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Queensland Alliance for Agriculture & Food Innovation

Phenotyping transpiration efficiency: Linking trait dissection to genetics

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Working together with the Queensland Government
Queensland Government

Outline

- What is Transpiration Efficiency (TE) and why it is important.
- Set up of phenotyping platform.
- Role of phenotyping within integrated approach to crop improvement.
- Concluding remarks.

What is Transpiration Efficiency (TE)?

$$TE = \frac{Biomass}{Transpiration}$$

$$TE = \frac{A}{gs}$$

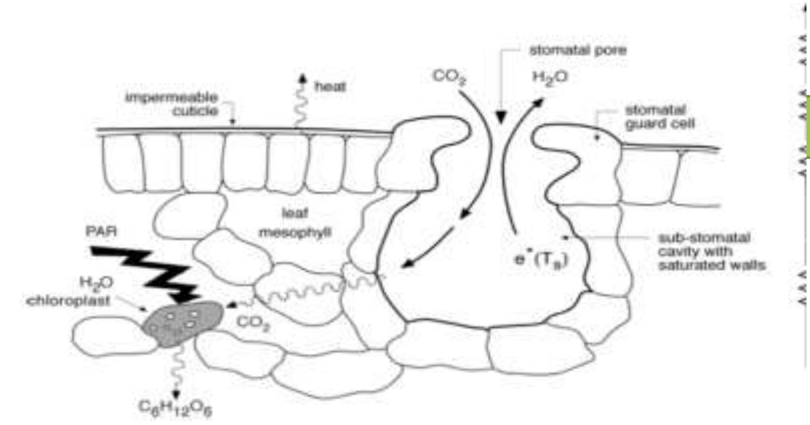
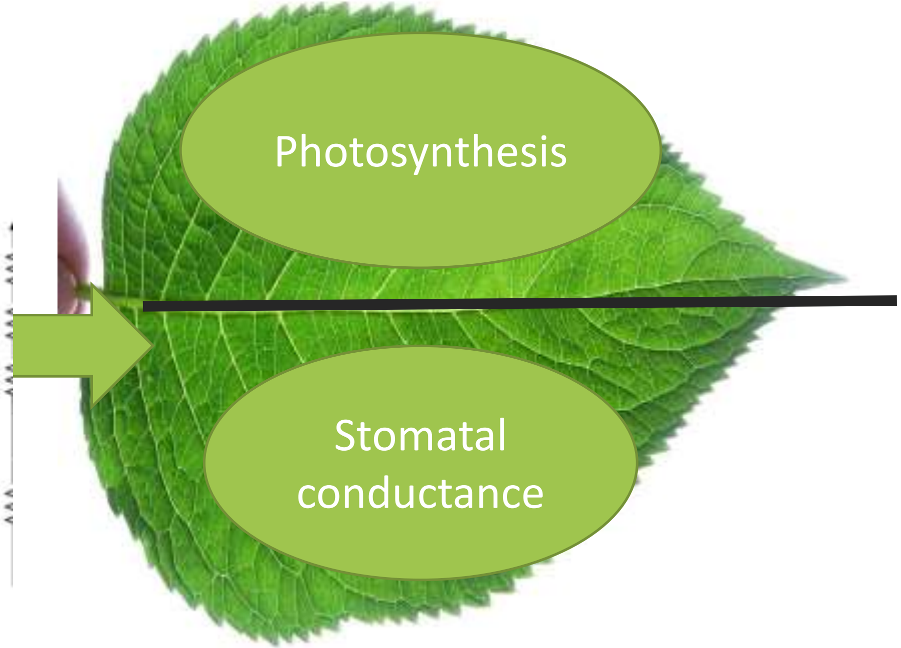


Figure 10. Schematic of a cross-section of a leaf. The resistance not defined in the text is the mesophyll resis



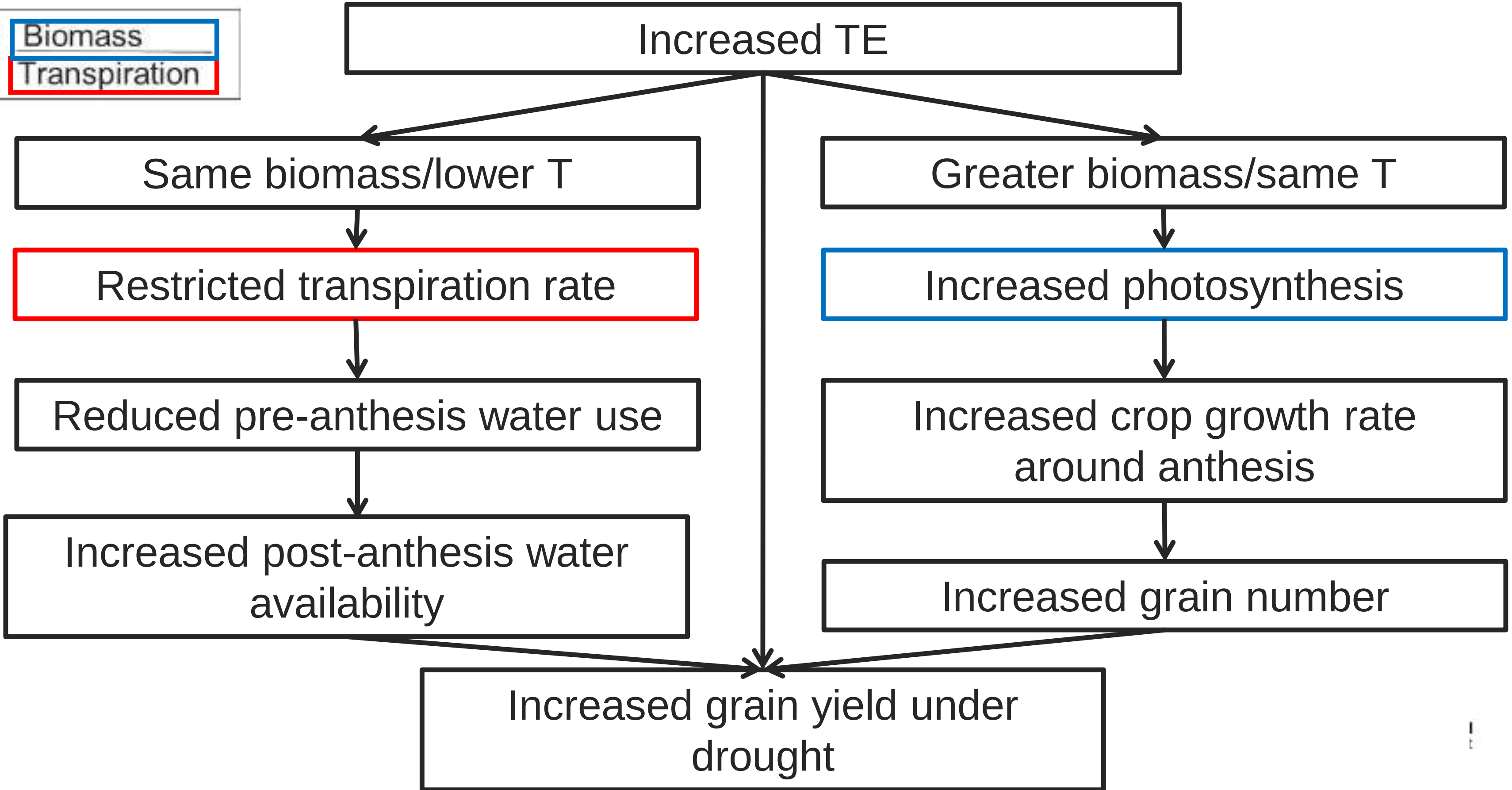
Photosynthesis

Stomatal conductance

Importance of TE

$$TE = \frac{\text{Photosynthesis}}{\text{Conductance}}$$

$$TE = \frac{\text{Biomass}}{\text{Transpiration}}$$



Increased TE

Same biomass/lower T

Restricted transpiration rate

Reduced pre-anthesis water use

Increased post-anthesis water availability

Greater biomass/same T

Increased photosynthesis

Increased crop growth rate around anthesis

Increased grain number

Increased grain yield under drought

Set up of phenotyping platform

Large lysimeters

- **Pot size**: 50+ L.
- **Capacity**: 128 lysimeters.
- **Harvest**: anthesis (maturity).
- **Use**: Detailed trait studies on TE and its components.

Set up of phenotyping platform

Small lysimeters

- **Pot size**: 4 L.
- **Capacity**: 560 lysimeters.
- **Harvest**: mid-vegetative.
- **Use**: High throughput phenotyping for TE.

- Each lysimeter is located on a load cell.
- Weights are recorded ever 10 minutes.
- Rewatering of each lysimeter is fully automated.

Set up of phenotyping platform

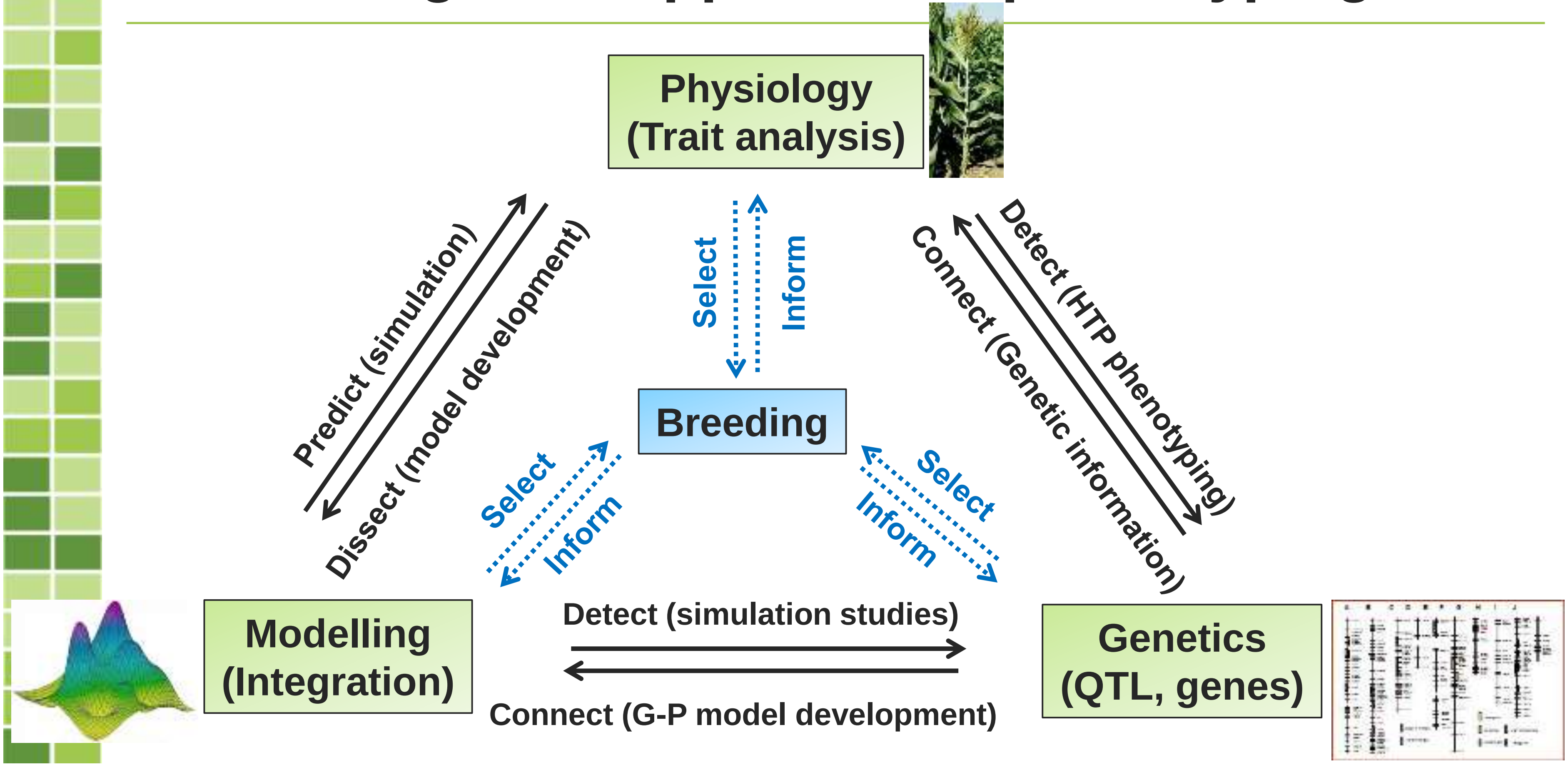
Transpiration during day

No transpiration at night

Watering event

- **Real time weights of individual lysimeters.**
- **Change in weight and amount of water added allow calculation of water use.**

Integrated approach to phenotyping



Physiology
(Trait analysis)

Select

Inform

Predict (simulation)

Dissect (model development)

Detect (HTP phenotyping)

Connect (Genetic information)

Breeding

Select

Inform

Select

Inform

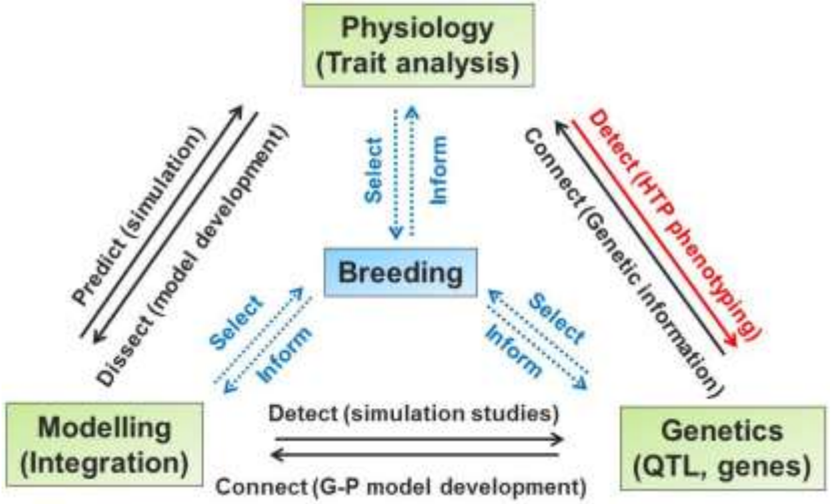
Modelling
(Integration)

Detect (simulation studies)

Connect (G-P model development)

Genetics
(QTL, genes)

Physiology to Genetics - Detect



Physiology (Trait analysis)

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Inform

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Modelling (Integration)

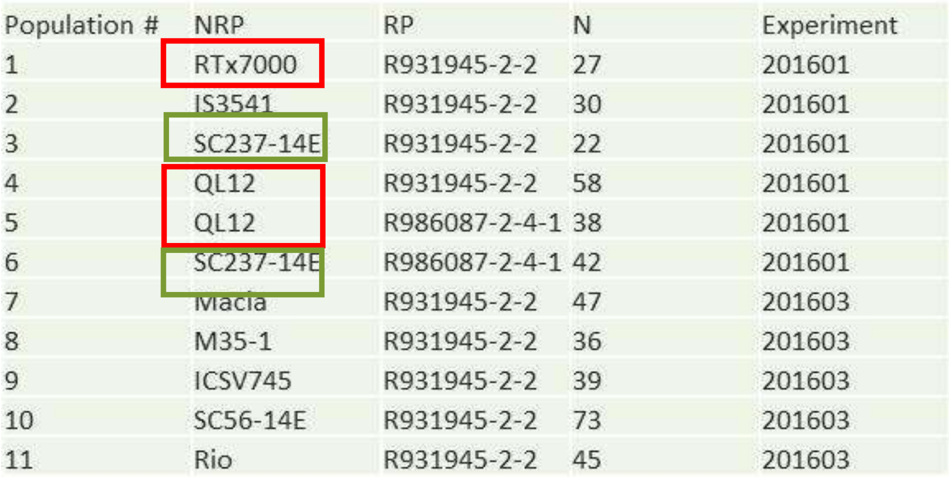
Detect (simulation studies)

Connect (G-P model development)

Genetics (QTL, genes)

- **Approach**: **High throughput phenotyping of mapping populations to detect QTL for TE.**
- **Platform**: **Small lysimeters**

Physiology to Genetics - Detect



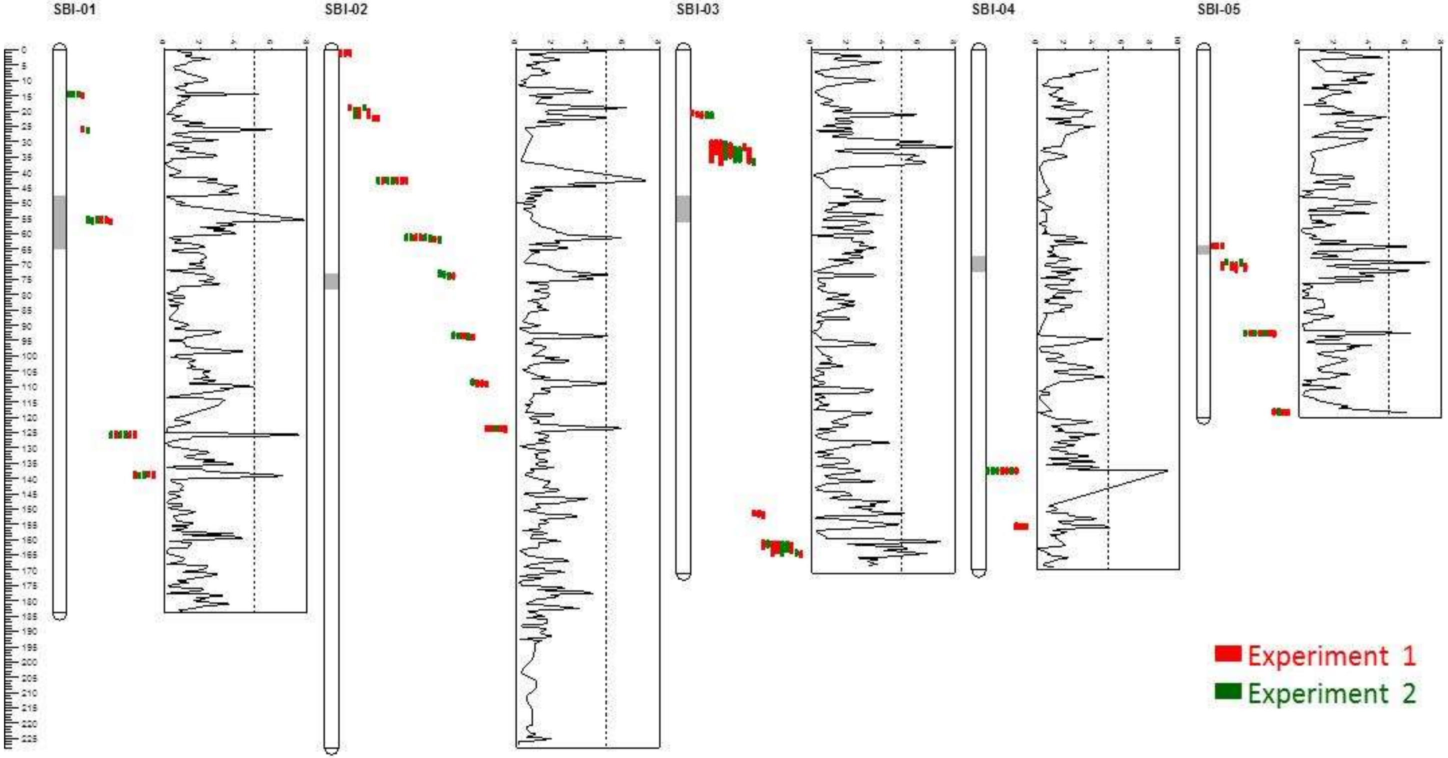
Population #	NRP	RP	N	Experiment
1	RTx7000	R931945-2-2	27	201601
2	IS3541	R931945-2-2	30	201601
3	SC237-14E	R931945-2-2	22	201601
4	QL12	R931945-2-2	58	201601
5	QL12	R986087-2-4-1	38	201601
6	SC237-14E	R986087-2-4-1	42	201601
7	Macia	R931945-2-2	47	201603
8	M35-1	R931945-2-2	36	201603
9	ICSV745	R931945-2-2	39	201603
10	SC56-14E	R931945-2-2	73	201603
11	Rio	R931945-2-2	45	201603

🟥	**Low TE**
🟩	**High TE**

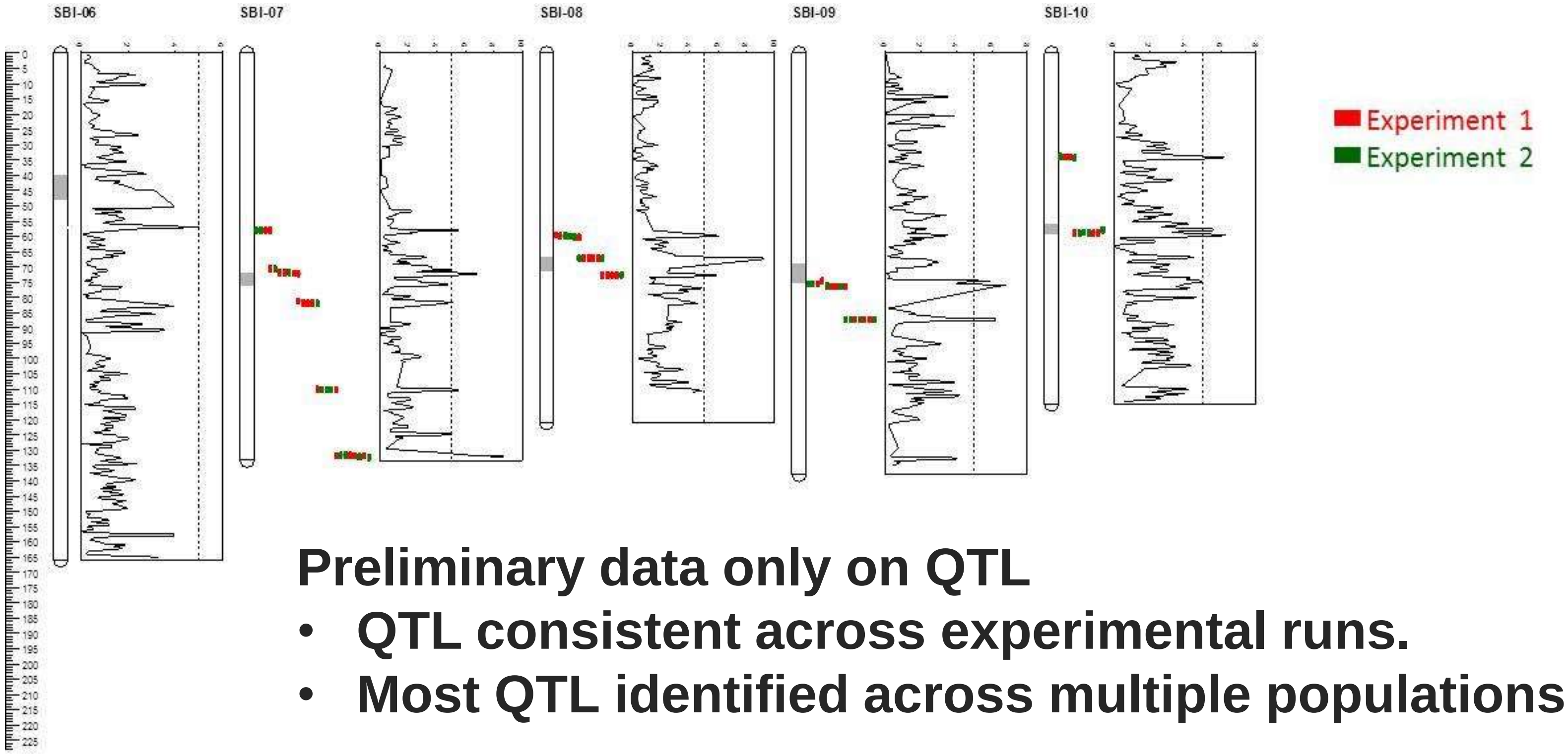
Subset of 11 NAM populations based on 9 exotic non recurrent parents (and 2 elite recurrent parents)

- **457 individuals in total.**
- **217 in experiment 1 (201601).**
- **240 in experiment 2 (201603).**

Physiology to Genetics - Detect



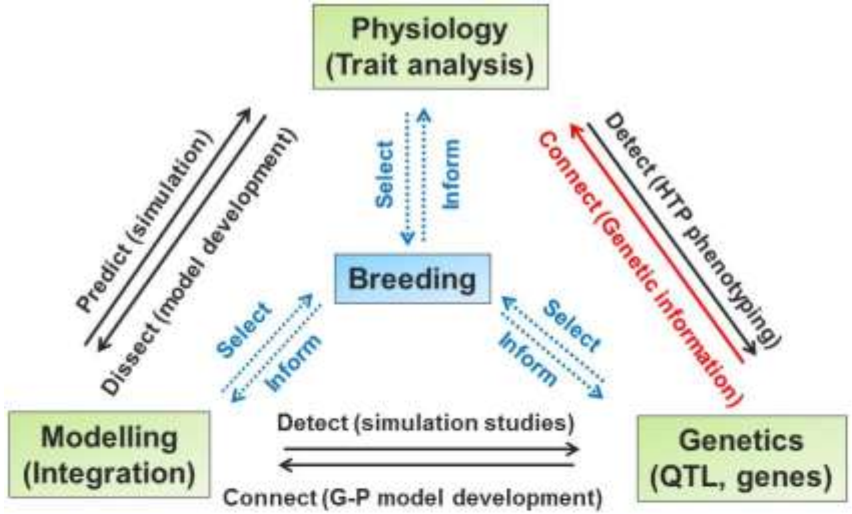
Physiology to Genetics - Detect



Preliminary data only on QTL

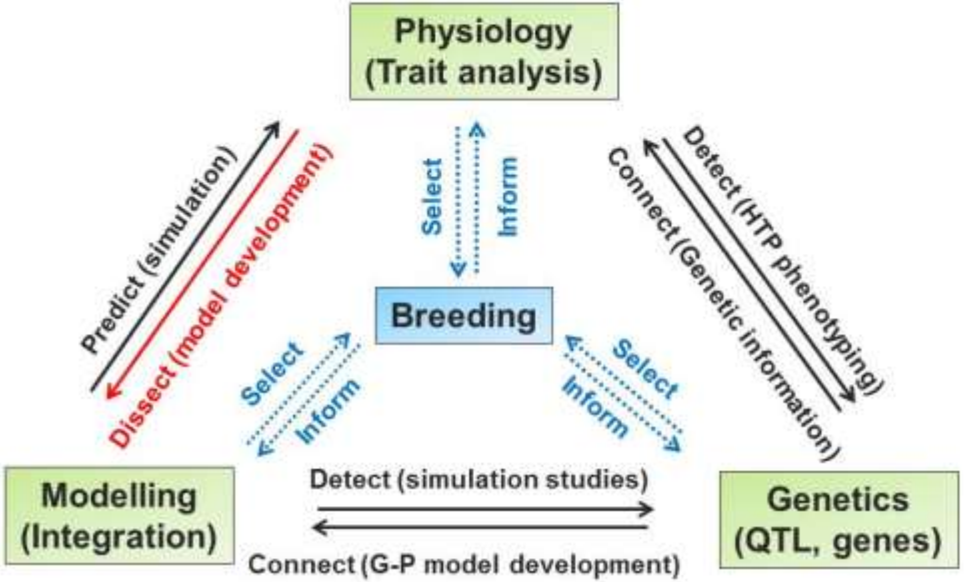
- **QTL consistent across experimental runs.**
- **Most QTL identified across multiple populations.**

Genetics to Physiology - Connect



Germplasm with contrasting alleles for TE QTL can be selected for detailed trait studies to determine the function of these QTL (eg. photosynthesis, transpiration).

Physiology to Modelling – dissect



Trait dissection studies:

- **Approach:** identify physiological processes that underpin genotypic differences in TE.
- **Application:** Science from trait dissection provides simulation models with biological functionality.
- **Platform:** Large lysimeters.

Physiology to Modelling – dissect

Can trait dissection meet the requirements for model development:

- **Relationships need to be generic.**
    - **allows robust parameterisation.**
- **Plant-level data need to be representative of leaf-level data.**
    - **allows connection across levels of biological organisation.**
- **Trait dissection needs to capture genotypic differences in the complex trait (TE).**
    - **dynamic models simulate complex traits as an emergent consequence of component traits.**

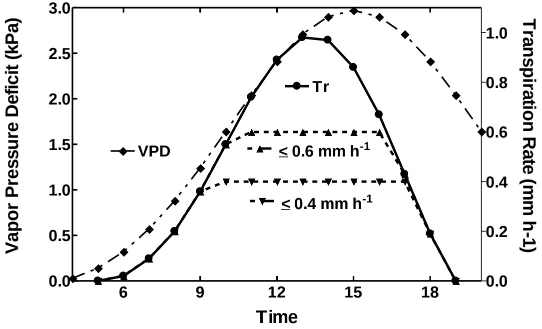
Example: transpiration rates.

$$TE = \frac{\text{Biomass}}{\text{Transpiration}}$$

Physiology to Modelling – dissect

$$TE = \frac{\text{Biomass}}{\text{Transpiration}}$$

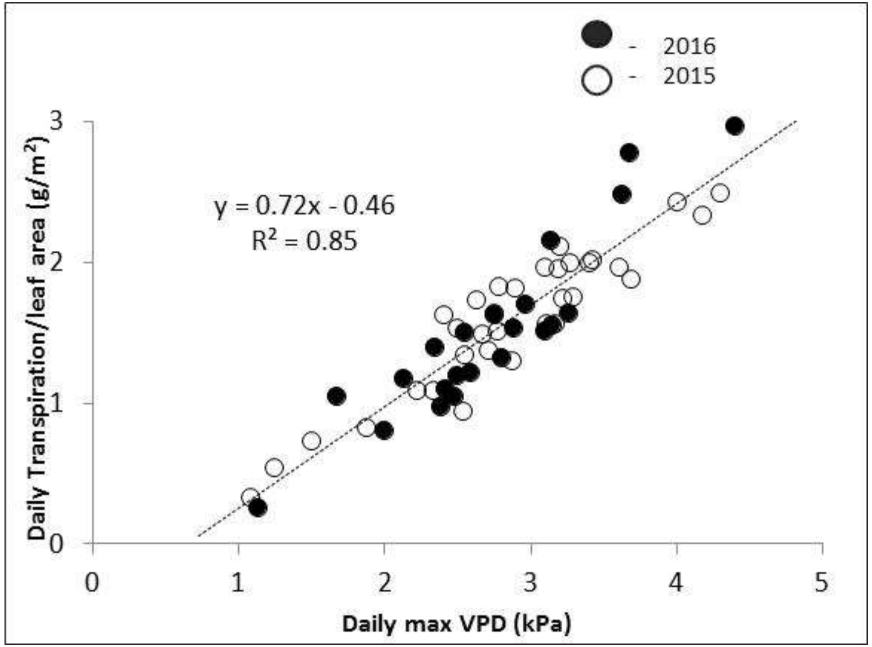
Are results sufficiently generic to parameterise crop models?
Example: response of transpiration to environmental conditions



Response of transpiration rates to VPD is consistent :

- **across experiments.**
- **across days within experiments.**

→Results are generic.



Physiology to Modelling – dissect

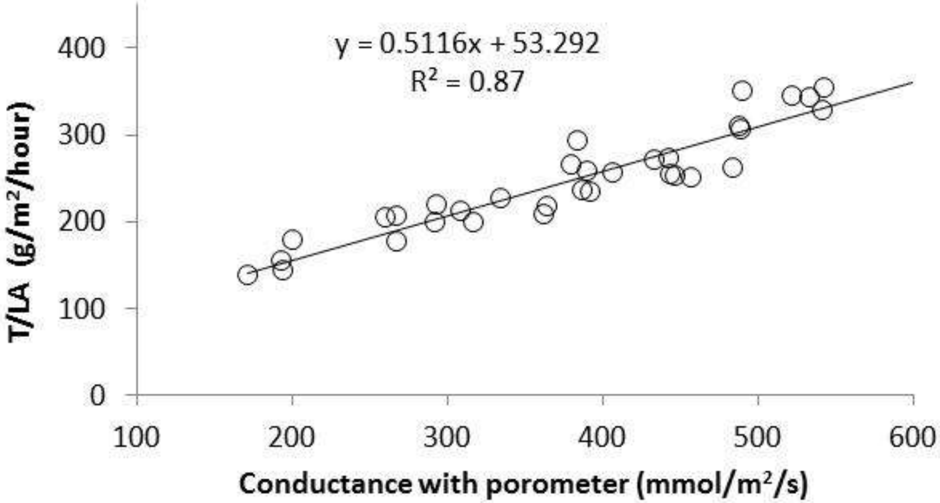
Are plant-level data representative of leaf-level data?
Example: transpiration-conductance

plant

$$TE = \frac{\text{Biomass}}{\text{Transpiration}}$$

leaf

$$TE = \frac{\text{Photosynthesis}}{\text{Conductance}}$$

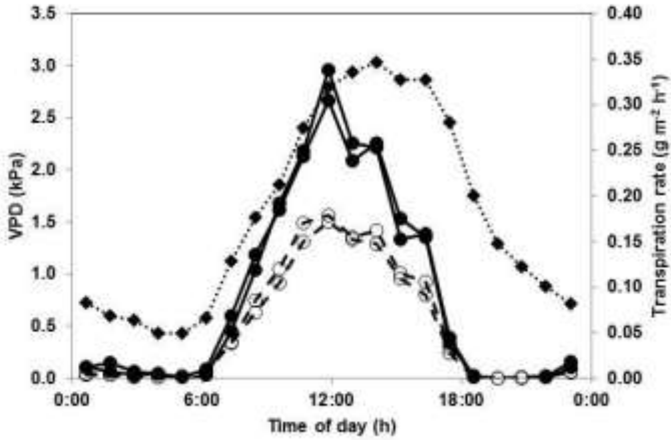


Plant-level measurements of transpiration per unit leaf area (T/LA) are representative of leaf-level measurements of conductance.

Physiology to Modelling – dissect

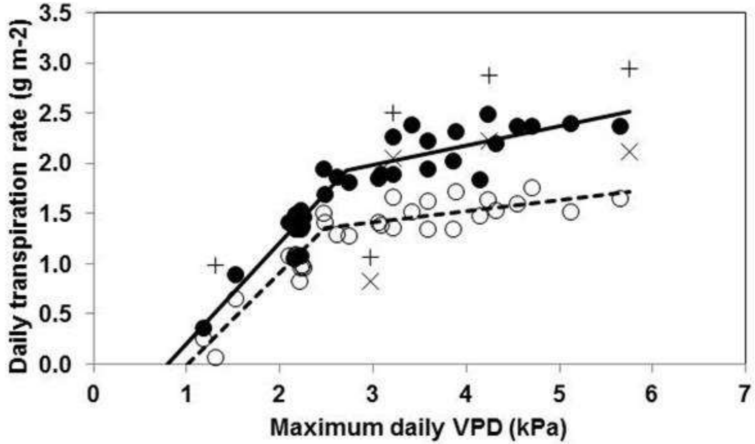
$$TE = \frac{\text{Biomass}}{\text{Transpiration}}$$

Can trait dissection capture genotypic differences in TE?
Example: transpiration rates



Hourly data Gatton 12 Nov 2011

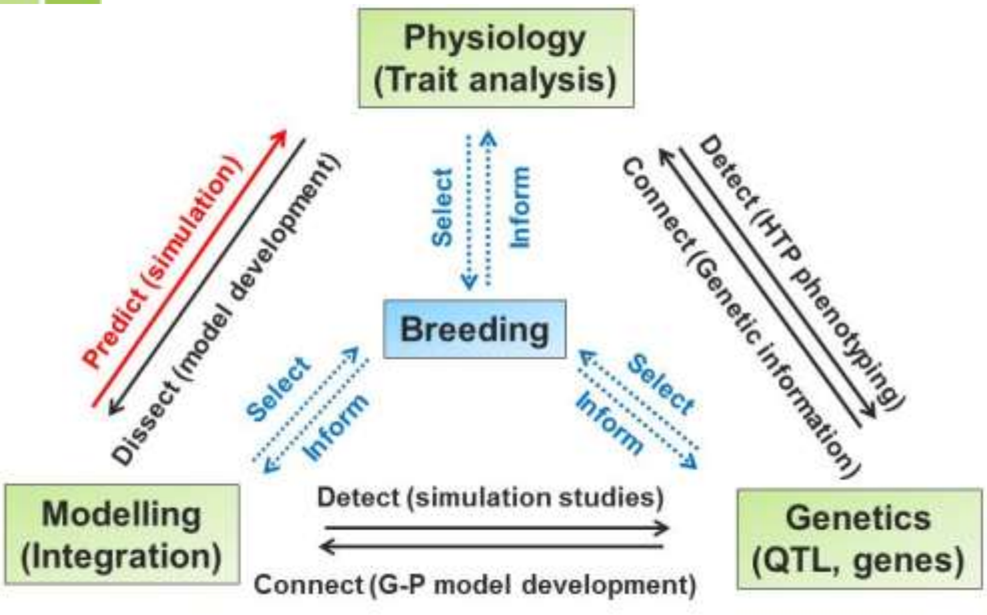
♦ VPD
○ 2 genotypes with high TE
● 2 genotypes with low TE



Daily data Gatton Sep-Dec 2011

Genotypic differences in TE are associated with consistent genotypic differences in transpiration rates.

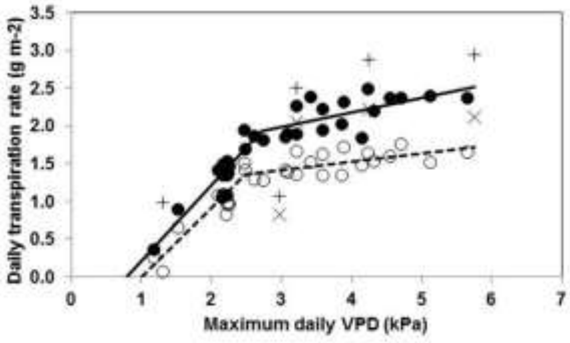
Modelling to Physiology – Predict



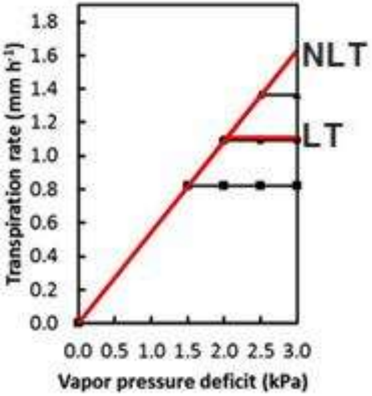
- **Science from trait dissection provides simulation models with biological functionality.**
- **This gives models predictive capability for trait evaluation in the target environments to unravel G × E × M interactions.**

Modelling to Physiology – Predict

Example: Transpiration of maize in the US

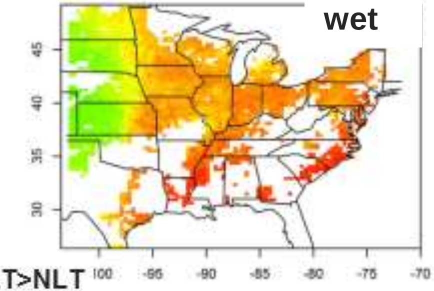


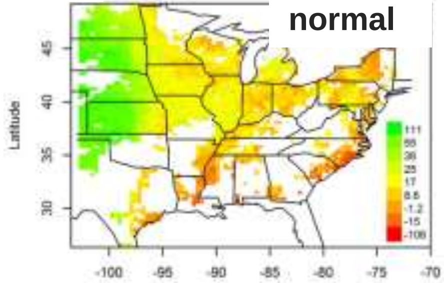
Trait dissection data

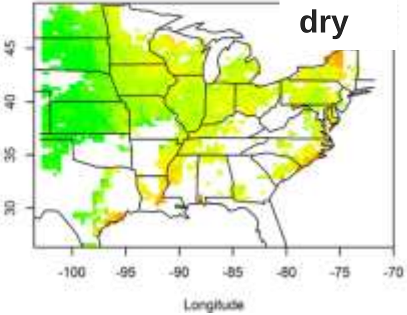


Parameterisation of maize model

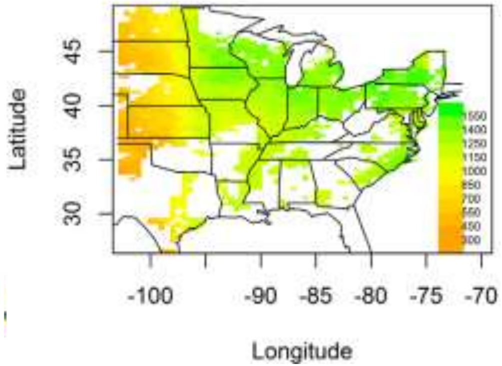
Green: LT>NLT
Red: NLT>LT







Applications
G × E simulations



Mean simulated maize yield in the
US for 63 years

Tool for breeders to evaluate the value of the trait to their breeding program.

Messina et al. 2015. Agron. J.

Concluding remarks

Phenotyping for TE in our lysimetry platform is part of an integrated approach that exploits synergies of combining phenotyping and crop modelling with genotyping.

- **Quantifies the role of TE in sorghum production.**
- **Informs decision making in the breeding program.**

Two platforms we have are complementary and serve different purposes.

- **Addition of imaging system would allow some trait dissection work to be done in the small lysimeters.**

Acknowledgements

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BioSystems
Engineering

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