Citation: Selvi GSA, Kahani F, Hittalmani S (2015) Stability Analysis of Rice Root QTL-NILs and Pyramids for Root Morphology and Grain Yield. J Rice Res 3: 153. doi:10.4172/2375-4338.1000153

Sl. No.	Season	Location	Conditions	Material used	Traits
1	1	MRS, Hebbal	low moisture stress	QTL-NILs	Shoot, root and yield traits
			well watered conditions	pyramids	
2	2	Farmers field	low moisture stress	QTL-NILs	Shoot and yield traits
		Pavagada, Tumkur	well watered conditions	pyramids	
3	3	MRS, Hebbal	low moisture stress	QTL-NILs	Shoot and root traits
			well watered conditions	pyramids	
4	3	ZARS, GKVK	low moisture stress	QTL-NILs	Shoot, root and yield traits
			well watered conditions	pyramids	
5	3	Farmers field	submerged	QTL-NILs	Shoot, root and yield traits
		Dodjala, Bangalore		pyramids	
6	3	Farmers field	aerobic, non-stress	QTL-NILs	Shoot, root and yield traits
		Shettigere, Bangalore		pyramids	

Table 4: List of field experiments conducted in this study.

Where,

n : number of environments

v : number of genotypes with $\sum_j I_j = 0$

The total variation is partitioned into genotypes, environment, environment (linear), genotype x environment (linear), pooled deviation and pooled error.

F test

a. To test the significance of differences among the genotypic means, the 'F' test followed was:

$F = MS_1 / MS_3$

Where, MS_1 : mean sum of squares of varieties

MS_3 : mean sum of squares of pooled deviation

b. To test individual from linear regression, the formula is as follows,

$$F = \sum_j \hat{\delta}^2_{ij} / (n-2) / MS_e$$

Where, n: number of environments

$\sum_j \hat{\delta}^2_{ij}$: sum of squares of deviations from the regression line

MS_e: pooled error

c. To test the hybrids/ varieties which do not differ for their regression on the environmental index, the appropriate test was,

$$t = \frac{b_i - 1}{SE(b)} \text{ or } \frac{b_i}{SE(b)}$$

$$SE(b) = \sqrt{\frac{\left[\sum Y^2 - \left(\sum Y\right)^2/n\right] - \left[\sum X^2 - \left(\sum X\right)^2/n\right]}{(n-2)\left[\sum X^2 - \left(\sum X\right)^2/n\right]}}$$

Where,

X : environmental index

n : number of environments

A joint consideration of the three parameters such as

1. The mean performance of the genotype over the environments (x)

2. The regression co-efficient (b)

3. The deviation from linear regression (S^2d) is used to define stability of a genotype.

The estimate of deviations from regression (S^2d) suggests that the degree of reliance that should be put to linear regression in interpretation of the data. If these values are significantly deviating from zero, the expected phenotype cannot be predicted satisfactorily. When, deviations (S^2d) are not significant, the conclusion may be drawn by the joint consideration of mean, yield and regression co-efficient (b) values as given below (Table 1).

While interpreting the results, S^2di is first looked into. A non-significant deviation from $S^2di=0$, then stability is interpreted based on bi and mean values. If bi=1, a genotype is considered to possess average stability i.e., same performance in all the growth conditions. If bi is more than unity, then the genotype is said to have less than average stability i.e., good performance under favorable environments. If bi is less than unity, then the genotype is said to possess above average stability i.e., good performance under poor environments. Thus, genotypes possessing unit regression coefficient and non-significant deviation from regression were considered ideal, widely adapted and stable genotypes.

Results

Environment- wise analysis of variance indicated a significant mean sum of squares for the QTL-NILs and the generated pyramids for most characters studied. Combined Analysis of Variance for the pyramids qRT24-9 x qRT11-7 (data not shown) indicated significant variance for genotype as well as for genotype x environment [33] model for stability analysis was applied as the genotype x environment component of variance was found significant. The performance of genotypes in different environments for five selected characters based on two-way analysis of variance and Bartlett's test are elaborated below (Table 5).

Plant height

The varying environmental indices indicated that there was a significant difference for plant height across environments and across genotypic entries. qRT6-2 x qRT19-1+7 was the shortest (47.74cm), while qRT6-2 x qRT11-7 was the tallest (62.77 cm). The bi and S^2di were found to be non-significant for all the genotypes studied.

Seed yield per plant

As indicated by the environmental indices and the environmental means, seed yield per plant showed significant differences across

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Genotypes	Source	df	PHT	NOT	NOP	PWT	PL	DFL	NS	NC	TWT	SWT0 0 1 513.460.L				

environments. qRT11-7 x qRT6-2 recorded the highest seed yield (9.95 g), while qRT11-7 x qRT18-1+7 recorded the least seed yields (6.92 g). The bi and s^2di were found to be non-significant for all the genotypes studied.

Total Biomass per plant

The varying environmental indices indicated that there were significant differences for total biomass across environments. qRT6-2 x qRT19-1+7 was the lightest (35.82 g), while qRT20-1+7 x qRT18-1+7 was the heaviest (50.92 g). The bi and s^2di were found to be non-significant for all the genotypes studied.

Maximum root length

As indicated by the environmental indices and the environmental means (11.86 to 18.63), maximum root length showed significant differences across genotypes. The QTL-NILs recorded the highest mean maximum root length (18.63 cm), while qRT11-7 x qRT6-2 recorded the least root length (11.86 cm). The bi and s^2di were found to be non-significant for all the genotypes studied (Table 6).

Total number of roots per plant

The varying environmental indices indicated that there were significant differences for total number of roots across environments. qRT6-2 x qRT11-7 had the highest mean number of roots (59.13), while qRT11-7 x qRT18-1+7 had the least mean number of roots (52.65). The bi and s^2di were found to be non-significant for all the genotypes studied.

Discussion

Phenotype of an individual is determined by the interaction of the genotype and environment surrounding it, the effects of genotype and environment on phenotype may not always be independent. The phenotypic response to change in environment is not the same for all the genotypes. The interplay in the genetic and non-genetic effects on development is termed as “genotype environment” interaction (Comstock and Moll, 1963) and is of major consequence to the breeder in the process of evolution of improved genotypes.

In the present study, twenty nine near isogenic lines of IR64