

are brought to the site of synthesis by the elongation factor (EFTu). Had there been no wobble pairing for all 61 codons that encode one amino acid each, there would have been a requirement of as many different types of t-RNAs. Wobble pairing has reduced this requirement. Lesser the variety of t-RNAs, faster the cognate tRNA appearing at the A site in the ribosome during translation. This also explains why synonymous codons are not randomly present in the genetic code (synonymous codons have same nucleotides at the first and second positions except few codons for serine, arginine and leucine). It seems, wobble pairing and non-randomness of synonymous codons are the consequences of a coevolutionary process leading to higher translation rate.

The program 'dinsearch' may have use in finding alien DNA sequences in genomes which have been acquired recently by horizontal gene transfer. Alien DNA sequences have been suggested to have different GC%, altered codon usage and encode polypeptides having different amino acid compositions in relation to the host genome<sup>11</sup>. Genome GC percentage is often correlated with the occurrence of the nucleotides at the third nucleotide position of synonymous codons. The first and/or the second nucleotide(s) of codons give information about amino acid composition of the poly-

peptide encoded by an ORF. Both GC% and amino acid composition are signatures of a genome. So the dinucleotide abundance at the third and first codon positions respectively, of adjacent codons in an ORF might be considered as a signature for the organism. Comparison of dinucleotide abundance of an alien sequence present in the genome with the reference genome signature will give better resolution than the one obtained on the basis of either the GC% value or the amino acid composition value of the alien sequence.

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DEBOJYOTI DAS<sup>1</sup>  
SIDDHARATHA SANKAR SATAPATHY<sup>2</sup>  
ALAK KUMAR BURAGOHAIN<sup>1</sup>  
SUVENDRA KUMAR RAY<sup>1,\*</sup>

<sup>1</sup>Department of Molecular Biology and Biotechnology,  
Tezpur University

<sup>2</sup>Department of Computer Science and Information Technology,  
Tezpur University,  
Tezpur 784 028, India

\*For correspondence.  
e-mail: suven@tezu.ernet.in

## Mapping QTLs underlying seedling vigour traits in rice (*Oryza sativa* L.)

Cultivars having high seedling vigour are desirable for crop establishment in the direct-seeded rice system and in temperate rice-growing areas<sup>1</sup>. High seedling vigour helps the genotypes to suppress the weeds, which is a serious problem in large rain-fed and upland areas in the tropics where dry seeding is practised.

The purpose of this study was to tag quantitative trait loci (QTLs) underlying seedling vigour-related traits using a DH mapping population derived from a cross between a high vigour *japonica* cultivar CT9993 and a low vigour *indica* cultivar IR62266. The linkage map of this population comprised 145 RFLPs, 153 AFLPs and 17 microsatellite markers covering 1788 cM in length with an average distance of 5.7 cM between adjacent markers<sup>2</sup>. In this experiment, seeds of 125 DH lines along with parents and one check,

Azucena were sown in black cylindrical pipes measuring 30 cm in length and 10 cm in diameter, which were filled with a mixture of FYM, coir pith and soil in 1 : 1 : 1 proportion. The experiment was laid out in completely randomized design with three replications. After germination, one seedling was allowed to grow in each pipe. Plants were watered daily throughout the experiment to maintain moisture field capacity. After 21 days, the pipes were submerged in water for one hour to loosen the soil and avoid any damage to the seedling. Later, the seedling was carefully removed from the pipe and washed with water to remove any adhering material without damaging any part of seedling. The observations for vigour-related traits were recorded (Table 1). Analysis of variance was done to partition the variance. Interval analysis was performed to

detect QTLs using MAPMAKER/QTL<sup>3</sup>. A locus with LOD > 3.00 was declared a putative QTL.

Analysis of variance of all the traits showed significant line differences, revealing desirable variation in the population. The ranges of the mean values of all traits extend beyond that of the parents, exhibiting transgressive segregation. Parent, CT9993, performed better for almost all the traits except for leaf number and root to shoot fresh weight ratio, when compared to parent IR62266.

A total of 29 QTLs for 14 morphological and growth-related traits were tagged to molecular markers (Table 2). The variance explained by each QTL ranged from 10.7 to 38.8. Significant QTLs were located on chromosomes 1 and 3. Four QTLs for total length were identified on chromosomes 3, 5, 10 and 12, which ex-

**Table 1.** Descriptive statistical analysis for vigour-related traits in CT9993/IR62266 DH mapping population of rice

Trait	Unit	CT9993 Mean	IR62266 Mean	Doubled haploid lines				
				Mean	SE ±	Min.	Max.	Skewness
<b>Morphological</b>								
Plant height	cm	13.600	6.850	9.770	0.146	4.700	16.700	0.343
Maximum root length	cm	20.600	9.200	16.468	0.336	7.000	28.000	0.130
Root number	–	5.000	4.000	4.204	0.078	1.000	8.000	–0.071
Leaf number	–	2.500	3.000	2.667	0.031	2.000	3.000	–0.712
Stem length	cm	4.400	1.950	2.603	0.030	1.300	4.500	0.216
Total length	cm	34.200	16.050	26.238	0.395	14.400	41.500	0.079
Total fresh weight	g	0.130	0.055	0.088	0.002	0.024	0.176	0.302
Total dry weight	g	0.015	0.006	0.011	0.000	0.002	0.026	1.022
Total shoot fresh weight	g	0.087	0.036	0.059	0.001	0.018	0.104	0.303
Total shoot dry weight	g	0.011	0.004	0.008	0.000	0.001	0.018	0.816
Root to shoot fresh weight ratio	–	0.496	0.546	0.502	0.014	0.031	1.691	1.224
<b>Growth-analysis</b>								
Leaf area ratio	cm <sup>2</sup> g <sup>-1</sup>	226.133	164.451	193.891	3.707	68.900	402.660	0.750
Second leaf area	cm <sup>2</sup>	1.960	0.513	1.251	0.032	0.070	3.250	0.684
Second specific leaf area	cm <sup>2</sup> g <sup>-1</sup>	133.912	91.101	116.243	2.600	18.500	269.600	0.362

Plant height: the vertical distance from the ground to the highest leaf-tip.

Stem length: the vertical distance from the ground to the apex.

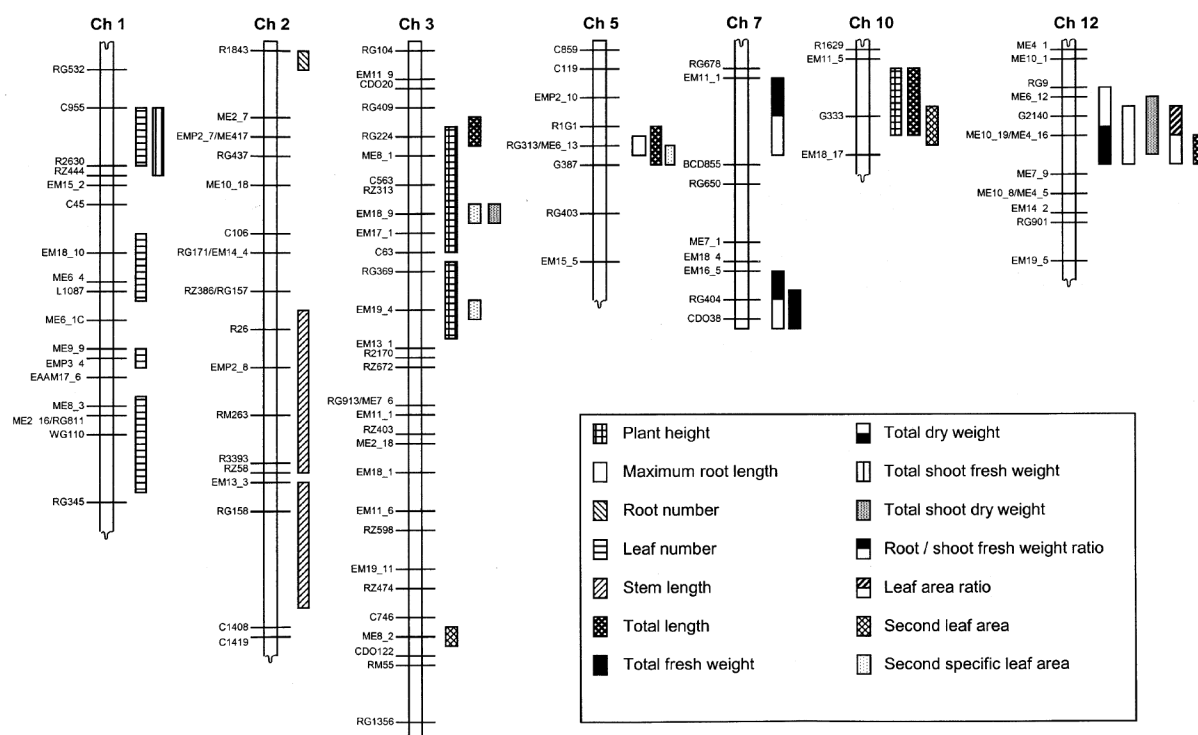
**Table 2.** Quantitative trait loci for vigour-related traits in CT9993/IR62266, DH mapping population of rice

Trait	QTL	Nearest marker	Chr. no.	Peak LOD <sup>a</sup>	% Variance explained	Additive effect <sup>b</sup>	Position <sup>c</sup>
<b>Morphological</b>							
Plant height	<i>qpht3-1</i>	RZ313	3	7.87	29.30	–1.2500	63.45
	<i>qpht3-2</i>	RG369	3	7.12	26.60	–1.1500	93.41
	<i>qpht10-1</i>	G333	10	5.04	20.30	–0.9600	123.49
Maximum root length	<i>qmrl5-1</i>	RG313	5	3.04	11.50	–1.7300	45.64
	<i>qmrl12-1</i>	ME4_16	12	4.51	16.60	2.0700	41.36
Root number	<i>qrn2-1</i>	R1843	2	3.06	10.70	–0.3700	0.01
Leaf number	<i>qln1-1</i>	C955	1	3.60	16.80	–0.2100	129.79
	<i>qln1-2</i>	EM18_10	1	3.81	14.63	–0.1800	178.98
	<i>qln1-3</i>	ME9_9	1	4.30	15.90	–0.1800	210.65
	<i>qln1-4</i>	ME2_16	1	5.42	19.67	–0.2000	237.74
Stem length	<i>qsl2-1</i>	EMP2_8	2	10.74	38.87	–0.2700	196.66
	<i>qsl2-2</i>	RG158	2	7.38	26.40	–0.2180	215.5
Total length	<i>qtl3-1</i>	RG409	3	3.24	13.50	–2.6200	35.16
	<i>qtl5-1</i>	RG313	5	3.84	14.36	–2.2400	45.64
	<i>qtl10-1</i>	G333	10	3.62	13.69	–2.1900	123.49
	<i>qtl12-1</i>	ME4_16	12	4.50	16.61	2.4100	41.36
Total fresh weight	<i>qtfw7-1</i>	RG404	7	4.00	16.16	0.0130	255.44
Total dry weight	<i>qtdw12-1</i>	ME4_16	12	5.35	19.36	0.0002	41.36
Total shoot fresh weight	<i>qtsfw1-1</i>	R2630	1	3.59	13.59	0.0073	149.35
Total shoot dry weight	<i>qtsdw3-1</i>	EM18_9	3	3.54	13.34	–0.0011	67.12
	<i>qtsdw12-1</i>	ME4_16	12	4.37	16.08	0.0009	41.36
Root to shoot fresh weight ratio	<i>qrsfwr7-1</i>	EM11_1	7	4.79	21.39	0.1300	168.68
	<i>qrsfwr7-2</i>	RG404	7	6.26	23.20	0.1150	255.44
<b>Growth-analysis</b>							
Leaf area ratio	<i>qlar12-1</i>	ME6_12	12	3.61	13.97	–23.6900	36.08
Second leaf area	<i>qsla3-1</i>	ME8_2	3	3.67	13.81	–0.1890	273.46
	<i>qsla10-1</i>	G333	10	3.04	13.11	–0.1830	127.49
	<i>qssla3-1</i>	EM18_9	3	3.89	15.13	–0.0009	69.12
Second specific leaf area	<i>qssla3-2</i>	EM19_4	3	3.36	12.66	–0.0008	133.55
	<i>qssla5-1</i>	ME6_13	5	3.11	11.80	–0.0007	47.63

<sup>a</sup>Maximum-likelihood (LOD) score for the QTL.

<sup>b</sup>Weight calculated by MAPMAKER/QTL. A negative weight mean that the IR62266 allele reduce the trait.

<sup>c</sup>Position of the QTL related to the nearest marker.



**Figure 1.** Chromosomal positions of QTLs that exceeded the critical LOD score of 3.00 for vigour-related traits in DH mapping population (CT9993/IR62266) of rice.

plained 13.5%, 14.3%, 13.6% and 16.6% of the total variance respectively (total is 57%). On chromosomes 5 and 12 two QTLs for maximum root length were found, overlapping with the QTLs for total length, which explained (11.5% + 16.6%) 28.1% of the total variance. One QTL associated with plant height, located on chromosome 10, overlapped with total length, explaining 20.3% of the total variance at a LOD of 5.07. The highest phenotypic variance was found for stem length (38.8%) on chromosome 2 with a LOD 10.7. On chromosome 12, a QTL for total dry weight was found partially overlapping with the QTLs for maximum root length, total shoot dry weight, leaf area ratio and total length. This QTL explained 19.3% of the total variance. Favourable alleles of *qmrl12-1*, *qtl12-1*, *qtdw12-1* and *qtsdw12-1* came from IR62266 but for *qlar12-1* the favourable allele was contributed by CT9993 (Figure 1). The QTL for total length reported in this study on chromosome 12 was close to a locus for the same traits in the same mapping population<sup>4</sup>. Six QTLs for growth-analysis traits were detected on chromosomes 3, 5, 10 and 12 where CT9993 contributed the favourable alleles for all the six QTLs. A QTL for leaf area ratio was found on chromosome 12,

it explained 14% of the total variance. While CT9993 contributed the favourite QTLs for all the growth-analysis traits and length-related traits (except *qmrl12-1* and *qtl12-1*), the IR62266 contributed the favourite alleles for all the weight-related traits (except *qtsdw3-1*). Identification of QTLs for seedling vigour-related traits would help enhance the selection efficiency at an earlier stage of the crop, so that much of the resources and time could be saved. If QTLs are found in the same genomic regions in both seedling and mature crop, the screening can be done at an early stage with the QTL markers. Apart from this elucidating the magnitude, number and location of the QTLs underlying the seedling vigour would help understand the genetics of the traits, leading to enhanced selection efficiency. Further, elucidating correlation of early vigour traits with the traits at maturity would help deduce certain early vigour traits, which could be satisfactorily used for early stage selection.

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ADNAN KANBAR<sup>1,2</sup>  
M. JANAMATTI<sup>1</sup>  
E. SUDHEER<sup>1</sup>  
M. S. VINOD<sup>1</sup>  
H. E. SHASHIDHAR<sup>1,\*</sup>

<sup>1</sup>Department of Genetics and Plant Breeding,  
University of Agricultural Sciences,  
Bangalore 560 065, India

<sup>2</sup>Department of Field Crops,  
Faculty of Agriculture,  
University of Damascus,  
Damascus, Syria

\*For correspondence.  
e-mail: heshashidhar@rediffmail.com

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