

Novel QTL Associated with Aerenchyma-Mediated Radial Oxygen Loss (ROL) in Rice (*Oryza sativa* L.) under Iron (II) Sulfide

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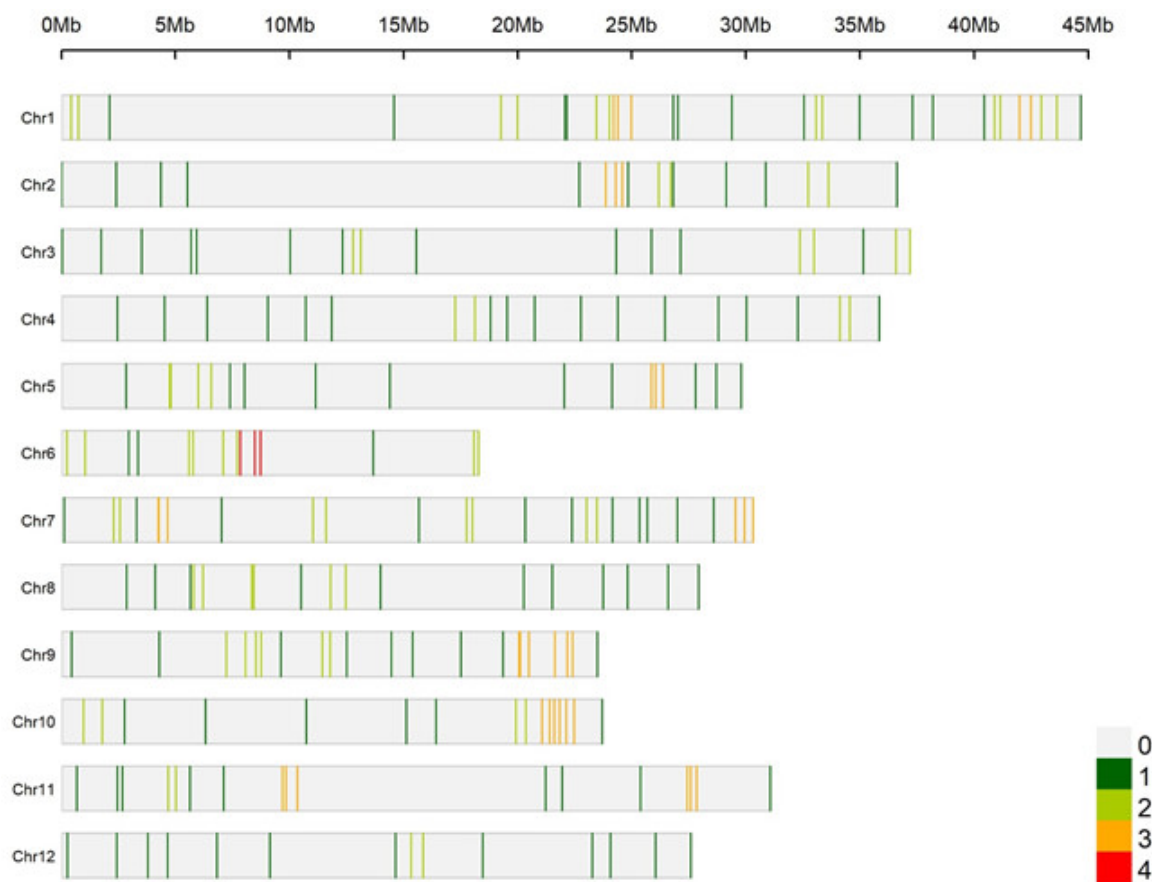


Figure S1. Density of Kompetitive Allele-Specific PCR (KASP) and Fluidigm markers across the rice genome.

Table S1. Results of Statistical Analysis of Traits in DH population

Trait	Sample Size	Mean	Variance	SE	Skewness	Kurtosis	Min	Max	W-test
ROL	117	27.79	55.99	7.481	0.2001	-0.2857	12.1	49	0.9791
RA	117	8.35	3.20	1.789	0.3287	-0.1947	4.283	13	0.9771
RL	117	6.71	11.18	1.057	-0.9184	0.8985	3.25	8.89	0.9407

ROL: radial oxygen loss; RA: root area; and RL: root length. W-test: the Shapiro–Wilk W-statistic for the test of normality of the distribution.

Table S2. Linkage groups and total length per chromosome

Chromosome ID	Chromosome Name	No. of markers	Length (cM)
1	Chromosome 1	29	207.95
2	Chromosome 2	17	189.28
3	Chromosome 3	20	204.8
4	Chromosome 4	21	201.48
5	Chromosome 5	17	139.66
6	Chromosome 6	11	60.54
7	Chromosome 7	27	210.84
8	Chromosome 8	17	102.5
9	Chromosome 9	19	101.21
10	Chromosome 10	13	109.7
11	Chromosome 11	16	130.12
12	Chromosome 12	13	134.52
Whole Genome	Whole Genome	220	1792.6

Table S3. List of ROL candidate genes and primers sequences used for qPCR validation.

Gene Name	Locus ID	Forward primer (5'→3')	Reverse primer (5'→3')	T _m °C (F/R)	G-C contents % (F/R)	Amplicon size (bp)
<i>OsTCP7</i>	LOC_Os02g42380	CCATGTCTACCAGCCCGTG	TTGCTGTGCCGGTCCTTC	60.15/60.28	63.16/61.11	150
<i>OsTRX</i>	LOC_Os02g42700	GCGGGCCATGCAAAATGATA	TGTCGGGGTTTTCATCAGTGT	59.61/59.86	50.00/47.62	102
<i>OsMYB21</i>	LOC_Os02g42850	GGTGGATCAACTACCTGCGG	TCCTAGACCACTTGTTGCCG	60.46/59.68	60.00/55.00	108
<i>OsPLIM2a</i>	LOC_Os02g42820	GGGCAGCTACAACCACTTGA	TCCTGTTCTTTCGCTGGC	60.25/60.32	55.00/55.00	102
<i>OsDEF7</i>	LOC_Os02g41904	CCACAGGTTCAAGGGCATGT	TTCTTGAGAAGCACTTGCG	60.54/59.69	55.00/50.00	120
<i>OsARF8</i>	LOC_Os02g41800	CAGTCGAGCCTCATGTACCC	CCCATTGTCAGGTCAGTGCT	59.90/59.96	60.00/55.00	95
<i>OsEXPA</i>	LOC_Os02g42650	AATTCGAGGATGGAGACGGC	CCCCCAGATGTGCTTCATGT	59.89/60.03	55.00/55.00	89
<i>OsNIP2</i>	LOC_Os02g41860	GTGATCGGGTACAAGCACCA	ATGAAGATCATGCCGCCGAA	60.04/60.18	55.00/50.00	110
<i>Osclb5</i>	LOC_Os02g42740	GTAAAAGGCGACCGACAGGA	CCTGGGAAAACGTCGTCAGA	60.04/59.97	55.00/55.00	88
<i>OsLRR2</i>	LOC_Os02g42412	CAGCAGCTGTGTTAGGATCAC	GAGGGCATGACCGAACATCT	58.99/59.82	52.38/55.00	92
<i>OsWBC8</i>	LOC_Os02g41920	TCACAGTGGTGGTGTACTGG	ACCCGACGTATCTCTTCACC	59.24/58.90	55.00/55.00	126
<i>OsActin1</i>	LOC_Os05g36290	CTAGCGGTGCAACAACCTGGT	ACCGGAGGATAGCATGAGGA	57.5/57.5	55.00/55.00	102