

IRRI Sequence analyses of the major rice QTL *Phosphate Uptake 1 (Pup1)*

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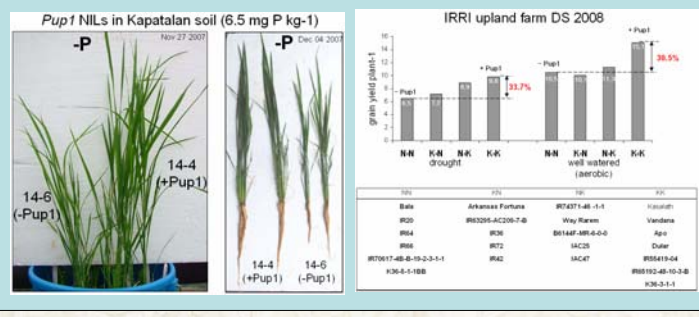
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The major rice QTL *Pup1* confers tolerance to phosphorus (P) deficiency under field conditions. We have sequenced the *Pup1* locus in the tolerant donor variety Kasalath. Sequence analyses revealed that the region contains more than 50% transposon-related elements and many insertions/deletions which led to the truncation of genes, integration of segments from other chromosomes, and *Pup1* specific gene models. Using RiceGAAS, 68 putative genes were predicted. Most of these genes are not conserved in the Nipponbare *Pup1* syntenic region. Due to the complex structure of the locus, the Kasalath gene models required detailed *in silico* and RT-PCR expression analyses. Our current data show that none of the putative *Pup1* genes can be directly related to P uptake or P metabolism. This suggests that *Pup1* confers P-deficiency tolerance via a yet unidentified mechanism. A set of best bet candidate genes has been short listed and generation of transgenic plants is ongoing. The *Pup1* sequence information has also been used for the development of *Pup1*-specific markers that are being applied in marker assisted breeding of *Pup1* introgression lines.

Pup1 phenotyping

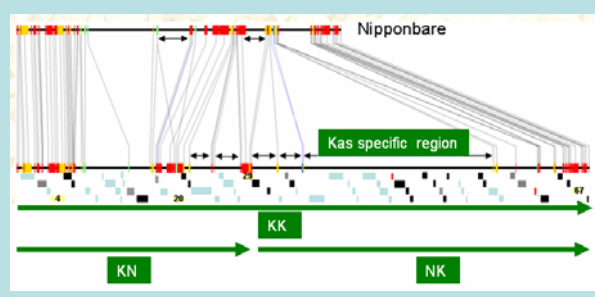
NIL 14-4 (+*Pup1*) showed growth advantage in P-deficient soil *Pup1* confers 30% yield advantage under upland (aerobic) conditions



Pup1 is a transposon-integration hot spot

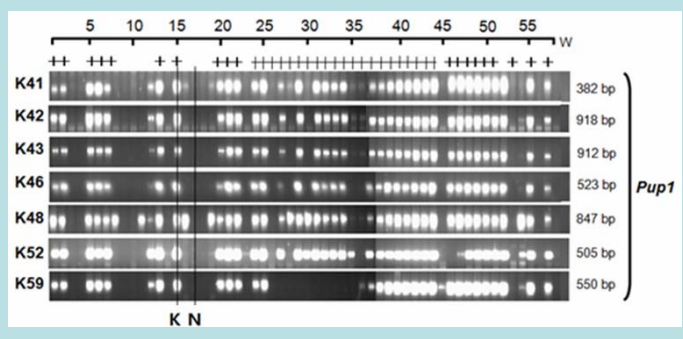
	Kasalath	Nipponbare	93-11
size of <i>Pup1</i> regions			
size of locus (bp)	278036 (incl. 'N')	154071	742472
gene number (incl. TE genes)			
RiceGAAS (incl. TE)	68	34	191
TIGR (incl. TE)	-	20	-
genes with clear annotation	12	11	nd
unclear annotation and gene model	21	nd	nd
genes not in database	2	nd	nd
retro-/transposon genes	33	9	nd
% non TE genes of total	24.99	11	nd
% TE of total sequence	25.22	26.5	nd
% annotated of total bp	50.21	37.5	nd
RepeatMasker analysis			
masked (bp)	148485	83192	335751
masked (%)	54.6	54.0	45.22
retrotransposons (%)			
total	37.7	43.23	31.47
Gypsy/DIRS1 type LTR	31.81	19.84	17.97
Ty1/Copia type LTR	1.41	16.94	11.07
others	4.48	6.45	2.21
DNA transposons (%)			
total	16.33	10.08	12.78
En-Spm	5.7	1.75	2.96
MuDR/IS305	2.62	0.88	1.93
Tourist/Harbinger	1.97	3.06	2.01
others	6.04	4.39	2.65
Nucmer alignment			
% Kasalath seq that aligns >100 bp with >80% homology	100	26.98	51.04

Pup1 molecular markers for germplasm screening and breeding

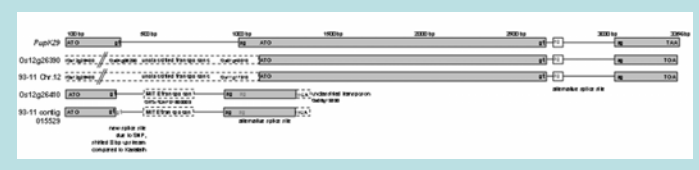


Kasalath allele distribution in 58 rice accessions

Pup1 is generally not present in irrigated rice varieties but highly conserved in rice varieties and breeding lines developed for rainfed environments (indicated by "+").



The Kasalath *OsPup1K29* gene corresponds to two genes in Nipponbare



OsPup1K29 RT-PCR analysis

