correlation with number of tillers per plant (0.967**) followed by harvest index (0.816**), test weight (0.661**), root dry weight (0.572**), kernel length (0.502**) and kernel breadth (0.363**) and it showed significant negative association with hulling (-0.620**), Milling (-0.523**), plant height (-0.539**) and root fresh weight and dry weight (-0.312**) under aerobic condition. In transplanted condition it exhibited highly significant positive association with biological yield per plant (0.843**) followed by harvest index (0.823**), number of tillers per plant (0.734**), test weight (0.457**), number of grains per panicle (0.379**) and kernel breadth (0.358**) and it showed significant negative association with kernel length breadth ratio (-0.551**), plant height (-0.495**) kernel length (-0.424**), days to 50 % flowering (-0.423**) and Milling (-0.417**).

In case of non-basmati genotypes, grain yield per plant showed significant positive correlation with biological yield per plant (0.836**) followed by harvest index (0.761**), plant height (0.432**), test weight (0.413**), number of grains per panicle (0.407**), number of tillers per plant (0.287**), root fresh weight (0.246*) and root volume (0.233*) and it showed significant negative association with Milling (-0.479**), kernel breadth (-0.376**) under aerobic condition. In transplanted condition biological yield per plant (0.665**) followed by number of tillers per plant (0.521**), root volume (0.453**), root fresh weight (0.385**), number of grains per panicle (0.371**), root dry weight (0.365**) and test weight (0.354**) showed significant positive correlation while root length exhibited significant negative correlation with grain yield per plant.

4.3.2 Days to 50 % flowering

In basmati genotypes, days to 50 % flowering showed highly positive and significant correlation with days to maturity (0.973**) followed by milling % (0.385**), head rice recovery % (0.322**) and root fresh and dry weight ratio (0.300**) under aerobic condition while in transplanted condition days to maturity (0.911**), plant height (0.580**), hulling% (0.405**), root fresh and dry weight ratio (0.369**), kernel length breadth ratio (0.348**) and panicle length (0.310**) showed significant positive correlation with grain yield.

Under non-basmati genotypes, days to 50 % flowering exhibited highly significant positive correlation with days to maturity (0.981**) followed by head rice recovery % (0.501**), kernel length (0.446**), root volume (0.404**) and root fresh weight (0.402**) and hulling % (0.363**) under aerobic condition, while it had positive and significant correlation with days to maturity (0.989**), milling % (0.545**) head rice recovery % (0.499**), number of tillers/plant (0.465**), kernel breadth (0.461**), harvest index % (0.332**) and hulling % (0.305**) whereas plant height (-0.340**) showed significant negative correlation with days to 50 % flowering in transplanted condition.

4.3.3 Days to maturity

Days to maturity in basmati genotypes exhibited significant positive correlation with days to 50 % flowering (0.973**), milling % (0.320**) under aerobic condition while in transplanted condition it showed significant positive correlation with days to 50 % flowering (0.911**), root fresh and dry weight ratio (0.412**), plant height (0.411**), root length (0.340**) and root volume (0.309**).

In case of non-basmati genotypes, days to maturity showed significant positive correlation with days to 50 % flowering (0.981**), head rice recovery % (0.524**), kernel

length (0.399**), hulling% (0.398**), root fresh weight (0.380**) and root volume (0.379**) under aerobic condition. In transplanted condition it exhibited significant positive correlation with days to 50 % flowering (0.989**), milling % (0.593**), head rice recovery % (0.562**), kernel breadth (0.504**) and number of tillers/plant (0.371**).

4.3.4 Plant height (cm)

Plant height showed significant positive correlation with hulling % (0.418**) followed by and panicle length (0.412**) and root length (0.331**) under aerobic condition while in transplanted condition panicle length (0.592**), days to 50% flowering (0.580**), hulling % (0.473**), days to maturity (0.411**), milling % (0.350**) and root length (0.308**) exhibited significant positive correlation with plant height in basmati genotypes.

In non-basmati genotypes, plant height exhibited significant positive correlation with root volume (0.579**), root fresh weight (0.571**), biological yield (0.530**), root fresh & dry weight ratio (0.430**), panicle length (0.368**) and number of grains/panicle (0.319**) under aerobic condition however it showed positive and significant correlation with panicle length (0.459**), biological yield per plant (0.423**) and number of grains per panicle (0.413**) under transplanted condition.

4.3.5 Panicle length (cm)

In basmati genotypes panicle length exhibited positive and significant correlation with root fresh weight (0.690**), hulling % (0.627**), head rice recovery % (0.552**), plant height (0.412**) and kernel length-breadth ratio (0.312**) under aerobic condition while in transplanted condition it showed positive and significant correlation with plant height (0.592**), number of tillers per plant (0.447**), hulling % (0.336**) and kernel length-breadth ratio (0.371**) and days to 50 % flowering (0.310**).

Panicle length showed significant positive correlation with root length (0.423**), plant height (0.368**) and number of grains/panicle (0.236*) under aerobic condition while in transplanted condition it exhibited significant positive correlation with plant height (0.459**), root fresh and dry weight ratio (0.421**), kernel length-breadth ratio (0.317**) and kernel length (0.264*) in non-basmati genotypes.

Table: 4.5 Phenotypic (below diagonal) & Genotypic (above diagonal) correlation coefficients under aerobic condition (Basmati genotypes)

	GY	DTF	DTM	PH	PL	NT/P	GN/PL	TW	BY/P	HI	HULL	MILL	HRR	KL	KB	KLBR	RL	RFW	RV	RDW	RFW/RDW
GY	1	0.091	0.112	-0.539**	-0.292*	0.967**	-0.029	0.661**	0.231	0.816**	-0.620**	-0.523**	-0.278*	0.502**	0.363**	0.136	-0.190	0.283*	0.287*	0.572**	-0.312**
DTF	0.082	1	0.973**	-0.004	0.008	0.182	0.183	-0.204	-0.093	-0.122	0.037	0.385**	0.322**	0.296*	0.157	0.141	0.152	0.223	0.244*	-0.255*	0.300*
DTM	0.097	0.944**	1	0.023	-0.071	0.217	0.248*	-0.206	0.019	-0.127	0.008	0.320**	0.241*	0.200	0.077	0.133	0.157	0.255*	0.223	-0.227	0.293*
PH	-0.425**	0.000	0.027	1	0.412**	-0.563**	-0.048	-0.625**	-0.207	-0.533**	0.418**	0.085	0.217	-0.115	-0.173	0.059	0.286*	0.015	0.331**	0.030	-0.042
PL	-0.009	0.017	-0.003	0.291*	1	-0.174	0.189	-0.359**	-0.258*	0.061	0.627**	0.074	0.552**	0.228	-0.078	0.312**	0.286*	0.690**	0.191	0.244*	0.206
NT/P	0.932**	0.157	0.188	-0.460**	0.054	1	0.129	0.595**	0.201	0.819**	-0.650**	-0.461**	-0.219	0.477**	0.281*	0.200	-0.094	0.418**	0.373**	0.550**	-0.224
GN/PL	0.029	0.182	0.246*	-0.018	0.215	0.135	1	-0.516**	0.097	0.020	-0.107	0.463**	0.560**	-0.320**	-0.407**	0.122	-0.020	0.060	0.109	0.111	-0.144
TW	0.677**	-0.160	-0.171	-0.532**	-0.055	0.621**	-0.390**	1	0.006	0.709**	-0.198	-0.532**	-0.590**	0.322**	0.495**	-0.192	-0.213	0.244*	-0.137	0.198	0.022
BY/P	0.431**	-0.041	0.000	-0.115	-0.017	0.351**	0.118	0.241*	1	-0.156	-0.323**	-0.257*	-0.333**	-0.209	-0.055	-0.123	-0.339**	-0.432**	-0.115	0.028	-0.239*
HI	0.613**	-0.123	-0.102	-0.489**	0.078	0.650**	0.015	0.543**	-0.268*	1	-0.378**	-0.472**	-0.140	0.428**	0.368**	0.040	-0.039	0.521**	0.035	0.518**	-0.128
HULL	-0.230	0.017	0.022	0.187	0.268*	-0.196	-0.046	-0.043	-0.110	-0.094	1	0.589**	0.045	-0.202	0.025	-0.231	0.495**	0.091	-0.335**	-0.437**	0.423**
MILL	-0.191	0.238*	0.261*	0.038	0.125	-0.144	0.287*	-0.249*	-0.060	-0.232*	0.562**	1	0.689**	-0.433**	-0.287*	-0.138	-0.015	-0.243*	-0.109	-0.465**	0.187
HRR	-0.062	0.211	0.164	0.124	0.174	-0.058	0.373**	-0.222	-0.020	-0.106	0.232	0.575**	1	-0.147	-0.218	0.084	-0.224	-0.175	0.150	0.008	-0.199
KL	0.428**	0.279*	0.192	-0.116	0.169	0.413**	-0.295*	0.292*	-0.136	0.381**	-0.106	-0.273*	-0.080	1	0.563**	0.408**	0.272*	0.423**	0.263*	0.328**	-0.016
KB	0.301*	0.152	0.075	-0.166	-0.025	0.240*	-0.368**	0.429**	-0.047	0.344**	0.072	-0.183	-0.147	0.539**	1	-0.523**	-0.125	0.060	-0.489**	0.020	0.076
KLBR	0.111	0.121	0.121	0.055	0.195	0.162	0.113	-0.160	-0.062	0.008	-0.184	-0.077	0.077	0.400**	-0.554**	1	0.409**	0.368**	0.814**	0.309**	-0.094
RL	-0.164	0.137	0.124	0.231	0.126	-0.116	-0.002	-0.164	-0.166	-0.078	0.103	-0.136	-0.121	0.229	-0.089	0.320**	1	0.168	0.707**	0.338**	-0.192
RFW	0.222	0.142	0.201	0.025	0.272*	0.285*	0.071	0.168	-0.229	0.386**	0.078	0.024	-0.020	0.348**	0.106	0.228	0.049	1	0.222	0.167	0.442**
RV	0.032	0.162	0.157	0.201	0.077	0.051	0.116	-0.109	-0.180	0.068	-0.123	-0.197	0.097	0.184	-0.228	0.436**	0.485**	0.174	1	0.691**	-0.500**
RDW	0.404**	-0.205	-0.190	0.016	0.192	0.403**	0.108	0.166	0.024	0.434**	-0.136	-0.248*	-0.020	0.294*	0.013	0.274*	0.273*	0.037	0.421**	1	-0.802**
RFW/RDW	-0.163	0.214	0.237*	-0.017	-0.003	-0.121	-0.099	0.022	-0.131	-0.078	0.156	0.176	-0.023	0.010	0.096	-0.095	-0.187	0.606**	-0.240*	-0.756**	1

**** = Significant at 1 % level, * = Significant at 5 % level**

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

Table: 4.6 Phenotypic (below diagonal) & Genotypic (above diagonal) correlation coefficients under transplanted condition (Basmati genotypes)

	GY	DTF	DTM	PH	PL	NT/P	GN/PL	TW	BY/P	HI	HULL	MILL	HRR	KL	KB	KLBR	RL	RFW	RV	RDW	RFW/RDW
GY	1	-0.423**	-0.261*	-0.495**	-0.112	0.734**	0.379**	0.457**	0.843**	0.823**	-0.240*	-0.417**	0.093	-0.424**	0.358**	-0.551**	-0.031	-0.003	0.027	-0.009	0.042
DTF	-0.361**	1	0.911**	0.580**	0.310**	-0.319**	0.101	-0.419**	-0.504**	-0.206	0.405**	0.164	0.265*	0.235*	-0.272*	0.348**	0.236*	0.085	0.119	-0.229	0.369**
DTM	-0.214	0.893**	1	0.411**	0.194	-0.057	0.08	-0.235*	-0.094	-0.328**	0.16	-0.114	0.05	0.219	-0.011	0.134	0.340**	0.238*	0.309**	-0.081	0.412**
PH	-0.364**	0.531**	0.375**	1	0.592**	-0.403**	0.136	-0.541**	-0.786**	-0.026	0.473**	0.350**	0.256*	0.244*	-0.177	0.280*	0.308**	0.294*	0.287*	0.290*	-0.004
PL	-0.105	0.193	0.15	0.419**	1	0.447**	-0.125	-0.386**	-0.416**	0.272*	0.336**	-0.014	0.262*	0.034	-0.458**	0.371**	0.175	0.247*	0.178	0.068	0.285*
NT/P	0.743**	-0.235*	-0.035	-0.239*	-0.237*	1	0.280*	0.434**	0.890**	0.378**	-0.097	-0.192	0.077	-0.276*	0.727**	-0.755**	0.205	0.197	0.289*	0.162	0.11
GN/PL	0.399**	0.105	0.093	0.163	-0.073	0.302**	1	0.045	0.211	0.400**	0.133	-0.253*	0.545**	-0.510**	0.156	-0.478**	0.079	0.189	0.241*	0.06	0.172
TW	0.441**	-0.407**	-0.227	-0.488**	-0.276*	0.367**	-0.027	1	0.753**	0	-0.417**	-0.375**	-0.318**	-0.169	0.515**	-0.485**	0.09	0.188	0.162	0.056	0.141
BY/P	0.567**	-0.213	0.006	-0.258*	-0.074	0.548**	0.249*	0.417**	1	0.423**	-0.706**	-0.939**	-0.128	-0.14	0.826**	-0.714**	0.478**	0.340**	0.438**	0.267*	0.176
HI	0.433**	-0.153	-0.218	-0.117	-0.028	0.211	0.137	0.011	-0.480**	1	0.349**	0.305**	0.388**	-0.625**	-0.234*	-0.231	-0.465**	-0.359**	-0.404**	-0.309**	-0.093
HULL	-0.208	0.236*	0.065	0.124	0.1	-0.138	0.011	-0.245*	-0.418**	0.287*	1	0.559**	0.630**	-0.420**	-0.598**	0.156	-0.284*	-0.273*	-0.364**	-0.465**	0.257*
MILL	-0.257*	0.081	-0.09	0.197	0.092	-0.127	-0.151	-0.237*	-0.343**	0.134	0.578**	1	0.297*	-0.182	-0.367**	0.138	-0.102	-0.310**	-0.397**	-0.605**	0.410**
HRR	0.117	0.174	-0.001	0.259*	0.102	0.044	0.369**	-0.213	-0.032	0.149	0.115	0.071	1	-0.198	-0.250*	0.064	0.121	-0.259*	-0.318**	-0.22	-0.156
KL	-0.323**	0.228	0.208	0.234*	0.012	-0.135	-0.457**	-0.156	-0.032	-0.334**	-0.248*	-0.113	-0.121	1	0.072	0.632**	0.277*	-0.018	0.06	0.355**	-0.572**
KB	0.289*	-0.249*	-0.011	-0.12	-0.301*	0.483**	0.13	0.481**	0.448**	-0.184	-0.363**	-0.241*	-0.136	0.059	1	-0.723**	0.489**	0.406**	0.474**	0.358**	0.136
KLBR	-0.428**	0.324**	0.123	0.231	0.235*	-0.472**	-0.415**	-0.454**	-0.358**	-0.074	0.112	0.107	0.032	0.623**	-0.739**	1	-0.176	-0.346**	-0.343**	-0.031	-0.534**
RL	0.006	0.192	0.283*	0.207	0.106	0.139	0.085	0.083	0.174	-0.143	-0.065	0.019	0.053	0.217	0.342**	-0.117	1	0.505**	0.517**	0.338**	0.226
RFW	0.011	0.07	0.206	0.243*	0.123	0.184	0.159	0.167	0.169	-0.186	-0.139	-0.127	-0.141	-0.002	0.315**	-0.261*	0.392**	1	1.019**	0.745**	0.398**
RV	-0.014	0.083	0.226	0.185	0.045	0.161	0.146	0.123	0.147	-0.185	-0.16	-0.212	-0.141	0.053	0.345**	-0.245*	0.402**	0.929**	1	0.801**	0.344**
RDW	-0.005	-0.187	-0.066	0.215	0.074	0.089	0.048	0.044	0.145	-0.184	-0.215	-0.269*	-0.1	0.312**	0.272*	-0.006	0.273*	0.621**	0.621**	1	-0.305**
RFW/RDW	0.03	0.229	0.276*	0.044	0.063	0.132	0.117	0.109	0.038	-0.008	0.072	0.158	-0.069	-0.378**	0.088	-0.337**	0.139	0.485**	0.403**	-0.367**	1

** = Significant at 1 % level, * = Significant at 5 % level

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

Table: 4.7 Phenotypic (below diagonal) & Genotypic (above diagonal) correlation coefficients under aerobic condition (non-Basmati genotypes)

	GY	DTF	DTM	PH	PL	NT/P	GN/PL	TW	BY/P	HI	HULL	MILL	HRR	KL	KB	KLBR	RL	RFW	RV	RDW	RFW/RDW
GY	1	-0.068	0.02	0.432**	0.054	0.287*	0.407**	0.413**	0.836**	0.761**	-0.127	-0.479**	-0.039	-0.03	-0.376**	0.122	0.229	0.246*	0.233*	0.165	0.059
DTF	-0.047	1	0.981**	-0.340**	-0.164	0.092	-0.557**	0.08	-0.014	-0.118	0.363**	0.126	0.501**	0.446**	0.223	0.294*	0.092	0.402**	0.404**	0.177	0.131
DTM	0.019	0.960**	1	-0.310**	-0.118	0.133	-0.414**	0.046	0.026	-0.012	0.398**	0.166	0.524**	0.399**	0.134	0.291*	0.065	0.380**	0.379**	0.172	0.12
PH	0.355**	-0.237*	-0.232	1	0.368**	-0.196	0.319**	0.058	0.530**	0.162	-0.362**	-0.755**	-0.364**	-0.11	-0.429**	0.066	0.294*	0.571**	0.579**	-0.03	0.430**
PL	0.064	-0.12	-0.103	0.451**	1	0.208	0.236*	-0.238*	0.126	-0.083	-0.125	-0.680**	-0.357**	0.153	-0.181	0.206	0.423**	-0.102	-0.094	0.235*	-0.270*
NT/P	0.391**	0.091	0.062	0.084	0.14	1	0.076	-0.161	0.364**	0.051	0.087	0.17	0.089	0.103	-0.14	0.152	0.131	-0.219	-0.229	-0.091	-0.112
GN/PL	0.475**	-0.480**	-0.362**	0.270*	0.198	0.285*	1	-0.427**	0.248*	0.436**	-0.173	-0.041	-0.487**	-0.278*	-0.531**	-0.024	-0.202	-0.206	-0.212	-0.17	-0.004
TW	0.491**	0.064	0.016	0.139	-0.128	0.23	-0.096	1	0.270*	0.385**	-0.646**	-0.207	0.111	0.138	0.166	0.032	0.176	0.048	0.088	0.526**	-0.283*
BY/P	0.818**	-0.006	0.009	0.393**	0.12	0.414**	0.364**	0.387**	1	0.283*	0.123	-0.431**	0.189	-0.039	-0.280*	0.082	0.11	0.331**	0.338**	0.249*	0.077
HI	0.727**	-0.086	0.005	0.16	-0.048	0.168	0.395**	0.366**	0.205	1	-0.399**	-0.364**	-0.334**	0.006	-0.371**	0.143	0.277*	0.027	0	-0.009	0.011
HULL	-0.046	0.189	0.205	-0.051	0.061	0.108	-0.028	-0.175	0.085	-0.188	1	0.553**	0.632**	-0.003	0.026	0.001	-0.276*	0.296*	0.301*	-0.444**	0.438**
MILL	-0.301*	0.057	0.117	-0.363**	-0.271*	-0.135	-0.09	-0.132	-0.234*	-0.248*	0.333**	1	0.770**	-0.004	0.167	-0.058	-0.958**	-0.322**	-0.303**	-0.255*	-0.048
HRR	-0.026	0.406**	0.375**	-0.141	-0.145	0.088	-0.315**	0.083	0.161	-0.257*	0.366**	0.373**	1	0.215	0.470**	0.005	-0.186	0.243*	0.245*	0.02	0.137
KL	-0.024	0.418**	0.356**	-0.054	0.124	0.097	-0.237*	0.152	-0.023	-0.001	0.08	-0.024	0.17	1	-0.131	0.912**	0.125	0.01	0.012	0.409**	-0.283*
KB	-0.281*	0.192	0.106	-0.252*	-0.14	-0.097	-0.399**	0.086	-0.201	-0.260*	-0.043	0.002	0.290*	-0.126	1	-0.526**	-0.239*	0.138	0.101	0.143	-0.038
KLBR	0.101	0.259*	0.248*	0.058	0.166	0.13	-0.018	0.074	0.072	0.104	0.091	-0.011	0.013	0.884**	-0.572**	1	0.206	-0.058	-0.038	0.288*	-0.231
RL	0.216	0.095	0.06	0.226	0.277*	0.039	-0.087	0.2	0.087	0.282*	-0.001	-0.239*	-0.119	0.088	-0.048	0.086	1	0.02	0.049	0.046	-0.071
RFW	0.212	0.321**	0.304**	0.303**	-0.103	-0.117	-0.089	0.06	0.276*	0.022	0.148	-0.109	0.162	-0.014	0.1	-0.063	-0.008	1	1.002**	-0.127	0.761**
RV	0.179	0.332**	0.330**	0.299*	-0.125	-0.17	-0.149	0.022	0.237*	0.014	0.087	-0.122	0.142	-0.016	0.08	-0.054	-0.001	0.961**	1	-0.051	0.715**
RDW	0.147	0.113	0.122	-0.076	0.139	-0.003	-0.089	0.444**	0.217	-0.017	-0.241*	-0.096	0.016	0.355**	0.026	0.285*	-0.073	-0.014	0.02	1	-0.725**
RFW/RDW	0.042	0.131	0.115	0.284*	-0.22	-0.108	-0.003	-0.250*	0.056	0.006	0.254*	-0.012	0.097	-0.262*	0.021	-0.232*	-0.005	0.713**	0.672**	-0.688**	1

**** = Significant at 1 % level, * = Significant at 5 % level**

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

Table: 4.8 Phenotypic (below diagonal) & Genotypic (above diagonal) correlation coefficients under transplanted condition (Non-basmati genotypes)

	GY	DTF	DTM	PH	PL	NT/P	GN/PL	TW	BY/P	HI	HULL	MILL	HRR	KL	KB	KLBR	RL	RFW	RV	RDW	RFW/RDW
GY	1	0.267*	0.196	0.433**	0.120	0.521**	0.371**	0.354**	0.665**	0.219	0.121	-0.090	0.153	0.142	-0.096	0.149	-0.391**	0.385**	0.453**	0.365**	-0.004
DTF	0.225	1	0.989**	-0.130	-0.055	0.465**	-0.082	0.053	0.004	0.332**	0.305**	0.545**	0.499**	0.267*	0.461**	-0.006	-0.256*	0.039	0.152	0.040	0.009
DTM	0.189	0.972**	1	-0.210	-0.048	0.371**	-0.068	0.010	-0.008	0.273*	0.259*	0.593**	0.562**	0.250*	0.504**	-0.038	-0.225	0.033	0.128	0.044	0.014
PH	0.350**	-0.116	-0.159	1	0.459**	-0.148	0.413**	0.248*	0.423**	-0.070	-0.093	-0.519**	-0.446**	0.181	-0.329**	0.290*	-0.041	0.131	0.130	0.118	-0.012
PL	0.123	-0.065	-0.043	0.397**	1	0.016	0.185	-0.083	0.075	0.055	-0.361**	0.033	-0.250*	0.264*	-0.195	0.317**	-0.162	0.156	0.069	-0.077	0.421**
NT/P	0.569**	0.259*	0.208	-0.115	0.064	1	-0.499**	0.047	0.173	0.354**	0.266*	0.334**	0.195	0.294*	-0.039	0.250*	-0.330**	0.538**	0.660**	0.330**	0.305**
GN/PL	0.367**	-0.078	-0.048	0.363**	0.148	-0.217	1	-0.458**	0.577**	-0.348**	-0.420**	-0.453**	0.025	-0.021	-0.110	0.042	-0.172	-0.121	-0.166	0.005	-0.180
TW	0.410**	0.024	-0.002	0.165	-0.055	0.260*	-0.360**	1	-0.128	0.535**	0.542**	0.250*	0.037	-0.022	0.078	-0.075	0.015	0.334**	0.364**	0.279*	0.023
BY/P	0.679**	-0.004	0.009	0.356**	0.117	0.326**	0.545**	-0.001	1	-0.581**	-0.139	-0.367**	0.033	0.191	-0.264*	0.276*	-0.274*	0.507**	0.579**	0.467**	0.111
HI	0.214	0.295*	0.237*	-0.063	-0.002	0.203	-0.311**	0.455**	-0.566**	1	0.300*	0.363**	0.110	-0.080	0.233*	-0.182	-0.065	-0.228	-0.244*	-0.221	-0.107
HULL	0.093	0.202	0.185	0.021	-0.101	0.082	-0.313**	0.308**	-0.040	0.152	1	0.317**	0.049	-0.215	0.445**	-0.406**	-0.591**	-0.306**	-0.137	-0.385**	0.143
MILL	-0.050	0.236*	0.280*	-0.060	0.141	0.064	-0.277*	0.078	-0.170	0.169	0.410**	1	0.726**	0.321**	0.379**	0.061	0.193	-0.559**	-0.580**	-0.222	-0.505**
HRR	0.120	0.432**	0.475**	-0.267*	-0.177	0.088	-0.017	-0.004	0.048	0.064	0.146	0.544**	1	0.198	0.524**	-0.091	0.361**	-0.316**	-0.249*	0.017	-0.581**
KL	0.121	0.249*	0.229	0.163	0.238*	0.145	-0.016	-0.039	0.142	-0.037	-0.153	0.184	0.150	1	-0.157	0.878**	0.393**	0.175	0.084	0.492**	-0.518**
KB	-0.129	0.385**	0.394**	-0.228	-0.102	-0.133	-0.117	0.017	-0.279*	0.239*	0.326**	0.082	0.321**	-0.125	1	-0.608**	-0.185	-0.355**	-0.205	-0.370**	0.063
KLBR	0.154	-0.016	-0.034	0.238*	0.242*	0.180	0.058	-0.058	0.255*	-0.160	-0.308**	0.094	-0.054	0.835**	-0.647**	1	0.415**	0.312**	0.164	0.577**	-0.451**
RL	-0.167	-0.135	-0.139	-0.021	-0.050	-0.027	-0.114	-0.022	-0.120	-0.035	-0.233*	0.052	0.209	0.202	-0.159	0.253*	1	-0.125	-0.194	0.361**	-0.910**
RFW	0.251*	0.020	0.028	0.203	0.177	0.192	-0.123	0.196	0.365**	-0.194	-0.027	-0.027	-0.122	0.109	-0.210	0.195	0.153	1	0.952**	0.844**	0.281*
RV	0.308**	0.102	0.114	0.243*	0.136	0.253*	-0.143	0.219	0.396**	-0.169	0.013	-0.045	-0.066	0.055	-0.146	0.120	0.107	0.930**	1	0.760**	0.331**
RDW	0.262*	0.037	0.067	0.126	-0.011	0.138	-0.017	0.181	0.364**	-0.191	-0.064	-0.060	0.017	0.337**	-0.227	0.387**	0.348**	0.657**	0.597**	1	-0.268*
RFW/RDW	-0.044	-0.020	-0.045	0.063	0.214	0.046	-0.124	-0.012	0.016	-0.053	0.059	0.058	-0.165	-0.278*	0.025	-0.235*	-0.267*	0.392**	0.367**	-0.420**	1

**** = Significant at 1 % level, * = Significant at 5 % level**

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

4.3.6 Number of tillers per plant

Under aerobic condition, number of tillers per plant showed significant positive correlation with harvest index % (0.819**), harvest index % (0.819**), test weight (0.595**), root dry weight (0.550**), kernel length (0.477**), root fresh weight (0.418**) and root volume (0.373**) while in transplanted condition it showed positive and significant correlation with biological yield per plant (0.890**) followed by kernel breadth (0.727**), panicle length (0.447**), test weight (0.434**), harvest index % (0.378**) and root volume (0.289*) in basmati genotypes.

Number of tillers per plant exhibited significant positive correlation with biological yield per plant (0.364**) while in transplanted condition it showed positive and significant correlation with root volume (0.660**), root fresh weight (0.538**), days to 50 % flowering (0.465**), days to maturity (0.371**), harvest index % (0.354**), milling % (0.334**), root dry weight (0.330**) and root fresh & dry weight ratio (0.305**) in non-basmati genotypes.

4.3.7 Number of grains per panicle

In basmati genotypes, number of grains per panicle exhibited positive and significant correlation with head rice recovery % (0.560**) milling % (0.463**) and days to maturity (0.248*) under aerobic condition and it showed significant positive correlation with head rice recovery % (0.545**), harvest index % (0.400**), number of tillers per plant (0.280*) and root volume (0.241*) in transplanted condition.

Number of grains per panicle showed positive and significant correlation with grain yield (0.407*), harvest index % (0.436**), plant height (0.319**) and panicle length (0.236*) under aerobic condition while in transplanted condition it had significant positive correlation with biological yield per plant (0.577**), plant height (0.413**) and grain yield (0.407*) in non-basmati genotypes.

4.3.8 Test weight

Test weight exhibited significant positive correlation with harvest index % (0.709**) followed by number of tillers per plant (0.595**), kernel breadth (0.495**), kernel length (0.322**) and root fresh weight (0.244*) under aerobic condition while in transplanted condition it showed significant positive association with biological yield (0.753**), kernel breadth (0.515**) grain yield (0.457**) and number of tillers per plant (0.434**) for basmati genotypes.

In non-basmati genotypes, test weight showed significant positive correlation with root dry weight (0.526**), grain yield (0.413**), harvest index % (0.385**) and biological yield per plant (0.270*) under aerobic condition while in transplanted condition it showed significant positive correlation with hulling % (0.542**), harvest index % (0.535**), grain yield (0.354**), root volume (0.364**), root fresh weight (0.334**), root dry weight (0.279*) and milling % (0.250*).

4.3.9 Biological yield/plant

Biological yield/plant in basmati genotypes was positively correlated with grain yield/plant (0.231) and number of tillers/plant (0.201) in aerobic condition while it had significant negative correlation with root fresh weight (-0.432**), head rice recovery (-0.333**) and hulling % (-0.323**) at genotypic level. In transplanted condition it showed significant positive correlation with number of tillers/plant (0.890**) followed by grain yield/plant (0.843**), kernel breadth (0.826**), test weight (0.753**), root length (0.478**), root volume (0.438**), harvest index % (0.423**) and root fresh weight (0.340**).

In non-basmati genotypes, biological yield had positive and significant correlation with plant height (0.530**) followed by number of tillers per plant (0.364**), root volume (0.338**), root fresh weight (0.331**), harvest index (0.283*), test weight (0.270*) and number of grains per plant (0.248*) under aerobic conditions while in transplanted condition it had significant positive correlation with grain yield (0.665**), root volume (0.579**), number of grains per plant (0.577**), root fresh weight (0.507**), root dry weight (0.467**) and plant height (0.423**).

4.3.10 Harvest index %

Harvest index % exhibited significant positive correlation with number of tillers/plant (0.819**) followed by grain yield/plant (0.816**), test weight (0.709**), root fresh weight (0.521**), root dry weight (0.518**), kernel length (0.428**) and kernel breadth (0.368**) in aerobic condition while in transplanted condition it showed significant positive correlation with grain yield/plant (0.823**), biological yield/plant (0.423**), number of grains per panicle (0.400**), head rice recovery % (0.388**), number of tillers/plant (0.378**), hulling % (0.349**) and milling % (0.305**) for basmati genotypes.

Character association of non-basmati genotypes revealed that harvest index showed positive and significant correlation with grain yield (0.761**), number of grains per plant (0.436**), test weight (0.385**), biological yield per plant (0.283*) and root volume under aerobic condition while it exhibited significant positive correlation with test weight (0.535**) followed by milling % (0.363**), number of tillers per plant (0.354**), days to flowering (0.332**) and hulling % (0.300*) under transplanted condition.

4.3.11 Hulling %

Under aerobic condition for basmati genotypes, character association revealed that hulling % exhibited significant positive correlation with panicle length (0.627**), milling % (0.589**), root length (0.495**), root fresh and dry weight ratio (0.423**) and plant height (0.418**). In transplanted condition it showed positive correlation with head rice recovery % (0.630**) followed by milling % (0.559**), plant height (0.473**), days to 50% flowering (0.405**), harvest index % (0.349**) and panicle length (0.336**).

Hulling % in non-basmati genotypes exhibited significant positive correlation with head rice recovery % (0.632**) followed by milling % (0.553**), root fresh and dry weight ratio (0.438**), days to maturity (0.398**), days to 50 % flowering (0.363**) and root volume (0.301*) under aerobic condition while in transplanted condition it had positive correlation with test weight (0.542**), kernel breadth (0.445**), milling % (0.317**) and days to 50 % flowering (0.305**).

4.3.12 Milling %

Milling % in aerobic basmati genotypes showed significant positive correlation with head rice recovery % (0.689**) followed by hulling % (0.589**), number of grains/panicle (0.463**), days to 50% flowering (0.385**) along with days to maturity (0.320**), whereas in transplanted condition it had significant positive correlation with hulling % (0.559**) followed by root fresh and dry weight ratio (0.410**), plant height (0.350**), harvest index % (0.305**) and head rice recovery (0.297*).

In non-basmati genotypes, milling % exhibited significant positive correlation with head rice recovery % (0.770**) and hulling % (0.553**) under aerobic condition, while in transplanted condition it showed significant positive correlation with head rice recovery % (0.726**) followed by days to maturity (0.593**), days to 50 % flowering (0.545**), kernel breadth (0.379**), harvest index % (0.363**), number of tillers per plant (0.334**), kernel length (.321**) and hulling % (0.317**).

4.3.13 Head rice recovery %

Under aerobic condition head rice recovery % showed significant positive correlation with milling % (0.689**), number of grains/panicle (0.560**), panicle length (0.552**) and days to 50% flowering (0.322**). It observed significant positive correlation with hulling % (0.630**), number of grains/panicle (0.545**) and harvest index (0.388**) in transplanted condition for basmati genotypes.

In non-basmati genotypes, head rice recovery % exhibited significant positive correlation with milling % (0.770**) followed by hulling % (0.632**), days to maturity (0.524**), days to flowering (0.501**) and kernel breadth (0.470**) under aerobic condition while in transplanted condition it had the same correlation with milling % (0.726**) followed by days to maturity (0.562**), kernel breadth (0.524**), days to 50 % flowering (0.499**) and root length (0.361**).

4.3.14 Kernel length (mm)

Kernel length observed significant positive correlation with kernel breadth (0.563**), grain yield/plant (0.502**), number of tillers/plant (0.477**), harvest index % (0.428**), root fresh weight (0.423**), kernel length-breadth ratio (0.408**), root dry weight (0.328**) and test weight (0.322**) in aerobic condition, while it had positive correlation with kernel length

breadth ratio (0.632**), root volume (0.355**) and root length (0.277*) under transplanted condition for basmati genotypes.

Kernel length exhibited significant positive correlation with kernel length-breadth ratio (0.912**), days to flowering (0.446**), root dry weight (0.409**) and days to maturity (0.399**) under aerobic condition, while it had positive and significant correlation with kernel length-breadth ratio (0.878**), root dry weight (0.492**), root length (0.393**), milling % (0.321**) and number of tillers per plant (0.294*) for non-basmati genotypes under transplanted condition.

4.3.15 Kernel breadth (mm)

Kernel breadth showed significant positive correlation with kernel length (0.563**), test weight (0.495**) and harvest index % (0.368**) under aerobic condition while in transplanted condition it showed positive correlation with biological yield/plant (0.826**), number of tillers/plant (0.727**), test weight (0.515**), root length (0.489**), root volume (0.474**), root fresh weight (0.406**) and root dry weight (0.358**) for basmati genotypes.

In non-basmati genotypes, kernel breadth exhibited significant positive correlation with head rice recovery % (0.470**) and significant negative correlation with number of grains per panicle (-0.531**), KLBR (-0.526**), plant height (-0.429**) and harvest index (-0.371**) under aerobic condition, while it showed significant positive correlation with head rice recovery % (0.524**) followed by days to maturity (0.504**), days to 50 % flowering (0.461**), hulling % (0.445**) and milling % (0.379**) under transplanted condition.

4.3.16 Kernel length breadth ratio

Under aerobic condition kernel length breadth ratio showed significant positive correlation with root volume (0.814**) followed by root length (0.409**), kernel length (0.408**), root fresh weight (0.368**), panicle length (0.312**) and root dry weight (0.309**). Whereas, in transplanted condition it showed significant positive correlation with kernel length (0.632**), panicle length (0.371**) and days to 50% flowering (0.348**) for basmati genotypes.

In non-basmati genotypes, kernel length-breadth ratio exhibited significant positive correlation with kernel length (0.912**), days to 50 % flowering (0.294*), days to maturity (0.291*) and root dry weight (0.288*) under aerobic condition while in transplanted condition it showed significant positive correlation with kernel length (0.878**) followed by root dry weight (0.577**), root length (0.415**), panicle length (0.317**) and root fresh weight (0.312**).

4.3.17 Root length (cm)

Root length exhibited significant positive correlation with root volume (0.707**), hulling % (0.495**), kernel length breadth ratio (0.409**) and root dry weight (0.338**) in aerobic condition, whereas in transplanted condition it showed significant positive correlation

with root volume (5.17**), root fresh weight (0.505**), kernel breadth (0.489**), biological yield/plant (0.478**), days to maturity (0.340**), root dry weight (0.338**) and plant height (0.308**) for basmati genotypes.

In non-basmati genotypes, root length showed significant positive correlation with panicle length (0.423**), plant height (0.294*) and harvest index (0.277*) under aerobic condition while in transplanted condition kernel length-breadth ratio (0.415**), kernel length (0.393**), root dry weight (0.361**) and head rice recovery % (0.361**) exhibited significant positive correlation with root length.

4.3.18 Root fresh weight (g)

Root fresh weight exhibited significant positive correlation with panicle length (0.690**), harvest index % (0.521**), root fresh and dry weight ratio (0.442**), kernel length (0.423**), number of tillers/plant (0.418**) and KLBR (0.368**) under aerobic condition, while in transplanted condition it showed significant positive correlation with root volume (1.019**) followed by root dry weight (0.745**), root length (0.505**), kernel breadth (0.406**), root fresh and dry weight ratio (0.398**), and biological yield per plant (0.340**) for basmati genotypes.

Root fresh weight showed significant positive correlation with root volume (1.002**) followed by root fresh and dry weight ratio (0.761**), plant height (0.571**), days to flowering (0.402**), days to maturity (0.380**) and biological yield per plant (0.331**) under aerobic condition while in transplanted condition root volume (0.952**), root dry weight (0.844**), number of tillers per plant (0.538**), biological yield (0.507**), test weight (0.334**) and kernel length-breadth ratio (0.312**) exhibited significant positive correlation with root fresh weight for non-basmati genotypes.

4.3.19 Root volume (ml)

In basmati genotypes, root volume had significant positive correlation with kernel length breadth ratio (0.814**), root length (0.707**), root dry weight (0.691**), number of tillers per plant (0.373**) and plant height (0.331**) in aerobic condition while it showed significant positive correlation with root fresh weight (1.019**), root dry weight (0.801**), root length (0.517**), kernel breadth (0.474**), biological yield/plant (0.438**) and root fresh and dry weight ratio (0.344**) in transplanted condition.

Root volume exhibited significant positive correlation with root fresh weight (1.002**), root fresh and dry weight ratio (0.715**), plant height (0.579**), days to 50 % flowering (0.404**), days to maturity (0.379**), biological yield per plant (0.338**) and hulling % (0.301*) under aerobic condition, whereas it showed significant positive correlation with root fresh weight (0.952**) followed by root dry weight (0.760**), number of tillers per plant (0.660**), biological yield per plant (0.579**), grain yield (0.453**), test weight (0.364**) and root fresh and dry weight ratio (0.331**) under transplanted condition.

4.3.20 Root dry weight (g)

Root dry weight exhibited significant positive correlation with root volume (0.691**), number of tillers/plant (0.550**), harvest index % (0.518**), root length (0.338**), kernel length (0.328**) and kernel length breadth ratio (0.309**) in aerobic condition while in transplanted condition it showed significant positive correlation with root volume (0.801**) followed by root fresh weight (0.745**), kernel breadth (0.358**), kernel length (0.355**) and root length (0.338**) for basmati genotypes..

In non-basmati genotypes, root dry weight showed significant positive correlation with test weight (0.526**), kernel length (0.409**), KLBR (0.288*) and biological yield/plant (0.249*) under aerobic condition while in transplanted condition it exhibited significant positive correlation with root fresh weight (0.844**) followed by root volume (0.760**), kernel length-breadth ratio (0.577**), kernel length (0.492**), biological yield (0.467**), root length (0.361**), root fresh and dry weight ratio (0.331**) and number of tillers per plant (0.330**).

4.3.21 Root fresh and dry weight ratio

Root fresh and dry weight ratio showed significant positive correlation with hulling % (0.423**), root fresh weight (0.442**), days to 50 % flowering (0.300*) and days to maturity (0.293*) under aerobic condition, while in transplanted condition, it showed significant positive correlation with milling % (0.410**), days to maturity (0.412**), root fresh weight (0.398**), days to 50 % flowering (0.369**) and root volume (0.344**) for basmati genotypes.

Under aerobic condition in non-basmati genotypes, root fresh and dry weight ratio exhibited significant positive correlation with root fresh weight (0.761**), root volume (0.715**), hulling % (0.438**) and plant height (0.430**) and root dry weight showed significant negative correlation with root fresh and dry weight ratio (-0.725**). Whereas, in transplanted condition panicle length (0.421**), root volume (0.331**), number of tillers per plant (0.305**) and root fresh weight (0.281*) showed significant positive correlation with root fresh and dry weight ratio for non-basmati genotypes.

4.4 Path co-efficient analysis

Path co-efficient analysis has been widely used in crop breeding programs to determine the nature of relationships between grain yield and its contributing components. Path analysis partitioned the correlation co-efficient into direct and indirect effects and helps to identify components with significant effects on yield to be used as selection criteria. The results of path analysis under both the production system are presented in table 4.9, 4.10, 4.11 and 4.12.

4.4.1 Basmati Genotypes

Under aerobic condition, kernel length exerted high positive direct effect on grain yield (4.128) and showed positive indirect effect through days to 50 % flowering (0.2592), test weight (0.2495), harvest index % (0.2445), number of tillers/plant (0.1815) and root fresh

weight (0.1591). Days to 50% flowering (0.8769) showed high positive direct effect on grain yield and it exhibited positive indirect effect through kernel length (1.281) and root dry weight (0.3106). Test weight (0.7756) had positive direct effect on grain yield and positive indirect effect via kernel length (1.3255) followed by kernel length breadth ratio (0.7206), harvest index (0.4044), number of tillers per plant (0.2266) and days to maturity (0.1629). Harvest index % (0.5707) exhibited positive direct effect on grain yield as well as positive indirect contribution through kernel length (1.7656), test weight (0.5497), number of tillers/plant (0.3118), root fresh weight (0.1959), root fresh and dry weight ratio (0.1309) and days to maturity (0.1002). Plant height (0.5338) expressed positive direct effect on grain yield and positive indirect effect through kernel breadth (0.7409). Biological yield/plant (0.5212) had positive direct contribution towards grain yield as well as positive indirect effect via kernel length breadth ratio (0.4612), root fresh and dry weight ratio (0.2440) and kernel breadth (0.2353). Number of tillers/plant (0.3808) showed positive direct effect on grain yield and positive indirect effect through kernel length (1.9637), harvest index % (0.4673), test weight (0.4616), root fresh and dry weight ratio (0.2290), days to 50% flowering (0.1600), root fresh weight (0.1571) and biological yield/plant (0.1048). Root fresh weight (0.3762) exhibited positive direct effect on grain yield as well as positive indirect effect via kernel length (1.7428), harvest index % (0.2971), days to 50% flowering (0.1957), test weight (0.1895) and number of tillers/plant (0.1590). Number of grains/panicle (0.2988) expressed positive direct effect on grain yield and positive indirect effect via kernel breadth (1.7467), days to 50% flowering (0.1607) and root fresh and dry weight ratio (0.1469). Root volume (0.1790) expressed positive direct effect on grain yield and positive indirect effect via kernel breadth (2.0953), kernel length (1.0823), root fresh and dry weight ratio (0.5113), days to 50% flowering (0.2144), plant height (0.1765) and number of tillers/plant (0.1422). Milling % (0.0371) showed positive direct effect on grain yield as well as positive indirect effect via kernel breadth (1.2285), root dry weight (0.5653), kernel length breadth ratio (0.5172), days to 50% flowering (0.3377) and number of grains per panicle (0.1383). High negative direct effect of kernel breadth (-4.2870) was observed on grain yield whereas it showed positive indirect effect through kernel length (2.3196), kernel length breadth ratio (1.9602), test weight (0.3839), harvest index % (0.2098), days to 50% flowering (0.1381) and number of tillers/plant (0.1069). KLBR (-3.7515) expressed negative direct effect on grain yield and showed positive indirect effect through kernel breadth (2.2400), kernel length (1.6815), root volume (0.1457), root fresh weight (0.1386) and days to 50% flowering (0.1240). Root dry weight (-1.2168) exerted negative direct effect on grain yield and showed positive indirect effect through kernel length (1.3513), root fresh and dry weight ratio (0.8204), harvest index % (0.2956), number of tillers/plant (0.2095), days to maturity (0.1798), test weight (0.1539) and root volume (0.1237). Root fresh and dry weight ratio (-1.0229) exhibited negative direct

effect on grain yield as well as positive indirect effect through root dry weight (0.9760), kernel length breadth ratio (0.3533), days to 50% flowering (0.2629) and root fresh weight (0.1662). Days to maturity (-0.7921) showed negative direct effect on grain yield and it had positive indirect effect via days to 50% flowering (0.8532), kernel length (0.8222) and root dry weight (0.2762). Hulling % (-0.0530) exhibited negative direct effect on grain yield while it showed positive indirect effect through KLBR (0.8679), root dry weight (0.5323) and plant height (0.2230). Head rice recovery % had negative direct effect on grain yield (-0.0437) and it showed positive indirect effect via kernel breadth (0.9327), days to 50% flowering (0.2826), root fresh and dry weight ratio (0.2036), number of grains/panicle (0.1672) and plant height (0.1156). Root length showed negative direct effect on grain yield (-0.0245) as well as positive indirect effect through kernel length (1.1212), kernel breadth (0.5377), root fresh and dry weight ratio (0.1960), plant height (0.1525), days to 50% flowering (0.1332) and root volume (0.1266). Panicle length (-0.0156) exerted negative direct effect on grain yield and it had positive indirect effect through kernel length (0.9404), kernel breadth (0.3330), root fresh weight (0.2595) and plant height (0.2200).

Different results were obtained under both the production system (aerobic and transplanted). In case of transplanted condition, kernel length breadth ratio (0.7482) exhibited positive direct effect on grain yield and showed positive indirect effect via root fresh weight (0.2910) and panicle length (0.0635). Biological yield/plant (0.4922) expressed positive direct effect on grain yield while it showed positive indirect effect through kernel breadth (0.2768), number of tillers/plant (0.2535), root volume (0.2127), harvest index % (0.1935), test weight (0.0981) and number of grains/panicle (0.0924). Root volume (0.4853) exerted positive direct effect on grain yield as well as positive indirect effect via biological yield/plant (0.2157), kernel breadth (0.1588), root dry weight (0.1421), root fresh and dry weight ratio (0.1388) and number of grains/panicle (0.1053). Harvest index % (0.4571) showed positive direct effect on grain yield and positive indirect effect through root fresh weight (0.3019), biological yield/plant (0.2084), number of grains/panicle (0.1749) and number of tillers/plant (0.1078). Number of grains/panicle (0.4376) expressed positive direct effect on grain yield and positive indirect effect via harvest index % (0.1827), biological yield/plant (0.1039) and root volume (0.1168). Root fresh and dry weight ratio (0.4032) exerted positive direct effect on grain yield whereas it observed positive indirect effect via root volume (0.1671), biological yield/plant (0.0869), number of grains/panicle (0.0755) and panicle length (0.0487). Kernel breadth (0.3349) exhibited positive direct effect on grain yield and it showed positive indirect effect via biological yield/plant (0.4067), root volume (0.2301) and number of tillers/plant (0.2072). Number of tillers/plant (0.2848) observed positive direct effect on grain yield and it had positive indirect effect through biological yield/plant (0.4381), kernel breadth (0.2436), harvest index % (0.1730), root volume (0.1400) and number of grains/panicle (0.1225).

Table 4.9 Direct (Bold) and indirect effects on grain yield by yield contributing and quality traits under aerobic condition (Basmati genotypes).

	DTF	DTM	PH	PL	NT/P	GN/PL	TW	BY/P	HI	HULL	MILL	HRR	KL	KB	KLBR	RL	RFW	RV	RDW	RFW/RDW
DTF	0.8769	-0.7707	-0.0021	-0.0001	0.0695	0.0548	-0.1581	-0.0482	-0.0694	-0.0020	0.0143	-0.0141	1.2181	-0.6749	-0.5305	-0.0037	0.0840	0.0438	0.3106	-0.3066
DTM	0.8532	-0.7921	0.0122	0.0011	0.0828	0.0742	-0.1596	0.0097	-0.0722	-0.0004	0.0119	-0.0105	0.8222	-0.3313	-0.4973	-0.0039	0.0959	0.0400	0.2762	-0.2998
PH	-0.0034	-0.0181	0.5338	-0.0064	-0.2145	-0.0145	-0.4847	-0.1076	-0.3042	-0.0221	0.0031	-0.0095	-0.4740	0.7409	-0.2221	-0.0070	0.0055	0.0592	-0.0361	0.0425
PL	0.0072	0.0566	0.2200	-0.0156	-0.0662	0.0564	-0.2786	-0.1346	0.0351	-0.0332	0.0027	-0.0241	0.9404	0.3330	-1.1700	-0.0070	0.2595	0.0341	-0.2968	-0.2111
NT/P	0.1600	-0.1722	-0.3006	0.0027	0.3808	0.0385	0.4616	0.1048	0.4673	0.0344	-0.0171	0.0096	1.9637	-1.2038	-0.7488	0.0023	0.1571	0.0669	-0.6693	0.2290
GN/PL	0.1607	-0.1966	-0.0259	-0.0029	0.0490	0.2988	-0.4001	0.0504	0.0112	0.0057	0.0172	-0.0245	-1.3176	1.7467	-0.4559	0.0005	0.0226	0.0196	-0.1351	0.1469
TW	-0.1787	0.1629	-0.3335	0.0056	0.2266	-0.1541	0.7756	0.0030	0.4044	0.0105	-0.0197	0.0258	1.3255	-2.1221	0.7206	0.0052	0.0919	-0.0246	-0.2415	-0.0225
BY/P	-0.0812	-0.0147	-0.1102	0.0040	0.0766	0.0289	0.0044	0.5212	-0.0890	0.0171	-0.0095	0.0146	-0.8623	0.2353	0.4612	0.0083	-0.1626	-0.0205	-0.0340	0.2440
HI	-0.1066	0.1002	-0.2845	-0.0010	0.3118	0.0059	0.5497	-0.0813	0.5707	0.0200	-0.0175	0.0061	1.7656	-1.5763	-0.1500	0.0010	0.1959	0.0063	-0.6304	0.1309
HULL	0.0326	-0.0067	0.2230	-0.0098	-0.2476	-0.0320	-0.1539	-0.1683	-0.2157	-0.0530	0.0219	-0.0020	-0.8311	-0.1076	0.8679	-0.0121	0.0342	-0.0599	0.5323	-0.4326
MILL	0.3377	-0.2538	0.0452	-0.0012	-0.1754	0.1383	-0.4124	-0.1339	-0.2691	-0.0312	0.0371	-0.0301	-1.7829	1.2285	0.5172	0.0004	-0.0915	-0.0195	0.5653	-0.1916
HRR	0.2826	-0.1909	0.1156	-0.0086	-0.0833	0.1672	-0.4578	-0.1737	-0.0797	-0.0024	0.0256	-0.0437	-0.6076	0.9327	-0.3143	0.0055	-0.0659	0.0269	-0.0099	0.2036
KL	0.2592	-0.1580	-0.0614	-0.0036	0.1815	-0.0955	0.2495	-0.1091	0.2445	0.0107	-0.0161	0.0065	4.1208	-2.4132	-1.5308	-0.0067	0.1591	0.0470	-0.3990	0.0163
KB	0.1381	-0.0612	-0.0922	0.0012	0.1069	-0.1217	0.3839	-0.0286	0.2098	-0.0013	-0.0106	0.0095	2.3196	-4.2870	1.9602	0.0031	0.0227	-0.0875	-0.0238	-0.0775
KLBR	0.1240	-0.1050	0.0316	-0.0049	0.0760	0.0363	-0.1490	-0.0641	0.0228	0.0123	-0.0051	-0.0037	1.6815	2.2400	-3.7515	-0.0100	0.1386	0.1457	-0.3754	0.0963
RL	0.1332	-0.1246	0.1525	-0.0045	-0.0357	-0.0059	-0.1650	-0.1767	-0.0222	-0.0262	-0.0006	0.0098	1.1212	0.5377	-1.5338	-0.0245	0.0632	0.1266	-0.4109	0.1960
RFW	0.1957	-0.2019	0.0078	-0.0107	0.1590	0.0180	0.1895	-0.2252	0.2971	-0.0048	-0.0090	0.0077	1.7428	-0.2585	-1.3817	-0.0041	0.3762	0.0398	-0.2032	-0.4518
RV	0.2144	-0.1769	0.1765	-0.0030	0.1422	0.0327	-0.1066	-0.0598	0.0201	0.0177	-0.0040	-0.0066	1.0823	2.0953	-3.0532	-0.0173	0.0836	0.1790	-0.8406	0.5113
RDW	-0.2238	0.1798	0.0159	-0.0038	0.2095	0.0332	0.1539	0.0146	0.2956	0.0232	-0.0172	-0.0004	1.3513	-0.0838	-1.1575	-0.0083	0.0628	0.1237	-1.2168	0.8204
RFW/RDW	0.2629	-0.2322	-0.0222	-0.0032	-0.0853	-0.0429	0.0170	-0.1243	-0.0730	-0.0224	0.0070	0.0087	-0.0655	-0.3247	0.3533	0.0047	0.1662	-0.0895	0.9760	-1.0229

Residual = 0.02438

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

Table 4.10 Direct (Bold) and indirect effects on grain yield by yield contributing and quality traits under transplanted condition (Basmati genotypes)

	DTF	DTM	PH	PL	NT/P	GN/PL	TW	BY/P	HI	HULL	MILL	HRR	KL	KB	KLBR	RL	RFW	RV	RDW	RFW/RDW
DTF	-0.0328	-0.2136	-0.0094	0.0531	-0.0909	0.0443	-0.0547	-0.2482	-0.0940	0.0511	-0.0001	-0.0732	-0.0139	-0.0912	0.2604	-0.0047	-0.0713	0.0578	-0.0406	0.1489
DTM	-0.0299	-0.2344	-0.0066	0.0332	-0.0162	0.0352	-0.0307	-0.0464	-0.1497	0.0202	0.0001	-0.0139	-0.0130	-0.0035	0.1000	-0.0068	-0.2002	0.1499	-0.0144	0.1660
PH	-0.0190	-0.0964	-0.0162	0.1013	-0.1147	0.0595	-0.0705	-0.3869	-0.0121	0.0596	-0.0002	-0.0705	-0.0145	-0.0594	0.2092	-0.0062	-0.2471	0.1395	0.0514	-0.0016
PL	-0.0102	-0.0455	-0.0096	0.1713	-0.1272	-0.0546	-0.0503	-0.2046	0.1241	0.0423	0.0000	-0.0723	-0.0020	-0.1534	0.2774	-0.0035	-0.2077	0.0864	0.0120	0.1147
NT/P	0.0105	0.0134	0.0065	-0.0765	0.2848	0.1225	0.0566	0.4381	0.1730	-0.0123	0.0001	-0.0213	0.0164	0.2436	-0.5650	-0.0041	-0.1659	0.1400	0.0288	0.0444
GN/PL	-0.0033	-0.0189	-0.0022	-0.0214	0.0798	0.4376	-0.0058	0.1039	0.1827	0.0168	0.0001	-0.1503	0.0302	0.0522	-0.3579	-0.0016	-0.1594	0.1168	0.0107	0.0695
TW	0.0137	0.0551	0.0087	-0.0661	0.1238	-0.0196	0.1303	0.3707	-0.0002	-0.0526	0.0002	0.0876	0.0100	0.1726	-0.3628	-0.0018	-0.1581	0.0784	0.0099	0.0570
BY/P	0.0165	0.0221	0.0127	-0.0712	0.2535	0.0924	0.0981	0.4922	0.1935	-0.0891	0.0005	0.0352	0.0083	0.2768	-0.5341	-0.0095	-0.2861	0.2127	0.0473	0.0712
HI	0.0067	0.0768	0.0004	0.0465	0.1078	0.1749	0.0000	0.2084	0.4571	0.0440	-0.0002	-0.1071	0.0370	-0.0785	-0.1729	0.0093	0.3019	-0.1963	-0.0547	-0.0377
HULL	-0.0133	-0.0375	-0.0076	0.0575	-0.0278	0.0581	-0.0543	-0.3477	0.1593	0.1262	-0.0003	-0.1739	0.0249	-0.2002	0.1164	0.0057	0.2300	-0.1766	-0.0824	0.1035
MILL	-0.0054	0.0268	-0.0057	-0.0024	-0.0547	-0.1106	-0.0488	-0.4622	0.1396	0.0705	-0.0006	-0.0820	0.0108	-0.1230	0.1031	0.0020	0.2606	-0.1929	-0.1072	0.1654
HRR	-0.0087	-0.0118	-0.0041	0.0449	0.0220	0.2383	-0.0414	-0.0628	0.1774	0.0795	-0.0002	-0.2759	0.0117	-0.0837	0.0478	-0.0024	0.2184	-0.1542	-0.0389	-0.0627
KL	-0.0077	-0.0513	-0.0040	0.0058	-0.0787	-0.2230	-0.0220	-0.0691	-0.2858	-0.0529	0.0001	0.0547	-0.0592	0.0242	0.4732	-0.0055	0.0155	0.0294	0.0629	-0.2305
KB	0.0089	0.0025	0.0029	-0.0784	0.2072	0.0682	0.0671	0.4067	-0.1072	-0.0754	0.0002	0.0690	-0.0043	0.3349	-0.5412	-0.0098	-0.3422	0.2301	0.0635	0.0549
KLBR	-0.0114	-0.0313	-0.0045	0.0635	-0.2151	-0.2093	-0.0632	-0.3514	-0.1056	0.0196	-0.0001	-0.0176	-0.0375	-0.2423	0.7482	0.0035	0.2910	-0.1665	-0.0055	-0.2153
RL	-0.0077	-0.0797	-0.0050	0.0300	0.0583	0.0348	0.0117	0.2351	-0.2125	-0.0359	0.0001	-0.0335	-0.0164	0.1639	-0.1315	-0.0199	-0.4251	0.2510	0.0599	0.0913
RFW	-0.0028	-0.0558	-0.0047	0.0423	0.0561	0.0828	0.0245	0.1673	-0.1639	-0.0345	0.0002	0.0716	0.0011	0.1361	-0.2586	-0.0101	-0.8419	0.4947	0.1320	0.1604
RV	-0.0039	-0.0724	-0.0046	0.0305	0.0822	0.1053	0.0211	0.2157	-0.1848	-0.0459	0.0002	0.0877	-0.0036	0.1588	-0.2566	-0.0103	-0.8582	0.4853	0.1421	0.1388
RDW	0.0075	0.0190	-0.0047	0.0116	0.0462	0.0264	0.0073	0.1314	-0.1411	-0.0586	0.0003	0.0606	-0.0210	0.1200	-0.0233	-0.0067	-0.6269	0.3889	0.1773	-0.1228
RFW/RDW	-0.0121	-0.0965	0.0001	0.0487	0.0313	0.0755	0.0184	0.0869	-0.0427	0.0324	-0.0002	0.0429	0.0339	0.0456	-0.3995	-0.0045	-0.3348	0.1671	-0.0540	0.4032

Residual = 0.00171

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

Root dry weight (0.1773) expressed positive direct effect on grain yield and showed positive indirect effect via root volume (0.3889), biological yield/plant (0.1314) and kernel breadth (0.1200). Panicle length (0.1713) observed positive direct effect on grain yield as well as positive indirect effect via kernel length breadth ratio (0.2774), harvest index % (0.1241) and root fresh and dry weight ratio (0.1147). Test weight (0.1303) showed positive direct effect on grain yield and positive indirect effect through biological yield/plant (0.3707), kernel breadth (0.1726) and number of tillers/plant (0.1238). Hulling % (0.1262) showed positive direct effect on grain yield while it showed positive indirect effect via root fresh weight (0.2300), harvest index % (0.1593), kernel length breadth ratio (0.1164) and root fresh and dry weight ratio (0.1035). Root fresh weight (-0.8419) exhibited negative direct contribution towards grain yield and showed positive indirect contribution via root volume (0.4947), biological yield/plant (0.1673), root fresh and dry weight ratio (0.1604), kernel breadth (0.1361) and root dry weight (0.1320). Head rice recovery % (-0.2759) exerted negative direct effect on grain yield and it had positive indirect effect via number of grains/panicle (0.2383), root fresh weight (0.2184) and harvest index % (0.1774). Days to maturity (-0.2344) exhibited negative direct effect on grain yield as well as it showed positive indirect effect through root fresh and dry weight ratio (0.1660), root volume (0.1499) and kernel length breadth ratio (0.1000). Kernel length (-0.0592) showed negative direct effect on grain yield whereas, it showed positive indirect effect through kernel length breadth ratio (0.4732). Days to 50% flowering (-0.0328) exhibited negative direct effect on grain yield and positive indirect effect through kernel length breadth ratio (0.2604) and root fresh and dry weight ratio (0.1489). Root length (-0.0199) exerted negative direct effect on grain yield whereas, it showed positive indirect effect via root volume (0.2510), biological yield/plant (0.2351) and kernel breadth (0.1639). Plant height (-0.0162) observed negative direct effect on grain yield and showed positive indirect effect via kernel length breadth ratio (0.2092), root volume (0.1395) and panicle length (0.1013). Milling % (-0.0006) expressed negative direct effect on grain yield whereas showed positive indirect effect via root fresh weight (0.2606), root fresh and dry weight ratio (0.1654), harvest index % (0.1396) and kernel length breadth ratio (0.1164). These results are given in table 4.9 and 4.10

4.4.2 Non-basmati Genotypes

In aerobic condition, kernel length (1.5725) exhibited high positive direct effect on grain yield as well as positive indirect effect via days to maturity (0.2906). Root volume (0.8616) exhibited positive direct effect on grain yield it showed positive indirect effects through days to maturity (0.2631), biological yield/plant (0.2200) and root fresh and dry weight ratio (0.2178). Days to 50% flowering (0.6518) expressed positive direct effect on grain yield and observed positive indirect effect through kernel length (0.7011) and root volume (0.3478). Biological yield per plant (0.6503) showed positive direct effect on grain

yield and positive indirect effect via root volume (0.2915), kernel breadth (0.1977), harvest index (0.1230) and number of grains/panicle (0.1032). Harvest index % (0.4339) exhibited positive direct contribution towards grain yield as well as positive indirect contribution through kernel breadth (0.2620), biological yield/plant (0.1843), number of grains per panicle (0.1816) and test weight (0.1243). Number of grains per panicle (0.4170) observed positive direct effect on grain yield and it had positive indirect effect through kernel breadth (0.3750), days to maturity (0.2636), harvest index% (0.1890), root fresh weight (0.1823) and biological yield/plant (0.1610). Test weight (0.3224) showed positive direct effect on grain yield and positive indirect effect through kernel length (0.2176), biological yield per plant (0.1753) and harvest index % (0.1672). Root fresh and dry weight ratio (0.3046) exhibited positive direct effect on grain yield and positive indirect effect via root volume (0.6159) and kernel length breadth ratio (0.4160). Plant height (0.1966) observed positive direct effect on grain yield and it showed positive indirect effect through kernel length (0.2410) and kernel length breadth ratio (0.1279). Root length (0.1088) exhibited positive direct effect on grain yield as well as positive indirect effect via kernel length (0.1973), kernel length and breadth ratio (0.1688) and harvest index % (0.1200). Hulling % (0.0700) showed positive direct effect on grain yield and it observed positive indirect effect via root volume (0.259), days to 50% flowering (0.2364), root fresh and dry weight ratio (0.1334) and plant height (0.1032). Head rice recovery % (0.0391) expressed positive direct effect on grain yield and positive indirect effect through kernel length (0.3384), days to 50% flowering (0.3263), root volume (0.2108), biological yield/plant (0.1226) and plant height (0.1037). Milling % exhibited positive direct effect on grain yield as well as positive indirect effect via root fresh weight (0.2849), plant height (0.2151) and kernel length breadth ratio (0.1036). Root dry weight (0.0104) exhibited positive direct effect on grain yield while it showed positive indirect effect via kernel length (0.6427), test weight (0.1696), biological yield/plant (0.1622), days to 50% flowering (0.1151) and root fresh weight (0.1123). Negative direct effect of kernel length breadth ratio (-1.7990) was observed on grain yield whereas it showed positive indirect effect through kernel length (1.4337), kernel breadth (0.3713) and days to 50% flowering (0.1919). Root fresh weight (-0.8857) exerted negative direct effect on grain yield while it showed positive indirect effect through root volume (0.8634), days to 50% flowering (0.2622), root fresh and dry weight ratio (0.2317), biological yield/plant (0.2150) and kernel length breadth ratio (0.1036). Kernel breadth (-0.7060) had negative direct effect on grain yield and positive indirect effect via kernel length breadth ratio (0.9461), days to 50% flowering (0.1454) and plant height (0.1222). Days to maturity (-0.6363) exerted negative direct effects on grain yield and it observed positive indirect effect via days to 50% flowering (0.6393), kernel length (0.6269) and root volume (0.3267). Plant height (-0.2850) observed negative direct effect on grain yield and positive indirect effect via root volume (0.4985), biological yield/plant (0.3448),

kernel breadth (0.3028), days to maturity (0.1975), number of grains per panicle (0.1332) and root fresh and dry weight ratio (0.1310). Number of tillers/plant (-0.0039) exhibited negative direct effect on grain yield and it showed positive indirect effect via biological yield/plant (0.239), root fresh weight (0.1942) and kernel length (0.1623).

In transplanted condition, kernel length (2.0531) expressed positive direct effect on grain yield and positive indirect effect via root fresh and dry weight (0.2299), days to 50% flowering (0.2196) and kernel breadth (0.2188). High positive direct effect of days to 50% flowering (0.8215) was observed on grain yield/plant whereas it showed positive indirect effect through kernel length (0.5489), number of tillers/plant (0.1413), harvest index% (0.1167) and hulling % (0.1144). Number of grains per panicle (0.5783) exhibited positive direct effect on grain yield and positive indirect effect through biological yield/plant (0.1607) and kernel breadth (0.1532). Panicle length (0.3791) showed positive direct effect on grain yield and positive indirect effect via kernel length (0.5421), kernel breadth (0.2726) and number of grains/panicle (0.1068). Hulling % (0.3749) observed positive direct effect on grain yield and positive indirect effect via kernel length-breadth ratio (1.2206), days to 50% flowering (0.2507) and harvest index% (0.1056). Harvest index % (0.3518) expressed positive direct effect on grain yield and positive indirect effect through kernel length-breadth ratio (0.5482), days to 50% flowering (0.2726), hulling % (0.1125) and number of tillers/plant (0.1078). Root fresh weight (0.3489) exhibited positive direct effect on grain yield as well as it had positive indirect effect through kernel breadth (0.4949), kernel length (0.3590), number of tillers/plant (0.1637), root dry weight (0.1554), biological yield/plant (0.1413) and root volume (0.1244). Number of tillers/plant (0.3041) expressed positive direct effect on grain yield as well as positive indirect effect via kernel length (0.6034), days to 50% flowering (0.3818), root fresh weight (0.1878) and harvest index% (0.1274). Biological yield per plant (0.2786) showed positive direct effect on grain yield and positive indirect effects through kernel length (0.3925), kernel breadth (0.3676), number of grains/panicle (0.335), and root fresh weight (0.1770). Root dry weight (0.1840) exhibited positive direct effect on grain yield and positive indirect effect via kernel length (1.0092), kernel breadth (0.5166), root fresh weight (0.2946), biological yield/plant (0.1301), root fresh and dry weight ratio (0.1191) and number of tillers/plant (0.1005). Milling % (0.1442) showed positive direct effect on grain yield while it had positive indirect effect through kernel length (0.6590), days to 50% flowering (0.4475), root fresh and dry weight ratio (0.2240), harvest index % (0.1278), hulling % (0.1190), head rice recovery % (0.1020) and number of tillers/plant (0.1016). Head rice recovery % (0.1404) showed positive direct effect on grain yield whereas it had positive indirect effect through days to 50% flowering (0.4101), kernel length (0.4067), kernel length and breadth ratio (0.2730), root fresh and dry weight ratio (0.2576) and milling % (0.1047). Root volume (0.1307) expressed positive direct effect on grain yield and showed positive indirect effect via root fresh weight (0.3321), kernel breadth (0.2862),

number of tillers/plant (0.2008), kernel length (0.1732), biological yield/plant (0.1614), root dry weight (0.1398) and days to 50% flowering (0.1249). Plant height (0.0021) observed positive direct effect on grain yield and positive indirect effect through kernel breadth (0.4593), kernel length (0.3724), number of grains/panicle (0.2387), days to maturity (0.2115), panicle length (0.1741) and biological yield/plant (0.1177). Negative direct effect of kernel length breadth ratio (-3.1143) was observed on grain yield whereas it had positive indirect effect through kernel length (1.8035), kernel breadth (0.8482), root fresh and dry weight ratio (0.2001), panicle length (0.1201), root fresh weight (0.1089) and root dry weight (0.1063). Kernel breadth (-1.3949) exhibited negative direct effect on grain yield and positive indirect effect via kernel length breadth ratio (1.8268), days to 50% flowering (0.3790) and hulling % (0.1667). Days to maturity (-1.0086) showed negative direct effect on grain yield and positive indirect effect via days to 50% flowering (0.8129), kernel length (0.5131) kernel length breadth ratio (0.1151) and number of tillers/plant (0.1127). Root fresh and dry weight ratio (-0.4437) exerted negative direct effect on grain yield and it showed positive indirect effect via kernel length breadth ratio (1.3546), panicle length (0.1597) and root length (0.1128). Root length (-0.1239) showed negative direct effect on grain yield and positive indirect effect through kernel length (0.8077), root fresh and dry weight ratio (0.4039), kernel breadth (0.2584) and days to maturity (0.2268). Test weight (-0.0696) observed negative direct effect on grain yield and positive indirect effect via kernel length-breadth ratio (0.2240), hulling % (0.2032), harvest index % (0.1882) and root fresh weight (0.1167). Above results are given in table 4.11 and 4.12.

4.5 Genetic Divergence Analysis

Results of ANOVA indicated the presence of substantial amount of variability among the genotypes but did not elaborate the degree of variability.

4.5.1 Clustering Pattern in Basmati Genotypes

Clustering was done according to the method suggested by Tocher and described by the Rao, 1952. Based on D^2 values 24 Basmati genotypes were grouped into 6 clusters in aerobic condition as well as transplanted condition (Fig. 16). In aerobic condition, maximum number of genotypes were grouped into cluster no. 1 (19) followed by cluster 2, cluster 3, cluster 4, cluster 5, and cluster 6 having single genotype each. Under transplanted condition, maximum genotypes were grouped into cluster 1 (16 genotypes) followed by cluster 2 (5 genotypes), cluster 3 (1 genotype), cluster 4 (1 genotype), cluster 5 (1 genotype) and cluster 6 (1 genotype). The genotypes were not distributed homogeneously in the clusters. Clustering pattern of basmati genotypes under aerobic condition and transplanted condition are presented in table 4.13 and 4.14.

Table 4.11 Direct (Bold) and indirect effects on grain yield by yield contributing and quality traits under aerobic condition (Non-basmati genotypes).

	DTF	DTM	PH	PL	NT/P	GN/PL	TW	BY/P	HI	HULL	MILL	HRR	KL	KB	KLBR	RL	RFW	RV	RDW	RFW/RDW
DTF	0.6518	-0.6240	0.0968	-0.0323	-0.0004	-0.2323	0.0257	-0.0092	-0.0513	0.0254	0.0044	0.0196	0.7011	-0.1574	-0.5295	0.0100	-0.3563	0.3478	0.0018	0.0399
DTM	0.6393	-0.6363	0.0884	-0.0232	-0.0005	-0.1728	0.0149	0.0170	-0.0051	0.0279	0.0057	0.0205	0.6269	-0.0949	-0.5234	0.0071	-0.3366	0.3267	0.0018	0.0366
PH	-0.2213	0.1975	-0.2850	0.0724	0.0008	0.1332	0.0187	0.3448	0.0702	-0.0254	-0.0260	-0.0142	-0.1724	0.3028	-0.1186	0.0320	-0.5060	0.4985	-0.0003	0.1310
PL	-0.1072	0.0751	-0.1050	0.1966	-0.0008	0.0984	-0.0766	0.0816	-0.0362	-0.0088	-0.0234	-0.0140	0.2410	0.1279	-0.3702	0.0460	0.0902	-0.0809	0.0025	-0.0824
NT/P	0.0599	-0.0846	0.0558	0.0410	-0.0039	0.0318	-0.0518	0.2369	0.0222	0.0061	0.0059	0.0035	0.1623	0.0989	-0.2734	0.0143	0.1942	-0.1972	-0.0010	-0.0340
GN/PL	-0.3631	0.2636	-0.0910	0.0464	-0.0003	0.4170	-0.1376	0.1610	0.1890	-0.0121	-0.0014	-0.0191	-0.4378	0.3750	0.0425	-0.0220	0.1823	-0.1827	-0.0018	-0.0013
TW	0.0519	-0.0293	-0.0165	-0.0467	0.0006	-0.1779	0.3224	0.1753	0.1672	-0.0452	-0.0072	0.0043	0.2176	-0.1169	-0.0580	0.0192	-0.0422	0.0757	0.0055	-0.0862
BY/P	-0.0092	-0.0167	-0.1511	0.0247	-0.0014	0.1032	0.0869	0.6503	0.1230	0.0086	-0.0149	0.0074	-0.0620	0.1977	-0.1480	0.0119	-0.2927	0.2915	0.0026	0.0236
HI	-0.0771	0.0074	-0.0461	-0.0164	-0.0002	0.1816	0.1243	0.1843	0.4339	-0.0279	-0.0126	-0.0131	0.0098	0.2620	-0.2580	0.0301	-0.0243	0.0003	-0.0001	0.0033
HULL	0.2364	-0.2532	0.1032	-0.0246	-0.0003	-0.0723	-0.2082	0.0798	-0.1731	0.0700	0.0191	0.0247	-0.0046	-0.0182	-0.0018	-0.0301	-0.2623	0.2597	-0.0046	0.1334
MILL	0.0824	-0.1058	0.2151	-0.1336	-0.0007	-0.0171	-0.0668	-0.2800	-0.1580	0.0387	0.0345	0.0301	-0.0059	-0.1179	0.1036	-0.1042	0.2849	-0.2608	-0.0027	-0.0146
HRR	0.3263	-0.3333	0.1037	-0.0702	-0.0003	-0.2032	0.0358	0.1226	-0.1451	0.0442	0.0266	0.0391	0.3384	-0.3318	-0.0086	-0.0202	-0.2154	0.2108	0.0002	0.0417
KL	0.2906	-0.2536	0.0312	0.0301	-0.0004	-0.1161	0.0446	-0.0256	0.0027	-0.0002	-0.0001	0.0084	1.5725	0.0927	-1.6401	0.0137	-0.0086	0.0106	0.0043	-0.0863
KB	0.1454	-0.0855	0.1222	-0.0356	0.0005	-0.2215	0.0534	-0.1821	-0.1610	0.0018	0.0058	0.0184	-0.2064	-0.7060	0.9461	-0.0260	-0.1222	0.0869	0.0015	-0.0116
KLBR	0.1919	-0.1851	-0.0188	0.0405	-0.0006	-0.0099	0.0104	0.0535	0.0622	0.0001	-0.0020	0.0002	1.4337	0.3713	-1.7990	0.0225	0.0510	-0.0328	0.0030	-0.0705
RL	0.0600	-0.0414	-0.0838	0.0832	-0.0005	-0.0844	0.0568	0.0713	0.1200	-0.0193	-0.0330	-0.0073	0.1973	0.1688	-0.3711	0.1088	-0.0174	0.0421	0.0005	-0.0218
RFW	0.2622	-0.2418	-0.1628	-0.0200	0.0008	-0.0858	0.0154	0.2150	0.0119	0.0207	-0.0111	0.0095	0.0153	-0.0974	0.1036	0.0021	-0.8857	0.8634	-0.0013	0.2317
RV	0.2631	-0.2412	-0.1649	-0.0185	0.0009	-0.0884	0.0283	0.2200	0.0001	0.0211	-0.0104	0.0096	0.0193	-0.0712	0.0685	0.0053	-0.8874	0.8616	-0.0005	0.2178
RDW	0.1151	-0.1096	0.0084	0.0463	0.0004	-0.0711	0.1696	0.1622	-0.0039	-0.0311	-0.0088	0.0008	0.6427	-0.1009	-0.5174	0.0050	0.1123	-0.0443	0.0104	-0.2207
RFW/RDW	0.0854	-0.0765	-0.1226	-0.0532	0.0004	-0.0018	-0.0913	0.0503	0.0047	0.0307	-0.0017	0.0054	-0.4453	0.0269	0.4161	-0.0078	-0.6738	0.6159	-0.0076	0.3046

Residual = 0.00659

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

Table 4.12 Direct and indirect effects on grain yield by yield contributing and quality traits under transplanted condition (Non-basmati genotypes)

	DTF	DTM	PH	PL	NT/P	GN/PL	TW	BY/P	HI	HULL	MILL	HRR	KL	KB	KLBR	RL	RFW	RV	RDW	RFW/RDW
DTF	0.8215	-0.9980	-0.0003	-0.0209	0.1413	-0.0474	-0.0037	0.0011	0.1167	0.1144	0.0785	0.0701	0.5489	-0.6435	0.0195	0.0317	0.0136	0.0199	0.0074	-0.0038
DTM	0.8129	-1.0086	-0.0004	-0.0183	0.1127	-0.0395	-0.0007	-0.0023	0.0961	0.0971	0.0854	0.0789	0.5131	-0.7035	0.1151	0.0279	0.0117	0.0167	0.0081	-0.0061
PH	-0.1070	0.2115	0.0021	0.1741	-0.0450	0.2387	-0.0173	0.1177	-0.0247	-0.0347	-0.0748	-0.0627	0.3724	0.4593	-0.8716	0.0051	0.0456	0.0170	0.0217	0.0054
PL	-0.0452	0.0488	0.0010	0.3791	0.0049	0.1068	0.0057	0.0208	0.0194	-0.1353	0.0047	-0.0351	0.5421	0.2726	-0.9522	0.0200	0.0545	0.0090	-0.0142	-0.1869
NT/P	0.3818	-0.3738	-0.0003	0.0061	0.3041	-0.2883	-0.0033	0.0481	0.1247	0.0996	0.0482	0.0274	0.6034	0.0540	-0.7514	0.0409	0.1878	0.0863	0.0608	-0.1352
GN/PL	-0.0674	0.0688	0.0009	0.0700	-0.1516	0.5783	0.0319	0.1607	-0.1225	-0.1575	-0.0654	0.0035	-0.0441	0.1532	-0.1261	0.0213	-0.0422	-0.0217	0.0009	0.0800
TW	0.0433	-0.0096	0.0005	-0.0313	0.0142	-0.2648	-0.0696	-0.0356	0.1882	0.2032	0.0360	0.0052	-0.0451	-0.1084	0.2240	-0.0019	0.1167	0.0476	0.0513	-0.0101
BY/P	0.0032	0.0083	0.0009	0.0284	0.0525	0.3335	0.0089	0.2786	-0.2043	-0.0522	-0.0529	0.0047	0.3925	0.3676	-0.8283	0.0340	0.1770	0.0757	0.0860	-0.0492
HI	0.2726	-0.2754	-0.0002	0.0209	0.1078	-0.2013	-0.0372	-0.1618	0.3518	0.1125	0.0524	0.0154	-0.1652	-0.3249	0.5482	0.0080	-0.0796	-0.0319	-0.0406	0.0473
HULL	0.2507	-0.2612	-0.0002	-0.1368	0.0808	-0.2430	-0.0377	-0.0388	0.1056	0.3749	0.0458	0.0068	-0.4407	-0.6202	1.2206	0.0732	-0.1069	-0.0179	-0.0709	-0.0633
MILL	0.4475	-0.5977	-0.0011	0.0125	0.1016	-0.2622	-0.0174	-0.1023	0.1278	0.1190	0.1442	0.1020	0.6590	-0.5281	-0.1830	-0.0239	-0.1949	-0.0758	-0.0408	0.2240
HRR	0.4101	-0.5666	-0.0009	-0.0947	0.0594	0.0143	-0.0026	0.0093	0.0385	0.0183	0.1047	0.1404	0.4067	-0.7304	0.2730	-0.0448	-0.1101	-0.0326	0.0031	0.2576
KL	0.2196	-0.2520	0.0004	0.1001	0.0894	-0.0124	0.0015	0.0533	-0.0283	-0.0805	0.0463	0.0278	2.0531	0.2188	-2.6390	-0.0487	0.0610	0.0110	0.0905	0.2299
KB	0.3790	-0.5086	-0.0007	-0.0741	-0.0118	-0.0635	-0.0054	-0.0734	0.0820	0.1667	0.0546	0.0735	-0.3221	-1.3949	1.8268	0.0230	-0.1238	-0.0268	-0.0682	-0.0281
KLBR	-0.0053	0.0387	0.0006	0.1201	0.0761	0.0243	0.0052	0.0768	-0.0642	-0.1523	0.0088	-0.0128	1.8035	0.8482	-3.0043	-0.0514	0.1089	0.0215	0.1063	0.2001
RL	-0.2104	0.2268	-0.0001	-0.0613	-0.1003	-0.0995	-0.0011	-0.0764	-0.0228	-0.2215	0.0278	0.0507	0.8077	0.2584	-1.2460	-0.1239	-0.0436	-0.0254	0.0664	0.4039
RFW	0.0320	-0.0337	0.0003	0.0592	0.1637	-0.0699	-0.0233	0.1413	-0.0802	-0.1148	-0.0805	-0.0443	0.3590	0.4949	-0.9380	0.0155	0.3489	0.1244	0.1554	-0.1246
RV	0.1249	-0.1290	0.0003	0.0260	0.2008	-0.0960	-0.0253	0.1614	-0.0859	-0.0512	-0.0837	-0.0350	0.1732	0.2862	-0.4934	0.0241	0.3321	0.1307	0.1398	-0.1471
RDW	0.0328	-0.0442	0.0002	-0.0291	0.1005	0.0027	-0.0194	0.1301	-0.0776	-0.1445	-0.0320	0.0023	1.0092	0.5166	-1.7349	-0.0447	0.2946	0.0993	0.1840	0.1191
RFW/RDW	0.0070	-0.0140	0.0000	0.1597	0.0927	-0.1043	-0.0016	0.0309	-0.0375	0.0535	-0.0728	-0.0815	-1.0637	-0.0882	1.3546	0.1128	0.0980	0.0433	-0.0494	-0.4437

Residual = 0.02108

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

Table 4.13: Clustering pattern of basmati genotypes under aerobic condition

Clusters	No. of genotypes	Name of Genotypes
Cluster 1	19	Basmati 370, Taraori Basmati, CSR-30, Type-3, HKR 15-482, Super Basmati, HKR 03-408, HKR15-483, HKR 15-488, HKR 15-487, HKR 08-408, HKR 06-434, HB-1, PB-1, Pusa 1718-14-2-150, HKR 14-410, HKR 06-443-66, HKR 16-459, HKR 16-464
Cluster 2	1	HB 2
Cluster 3	1	HKR 15-455
Cluster 4	1	Pusa 1557-06-08126-162-156
Cluster 5	1	Pusa 1656-10-705
Cluster 6	1	PB 1121

Table 4.14: Clustering pattern of basmati genotypes under transplanted condition

Clusters	No. of genotypes	Name of genotypes
Cluster 1	16	Taraori Basmati, CSR-30, Type-3, HKR 15-482, Super Basmati, HKR 03-408, HKR 15-483, HKR 15-488, HKR 15-487, HKR 08-408, HKR 06-434, HB-1, HKR 15-455, HKR 14-410, HKR 16-459, HKR 16-464
Cluster 2	5	PB 1121, Pusa 1557-06-08126-162-156, Pusa 1718-14-2-150, Pusa 1656-10-705, HKR 06-443-66
Cluster 3	1	Basmati370
Cluster 4	1	PB - 1
Cluster 5	1	HKR 16-464
Cluster 6	1	HB-2

4.5.2 Dendrogram

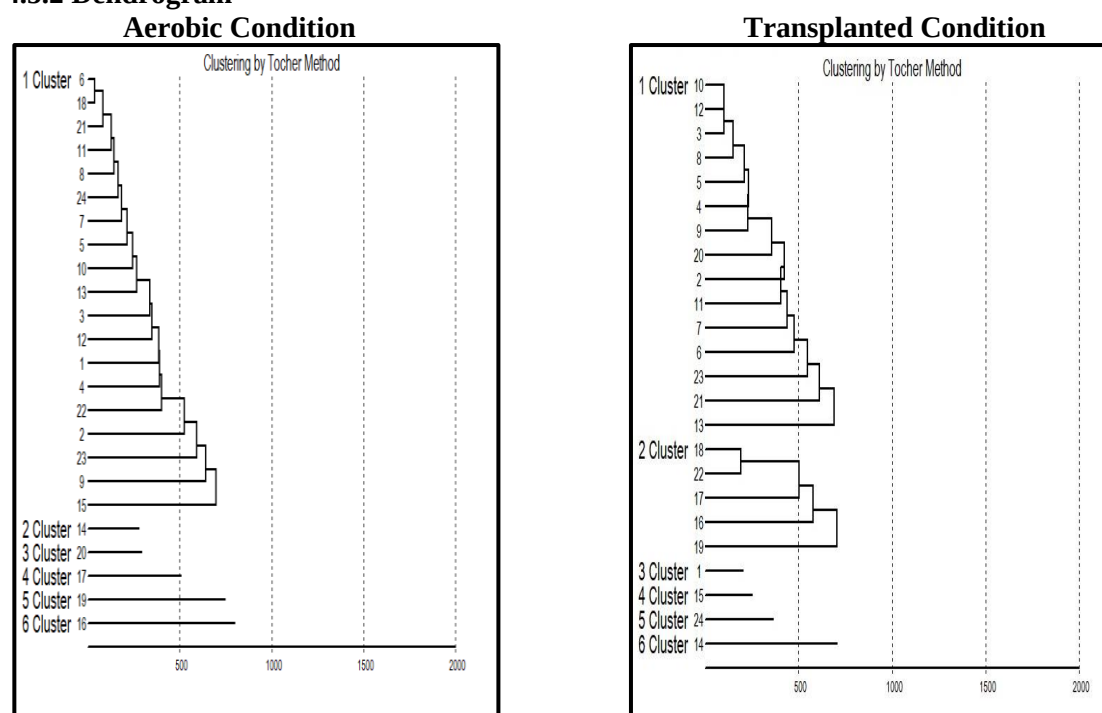


Fig 16: Group constellation of Basmati genotypes under aerobic and transplanted conditions by Torcher's method

4.5.3 Intra and Inter-cluster average D^2 values for Basmati genotypes

In aerobic condition, maximum intra-cluster distance was observed for cluster 1 (21.36) while maximum inter-cluster D^2 values were recorded between cluster 5 and cluster 6 (51.79) followed by cluster 2 and cluster 5 (47.79), cluster 3 and cluster 5 (41.58), cluster 1 and cluster 5 (40.37), cluster 4 and cluster 6 (39.72), cluster 1 and cluster 6 (34.92), cluster 3 and 6 (32.73), cluster 1 and 4 (31.89), cluster 2 and cluster 4 (31.12), cluster 1 and cluster 2 (30.02), cluster 4 and cluster 5 (28.99), cluster 2 and cluster 6 (28.77), cluster 1 and cluster 3 (28.34), cluster 3 and cluster 4 (22.5) and cluster 2 and cluster 3 (17.12).

Maximum intra cluster distance was recorded for cluster 2 (27.42). Maximum inter-cluster distance was recorded for cluster 2 and cluster 4 (69.89) followed by cluster 2 and cluster 5 (69.03), cluster 2 and cluster 3 (63.82), cluster 1 and cluster 2 (51.66), cluster 5 and cluster 6 (49.39), cluster 2 and cluster 6 (45.88), cluster 4 and cluster 6 (44.39), cluster 1 and cluster 6 (39.84), cluster 1 and cluster 3 (31.31), cluster 3 and cluster 6 (31.10), cluster 1 and cluster 4 (29.89), cluster 3 and cluster 5 (29.53), cluster 1 and cluster 5 (28.49), cluster 3 and cluster 4 (24.26) and cluster 4 and cluster 5 (19.07) in transplanted condition. The inter and intra-cluster distances between six clusters are depicted in tables 4.15 and 4.16

Table 4.15: Intra (diagonal) and Inter-Cluster distances under aerobic condition in Basmati Genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	21.36	30.02	28.34	31.89	40.37	34.92
Cluster 2		0	17.12	31.12	47.79	28.77
Cluster 3			0	22.5	41.58	32.73
Cluster 4				0	28.99	39.72
Cluster 5					0	51.79
Cluster 6						0

Table 4.16: Intra (diagonal) and Inter-Cluster distances under transplanted condition in Basmati Genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	22.33	51.66	31.31	29.89	28.49	39.84
Cluster 2		27.42	63.82	69.89	69.03	45.88
Cluster 3			0	24.26	29.53	31.1
Cluster 4				0	19.07	44.39
Cluster 5					0	49.39
Cluster 6						0

4.5.4 Cluster means for basmati genotypes grown under aerobic and transplanted conditions

The results of cluster mean for 21 yield and quality traits grown under aerobic and transplanted conditions for basmati genotypes are shown in table 4.17 and 4.18.

The results revealed that cluster mean for grain yield/plant (18.87 g), number of tillers/plant (14.28) and root dry weight (6.10g) was recorded highest in cluster 4 while minimum cluster mean for grain yield/plant (11.27 g), number of tillers/plant (9.06) and root dry weight (3.5 g) was recorded in cluster 5 under aerobic condition. Cluster 6 showed highest cluster mean value for kernel length breadth ratio (4.76), root length (15.99 cm), root fresh weight (27.02g) and root dry weight (25.67g) while minimum for kernel breadth (1.5mm). Maximum cluster means for Days to 50 % flowering (102.18), days to maturity (140.54), kernel length (7.37) and kernel breadth (1.84) were recorded in cluster 1. Cluster 2 recorded maximum cluster mean for number of grains/panicle (111.35), hulling % (77%), milling % (68.63) and root fresh and dry weight ratio (6.15) while it showed minimum cluster mean for test weight (21.13g) and kernel length (6.54mm). The highest cluster mean for panicle length (27.51cm), harvest index % (45.19 %) and head rice recovery % (59.03) was observed in cluster 3 along with minimum cluster mean for plant height (104.54cm) and biological yield/plant (32.83 g). Cluster 4 showed lowest cluster mean for days to 50% flowering. Maximum cluster mean for plant height (147.99 cm) was recorded in cluster 5.

Under transplanted condition, highest cluster means for days to 50% flowering (105.33), plant height (163.92 cm), panicle length (29.15cm), milling % (70.03%), root length (18.20cm), root fresh weight (27.81 g), root volume (24.03) and root fresh and dry weight ratio (5.96) were recorded by cluster 3 while it showed lowest cluster mean for number of tillers/plant (12.23), biological yield/plant (41.57g) and kernel breadth (1.70mm). Cluster 6 showed maximum cluster means for grain yield/plant (21.86 g), number of tillers/plant (14.59), number of grains/panicle (115.33), biological yield/plant (51.91g), harvest index % (42.41%) and it recorded minimum cluster mean for panicle length (27.14cm), kernel length (6.57mm) and kernel length breadth ratio (3.58). In cluster 4 minimum cluster mean values for different traits were recorded i.e., plant height (118.97cm), number of grains/panicle (70.33), test weight (21.07 g), harvest index % (30.88%), head rice recovery % (48.17%), root length (15.95 cm), root fresh weight (18.75 cm), root volume (17.51 ml) and root dry weight (3.16 g) but for plant height (142.67cm) it recorded maximum cluster mean value. Cluster means were found highest for head rice recovery % (58.46), kernel length (7.68mm), kernel breadth (1.90mm), root length (18.20cm), and root dry weight (6.46 g) in cluster 4 while lowest for hulling % (76%), milling % (68%) and root fresh and dry weight ratio (3.73). Cluster 1 showed minimum cluster mean for grain yield/plant (14.5 g) and maximum for kernel length breadth ratio (4.17). Days to 50% flowering (95.20), days to maturity (135.73) were minimum but test weight (30.27g) was recorded maximum in cluster 2.

Table 4.17: Cluster means of different traits for basmati genotypes grown under aerobic condition

Characters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
GY	15.57	14.45	14.83	18.87	11.27	15.74
DTF	102.18	101.00	92.00	82.67	83.67	99.67
DTM	140.54	140.33	131.33	126.33	122.33	140.00
PH	128.18	117.57	104.54	115.99	147.99	128.10
PL	27.07	26.79	27.79	26.77	26.87	27.51
NT/P	12.64	11.79	12.76	14.28	9.16	13.05
GN/PL	80.64	111.35	104.62	67.02	67.49	97.62
TW	24.91	21.13	23.47	29.13	23.80	23.80
BY/P	42.19	46.19	32.83	54.15	38.19	46.89
HI	35.84	31.35	45.19	40.34	29.58	33.57
HULL	76.46	77.00	76.73	75.13	76.73	75.95
MILL	65.78	68.63	66.86	61.42	65.55	65.34
HRR	54.98	56.55	59.03	44.30	56.78	54.76
KL	7.37	6.54	7.10	7.10	6.89	7.15
KB	1.84	1.63	1.71	1.80	1.76	1.50
KLBR	4.01	4.01	4.14	3.94	3.91	4.76
RL	14.84	13.74	15.15	13.91	13.20	15.99
RFW	25.50	24.48	25.97	23.11	20.86	27.02
RV	18.82	18.13	16.93	15.87	16.67	25.67
RDW	4.50	3.98	5.07	6.10	3.57	4.98
RFW/RDW	5.86	6.15	5.23	3.83	5.86	5.52

Table 4.18: Cluster means of different traits for basmati genotypes grown under transplanted condition

Characters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
GY	14.50	16.49	15.31	15.05	17.05	21.86
DTF	102.96	95.20	105.33	101.67	99.00	102.00
DTM	140.76	135.73	142.00	142.67	139.33	142.00
PH	142.61	123.28	163.92	118.97	148.11	130.89
PL	27.67	27.22	29.15	28.32	28.00	27.14
NT/P	12.32	13.34	12.23	12.31	13.70	14.59
GN/PL	79.72	78.52	110.03	70.33	86.27	115.33
TW	24.01	30.27	22.40	21.07	21.73	27.23
BY/P	44.46	50.09	41.57	48.83	50.37	51.91
HI	33.15	33.13	36.99	30.88	33.85	42.41
HULL	76.39	76.01	76.40	76.33	76.00	76.38
MILL	69.88	69.48	70.03	69.67	68.00	69.05
HRR	56.11	52.58	57.46	48.17	58.46	56.55
KL	7.45	7.13	6.77	7.10	7.68	6.57
KB	1.79	1.90	1.70	1.73	1.90	1.84
KLBR	4.17	3.75	3.98	4.11	4.04	3.58
RL	17.20	17.48	18.20	15.95	18.20	16.24
RFW	21.17	24.04	27.81	18.75	23.99	19.78
RV	19.13	21.21	24.03	17.51	22.48	17.89
RDW	4.48	4.73	4.71	3.16	6.46	3.98
RFW/RDW	4.47	5.17	5.96	5.90	3.73	4.97

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

4.5.5 Contribution of Each Trait towards Genetic Divergence

The results of contribution of each trait towards genetic divergence under aerobic and transplanted conditions were shown in table 4.19. Kernel length (25%) contributed maximum followed by plant height (21.01%), root fresh and dry weight ratio (18.84%), days to 50 % flowering (9.78%), number of grains/panicle (8.33%), kernel length breadth ratio (6.16%), root fresh weight (4.71%), root dry weight (3.26%), biological yield/plant (1.09%), harvest index % (0.72%), days to maturity, kernel breadth and root length 0.36 % in aerobic condition (Fig. 17).

Under transplanted condition test weight (54.71%) contributed maximum toward genetic divergence (Fig.18) followed by kernel length (32.97%), kernel breadth (3.26%), number of grains/panicle (2.9%), days to maturity (1.81%), root fresh and root dry weight (1.45%), root dry weight (1.09%), kernel length breadth ratio (0.72%), root length (0.36%), plant height (0.36%) and harvest index % (0.36%).

Table 4.19: Relative contribution of 21 yield and quality traits towards genetic divergence under aerobic and transplanted condition for Basmati genotypes

Source	Aerobic condition		Transplanted condition	
	Times Ranked 1st	Contribution %	Times Ranked 1st	Contribution %
Grain yield/plant (g)	0	0.00%	0	0.00%
Days to 50% Flowering	27	9.78%	5	1.81%
Days to maturity	1	0.36%	0	0.00%
Plant height (cm)	58	21.01%	1	0.36%
Panicle length (cm)	0	0.00%	0	0.00%
Number of tillers/plant	0	0.00%	0	0.00%
Number of grains/panicle	23	8.33%	8	2.90%
Test weight (g)	0	0.00%	151	54.71%
Biological yield/plant (g)	3	1.09%	0	0.00%
Harvest index %	2	0.72%	1	0.36%
Hulling %	0	0.00%	0	0.00%
Milling %	0	0.00%	0	0.00%
Head rice recovery %	0	0.00%	0	0.00%
Kernel length (mm)	69	25.00%	91	32.97%
Kernel breadth (mm)	1	0.36%	9	3.26%
Kernel length breadth ratio	17	6.16%	2	0.72%
Root length (cm)	1	0.36%	1	0.36%
Root fresh weight (g)	13	4.71%	0	0.00%
Root volume (ml)	0	0.00%	0	0.00%
Root dry weight (g)	9	3.26%	3	1.09%
Root fresh and dry weight ratio	52	18.84%	4	1.45%

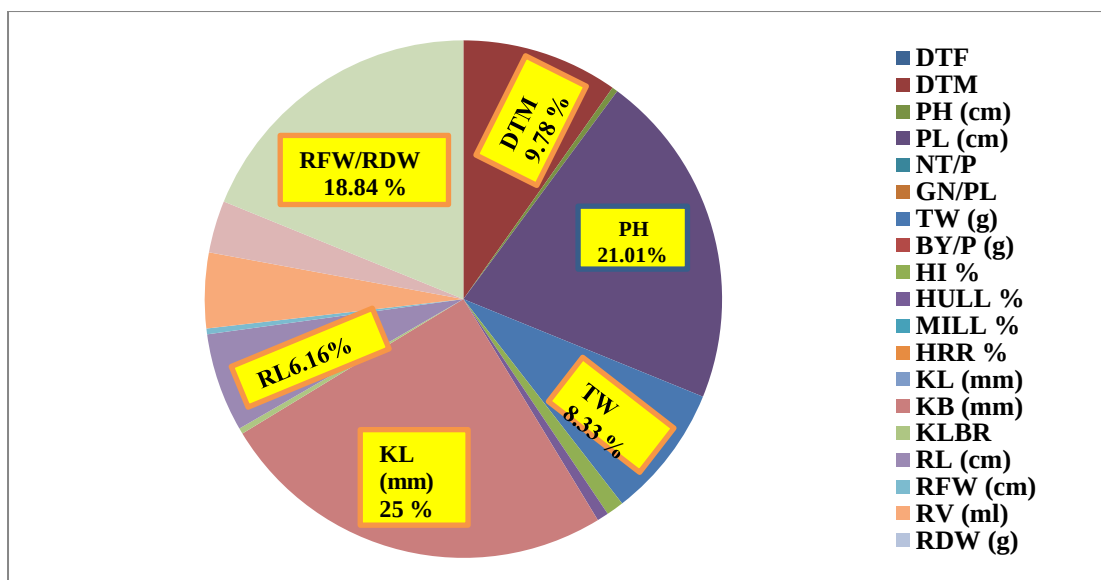


Fig. 17: Pie diagram showing % contribution of traits in genetic divergence under aerobic condition in basmati genotypes

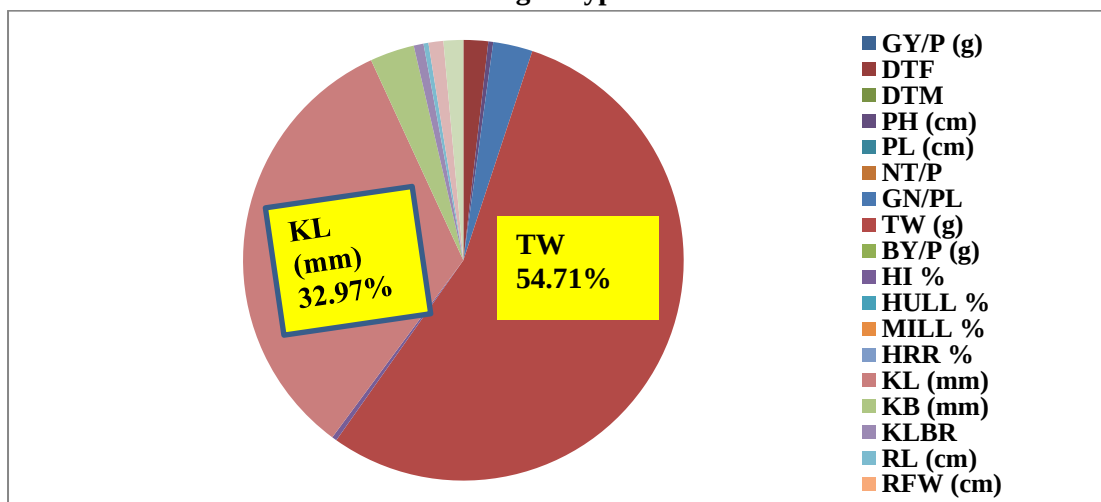


Fig. 18: Pie diagram showing % contribution of traits in genetic divergence under aerobic condition in basmati genotypes

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

4.5.6 Clustering pattern in non-basmati genotypes

Based on D^2 values, non-basmati genotypes were clustered into 4 and 6 groups in aerobic condition and transplanted condition respectively (Fig 19). In aerobic condition maximum genotypes were grouped in cluster 1 (19 genotypes) followed by cluster 2 (3 genotypes), cluster 3 and cluster 4 had single genotype each.

Under transplanted condition, clustering pattern showed that maximum number of genotypes were found in Cluster 1 (19 genotypes) followed by cluster 2, 3, 4, 5 and 6 having

single genotype each. Clustering pattern of non-basmati genotypes under aerobic condition and transplanted condition are presented in table 4.20 and 4.21.

Table 4.20: Clustering pattern of non-basmati genotypes under aerobic condition

Clusters	No. of genotypes	Name of the genotypes
Cluster 1	19	CR Dhan-201, IR 95780-43-1-1-1, IR 99784-255-91-1-5, HKR 14-30, HKR 16-29, HKR 17-33, HKR 17-35, PAU 7551-1-1-1, HKR 17-44, HKR 48, HKR 14-30, HKR 16-29, HKR 17-33, HKR 17-34, HKR 17-35, RDR 1158, HKR 47
Cluster 2	3	HKR 16-58, HKR 16-35, IR 64
Cluster 3	1	IR 14L521
Cluster 4	1	PR 126

Table 4.21: Clustering pattern of non-basmati genotypes under transplanted condition

Clusters	No. of genotypes	Name of genotypes
Cluster 1	19	IR 14L521, CR Dhan 201, PAU 7551-1-1-1, RP 5591-123-16-2,, IR 98976-20-1-2-2,, HKR 17-44, HKR 16-35, HKR 16-58, HKR 14-30, HKR 16-29, HKR 17-33, HKR 17-34, HKR 17-35, RDR 1158, NVSR 474, IR 64, HKR 47, PR 126
Cluster 2	1	IR 99784-11-8-1-2
Cluster 3	1	HKR 48
Cluster 4	1	GOVIND
Cluster 5	1	IR 9897620-1-1-1
Cluster 6	1	IR 95780-43-1-1-1

4.5.7 Dendrogram

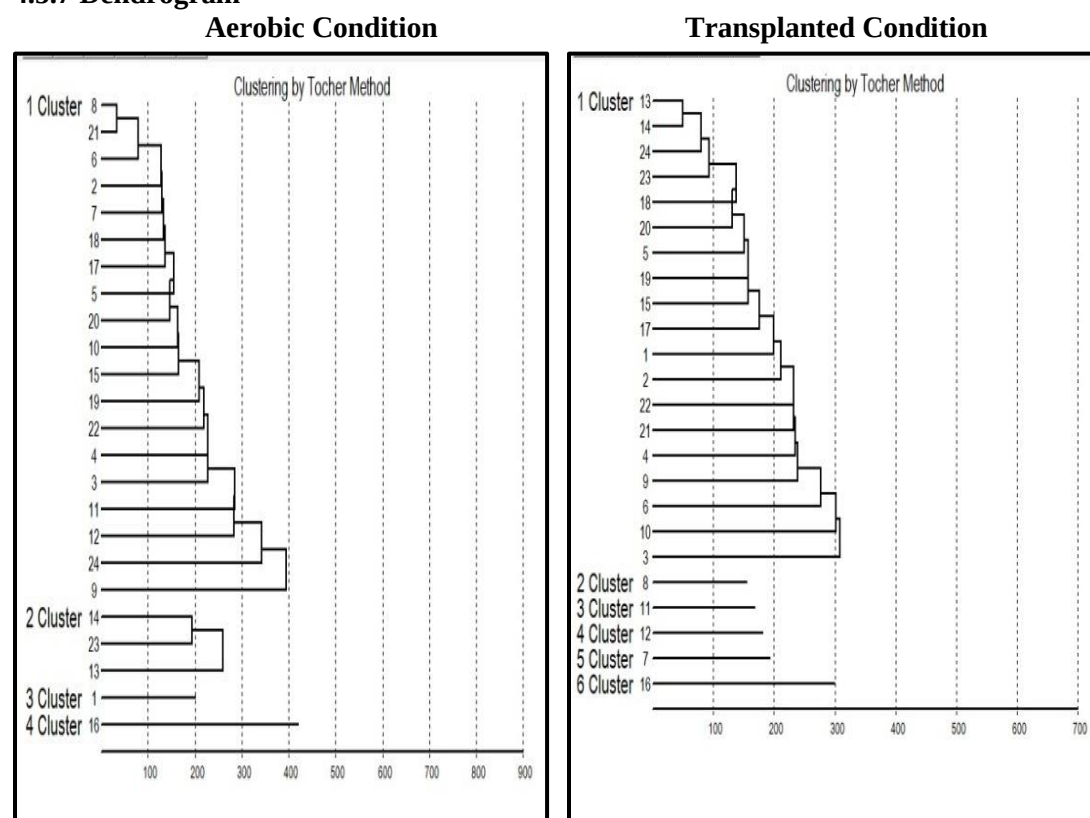


Fig: 19: Group constellation of non-basmati genotypes under aerobic and transplanted conditions by Torcher's method

4.5.8 Intra and inter-cluster average D^2 values for non-basmati genotypes

Clustering pattern revealed that cluster 2 (18.03) recorded maximum intra cluster distance. Inter-cluster distance was maximum between cluster 3 and cluster 4 (31.83) followed by cluster 2 and cluster 4 (28.04), cluster 2 and cluster 3 (27.19), cluster 1 and cluster 4 (25.21), cluster 1 and cluster 2 (22.58) and cluster 1 and cluster 3 (21.2) in aerobic condition.

Maximum intra cluster distance was recorded for cluster 1 (15.67). In case of inter-cluster distances it was observed that cluster 5 and cluster 6 (24.89) showed maximum distance followed by cluster 4 and cluster 6 (24.65), cluster 2 and cluster 6 (22.95), cluster 3 and cluster 6 (22.85), cluster 1 and cluster 4 (22.04), cluster 2 and cluster 5 (22.01), cluster 2 and cluster 4 (21.32), cluster 1 and cluster 5 (20.54), cluster 1 and cluster 6 (20.42), cluster 1 and cluster 3 (20.2), cluster 1 and cluster 2 (20.14), cluster 2 and cluster 3 (19.82), cluster 5 and cluster 3 (18.97), cluster 4 and cluster 5 (16.33) and cluster 3 and cluster 4 (13.45) under transplanted condition. Intra and inter cluster distances under aerobic and transplanted condition are given in table 4.22 and 4.23.

Table 4.22: Intra (diagonal) and Inter-Cluster distances under aerobic condition of non-basmati genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	16.08	22.58	21.2	25.21
Cluster 2		18.03	27.19	28.04
Cluster 3			0	31.83
Cluster 4				0

Table 4.23: Intra (diagonal) and Inter-Cluster distances under transplanted condition of non-basmati genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	15.67	20.14	20.2	22.04	20.54	20.42
Cluster 2		0	19.82	21.32	22.01	22.95
Cluster 3			0	13.45	18.97	22.85
Cluster 4				0	16.33	24.65
Cluster 5					0	24.89
Cluster 6						0

4.5.9 Cluster means for non-basmati genotypes grown under aerobic and transplanted condition

The results of cluster mean for 21 yield and quality traits grown under aerobic and transplanted conditions for basmati genotypes are shown in table 4.24 and 4.25.

In aerobic condition, cluster 3 recorded highest cluster mean value for grain yield/plant (33.87 g), plant height (112.75 cm), panicle length (27.49 cm), number of tillers/plant (13.91), number of grains/panicle (122.73), test weight (28.83 g), biological yield/plant (63.67 g), harvest index % (53.19%), hulling % (77.13%), root length (16.29 cm) and root fresh weight (23.85 g) while lowest for days to 50% flowering (84.33), milling % (62.18%) and kernel length breadth ratio (2.03). Milling % (67.74%), head rice recovery % (61.75%) and kernel breadth (2.27 mm) recorded maximum cluster mean while grain yield/plant (19.33 g), plant height (86.61 cm), panicle length (23.81 cm), number of tillers/plant (12.5), number of grains/panicle (98.07), test weight (25.5), biological yield/plant (49.30), harvest index % (39.22%), kernel length (5.53 mm), kernel length breadth ratio (2.44), root length (13.83 cm), root fresh weight (22.01 g), root volume (19.82) and root dry weight (4.47) recorded minimum cluster mean values in cluster 4. Days to maturity had highest (127.11 days) cluster mean value in cluster 2 and lowest (116.98) in cluster 1. Cluster 2 showed maximum cluster mean value for days to 50% flowering (94.67), kernel length (6.55 mm), kernel length breadth ratio (3.18), root volume (21.81 ml) and root dry weight (5.71 g) and minimum for root fresh and dry weight (4.35). Root fresh and dry weight (4.98) ratio recorded highest in cluster 1.

Under transplanted condition, cluster 5 recorded maximum cluster mean value for number of tillers/plant, test weight (26.53 g), harvest index % (55.09%), kernel length (6.53 mm), kernel length breadth ratio (3.21), root length (18.65 cm), root fresh weight (26.57 g) and root volume (23.2 ml) while minimum for grain yield/plant (23.37 g), number of grains/panicle (102.13) and biological yield/plant (42.57 g). Days to 50% flowering (92), days to maturity (125.67), head rice recovery % (58.49%) and kernel breadth (2.32 mm) had maximum cluster mean value and plant height (107.51 cm), panicle length (25.32 cm), test weight (25.5 g), kernel length (5.57 mm), kernel length breadth ratio (2.4), root fresh weight (22.24 g) and root dry weight (3.43 g) recorded minimum cluster mean in cluster 6. Milling % (65.33%) and root dry weight (4.15 g) recorded maximum cluster mean in cluster 1. Cluster 4 showed lowest cluster mean values for days to 50% flowering (77), days to maturity (110.33), harvest index % (47.50%), root volume (18.93 ml) and root fresh and dry weight (5.94) while highest for hulling % (77.33%). Maximum cluster mean for grain yield/plant (30.9 g), biological yield/plant (62.71 g), hulling % (77.73%), root fresh and dry weight ratio (6.94) while minimum for head rice recovery % (42.96%) and root length (11.67 cm) was recorded in cluster 2. Cluster 3 recorded lowest cluster mean value for number of tillers/plant (10.2), hulling % (72.2%), milling % (61.66%), kernel breadth (2 mm) while highest for plant height (124.95 cm), panicle length (28.51 cm) and number of grains/panicle (147.07).

Table 4.24: Cluster means of different traits for non-basmati genotypes grown under aerobic condition

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
GY	23.80	24.66	33.87	19.33
DTF	84.74	94.67	84.33	85.33
DTM	116.98	127.11	118.00	117.00
PH	110.18	101.16	112.75	86.61
PL	25.31	25.00	27.49	23.81
NT/P	12.55	12.87	13.91	12.50
GN/PL	112.22	103.16	122.73	98.07
TW	26.18	27.43	28.83	25.50
BY/P	52.66	52.36	63.67	49.30
HI	45.23	46.93	53.19	39.22
HULL	76.31	75.86	77.13	76.73
MILL	64.58	64.51	62.18	67.74
HRR	53.84	56.43	54.63	61.75
KL	6.30	6.55	6.00	5.53
KB	2.06	2.06	2.03	2.27
KLBR	3.06	3.18	2.95	2.44
RL	15.21	15.76	16.29	13.83
RFW	23.09	23.80	23.85	22.01
RV	20.93	21.81	21.07	19.82
RDW	4.83	5.71	5.34	4.47
RFW/RDW	4.98	4.35	4.50	4.93

Table 4.25: Cluster means of different traits for non-basmati genotypes grown under transplanted condition

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
GY	28.08	30.90	25.87	24.17	23.37	24.77
DTF	90.54	88.67	81.00	77.00	84.33	92.00
DTM	122.82	120.33	114.00	110.33	116.33	125.67
PH	122.32	121.78	124.95	117.71	114.55	107.51
PL	26.42	25.93	28.51	25.56	26.65	25.32
NT/P	12.22	12.93	10.20	10.83	13.00	11.27
GN/PL	130.75	138.60	147.07	127.60	102.13	129.93
TW	26.51	25.93	26.03	26.40	26.53	25.50
BY/P	56.02	62.71	50.95	50.84	42.57	47.33
HI	50.42	49.26	50.74	47.50	55.09	52.30
HULL	75.71	77.73	72.20	77.33	74.73	76.80
MILL	65.33	61.67	61.66	65.12	62.67	63.67
HRR	55.44	42.96	45.75	47.71	46.29	58.49
KL	6.50	6.00	6.20	6.20	6.53	5.57
KB	2.09	2.03	2.00	2.06	2.04	2.32
KLBR	3.10	2.96	3.10	3.01	3.21	2.40
RL	17.84	11.67	17.82	18.05	18.65	16.61
RFW	24.43	24.83	24.97	22.80	26.57	22.24
RV	21.85	23.00	19.53	18.93	23.20	21.00
RDW	4.15	3.58	4.14	3.83	4.03	3.43
RFW/RDW	5.94	6.94	6.05	5.94	6.61	6.51

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

4.5.10 Per cent contribution of each trait towards Genetic Divergence in non-basmati genotypes

D² analysis revealed the per cent contribution of each trait towards genetic divergence; test weight (19.20 %) contributed maximum towards genetic divergence followed by days to 50 % flowering (17.39 %), kernel length (13.41 %), root fresh weight (10.51 %), root dry weight (9.06 %), harvest index % (6.88 %), kernel length-breadth ratio (5.07 %), root length (4.35 %), number of tillers per plant (3.62 %), root fresh and dry weight ratio (3.26 %), biological yield (2.54 %), number of grains per panicle (1.81 %), days to maturity (1.09 %), panicle length (0.72 %), grain yield (0.72 %) and head rice recovery % (0.32 %) in aerobic condition. (Fig. 20)

Under transplanted condition, days to 50 % flowering (40.94 %) recorded maximum towards genetic divergence followed by kernel length (19.20 %), number of grains per panicle (8.33 %), test weight (7.25 %), root volume (3.99 %), kernel breadth (3.62 %), head rice recovery % (3.62 %), biological yield (2.90 %), plant height (2.17 %), kernel length-breadth ratio (1.81 %), number of tillers per plant and harvest index % (1.45 %), grain yield and days to maturity (0.72 %), panicle length (0.36%), milling % (0.36%) and root length (0.36 %). Per cent contribution of each trait towards genetic divergence in non-basmati genotypes is given in table 4.26 and Fig. 21

Table 4.26: Relative contribution of 21 yield and quality character towards genetic divergence under aerobic and transplanted condition in non-basmati genotypes

Source	Aerobic condition		Transplanted condition	
	Times Ranked 1st	Contribution %	Times Ranked 1st	Contribution %
Grain yield/plant (g)	2	0.72%	2	0.72%
Days to 50% Flowering	48	17.39%	113	40.94%
Days to maturity	3	1.09%	2	0.72%
Plant height (cm)	0	0.00%	6	2.17%
Panicle length (cm)	2	0.72%	1	0.36%
Number of tillers/plant	10	3.62%	4	1.45%
Number of grains/panicle	5	1.81%	23	8.33%
Test weight (g)	53	19.20%	20	7.25%
Biological yield/plant (g)	7	2.54%	8	2.90%
Harvest index %	19	6.88%	4	1.45%
Hulling %	0	0.00%	0	0.00%
Milling %	0	0.00%	1	0.36%
Head rice recovery %	1	0.36%	10	3.62%
Kernel length (mm)	37	13.41%	53	19.20%
Kernel breadth (mm)	0	0.00%	10	3.62%
Kernel length breadth ratio	14	5.07%	5	1.81%
Root length (cm)	12	4.35%	1	0.36%
Root fresh weight (g)	29	10.51%	0	0.00%
Root volume (ml)	0	0.00%	11	3.99%
Root dry weight (g)	25	9.06%	0	0.00%
Root fresh and dry weight ratio	9	3.26%	2	0.72%

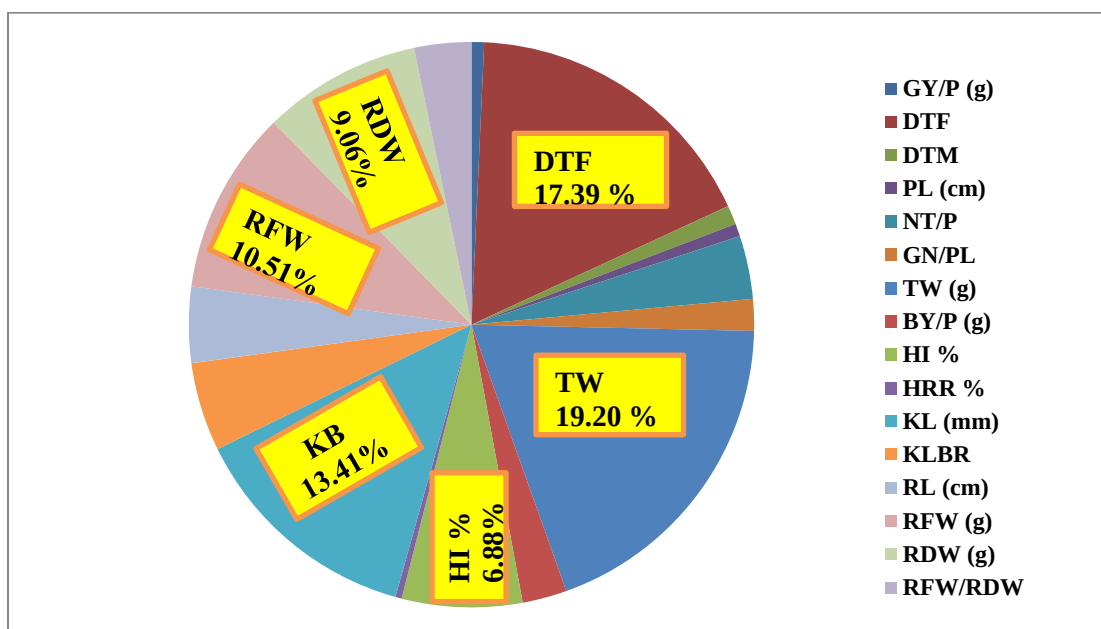


Fig. 20: Pie diagram showing % contribution of traits in genetic divergence under aerobic condition in non-basmati genotypes

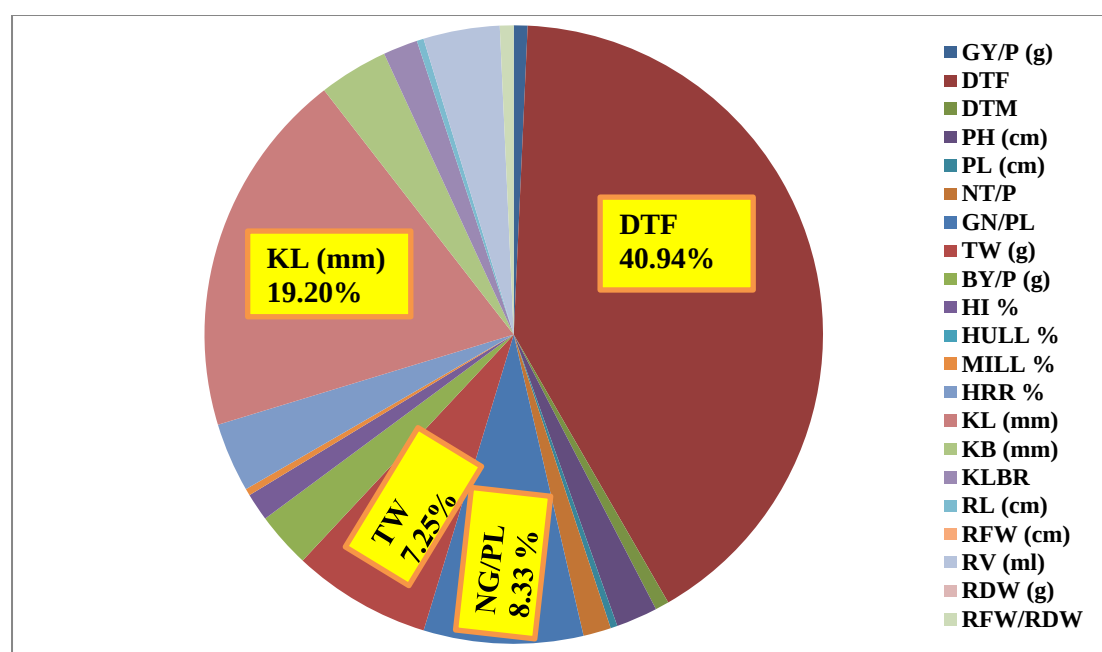


Fig. 21: Pie diagram showing % contribution of traits in genetic divergence under transplanted condition in non-basmati genotypes

(GY= grain yield per plant, DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, PL= Panicle length, NT/P= Number of tillers per plant, GN/PL= Number of grains per panicle, TW=1000 seed weight, BY/P = biological yield per plant, HI= Harvest Index %, HULL= Hulling(%), MILL =Milling %, HRR= Head rice recovery %, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length - breadth ratio, RL= Root length, RFW= Root fresh weight per plant, RV= Root volume, RDW= Root dry weight per plant, RFW/RDW= Root fresh and dry weight ratio)

Rice (*Oryza sativa* L.) is second most important cereal crop grown after maize and it provides food for two third of world population (Kahani *et al.* 2015). It is grown under diversified ecologies with differential consumer's preferences and recognized as the “Grain of life” as it unites cultures and regions (Kondi *et al.* 2021). Conventional rice cultivation requires huge amount of water (3000-5000 litres of water to produce 1 Kg of rice) and is labour intensive. Changing climatic conditions, limited natural resources and growing population are serious threats to ensure food security (Zeng *et al.* 2017). Therefore, to counter this, it is high time to develop high yielding quality rice, climate resilient varieties with new production technologies to optimise water and other inputs.

Aerobic rice cultivation has emerged as water saving establishment method where crop is sown directly into field (dry or water-soaked seed) that are non-puddled and non-flooded. Under aerobic conditions the fields are kept moist during growing season and it saves up to 50 % of irrigation water as compared to traditional cultivation where fields are kept in flooded conditions. Lack of stable yielding and adapted aerobic varieties is a serious concern to attain sustainable rice production under limited resources. Keeping in mind the constraints of traditional method and merits of aerobic rice, it is high time to spot those genotypes which will perform equally or at par under both aerobic and transplanted conditions.

Results of the present investigation entitled “**Characterization for yield and quality traits under aerobic and transplanted conditions in rice (*Oryza sativa* L.)**” are discussed under following titles:

5.1 Analysis of variance

5.2 Identification of promising rice genotypes suitable for aerobic and transplanted conditions on mean basis

5.3 Genetic variability, Heritability and Genetic advance

5.4 Correlation co-efficient analysis

5.5 Path co-efficient analysis

5.6 Genetic divergence analysis (D^2 statistics)

5.1 Analysis of variance

The analysis of variance (ANOVA) revealed that mean sum of squares due to genotypes were significant under aerobic and transplanted conditions for all the 21 morphological and quality traits (for basmati and non-basmati genotypes) indicated the presence of considerable genetic variability among the genotypes which can be exploited in

future breeding programmes. Similar findings were also reported by Hijam *et al.* (2012), Kumar *et al.* (2012), Singh *et al.* (2012), Bahera *et al.* (2018) and Bhargavi *et al.* (2021).

5.2 Identification of promising genotypes suitable for aerobic and transplanted conditions on mean basis

Yield is a polygenic trait and depends on multiple factors. Improvement in yield potential of genotypes is the main aim of any breeding programme. In the present study suitable genotypes were selected on the basis of grain yield/plant for basmati and non-basmati genotypes under both production systems. Under basmati group, genotypes HKR 15-455, HKR 16-459, Pusa 1557-06-08-126-162-156 and HKR 15-488 were identified as promising as they were performing significantly higher than the check Haryana Basmati 2 under both the conditions (aerobic and transplanted). Moreover for quality parameters two genotypes HKR 15-488 and HKR 16-459 were found promising since they had better quality attributes as compared to Taraori Basmati (quality check) under both the conditions.

In non-basmati group, genotypes viz. IR14L521, HKR 16-35 and NVSR 2107 were selected as promising genotypes on the basis of mean grain yield/plant as these genotypes significantly out yielded the check HKR 47 and HKR 48 under aerobic and transplanted conditions. Grain yield per plant in transplanted condition was observed higher than aerobic condition. Similar findings were reported by Sahu *et al.* (2017). Therefore, these genotypes can be utilized in breeding programme for developing suitable genotypes for both aerobic and transplanted conditions.

5.3 Genetic variability, Heritability and Genetic Advance

5.3.1 Genetic and Phenotypic co-efficient of variation

Presence of genetic variability in the planting material is essential for execution of a successful breeding programme. Greater is the variability in base material more will be the probability of selecting promising and desired types. Phenotypic co-efficient of variation was observed slightly higher than genotypic co-efficient of variation for all the traits studied under both the production systems (aerobic and transplanted) which indicated the environmental influence on the expression of these traits.

In basmati group, under both the conditions (aerobic and transplanted) moderate genotypic coefficient of variation and phenotypic coefficient of variation were observed for grain yield/plant, plant height and number of grains/panicle. Results obtained under aerobic condition were in accordance with Kumar *et al.* (2012) for plant height along with number of grains/panicle and Osman *et al.* (2012) for grain yield/plant. Similar results were observed by Naseer *et al.* (2015) for plant height, Bagati *et al.* (2016) for number of grains/panicle and Akhter *et al.* (2018) for grain yield/plant under transplanted condition.

Under non-basmati group, moderate genotypic coefficient of variation and phenotypic coefficient of variation was observed for grain yield/plant, root fresh weight, root volume and

root dry weight under both conditions (aerobic and transplanted). These results were in accordance with Kumari and Parmar (2020) for grain yield/plant in aerobic condition and Qamar *et al.* (2005) in transplanted condition.

5.3.2 Heritability and Genetic advance as per cent of mean

Not all the variation present in a population is due to genetic factors, it is the result of genotype and environment interaction. The extent variation due to the genetic components is estimated through heritability whereas genetic advance measures the gain in genetic value over the parents. Heritability coupled with high genetic advance estimation determines the influence of environment on the expression of genetic factors and offers most suitable conditions for selection.

In the present investigation, high heritability coupled with high genetic advance as percent of mean were observed for grain yield/plant, plant height, number of grains/panicle and root dry weight under aerobic and transplanted conditions for basmati genotypes. These results were supported by findings of Kumar *et al.* (2012) for plant height along with number of grains/panicle and Osman *et al.* (2012) for grain yield/plant under aerobic condition. Similar results were obtained by Naseer *et al.* (2015) for plant height together with number of grains/panicle and Akhter *et al.* (2018) for grain yield/plant under transplanted condition.

Under non-basmati group, grain yield per plant, root fresh weight, root volume and root dry weight had high heritability coupled with high genetic advance as percent of mean under aerobic condition. These results were supported by Hijam *et al.* (2012) for root fresh weight, root volume and root dry weight, Kumari and Parmar (2020) for grain yield/plant. In transplanted condition, none of the trait had high heritability with high genetic advance as percent of mean. However, days to 50 % flowering, grain yield/plant, test weight, number of grains/panicle showed high heritability coupled with moderate genetic advance as percent of mean. Similar kind of results were observed by Qamar *et al.* (2005) for grain yield/plant and Islam *et al.* (2015) for days to 50 % flowering, test weight, number of grains/panicle. Therefore, selection of these traits would be effective for grain yield improvement under aerobic and transplanted conditions, respectively.

5.4 Correlation co-efficient analysis

Improvement in any trait requires meticulous selection process. Thus knowledge of interrelationship between yield and its component traits improves the efficacy of breeding programme through the use of effective selection indices (Kumar *et al.* 2020). Correlation coefficient analysis measures degree and direction of the relationship between two variables. These associations can be exploited to develop improved genotypes. Correlation coefficient analysis showed that most of the genotypic correlation coefficients were higher than the phenotypic correlation coefficients implying that even though there were inherent associations between the characters, they were highly influenced by external environments.

Basmati Genotypes

In aerobic condition, grain yield/plant exerted significant positive correlation with number of tillers/plant, test weight, harvest index %, kernel length, kernel breadth, root fresh weight, root volume and root dry weight. The results were in accordance with Akram *et al.* (2013) for number of tillers/plant and test weight; Sandhu *et al.* (2013) for root fresh weight, root volume and root dry weight.

Under transplanted condition, grain yield/plant exhibited significant positive correlation with number of tillers/plant, number of grains/panicle, test weight, biological yield/plant, harvest index % and kernel breadth. Abarshahr *et al.* (2011) and Singh *et al.* (2020) also observed that grain yield/plant showed significant positive association with number of grains per panicle and test weight. Priya *et al.* (2017) reported that grain yield/plant had significant positive correlation with kernel breadth. Sahu *et al.* (2017) observed similar kind of results for biological yield/plant and harvest index %. Khokhar and Sarial (2018) reported that grain yield/plant showed significant positive correlation with number of tillers per plant and biological yield/plant. Head rice recovery % and root volume showed positive correlation with grain yield/plant which is in accordance with Khokhar and Sarial (2018) and Khushwaha *et al.* (2020) respectively.

Under both the conditions (aerobic and transplanted), number of tillers/plant biological yield/plant, test weight, kernel breadth, root volume and harvest index were exhibited significant positive correlation with grain yield/plant. These results were supported by Singh *et al.* (2020) and Priya *et al.* (2017). So, in future emphasis should be given on these traits for enhancing yield.

Non-Basmati Genotypes

Under aerobic condition grain yield/plant exhibited significant positive correlation with plant height, number of tillers/plant, number of grains/panicle, test weight, biological yield/plant, harvest index %, root length, root fresh weight and root volume. Similar findings were observed by Murthy *et al.* (2011) for biological yield/plant, harvest index % and plant height; Haider *et al.* (2012) for root length, number of grains/panicle and test weight; Sravan *et al.* (2012) for test weight, biological yield/plant and harvest index %; Malath and Gomathinayagam (2013) for number of grains/panicle and root length; Priyanka *et al.* (2016) for plant height, number of tillers/plant, number of grains/panicle and harvest index %. However, results were also in accordance with Mohankumar *et al.* (2011) for root fresh weight and root volume; and Vengatesh and Govindaraso (2018) for root length, root fresh weight and root volume.

In transplanted condition, grain yield/plant showed significant positive correlation with days to 50 % flowering, plant height, number of tillers/plant, number of grains/panicle, test weight, biological yield/plant, root fresh weight, root dry weight and root volume. Qamar

et al. (2005) reported that grain yield/plant showed significant positive correlation with days to 50% flowering and number of tillers/plant. Bhageri *et al.* (2011) observed similar kind of results for number of grains/panicle; Augustina *et al.* (2013) for root fresh weight and root volume; Rashid *et al.* (2017) for plant height and number of grains/panicle; Bhattacharya and Chakraborty (2019) observed similar findings for biological yield/plant and test weight.

Under both the condition (aerobic and transplanted) grain yield per plant showed significant positive correlation with plant height, number of tillers/plant, number of grains/panicle, test weight, biological yield/plant, root fresh weight and root volume. Therefore, these traits might be given more attention for improving rice yield.

5.5 Path co-efficient analysis

Path co-efficient analysis explains whether the relationship of grain yield with its component traits is due to the direct effects of component traits or is the actual result of their indirect effects through some other traits. When correlation co-efficient between a factor and direct effect is nearly same then only correlation will explain the true association. In such condition, direct selection via these traits will be fruitful. If correlation coefficient is positive and direct effect is negative, then it shows association because of indirect effects. So, continuous selection of other factors is necessary in this situation. If correlations is negative but direct effect is positive and high, then limited simultaneously selection needs to consider invalidating undesirable indirect effect.

Basmati genotypes

Under aerobic condition, days to 50% flowering and plant height showed positive direct effect and head rice recovery % had negative effect on grain yield. Similar findings were reported by Khokhar and Sarial (2018). Number of tillers/plant and number of grains/panicle exhibited positive direct effect on grain yield/plant. These results were in accordance with Islam *et al.* (2020). Test weight, biological yield/plant and harvest index showed positive direct effect on grain yield. Alike outcomes were observed by Sravan *et al.* (2012) for all three traits and Khokhar and Sarial (2018) for biological yield/plant and test weight. Kernel length showed high positive direct effect while kernel breadth and kernel length breadth ratio exhibited high negative direct effect on grain yield. These results were favoured by the findings of Aditya *et al.* (2016).

Under transplanted condition, days to 50% flowering, days to maturity and plant height exhibited negative direct effect on grain yield. Similar results were reported by Nayak *et al.* (2001) and Khokhar and Sarial (2018). Panicle length, number of tillers per plant, number of grains per panicle, test weight, biological yield/plant, harvest index %, hulling %, kernel breadth, root volume and kernel length breadth ratio exhibited positive direct effect on grain yield. Similar findings were reported by Allam *et al.* (2015) for panicle length; Priya *et al.* (2017) for number of tillers/plant and kernel length breadth ratio; Nayak *et al.* (2001) and

Priya *et al.* (2017) for number of grains per panicle and test weight; Akhter *et al.* (2018) for biological yield/plant; Pratap *et al.* (2012) and Roy *et al.* (2015) for harvest index %; Nandan *et al.* (2010) for hulling % and Khushwah *et al.* (2020) for kernel breadth and root volume. Milling % and head rice recovery % showed negative direct effect on grain yield which were supported by Nandan *et al.* (2010) and Khokhar and Sarial (2018) respectively.

Non-basmati Genotypes

Under aerobic condition, days to 50% flowering, number of grains/panicle, test weight, biological yield/plant, harvest index %, hulling %, milling %, head rice recovery %, and root dry weight expressed positive direct effect on grain yield. These results were in accordance with Priyanka *et al.* (2016) for panicle length, harvest index % and biological yield/plant; Adithya and Bhartiya (2013) for number of grains/panicle; Ekka *et al.* (2011) for days to 50% flowering, test weight, panicle length, milling % and head rice recovery %; Khokhar and Sarial (2018) for hulling % and Manickavelu *et al.* (2006) for root dry weight. However, number of tillers/plant, kernel breadth and plant height exhibited negative direct effects on grain yield. Similar results were obtained by Srijan *et al.* (2018) for number of tillers/plant and Ekka *et al.* (2011) for kernel breadth and plant height.

Under transplanted condition, days to 50% flowering, plant height, panicle length, number of tillers/plant, number of grains/panicle, biological yield/plant, harvest index %, hulling %, milling %, head rice recovery %, kernel length, root fresh weight and root dry weight exhibited positive direct effect on grain yield. Similar findings were reported by Bagheri *et al.* (2011) for plant height, panicle length and number of grains/panicle; Hossain *et al.* (2015) for number of tillers/plant, root fresh weight and days to 50% flowering; Manickavelu *et al.* (2006) for root dry weight; Veni *et al.* (2013) for head rice recovery %; Khatiyaar *et al.* (2019) for biological yield/plant and harvest index %; Khokhar and Sarial (2018) for hulling %, milling % and Gunasekaran *et al.* (2017) for kernel length. Moreover, test weight, kernel breadth and kernel length breadth ratio showed negative direct effect on grain yield. Similar results were observed by Veni *et al.* (2013) for test weight and Gunasekaran *et al.* (2017) for kernel breadth and kernel length breadth ratio.

5.6 Genetic divergence analysis (D^2 statistics)

For success of long term breeding programme and exploitation of genetic resources, demands data of genetic diversity present between cultivars (Kondi *et al.* 2021). Genetic divergence among the parents is essential to increase the possibility of selecting better segregants for different traits. Genetic diversity not only helps in selection of parents to get superior recombinants but also in understanding the pattern of variation for different traits. Mahalanobis D^2 statistics is an important tool to identify genetic diverse parents based on quantitative traits.

Basmati genotypes

In the present investigation 24 basmati genotypes under aerobic condition were grouped into six clusters in accordance with the D^2 statistics by Tocher method. Maximum numbers of the genotypes (19) were present in cluster 1 followed by cluster 2, cluster 3, cluster 4, cluster 5, and cluster 6 having one genotype each. The results were in accordance with Abarshahr *et al.* (2011); Khokhar and Sarial (2016) and Perween *et al.*, under aerobic condition.

Under transplanted condition, genotypes were clustered into 6 six clusters. The highest numbers of genotypes (16) were included in cluster 1 followed by genotypes (5) in cluster 2 and one genotype each in cluster 3, cluster 4, cluster 5 and cluster 6. Shahidullah *et al.* (2009) grouped 40 rice accessions into six clusters under transplanted condition. Kumar *et al.* (2014) clustered 23 genotypes of basmati into five groups. Supriya *et al.* (2017) screened 25 scented rice genotypes under transplanted condition and genotypes were grouped into six different clusters. Devi *et al.* (2020) assessed 33 elite genotypes of rice for yield and quality parameters and grouped them into eight clusters. Perween *et al.* (2020) examined 48 genotypes of rice and clustered them into eleven clusters under aerobic condition. Group constellation of genotypes under both the conditions (aerobic and transplanted) did not follow their geographical distribution. Therefore, the kind of genetic diversity found among the genotypes belonging to the same geographic origin might be due to differences in adaption, selection criteria, selection pressure and environmental conditions. Therefore, for selecting suitable genotypes for hybridization programme should be based on genetic diversity rather than geographical diversity (Gohil and Pandya, 2008).

Under aerobic condition, cluster 4 had maximum cluster mean value for grain yield, days to 50% flowering, number of tillers/plants, test weight and biological yield/plant. Cluster 2 recorded maximum cluster mean for hulling % and milling % whereas, cluster 1 had maximum cluster mean for kernel length and kernel breadth. In transplanted condition, cluster 6 recorded highest mean values for grain yield, number of tillers/plant, number of grains/panicle, biological yield and harvest index %. Cluster 3 showed highest cluster mean value for hulling % and milling % whereas cluster 5 had maximum cluster mean value for kernel length and kernel breadth. Genotypes of the above identified clusters could be evaluated in larger trials to improve grain yield and other desirable traits in respective production systems.

Under aerobic condition, cluster 1 showed highest intra cluster distance (21.36). Between cluster 5 and cluster 6 maximum inter cluster distance (51.79) was recorded followed by cluster 2 and cluster 5 (47.79), cluster 3 and 5 (41.58), cluster 1 and cluster 5 (40.37) and cluster 4 and cluster 6 (39.72). Maximum intra cluster distance was observed for cluster 2 (27.42) in transplanted condition. Highest inter cluster distance were recorded

between cluster 2 and cluster 4 (69.89) followed by cluster 2 and cluster 5 (69.03), cluster 2 and cluster 3 (63.82), cluster 1 and cluster 2 (51.66) and cluster 5 and cluster 6 (49.39). Under both the conditions, in general inter cluster distances were higher than the intra-cluster distances indicating the presence of accountable diversity among the genotypes. These findings were in accordance with Perween *et al.* (2020) under both the conditions (aerobic and transplanted).

Kernel length contributed maximum towards genetic divergence followed by plant height root fresh weight and dry weight ratio, days to 50% flowering and number of grains/panicles under aerobic condition. These results were in accordance with Krishna *et al.* (2020) for kernel length. Test weight contributed maximum towards genetic divergence followed by kernel length, number of grains/panicle and days to 50% flowering under transplanted condition. Similar results were observed by Kumar *et al.* (2014) and Tejaswini *et al.* (2020) for test weight and Deepika *et al.* (2020) for kernel length, number of grains/panicle and days to 50% flowering under transplanted condition.

Non-basmati Genotypes

Under aerobic condition, 24 genotypes were grouped into 4 clusters. Cluster 1 had maximum number of genotypes (19) followed by cluster 2 having 3 genotypes, cluster 3 and clusters 4 had single genotype each. Kandamoorthy and Govindarasu (2005) evaluated 30 early genotypes and group them into three clusters under aerobic condition. Ramanjaneyulu *et al.* (2014) screened 10 genotypes and grouped them into four clusters. Chandra and Nilanjaya (2016) clustered 25 genotypes into six clusters under aerobic condition.

Under transplanted condition, genotypes were grouped into 6 six clusters. Cluster1 was the largest with 19 genotypes followed by cluster 2, cluster 3, cluster 4, cluster 5 and cluster 6 having single genotype each. Based on relative magnitude of D^2 values, Joshi *et al.* (2018) grouped 19 genotypes into four clusters. Nikhil and Rangare (2012) investigated 40 rice genotypes using Mahalanobis D^2 statistics and formed seven clusters. Chandermohan *et al.* (2016) evaluated 44 genotypes and clustered them into eleven clusters based on their D^2 values.

Cluster 3 had maximum cluster mean values for grain yield/plant, number of tillers/plant, number of grains/panicle and hulling % under aerobic condition. Genotypes of above cluster could be used in future breeding programme to improve grain yield and its component traits. In transplanted condition, on the basis of cluster mean, clusters identified for selecting parents for future hybridization programme are accordingly; cluster 2 for grain yield; Cluster 5 for number of tillers/plant and test weight; cluster 3 for panicle length and number of grains/panicle while cluster 4 to incorporate early maturity.

Under aerobic condition, maximum intra cluster distance was observed in cluster 2 (18.03). Maximum inter cluster distance (31.83) was recorded between cluster 3 and cluster 4

followed by cluster 2 and cluster 4 (28.04), cluster 2 and 3 (27.19) and cluster 1 and cluster 4 (25.21). In transplanted condition maximum intra cluster distance was observed in cluster 1 (15.67). Maximum inter cluster distance were recorded between cluster 5 and cluster 6 (24.89) followed by cluster 4 and cluster 6 (24.65), cluster 2 and cluster 6 (22.95), cluster 3 and cluster 6 (22.85) and cluster 1 and cluster 4 (49.39). However, under both the conditions (aerobic and transplanted) intra cluster distances were relatively lower than inter cluster distances indicating that genotypes within these clusters were genetically similar to each other than the genotype present in different clusters (Sahidullah *et. al.* 2009). Higher inter cluster distances than the intra-cluster distances were recorded indicating the presence of significant diversity among the genotypes. Similar findings were observed by Kumari *et al.* (2014) in aerobic condition and Chandra and Nilanjaya (2016) in both the conditions (aerobic and transplanted).

Under aerobic condition test weight, days to 50% flowering, kernel length, root fresh weight and root dry weight contributed maximum towards genetic divergence. These results were in accordance with Kandamoorthy and Govindasasu (2005) for days to 50% flowering and Sreedhar S. (2018) for test weight. In transplanted condition, days to 50% flowering, kernel length, number of grains per panicle and test weight had contributed maximum towards genetic divergence. These results were in accordance with Chandermohan *et al.* (2016) for days to 50% flowering, test weight and number of grains per panicle.

CHAPTER-VI

SUMMARY AND CONCLUSION

The present investigation entitled “**Characterization for yield and quality traits under aerobic and transplanted conditions in rice (*Oryza sativa* L.)**” was conducted during *kharif* 2020 at research farm of Chaudhary Charan Singh Haryana Agricultural University, Rice Research Station, Kaul with the following objectives:

1. To estimate genetic variability parameters among the rice genotypes under aerobic and transplanted conditions for yield and quality traits
2. To review character association and path analysis for yield and quality traits under aerobic and transplanted conditions
3. To assess genetic divergence among the rice genotypes

The experimental materials consisted of forty-eight (48) rice genotypes (24 basmati and 24 non-basmati genotypes) collected from Chaudhary Charan Singh Haryana Agricultural University, Rice Research Station, Kaul. The genotypes were grown under two production systems viz; aerobic and transplanted conditions in three replications each using randomized block design (RBD). Plot size consisted of single rows of 5 m length with spacing of 20 x 15 cm between rows and plants of each genotype.

Observations were recorded on five randomly selected plants from each row for every genotype on 21 morphological and quality traits viz; days to 50% flowering, days to maturity, plant height (cm), number of tillers per plant, panicle length (cm), number of grains per panicle, test weight (g), biological yield/plant (g), harvest index %, hulling %, milling %, head rice recovery %, kernel length (mm), kernel breadth (mm), kernel length-breadth ratio, root length (cm), root fresh weight (g), root volume (ml), root dry weight (g) and root fresh and dry weight ratio. Replicated data were used for analyses to estimate co-efficient of variability, heritability, genetic advance as percent of mean, correlation co-efficient analysis, path co-efficient analysis and genetic divergence Mahalanobis according to standard statistical porocedure under both production systems. Findings of present investigation are given below for basmati and non-basmati genotypes under aerobic and transplanted condition.

Basmati Genotypes

Analysis of variance (ANOVA) revealed that mean sum of squares due to genotypes were highly significant under both aerobic and transplanted conditions for all the traits indicating the existence of enough variability in planting material. Genotypes viz; HKR 15-455, HKR 16-459, Pusa 1557-06-08-126-162-156 and HKR 15-488 were observed suitable for yield parameters as they out yielded the check Haryana Basmati -2 under both aerobic and transplanted conditions. However, two genotypes HKR 15-488 and HKR 16-459 also

observed promising for quality parameters over Taraori Basmati (quality check) under both the conditions. Phenotypic co-efficient of variation was observed slightly higher than genetic co-efficient of variation for all the traits studied which indicated the influence of environmental factors on expression of these traits. Moderate GCV and PCV were observed for grain yield/plant, plant height and number of grains/panicle under aerobic and transplanted conditions. High heritability coupled with high genetic advance as percent of mean were recorded for grain yield/plant, plant height, number of grains/panicle and root dry weight under aerobic and transplanted conditions. Therefore, selection of these traits can improve rice yield. Correlation analysis indicated that grain yield per plant exhibited significant positive correlation with number of tillers/plant, test weight, harvest index % and kernel breadth under both aerobic and transplanted condition. However it also showed significant positive correlation with kernel length, root fresh weight, root volume and root dry weight under aerobic condition and number of grains/panicle and biological yield/plant, under transplanted condition respectively. These traits might be utilized in crop improvement programmes. In aerobic condition, high positive direct effect on grain yield was expressed by kernel length, followed by days to 50% flowering, test weight, harvest index %, plant height, biological yield/plant, number of tillers/plant and root fresh weight while in transplanted condition major positive direct effect on grain yield/plant was exhibited by kernel length breadth ratio followed by biological yield/plant, root volume, harvest index %, number of grains/panicle, root fresh and dry weight ratio and kernel breadth. Genotypes were grouped into six clusters each under both aerobic and transplanted conditions according to D^2 values. Cluster 1 was the largest with 19 genotypes and cluster 2, cluster 3, cluster 4, cluster 5 and cluster 6 had single genotype each. Highest inter cluster distance was recorded between cluster 5 and cluster 6 (51.79) followed by cluster 2 and cluster 5 (47.79) under aerobic condition. In transplanted condition, maximum numbers of genotypes (16) were presented in cluster 1 followed by cluster 2 with 5 genotypes while cluster 3, cluster 4, cluster 5 and cluster 6 had single genotype each. Maximum inter cluster distance were recorded between cluster 2 and cluster 4 (69.89) followed by cluster 2 and cluster 5 (69.03). Kernel length, number of grains/panicle and days to 50% flowering exerted major contribution towards total divergence under both aerobic and transplanted conditions.

Non-Basmati Genotypes

In non-basmati genotypes, IR14L521, HKR 16-35 and NVSR 2107 were identified superior on the basis of grain yield/plant under aerobic and transplanted conditions as these genotypes performed significantly higher than the check HKR 47 and HKR 48 respectively. ANOVA showed that mean sum of squares due to genotypes were recorded significant for all the traits under both the conditions, which indicated the presence of sufficient variability in the evaluated genotypes. Phenotypic coefficient of variation was observed slightly higher than

genotypic co-efficient of variation for all the characters under aerobic and transplanted conditions. Moderate GCV and PCV was noticed for grain yield/plant, root fresh weight, root volume and root dry weight under aerobic and transplanted conditions. High heritability coupled with high genetic advance as percent of mean was recorded for grain yield/plant under both aerobic and transplanted conditions and therefore, can be utilized as selection criteria. However, root fresh weight, root volume, root dry weight and root fresh and dry weight ratio showed high heritability coupled with high genetic advance as % of mean under aerobic condition. High heritability coupled with moderate genetic advance as percent of mean were expressed by days to 50% flowering and number of grains/panicles under transplanted condition. Grain yield/plant exhibited significant positive correlation with biological yield/plant followed by harvest index %, plant height, test weight and number of grains/panicles, number of tillers/plant, root fresh weight and root volume under both conditions. Path analysis revealed that high positive direct effect on grain yield/plant was exerted by kernel length followed by number of grains/panicles, days to 50% flowering and biological yield/plant, harvest index % and root volume under both conditions. According to D² statistics, 4 clusters were formed under aerobic condition. Cluster 1 consisted of maximum 19 genotypes followed by cluster 2 having 3 genotypes. Cluster 3 and cluster 4 had single genotype each. Maximum inter cluster distance (31.83) was recorded between cluster 3 and cluster 4 followed by cluster 2 and cluster 4 (28.04). In transplanted condition, genotypes were grouped into six clusters and cluster 1 was the largest cluster consisting of 19 genotypes. Cluster 2, cluster 3, cluster 4, cluster 5 and cluster 6 had one genotype each. Days to 50% flowering, kernel length and test weight contributed maximum towards genetic divergence under both aerobic and transplanted condition.

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ABSTRACT

Title of Thesis	:	Characterization for yield and quality traits under aerobic and transplanted conditions in rice (<i>Oryza sativa</i> L.)'
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The present experiment was carried out at Rice Research Station, Kaul, CCS Haryana Agricultural University Hisar, during Kharif, 2020 to estimate co-efficient of variability, heritability, genetic advance as percent of mean, character association, path co-efficient analysis and genetic divergence for yield and quality traits grown under aerobic and transplanted conditions. A total of 48 genotypes (24 basmati and 24 non-basmati genotypes) were grown in single row (5m long) of each genotype in each replication using randomized block design with spacing 20 x15 cm between rows and plants respectively. Observations were recorded on five randomly selected plants for each genotype on 21 morphological and quality traits. Mean sum of squares due to genotypes were highly significant for all the traits indicating the presence of sufficient variability under both the conditions. Narrow range of GCV and PCV indicated major role of genetic factors in expression of traits than environmental factors. In basmati genotypes, high heritability coupled with high genetic advance as per cent of mean was observed for grain yield/plant, plant height, number of grains/panicle and root dry weight under both conditions. While in non-basmati genotypes, grain yield/plant had high heritability coupled with high genetic advance as percent of mean revealed the importance of additive gene action in expression of the trait. Grain yield/plant showed significant positive correlation with number of tillers/plant, test weight, harvest index % and kernel breadth under both conditions for basmati genotypes, whereas in non-basmati genotypes grain yield/plant exhibited significant positive correlation with biological yield/plant followed by harvest index %, plant height, test weight, number of grains/panicle, number of tillers/plant, root fresh weight and root volume under both conditions suggesting that for improving grain yield direct selection of genotypes for these traits will be more fruitful. Path analysis revealed that biological yield/plant and harvest index % exhibited major positive direct effect on grain yield under both conditions for basmati genotypes whereas, in non-basmati genotypes kernel length followed by number of grains/panicle, days to 50% flowering and biological yield/plant, harvest index % and root volume exerted high positive direct effect on grain yield. Group constellation of genotypes under both the conditions (aerobic and transplanted) did not follow their geographical distribution. On the basis of grain yield HKR 15-455, HKR 16-459, Pusa 1557-06-08-126-162-156 and HKR 15-488 were identified superior than check Haryana Basmati -2 whereas HKR 15-488 and HKR 16-459 were identified as suitable genotypes for quality parameters over check Taraori Basmati. Genotypes, IR14L521, HKR 16-35 and NVSR 2107 were observed suitable under both aerobic and transplanted conditions as these genotypes performed significantly higher than the check HKR 47 and HKR 48 respectively.

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I, Bhawana, Admission No. 2019A85M, hereby undertake that I give full copyrights of my thesis entitled, “**Characterization for yield and quality traits under aerobic and transplanted conditions in rice (*Oryza sativa* L.)**” to the Chaudhary Charan Singh Haryana Agricultural University, Hisar. I also undertake that the patent, if any, arising out of the research work conducted during the programme shall be filed by me only with due permission of the competent authority of CCS HAU, Hisar (Haryana).

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