



Genetic variability and association analysis for grain yield components among *SALTOL* QTL introgressed rice genotypes under normal and saline environments

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Parameters of genetic variability and correlation and path coefficient analyses for nine quantitative traits were studied after evaluation of *SALTOL* QTL derived rice genotypes across normal and saline stress environments for two years. Analysis of variance showed highly significant differences due to environments for all the characters studied. Based upon the overall parameters of genetic variability and genetic advance, phenotypic selection for the traits like biological and grain yield in both conditions, whereas for tillers number, spikelet fertility and harvest index under salt stress is likely to be more effective in trait improvement. In both environments, grain yield was positively correlated with plant height, biological yield, 1000 grain weight, spikelet fertility and harvest index. Spikelet fertility was positively correlated with panicle length and biological yield under salinity only. At genotypic level, the traits like total tillers/plant, panicle length and harvest index exerted positive direct effects on grain yield in both environments. While biological yield and spikelet fertility exerted positive direct effects in normal environment, both these traits caused negative effects under salinity stress. Similarly, positive correlation of 1000 grain wt. with grain yield was revealed through its direct effect per se and indirect effects via productive tillers, panicle length and harvest index under salt stress. The overall analysis revealed that traits such as biological yield, spikelet fertility and harvest index could be effective indirect selection criteria for yield improvement under both normal and saline environments in the novel rice material.

(Key words: Genetic variability, *SALTOL* QTL, Correlation and path analysis, Salinity, Microplots)

Soil salinity is one of the major abiotic stresses affecting crop productivity in the world. In India about 6.73 m ha land is salt affected (Sharma *et al.*, 2004) Though irrigated lands are further expected to suffer from secondary inland salinization, the situation is likely to be aggravated by climate change causing a rise in sea level (Wassmann *et al.*, 2004). Though rice (*Oryza sativa* L.) is the most important crop and feasible option in the coastal areas, it is likely to suffer the most due to this stress situation especially in countries with long sea shore line (Swaminathan and Kesvan, 2012). Under such situation, search and systematic breeding for salt tolerance is quite beneficial. Large intra-specific variation in rice for tolerance to salinity stress has been reported and harnessed in the form of development and dissemination of salt tolerant varieties in various countries including India (Gregorio *et al.*, 2002; Singh *et al.*, 2010). In the quest for modern rice breeding for salt tolerance, a gene called as *SALTOL* quantitative trait locus (QTL) has been mapped on chromosome 1 and successfully transferred to different rice genotypes at IRRI, Philippines (Bonilla *et al.*, 2002; Thomson

et al., 2010. Large number of rice lines containing *SALTOL* QTL have been developed at IRRI, Philippines through marker assisted breeding (MAB). In order to harness the productivity potential of such novel material, it is important to understand the magnitude and nature of genetic variability and association of various agro-morphological traits with grain yield under normal as well as saline environments.

It becomes necessary to split overall genetic variability into its heritable and non-heritable components with the help of certain genetic parameters, which may enable the breeders to plan a proper breeding programme. The heritability and genetic advance are important selection parameters and are more helpful in predicting the genetic gain under effective selection (Bisne *et al.*, 2009). Correlation coefficients indicate the magnitude of association between two traits. However, path coefficient analysis partitions the correlation coefficients into its direct and indirect effects, so that the contribution of each character to yield could be estimated for picking up appropriate traits for indirect selection. Since the nature and extent of

genetic variability and association parameters are expected to be influenced by the genetic material under study and the prevailing environmental factors, we attempted to study these parameters in *SALTOL* QTL material. The study was also carried out in normal as well as saline conditions to understand the pattern of alterations for the above mentioned parameters in the two environments. Since evaluation under natural salinity affected fields is often marred by spatial heterogeneity for salt stress, the study of this novel material was conducted under precisely controlled state of the art facility of micro-plots environments.

MATERIALS AND METHODS

A total of 21 rice genotypes possessing *SALTOL* gene/QTL introgressed with *SALTOL* QTL developed at International Rice Research Institute (IRRI), Philippines were included in the study. The experiment was carried out in artificially created microplots or lysimeters at Central Soil Salinity Research Institute (CSSRI), Karnal, India during two consecutive years of Kharif 2009 and 2010. The genotypes were evaluated under control (no stress, pH~8.2, $EC_e \sim 0.7 \text{ dS m}^{-1}$) and saline ($EC_{iw} \sim 10 \text{ dS m}^{-1}$) environments of precisely controlled microplots at CSSRI, Karnal each in a randomized complete block design with three replications. Observations on five randomly selected plants were made for plant height (cm), total tiller number/plant, productive tiller number/plant, panicle length (cm), 1000- grain weight (g) and spikelet fertility (%) during different crop stages. At maturity, data on whole plot basis were recorded for biological yield (t/ha) which includes both grain and straw yields, grain yield (t ha^{-1}), and harvest index (%). Genetic parameters of variability like mean, analysis of variance, phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV), heritability (Broad sense) and genetic advance as per cent of mean were computed by the formula as suggested by Burton (1952) and Johanson *et al.*, (1955). Phenotypic and genotypic correlation coefficients were computed as per Miller *et al.*, (1958) and path coefficient analysis was performed according to Dewey and Lu (1959).

RESULTS AND DISCUSSIONS

Genetic variability parameters

The analysis of variance showed highly significant differences due to environments for all the characters studied. The mean sum of square for all the 9 characters was significant indicating

the presence of substantial amount of variability in the *SALTOL* QTL derived rice germplasm. The Table 1 shows the comparative % reduction of mean values for different traits under salinity stress. It was found that grain yield (74% reduction) was the most sensitive trait under tested salinity stress followed by biological yield (57%), harvest index and spikelet fertility (43%), productive tillers/plant and plant height (25%) total tillers/plant and panicle length (25%). This is expected because grain yield is the final product which is ultimately affected due to accumulation of reduction effects in respect of the component traits. The magnitude of phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for the characters studied, indicating that these characters were influenced by the tested environmental conditions. Phenotypic variance was higher than the genotypic variances for all the characters indicated the influences of environmental factors on these traits. Similar findings were earlier reported (Singh and Chakraborty, 1996; Devi *et al.*, 2006). In addition, magnitudes of PCV, GCV and variances were observed higher under salinity compared to normal conditions, which is expected under abiotic stress conditions. Among traits, grain yield, biological yield, and harvest index in both conditions whereas tillers number and spikelet fertility under stress recorded higher values of PCV (>25%) which substantiates genotypic differences for the traits under study. Similar results for high PCV and GCV are also earlier reported for grain yield (Bose *et al.*, 2005; Panwar, 2005; Kumar *et al.*, 2006) and for plant height, panicle length and spikelet fertility (Panwar, 2005).

Heritability estimates provide the information regarding the amount of transmissible genetic variation out of total variation and determines response to selection. The characters plant height, panicle length and biological yield in both environments whereas tillers number, grain yield and harvest index under stress exhibited high broad sense heritability of more than 70% (Table 1). Therefore, there is good scope of genetic improvement of these characters through selection. High broad sense heritability has been reported for grain yield (Hosseini *et al.*, 2005), productive tillers and plant height (Das *et al.*, 2005, Jayashudha and Sharma, 2010, Satyanarayana *et al.*, 2005) and for panicle length (Satyanarayana *et al.*, 2005). Genetic advance denotes the scope of improvement in the selection gain in the new population over the original

Table 1. Genetic variability parameters under normal and saline stress environments

Characters	Environment	Plant Height (cm)	Total tillers /plant (cm)	Productive tillers/plant	Panicle length (cm)	Biological Yield (t ha ⁻¹)	1000 Grain Wt.(g)	Grain Yield (t ha ⁻¹)	Spikelet Fertility (%)	Harvest Index (%)
Grand Mean	Normal	101.49	7.96	7.64	23.53	13.37	22.71	4.46	79.13	33.39
	Saline	75.74	6.58	5.64	19.71	5.68	14.43	1.13	44.89	18.74
% reduction	Reduction	25.13	17.33	26.09	16.23	57.51	37.46	74.64	43.25	43.87
CD (P < 0.05)	Normal	4.52	1.38	1.45	1.71	3.30	2.37	1.81	10.67	9.84
	Saline	7.24	1.10	1.17	2.48	1.28	3.22	0.46	19.62	6.21
CV (%)	Normal	2.70	10.51	11.47	4.40	14.97	6.33	24.64	8.17	17.86
	Saline	5.79	10.13	12.62	7.62	13.58	13.52	24.61	26.48	20.07
SE	Normal	2.24	0.68	0.72	0.85	1.63	1.17	0.90	5.28	4.87
	Saline	3.58	0.54	0.58	1.23	0.63	1.59	0.23	9.71	3.07
GCV (%)	Normal	8.79	9.71	9.20	9.17	24.74	8.28	34.82	11.35	21.33
	Saline	13.97	25.34	21.08	20.45	23.51	13.10	51.90	38.61	39.75
PCV (%)	Normal	9.19	14.31	14.71	10.17	28.92	10.42	42.65	13.98	27.82
	Saline	15.12	27.29	24.57	21.83	27.15	18.82	57.44	46.83	44.52
σ^2G	Normal	79.53	0.60	0.49	4.66	10.94	3.54	2.41	80.68	50.74
	Saline	111.98	2.78	1.41	16.26	1.78	3.57	0.34	300.61	55.51
σ^2P	Normal	87.04	1.30	1.26	5.73	14.95	5.61	3.62	122.49	86.33
	Saline	131.23	3.23	1.92	18.51	2.38	7.38	0.42	442.01	69.66
Heritability (%)	Normal	91.37	46.06	39.17	81.29	73.19	63.17	66.62	65.86	58.78
	Saline	85.33	86.23	73.61	87.81	74.97	48.43	81.64	68.01	79.69
GA (as % of mean)	Normal	16.85	13.22	11.55	16.59	42.47	13.21	57.01	18.48	32.81
	Saline	20.27	41.12	29.21	33.44	28.92	11.83	32.62	38.63	35.42

Table 2. Inter-trait phenotypic (P) and genotypic (G) correlation coefficients in normal environment

Characters		Plant Height	Total tillers /plant	Productive tillers /plant	Panicle Length	Biological Yield	1000 Grain Weight	Spikelet fertility	Harvest Index	Grain Yield
Plant Height	P	1.00								
	G	1.00								
Total tillers	P	0.29	1.00							
	G	0.36	1.00							
Productive tillers	P	0.26	0.96**	1.00						
	G	0.24	0.99**	1.00						
Panicle Length	P	0.60**	0.15	0.16	1.00					
	G	0.65**	0.47*	0.37	1.00					
Biological Yield	P	0.56**	0.52*	0.51*	0.16	1.00				
	G	0.76**	0.50*	0.46*	0.31	1.00				
1000 Grain Weight	P	0.41	0.31	0.29	0.24	0.45*	1.00			
	G	0.51*	0.19	0.20	0.35	0.51*	1.00			
Spikelet fertility	P	0.42	0.11	0.08	0.07	0.40	0.18	1.00		
	G	0.46*	-0.02	-0.08	-0.2	0.51**	0.26	1.00		
Harvest Index	P	0.44*	0.18	0.17	0.26	0.04	0.32	0.19	1.00	
	G	0.44*	0.02	-0.01	0.24	0.02	0.34	0.06	1.00	
Grain Yield	P	0.69**	0.54*	0.52*	0.23	0.78**	0.53*	0.44*	0.59**	1.00
	G	0.90**	0.41	0.36	0.41	0.84**	0.59**	0.51*	0.57**	1.00

*and ** denote significance at 5% and 1% levels, respectively

population. The high genetic advance as % of mean (> 20%) was registered for grain yield, biological yield and harvest index in both environments whereas for all remaining traits except 1000 grain weight under salinity stress. High heritability coupled with high genetic advance indicates the preponderance of additive gene action and such characters could be improved through selection. Therefore, the improvement of these traits through selection is the most important way to achieve the genetic gain generation after generation. Heritability estimates along with genetic advance are more helpful in predicting the genetic gain under selection than heritability estimates alone (Bisne, 2009) and it is interpreted that the characters showing high heritability with high genetic advance are controlled by additive gene action (Panse and Sukhatme, 1967). Such traits are amenable to simple selection methods. Based upon the overall parameters of genetic variability and advance, phenotypic selection for biological and grain yield in both conditions, whereas for tillers number, spikelet fertility and harvest index under salt stress is likely to be more effective in trait improvement.

Correlation and path coefficient analysis

The inter-trait correlation coefficients calculated for both environments revealed that the

magnitudes of genotypic correlation coefficients for most of the characters were higher than their phenotypic counterparts (Table 2 and 3). This indicates lesser influence of external environment in affecting correlations among traits. The results of both phenotypic and genotypic correlation coefficients in both environments revealed that grain yield was positively correlated with plant height, biological yield, 1000 grain weight, spikelet fertility and harvest index. Regarding correlations among component traits, it was observed that plant height was positively correlated with panicle length, biological yield, spikelet fertility and harvest index in both environments. Under normal conditions only, biological yield was positively correlated with tillers number, and 1000 grain wt. Under salt stress only, tillers number was negatively correlated with 1000 grain wt. The trait 1000 grain wt. developed positive association with spikelet fertility and harvest index. Spikelet fertility was positively correlated with panicle length and biological yield only under salinity condition. The positive correlation of grain yield with harvest index is in conformity with previous studies (Xiang *et al.*, 1986; Lu *et al.*, 1988) and similar correlation with spikelet fertility, plant height and 1000 grain weight is also in agreement with earlier findings (Prasad *et al.*, 1988; Panwar *et al.*, 1989).

Table 3. Inter-trait phenotypic (P) and genotypic (G) correlation coefficients in saline environment

Characters		Plant Height	Total tillers/ plant	Productive tillers/ plant	Panicle Length	Biological Yield	1000 Grain Weight	Spikelet fertility	Harvest Index	Grain Yield
Plant Height	P	1.00								
	G	1.00								
Total tillers	P	0.061	1.00							
	G	-0.19	1.00							
Productive tillers	P	0.22	0.82**	1.00						
	G	0.07	0.89**	1.00						
Panicle Length	P	0.67**	0.09	0.32	1.00					
	G	0.73**	0.13	0.41	1.00					
Biological Yield	P	0.49*	0.17	0.27	0.37	1.00				
	G	0.82**	-0.07	0.07	0.53*	1.00				
1000 Grain Weight	P	0.38	-0.52*	-0.37	0.24	0.33	1.00			
	G	0.59**	-0.75**	-0.55**	0.22	0.61**	1.00			
Spikelet fertility	P	0.47*	-0.13	0.05	0.26	0.34	0.56**	1.00		
	G	0.81**	-0.31	-0.07	0.59**	0.77**	0.80**	1.00		
Harvest Index	P	0.35	-0.33	-0.14	0.23	0.27	0.61**	0.68**	1.00	
	G	0.78**	-0.41	-0.17	0.38	0.79**	0.81**	0.93**	1.00	
Grain Yield	P	0.48*	-0.12	0.04	0.29	0.68**	0.59**	0.66**	0.84**	1.00
	G	0.80**	-0.31	-0.10	0.40	0.91**	0.77**	0.92**	0.97**	1.00

*and ** denote significance at 5% and 1% levels, respectively

Table 4. Phenotypic (P) and genotypic (G) path coefficients in normal environment

Characters		Plant Height	Total tillers/ plant	Productive tillers/ plant	Panicle Length	Biological Yield	1000 Grain Weight	Spikelet fertility	Harvest Index
Plant Height	P	0.12*	0.03	0.03	0.07	0.07	0.05	0.05	0.05
	G	-0.31	-0.11	-0.07	-0.2	-0.24	-0.16	-0.14	-0.14
Total tillers	P	0.03	0.09	0.09	0.01	0.05	0.03	0.01	0.02
	G	0.11	0.31	0.31	0.15	0.16	0.06	-0.01	0.01
Productive tillers	P	-0.01	-0.02	-0.02	0.00	-0.01	-0.01	0.00	0.00
	G	-0.09	-0.36	-0.36	-0.13	-0.17	-0.07	0.03	0.00
Panicle Length	P	-0.06	-0.01	-0.02	-0.10	-0.02	-0.02	-0.01	-0.02
	G	0.12	0.09	0.07	0.19	0.06	0.07	-0.04	0.05
Biological Yield	P	0.38	0.35	0.34	0.10	0.67	0.30	0.27	0.03
	G	0.74	0.48	0.45	0.3	0.96	0.49	0.49	0.02
1000 Grain Weight	P	0.01	0.01	0.01	0.00	0.01	0.02	0.00	0.01
	G	-0.03	-0.01	-0.01	-0.02	-0.03	-0.05	-0.01	-0.02
Spikelet fertility	P	0.01	0.00	0.00	0.00	0.01	0.00	0.02	0.00
	G	0.07	0.00	-0.01	-0.03	0.08	0.04	0.15	0.01
Harvest Index	P	0.23	0.09	0.09	0.13	0.02	0.17	0.1	0.52
	G	0.28	0.01	-0.01	0.16	0.01	0.22	0.04	0.63
Correlation with yield	P	0.70	0.54	0.52	0.23	0.79	0.53	0.44	0.59
	G	0.90	0.41	0.36	0.41	0.84	0.59	0.51	0.57

*Bold figures indicates direct effect; Residual effect = 0.2346

Table 5. Phenotypic (P) and genotypic (G) path coefficients in saline environment

Characters		Plant Height	Total tillers/ plant	Productive tillers/ plant	Panicle Length	Biological Yield	1000 Grain Weight	Spikelet fertility	Harvest Index
Plant Height	P	0.04*	0.00	0.01	0.02	0.02	0.01	0.02	0.01
	G	0.04	-0.01	0.00	0.03	0.03	0.02	0.03	0.03
Total tillers	P	0.00	0.08	0.06	0.01	0.01	-0.04	-0.01	-0.02
	G	-0.44	2.33	2.08	0.31	-0.17	-1.74	-0.71	-0.94
Productive tillers	P	-0.01	-0.02	-0.02	-0.01	-0.01	0.01	0.00	0.00
	G	-0.08	-1.00	-1.12	-0.45	-0.07	0.61	0.07	0.19
Panicle Length	P	-0.05	-0.01	-0.02	-0.08	-0.03	-0.02	-0.02	-0.02
	G	0.73	0.13	0.41	1.00	0.53	0.22	0.59	0.38
Biological Yield	P	0.23	0.08	0.13	0.17	0.47	0.15	0.16	0.13
	G	-0.64	0.06	-0.05	-0.41	-0.78	-0.47	-0.6	-0.62
1000 Grain Weight	P	0.02	-0.02	-0.02	0.01	0.01	0.04	0.02	0.03
	G	1.2	-1.51	-1.11	0.45	1.23	2.02	1.63	1.64
Spikelet fertility	P	-1.24	0.64	0.15	-1.42	-1.15	-2.42	-0.56	-1.37
	G	-2.24	0.84	0.18	-1.62	-2.12	-2.22	-2.76	-2.57
Harvest Index	P	0.25	-0.23	-0.1	0.16	0.19	0.43	0.49	0.71
	G	2.23	-1.16	-0.49	1.09	2.27	2.32	2.67	2.86
Correlation with yield	P	0.49	-0.12	0.04	0.30	0.68	0.60	0.67	0.84
	G	0.80	-0.31	-0.10	0.40	0.91	0.77	0.92	0.97

* Bold figures indicates direct effect; Residual effect = 0.2591

The goal of the path analysis is to know the cause and effect relationships and to understand the influence of specific traits on resultant grain

yield. The partitioning of correlation coefficients into direct and indirect effects is shown in Tables 4 and 5. It was observed that at genotypic level, the traits

total tillers/plant, panicle length and harvest index exerted positive direct effects on grain yield in both environments. However, productive tillers in both environments caused negative direct effects. Whereas biological yield and spikelet fertility exerted positive direct effects in normal environment, both these traits caused negative effects under salinity stress. Under salt stress, the positive correlation of plant height, and spikelet fertility with grain yield was explained by its contribution via panicle length, 1000 grain wt. and harvest index. Similarly, positive correlation of 1000 grain wt. with grain yield was revealed through its direct effect per se and indirect effects via productive tillers, panicle length and harvest index under salt stress. Regarding related literature on this aspect, higher positive direct effects of harvest index (Murty and Babu, 1992; Surek *et al.*, 1998) and biological yield (Peiyan, 1988, Surek *et al.*, 1998) have been reported. The residual effect was found to be about 0.25 in both normal and saline environments indicating that most of the variation was accounted for by the traits studied.

It is important to know the specific traits which could be useful for attempting fruitful selection in the marker assisted breeding derived material. Considering the genetic variability parameters in conjunction with association and path analysis, it is concluded that the traits biological yield, spikelet fertility and harvest index could be effective selection criteria for yield improvement in such genetic material under both normal and saline environments.

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