

PHENOTYPIC AND GENOTYPIC EVALUATION OF ROOT QTL EFFECTS ON SEEDLING VIGOR IN RICE (*ORYZA SATIVA* L.)

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KEYWORDS

Rice germplasm
Seed weight
Seedling emergence
Microsatellite markers

Received on :

12.05.2016

Accepted on :

13.08.2016

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ABSTRACT

The present study was undertaken to assess seedling vigor in 46 rice germplasm and its association with SSR markers linked to root QTL traits and revealed significant genotypic variability existed with highest heritability (99.92 %) for seedling fresh weight. High seedling vigor (3216.28) was expressed in Dinesh followed by Jaldidhan, Moroberekan, Nagina22, Nipponbare, Suraksha, VL Dhan 208 and VL Dhan 221. Dinesh, Moroberekan, Nipponbare and VL Dhan 208 had multiple root QTL. High vigor genotypes showed more number of QTL for root traits, which confirms that root traits has significant role in expressing high vigor for early establishment. However, genotypes Jaldidhan, Nagina 22, Suraksha and VL Dhan 221 though not having root QTL but expressed better vigor. These cultivars may be explored further for additional QTL with strong vigor traits and are desirable in breeding for direct-sown system.

INTRODUCTION

Seedling vigor is the most important trait attribute which helps in rapid seedling establishment, optimum plant stand and increasing weed competitive ability that plays a key role in direct sown rice. In cropping practice of rice, many farmers particularly in the tropics are shifting from transplanting to direct sowing system (Erguiza *et al.*, 1990). Compared to wet and water seeding, dry direct seed rice is more advantageous in many situations: less labour intensive, time saving in sowing the crop, consumes less water, suitable for lowland, crops mature 7-14 days earlier and there is less methane emission (Chauhan, 2012).

The cultivars with deep root system have better penetrating ability to extract water and nutrients which in-turn better shoot growth (Devendra *et al.*, 2015). There is genotypic variability in rice germplasm with regard to root characters which is an important trait in relation to seed vigor. Assessment of variability, heritability, character association and contribution of characters to seed vigor is prerequisite for exploitation of genetic potential. Roots are important parts of the plant architecture that is involved in foraging for the available water and nutrients in the rhizosphere (Malamy, 2005). Rice with its poor water use efficiency needs about 5000 liters of water to produce 1 kg of rice and availability of water is the major limiting factor in rice production in irrigation and rain-fed ecosystems due to shrinking ground water resources. A deep and thick root system is generally considered as a favourable trait allowing the crop to maintain its water status even under water stress (Nguyen *et al.*, 1997). It is possible to provide

selection for cultivar with good root traits at seed germination stage based on the quality of the plant root system. Quality of the embryonic roots is important for the plant growth and also root development. But due to the absence of easy, reliable and efficient screening techniques under field conditions, it has been a very difficult task to breed varieties with increased root length and other improved root traits related to seed vigor. To circumvent the screening problems, molecular genetic markers could be employed to identify the genotypes having desired root characteristics associated with seed vigor.

Analysis of QTL for root thickness, volume, and distribution has been performed with different rice mapping populations (Price *et al.*, 2002). These studies were based on RILs, DHLs, BILs or NILs produced using Indica lowland varieties (IR 64, IR 1552, IR 62266, IR 58821, IR 52561, CO 39 and Zhenshan 97), Indica upland varieties (Bala and Kalinga III), Japonica lowland varieties (Akihikari and Yuefu) and Japonica upland varieties *viz.*, CT9993, IAC165, IRAT109 and Azucena (Ulaganathan 2007). A total of 861 root development QTL and associated microsatellite markers located on different chromosomes were identified. The present study focused on QTL reported for root traits and validation in the 46 germplasm lines for their association with seedling vigor.

MATERIALS AND METHODS

Plant material and methodology

Forty six rice genotypes of different duration and grain types were evaluated for seedling vigor and seedling root traits in

completely randomized design with three replication at Department of Seed Science and Technology, College of Agriculture, ANGRAU, Rajendranagar, Hyderabad. All laboratory observations were recorded in each replication was considered for statistical analysis. Fifteen putative QTL contributing to seedling root traits with phenotypic variation more than 20 percent were selected and associated with 30 SSR markers (www.gramene.org).

Estimation of physio-morphological traits

In order to assess and quantify the genetic variability among the genotypes for the characters under study, the following parameters were estimated as given below. 100 seed weight(g), germination test using 100 seeds at 25°C (ISTA 2009), electrical conductivity in dsm^{-1} to assess the leakage of solutes (Dadlani and Agarwal, 1983), Mean germination time in days (Ellis and Roberts, 1980), root and shoot length (cm), root shoot ratio, seedling length (cm), root fresh weight (mg), shoot fresh weight (mg), seedling fresh weight (mg), seedling dry weight (mg) and seedling vigour index (SVI-I and SVI-II) based on shoot and root length and on dry weight basis as per Abdul Baki and Anderson (1973).

Estimation of genetic parameters

Mean, standard error, range were analyzed according to Singh and Chaudhary (1985). Both genotypic and phenotypic coefficients of variability were calculated as the following formula proposed by Singh and Chaudhary (1985). The GCV and PCV values were classified into low (0 - 10), medium (10 - 20) and high (20 and above) as described by Sivasubramanian and Menon (1973). Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance as suggested by Allard (1999) and expressed as percentage. Heritability estimates were classified into low (0-29), moderate (30-60) and high (61-100) by following Hanson *et al.* (1956). Expected genetic advance (GA) and percentage of GA calculated according to Shukla *et al.* (2006). Genotypic and phenotypic correlation coefficients were calculated and the range of genetic advance as per cent of mean was classified into low (0-30), medium (30-60) and high (above 60) as suggested by Johnson *et al.* (1955).

SSR genotyping and trait correlation analysis

Genomic DNA of 46 rice genotypes including checks for root QTLs were isolated using CTAB method using the procedure given by Zhang (1995). Markers were scored for the presence and absence of the corresponding bands of the genotypes. The score 1 and 0 indicates the presence and absence of bands, respectively. In case of binary coding, a data matrix comprising 1 and 0 formed depending on the character and this data matrix was subjected to further analysis.

The correlation of the marker with the trait was determined by the presence of number of marker alleles corresponding to positive and negative control in morphologically characterized low and high vigorous genotypes. The analysis of variance for different characters was carried out using the mean data in order to partition variability due to different sources by following Panse and Sukhatme (1961). All the Statistical analysis was performed using INDOSTAT software. Correlations among the parameters were calculated according to Gomez and Gomez (1983).

RESULTS

The analysis of variance of rice genotypes showed highly significant variation for seedling vigor traits (Table 1). Three genotypes BPT 5204, Kalinga III and Sampada had light seed weight, while the rest of the genotypes have medium to heavy seed weight. Of all the genotypes IR 28, Sahbagidhan, Vandana, VL Dhan 208 recorded low EC Values and highest germination percentage. High MGT was observed in Heera, Krishnahamsa, RP2421 and Vandana. Bharani deep, Dinesh, Narendra 118, Sahbhagidhan, Sasyasree and VL Dhan 221 recorded high root length. High shoot length was observed in Dinesh, Heera, Jaldidhan, Narendra 118, PNR 381, Sabita, Vandana, and VL Dhan 221. Similarly highest root shoot ratio was found in Adithya, BPT 5204, Govind, NDR 97, Pant Dhan 16, Sahbhagidhan, Sasyasree, Sampada and Swarna. Highest seedling length was observed in Bharani Deep, Dinesh, Sabita, Sahbhagidhan, Narendra 118, and VL Dhan 221. Among all the genotypes, Akshayadhan, Dinesh, Jaldidhan, Moroberekan, Nagina 22, Suraksha and VL Dhan 208 recorded highest fresh shoot weight and Adithya, NDR 97, Sasyasree, Swarna and Vikas recorded high fresh root and seedling weight, except Moroberekan above genotypes recorded high seedling dry weight. Highest SVI I was found in Bharani Deep, Dinesh, Sabita, Sahbhagidhan, Sasyasree, VL Dhan 208 and VL Dhan 221, where as high SVI II was noted in Dinesh, Jaldidhan, Moroberekan, Nagina 22, Nipponbare, Suraksha, VL Dhan 208 and VL Dhan 221.

Of all traits root shoot ratio, root fresh weight, seedling dry weight, SVI I and SVI II showed high GCV per cent while root length, shoot length, root shoot ratio, root fresh weight, seedling dry weight, SVI I and SVI II recorded high PCV per cent. Among all the characters, highest heritability was recorded for seedling fresh weight. Correlation coefficient revealed significant positive correlation among all traits except for electrical conductivity and root shoot ratio (Table 2). The results pertaining to genetic variability parameters *viz.*, mean, genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), broad sense heritability (h^2) and genetic advance as per cent of mean (GAM) for seed vigor characteristics are presented in table 3. In the present investigation, high heritability coupled with high GAM was observed for SVI II (95.3 and 54.66).

The 15 reported QTL related to eight seedling root traits were screened with 30 SSR markers in 46 rice germplasm to identify its role in associated traits of seedling vigor (Table 5). For QTL1-1 four SSR markers were selected (RM212, RM265 and RM315) for QTL1-2 four SSR markers were selected (RM212, RM265, RM315 and RM11934), for QTL5-1 two SSR markers RM17855 and RM592 were selected, similarly two markers (RM20487 and RM20503) were selected for the QTL6-1. For the root penetration related QTL, QTL2-1 four marker was selected (RM221, RM318, RM13923 and RM13924), whereas for QTL3-1 two SSR markers were selected (RM231 and RM14436). Similarly for QTL 11-2 peak marker RM206 was selected. Another QTL7-1 associated with three markers (RM351, RM234 and RM248) were selected.

Among the root thickness controlling QTL9-1, a peak marker RM242 was selected, for QTL10-1 two SSR markers were selected (RM24903 and RM24904). Whereas for QTL12-1

Table 1: Genotypes used as experimental material under study

S.No.	Genotype	Parentage	Released for
1.	Adithya	M63-83/Cauvery	Rainfed upland
2.	Akshyadhan	BR 827-35/SC 5109-2	Irrigated medium
3.	Anjali	RR 19-2/RR 149-1129	Rainfed upland
4.	Bala	TN 1 / N22	Rainfed upland
5.	Bharani deep	C 1064-5/IR 9129-320-3-3-3//IR 54	Rainfed upland
6.	BPT 5204	GEB 24/TN 1//Mahsuri	Rainfed shallow lowland
7.	CO 39	Kannagi / Cul 340	Irrigated Medium
8.	Dinesh	Jaladhi 2/ Pankaj	Deep water
9.	DRR Dhan 38	BPT 5204 / KMR3	Irrigated medium
10.	Erramalla	BC 5-55/W 12708	Irrigated Early
11.	Govind	IR 20/ IR24	Rainfed upland
12.	Heera	CR 404-48/CR 289-1208	Rainfed upland
13.	IR 28	IR 833-6-1-1-1/ IR 1561-149-1//IR 1737	Irrigated mid –early
14.	IR 50	IR 2153-14-6-6-2/IR 28//IR 2070-625-1-25	Irrigated Early
15.	Jalididhan	Dular / N22	Rainfed upland
16.	Kalinga III	AC 540/ Ratna	Rainfed upland
17.	Krishnahamsa	Rasi /Fine Gora	Boro
18.	Moroberekan	African landrace	Rainfed upland
19.	Nagina 22	Pureline selection from Rajbhog	Rainfed upland
20.	Narendra 118	IR 36/ Hansraj	Rainfed upland
21.	NDR 97	N22 / Ratna	Rainfed upland
22.	Nipponbare	C 1064/IR 9129-320-3-3-3//IR 54	-
23.	Pantdhan 16	BG 380/BG 367-4	Rainfed upland
24.	PNR 381	T3 mutant/ Bas 370	Rainfed upland
25.	Rasi	TN 1/CO 39	Irrigated early
26.	Ravi	M 63-83 // RP 79-5/Rikuto Norin 21	Rainfed upland
27.	RP 2421	IR 36/Kathawar	Irrigated hills
28.	Sabita	Pure line sel from Boyan	Semi deep water
29.	Sampada	Vijaya / C14-8	Irrigated medium
30.	Sasyasree	IR 8/ TKM 6	Irrigated mid-early
31.	Sahbagidhan	IR 55419-04*2 / Way Rarem	Rainfed upland
32.	Salivahana	RP 5-32/Pankaj	Rainfed shallow lowland
33.	Sukardhan	IR 32429/ 122-3-1-2-1//IR 31868-64-2-3-3-3	Upland hills
34.	Suraksha	Sasyasree/ MR 1523	Irrigated medium
35.	Swarna	Vasistha / Mahsuri	Rainfed shallow lowland
36.	Tellahamsa	HR 12/TN 1	Irrigated early
37.	Tulasi	Rasi / Fine Gora	Rainfed upland
38.	Vandana	C22 / Kalakeri	Rainfed upland
39.	Varalu	WGL 20471/ CR 544-1-2	Rainfed upland
40.	Vikas	IR 8 / TKM 6	Sodic/saline
41.	Vivekdhan 62	China 4 / BG 367-4	Irrigated hills
42.	VL Dhan 65	Himalaya 2/ VL Dhan 16	Irrigated hills
43.	VL Dhan 82	VL Dhan 221/ UPR 82-1-7	Irrigated hills
44.	VL Dhan 208	VR 410-19/VR 212	Rainfed upland
45.	VL Dhan 221	IR 2053-521-1-1-1/CH 1039	Rainfed upland
46.	Udayagiri	IR 138/ IR 13543-66	Rainfed upland

related to root thickness and number of roots at depth, two SSR markers were selected (RM27508 and RM247). Two QTL, QTL4-1 and QTL11-1 are related to maximum root length; QTL4-1 was associated with two markers (RM16550 and RM16553) and for QTL11-1 a peak marker RM229 was selected. Adventitious root length related QTL5-2 was selected with two markers (RM18820 and RM18918). Another QTL8-1 associated with adventitious root number had RM44 and RM339 as the left and right flanking markers which were selected as the two SSR markers for analysis.

Association of SSR's located in the interval of root QTL with seedling vigor traits

A total of 30 SSR markers which were dispersed throughout the 12 chromosomes were used to assess the association of

markers with seedling root traits in 46 different rice genotypes by taking high and low trait parents as positive and negative control respectively. For some traits Azucena primitive rice genomic DNA was taken as a positive control as it had been identified with major root QTL. All the 30 markers were amplified, out of them a total of 16 markers were found to be polymorphic and remaining 14 markers showed monomorphic marker allele across the genotypes tested.

SSR marker- trait correlation

Among the 16 markers which were found to be polymorphic, RM351 and RM44 were identified as best marker which showed highest correlation between genotypic and phenotypic data (Table 5).

QTL for seedling root traits

Table 2 : ANOVA for seedling vigor related traits among rice genotypes

Source of variance	Df	Seed weight (g)	EC (dSm ⁻¹)	First count (%)	Final count (%)	Mean germination	Shoot Length (cm)	Root Length (cm)	Seedling Length (cm)	Root: Shoot (cm)	Root fresh ratio(mg)	Shoot fresh weight (mg)	Seedling fresh (mg)	Seedling dry weight (mg)	SVII	SVIII
Treatments	45	0.34**	0.01**	276.80**	257.57**	0.57**	16.26**	25.48**	16.25**	0.36**	385.56**	19695.19**	21460.03**	4169.357**	743678.1**	430376.80**
Error	92	0.001	0.001	5.305	2.915	0.012	0.963	0.654	1.715	0.017	4.241	8.369	7.113	70.979	35162.500	6963.908
CV (%)		0.811	0.482	2.689	1.912	3.807	8.639	5.346	4.945	9.344	4.213	0.463	0.389	5.473	6.038	6.035

** = Significant at 5% LSD

A total of 15 QTL were selected for the eight seedling root traits. These QTL were analysed with suitable selected SSR markers, QTL associated with different seedling root traits were found to be present in some genotypes were selected for analysis. QTL associated with different genotypes were indicated in the table 5. For the QTL1-1, three markers among them only RM315 was polymorphic in nature. RM315 showed marker allele of positive control at 220 bp in Azucena and negative control at 210 bp allele in Bala. For QTL1-2 among the four markers used for analysis RM315 and RM11934 were found to be polymorphic, RM315 showed allele for positive control of 220 bp in Azucena and allele of negative control was 210 bp in IR64, whereas RM11934 showed positive control allele 160 bp in Azucena and negative control allele was 170 bp in IR64. Similarly for the QTL2-1 two markers (RM318 and RM13924) showed polymorphic banding pattern. RM318 showed marker allele of positive control was 170 bp in Azucena and allele of negative control was 200 bp in Bala (Figure 1).

For the QTL3-1, two markers were analyzed using Azucena and IR64 as positive and negative controls viz., RM231 and RM14436. Marker RM231 showed polymorphic banding pattern with their positive controls at 170 bp and 160 bp respectively (Figure 2). Markers RM592 was found to be polymorphic which showed allele of positive control at 210 bp in Azucena and allele of negative control at 270 bp in IR64 for the QTL5-1, while marker RM18820 was polymorphic showing allele of positive control at 290 bp in Azucena and allele of negative control at 270 bp in IR64 for the QTL5-2.

Similarly for the QTL QTL7-1, QTL9-1, QTL11-1, QTL11-2 and QTL12-1, eight markers were analysed using Azucena as positive and Bala as negative control. For the QTL7-1, all three markers (RM351, RM234 and RM248.) got amplified and found to be polymorphic. The marker RM351 showed allele of positive and negative control at 190 bp and 180 bp respectively, RM234 showed positive control allele at 140 bp and negative control allele at 130 bp (Figure 1). For the QTL9-1 peak marker RM242 showed allele of positive control at 290 bp and allele of negative control at 260 bp. The marker RM229 showed positive control allele at 100 bp and negative control allele at 120 bp, for QTL11-1 and RM206 showed positive control allele at 210 bp and negative control allele at 180 bp for QTL 11-2. In the same way for the QTL12-1, from the two markers analyzed (RM27508 and RM247) RM247 showed positive control allele at 120bp and negative control allele at 110 bp.

Among two markers analyzed for QTL8-1 viz., RM44 and RM339, RM339 was monomorphic and showed band approximately at 120 bp and RM44 was polymorphic showing allele of positive control at 110 bp and allele of negative control at 120 bp (Figure 2). QTL6-1 when analysed using two markers (RM 20487 and RM20503) both were found to be monomorphic. RM24903 and RM24904 were used to analyse QTL10-1 and were found to be monomorphic.

The putative QTL1-1 was found in seven genotypes viz., Vivekdhan 62, Swarna, Dinesh, Pantdhan16, VL Dhan 208, Nipponbare and Moroberekan. Similarly, QTL2-1 was associated with Sabita, Nipponbare and Moroberekan. Presence of QTL3-1 was identified in Nipponbare and

Table 3 : Mean, range and genetic parameters for early vigor related traits in 46 rice genotypes

Character	Mean	GCV	PCV	Heritability	GAM
100-Seed weight (g)	2.29	14.6	14.62	99.69	30.03
Electrical Conductivity (dSm ⁻¹)	1.2	5.52	5.54	99.24	11.32
Mean germination (days)	2.89	15	15.47	93.94	29.94
First count (%)	85.67	11.1	11.43	94.46	22.23
Final count (%)	89.31	10.32	10.49	96.68	20.89
Root length (cm)	15.13	19.02	19.75	92.68	37.71
Shoot length (cm)	11.36	19.88	21.68	84.12	37.56
Seedling length (cm)	26.48	15.67	16.43	90.94	30.77
Root Shoot ratio	1.38	24.45	26.18	87.17	47.02
Root fresh weight (mg)	48.89	23.06	23.44	96.77	46.73
Shoot fresh weight (mg)	636.89	12.72	12.73	99.87	26.18
Seedling fresh weight (mg)	685.78	12.33	12.34	99.92	25.39
Seedling dry weight (mg)	153.94	24.01	24.63	95.06	48.23
Seed vigor Index I	2378.97	20.87	21.51	94.18	41.73
Seed vigor Index II	1382.096	27.18	27.84	95.3	54.66

Where, GCV = Genotypic Coefficient of Variability; PCV = Phenotypic Coefficient of Variability; GAM = Genetic Advance as per Mean

Table 4: Phenotypic correlation among seedling vigor traits in rice genotypes

Character	Seed weight (g)	EC (dSm ⁻¹)	First count (%)	Final count (%)	MGT (days)	Root length (cm)	Shoot length (cm)	Seedling length (cm)	Root: Shoot ratio	Fresh root weight (mg)	Fresh shoot weight (mg)	Seedling fresh weight (mg)	Seedling dryweight (mg)	SVII	SVIII
Seed weight	1	0.082	0.082	0.046	-0.048	0.251	0.377**	0.382**	-0.158	0.313*	0.257	0.288*	0.320*	0.315*	0.300*
EC (dSm ⁻¹)		1	-0.423**	-0.446**	-0.247	-0.330*	-0.113	-0.291*	-0.204	-0.051	-0.288*	-0.283	-0.271	-0.402**	-0.370*
First count (%)			1	0.970**	0.530**	0.364*	0.148	0.334*	0.133	0.229	0.336*	0.353*	0.228	0.698**	0.516**
Final count (%)				1	0.551**	0.386**	0.162	0.356*	0.152	0.181	0.336*	0.346*	0.217	0.711**	0.513**
MGT (days)					1	0.151	0.164	0.195	-0.015	0.256	0.066	0.098	0.071	0.383**	0.226
Root length (cm)						1	0.285	0.849**	0.566**	0.510**	0.213	0.273	0.274	0.786**	0.381**
Shoot length (cm)							1	0.749**	-0.603**	0.03	0.451**	0.436**	0.443**	0.639**	0.466**
Seedling length (cm)								1	0.058	0.369*	0.396**	0.429**	0.435**	0.896**	0.520**
Root Shoot ratio									1	0.359*	-0.246	-0.187	-0.172	0.085	-0.109
Fresh root weight (mg)										1	0.25	0.374**	0.398**	0.366*	0.404**
Fresh shoot weight (mg)											1	0.992**	0.942**	0.486**	0.933**
Seedling fresh weight (mg)												1	0.956**	0.515**	0.948**
Seedling dry weight (mg)													1	0.465**	0.944**
SVII														1	0.657**
SVIII															1

Moroberekan. QTL5-1 was found to be present in Anjali, Tulasi, VL Dhan 208 and Moroberekan. QTL5-2 was present in DRR Dhan 38, Govind, Tulasi, Pantdhan16, VL Dhan 82, Nipponbare and Moroberekan. QTL7-1 was found only in Nipponbare. Adventitious root number controlling QTL8-1 was found in Vandana, Sahbagidhan, Sampada, VL Dhan 208, Nipponbare and Moroberekan. QTL 9-1 for root thickness was found in Vandana, Erramallelu, Krishnahamsa, DRR Dhan 38, Vivekdhan 62, IR 28, Sasyasree, Akshyadhan, Swarna, Dinesh, Ravi, Tulasi, Tellahamsa, IR50, Sampada, PNR 381, Vikas, Salivahana, Rasi, BPT 5204, Jaldidhan, VL Dhan 208, Udayagiri, and CO 39. Moroberekan is the only genotype found to have QTL11-2. QTL12-1 controlling root thickness was found in Vandana, Heera, Anjali, RP 2421, DRR Dhan 38, Varalu, Sahbagidhan, Tulasi, Rasi and Moroberekan.

DISCUSSION

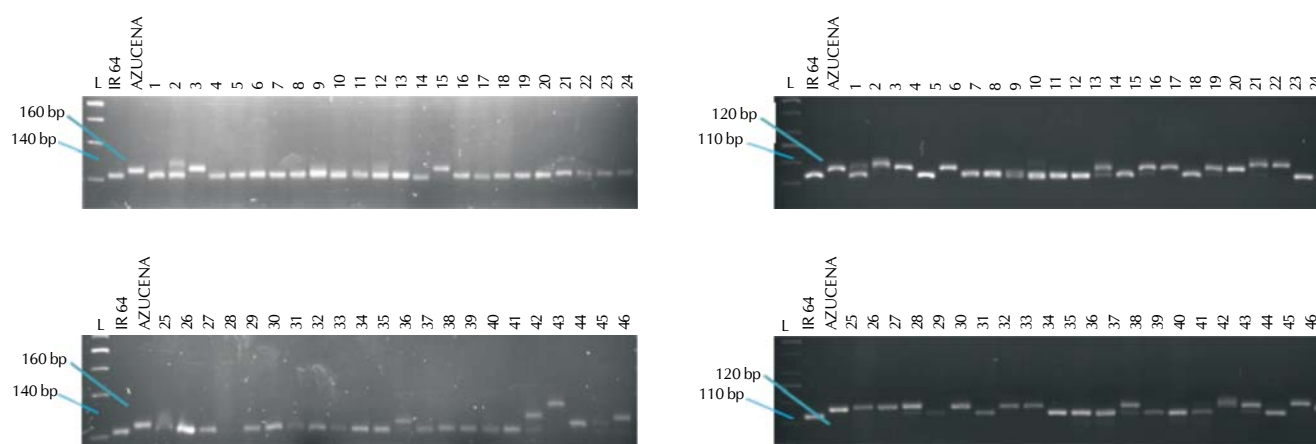
Seedling vigor is an important trait for better crop establishment in direct seeded rice and associated traits are quantitatively inherited (Zhang 1995). Most of the previous experiments

were done at controlled conditions because of tedious and lacks of consistency in phenotyping at field level. Based on seed vigor analysis the high vigor genotypes are Dinesh, Jaldidhan, Moroberekan, Nagina 22, Nipponbare, Suraksha, VL Dhan 208 and VL Dhan 221 and 9 low vigor genotypes are Bala, BPT 5204, Erramallelu, Govind, IR 50, Krishnahamsa, Sampada, Suraksha and Udayagiri, while the rest 30 are medium vigor genotypes. Similar type of results were obtained by Sujay (2007) for 100-seed weight, germination, shoot length, root length, seedling dry weight and seed vigor index II. Cui *et al.* (2002) determined significant correlation among the five seedling vigor traits *viz.*, germination rate, total dry weight, shoot dry weight, root dry weight and maximum root length.

Some high vigor genotypes have multiple QTL for root traits this may be one of the reason for their vigorous nature. The presence of multiple QTL in Moroberekan(9), VL Dhan 208(6), Nippon bare(6) and Dinesh(2) for traits like root shoot ratio, root thickness, seminal root length, root penetration, adventitious root length and number of roots at depth. Multiple QTL controlling seedling vigor on chromosome 5 was reported by Hu *et al.* (2004). The additive effect of all these QTL results

Table 5: Genotypic and phenotypic correlation, QTL, traits and reported population for root traits in rice

S.no	Polymorphic Primers	Phenotypic correlation (%) / R ²	Details of reported QTL	Trait	Reported population
1	RM315	30.55	QTL 1-1, QTL 1-2	Seminal root length, root shoot ratio and root thickness	Azucena/Bala, IR64/Azucena
2	RM11934	48.61	QTL 1-2	Seminal root length	IR64/Azucena
3	RM318	34.72	QTL2-1	Root penetration	Azucena/Bala
4	RM221	52.78	QTL2-1	Root penetration	Azucena/Bala
5	RM231	46.5	QTL3-1	Root penetration	IR64/Azucena
6	RM14436	56.25	QTL3-1	Root penetration	IR64/Azucena
7	RM592	34.72	QTL5-1	Seminal root length	IR64 x Azucena
8	RM18820	18.06	QTL5-2	Advanteous root length	IR64/Azucena
9	RM234	45.14	QTL7-1	Root penetration, max root length	Azucena/Bala
10	RM351	57.64	QTL7-1	Root penetration, max root length	Azucena/Bala
11	RM248	29.17	QTL7-1	Root penetration, max root length	Azucena/Bala
12	RM44	57.64	QTL8-1	Advanteous root length	IR64/Azucena
13	RM242	18.75	QTL9-1	root thickness	Azucena/Bala
14	RM229	38.89	QTL11-1	root length	Azucena/Bala
15	RM206	28.47	QTL12-1	Root thickness, no of roots at depth	Azucena /Bala
16	RM247	11.81	QTL12-1	Root thickness, no of roots at depth	Azucena /Bala



1. Narendra 118, 2. Sabitha, 3. Vandana, 4. Heera, 5. Anjali, 6. Rp 2421, 7. Erramallelu, 8. Krishnahamsa, 9. DRR 38, 10. Varalu, 11. VL Dhan 65, 13. Suraksha, 14. IR 28, 15. Sabhagidhan, 16. Govind, 17. Sasyasree, 18. Akshadhan, 19. Swrna, 20. Dinesh, 21. Ravi, 22. Tulasi, 23. Tellahamsa, 24. IR 50, 25. Sampada, 26. PNR 381, 27. Kalinga 111, 28. Vikas, 29. Shalivahana, 30. Rasi, 31. BPT 5204, 32. Pant Dhan 16, 33. NDR 97, 34. Jaldidhan, 35. Adithya, 36. VL Dhan 208, 37. VL Dhan 221, 38. Sukardhan, 39. Udayagiri, 40. Vivekdhan 82, 41. Nagina 22, 42. Bharani Deep, 43. Nipponbare, 44. Moroberekan, 45. Bala, 46. Co 39

Figure 1 : Banding pattern of the markers RM 44 and RM 231 in 46 rice genotypes

in enhanced seedling vigor and better crop establishment. High heritability and correlation of root traits with early vigor results in enhanced field emergence (Seshu and Dadlani, 1993). The congruence of these multiple in expression of vigor trait like germination rate, root traits may be due to pleiotropy or linkage between the traits. Similarly, IRR1 (1979) found that Moroberekan was cited with unique combination of showing deep root growth and better vigor but low drought tolerance when root depth was restricted.

Even though none of the root QTL present in genotypes like Jaldidhan, Nagina 22, Suraksha and VL Dhan 221, they are high vigours. It is clearly evident that other than root QTL, traits like coleoptile length, elongated mesocotyl may play a significant role in trait determination. Similarly some medium vigor genotypes were found to have few QTL but low vigor genotypes were not found with even a single QTL. The present study clearly showed that among the 46 genotypes evaluated for seedling vigor traits, eight genotypes like Dinesh, Jaldidhan, Moroberekan, Nagina 22, Nipponbare, Suraksha, VL Dhan

208 and VL Dhan 221 were found to be highly vigorous. Among the high vigorous genotypes *viz.*, Dinesh, Moroberekan, Nagina 22, Nipponbare, VL Dhan 208 having multiple root QTL compared to other medium and low vigor genotypes. So, better root growth is one the possible reasons for better seedling vigor and initial establishment, which is imperative trait for direct seeded rice. Majority of root QTL were developmental stage specific and identification of QTL

for seedling root-related traits would help to enhance the selection efficiency at an earlier stage of the crop, so that much of the resources and time could be saved. Selection of cultivar at the seed germination stage based on the quality of embryonic roots which is important for the plant growth and also roots development (Reddy *et al.*, 2013). Hence, these results clearly indicate that some root QTL support seedling vigor, utilizing root QTL through MAS may help to elucidate genotypes having better vigor and can be exploited in pyramiding directly utilize in breeding programme and

ultimately improves grain yield.

ACKNOWLEDGEMENT

We thank ICAR-Indian Institute of Rice Research for financial support and lab facilities for the study

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