

## AN ANALYSIS OF GENETIC ASSOCIATION BETWEEN YIELD AND QUALITY TRAITS IN SEGREGATING POPULATION OF *ORYZA SATIVA* L.

GHOURI, F.<sup>1</sup> – NAEEM, M.<sup>2\*</sup> – IQBAL, M.<sup>2</sup> – ALLAH, S. U.<sup>3</sup> – SHAHID, M. Q.<sup>1\*</sup>

<sup>1</sup>College of Agriculture, South China Agricultural University, Guangzhou, Guangdong 510642, China

<sup>2</sup>Department of Plant Breeding and Genetics, UCA & ES, The Islamia University of Bahawalpur, Bahawalpur, Pakistan

<sup>3</sup>Department of Plant Breeding and Genetics, College of Agriculture, BZU Bahaddar Sub-Campus, Layyah, Pakistan

\*Corresponding authors

e-mail: mniub@iub.edu.pk (M. Naeem); shahidmq@gmail.com (M. Q. Shahid); phone: +92-62-925-5539; fax: +86-20-8528-0205

(Received 22<sup>nd</sup> Jan 2020; accepted 6<sup>th</sup> May 2020)

**Abstract.** Limited information has been reported on the genetic association of morphological and quality traits of *Oryza sativa* L. From a total of 50 genotypes, evaluated for genetic diversity using SSR markers, six diverse genotypes were selected for the generation of three crosses. Progenies of these crosses were grown to develop three F<sub>2</sub> populations. Morphological and quality traits were recorded and analysed for genotypic and phenotypic correlations followed by the path coefficient analysis from the genotypic correlation. Strongest association was observed for yield per plant and alkali spread value (ranging from -0.73 to -0.91 for different crosses). It was depicted from path coefficient analysis that length width ratio had a maximum direct effect on yield (ranging from 0.61 to 0.67 for different crosses), and also had a relatively high magnitude of the indirect effect to the yield via plant height, panicle length protein content and length width ratio. Although, minute differences were detected in the strength of association and direct/indirect effects for different populations, the direction of the association always remained the same. The present study showed that direct and indirect effects of traits should be considered for the selection of yield improvement instead of correlation, as a trait having high correlation may have a low direct effect and vice versa.

**Keywords:** *Oryza sativa* L., correlation, path coefficient analysis, qualitative traits, basmati rice

### Introduction

Rice is the staple food for about half of the world population. Rice is a healthful cereal grain which owns unusual dietary requirements. In 2018-19 world's rice production is expected to be 510 million tonnes while world's consumption is also expected to be 503 million tonnes (FAO, 2018). Asia produced and consumed more than 90% of the world's rice (Memon et al., 2015) as three billion Asians fulfil their 35-60% of caloric requirement through rice (Guyer et al., 1998). The cooking and eating qualities of rice are important in defining its economic value in export market and for user acceptance (Pingali, 1997). The Quality of rice grain is intricate characteristic comprising several components such as appearance, cooking and eating qualities (Rabiei et al., 2004). Physicochemical properties of rice are calculated on the basis of amylose content, protein contents and alkali spread value (Rohilla et al., 2000). Quality and yield of rice grain can be enhanced by understanding the genetic mechanism

controlling these traits and association between these traits which is not very well elaborated in previous studies. Correlation studies reported in past have been conducted in homozygous populations but in this study we have conducted correlation studies in segregating populations.

Complex inheritance pattern of grain yield and quality traits necessitate their thorough understanding in order to strengthen rice breeding program. Studies of genetic correlation between yield and quality traits gave understanding about the extent and direction of association between these traits. However direct and indirect effect of different yield related traits are determined by path coefficient analysis. Genetic attributes could be ranked according to their contribution by the breeder (Dewey and Lu, 1959). Dewey and Lu (1959) developed a statistical technique for path analysis which helps in understanding the cause of association and provide information about cause and effect situation. Path analysis assists plant breeders in making selection as it dissects the correlation of different traits into direct and indirect effects (Dewey and Lu, 1959; Milligan et al., 1990; Samonte et al., 2005).

The main objective of this study was to (i) assess genetic variability and correlation among yield and quality traits of various segregating populations for selecting superior genotypes, (ii) to assess the direct and indirect contribution of yield components to yield (iii) to assess the type of connection between quality and yield traits of rice.

## Materials and methods

The present study was conducted in the experimental area of Department of Plant BREEDING and Genetics, University College of Agriculture and Environmental Sciences, the Islamia University of Bahawalpur, Pakistan.

### *Development of plant material for genetic diversity studies*

Thirty rice varieties were grown in nursery during stat of May 2013 up to three leaf stage. Of each genotype 4 cm leaf sample was collected and preserved in liquid nitrogen prior to DNA extraction by CTAB method (Ul-Allah et al., 2017). Twenty  $\mu$ l PCR reaction mixture included DNA 2  $\mu$ l, 0.2  $\mu$ l Taq polymerase enzyme, 1.5  $\mu$ l of each primer, 2.5  $\mu$ l of 2.5 mM dNTPs, 3  $\mu$ l  $MgCl_2$  and 2  $\mu$ l PCR buffer along with 9.3  $\mu$ l of  $ddH_2O$ . One hundred SSR markers (*Table 1*) were used for diversity studies. PCR product was studied on 1.5% agarose gel with Ethidium bromide as fluorescent dye. Banding pattern was scored in binary fashion for the calculation of similarity index which was deployed for the construction of dendrogram by using un-weighted pair group method with arithmetic mean (UPGMA).

### *Selection of diverse genotypes and development of populations*

Based on dendrogram generated by UPGMA, six genetically diverse genotypes i.e., Basmati Pak, Basmati-198, Basmati-385, Super Basmati, Basmati-2000 and Shaheen Basmati were grown in field in end of May, 2013. Cross combinations were made among genotypes widely assorted in dendrogram in following fashion (Basmati Pak  $\times$  HuoYou8166, Basmati-385  $\times$  HuoYou8305 and Basmati-198  $\times$  HuoJingXian) to generate  $F_1$  seed.  $F_2$  seed harvested from  $F_1$  generation during September 2014 was sown in field during May 2015 adapting nursery sowing followed by field transplantation maintaining plant to plant and row to row distance of 30 cm. Soil was

sandy-loam with 50:30:20 sand, silt and clay proportion. Ten rows (each having fifteen plants) of each segregating population plus five rows of each parent were grown keeping single plant per hill in non-replicated fashion. All agronomic practices and crop protection measures were observed as per standard recommendations. Weeds, insect pests and diseases were controlled following standard recommendations.

**Table 1.** List of primers used in present study

Locus name	Chr	Forward primer sequence	Reverse primer sequence	Reference
RM1	1	GCGAAAACACAATGCAAAAA	GCGTTGGTTGGACCTGAC	Panaud et al., 1996
RM2	7	ACGTGTCACCGCTTCCTC	ATGTCCGGGATCTCATCG	Panaud et al., 1996
RM3	6	ACACTGTAGCGGCCACTG	CCTCCACTGCTCCACATCTT	Panaud et al., 1996
RM7	3	TTCGCCATGAAGTCTCTCG	CCTCCCATCATTTTCGTTGTT	Panaud et al., 1996
RM8	2	CACGTGGCGTAAATACACGT	GGCCAAACCCTAACCCCTG	Panaud et al., 1996
RM10	7	TTGTCAAGAGGAGGCATCG	CAGAATGGGAAATGGGTCC	Panaud et al., 1996
RM11	7	TCTCCTTTCCTCCGATC	ATAGCGGGCGAGGCTTAG	Panaud et al., 1996
RM13	5	TCCAACATGGCAAGAGAGAG	GGTGGCATTTCGATTCCAG	Panaud et al., 1996
RM16	3	CGTAGGGCAGCATCTAAA	AACACAGCAGGTACGCGC	Panaud et al., 1996
RM17	12	TGCCCTGTTATTTTCTTCTC	GGTGATCCTTTCCCATTTCA	Panaud et al., 1996
RM18	7	TTCCCTCTCATGAGCTCCAT	GAGTGCCTGGCGCTGTAC	Panaud et al., 1996
RM19	12	CAAAAACAGAGCAGATGAC	CTCAAGATGGACGCCAAGA	Panaud et al., 1996
RM21	11	ACAGTATTCCGTAGGCACGG	GCTCCATGAGGGTGGTAGAG	Panaud et al., 1996
RM22	3	GGTTTGGGAGCCATAATCT	CTGGGCTTCTTCACTCGTC	Panaud et al., 1996
RM26	5	GAGTCGACGAGCGGCAGA	CTGCGAGCGACGGTAACA	Chen et al., 1997
RM27	2	TTTTCTTCTCACCCACTTCA	TCTTTGACAAGAGGAAAGAGGC	Chen et al., 1997
RM30	6	GGTTAGGCATCGTCACGG	TCACCTCACCACACGACACG	Chen et al., 1997
RM31	5	GATCACGATCCACTGGAGCT	AAGTCCATTACTCTCCTCCC	Chen et al., 1997
RM36	3	CAACTATGCACCATTGTGCG	GTACTCCACAAGACCGTACC	Chen et al., 1997
RM38	8	ACGAGCTCTCGATCAGCCTA	TCGGTCTCCATGTCCAC	Chen et al., 1997
RM39	5	GCCTCTCTCGTCTCCTTCT	AATTCAAACCTGCGGTGGC	Chen et al., 1997
RM41	9	AAGTCTAGTTTGCCTCCC	AATTTCTACGTCGTCGGGC	Chen et al., 1997
RM42	8	ATCCTACCGCTGACCATGAG	TTTGGTCTACGTGGCGTACA	Chen et al., 1997
RM44	8	ACGGGCAATCCGAACAACC	TCGGGAAAACCTACCCTACC	Chen et al., 1997
RM47	7	ACTCCACTCCACTCCCCAC	GTCAGCAGGTCCGACGTC	Chen et al., 1997
RM49	3	TTCGGAAGTTGGTTACTGATCA	TTGGAGCGGATTCCGGAGG	Chen et al., 1997
RM50	6	ACTGTACCGGTCGAAGACG	AAATTCACGTCAGCCTCC	Chen et al., 1997
RM51	7	TCTCGATTCAATGTCCTCGG	CTACGTCATCATCGTCTTCCC	Chen et al., 1997
RM55	3	CCGTCGCCGTAGTAGAGAAG	TCCCGTTATTTAAGGCG	Chen et al., 1997
RM60	3	AGTCCCATGTTCCACTTCCG	ATGGCTACTGCCTGACTAC	Chen et al., 1997
RM70	7	GTGGACTTCATTTCAACTCG	GATGTATAAGATAGTCCC	Chen et al., 1997
RM71	2	CTAGAGGCGAAAACGAGATG	GGGTGGGCGAGGTAATAATG	Temnykh et al., 2000
RM72	8	CCGGCGATAAAACAATGAG	GCATCGGTCTAACTAAGGG	Temnykh et al., 2000
RM80	8	TTGAAGGCGCTGAAGGAG	CATCAACCTCGTCTTACC	Chen et al., 1997
RM82	7	TGCTTCTTGTC AATTTCGCC	CGACTCGTGGAGGTACGG	Chen et al., 1997
RM83	12	ACTCGATGACAAGTTGAGG	CACCTAGACACGATCGAG	Chen et al., 1997
RM85	3	CCAAAGATGAAACCTGGATTG	GCACAAGGTGAGCAGTCC	Temnykh et al., 2000
RM87	5	CCTCTCCGATACACCGTATG	GCGAAGGTACGAAAGGAAAG	Temnykh et al., 2000
RM88	8	ACTCATCAGCATGGCCTTGCTC	TAATGCTCCACCTTACCAC	Temnykh et al., 2000
RM201	9	CTCGTTTATTACCTACGTACC	CTACCTCCTTTCTAGACCGATA	Chen et al., 1997
RM202	11	CAGATTGGAGATGAAGTCTCC	CCAGCAAGCATGTCAATGTA	Chen et al., 1997
RM204	6	GTGACTGACTTGGTCATAGGG	GCTAGCCATGCTCTCGTACC	Chen et al., 1997
RM205	9	CTGGTCTGTATGGGAGCAG	CTGGCCCTTACGTTTCAGTG	Chen et al., 1997
RM206	11	CCCATGCGTTTAACTATTCT	CGTTCCATCGATCCGTATGG	Chen et al., 1997
RM207	2	CCATTCGTGAGAAGATCTGA	CACCTCATCCTCGTAACGCC	Chen et al., 1997
RM209	11	ATATGAGTTGCTGTCTGTGCG	CAACTTGCATCCTCCCCTCC	Chen et al., 1997

Locus name	Chr	Forward primer sequence	Reverse primer sequence	Reference
RM210	8	TCACATTCGGTGGCATTG	CGAGGATGGTTGTTCACCTTG	Chen et al., 1997
RM214	7	CTGATGATAGAAAACCTCTTCTC	AAGAACAGCTGACTTCACAA	Chen et al., 1997
RM215	9	CAAAATGGAGCAGCAAGAGC	TGAGCACCTCCTTCTCTGTAG	Chen et al., 1997
RM216	10	GCATGGCCGATGGTAAAG	TGTATAAAAACCACACGGCCA	Chen et al., 1997
RM217	6	ATCGCAGCAATGCCTCGT	GGGTGTGAACAAAGACAC	Chen et al., 1997
RM219	9	CGTCGGATGATGTAAGCCT	CATATCGGCATTTCGCCTG	Chen et al., 1997
RM222	10	CTTAAATGGGCCACATGCG	CAAAGCTTCCGGCCAAAAG	Chen et al., 1997
RM223	8	GAGTGAGCTTGGGCTGAAAC	GAAGGCAAGTCTTGGCACTG	Chen et al., 1997
RM224	11	ATCGATCGATCTTACGAGG	TGCTATAAAAAGGCATTCGGG	Chen et al., 1997
RM225	6	TGCCCATATGGTCTGGATG	GAAAGTGGATCAGGAAGGC	Chen et al., 1997
RM228	10	CTGGCCATTAGTCCTTGG	GCTTGC GGCTCTGCTTAC	Chen et al., 1997
RM229	11	CACTCACACGAACGACTGAC	CGCAGGTTCTTGTGAAATGT	Chen et al., 1997
RM230	8	GCCAGACCGTGGATGTTT	CACCGCAGTCACTTTTCAAG	Chen et al., 1997
RM234	7	ACAGTATCCAAGGCCCTGG	CACGTGAGACAAAGACGGAG	Chen et al., 1997
RM235	12	AGAAGCTAGGGCTAACGAAC	TCACCTGGTCAGCCTCTTTC	Chen et al., 1997
RM239	10	TACAAAATGCTGGGTACCCC	ACATATGGGACCCACCTGTC	Chen et al., 1997
RM241	4	GAGCCAAATAAGATCGCTGA	TGCAAGCAGCAGATTTAGTG	Chen et al., 1997
RM242	9	GGCCAACGTGTGTATGTCTC	TATATGCCAAGACGGATGGG	Chen et al., 1997
RM244	10	CCGACTGTTCGTCTTATCA	CTGCTCTCGGGTGAACGT	Chen et al., 1997
RM245	9	ATGCCGCCAGTGAATAGC	CTGAGAATCCAATTATCTGGGG	Chen et al., 1997
RM246	1	GAGCTCCATCAGCCATTGAG	CTGAGTGCTGCTGCGACT	Chen et al., 1997
RM247	12	TAGTGCCGATCGATGTAACG	CATATGGTTTTGACAAAGCG	Chen et al., 1997
RM248	7	TCCTTGTGAAATCTGGTCCC	GTAGCCTAGCATGGTGCATG	Chen et al., 1997
RM250	2	GGTTCAAACCAAGCTGATCA	GATGAAGGCCCTTCCACGCAG	Chen et al., 1997
RM253	6	TCCTTCAAGAGTGCAAAACC	GCATTGTCATGTCGAAGCC	Chen et al., 1997
RM254	11	AGCCCCGAATAAATCCACCT	CTGGAGGAGCATTTGGTAGC	Chen et al., 1997
RM255	4	TGTTGCGTGTGGAGATGTG	CGAAACCGCTCAGTTCAAC	Chen et al., 1997
RM256	8	GACAGGGAGTGATTGAAGGC	GTTGATTTTCGCCAAGGGC	Chen et al., 1997
RM257	9	CAGTTCGAGCAAGAGTACTC	GGATCGGACGTGGCATATG	Chen et al., 1997
RM258	10	TGCTGTATGTAGCTCGCACC	TGGCCTTTAAAGCTGTGCG	Chen et al., 1997
RM259	1	TGGAGTTTGAGAGGAGGG	CTTGTTCATGGTGCCATGT	Chen et al., 1997
RM260	11	ACTCCACTATGACCCAGAG	GAACAATCCCTTCTACGATCG	Chen et al., 1997
RM261	4	CTACTTCTCCCCTTGTGTCG	TGTACCATCGCAAATCTCC	Chen et al., 1997
RM262	2	CATTCCGTCCTCGGCTCAACT	CAGAGCAAGGTGGCTTGC	Chen et al., 1997
RM263	2	CCCAGGCTAGCTCATGAACC	GCTACGTTTGAGCTACCACG	Chen et al., 1997
RM264	8	GTTGCGTCTACTGCTACTTC	GATCCGTGTCGATGATTAGC	Chen et al., 1997
RM266	2	TAGTTTAACCAAGACTCTC	GGTTGAACCCAAATCTGCA	Chen et al., 1997
RM267	5	TGCAGACATAGAGAAGGAAGTG	AGCAACAGCACAACCTTGATG	Chen et al., 1997
RM269	10	GAAAGCGATCGAACCCAGC	GCAAATGCGCCTCGTGTG	Chen et al., 1997
RM270	12	GGCCGTTGGTTCTAAAATC	TGCGCAGTATCATCGGCGAG	Chen et al., 1997
RM271	10	TCAGATCTACAATCCATCC	TCGGTGAGACCTAGAGAGCC	Chen et al., 1997
RM272	1	AATTGGTAGAGAGGGGAGAG	ACATGCCATTAGAGTCAGGC	Chen et al., 1997
RM273	4	GAAGCCGTCGTGAAGTTACC	GTTTCTACTCTGATCGCGAC	Chen et al., 1997
RM274	5	CCTCGCTTATGAGAGCTTCG	CTTCTCCATCACTCCCATGG	Chen et al., 1997
RM275	6	GCATTGATGTGCCAATCG	CATTGCAACATCTTCAACATCC	Chen et al., 1997
RM276	6	CTCAACGTTGACACCTCGTG	TCCTCCATCGAGCAGTATCA	Chen et al., 1997
RM278	9	GTAGTGAGCCTAACAAATAATC	TCAACTCAGCATCTCTGTCC	Chen et al., 1997
RM279	2	GCGGGAGAGGGATCTCCT	GGCTAGGAGTTAACCTCGCG	Chen et al., 1997
RM280	4	ACACGATCCACTTTGCGC	TGTGTCTTGAGCAGCCAGG	Chen et al., 1997
RM281	8	ACCAAGCATCCAGTGACCAG	GTTCTTCATACAGTCCACATG	Chen et al., 1997
RM282	3	CTGTGTCGAAAGGCTGCAC	CAGTCTGTGTTGCAGCAAG	Chen et al., 1997
RM283	1	GTCTACATGTACCCTTGTGGG	CGGCATGAGAGTCTGTGATG	Chen et al., 1997
RM284	8	ATCTCTGATACTCCATCCATCC	CCTGTACGTTGATCCGAAGC	Chen et al., 1997
RM285	9	CTGTGGGCCCAATATGTCAC	GGCGGTGACATGGAGAAAG	Chen et al., 1997

### ***Morphological and quality traits evaluation***

At maturity data was recorded on one hundred fifty randomly selected guarded plants from each population for plant height, panicle length, and yield per plant. Seed samples were collected separately for the estimation of Amylose content, Alkali Spread Value, protein content and grain length/width ratio. Chemical analysis of Protein contents were accomplished according to AACC method 2000.

### ***Correlation analysis***

Correlation coefficient among the characters under study was estimated according to the statistical techniques given by Gomez and Gomez (1984).

$$r = \frac{\sum XY - \sum X \cdot \sum Y/n}{\sqrt{[\sum X^2 - (\sum X)^2/n] \cdot [\sum Y^2 - (\sum Y)^2/n]}}$$

where n is number of observations, X is first variable, Y is second variable, while genotypic correlation was calculated according to formula

$$r = \frac{CoVF_2 - \overline{CoVp}}{\sqrt{[VF_{2(x)} - Vp(X)] \cdot [VF_2 - \overline{CoVp}(Y)]}}$$

### ***Path analysis***

Path coefficient analysis was performed according to the method given by Dewey and Lu (1959) for the yield and quality traits of Rice, keeping yield per plant as resultant variable and rest of the traits as causal variables.

## **Results**

### ***Genetic diversity studies***

Thirty rice genotypes having wide range of phenotypic variability (*Table 2*) for all of the traits under study were subjected to Simple sequence repeat (SSR) based genetic diversity study (*Fig. 1*). Cluster analysis revealed the genetic relatedness among 30 genotypes of rice as shown in the dendrogram (*Fig. 2*). One hundred SSR markers equally distributed on twelve chromosomes were randomly selected from the genetic map of Rice which revealed polymorphism percentage of 11.3 to 77.5%. Distribution of these genotypes in the dendrogram shows the genetic variation among the genotypes. Cluster analysis grouped the genotypes into four clusters with reference to yield and yield related traits having smallest cluster (Cluster I) with two varieties, Huo Jing Xian and HuoYou8187 and the largest cluster (Cluster IV) having nine varieties, while second and third clusters possesses eight varieties each. Huojing xian, Huoyou-8187, Huoyou-8305, Basmati-Pak, Basmati-198 and Basmati-385 on the bases of genetic divergence owing to variation in yield were selected for making three cross combinations.

### Correlation analysis

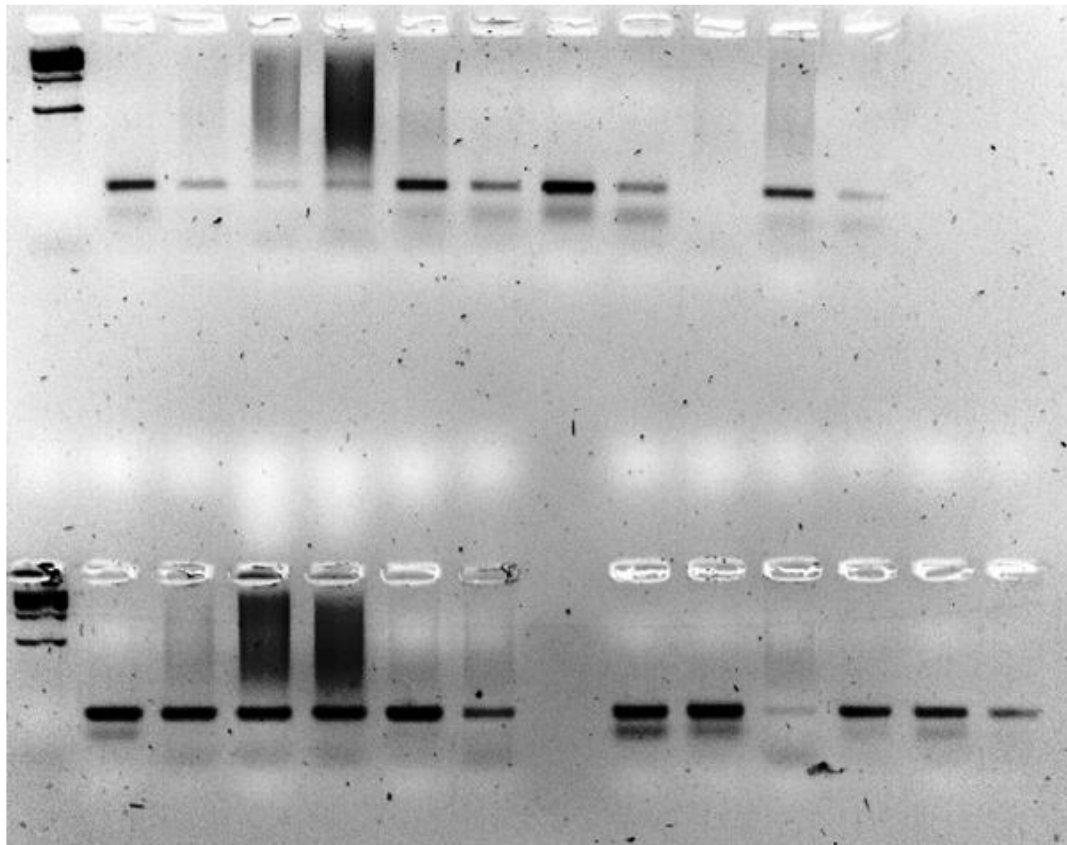
Genetically diverse F<sub>2</sub> population (Fig. 3) for all of the traits studied was obtained from above mentioned cross combinations. Populations from all three cross combinations are significantly different from each other for plant height, panicle length, yield per plant, alkali spread value, amylose content, L/W ratio and protein content. All the characters studied were significantly correlated with yield per plant with few exceptions (discussed below). Genotypic and phenotypic correlation coefficients of three cross combinations populations for various traits are presented in Table 3. Highest positive phenotypic correlation for plant height was observed with protein content values 0.61 in Basmati-198 × HuoJingXian, while it was minimum with L/W ratio 0.01 in the same cross. Phenotypic correlation of plant height was lowest with Alkali spread value -0.48 while genotypic correlation between plant height and amylose content was highest having numerical value -0.71. Highest positive phenotypic correlation for panicle length was with Yield per plant 0.73 while genotypic correlation between panicle length and ASV was -0.64. Panicle length show minimum genotypic correlation with protein content and L/W ratio having numerical values 0.04 and -0.05 respectively. Yield per plant being the most important character of plant showed strongest phenotypic and genotypic correlation with ASV -0.91 while the genotypic and phenotypic correlation between YPP vs panicle length 0.14 and YPP vs Plant height -0.54 respectively, were minimum. Genotypic correlation of ASV was strongest with YPP -0.91, but phenotypic correlation of ASV was weakest with panicle length -0.31. Alkali Spread Value showed strongest positive phenotypic correlation with amylose content 0.87. Length Width ratio show strongest positive phenotypic correlation with protein content 0.86 while strongest negative phenotypic correlation of L/W ratio was found with amylose content -0.89. Contrary to this weakest genotypic correlation of L/W ratio was observed with panicle length -0.05. Protein content shows highest positive phenotypic correlation with L/W ratio i.e. 0.72 and strongest negative genotypic correlation with ASV -0.91. Strong negative (-0.73) phenotypic correlation was observed between protein content and ASV while weakest positive (0.04) genotypic correlation was found between protein content and panicle length.

**Table 2.** Mean values of various traits of parent, studied in this experiment

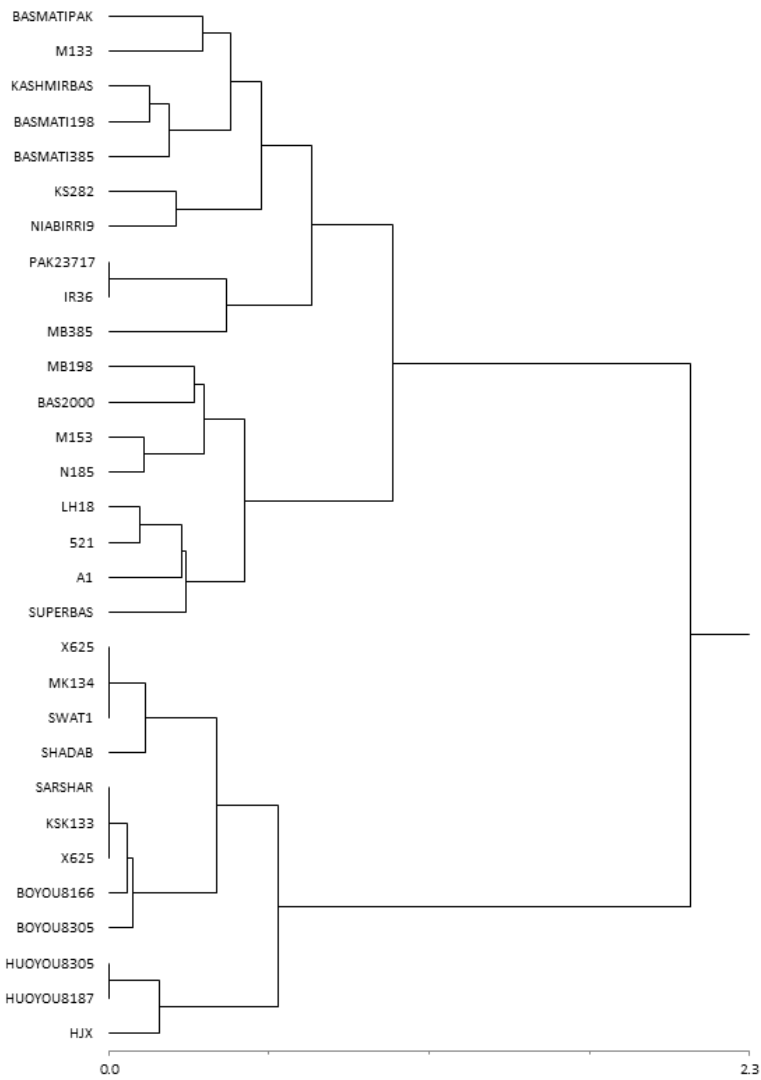
S. No	VAR/TR	PH	PL	YPP	ASV	Aamyl	L/W ratio	Protein
1	BASMATIPAK	132.98 <sup>a</sup>	22.68 <sup>b</sup>	14.04 <sup>a</sup>	5.59 <sup>b</sup>	25.67 <sup>cd</sup>	4.63 <sup>cd</sup>	7.79 <sup>cd</sup>
2	M133	139.07 <sup>a</sup>	21.86 <sup>a</sup>	14.71 <sup>a</sup>	5.33 <sup>ab</sup>	25.63 <sup>cd</sup>	4.65 <sup>cd</sup>	7.75 <sup>def</sup>
3	KASHMIRBAS	136.63 <sup>a</sup>	21.97 <sup>ab</sup>	14.08 <sup>ab</sup>	5.51 <sup>ab</sup>	25.79 <sup>cd</sup>	4.67 <sup>cd</sup>	7.75 <sup>def</sup>
4	BASMATI198	136.53 <sup>a</sup>	23.18 <sup>bc</sup>	14.23 <sup>ab</sup>	5.55 <sup>b</sup>	25.67 <sup>cd</sup>	4.93 <sup>f</sup>	7.83 <sup>efg</sup>
5	BASMATI385	137.60 <sup>a</sup>	23.22 <sup>b</sup>	14.99 <sup>ab</sup>	5.66 <sup>bc</sup>	25.06 <sup>bc</sup>	4.93 <sup>f</sup>	7.68 <sup>cd</sup>
6	KS282	140.84 <sup>a</sup>	21.97 <sup>ab</sup>	14.63 <sup>ac</sup>	5.37 <sup>ab</sup>	25.10 <sup>bc</sup>	4.87 <sup>ef</sup>	7.90 <sup>g</sup>
7	NIABIRRI9	128.03 <sup>b</sup>	22.68 <sup>bc</sup>	14.65 <sup>ac</sup>	5.42 <sup>ab</sup>	25.26 <sup>bc</sup>	4.97 <sup>efg</sup>	7.94 <sup>g</sup>
8	PAK23717	127.36 <sup>ab</sup>	21.74 <sup>ab</sup>	12.12 <sup>abc</sup>	5.43 <sup>ab</sup>	24.88 <sup>bc</sup>	4.94 <sup>ef</sup>	7.64 <sup>ef</sup>
9	IR36	116.89 <sup>abc</sup>	21.02 <sup>a</sup>	11.58 <sup>abc</sup>	6.25 <sup>c</sup>	26.44 <sup>d</sup>	4.74 <sup>c</sup>	7.25 <sup>ab</sup>
10	MB385	116.48 <sup>abc</sup>	23.17 <sup>abc</sup>	10.71 <sup>acd</sup>	5.87 <sup>cd</sup>	27.05 <sup>de</sup>	4.67 <sup>cd</sup>	7.21 <sup>ab</sup>
11	MB198	117.48 <sup>abc</sup>	22.71 <sup>bc</sup>	13.50 <sup>ad</sup>	5.27 <sup>ab</sup>	27.48 <sup>e</sup>	4.76 <sup>d</sup>	7.19 <sup>ab</sup>
12	BAS2000	115.75 <sup>abc</sup>	23.47 <sup>bc</sup>	13.61 <sup>ad</sup>	5.27 <sup>ab</sup>	25.39 <sup>bc</sup>	4.57 <sup>c</sup>	7.18 <sup>ab</sup>
13	M153	115.46 <sup>abc</sup>	24.27 <sup>cd</sup>	13.70 <sup>abcd</sup>	5.48 <sup>ab</sup>	26.38 <sup>cd</sup>	4.84 <sup>d</sup>	7.15 <sup>a</sup>

S. No	VAR/TR	PH	PL	YPP	ASV	Aamyl	L/W ratio	Protein
14	N185	115.36 <sup>bc</sup>	22.36 <sup>b</sup>	13.65 <sup>abcd</sup>	6.74 <sup>cd</sup>	26.49 <sup>cd</sup>	4.26 <sup>a</sup>	7.13 <sup>a</sup>
15	LH18	115.36 <sup>bc</sup>	22.58 <sup>bc</sup>	13.50 <sup>abcd</sup>	6.32 <sup>c</sup>	26.47 <sup>cd</sup>	4.38 <sup>ab</sup>	7.10 <sup>a</sup>
16	521	115.94 <sup>bc</sup>	23.46 <sup>cd</sup>	13.45 <sup>abd</sup>	6.38 <sup>c</sup>	24.55 <sup>b</sup>	4.27 <sup>a</sup>	7.08 <sup>a</sup>
17	A1	113.14 <sup>c</sup>	22.73 <sup>bc</sup>	13.20 <sup>abd</sup>	5.27 <sup>ab</sup>	24.49 <sup>b</sup>	4.39 <sup>ab</sup>	7.43 <sup>cd</sup>
18	SUPPERBAS	113.18 <sup>c</sup>	23.46 <sup>c</sup>	13.10 <sup>abde</sup>	5.95 <sup>b</sup>	25.63 <sup>cd</sup>	4.71 <sup>e</sup>	7.24 <sup>ab</sup>
19	X625	113.27 <sup>c</sup>	24.24 <sup>d</sup>	12.74 <sup>f</sup>	5.27 <sup>ab</sup>	25.48 <sup>bc</sup>	4.75 <sup>e</sup>	7.29 <sup>c</sup>
20	MK134	111.28 <sup>cd</sup>	22.36 <sup>bc</sup>	12.64 <sup>f</sup>	6.46 <sup>cd</sup>	23.47 <sup>a</sup>	4.57 <sup>c</sup>	7.35 <sup>c</sup>
21	SWAT1	110.27 <sup>cd</sup>	22.68 <sup>bc</sup>	12.70 <sup>f</sup>	6.25 <sup>bc</sup>	23.84 <sup>cb</sup>	4.26 <sup>a</sup>	7.36 <sup>cd</sup>
22	SHADAB	109.27 <sup>cd</sup>	23.74 <sup>c</sup>	11.74 <sup>fg</sup>	7.46 <sup>d</sup>	24.57 <sup>b</sup>	4.27 <sup>a</sup>	7.25 <sup>ab</sup>
23	SARSHAR	108.13 <sup>cde</sup>	22.47 <sup>bc</sup>	10.72 <sup>fgh</sup>	5.47 <sup>ab</sup>	24.65 <sup>b</sup>	4.37 <sup>ab</sup>	7.28 <sup>ab</sup>
24	KSK133	108.17 <sup>cde</sup>	22.37 <sup>b</sup>	10.64 <sup>fgh</sup>	5.61 <sup>bc</sup>	23.48 <sup>a</sup>	4.28 <sup>a</sup>	7.55 <sup>e</sup>
25	X625	108.34 <sup>cde</sup>	23.58 <sup>c</sup>	10.54 <sup>fgh</sup>	5.82 <sup>bc</sup>	24.59 <sup>b</sup>	4.76 <sup>ed</sup>	7.45 <sup>cd</sup>
26	BOYOU8166	107.48 <sup>d</sup>	24.57 <sup>d</sup>	9.78 <sup>fhi</sup>	5.96 <sup>bc</sup>	24.65 <sup>bc</sup>	4.56 <sup>c</sup>	7.39 <sup>cd</sup>
27	BOYOU8305	107.47 <sup>ef</sup>	22.16 <sup>ab</sup>	9.54 <sup>fghi</sup>	6.57 <sup>c</sup>	25.58 <sup>d</sup>	4.36 <sup>ab</sup>	7.85 <sup>gh</sup>
28	HUOYOU8305	106.37 <sup>ef</sup>	22.38 <sup>b</sup>	8.49 <sup>hij</sup>	5.68 <sup>bc</sup>	23.52 <sup>a</sup>	4.57 <sup>c</sup>	7.73 <sup>fg</sup>
29	HUOYOU8187	106.48 <sup>ef</sup>	24.27 <sup>b</sup>	8.43 <sup>hij</sup>	4.90 <sup>a</sup>	24.48 <sup>bc</sup>	4.95 <sup>ef</sup>	7.63 <sup>f</sup>
30	HJK	105.37 <sup>ef</sup>	23.57 <sup>cd</sup>	7.21 <sup>117</sup>	5.27 <sup>ab</sup>	23.44 <sup>a</sup>	4.37 <sup>ab</sup>	7.46 <sup>cd</sup>

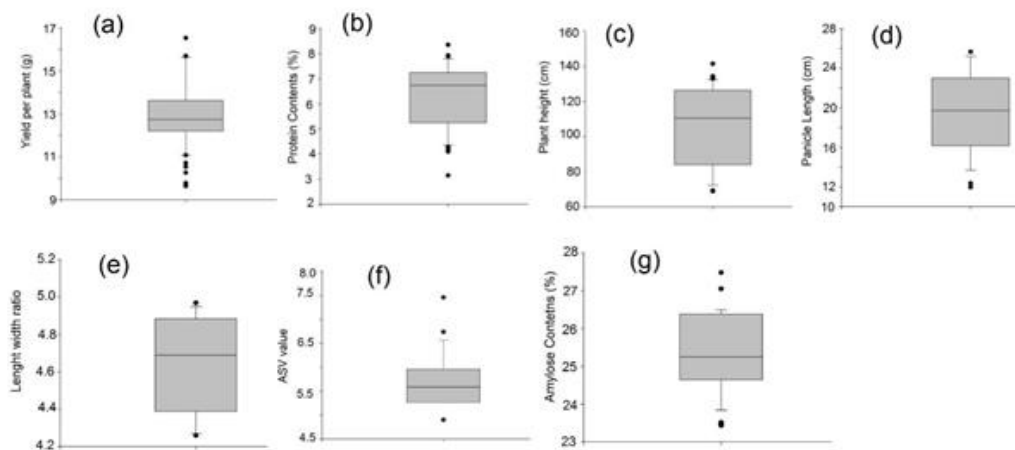
PH: plant height, PL: penical length, YPP: yield per plant, ASV: Alkali spread value, L/W ratio: length width ratio, Protein: protein content. <sup>a,b,c,d</sup> values with similar alphabets are statistically same



**Figure 1.** Gel electrophoresis image of RM-229 with rice genotypes in present study



**Figure 2.** UPGMA cluster analysis showing the diversity and relatedness among the 30 rice genotypes studied



**Figure 3.** Cumulative range of variability in  $F_2$  population of all three crosses for various traits in present study



**Table 3.** Phenotypic and genotypic correlation among different yield and quality traits of rice in three different  $F_2$  populations

Variables	PH	PL	YPP	ASV	Aamyl	L/W Ratio	Protein
<b>Basmati Pak × HuoYou8166</b>							
PH	<b>1.00</b>	0.12	-0.70**	-0.69**	-0.71**	0.05	0.49*
PL	0.19	<b>1.00</b>	0.16	-0.35	-0.27	-0.26	0.05
YPP	-0.68	0.67**	<b>1.00</b>	-0.91**	-0.86**	0.56**	-0.11
ASV	-0.67**	-0.31	-0.87**	<b>1.00</b>	0.75**	-0.83**	-0.85**
Aamyl	-0.66**	-0.23	-0.82**	0.92**	<b>1.00</b>	-0.57**	-0.89**
L/W Ratio	0.09	-0.21	0.82*	-0.79**	-0.50*	<b>1.00</b>	0.62**
Protein	0.56**	0.15	-0.15	-0.83**	-0.84**	0.86**	<b>1.00</b>
<b>Basmati-385 × HuoYou8305</b>							
PH	<b>1.00</b>	0.17	-0.61**	-0.65**	-0.65**	0.05	0.49*
PL	0.42*	<b>1.00</b>	0.14	-0.64**	-0.58**	-0.05	0.04
YPP	-0.56**	0.53**	<b>1.00</b>	-0.83**	-0.72**	0.73**	-0.15
ASV	-0.59**	-0.43*	-0.79**	<b>1.00</b>	0.79**	-0.69**	-0.91**
Aamyl	-0.54*	-0.25	-0.73**	0.87**	<b>1.00</b>	-0.85**	-0.87**
L/W Ratio	0.10	-0.24	0.81**	-0.67**	-0.82**	<b>1.00</b>	0.68**
Protein	0.59**	0.13	-0.17	-0.86**	-0.83**	0.81**	<b>1.00</b>
<b>Basmati-198 × HuoJingXian</b>							
PH	<b>1.00</b>	0.21	-0.61**	-0.50*	-0.57**	0.04	0.42*
PL	0.39	<b>1.00</b>	0.23	-0.49*	-0.38	-0.36	0.05
YPP	-0.54**	0.73**	<b>1.00</b>	-0.91**	-0.85**	0.48*	-0.12
ASV	-0.48**	-0.42*	-0.85**	<b>1.00</b>	0.51*	-0.81**	-0.82**
Aamyl	-0.55**	-0.34	-0.81**	0.55*	<b>1.00</b>	-0.89**	-0.91**
L/W Ratio	0.01	-0.28	0.70**	-0.76**	-0.87**	<b>1.00</b>	0.72**
Protein	0.61**	0.17	-0.19	-0.73**	-0.82**	0.81**	<b>1.00</b>

Lower diagonal represents phenotypic correlation and upper diagonal represent genotypic correlation. Bold numerical values are diagonals. PH: plant height, PL: panicle length, YPP: yield per plant, ASV: Alkali spread value, L/W ratio: length width ratio, Protein: protein content. \*Significant at the 5% level. \*\*Significant at the 1% level

### Path co-efficient analysis

Genetic correlation of different quality traits and yield components was further dissected to investigate the direct and indirect effects of each trait that it has on grain yield (Table 4). Direct effects explain the contribution of individual trait with grain yield while indirect effect explains the influence of a character on yield in association of other characters.

### Direct effects

Direct effect is the contribution of the trait that directly determined the yield. The traits that have positive direct effect, with increase in them the yield will also increases. While increase in the characters having negative effect toward yield will results in decrease of yield. In the present population the results show that all the traits show positive direct effect in the yield except ASV. Highest positive direct effect was showed by L/W ratio (0.67) followed by panicle length (0.41), amylose content (0.36) while lowest positive direct effect was contributed by plant height (0.22). Alkali spread value show negative direct effect with maximum value (-0.49) and minimum value (-0.21).

**Table 4.** Direct and indirect effect matrix. Dependent variable is YPP. The last column shows genotypic correlations of independent variables with YPP among different yield and quality traits of rice in three different  $F_2$  populations

Variables	PH	PL	ASV	Aamyl	l/w ratio	Protein	YPP
<b>Basmati Pak × HuoYou8166</b>							
PH	0.19	0.07	-0.33	-0.31	-0.03	-0.29	-0.70
PL	0.04	0.32	-0.18	0.01	0.04	-0.07	0.16
ASV	0.12	-0.27	-0.49	0.19	0.28	-0.74	-0.91
Aamyl	0.10	0.07	-0.82	0.33	-0.73	0.19	-0.86
L/w ratio	-0.01	-0.03	-0.34	0.56	0.61	-0.23	0.56
Protein	-0.02	0.02	-0.18	0.32	-0.15	-0.1	-0.11
<b>Basmati-385 × HuoYou8305</b>							
PH	0.22	0.09	-0.27	-0.31	-0.02	-0.32	-0.61
PL	0.04	0.41	-0.24	0.02	0.05	-0.05	0.14
ASV	0.11	-0.15	-0.21	0.51	-0.57	-0.52	-0.83
Aamyl	0.13	0.06	-0.73	0.32	-0.68	0.22	-0.72
L/W ratio	0.03	-0.04	-0.32	0.73	0.67	-0.35	0.73
Protein	0.06	0.08	-0.15	0.21	-0.22	-0.13	-0.15
<b>Basmati-198 × HuoJingXian</b>							
PH	0.20	0.08	-0.35	-0.28	-0.04	-0.26	-0.61
PL	0.03	0.36	-0.20	0.02	0.06	-0.04	0.23
ASV	0.18	-0.56	-0.44	0.27	0.36	-0.63	-0.91
Aamyl	0.09	0.05	-0.78	0.36	-0.84	0.27	-0.85
L/w ratio	-0.03	-0.04	-0.43	0.57	0.65	-0.24	0.48
Protein	-0.01	0.05	-0.12	0.26	-0.14	-0.16	-0.12

PH: plant height, PL: penical length, YPP: yield per plant, ASV: Alkali spread value, L/W ratio: length width ratio, Protein: protein contents

### Indirect effects

Plant height has positive indirect effect through panicle length which ranges 0.07-0.09. Negative indirect effect of plant height was present for all other traits which was minimum (-0.02) for L/W ratio while negative indirect effect was maximum (-0.35) for ASV. Panicle length has positive indirect effect with plant height, amylose content and L/W ratio which was highest for L/W ratio having value 0.06 while panicle length has minimum indirect positive effect with amylose content (0.01). Negative indirect effect of panicle length observed with ASV and protein content, being maximum for ASV (-0.24) and minimum for protein content (-0.04). Negative indirect effect of ASV was resulted with panicle length ranges (-0.15 to -0.56) and protein content ranges (-0.52 to -0.72). ASV showed positive indirect effect with plant height, amylose content and L/W ratio which is highest for L/W ratio (0.57) and lowest for (0.11). Amylose content has all the positive indirect effects except ASV and L/W ratio. Direct positive effect of amylose content was maximum through protein content (0.27) and was minimum through panicle length (0.05). Negative indirect was highest through L/W ratio (-0.84) while minimum was also through L/W ratio (-0.68). L/W ratio has all the negative indirect effect except through amylose content, the maximum negative indirect effect contributed through ASV (-0.43) while minimum through plant height (-0.01). Positive indirect effect of protein content presented through panicle length and amylose content

which ranges (0.02-0.32). Negative indirect effect of Protein content ranges (-0.02 to -0.22) that are contributed through plant height, ASV and L/W ratio.

## Discussion

The study was conducted to add in the existing knowledge of relationship between yield and quality traits. For the improvement of complex quantitative traits, the knowledge of inter relationship for yield contributing and quality traits are important for a breeder to evolve high yielding cultivars with improved quality traits. Negative correlation of plant height with paddy yield show higher photosynthetic accumulation in the vegetative parts due to tallness rather their accumulation in the reproductive parts (Zahid et al., 2006; Akinwale et al., 2011). Furthermore, dwarf genes have also been reported to have pleiotropic effect on yield (Zahid et al., 2006; Parsad et al., 2001; Tahir et al., 1988). However, the results were contradictory to Ranawake and Amarasinghe (2014) who reported that increase in plant height results in increased rate of photosynthesis in plant which transfer more photosynthates to grains. The contrary results may be attributed to genetic differences and environmental factors. Negative correlation between panicle length and plant height was also observed by Jayasudha and Sharma (2010) and Eradasappa et al. (2007), this may be as a result of compromise between reproductive and vegetative growth. Increase amylose content of grain will increase grain yield in rice. Positive correlation between amylose content and protein shows that increase in one character will lead to increase the in others traits and vice versa Anandan et al. (2011). For the improvement of yield direct selection through plant height will result in the reduction of grain yield per plant due its negative direct effect (Naseem et al., 2014; Hairmasis et al., 2010; Akhtar et al., 2011). Panicle length has positive direct effect on yield so increase in panicle length will enhance yield. All the genetic coefficients of correlation were less than the phenotypic coefficient of correlation in present investigation which indicates the effect of environment in the observed correlation. Panicle length was positively correlated with grain yield which showed that improvement of this character will led to improved varieties with higher yield. Plant height and quality traits like alkali spread value, amylose content and protein content decrease with the increase of yield so higher yielding varieties will produce lower amylose, ASV content and protein contents (Sarkar et al., 2007; Sabesan et al., 2009). Protein contents have negative correlation with grain yield, but this correlation was negative, therefore, selection for higher yield may not have significant impact on protein contents. Here, it is important to notice that amylose content and plant height have negative correlation with grain yield of rice but when its correlation is divided into direct and indirect effects, direct effect of these traits was in positive direction. Similar findings have also been shown in cotton case of seeds per locule and lint percentage (Ul-Allah et al., 2017). In such conditions, selection become complicated and indirectly effecting traits must be considered for an effective selection. It is concluded that plant height and panicle length are the key yield influencing traits, while protein content and amylose content are the basic quality traits which also influence yield.

This reflect that with the increase in panicle length, number of spikelets may increase that result in increase of paddy yield (Ashfaq et al., 2012; Ramkrishnan et al., 2006). Increase amylose content of grain will increase grain yield in rice. Positive correlation

between amylose content and protein shows that increase in one character will leads to increase the others (Anandan et al., 2011).

Path coefficient analysis simplify the complex multiple effect of different traits on resultant traits (Ul-Allah et al., 2017) as it breaks the correlation into direct and indirect effects. Main purpose of the analysis is to identify that how different traits effect each other and modify the effect of other trait to the final yield. Plant height has positive direct effect on yield per plant as with the increase in plant height, plant produce photosynthates but due to accumulation of photosynthetic assimilate in vegetative parts, magnitude of its direct effect is low and indirect effect of plant height through various other traits lead to overall negative correlation. Plant height has indirect effect with panicle length toward the increment of yield as due to increase of plant height, panicle length also increases, which leads to higher yield. Similar correlation far panicle and plant height was identified by Jayasudha and Sharma (2010) and Eradasappa et al. (2007). Amylose content, ASV, length to width ratio and protein content have overall negative correlation with yield per plant as more photosynthates will accumulates in the vegetative parts and does not moves towards sink (Tahir et al., 1988; Zahid et al., 2006). Similar result was reported by Parsad et al. (2001). More the length of panicle more grain will produce which leads to increased grain yield (Immanue et al., 2011).

The negative direct effect of alkali spread value shows that it directly decreases the yield and also indirectly along with L/B ratio decreases the yield. Length to width ratio has positive direct effect on the yield while overall correlation with grain yield was positive, which means that with the increase in L/B ratio grain yield will increase. Nandan et al. (2010) suggested that the difference was due to different genotypes and environmental conditions. Protein content has positive direct effect on the yield and negative indirect effect via plant height, ASV and L/W ratio. While combined effect of protein with all other traits on the yield is positive.

## Conclusion

It is concluded from this study that traits having positive correlation with yield may have negative direct effect and vice versa. Therefore, selection of traits for yield improvement should be made carefully by looking at direct effect of specific trait to yield as one trait with smaller direct effect may have higher correlation due to higher indirect effect of other traits. Information created from this research will help plant breeder for effective selection of traits in developing high yielding rice cultivars. High yield rice cultivars will contribute to sustainable profit of the farmers by getting higher yield without any extra inputs.

**Acknowledgements.** This work was supported by the National Natural Science Foundation of China (NSFC) (grant number 31850410472).

## REFERENCES

- [1] AACC International (2000): Approved Methods of the American Association of Cereal Chemists. 10th Ed. Methods 22-05, 38-12A, 46-12, 54-30A, 54-40A, 56-11, and 56-70. – AAAC, St. Paul, MN.

- [2] Akhtar, N., Nazir, M. F., Rabanawaz, A., Mahmood, T., Safdar, M. E., Asif, M., Rehman, A. (2011): Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.). – J. Anim. Plant Sci. 21(4): 660-664.
- [3] Akinwale, M. G., Gregorio, G., Nwilene, F., Akinyele, B. O., Ogunbayo, S. A., Odiyi, A. C. (2011): Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). – African J. Plant Sci. 5: 207-12.
- [4] Anandan, A. G., Eswaran, R. R., Prakash, M. (2011): Genotypic variation and relationships between quality traits and trace elements in traditional and improved rice (*Oryza sativa* L.). – Genotypes J. Food Sci. 76: 122-130.
- [5] Ashfaq, M., Khan, A. S., Khan, S. H. U., Ahmad, R. (2012): Association of various morphological traits with yield and genetic divergence in rice (*Oryza sativa* L.). – Int J. Agric. Biol. 14: 55-62.
- [6] Chen, X., Temnykh, S., Xu, Y., Cho, Y. G., Mccouch, S. R. (1997): Development of a microsatellite framework map providing genome-wide coverage in rice (*Oryza sativa* L.). – Theor. Appl. Genet. 95: 553-567.
- [7] Dewey, R. D., Lu, K. H. (1959): A correlation and path coefficient analysis of components of crested wheat grass seed production. – Argon. J. 51: 515-518.
- [8] Eradasappa, E., Nadarajan, N., Ganapathy, K. N., Shanthala, J., Satish, R. G. (2007): Correlation and path analysis for yield and its attributing traits in rice (*Oryza sativa* L.). – Crop Research 34: 156-159.
- [9] FAO (2018): Rice market monitor 21(1). – [www.fao.org/3/I9243EN/i9243en.pdf](http://www.fao.org/3/I9243EN/i9243en.pdf).
- [10] Gomez, K. A., Gomez, A. A. (1984): Statistical Procedures for Agricultural Research. 2nd Ed. – John Wiley and Sons, New York.
- [11] Guyer, D., Tuttle, A., Rouse, S., Volrath, S., Johnson, M., Potter, S., Gorlach, J., Goff, S., Crossland, L., Ward, E. (1998): Activation of latent 171 transgenes in Arabidopsis using a hybrid transcription factor. – Genetics 149: 633-639.
- [12] Hairmasis, A., Kustianto, B., Suwarno, S. (2010): Correlation analysis of agronomic characters and grain yield of rice for tidal swamp areas. – Indonesian J Agric Sci 11(1): 11-15.
- [13] Immanue, S. C., Nagarajan, P., Thiagarajan, K., Bharathi, M., Rabindran, R. (2011): Genetic parameters of variability, correlation and path coefficient studies for grain yield and other yield related attributes among rice blast disease resistant genotypes of rice (*Oryza sativa* L.). – African J. Biotech. 10(17): 3322-3334.
- [14] Jayasudha, S., Sharma, D. (2010): Genetic parameters of variability, correlation and path-coefficient for grain yield and physiological traits in rice (*Oryza sativa* L.) under shallow lowland situation. – Electronic J. Plant Breeding 1(5): 33-38.
- [15] Memon, Q. A., Wagan, S. A., Wagan, T. A., Memon, I. H., Wagan, Z. A., Memon, H., Wagan, Z. A., Jamro, A., Wagan, S. A., Memon, I. H., Memon, A. H. (2015): Economic analysis of hybrid rice in Taluka Golarchi District Baddin Sindh, Pakistan. – International Journal of Business and Economics Research 4(6): 264-269.
- [16] Milligan, S. B., Gravois, K. A., Bischoff, K. P., Martin, F. A. (1990): Crop effects on genetic relationships among sugarcane traits. – Crop Sci. 30: 927-931.
- [17] Nandan, R., Sweta, Singh, S. K. (2010): Character association and path analysis in rice (*Oryza sativa* L.) genotypes. – World J. Agric Sci. 6(2): 201-206.
- [18] Naseem, I., Khan, A. S., Akhter, M. (2014): Correlation and path coefficient studies of some yield related traits in rice (*Oryza sativa* L.). – International Journal of Scientific and Research Publications 4(4): 2250-3153.
- [19] Panaud, O., Chen, X., Mccouch, S. R. (1996): Development of microsatellite markers and characterization of simple sequence length polymorphism (SSLP) in rice (*Oryza sativa* L.). – Mol. Gen. 252: 597-607.
- [20] Parsad, B., Patwary, A. K., Biswas, P. S. (2001): Genetic variability and selection criteria for fine rice (*Oryza sativa* L.). – Asian J. Plant Sci. 1: 245-247.

- [21] Pingali, P. L. (1997): From subsistence to commercial production systems: the transformation of Asian agriculture. – American Journal of Agricultural Economics 79: 628-34.
- [22] Rabiei, B., Valizadeh, M., Ghareyazie, B., Moghaddam, M., Ali, A. J. (2004): Identification of QTLs for rice grain size and shape of Iranian cultivars using SSR markers. – Euphytica 137: 325-332.
- [23] Ramkrishnan, S. H., Anandakumar, C. R., Saravanan, S., Malini, N. (2006): Association analysis of some yield traits in rice (*Oryza sativa* L.). – Journal of Applied Science Research 2: 402-404.
- [24] Ranawake, A. L., Amarasinghe, G. S. (2014): Relationship of yield and yield related traits of some traditional rice cultivars in Sri Lanka as described by correlation analysis. – Journal of Scientific Research and Reports 3(18): 2395-2403.
- [25] Rohilla, R., Singh, V. P., Singh, U. S., Singh, R. K., Khush, G. S. (2000): Crop Husbandry and Environmental Factors Affecting Aroma and Other Quality Traits. –In: Sing, R. K., Singh, U. S., Khush, G. S. (eds.) Aromatic Rices. Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi, India, pp 201-216.
- [26] Sabesan, T., Suresh, R., Saravanan, K. (2009): Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamilnadu. – Electronic Journal of Plant Breeding 1: 56-59.
- [27] Samonte, P. B. O. S., Sherwin, A. L., Tagle, J. S., Lales, G. M., Villegas, E. A. (2005): Path analysis of traits affecting grain yield and its components in corn. – The Philippine Agric. Scientist. 88(4): 400-407.
- [28] Sarkar, K. K., Bhutia, K. S., Senapathi, B. K., Roy, S. K. (2007): Genetic variability and character association of quality traits in rice (*Oryza sativa* L.). – Oryza 44(1): 64-67.
- [29] Tahir, H., Jilliani, G., Iqbal, M. Z. (1988): Integrated use of organic and inorganic N fertilizers in rice wheat cropping system. – Pakistan Journal of Soil Science 3: 19-23.
- [30] Temnykh, S., Park, W. D., Ayeres, N., Cartinhour, S., Hauck, N., Lipovich, L., C. H. O., Y. G., Ishit, T., Mccouch, S. R. (2000): Mapping and genome organization of microsatellite sequences in rice (*Oryza sativa* L.). – Theor. Appl. Genet. 100: 697-712.
- [31] Ul-allah, S., Iqbal, M., Naeem, M., Zahid, W. (2017): Genetic dissection of association among within boll yield components and their relationship with seed cotton yield in F3 populations of *Gossypium hirsutum* L.). Plant Genetic Resources 15: 157-164.
- [32] Zahid A. M. A., Akhtar, M., Sabir, M., Manzoor, Z. T., Awan, H. (2006): Correlation and path analysis studies of yield and economic traits in Basmati rice (*Oryza sativa*, L.). – Asian J. of Plant Science 5: 643-645.