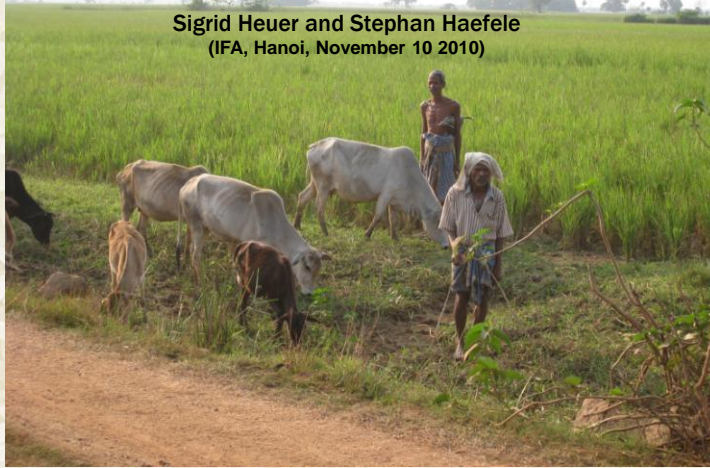


**Marker-assisted breeding & molecular characterization
of the major rice QTL *Phosphorus uptake 1 (Pup1)***

Sigrid Heuer and Stephan Haefele
(IFA, Hanoi, November 10 2010)

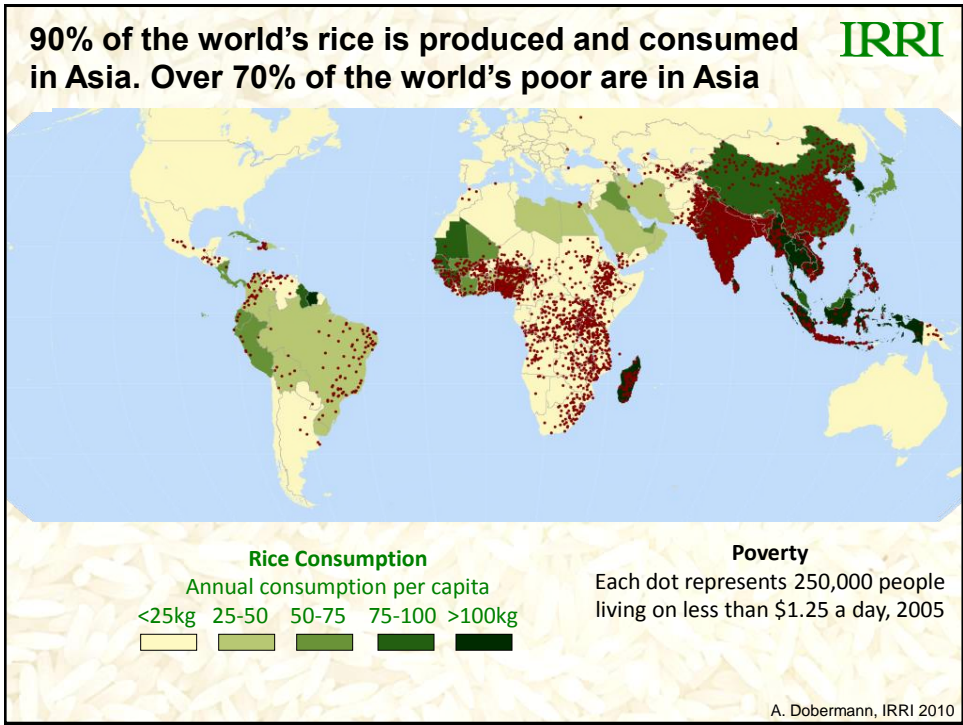


Rice
Science
for a Better
World

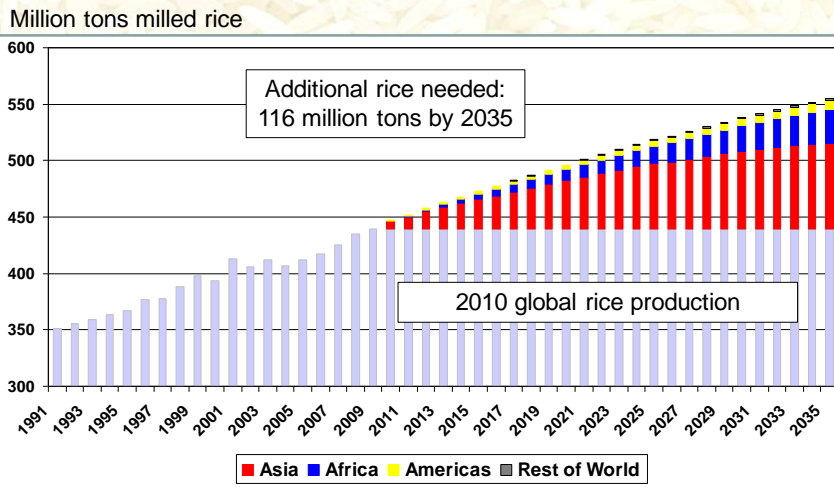
IRRI in Los Baños, Philippines



- 250 ha research station (irrigated and upland)
- 1200 staff in >25 countries
- Total budget 2009: US\$50 M (2008: US\$ 33.5 M)



Increasing rice production on less land, with less water, and less inputs



(i) Irrigated systems: ~80 Mha (50% area, **75%** production)

(ii) Rainfed systems: ~75 Mha (50% area, **25%** production)

A. Dobermann, IRRI 2010

Breeding activities and focus at IRRI: Overview

● **Intensive irrigated systems**

- high yield (any new variety has to out-yield checks)
- hybrid rice (new consortium with private sector) **I. Enhancing yield**
- C4 rice, golden rice, high iron rice
- disease resistance (blast, BB, tungro, sheath blight, brown spot...); rats

● **Rainfed drought-prone and stress environments (upland + lowland)**

- submergence and drought
- salinity and acidity
- phosphorus and zinc deficiency **II. Reducing stress-related yield losses**
- heat and cold (AfricaRice)
- iron and aluminum toxicity
- all diseases + nematodes ...

● **Technologies/agronomy**

- variety testing in multi-location trials
- crop management and fertilizer trials
- alternate-wetting and drying technology (water saving)
- direct seeding (anaerobic germination)
- weed control (early vigor, water management) **III. Improved management and nutrient use**

Major crops: Share of global fertilizer use (2007)

Crop	Area (Mha)	Yield (t ha ⁻¹)	Total fertilizer use (N + P ₂ O ₅ + K ₂ O)		Total N use		Total P ₂ O ₅ use		Total K ₂ O use	
			(% of total)	(Mt)	(% of total)	(Mt)	(% of total)	(Mt)	(% of total)	(Mt)
Maize	158	5.0	15.3	25.8	16.8	16.9	12.4	4.9	14.2	4.1
Wheat	214	2.8	15.1	25.5	17.3	17.4	16.2	6.4	6.0	1.7
Rice	156	4.2	14.4	24.3	15.6	15.7	12.3	4.8	13.3	3.8
Other cereals	-	-	4.8	8.1	5.1	5.1	5.1	2.0	3.3	0.9
Sum			49.7	83.8	54.8	55.1	46.0	18.1	36.7	10.6

	nutrient-recovery rate (rice, 1 st season):	nutrients not used in season (rice; Mt):
N	30-50%	11.0 - 7.85
P ₂ O ₅	25%	3.6
K ₂ O	35-50%	2.47 - 1.9

→ at least **13.4 Mt** of the applied **24,3 Mt** fertilizer is **not used** (rice in 1st season)



- waste of resources (especially P^{*})
- waste of energy
- source of pollution (especially N)
- contribution to climate change
- high costs for (poor) farmers

* **IFDC report**, S.J Van Kauwenbergh (2010):

- world rock P reserves: 340,000 – 460,000 mmt
- this will last for 300-400 years

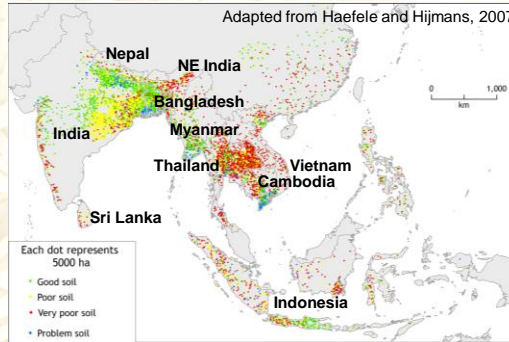
How can we improve nutrient uptake and use efficiency ?

- Site specific nutrient management/ slow release fertilizers
- Increased uptake efficiency of fertilizer (reduced net loss of fertilizer nutrients)
- More roots and/or different root architecture
- Better mobilization of “fixed” nutrients (P, K)
- High affinity transporters
- Increased internal efficiency
- Improve plant metabolism / photosynthesis
- Increase harvest index / new plant type
- Biological N fixation by exo- and/or endo-symbiosis
- Tolerant genotypes (reduce yield losses due to biotic and abiotic stresses)
-

Poor soils in poor countries

60% of rainfed rice in Asia is grown on problem soils

Adapted from Haefele and Hijmans, 2007



- applied P fertilizer not plant available due to P-fixation in soil
- root growth impaired due to low pH, Al and Fe toxicity
- yield loss due to drought and submergence stress
- tolerant genotypes are needed to reduce production risk before farmers invest in fertilizer

Nutrient uptake by roots : Phosphorus

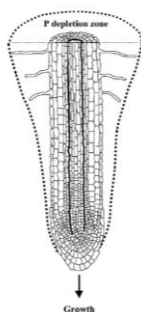
e.g., maize

Table 3. Percent of nutrients taken up by a corn crop normally supplied by root interception, mass flow and diffusion

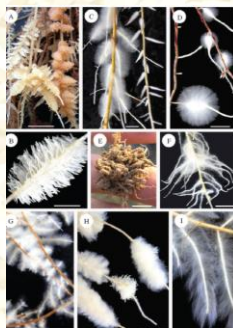
Nutrient	Root interception	% of uptake possible		
		Mass flow	Diffusion	
Nitrogen	<1	80	19	
Phosphorous	2	5	93	
Potassium	2	18	80	
Calcium	150	375	0	
Magnesium	33	600	0	
Sulfur	5	300	0	

http://www.spectrumanalytic.com/support/library/ff/The_Nutrient_Uptake_Process.htm

Induction of root growth under low P

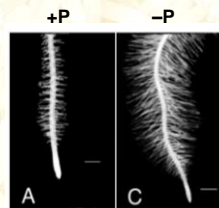


Cluster roots



Lambers et al (2006)
Annals of Botany

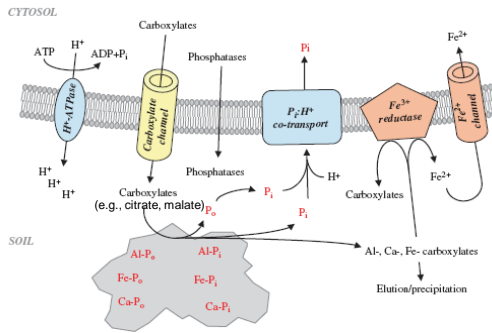
Root hair growth (*Arabidopsis*)



adapted from Zhang et al (2003)
J Experimental Botany

- A: *Banksia prionotes*
- B: *Hakea prostrata*
- C: *Lepidosperma squamatum*
- D: *Tetrasia* sp.
- E: *Aspalathus linearis*
- F: *Aspalathus linearis* in nutrient solution
- G: *Thamnochorus fracternus*
- H: *Mastersonia digitata*
- I: *Chondropetalum tectorum*

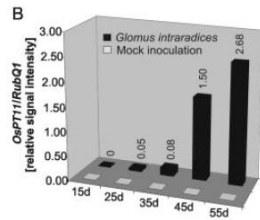
- Mobilization of phosphorus by root exudates



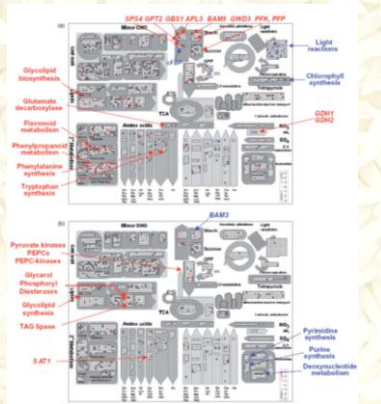
Lambers et al (2006), Annals of Botany

- Induction of high-affinity P transporters

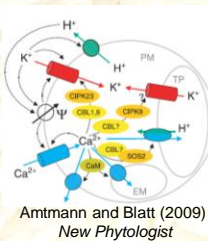
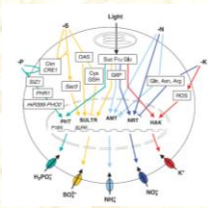
- P-uptake in interaction with Mycorrhiza, e.g., OsPT11



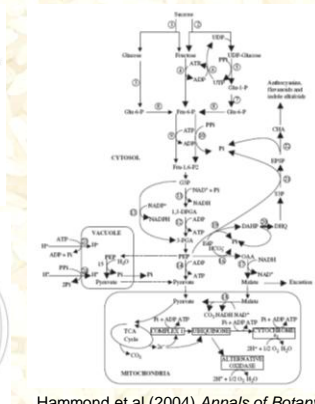
Molecular studies reveal insight in the regulation of nutrient uptake



Morcuende et al (2007), Plant Cell Environment



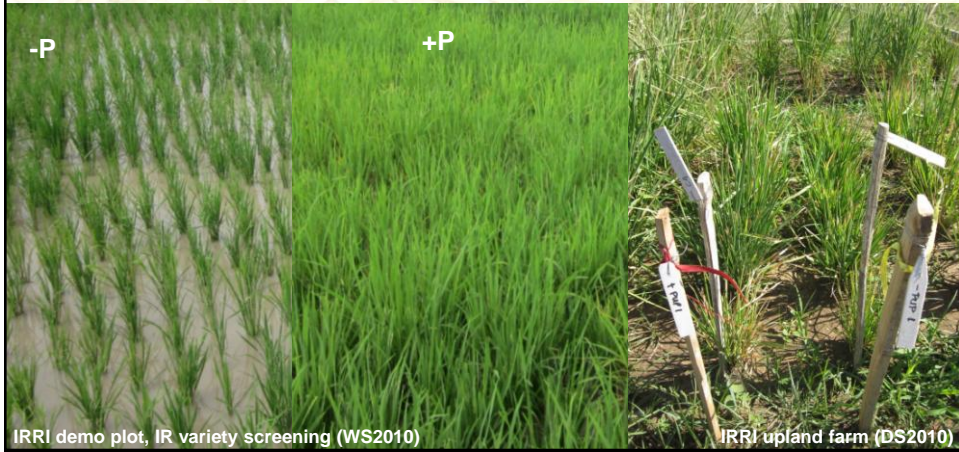
Amtmann and Blatt (2009) New Phytologist



Hammond et al (2004) Annals of Botany

Many pathways/genes with complex regulation - manipulate to enhance P uptake ?

The major QTL Phosphorus uptake 1 (*Pup1*): A different story

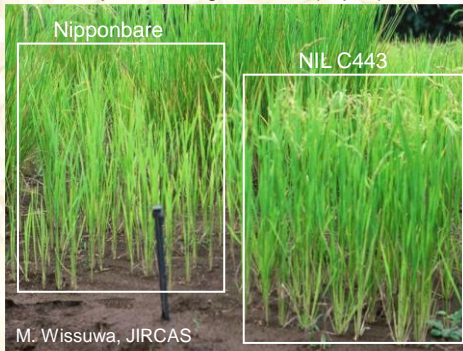


IRRI demo plot, IR variety screening (WS2010)

IRRI upland farm (DS2010)

Pup1 mapping

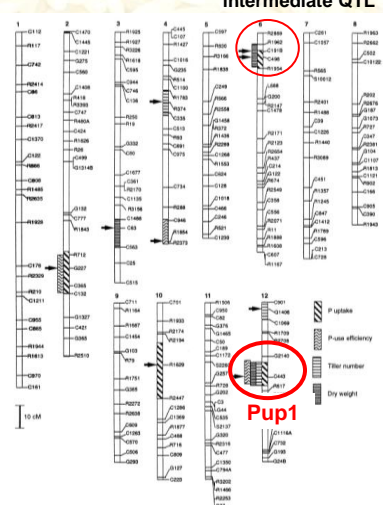
Pup1 near isogenic lines (Japan)

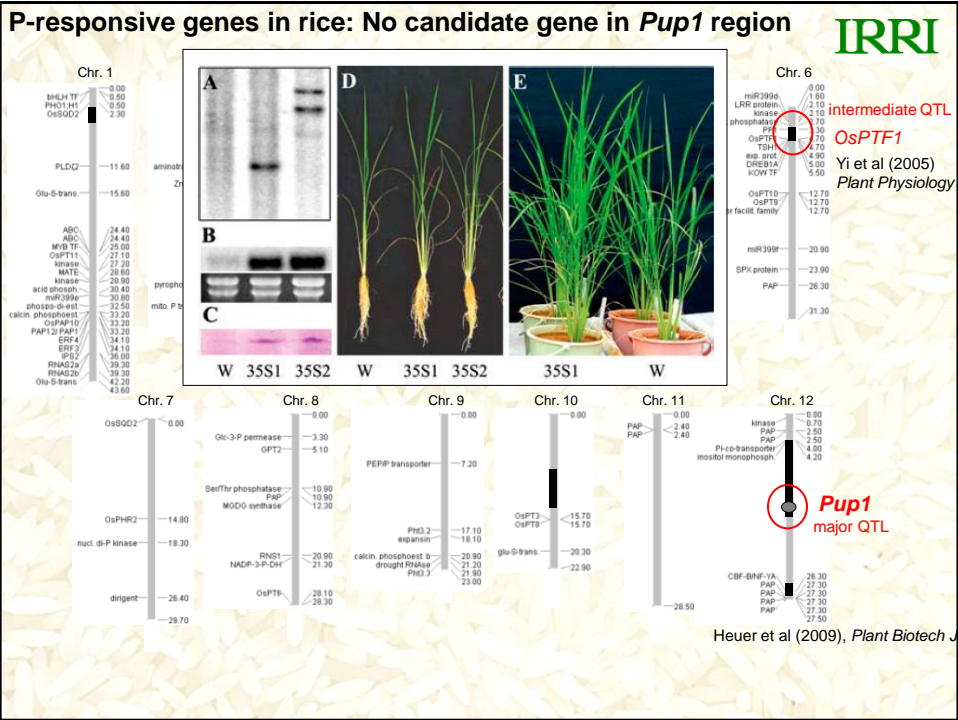


P-uptake: LOD 10.7 (28%)
 dry weight: LOD 10.5 (27%)
 tiller number: LOD 7.9 (21%)
 (P-use efficiency: LOD 6.6 (19%) NB allele)

		+P	-P
P uptake (mg root weight ⁻¹)	Nipponbare	13.7	1.8
	NIL-C443	13.9	3.2
	Kasalath	10.9	3.2

intermediate QTL





How is *Pup1* functioning?

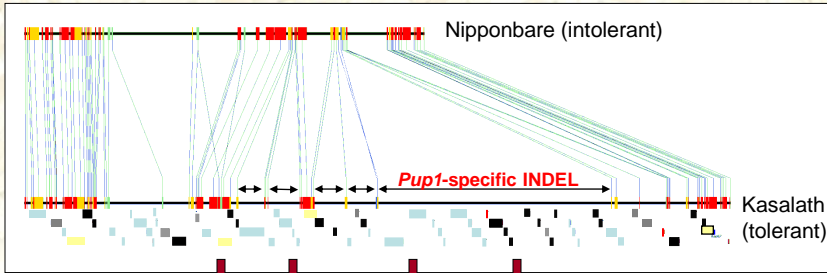
- no effect of *Pup1* on root growth in hydroponics
- root length? No
- longer root hairs? Yes in two *Pup1* NILs but not in NIL6-4
- organic acid exudation? **No**
- interaction with mycorrhiza? No difference in autoclaved soil
- **Microarray studies of contrasting *Pup1* materials**
 - (i) high affinity P transporters are up-regulated in tolerant and intolerant lines
 - (ii) main differences are related to cell walls

Novel genes or P-uptake mechanisms?

➔ **Sequencing of the *Pup1* region in tolerant donor (Kasalath)**

Sequence comparison of the *Pup1* genomic region

IRRI



1. Identification of candidate genes
2. gene validation by transgenic approaches

Phenotyping in P-deficient soil



Effect of *Pup1* transgene

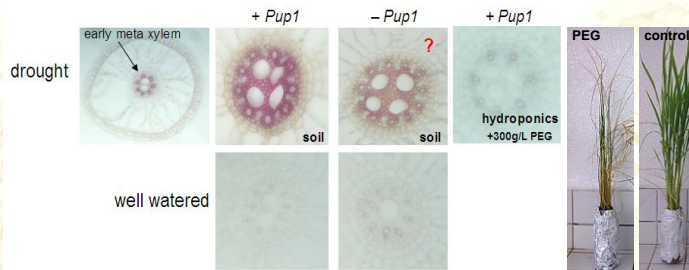


Pup1 is a novel, regulatory gene located in the INDEL region

Other *Pup1* candidate genes:

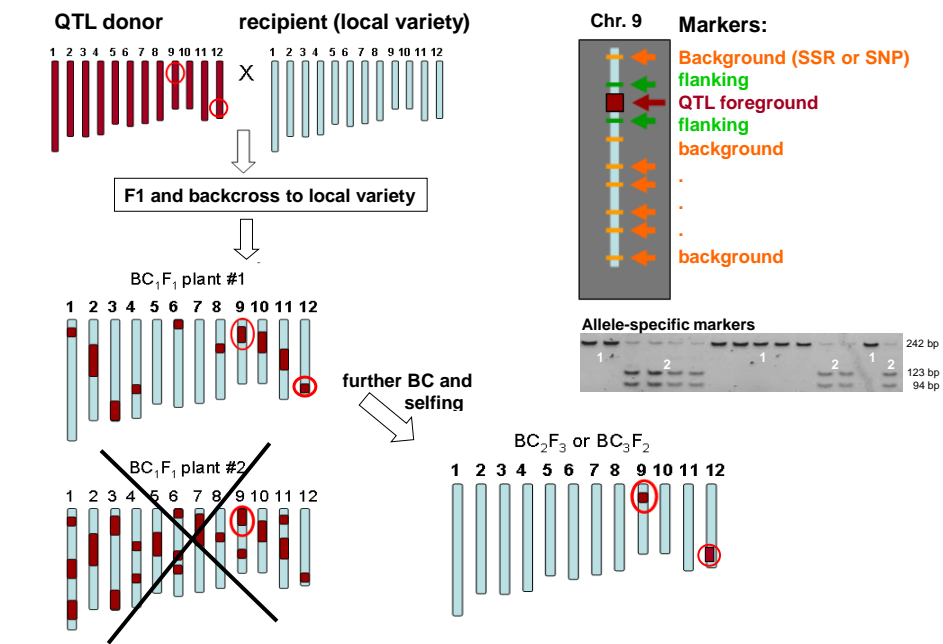
IRRI

Lignification of roots under drought - role of *Pup1* dirigent gene?



Marker-assisted backcrossing:
Targeted introgression of high-value genes/QTLs
into widely grown and well adapted mega varieties

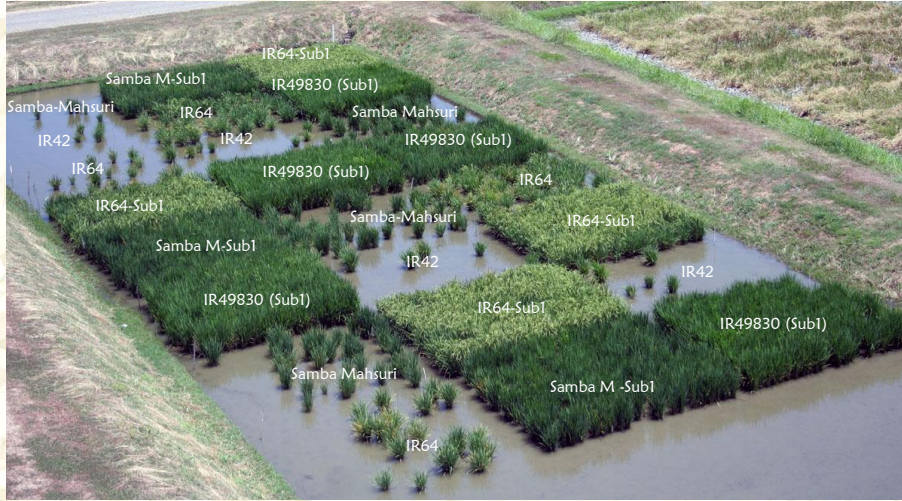
Marker assisted backcrossing (MABC)



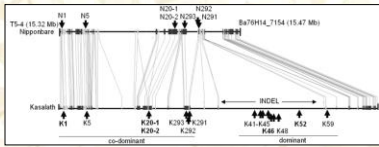
First MABC product at IRRI: *Sub1* mega varieties



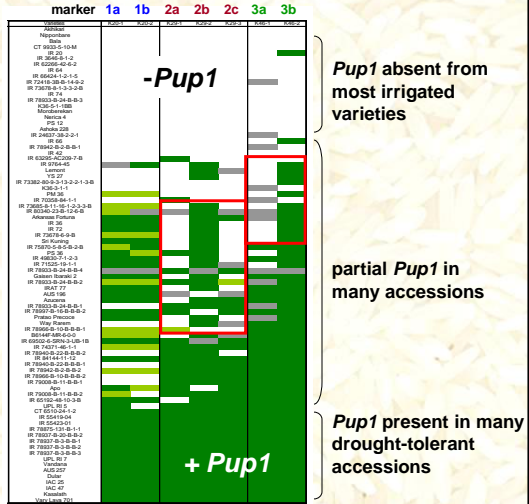
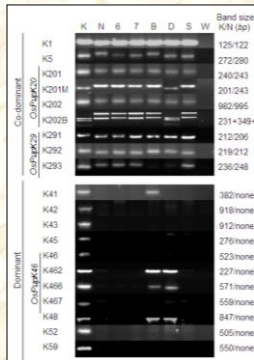
Recovery of *Sub1* varieties after 17 days complete submergence



***Pup1* gene-based markers**

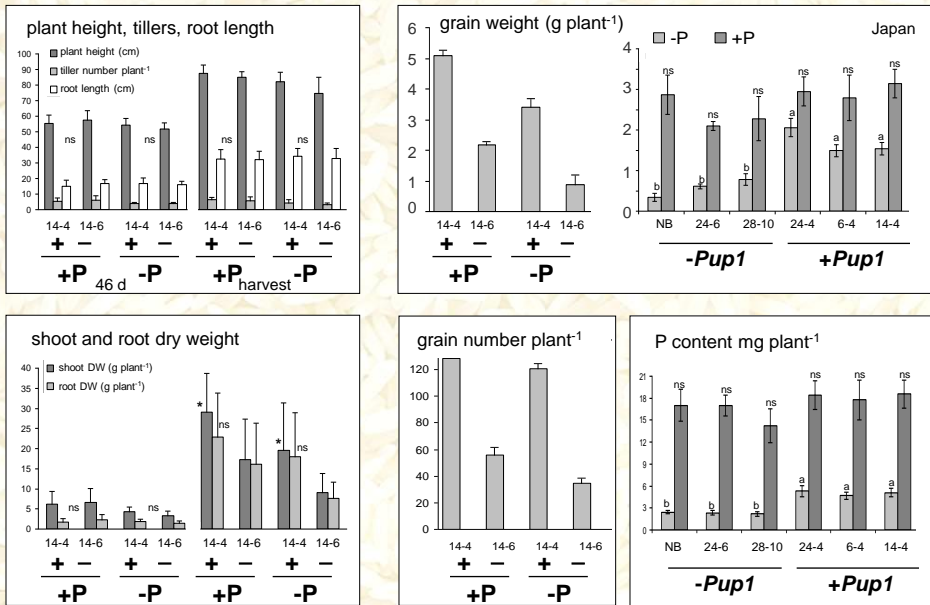


***Pup1* survey**



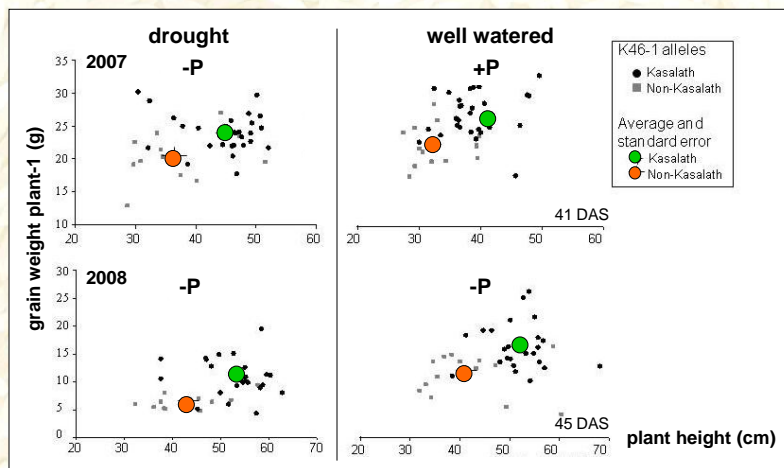
Pup1 phenotyping

Phenotyping in P-deficient soil, aerobic/drought



Chin et al (2010), *Theor Appl Genet*

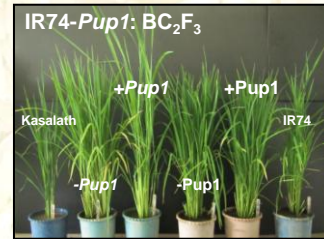
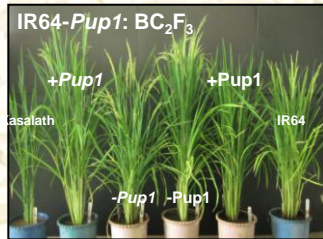
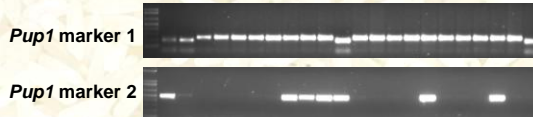
IRRI upland farm experiments (drought/ ww but high residual P)



Pup1 in mega varieties

IRRI

BC₂F₃ genotyping



Summary and outlook:

IRRI

- *Pup1* does not function via known P-uptake mechanisms
- *Pup1* major gene is a novel regulatory gene with large effect on root growth; other *Pup1* genes are under validation (cell wall related)
- mapping of QTLs + MABC into mega varieties is a straight forward and successful breeding approach --- candidate gene approach is limited to known mechanisms/genes
- important:
 - (i) Good QTL donor (IRRI's strongest QTLs come from un-adapted germplasm)
 - (ii) QTLs must have effect in different environments and genetic backgrounds
- *Pup1* is most likely best suitable for aerobic, drought-prone environments
- For intensive systems we need to
 - (i) clearly define targeted mechanisms (higher and/or faster nutrient uptake? Higher internal nutrient-use efficiency?...)
 - (ii) develop well defined screening protocols to identify donor varieties for this trait