



WHOLE PLANT MODELLING PROJECT (WPM)

Whole plant physiology modelling for drought tolerance in cereals

Embrapa

**F. Duraes
A. Bryan Heinemann
C. Morais
F. Giacomini
E. Bastos
E. Gama**

Csiro

S. Chapman

UQ

G. Hammer

Agropolis Inra

F. Tardieu

C. Welcker

Agropolis Cirad

M. Dingkuhn

D. Luquet

JC. Combres

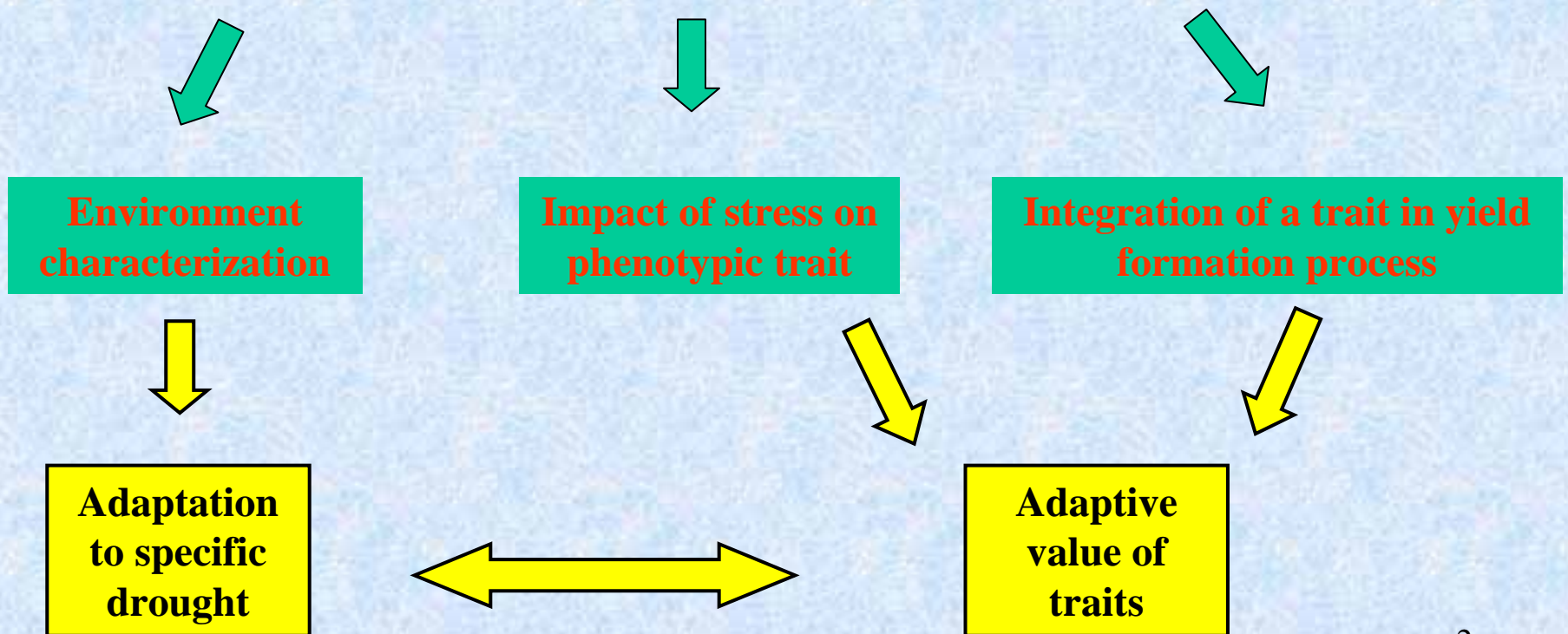
M. de Raïssac

***Generation Challenge Program
Rome, 29/09/05 – 01/10/05***



Background

- **Drought phenotyping workshop held in Montpellier (July 2004)**
 - Importance of modelling in phenotyping for drought





Whole Plant Modelling Project

Insertion in GCP



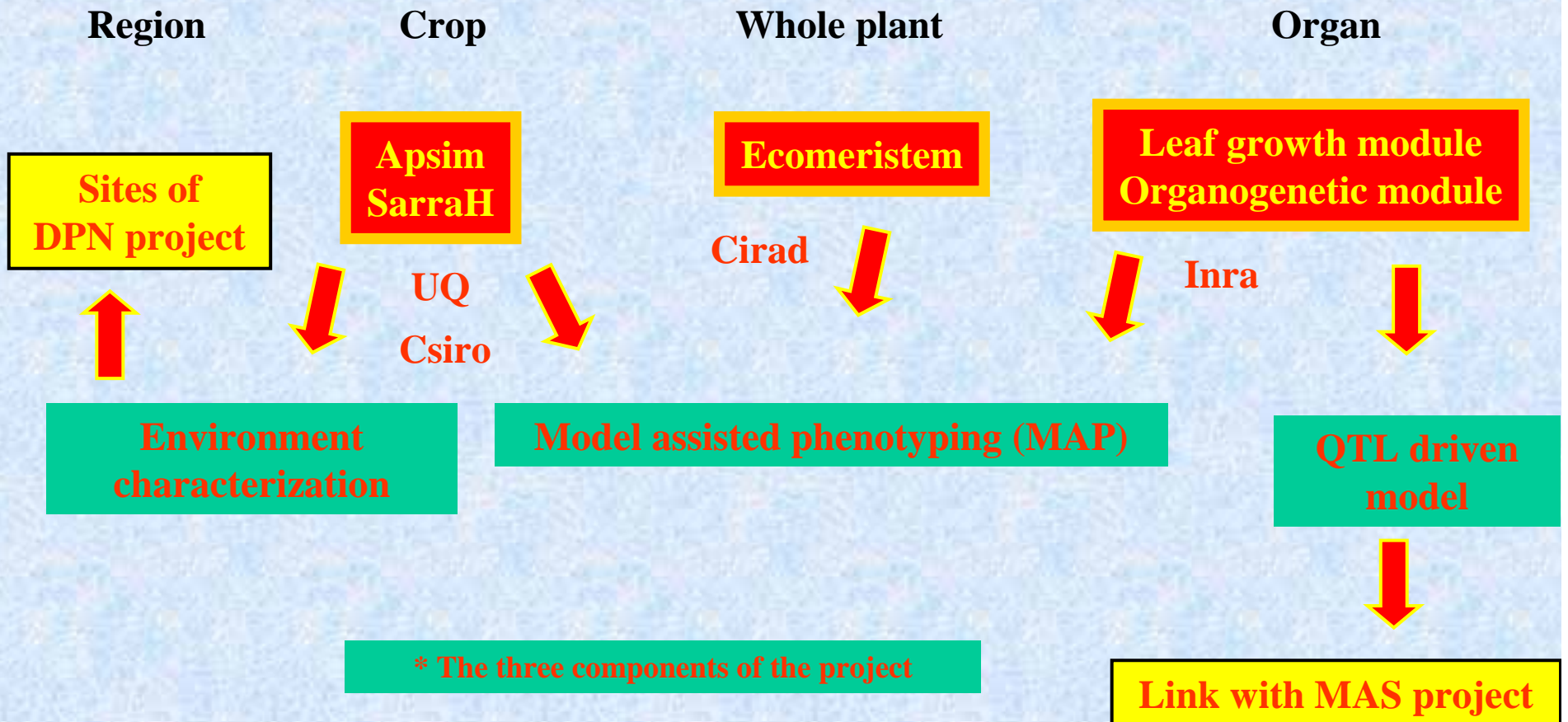
- **A balance between application and tool improvement**
 - Applying current models to support phenotyping for drought in real conditions of a breeding program : the Embrapa drought phenotyping network
 - **Maize, sorghum and upland rice**
 - Creating stronger links between breeders, physiologists and modellers
 - Improving whole plant models and modelling capacity in GCP
 - **Model driven by genetic information**

1. **Cereal crops**
2. **Drought types**
3. **Model Assisted Phenotyping**



Whole Plant Modelling Project

Models





Environment characterization by models

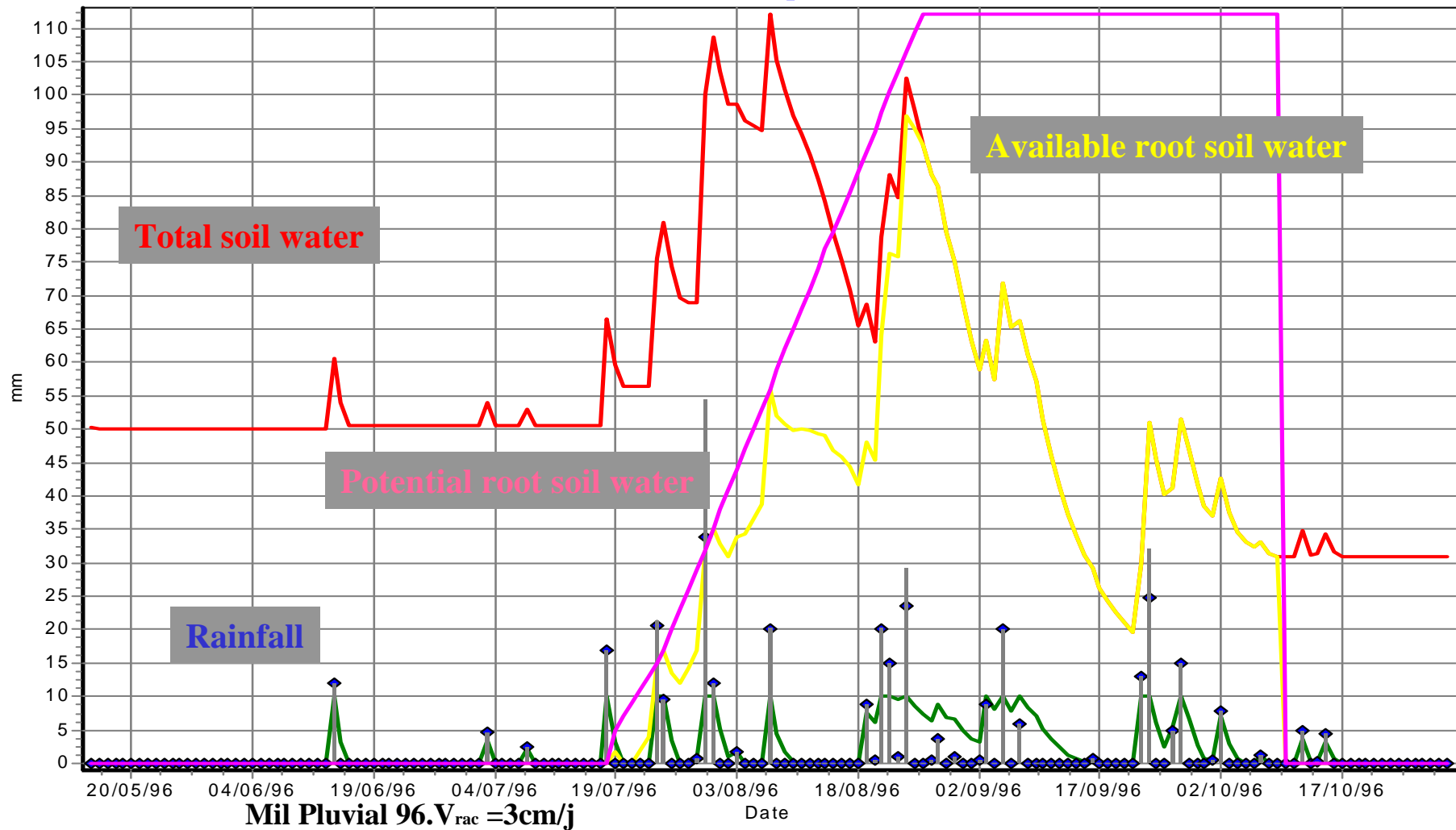
- **Objectives**
 - **To characterize, timing, duration and intensity of water stress in Embrapa sites of phenotyping, using crop models**
 - **To cluster at a regional level and to define TPE**



Environment characterization by models

SarraH outputs

Simulation effectuée avec la plateforme ECO-TRIP V3.0.1.1 - Modèle Mil V2 BHY



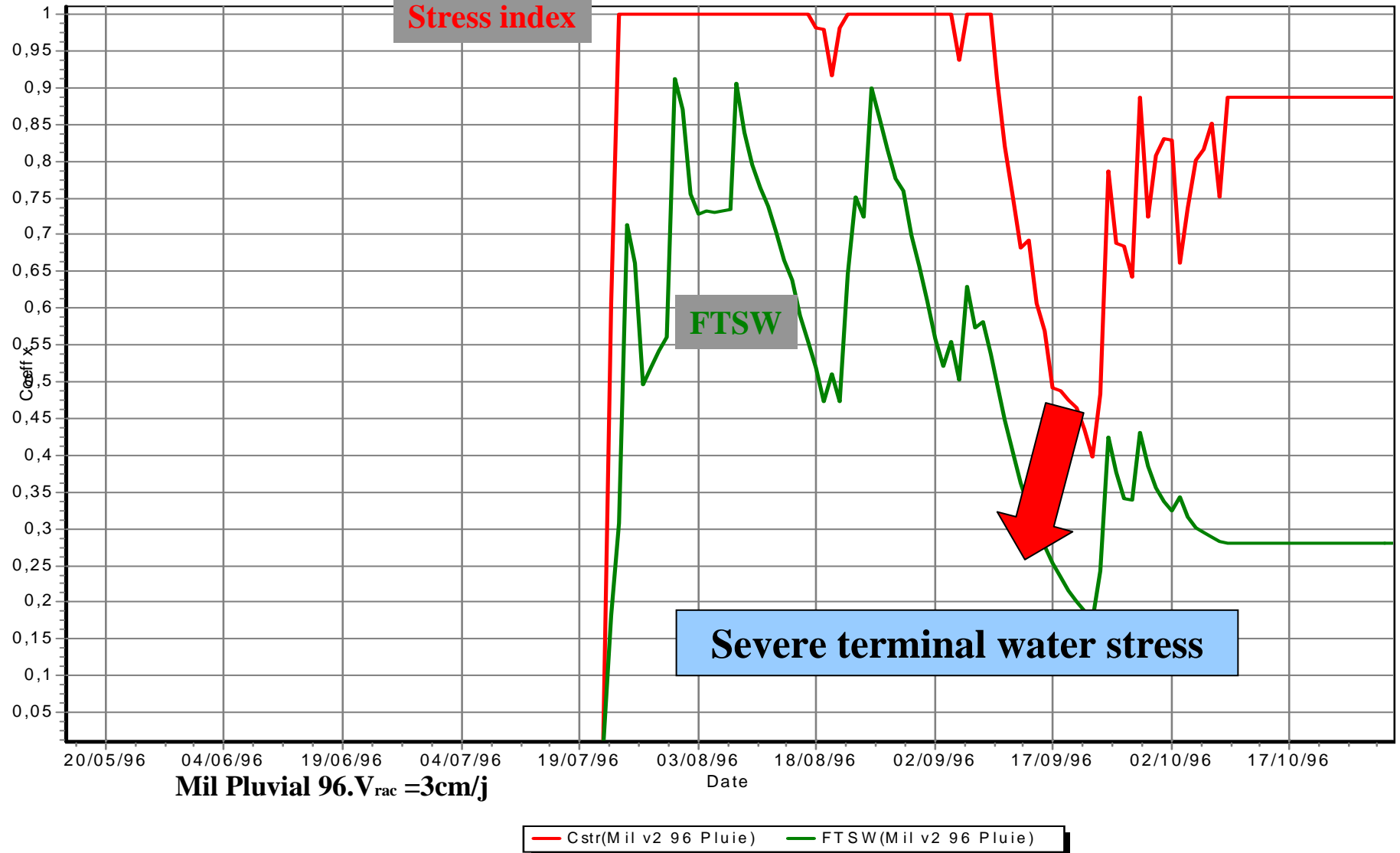
— StockTotal(Mil v2 96 Pluie) — StockSurface(Mil v2 96 Pluie) — StockRac(Mil v2 96 Pluie) ◆ EauDispo(Mil v2 96 Pluie)
■ Pluie(Mil v2 96 Pluie) — RURac(Mil v2 96 Pluie)



Environment characterization by models

SarraH outputs

Simulation effectuée avec la plateforme ECOTROP v3.0.1.1 - Modèle Mil V2 BHY

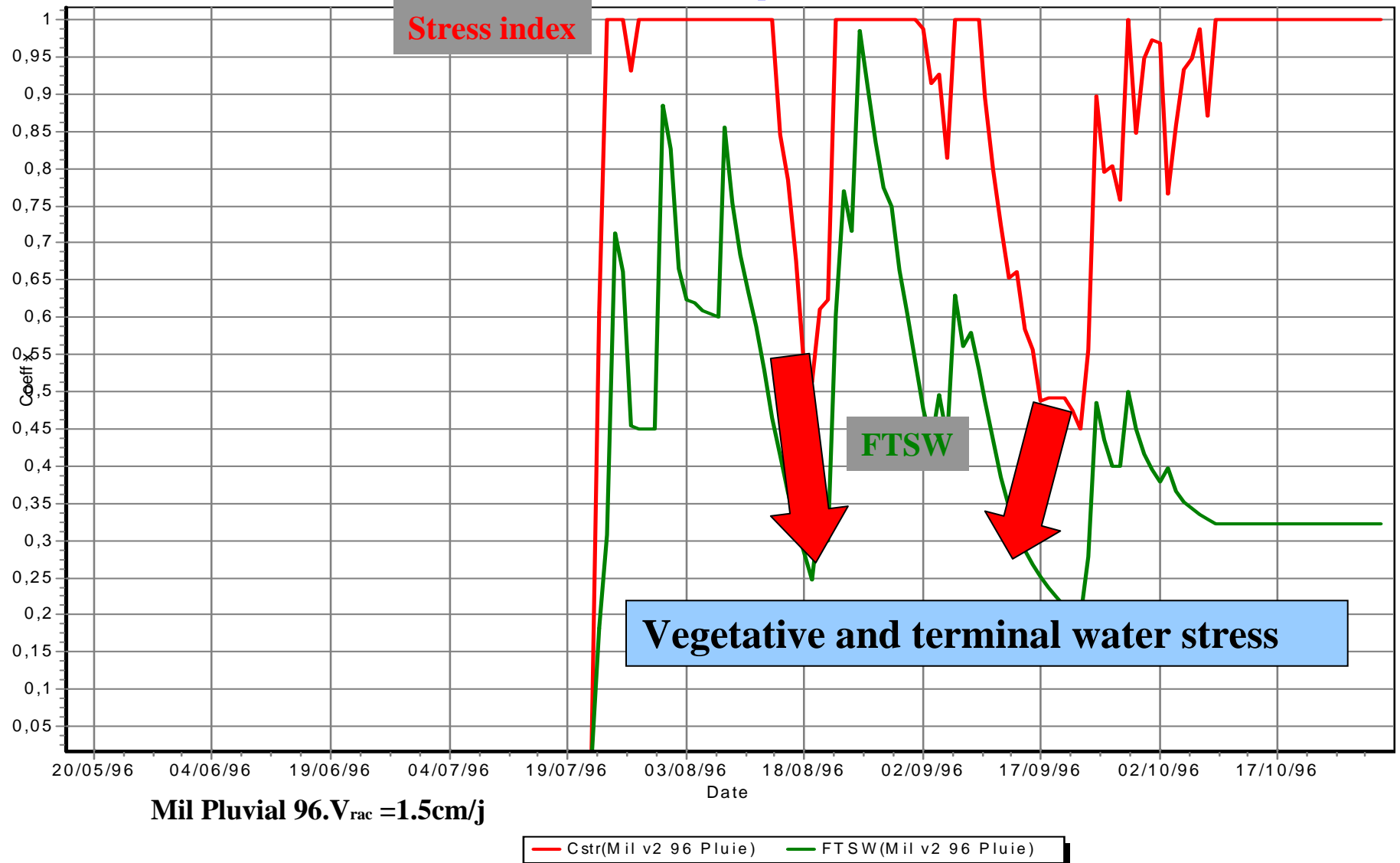




Environment characterization by models

SarraH outputs

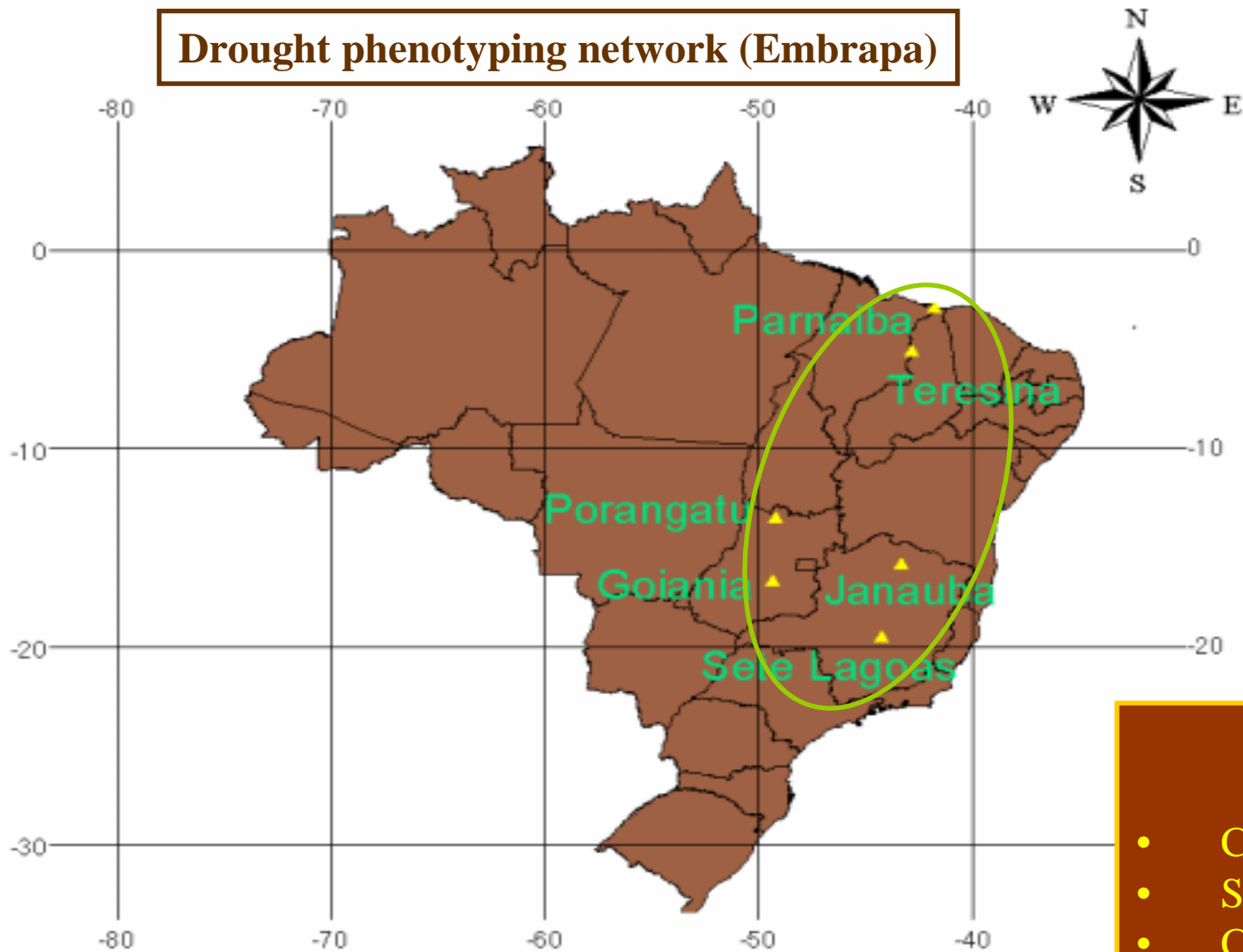
Simulation effectuée avec la plateforme ECO-POP V3.0.1.1 - Modèle Mil V2 BHY





Environment characterization by models

Drought phenotyping network (Embrapa)

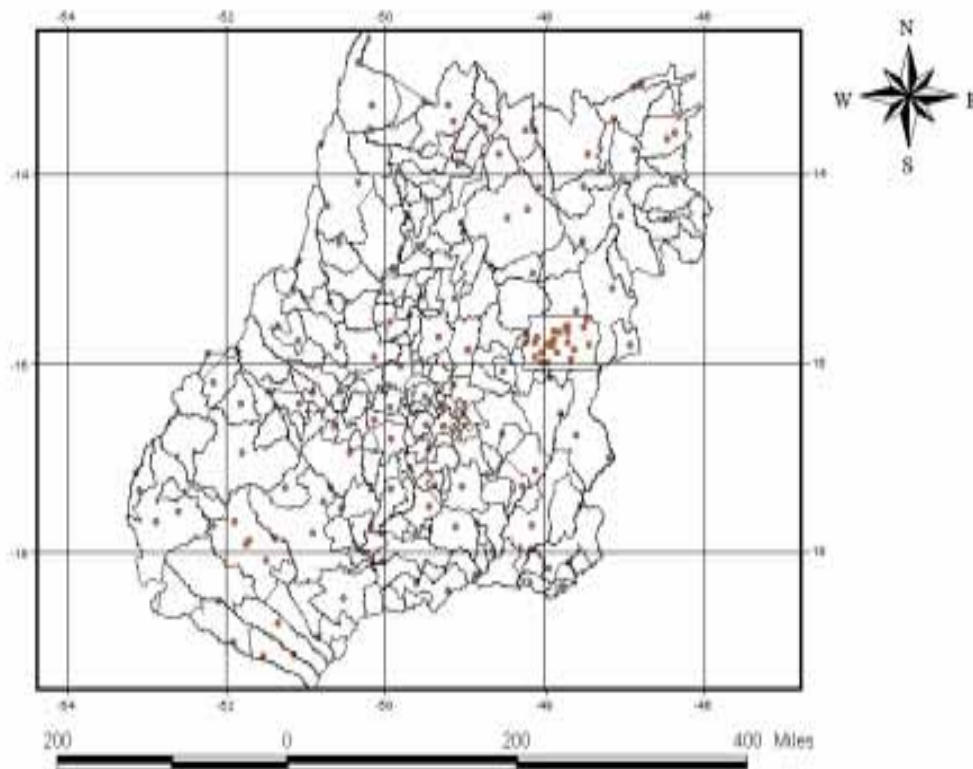


Data collection

- Climate
- Soil
- Crop



Environment characterization by models



Daily meteorological data

Goias

- Rainfall, 124 points >20 years
- Radiation, 26 points > 5 years
- Temperature, 14 points > 30 years

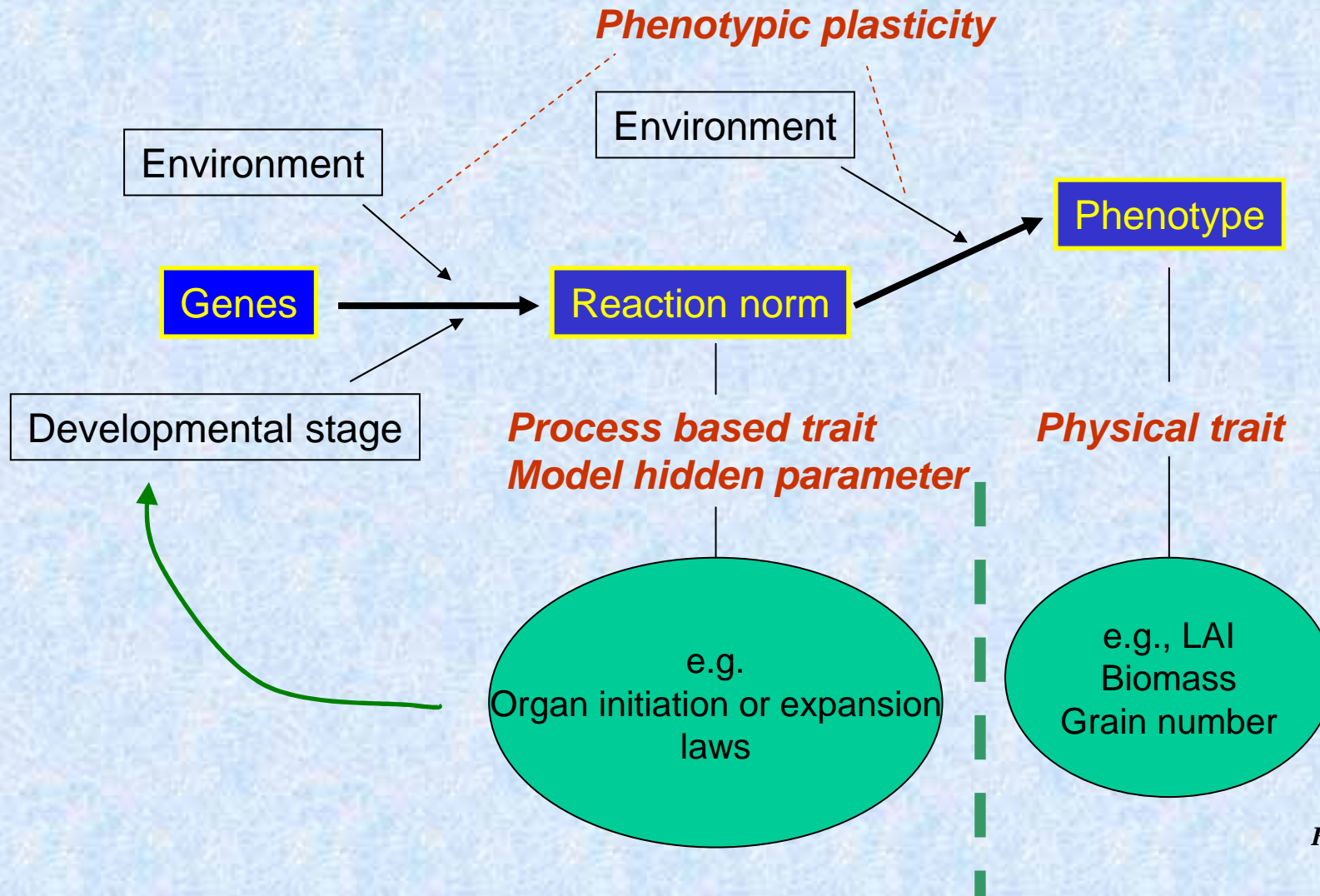
Data curation and
model running



Stress profiles
Clusters
TPE



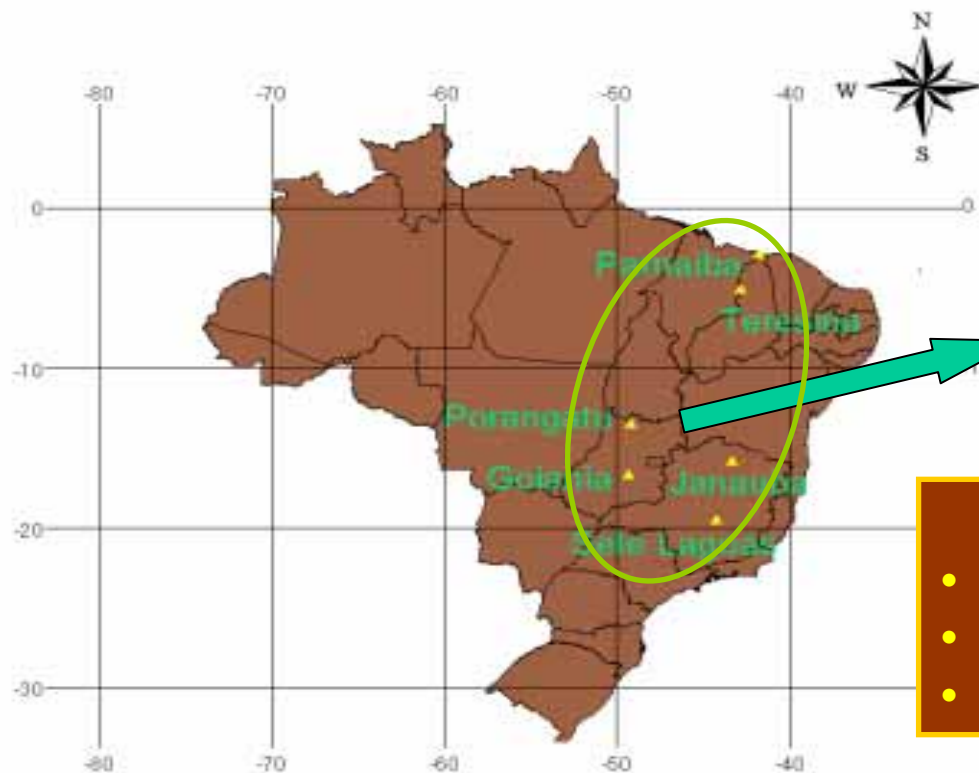
Model assisted phenotyping (MAP)



From M. Dingkuhn



Model assisted phenotyping (MAP)



- Crop x Genotype x site x season**
- Maize, sorghum, rice
 - 4 materials / crop
 - Dry and wet seasons experiments

Model

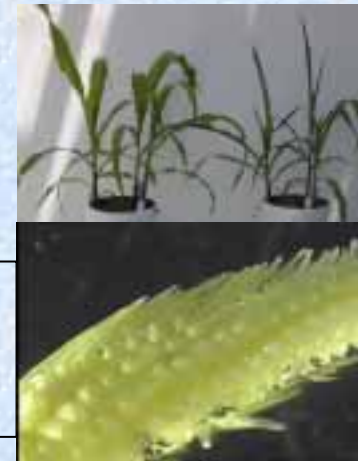
**Process based parameter estimation
Adaptive value assessment
Ideotype definition**

QTL driven Models

Maize case study

Process-based model of growth maintenance under water deficit

Established for leaves,
Common mechanisms with silks
(INRA - CIMMYT), "genes" project



- Can a QTL-driven model predict yields without G X E interaction ?
 - What are the contributions to yield of QTLs of growth maintenance of leaf and reproductive organs under different drought scenarios ?
- no QTL x E (valid in fields, and greenhouse) (INRA)

$$LER = ((T - T_p) \cdot (a - b \cdot VPD - c \cdot [-\Psi_{soil}]))$$

$$a = \bar{a} + \sum_i \alpha_i QTL_i$$

$$b = \bar{b} + \sum_i \beta_i QTL_i$$

$$c = \bar{c} + \sum_k \chi_k QTL_k$$

- Combination of LER QTL driven model and crop model (APSIM, Queensland)
- Test on CIMMYT data
- Simulation of the contribution of QTLs to yields
 - if leaves and silks are independent traits (pyramiding necessary),
 - if they are genetically linked.

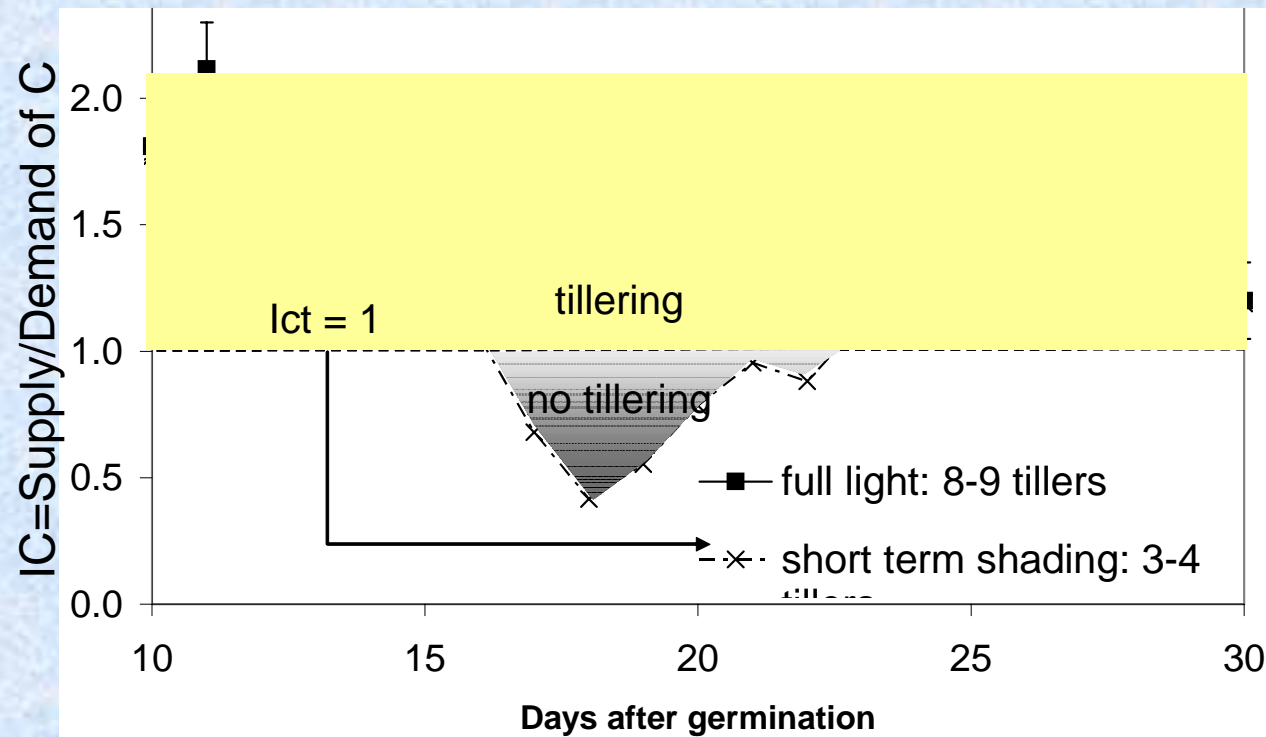


QTL driven Models

Rice case study

Linking process based model parameters to rice QTLs (water stress)

Genotypic tillering potential as an Ecomeristem parameter (ICt)



-IR 64
-Field and controlled experiments (CIRAD, IRRI)
-Same critical IC

-ICt genotype dependant
Dingkuhn and al, 2005,AJAR

2006: Ict (& other process-based parameters) used for QTL detection (water stress) for IR64 X Azucena mapping population...



Conclusions

- **Some main challenges taken up :**
 - Improvement of phenotyping methodology
MAP concept
 - Better interaction between breeders, physiologists and modellers
multidisciplinary approaches
 - Progress in genetic driven modelling
physiological models including QTLs information
 - Extension of this “proof of concept” project to other crops (legumes and tubers) and regions
Final workshop in May 2007