

Assessment of genetic variability in recombinant inbred lines of rice derived from high temperature tolerant parent

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ABSTRACT

An investigation was carried out utilizing 148 recombinant inbred lines of rice derived from cross between IR 64 and high temperature stress / heat tolerant donor N 22 at Agricultural College and Research Institute, Madurai, Tamil Nadu. The aim of the study was to assess the extent of variability in order to identify high temperature tolerant lines that could be utilized either directly or in hybridization programme to keep pace with the global climate changes. The variability studies indicated that single plant yield, number of ill-filled grains panicle⁻¹, number of productive tillers plant⁻¹, number of filled grains panicle⁻¹, 1000 grain weight, flag leaf length and flag leaf width had relatively high PCV and GCV estimates. High genetic advance along with high heritability were found for all the characters except days to 50 per cent flowering and number of ill-filled grains indicating the presence of additive gene action for controlling these traits. High positive direct effect with single plant yield was exerted by the traits viz., number of productive tillers plant⁻¹, number of filled grains panicle⁻¹ and spikelet fertility.

Key words: rice, recombinant inbred lines, high temperature, variability, yield trait

Rice is life for millions of Asians and provides 75 per cent of calories and 55 per cent protein in the average daily diet of the people (Bhuiyan *et al.*, 2002). An increase in rice production by 0.6-0.9% annually until 2050 is needed to meet the demand (Carriger and Vallee, 2007). It is predicted that the carbon dioxide concentration (CO₂) in the atmosphere will double within this century compared to that at the beginning of last century and that the increase in CO₂ and other greenhouse gases will cause global warming of 1.5 to 5.8°C by the end of this century (IPCC, 2001). Such global environmental change is considered to have an enormous impact on Asian rice production. For every 75 ppm increase in CO₂ concentration, rice yield will increase by 0.5 t ha⁻¹, but the yield will decline by 0.6 t ha⁻¹ for every 1°C increase in temperature (Sheely *et al.*, 2005). Predicted rate of increase in night temperature has a negative impact on rice production with significant yield losses (Mohammed and Tarpley, 2009). As water is becoming a limiting factor, there is a gradual shift in crop cultivation from irrigated system to water saving technologies like direct seeded rice, aerobic rice, alternate wetting and drying etc., which

would be more vulnerable to adverse effects of high temperatures. Hence, there is an urgent need to address high temperature induced yield losses and effort to breed rice for hot environments (Wassmann and Dobermann, 2007).

The success of any breeding programme depends on the selection of parents for hybridization and involves the steps like creating genetic variability, practising selection and utilization of selected genotypes to evolve promising varieties. Breeding for heat tolerance in rice is an emerging area of study to address the issues elaborated earlier. A scrutiny of meteorological data over the past 10 years at Agricultural College and Research Institute, Madurai has indicated that March, April, May, June and July are prone to high temperature stress with the average maximum temperature reaching 37-38°C. Farmers in these regions tend to grow summer rice for varied reasons if they have irrigation facility. This crop will be prone to high temperature stress at booting or flowering or grain filling stages. Under this context, the present study was undertaken using breeding lines derived from

crosses involving heat tolerant donor (N 22) to assess the variability and determine the association of yield, and its contributing traits of existing recombinant inbred lines for yield.

MATERIALS AND METHODS

The present investigation was carried out at Agricultural College and Research Institute, Madurai, Tamil Nadu. The experimental material consisting of 148 recombinant inbred lines (F_6) derived from the cross between IR 64 (heat susceptible) and N 22 (heat tolerant). The seeds were sown in nursery bed during December 2012 and transplanted to the main field on 28th day after sowing. The seedlings were planted in randomised block design adopting a spacing of 20 x 15 cm and the genotypes were replicated twice. In each replication, each genotype was planted in four rows. The normal recommended crop management practices were followed. The observations were recorded on five randomly selected plants per replication based on the descriptions provided in Standard Evaluation System for rice by IRRI in 1996 for the following 11 biometrical traits *viz*; days to 50 per cent flowering, plant height, number of productive tillers plant⁻¹, panicle length, flag leaf length, flag leaf width, number of filled grains panicle⁻¹, number of ill-filled grains panicle⁻¹, spikelet fertility, 1000 grain weight and single plant yield. The genetic parameters were estimated based on the method suggested by Burton (1952). The genotypic and

phenotypic correlations were estimated following Johnson *et al.* (1955) and path analysis was carried out following Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the 148 RILs for all the characters studied. Wide range of variation observed for all the characters provided a large scope of selection on the basis of phenotypic value of the component characters. The phenotypic variance was higher than the corresponding genotypic variance for all the characters. The estimates of phenotypic and genotypic coefficients of variation were high for single plant yield, number of illfilled grains panicle⁻¹, number of productive tillers plant⁻¹, number of filled grains panicle⁻¹, 1000 grain weight, flag leaf length and flag leaf width. The characters plant height, spikelet fertility, days to 50 per cent flowering and panicle length showed moderate genotypic and phenotypic variances (Table 1). A close proximity between GCV and PCV for all the characters except number of filled grains panicle⁻¹ and spikelet fertility indicated less influence of environment on such characters. So, the expressions of these traits are mainly due to the genetic constitution of the populations and the effect of environment was not so effective in case of expression of these traits. Relatively high environmental variance and high difference between PCV and GCV for the traits number of filled grains

Table 1. Variability, heritability and genetic advance for 11 characters in rice

Characters	Mean	PV	GV	GCV	PCV	ECV	Heritability	Genetic advance as per cent of mean
Days to 50 per cent flowering	69.78	93.33	86.73	13.34	13.85	3.68	82.90	26.50
Plant height (cm)	112.35	481.53	478.38	19.48	19.85	0.84	89.81	30.11
Number of productive tillers plant ⁻¹	21.27	60.51	60.21	36.46	36.96	2.58	92.50	41.93
Panicle length(cm)	25.66	10.35	10.27	12.48	12.74	1.12	93.19	20.61
Flag leaf length(cm)	26.32	35.17	35.17	22.52	22.83	0.37	91.97	36.39
Flag leaf width(cm)	1.21	0.063	0.063	20.72	20.87	0.06	85.56	32.68
Number of filled grains panicle ⁻¹	114.59	1932.91	1928.21	33.31	38.56	4.89	76.76	18.84
Number of unfilled grains panicle ⁻¹	23.91	425.23	425.13	46.22	46.43	1.32	89.98	27.60
Spikelet fertility (%)	83.97	138.19	130.87	13.62	17.99	3.22	84.70	15.30
1000 grain weight (g)	20.43	24.61	24.52	24.24	24.61	1.44	91.56	39.84
Single plant yield (g)	33.35	474.31	469.98	65.00	65.29	6.24	80.09	43.28

PV - Phenotypic variance, GV-Genotypic variance, GCV-Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, ECV - Environment coefficient of variation

panicle⁻¹ (5.25) and spikelet fertility (4.37) which indicated that these characters were influenced by the environmental conditions rather than the genetic constitution of the population.

All the above characters had high heritability which indicated the characters to be under the genetic control, mostly. High genetic advance along with high heritability were found for panicle length (93.19 and 20.61, respectively), number of productive tillers plant⁻¹ (92.50 and 41.93, respectively), flag leaf length (91.97 and 36.39, respectively), 1000 grain weight (91.56 and 49.84, respectively), number of ill-filled grains panicle⁻¹ (89.98 and 27.60, respectively), plant height (89.81 and 30.1, respectively), flag leaf width (85.56 and 32.68, respectively), days to 50 per cent flowering (82.90 and 26.50, respectively) and single plant yield (80.09 and 43.28, respectively) indicating the presence of additive gene action for controlling these traits. Therefore, direct selection on the basis of phenotype of these characters

would be beneficial. The remaining characters *viz.*, number of filled grains panicle⁻¹ and spikelet fertility were controlled by non-additive gene action and in this case heterosis breeding might be used rather than selection for the improvement of these traits. Similar results were also reported (Sabesan *et al.*, 2009, Anbanandan *et al.*, 2009 and Singh *et al.*, 2011)

Yield is a complex product being influenced by several interdependent quantitative characters. Thus, developing a breeding protocol for yield improvement may not be effective unless the other yield components influencing it directly or indirectly are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Correlation analysis among yield and its contributing characters revealed that the genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients

Table 2. Genotypic and phenotypic correlation coefficient among 11 characters in rice

Characters	DFE	PHT	NPT	PL	FLL	FLW	NFG	NUG	SF	1000 GW	SPY	
DFE	G	1.000	0.028	-0.272**	0.037	-0.158	0.024	0.011	0.229*	-0.143	-0.105	-0.246**
	P	1.000	0.025	-0.262**	0.034	-0.151	0.023	0.008	0.222*	-0.126	-0.101	-0.235**
PHT	G		1.000	-0.111	0.585**	0.320**	0.095	0.261**	0.054	0.126	0.029	0.098
	P			-0.107	0.582**	0.324**	0.107	0.259**	0.059	0.119	0.028	0.097
NPT	G			1.000	-0.039	-0.107	0.085	0.155	-0.113	0.297**	0.080	0.739**
	P				-0.035	-0.107	0.085	0.155	-0.112	0.287**	0.080	0.734**
PL	G				1.000	0.518**	0.287**	0.250**	0.024	0.116	0.024	0.152
	P					0.516	0.286**	0.248**	0.023	0.112	0.024	0.153
FLL	G					1.000	0.336**	0.191*	0.081	0.009	0.019	0.049
	P						0.334**	0.190*	0.081	0.009	0.019	0.049
FLW	G						1.000	0.250**	-0.021	0.038	0.102	0.151
	P							0.248**	-0.021	0.037	0.101	0.150
NFG	G							1.000	0.125	0.333**	0.083	0.480**
	P								0.125	0.322**	0.083	0.477**
NUG	G								1.000	-0.670**	-0.127	-0.087
	P									-0.652**	-0.126	-0.086
SF	G									1.000	0.150	0.430**
	P										0.652**	0.421**
1000 GW	G										1.000	0.128
	P											0.127
SPY	G											1.000
	P											

DFE- Days to 50 per cent flowering, PHT- Plant height, NPT- Number of productive tillers plant⁻¹, PL - Panicle length, FLL - Flag leaf length, FLW - Flag leaf width, NFG - Number of filled grains panicle⁻¹, NUG - Number of unfilled grains panicle⁻¹, SF - Spikelet fertility, 1000 GW - 1000 grain weight, SPY- Single plant yield

* Significant at 5 per cent and ** significant at 1 per cent

indicating the association is largely due to genetic reason (Table 2). In some cases phenotypic correlation coefficients were higher than genotypic correlation indicating suppressing effect of the environment which modified the expression of the characters at phenotype level.

Significant positive genotypic and phenotypic correlation was found between days to 50 per cent flowering and number of unfilled grains panicle⁻¹, plant height and panicle length, flag leaf length and number of filled grains panicle⁻¹, number of productive tillers plant⁻¹ and spikelet fertility, single plant yield and flag leaf length, plant height, flag leaf width and number of filled grains panicle⁻¹, flag leaf width and number of filled grains panicle⁻¹, flag leaf length, panicle length, number of filled grains panicle⁻¹ and spikelet fertility, single plant yield, plant height, panicle length and flag

Path coefficient analysis showed that number of productive tillers plant⁻¹ (0.6369) had the maximum direct effect on yield and it also exhibits considerable indirect effect via number of filled grains panicle⁻¹ and spikelet fertility (Table 3). Further, number of filled grains panicle⁻¹ (0.2886) and spikelet fertility (0.1774) which showed direct effect on yield also contributed indirectly via number of productive tillers plant⁻¹ and spikelet fertility. Days to 50 per cent flowering showed the highest direct negative effect on yield (-0.0727) followed by flag leaf length (-0.0021) and flag leaf width (-0.0003). Number of productive tillers plant⁻¹, number of filled grains panicle⁻¹ and spikelet fertility showed significant positive correlation (both genotypic and phenotypic correlation) with yield along with positive direct effect on yield which might be taken into consideration to develop breeding strategy for yield

Table 3. Path analysis showing direct and indirect effects of 10 characters on yield

	DDF	PHT	NPT	PL	FLL	FLW	NFG	NUG	SF	1000 GW	SPY
DDF	-0.0727	0.0008	-0.1732	0.0025	0.00033	-0.00001	0.0033	0.0186	-0.0254	-0.0029	-0.246**
PHT	-0.0020	0.0291	-0.0709	0.0401	-0.00067	-0.00004	0.0753	0.0044	0.0224	0.0008	0.098
NPT	0.0197	-0.0032	0.6369	-0.0026	0.00023	-0.00003	0.0448	-0.0092	0.0526	0.0027	0.739**
PL	-0.0027	0.0170	-0.0246	0.0685	-0.00109	-0.00011	0.0722	0.0019	0.0207	0.0068	0.152
FLL	0.0114	0.0093	-0.0682	0.0355	-0.00210	-0.00013	0.0550	0.0065	0.0016	0.0054	0.049
FLW	-0.0017	0.0027	0.0540	0.0196	-0.00071	-0.00039	0.0722	-0.0017	0.0067	0.0028	0.151
NFG	-0.0008	0.0075	0.0989	0.0171	-0.00040	-0.00010	0.2886	0.0102	0.0590	0.0023	0.480**
NUG	-0.0166	0.0015	-0.0717	0.0016	-0.00017	0.00001	0.0361	0.0813	-0.1188	0.0035	-0.087
SF	0.0104	0.0036	0.1890	0.0079	-0.00002	-0.00001	0.0960	-0.0544	0.1774	0.0042	0.430**
1000 GW	0.0074	0.0008	0.0508	0.0016	-0.00003	-0.00003	0.0238	-0.0104	0.0261	0.0284	0.128

** Significant at 1 per cent, DDF- Days to 50 per cent flowering, PHT- Plant height, NPT- Number of productive tillers plant⁻¹, PL - Panicle length, FLL- Flag leaf length, FLW - Flag leaf width, NFG - Number of filled grains panicle⁻¹, NUG - Number of unfilled grains panicle⁻¹, SF - Spikelet fertility, 1000 GW - 1000 grain weight, SPY- Single plant yield

leaf characters. This means increase in one character will cause increase in the correlated character also. Significant negative correlation was observed between days to 50 per cent flowering and number of productive tillers plant⁻¹, single plant yield. Grain yield showed significant positive correlation with number of productive tillers plant⁻¹, number of filled grains panicle⁻¹ and spikelet fertility upon which emphasis may be given during selection.

improvement (Nandeshwar *et al.*, 2010, Pal *et al.*, 2011 and Rahman *et al.*, 2012).

Knowledge on genetic variability of the available population, which is partitioned from the environmental effect is very essential for any crop improvement programme as it will increase the efficiency of selection. In the present study, it has been found that the number of productive tillers plant⁻¹, number of filled grains panicle⁻¹ and spikelet fertility showed high positive direct effect along with positive genetic correlation on yield. These genotypes offer

scope for further utilization by hybridization or direct selection to develop high temperature stress tolerant line to combat with the global climatic changes.

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