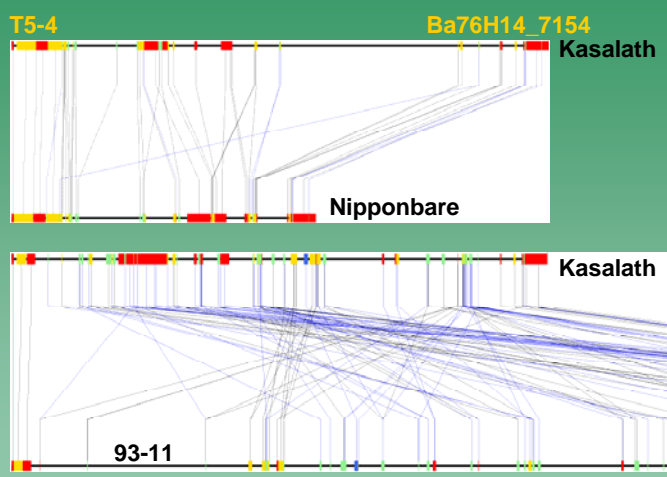


Comparative genomic analysis and assessment of candidate genes at the Pup1 locus, a major QTL for phosphorus deficiency tolerance in rice.

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The Pup1 locus is a major QTL for tolerance of phosphorus (P) deficiency located on Chr.12. The Pup1 region was fine-mapped in a Nipponbare x Kasalath population and recently sequenced in the tolerant donor *Aus* variety Kasalath. Sequence analyses revealed major differences in size and gene models compared to the corresponding region in Nipponbare (*japonica*) and 93-11 (*indica*). None of the predicted Pup1 Kasalath genes has formerly been associated with P-response and it is currently unclear how Pup1 confers tolerance. Candidate genes are now being analyzed to elucidate their function.

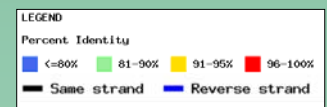
The Pup1 region in Kasalath, Nipponbare, and 93-11 is highly variable with respect to size, structure, and gene models:



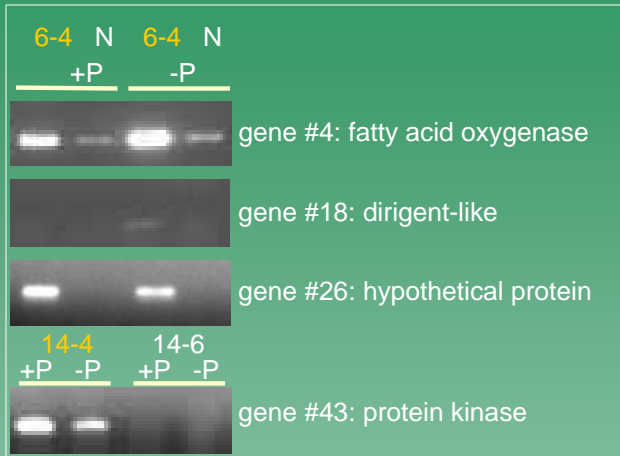
	Kasalath	Nipponbare	93-11
Size of Pup1 region	272 ^a kb	154.1 kb	752.7 ^a kb
Number annotated genes ^b : TIGR, BGI	-	22	32
RiceGAAS	70	34	191
Total nucleotides annotated genes: TIGR, BGI	-	60.7 kb	32.1 kb
RiceGAAS	135.3 kb	76.6 kb	250.5 kb
Repeat elements, transposons and retrotransposons (Repeat Masker)	140.6 kb (52%)	80.1 kb (52%)	340.2 kb (45%)
Total annotated sequence: TIGR, BGI	-	140.9 kb	372.3 kb
RiceGAAS	275.9 kb	156.8 kb	590.8 kb
intergenic and non-annotated sequence: TIGR, BGI	-	13.2 kb	380.4 kb
RiceGAAS	(3940 nt) ^{***}	(2737 nt) ^{***}	162 kb

^awith gaps of unknown length; ^bincl. genes annotated as transposons; ^{***}double annotation of sequences

Genomic regions are defined by the fine mapping markers T5-4 and Ba76H14_7154 and sequences are aligned using Nucmer software (Kurtz et al. 2004). The data show the importance of sequencing QTLs in the tolerant donor variety.

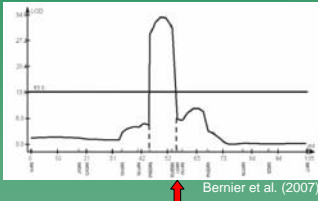


Pup1 candidate genes: Expression analysis and relation to other stresses



RT-PCR analysis of Pup1 candidate genes in near isogenic Pup1 lines grown under +P and -P field conditions. Transformation of the genes is ongoing (RNAi and overexpression).
 6-4/14-4: +Pup1 NILs; 14-6: -Pup1 NIL; N=Nipponbare.

Drought QTL on Chr.12



Pup1 at 55 cM (15.3 Mb)

Chr.12 regions overlapping with Pup1 have been mapped in QTL studies on drought and biotic stresses, e.g. blast. We are currently analyzing whether Pup1 candidate genes are drought responsive and Pup1 NILs are being tested for their tolerance of drought and biotic stresses.

The analysis of Pup1 candidate genes in conjunction with the development of PCR-based markers (available) and a robust phenotyping system (ongoing) will ultimately lead to a better understanding of P-deficiency tolerance and the development of higher-yielding improved rice varieties for rainfed systems. For a recent review on our work, see Ismail et al. (2007).

References cited:
 Bernier et al. (2007). Crop Science 47:507-518
 Ismail et al. (2007). Plant Mol Biol in press (online DOI 10.1007/s11103-007-9215-2)
 Kurtz et al. (2004). Genome Biology 5:R12