



HAL
open science

Pleiotropy and cryptic genetic variation govern the phenotypic space in Arabidopsis response to water deficit

Denis Vile, François Vasseur, Sebastien Tisne, Christine Granier

► **To cite this version:**

Denis Vile, François Vasseur, Sebastien Tisne, Christine Granier. Pleiotropy and cryptic genetic variation govern the phenotypic space in Arabidopsis response to water deficit. 23rd International Conference on Arabidopsis Research (ICAR) 2012, Jul 2012, Vienna, Austria. 2012. hal-01190041

HAL Id: hal-01190041

<https://hal.science/hal-01190041>

Submitted on 1 Sep 2015

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

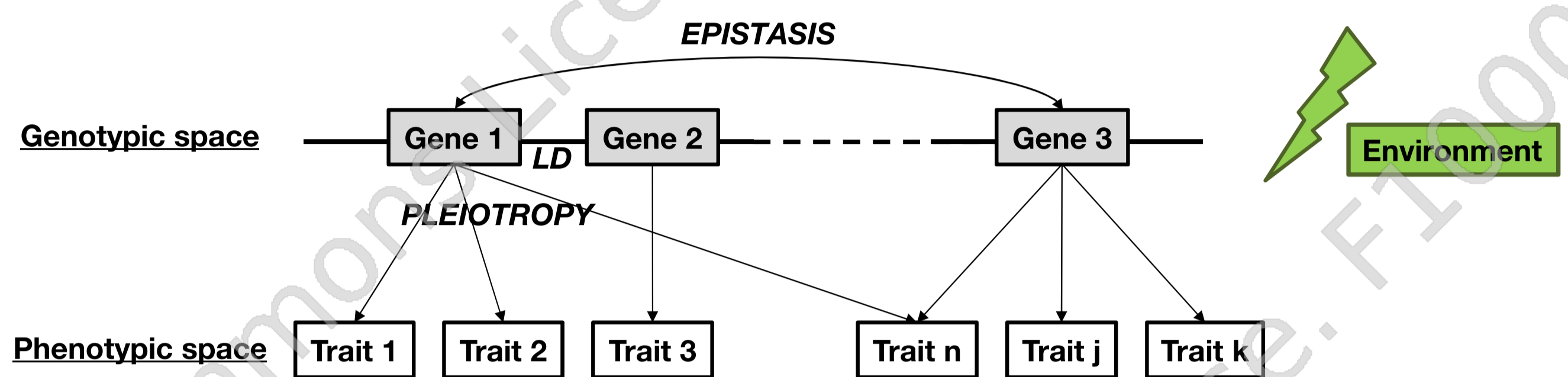
L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Pleiotropic genes have been identified to control simultaneously different processes involved in key functions such as plant growth and reproduction. We developed a modeling approach to uncover the variation of whole rosette development of *A. thaliana*, a fitness related trait.

A modeling approach to uncover phenotypic variation of plant growth

Growth is a multi-level integrated trait. The genetic determinisms of plant growth occurring at each underlying level can lead to cryptic genetic variation, *i.e.* standing genetic variation which is not observed when looking at the integrated complex trait¹. This results in a neutral phenotypic space in the absence of genetic or environmental perturbation.

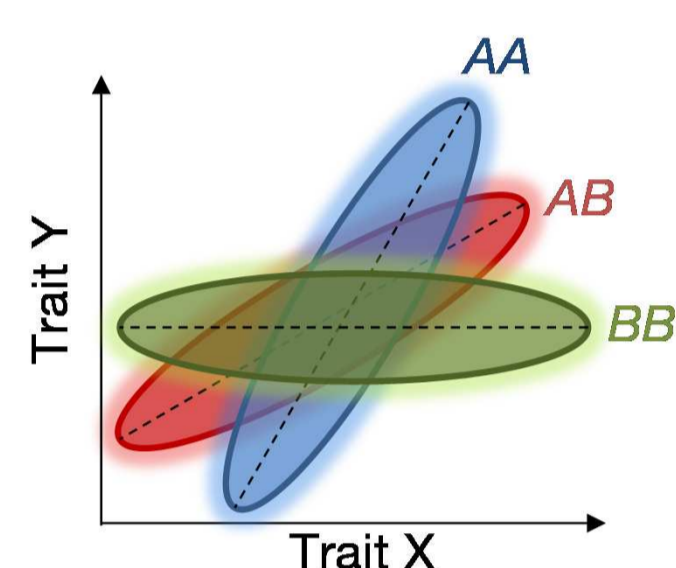
Disentangling multivariate genetic architecture



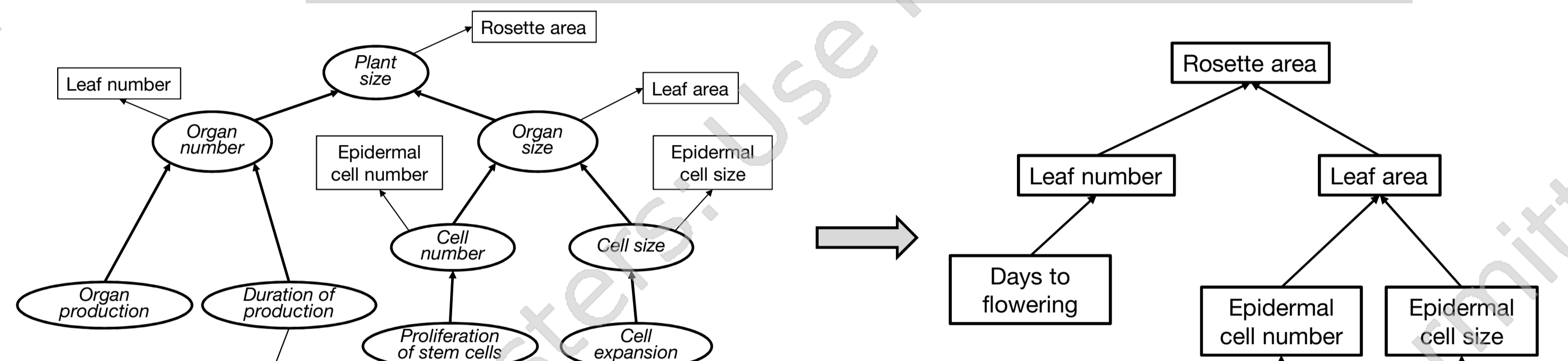
- QTL detection

- **QTL of bivariate relationships:** genome-wide detection of relationship QTL^{2,3} (rQTL).
- **Detection of QTL affecting multivariate relationships:** genome-wide variance-covariance (G-)matrices comparisons^{4,5}.

Relationship QTL



A structural equation model (SEM) of plant growth



Reduced path model of plant growth

Mutations of pleiotropic genes are suspected to sensitize such multi-level systems to produce new phenotypes, out of the neutral phenotypic space, in interaction with standing cryptic genetic variation.

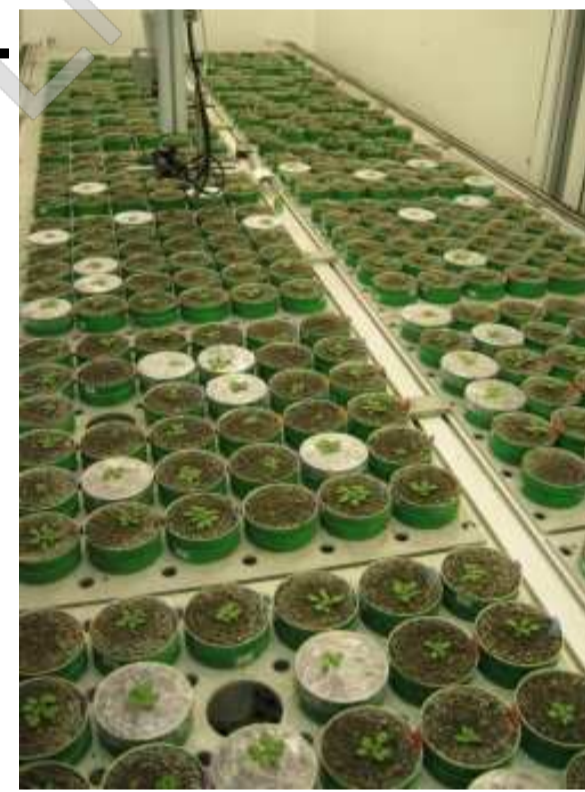
→ Incorporating genetic architecture into SEM⁶

Plant material and growth conditions

We analyzed the effects of the mutation found at *ERECTA* in the Landsberg *erecta* (Ler) accession in two populations of recombinant inbred lines.

120 RI lines (480 individuals, $n = 4$) per population were grown in PHENOPSIS under highly controlled climatic conditions (12 h photoperiod; 20-21 °C; 70% air RH; 220 $\mu\text{mol m}^{-2} \text{s}^{-1}$ PAR), and under well-watered (WW) and water deficit (WD) conditions.

	Ler x An-1 (LA)	Ler x Cvi (LC)
Well-watered	LA:WW	LC:WW
Water deficit	LA:WD	LC:WD



Measurements of traits

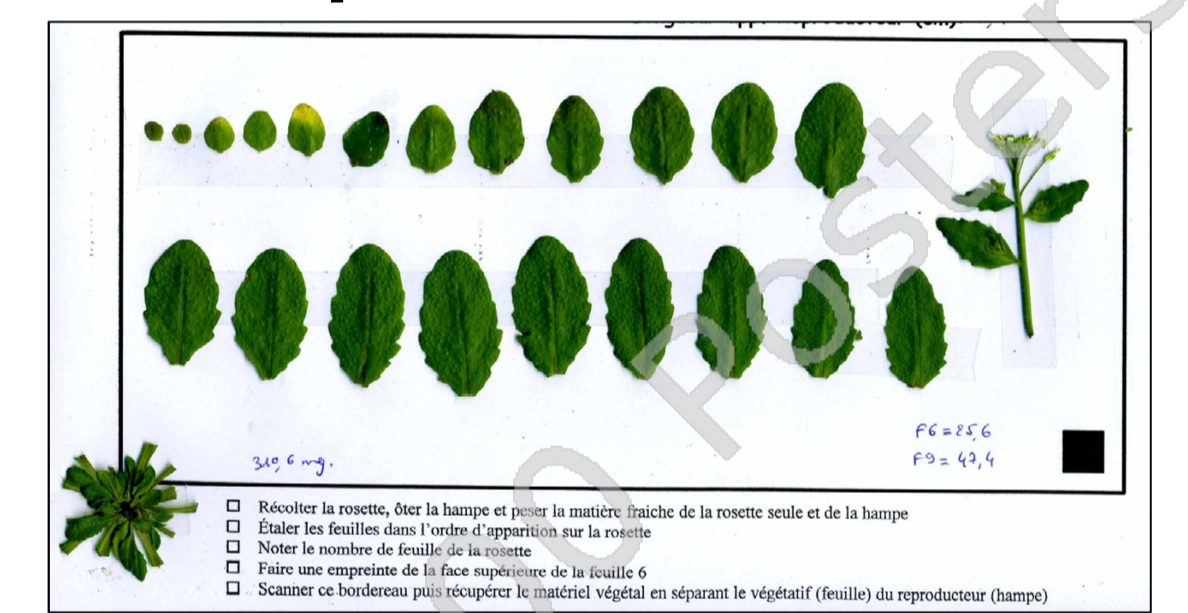
PHENOPSIS: an automated phenotyping platform⁷

Daily growth dynamics

Multi-scale quantification of rosette development

At flowering:

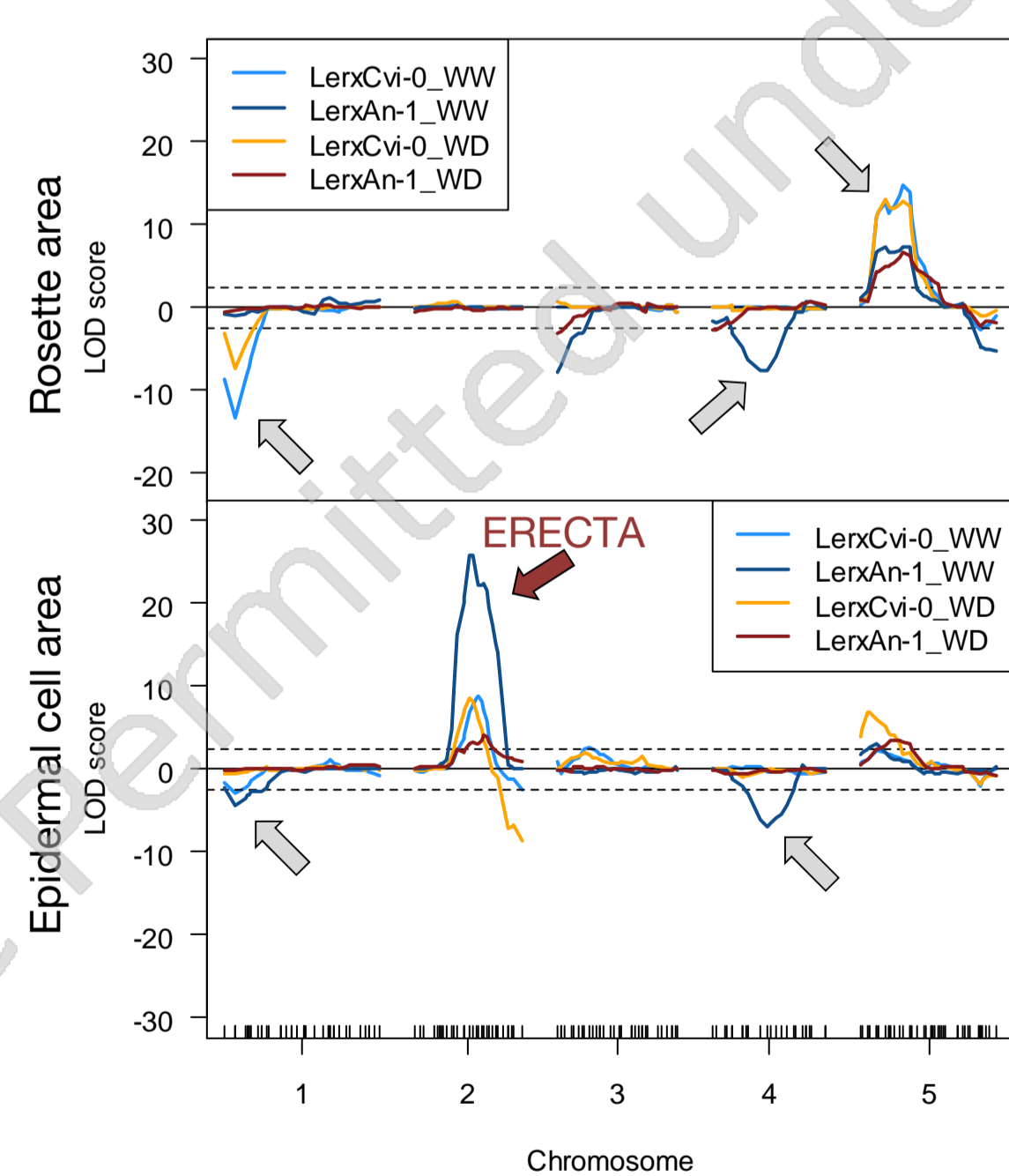
- Rosette area = Σ individual leaf area
 - Number of vegetative leaves
 - Epidermal cell density of 6th leaf
- cell number and cell area



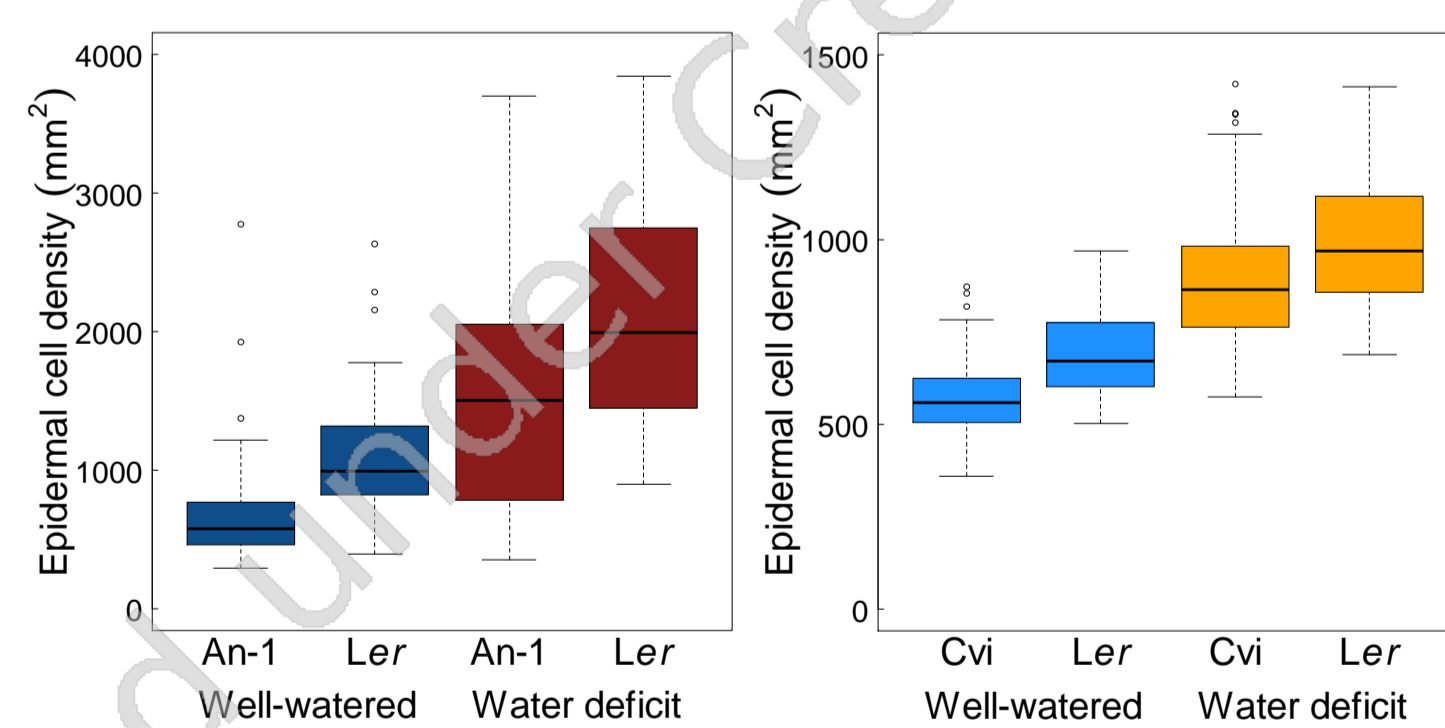
The interactive role of *ERECTA* on plant growth and plant response to water deficit

The *ERECTA* gene has marked effects on development and physiology, and on plasticity due to its interactive effects with the environment and other genes⁸.

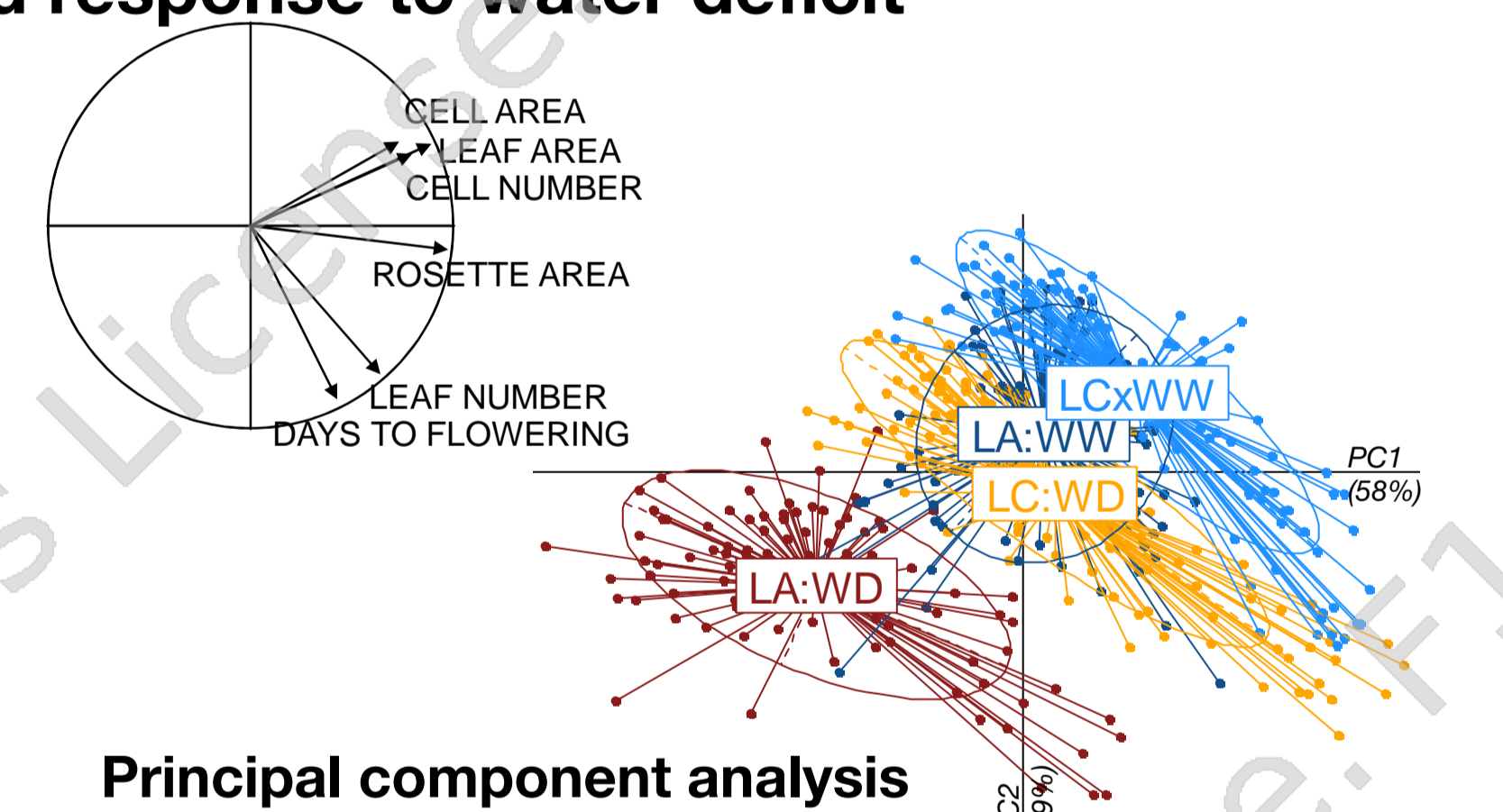
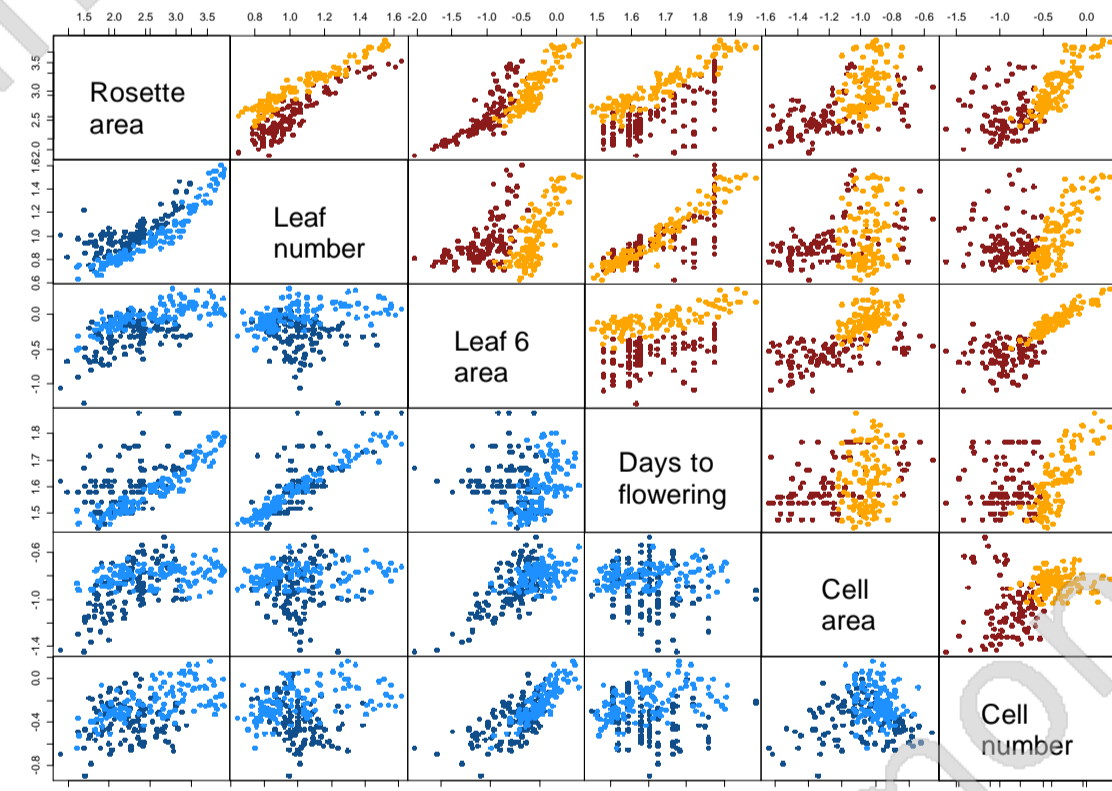
QTL analysis detected common and population-specific genetic architecture in response to water deficit



ERECTA has similar effects of on cell patterning whatever the population or soil water status, but significant variance differences are visible.

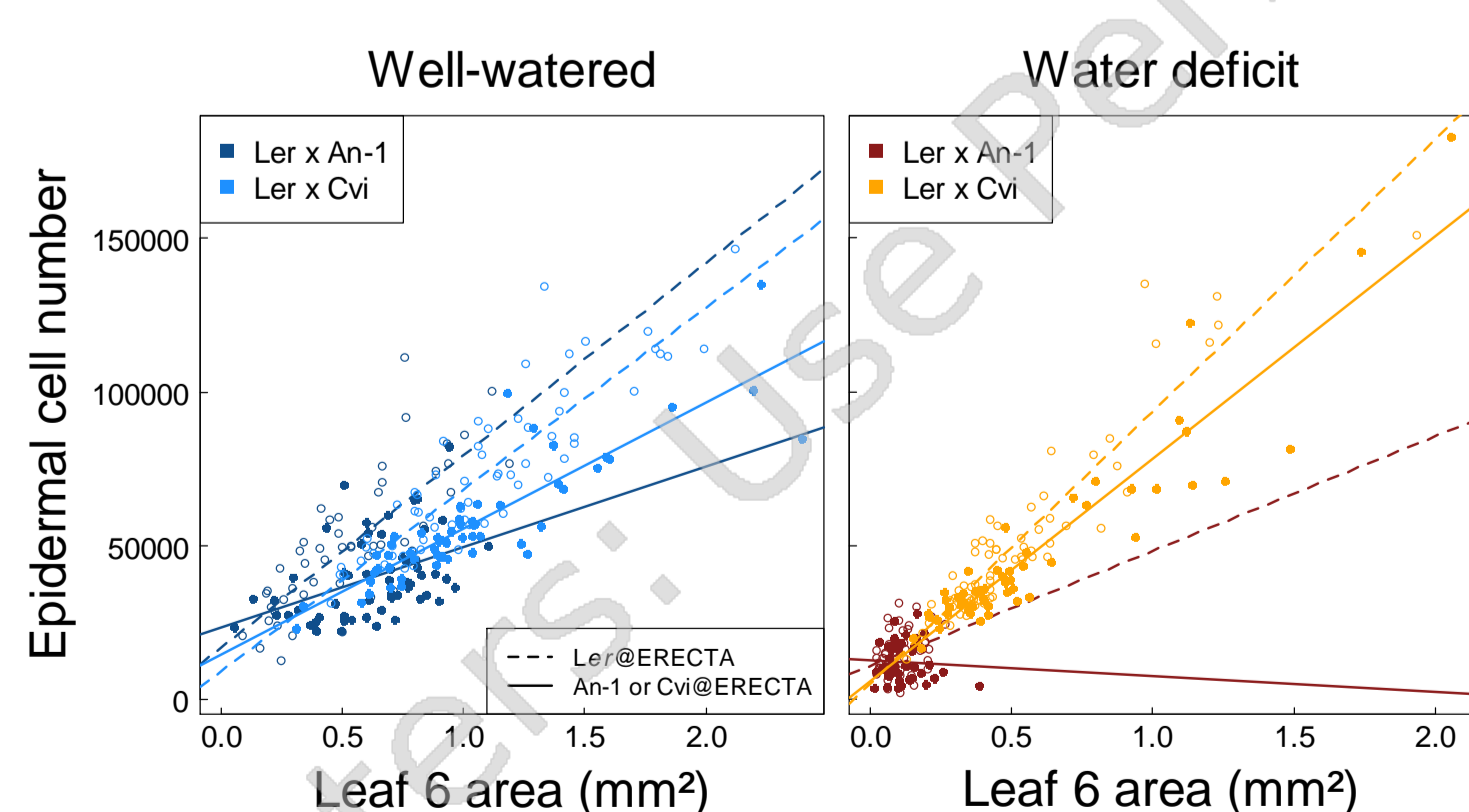


Multivariate relationships between growth-related variables: differences between RI lines populations and response to water deficit



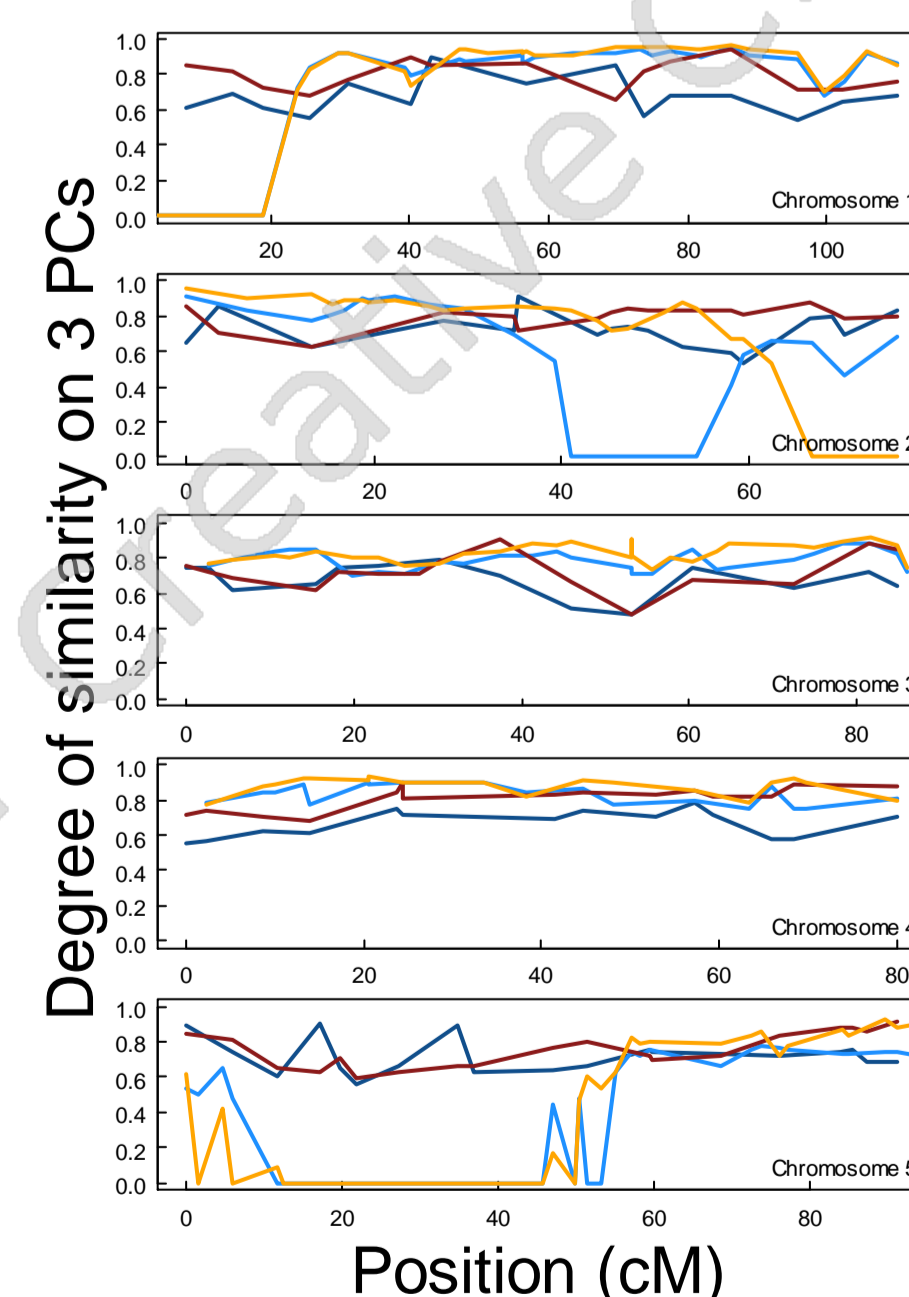
Principal component analysis

rQTL effect of *ERECTA*: comparable under well-watered conditions, but population specific under water deficit.



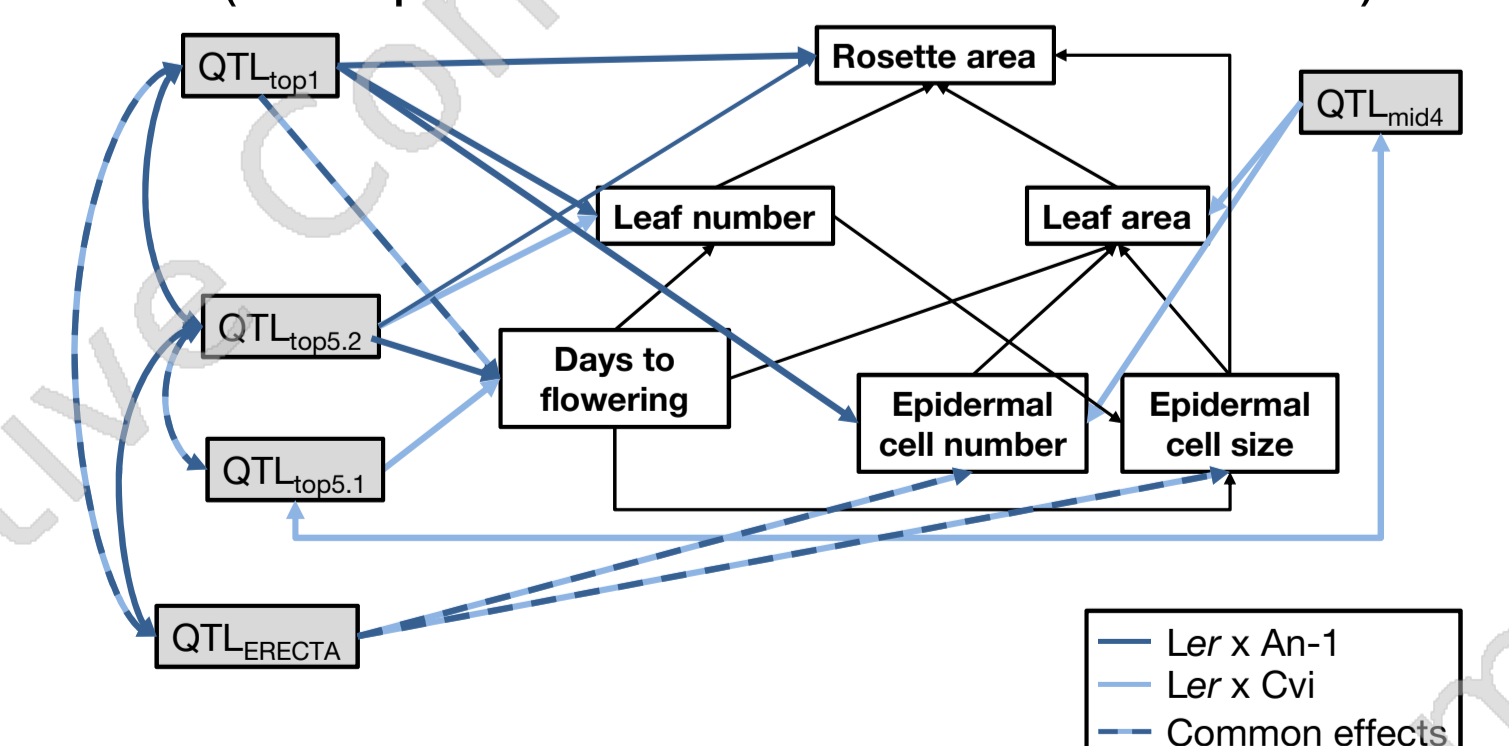
In response to water deficit, *ERECTA* affects the coordinated response of rosette development, in interaction with other QTL, depending on the population in which the mutation segregates⁸ (Vasseur *et al.* in prep.).

Comparison of variance-covariance matrices



A genome-wide analysis of the multidimensional data underlying plant growth revealed similar and contrasted levels of similarity depending on the allelic values in the two populations and on the watering conditions. This suggests background-dependent responses to environmental stresses.

Towards path models including QTL effects and interactions (example under well-watered conditions)



Genetic as well as ecophysiological relationships are explicitly integrated into path models. Our results show that the effects of major effect mutations are highly dependent on the genetic background.

Integrating pleiotropy and epistasis into the modeling of plant growth will provide valuable information into the processes underlying plant performance in response to environmental constraints.

Literature cited

- ¹Gibson G and Dworkin L (2004). *Nature Rev. Gen.* 5: 681-690.
- ²Tisné S *et al.* (2008). *Plant Physiol.* 148: 1117-1127.
- ³Pavlicev M *et al.* (2008). *Evolution* 62: 199-213.
- ⁴Stinchcombe JR *et al.* (2009). *Genetics* 182: 911-922.
- ⁵Jouan-Rimbaud D. *et al.* (1998). *Chemometr. Intell. Lab.*, 40, 129-144.
- ⁶Li R *et al.* (2006). *PLoS Genetics* 2: e114.
- ⁷Granier C. *et al.* (2006). *New Phytol.* 169: 623-35.
- ⁸Tisné S *et al.* (2010). *Plant Cell & Environ.* 33: 1875-1887.

