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VARIABILITY AMONG RECOMBINANT INBRED LINES DERIVED FROM THE CROSS BPT5204 × HPR14 FOR GRAIN PROTEIN CONTENT, AMYLOSE CONTENT, GRAIN YIELD AND YIELD ATTRIBUTING TRAITS IN RICE (*ORYZA SATIVA L.*)

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ABSTRACT

Rice is a staple food for vast majority of population through out world. In a study an eperiment was conducted to check the variability among the recombinant inbreed lines for the mapping population. Genetic variability, Heritability and genetic advance study for protein content, amylase content, Seed yield and its components was conducted in recombinant inbreed lines (in F9 generation) of Oryza sativa indica L. at the K-block, UAS, Bengaluru, India. Genetic Variance was less than enviormental variance for all the traits. High broad sence heritability and genetic gain were recorded for grain protein content, amylase content, grain yield and yield attributing traits. These results suggest that there is sufficient genetic variability for all the traits studied in the recombinant inbreed lines, Suggesting suitability of the population for mapping.
***Keywords* :** Grain protein content, Amylase content, Grain yield and Yield attributing traits in rice

Introduction

The cooking as well as eating quality of rice is an important trait for consumer preference and fetching high price to farmer (Cramer *et al.,* 1993; Unnevehr, 1986). Volume expansion and taste of rice is one of the major characters to be selected by food industry (Gujral and Kumar, 2003). The rice which is soft and sticky on cooking are highly proffered over other rice (Kaosaard and Juliano, 1991). There is considerable variation among the traits and parameter used to evaluate may varies across the countries. Eventually, out of all the traits four traits which represent quality are considered (Yu *et al.,* 2008) These four traits are milled rice properties, enhanced cooking quality, texture or appearance and nutritive content of rice grain.

Generally from rice seed external and bran layer is milled up or remove to make it fit for consumer choice. And the trait like broken kernel rate is taken with utmost care as it defines the quality and price of rice in market. Trait such as mild rice appearance is more attractive alternative quality character for consumer.

This is a cook quality which is responsible for the easiness of cooking, firmness and stickiness of the rice when cooked. This lead to difference in grades for milling based on the ratios of these rates. Once the rice is milled the appearance factor depends upon with size, shape (long vs. round), chalkiness, and translucency. Starch present in the endosperm along with the protein and lipid is major factor for determining the properties of rice in term of quality standards (Zhong kai *et al.,* 2002). In this study the trail was conducted to know the variability of recombinant inbreed lines derived from parents (i.e cross of BPT5204 and HPR14) for different traits like GPC, AC, grain yield and yield attributing character. All the RILs were sown under aerobic condition to know the effect of aerobic environment on above mentioned trait of rice.

Material and Methods

Experimental Material

The experimental material consisted of 288 F9 RIL's derived from cross BPT5204 × HPR14. A core set of 288 RIL's were developed using power core software (Kim *et al.,* 2007) from previous data of grain protein content, amylose content and agronomic traits of 2000 RIL's evaluated under wetland condition at mandya during 2009. The plant material was developed by Dr. Shailaja Hittalmani at Department of Genetics and Plant Breeding, University of Agricultural Sciences, GKVK, Banglore and has been evaluated over the years by Banu *et al.* (2011) Samak *et al.* (2009), Shasidharan *et al.* (2007) for grain protein and amylose content along with agronomic traits.

Experimental design and Layout

A set of 288 F9 recombinant inbred lines (RIL's) of rice were sown by direct seeding in Bangalore under aerobic condition. Beta-lattice augmented design was followed with parents as check after every tenth row at spacing of 25 X 20 cm; each plant is sown in replication of ten within a row. Fertilizer applications were done in accordance with required level of NPK i.e. 100:50:50 per hectare. Urea was applied to soil to soil at 30 and 60 days from sowing in three different doses (i.e. 50%, 25% and 25% respectively). SSP and MOP is been provided to crop as a phosphate and potassium source to the crop. Aerobic condition were maintained in a plots where regulated irrigation was provided as per practice (Anon, 2008). RILs with their parents were used to measure traits as mentioned above. The crop was shown for investigation in summer season of 2011.

Observations recorded

Randomly five selected individual plants are chosen for recording observation along with checks. The observations recorded for Plant height, Number of tillers per plant, Number of productive tillers per plant Days to 50 per cent flowering, Days to maturity, Seed yield (g) per plant Straw yield (g) per plant..

Total protein and amylose content (%) estimation.

NIR system, FOSS, Denmark generally referred to as near infrared reflectance spectroscopy was utilized to measure percentage of protein and amylase content. is utilized for estimation of grain protein content and amylose content in RIL's. A data from generation F3 and F4 is utilized to standardized the panel. On the basis of which total content of protein and amylase is recorded. Amylose content and protein content were predicted from models of developed spectrum at UAS, Banglore with 3000 sample

Statistical analysis

Various software packages such as GENERES and STATISTICA is used for Statistical analysis.

Correlation studies

Correlation coefficient was calculated as described by Al-Jibourie *et al*. (1958).

Analysis of variance (ANOVA)

ANOVA is calculated by taking mean values of five plants (Rana *et al*., 1991). ANOVA is calculated using software AUGMENT1 at 5 % and 1 % significant level (Agrawal and Sapra, 1995). Shown in table 1.

Test of normality

Normal distribution

The normal distribution is determined by the standard formula (Altman D.G and Bland J.M 1995)

Skewness

The skewness is calculated with the formula as described in Fisher *et al*., 1932.

Kurtosis

The kurtosis is calculated with the formula as described in Robson, 1956

Result and Discussion

The PCV and GCV were found to be high or moderate for the traits. No characters were reported with low PCV and GCV. Similar result for seed yield is seen in studies of Bisne *et al.,* 2009, Akinwale *et al*., 2011. The entire trait shows high heritability (>60%). Hence traits are suitable for mapping and selection. Shown in table 2.

The Genetic advance for days to maturity, days to flowering and straw yield was as low (>0-10 %). The lowest GA is reported in days to maturity. Moderate GA is been reported in amylase content, plant height and harvesting index where as high GA is observed for protein content, number of tillers, productive number of tillers and seed yield. Traits with low genetic advance and heritability are controlled by non additive gene function and is not suitable for selection.

The frequency distributions of RILs were found to fall under continuous variation. Plant height shows a skewed variation towards male parent (HPR18) where as slightly skewed pattern towards female parents were seen in AC & PC traits (Singh and Rai, 1981). Skewed distribution is seen for e.g. number of tiller and productive number of tillers. The trait was skewed towards male parent. (Chauhan, 1996; Elayaraja *et al.,* 2005 and Bisne *et al*., 2009) Shown in table 3.

Most of morphological, quality and yield traits observed under the present study exhibit high genetic variability, heritability and genetic advance. This makes this population best for direct selection for yield along with quality traits for improvement of rice crop (Singh and Singh, 2007). In present studies traits such as protein content, yield, yield attributing traits and amylase content show transgressive segregants in both directions (Xiao *et al.,* 1996; Yadav *et al.,* 1997 and Ali *et al.,* 2000).

Above observation suggest that importance of the character for selection of improving yield and quality content.

Correlation studies

Protein content and amylase content was found to be negatively correlation with each other. Highly significant negative correlation was observed for protein content and amylase content (Simmonds *et al*. (1995), Singh *et al*. (1998), Song and Zhang, (1992), Yang *et al*. (2004), Zuo *et al*. (2001)). Also amylase content is found positively correlated with seed yield. The result was similar to Singh et al 1998. Straw yield and productive number of tiller were found to be negatively correlated. Shown in table 4.

Test of normality

The trait with skewed distribution by dominant geen whether remains dominant even if the trait shows increasing or decreasing affect (Pooni *et al*., 1977, Fisher *et al*., 1932, Robson, 1956). The trait showing no gene interaction have a negative or close to zero kurtosis and in the presence of gene interaction it tend to be positive (Pooni *et al*., 1977; Choo and Reinbergs, 1982; Kotch *et al*., 1992). RILs population were positively skewed (towards HPR14) for protein content indicating the population has more genomic region from HPR14. Linkage disequilibrium, linkage drag, natural selection and meiotic distortion may be the reason behind the RILs deviating from normal distribution.

Table 1: Estimates of mean sum of squares for ten quantitative traits among RILs derived from the cross BPT5204 × HPR14.

Components	DOF	PC	AC	DF	DM	NT	PT	PHT	STY	SY	HI
Treatments	289	6.2**	1565**	131**	183.6**	39.5**	32**	841.2**	1382.5**	33.83**	0.01**
Checks	1	658.8**	618.9**	6657**	18235**	370**	777.6**	8954.8**	1576.5**	447.01**	0.1**
T.ENTRY	287	3.7	13.6	99	117.1	38.5	29.4	650	1386.1	31.07	0.01
CHK V Test	1	66.3**	2.6**	2990**	1219**	3.1**	41.9**	475888**	154.4**	414.52**	0.0008**
Error	58	0.06	2	11	1.9	2	1.8	48.2	3.8	2.36	0.0002

'*' @ 5% significant '**' @ 1% significant
DOF= Degree of freedom, PC = protein content, AC = Amylose content
DF= Days to flowering, DM= Days to maturity, NT= Number of tillers
PT= Number of productive tillers, PHT= Plant Height, STY= Straw yield
SY= Seed yield, HI =Harvesting Index, PT= Number of productive tillers

Table 2: Estimates of variability and genetic parameters for ten quantitative traits among RILs derived from the cross BPT5204 × HPR14.

	Parents		Range							
Trait	BPT5204	HPR14	Max-imum	Mini-mum	Grand mean	GCV (%)	PCV (%)	Heritability	GA (%)	CD (0.05
PC (%)	7.42	14.05	14.7	4.2	9.58	24.41	26.11	87.44	23.5	2.48
AC (%)	19.6	26.02	32.9	3	23.0	16.03	17.19	86.93	15.74	4.01
DF	102.2	81.13	124	70	99.4	11.01	11.54	91.06	8.92	9.36
DM	152	116	148	109	128.6	10.47	10.53	98.93	3.13	3.9
NT	20.47	15.5	39	5	17.73	34.52	35.47	94.71	22.47	4.04
PHT (cm)	76.1	100.53	178	54	119.2	23.6	24.31	94.26	15.98	19.4
PT	16.73	9.53	36	3	14.05	39.14	40.3	94.33	26.34	3.77
STY (g/plant)	53.92	64.17	360.5	14.88	57.27	64.83	64.92	99.71	9.99	5.52
SY (g/plant)	25.71	20.25	46	8.18	20.09	27.92	28.95	93.02	20.72	4.3
HI	0.32	0.24	0.56	0.05	0.28	37.96	38.29	98.2	16.07	0.04

PC= Protein content AC= Amylose content GCV= Genotypic coefficient of variation PCV= Phenotypic coefficient of variation GA= Genetic advance
CD=Critical difference at 0.05 significant level

Table 3: Estimate of skewness and kurtosis for different characters in 288 RIL's of cross BPT5204 × HPR14

Traits	Skewness	Kurtosis
Protein content (%)	-0.16	-0.07
Amylose content (%)	-0.72	3.62
Days to 50 % flowering	-0.13	0.13
Plant height	-0.8	0.18
No. of tillers per plant	0.47	0.37
No. of productive tiller per plant	0.64	0.71
Days to maturity	-0.26	-0.31
Seed yield (g/plant)	1.08	2.70
Straw yield (g/plant)	3.30	19.10
Harvesting Index	0.21	-0.31

Table 4: Correlation coefficients for ten quantitative traits among RILs derived from the cross BPT5204 ×HPR14.

	Protein content	Amylose content	DF	PHT	NT	PT	DM	Seed yield	Straw yield	HI
P C (%)	1									
A C (%)	-0.45**	1								
DF	0.11	-0.09	1							
PHT (cm)	-0.30**	0.11	0.11	1						
NT	-0.01	0.05	-0.07	0.08	1					
PT	0.02	-0.05	0.06	-0.16**	-0.84**	1				
DM	0.14*	-.13*	-0.11	-0.25**	-0.15**	0.11*	1			
S Y (g/plant)	-0.68**	0.42**	-0.13*	0.19**	0.05	-0.04	-0.08	1		
STY (g/plant)	-0.19**	0.07	-0.01	0.46**	0.63**	-0.63**	-0.20**	0.12*	1	
HI	-0.39 **	0.29**	-0.08	-0.36**	-0.56**	0.58**	0.12*	0.34**	-0.70**	1

PC = Protein content AC= Amylose content PHT = Plant height PT = Productive number of tiller
DF = Days to flowering, DM = Days to maturity NT = Number of tille, SY = Seed yield, STY = Straw yield
HI = Harvesting index

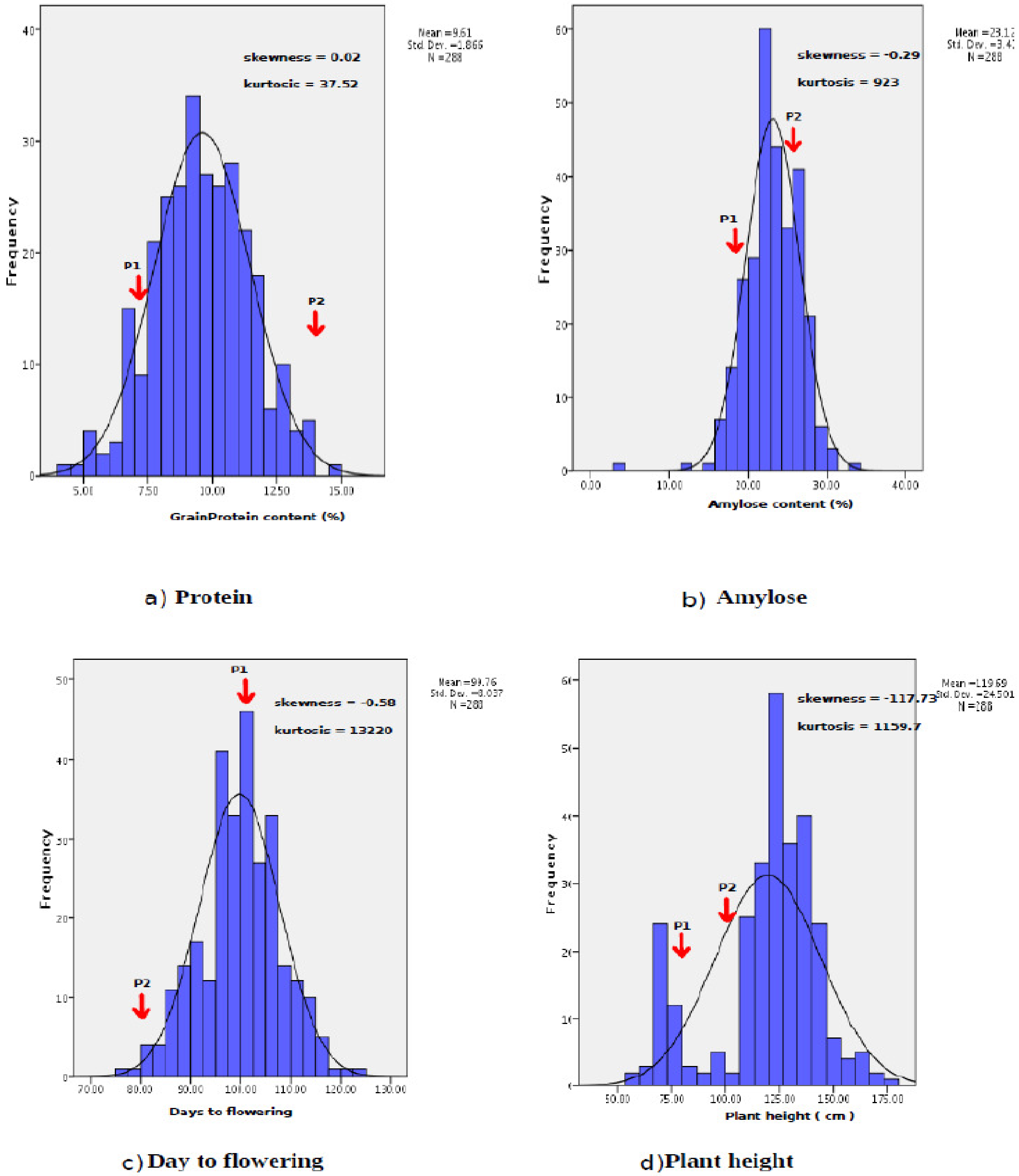


Fig. 1: [a-d]: Frequency distribution of 288 RIL's protein content, amylose content, days to flowering and plant height. P1 = Trait value for BPT5204 , P2 = Trait value for HPR14.

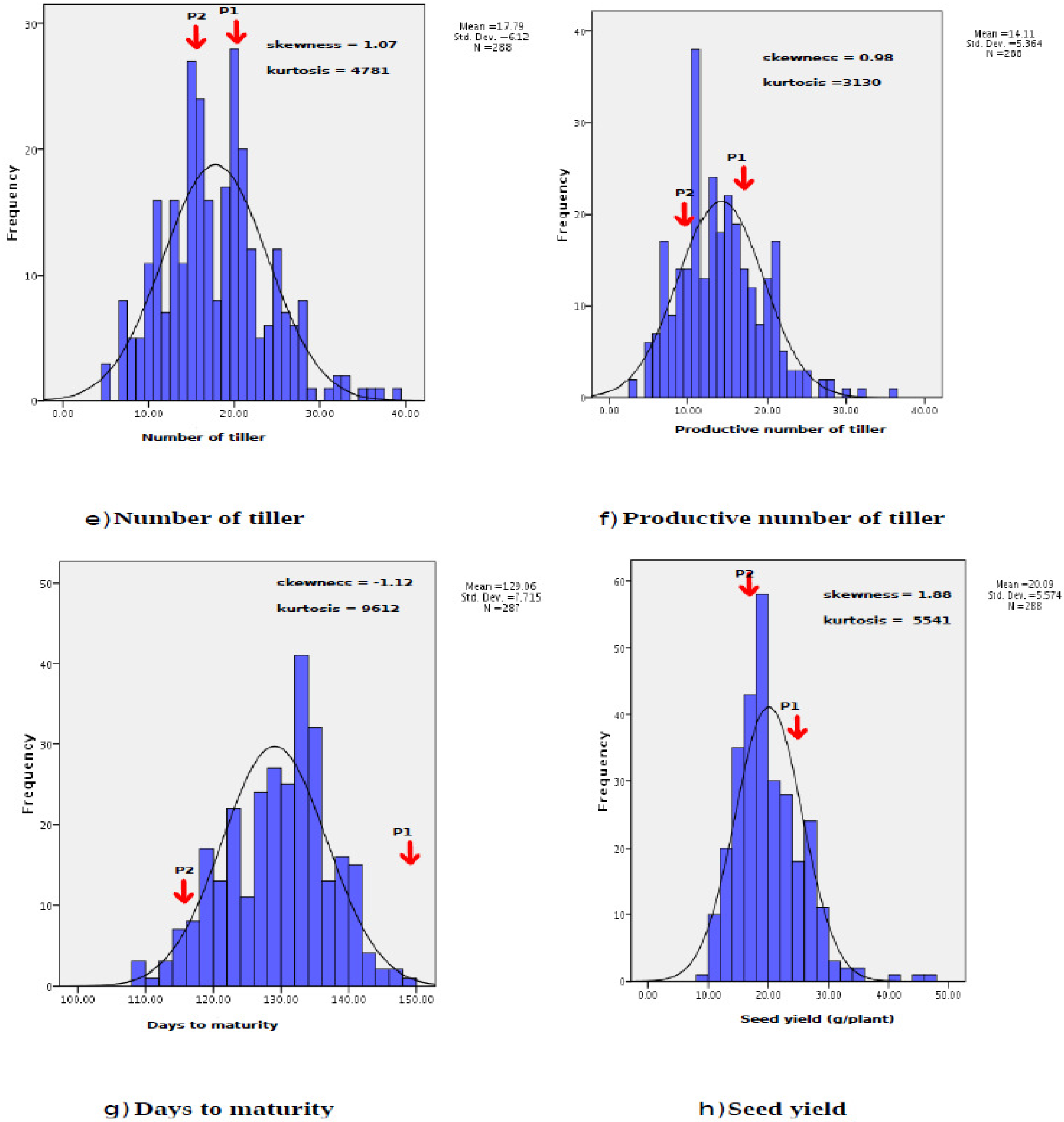
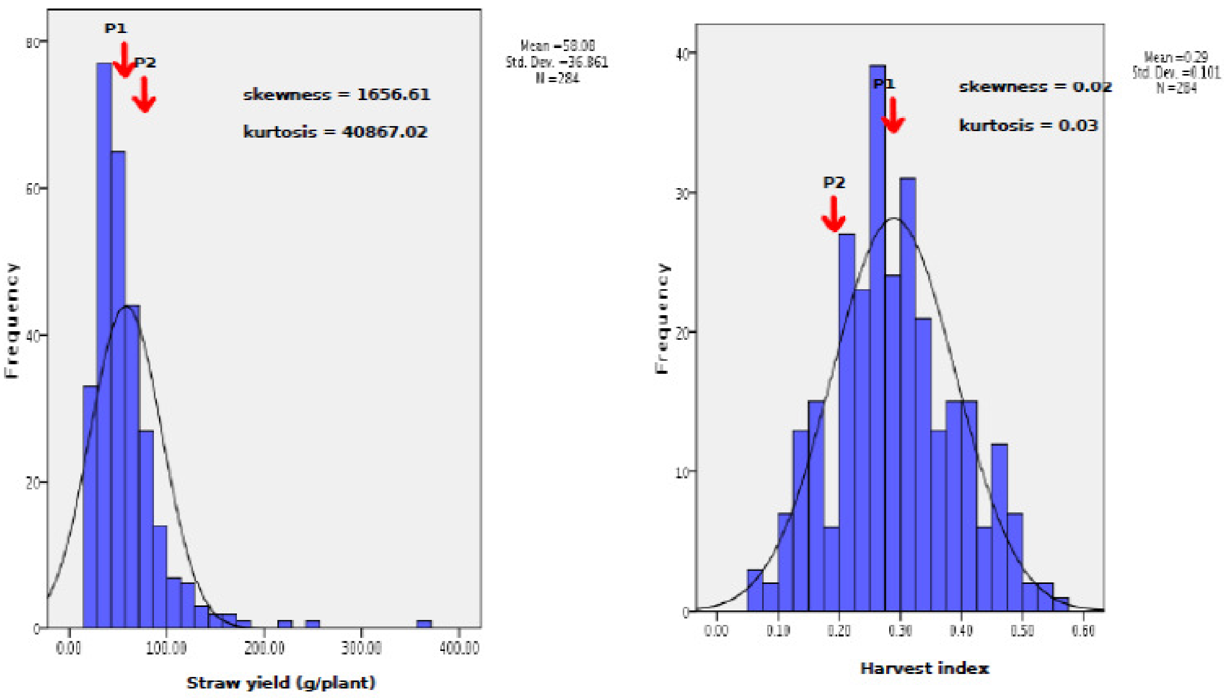


Fig. 2:[e-h]: Frequency distribution of 288 RIL's Number of tiller, productive number of tiller, days to maturity and seed yield.
P1 = Trait value for BPT5204 , P2 = Trait value for HPR14.



i) Straw yield j) Harvest index

Fig. 3:[i-j]: Frequency distribution of 288 RIL's straw yield and harvest index.
P1 = Trait value for BPT5204 , P2 = Trait value for HPR14.

Author's Contribution: All the authors are equally contributed.

Declaration: The authors do not have any conflict of interest

References

Agrawal, R.C. and Sapra R.L. (1995), Augment 1: A microcomputer based program to analyze augmented randomized complete block design. *Indian J. Plant Genetic Res*., 8(1): 61 – 69.

Akinwale, M.G.; Gregorio, G.; Nwilene, F.; Akinyele, B.O.; Ogunbayo, S.A. and Odiyi, A.C. (2011). Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *Afr. J. Plant Sci*., 5: 207-212.

Ali, M.L.; Pathan, M.S.; Zhang, J.; Bai, G.; Sarkarung, S.; and Nguyen, H.T.; (2000). Mapping QTLs for root traits in recombinant inbred population from two indica ecotypes in rice. *Theor. Appl. Genet*., 101: 756-766.

Altman, D.G. and Bland, J.M. (1995). Statistics notes: the normal distribution BMJ, 310(6975): 298.

Al-Jibouriea, H.; Miller, P.A. and Robinson, H.F. (1958). Genotyping and enviornmental variances and covariances in an upland cotton cross of interspecific origin. *Agro. J.,* 50: 633- 636.

Anonymous (2008). Package of Practice of field crops, *Univ. Agric. Sci*.; GKVK, Bangalore, p. 67-71.

Banu, H. (2011). Assesment of selected RILs for yield, its components and quality traits in aerobic rice (*Oryza sativa L.*). Thesis, University of Agriculture Sci. s, Bangalore.

Bisne, R.; Sarawgi A.K. and Verulkars, B. (2009). Study of heritability genetic advance and variability for yield contributing characters in rice. Bangladesh *J. Agril. Res*., 34: 175-179.

Chauhan, J.S. (1996). Genotypic and phenotypic correlations between grain yield and other associated characters in early duration elite breeding cultures of rice. *Oryza*, 33: 26-30.

Choo, T.M. and Reinbergs, E. (1982), Analyses of Skewness and Kurtosis for Detecting Gene Interaction in a Doubled Haploid Population1. Crop Science, 22: 231-235.

Cramer, G.L.; Wailes, E.J. and Shui, S. (1993). Impacts of liberalizing trade in the world rice market. *American J. of Agri. Eco.,* 75: 219–226.

Elayaraja, K.; Prakash, M.; Saravana, K.; Kumar, B.S. and Ganesan, J. (2005). Studies on variability, heritability and genetic advance for certain quantitative characters in mutant population of rice (*O. sativa* L.). *Crop Res.* (Hisar), 29: 134-137.

Fisher, R.A.; Immer, F.R. and Tedin, O. (1932). The genetical interpretation of statistics of the third degree in the study of quantitative inheritance. Genetics, 17: 107–124.

Gujral, H.S. and Kumar, V. (2003). Effect of accelerated aging on the physicochemical and textural properties of brown and milled rice. *J. Food Engineer.;* 59: 117-121.

Johnson, H.W.; Robinson, H.I. and Comstock, R.E. (1955). Estimation of genetic and environmental variability in soybean. Agron. J., 47: 314 – 318

Kaosaard, M. and Juliano, O. (1991). Assessing rice quality characteristics and prices in selected international markets. *Rice Grain Marketing and Quality Issues*. Manila, Philippines: International Rice Research Institute.

Kim, K.W.; Chung, H.K.; Cho, G.T.; Ma, K.H.; Chandrabalan, D.; Gwag, J.G. and Park, Y.J. (2007). Power Core: a program applying the advanced M strategy with a heuristic search for establishing core sets. *Bioinfo.; 23*(16): 2155-2162.

Kotch, G.P.; Ortiz, R. and Ross, W.M. (1992). Genetic analysis by use of potato haploid populations. Genome, 35: 103–108.

Patil, P.V.; Sarawgi, A.K. and Shrivastava, M.N. (2003). Genetic analysis of yield and quality traits in traditional aromatic accessions of rice. *J. Maharashtra Agric. Univ*.; 28(3): 225-258.

Pooni, H.S.; Jinks J.L. and Cornish, M.A. (1977). The causes and consequences of non-normality in predicting the properties of recombinant inbred lines. Heredity, 38: 329–338.

Rana, R.S.; Sapra, R.L.; Agrawal, R.C. and Gambhir, R. (1991). Germplasm evaluation; Augumented design. In: Plant genetic resources; documentation and information management. National bureau of plant genetic resource, New Delhi, pp. 37 – 44.

Robson, D.S. (1956). Application of K4 statistics to genetic variance component analysis. *Biometrics*, 12: 433–444.

Samak, A. (2007). DNA marker assisted selection of grain protein content in RILs and identification of genomic region for important yield traits in rice (*Oryza sativa L.*). Thesis, *Uni. sativa* L.). *Afr. J. Plant Sci*.; 5: 207-212.

Shashidhara, N. (2007). Evaluation of rice (*Oryza sativa* L.) segregating population for total grain protein content, grain quality and yield traits under aerobic and submerged conditions. *Thesis, Uni. Agri. Sci.; bangalore.*

Shinha, S.K.; Tripathi, A.K. and Bisen (2004). Study of genetic variability and correlation coefficient analysis in midland landraces of rice. *Annal of Agric. Res.* 25(1): 1-3.

Simmonds, N.W. (1995). The relation between yield and protein in cereal grain. *J. Sci. Food and Agri.,* 67(3): 309-315.

Singh, S.; Dhaliwal, Y.S.; Nagi, H.P.S. and Kalia, M. (1998). Quality characteristics of six rice varieties of Himachal Pradesh. *Journal of Food Science and Technology*, 27(5): 345-348.

Song, W.C. and Zhang, Y.H. (1992). Rice tetraploidy and its effect on agronomic traits and nutritional constituents. *Acta Agron. Sinica,* 18(2): 137-144.

Unnevehr, L.J. (1986). Consumer demand for rice grain quality and returns to research for quality improvement in Southeast Asia. *American Journal of Agricultural Economics*, 68: 634–641.

Xiao, J.; Li, J.; Yuan, L.; and Tanksley, S.D. (1996). Identification of QTLs affecting traits of agronomic importance in a recombinant inbred population derived from a sub specific rice cross. *Therot. Appl. Genet*., 92(2): 230-244.

Yadav, R.; Courtois, B.; Huang, N. and Mclaren, G. (1997). Mapping genes controlling root morphology and root distribution in double haploid population of rice. *Theor. Appl. Genet*., 94: 619-632.

Yang, L.J.; Xu, L. and Li, J.Y. (2004). Analysis of correlation between protein content, amylose content in the unpolished rice and 1000-grain weight in six different varieties' rice. J. of Shanghai Normal University (Natural Sciences). 10: 55-58.

Yu, T.; Jiang, W.; Ham, T.; Chu, S.; Lestari, F.; AND Lee, J. (2008). Comparison of grain quality traits between japonica rice cultivars from Korea and Yunnan Province of China. *J. Crop Sci. Biotechnol.;* 11: 135–140.

Zhong Kai, Z.; Kevin, R.; Stuart, H.; and Chris, B. (2002). Composition and functional properties of rice. *International Journal of Food Sci. & Tech.;* 37: 849–868.

Zuo, Q.F.; Liu, Y.B.; Pan, X.Y.; Zhu, J. and Xie, P. (2001). Genetic correlation analysis of yield and quality characters of rice (*Oryza sativa* L.) in multiple environments. *Acta Agricultuerae Universitatis Jiangxiensis*. 23(1): 16-23.