Growth maintenance under water deficit in maize, rice and wheat

GCP project 15, François Tardieu (INRA) PI.

Rationale

1. Yield = growth maintenance of organs (leaves, roots, grains) under water deficit ("tolerance").

   Phenotyping in controlled conditions at early stages ?

2. Growth = same processes in all organs, all species

   Common genetic determinisms ?

3. Comparative biology/genetics on a relatively simple trait

   - multi species
   - multi organs
   - genetics + transcripts + models
   - controlled conditions ➔ field.

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GCP project 15

Rationale :

1. Yield = growth maintenance of organs (leaves, roots, grains)

2. Growth = Common genetic determinisms ?

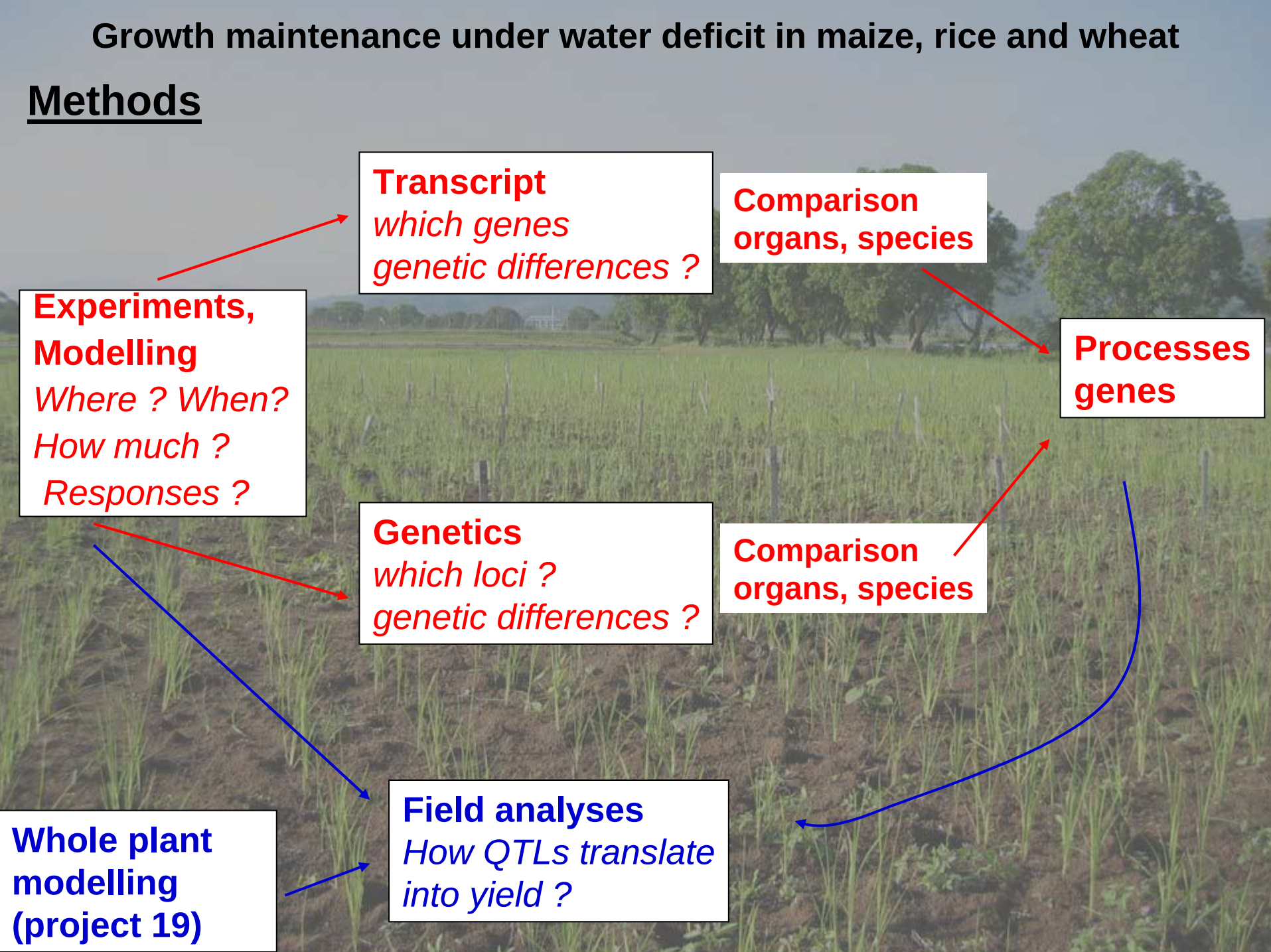
3. Comparative Biology

	Genetics, modelling			Whole plant yield, modelling	Transcripts
	Leaves	Roots	reproductive		
Maize	INRA	ETH	CIMMYT, INRA	CIMMYT, KARI IARI, INRA	CIMMYT Biogemma+ all
Rice	IRRI, INRA		IRRI	IRRI	IRRI
Wheat	CIMMYT, ACPFG		ACPFG		ACPFG

same populations (RILs, BCs for all traits in each species

Growth maintenance under water deficit in maize, rice and wheat

Methods



Experiments,
Modelling
Where ? When?
How much ?
Responses ?

Example 1: rice
IRRI and INRA

Response to drought and to air humidity have a genetic variability

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Modelling
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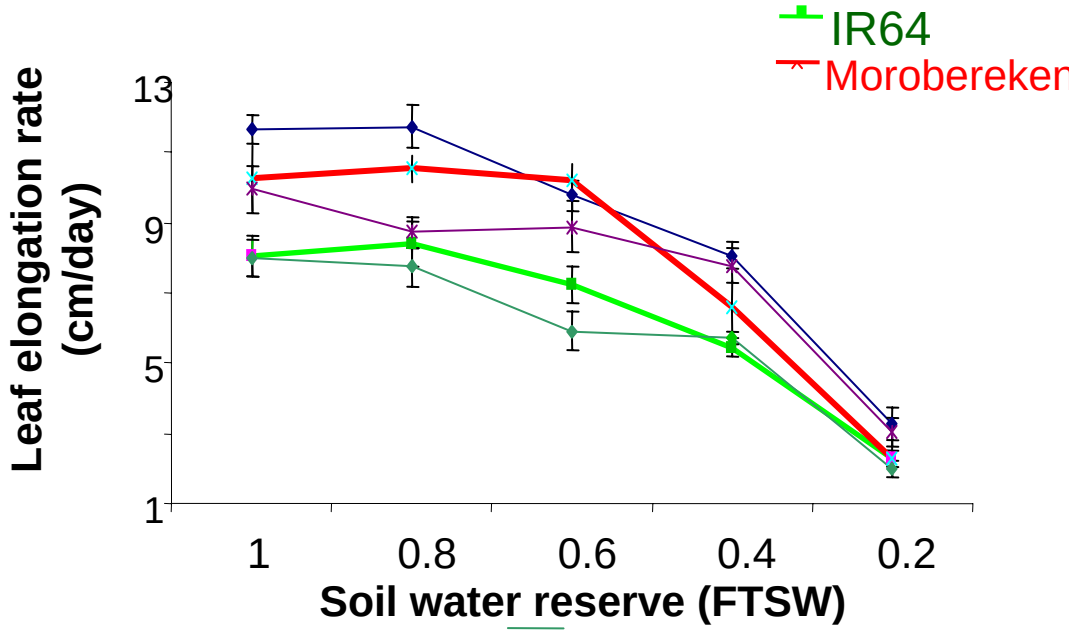
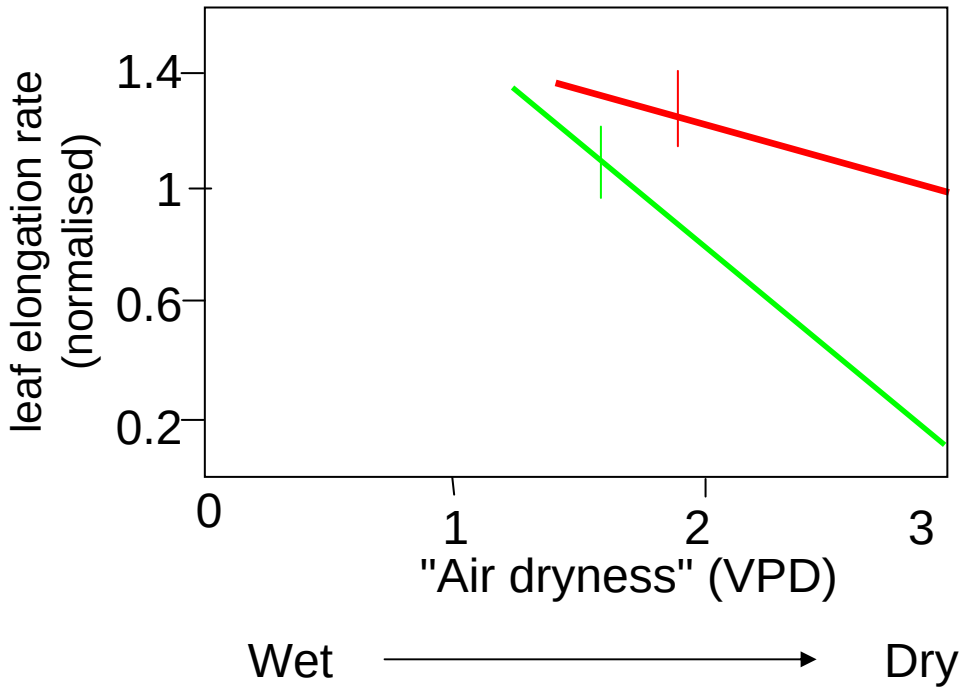


Example 1: rice
IRRI and INRA

Response to drought and to air humidity have a genetic variability among accessions



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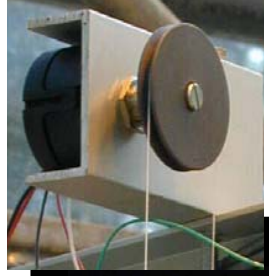

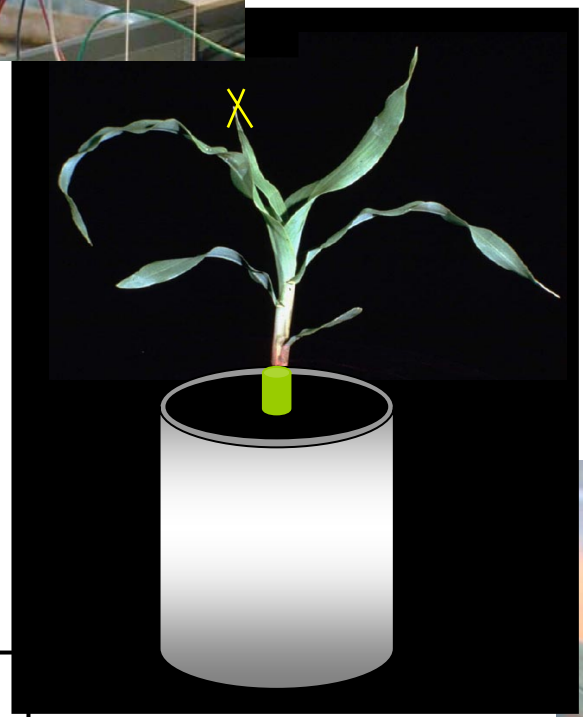

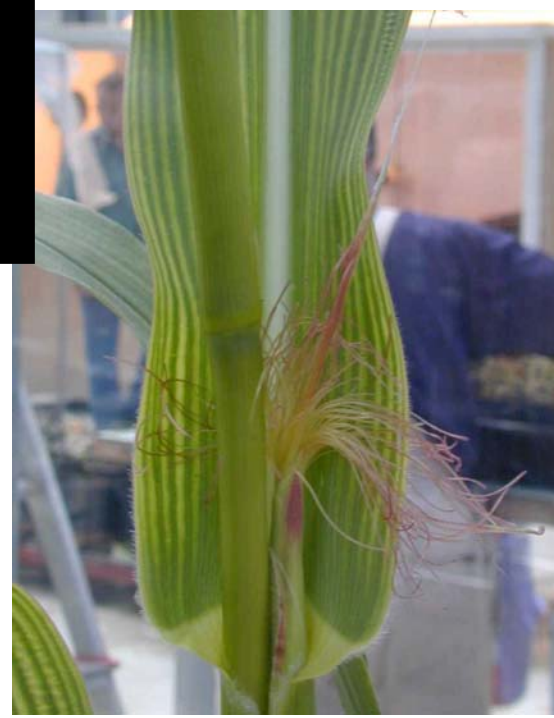

Example 2: Maize

Leaves and silks have a huge response to plant hydraulics (water transfer)

➔ candidate genes !

Experiments,
Modelling
Where ? When?
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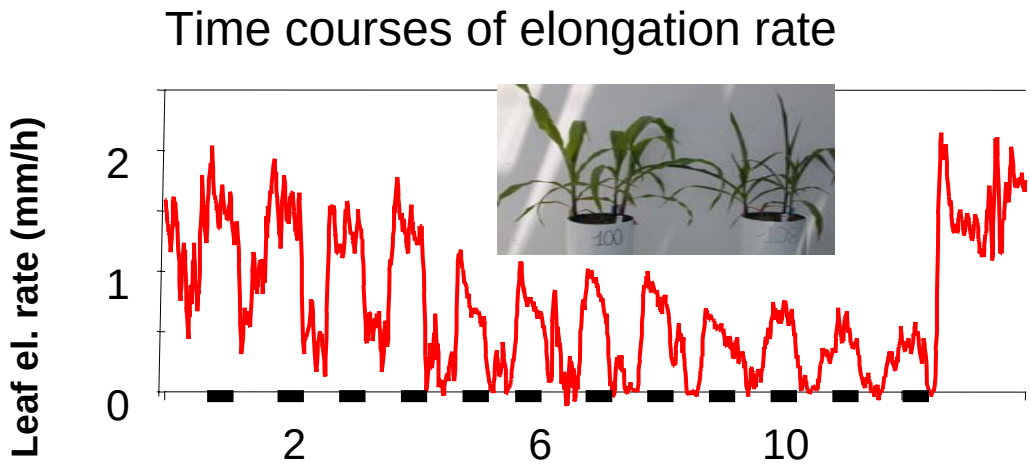
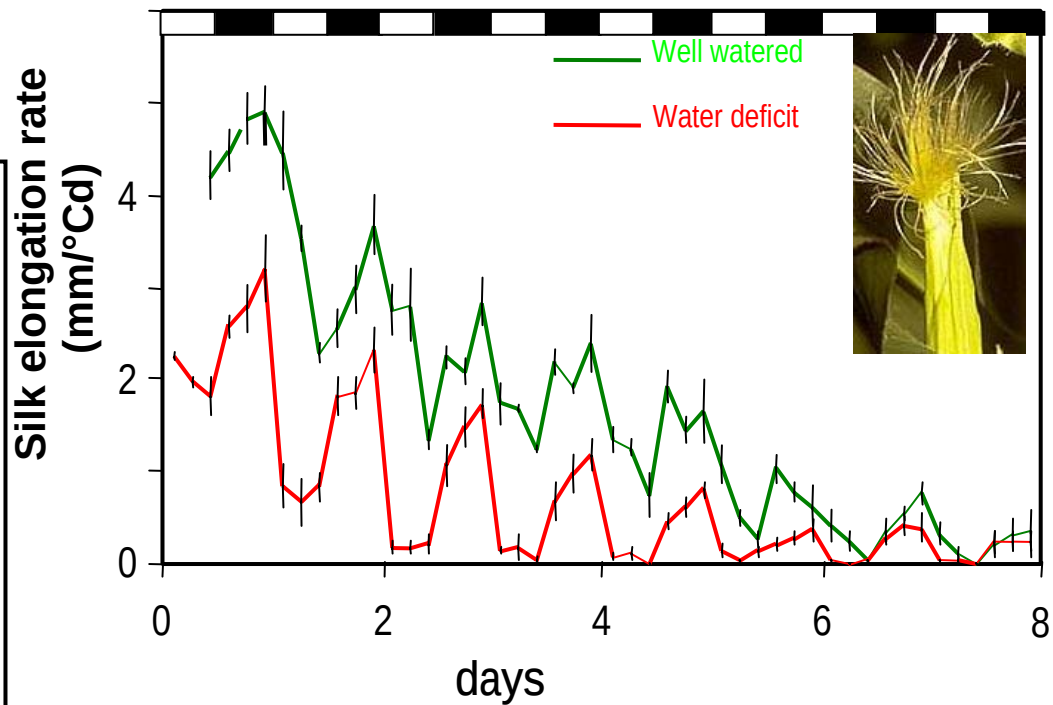
Responses ?





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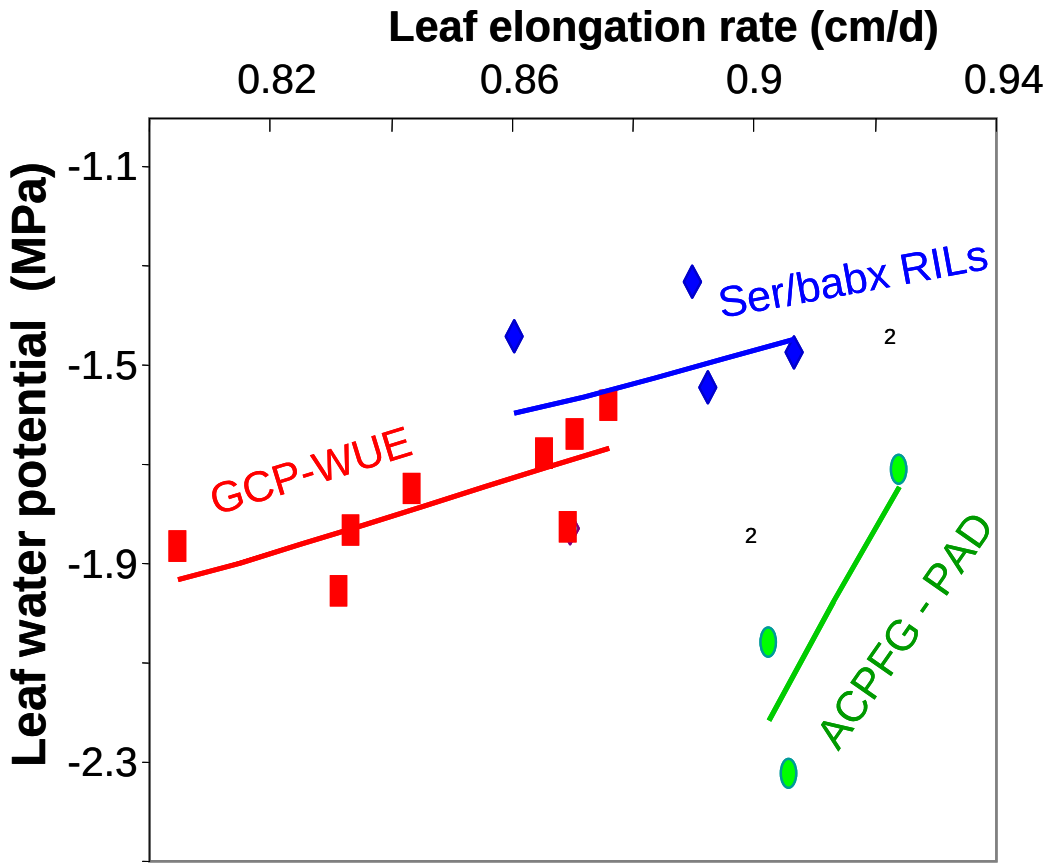


Example 3: Wheat
ACPFG and CIMMYT

In 3 populations, variability of elongation rate associated with that of leaf water status

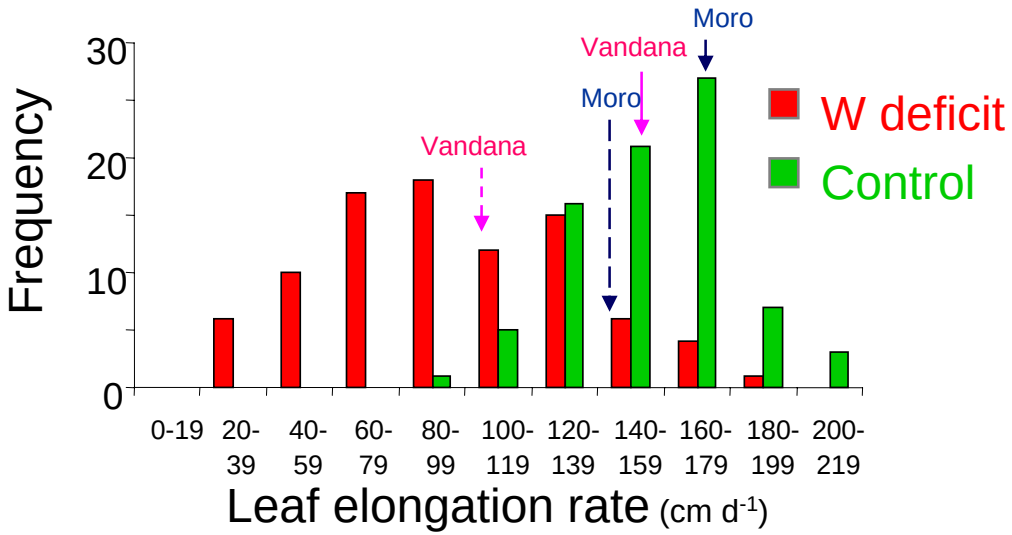
Experiments,
Modelling
Where ? When?
How much ?
Responses ?

Processes, pathways ➔ candidate genes :
Plant hydraulics is back

Experiments, Modelling → **Genetics** *which loci ? genetic differences ?* → Comparison organs, species → Processes genes

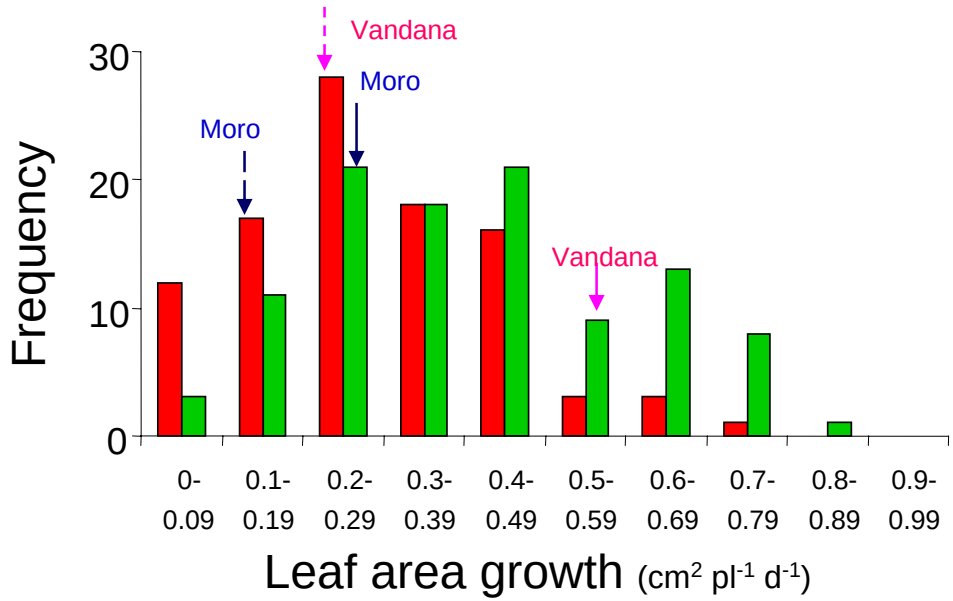
Example 1: Genetic analysis of a BC (rice) IRRI:

QTLs of leaf elongation rate



and

QTLs of leaf area in the field



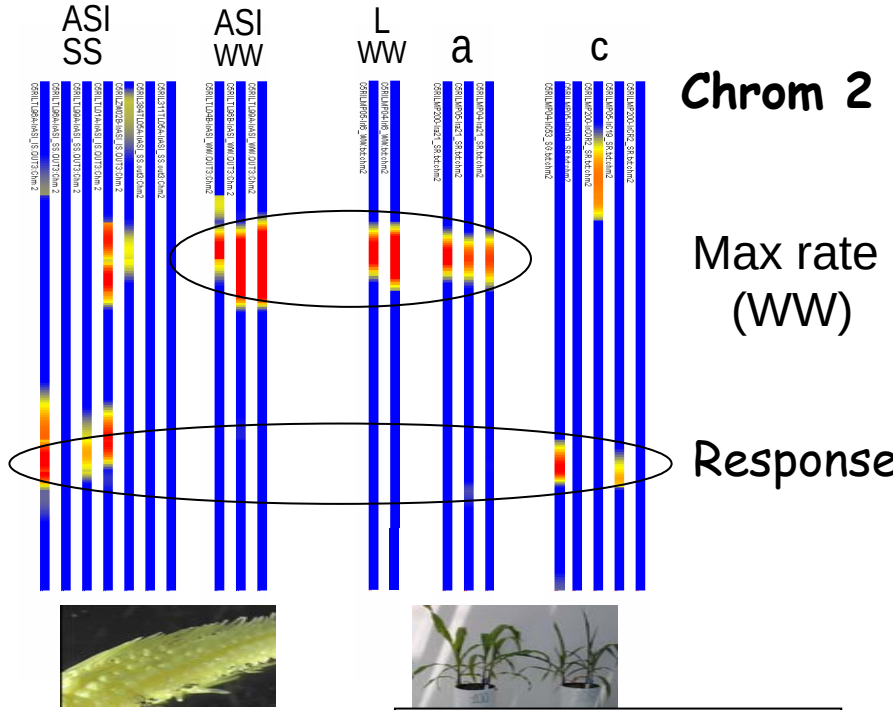
Experiments, Modelling → **Genetics** *which loci ? genetic differences ?* → Comparison organs, species → Processes genes

Example 2: Maize

INRA - CIMMYT

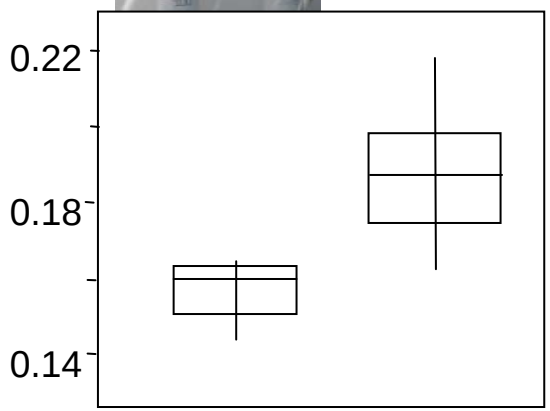
Half of QTLs in common leaf growth and silk growth (ASI)

- maximum rate
- responses to water deficit



Check in Insertion lines (Biogemma, Tuberosa) and BCA (INRA) :

max rate and responses

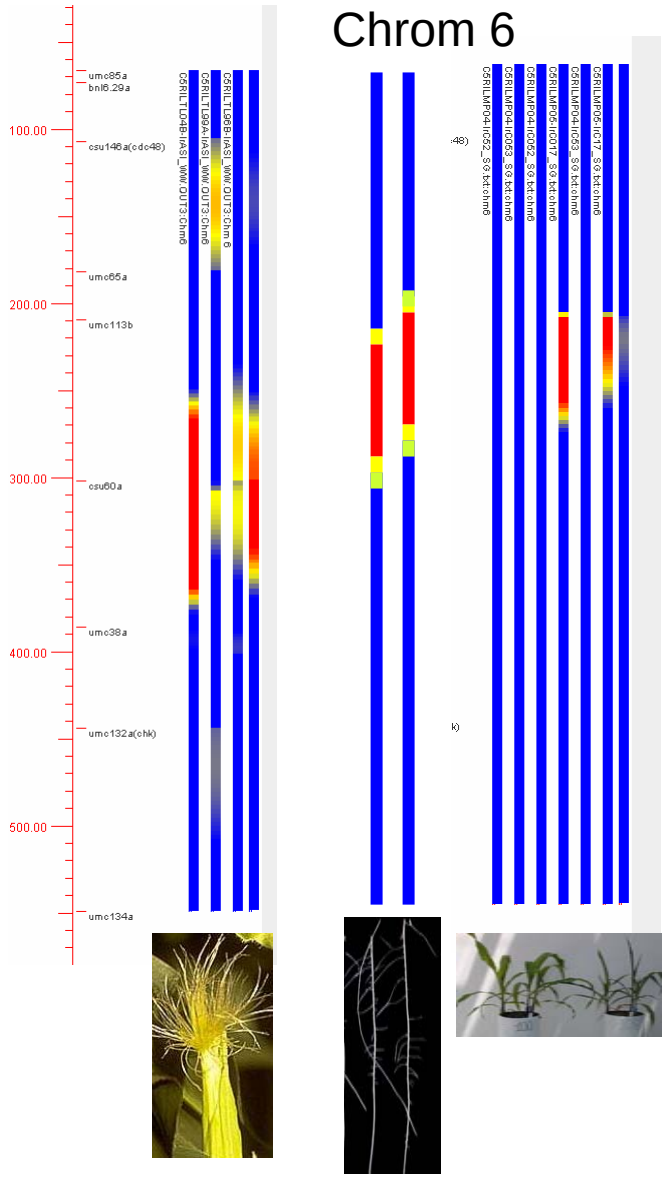


Experiments, Modelling → **Genetics** *which loci ? genetic differences ?* → Comparison organs, species → Processes genes

Example 2: Maize

ETH - INRA - CIMMYT

QTLs in common :
root growth and silk growth (ASI)
(and leaf growth)



ETH, QTLs of response of axile and lateral growth rates

Maize : roots, leaves, silks. 4 genotypes (+4), field and chambre

Rice : leaves, 4 genotypes, 3 treatments

Wheat : leaves and pedicels, 3 genotypes, 5 treatments

All material collected,
transcript analysis under way

Validation

Experiments, Modelling
Where ? When?
How much ?
Responses ?

Transcript
which genes
genetic differences ?

Genetics
which loci ?
genetic differences ?

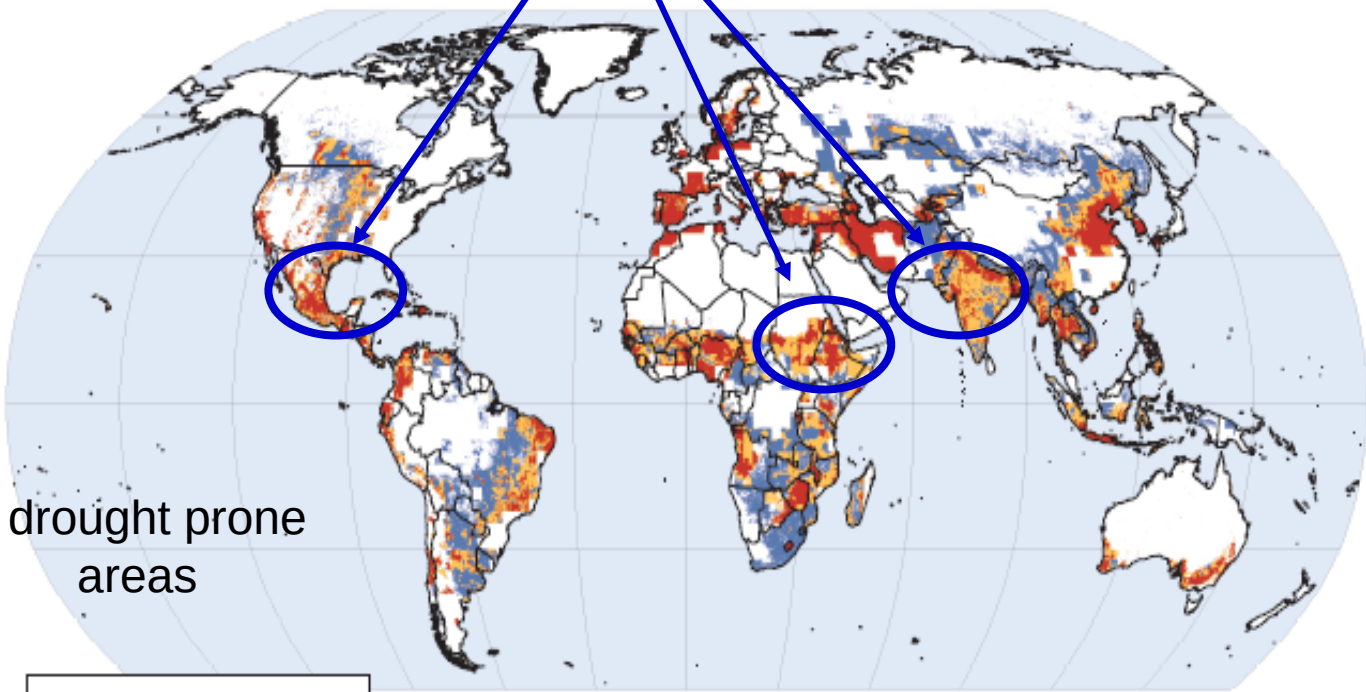
Comparison organs, species

Comparison organs, species

Processes genes

Whole plant modelling (project 19)

Field analyses
How QTLs translate into yield ?



In drought prone areas

Validation

Experiments, Modelling
Where ? When?
How much ?
Responses ?

Transcript
which genes
genetic differences ?

Genetics
which loci ?
genetic differences ?

Comparison organs, species

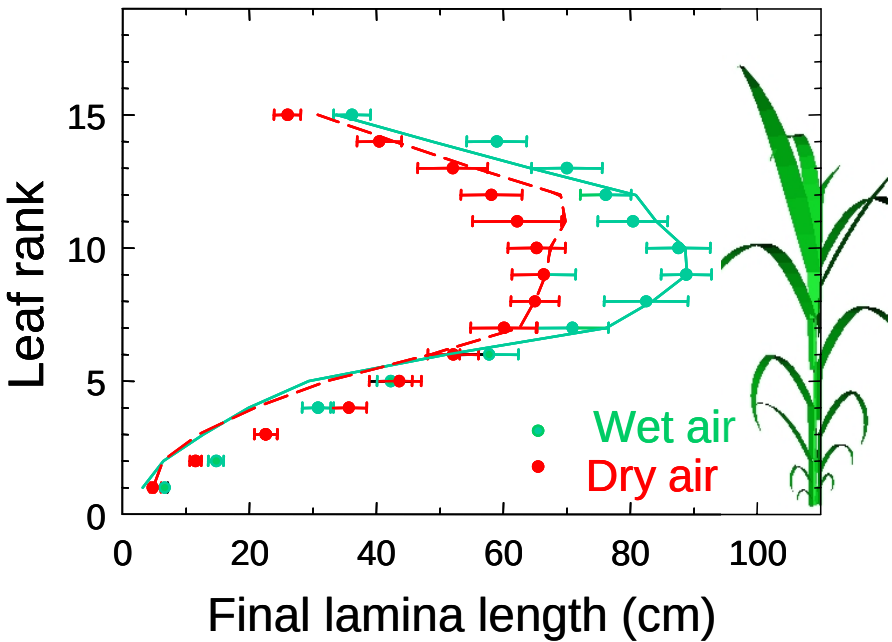
Comparison organs, species

Processes genes

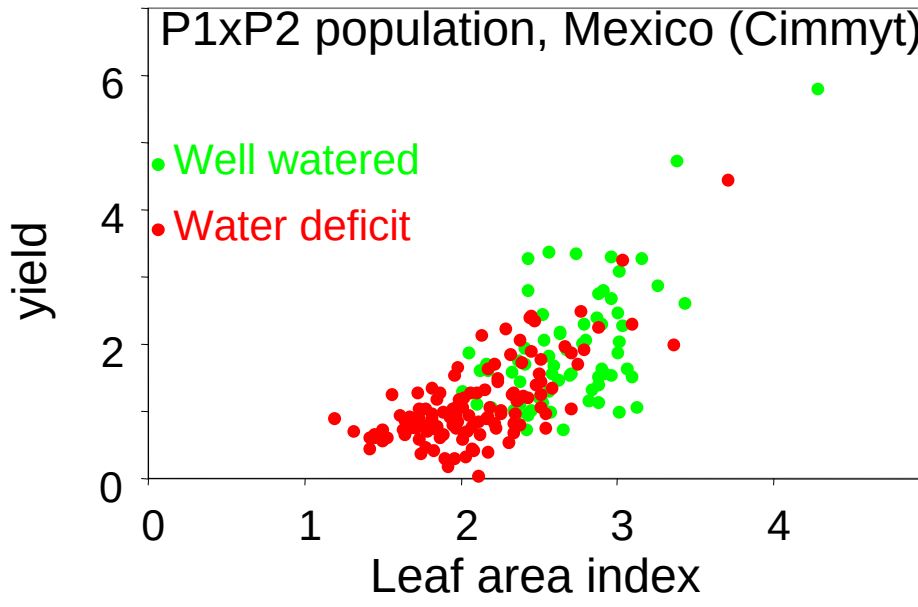
Whole plant modelling (project 19)

Field analyses
How QTLs translate into yield ?

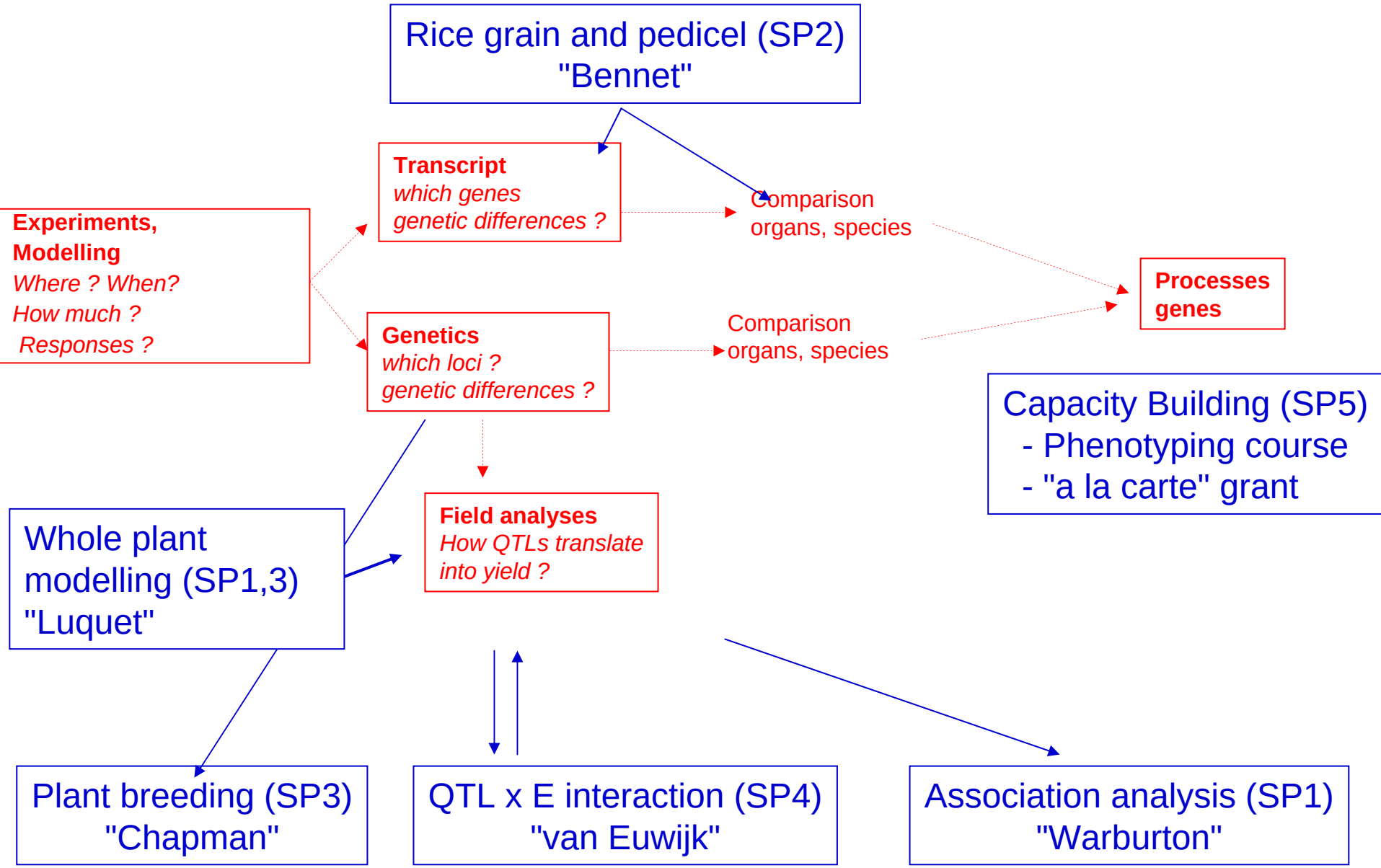
What do we expect ?
modelling leaf area (and QTLs)



What do get ?
Impact of leaf area on yield



Link with other projects



Product delivery and impact :

Deliverables will be delivered, but still work after for interpretations and checks

Nature		date
Methods models	when where sample ? involved pathways phenotyping technologies	2007
QTLs	Maize leaves silks roots Maize field rice leaves wheat leaves Modelling ; QTL x E	2007 2008 2008 2008 after
gene lists	maize leaves silks roots rice leaves wheat leaves	2008 2008 2008
pathways, positional analysis, checks gene effects (transgenics / association / IL)		2008 / after after