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URUGUAY



FACULTAD DE  
**AGRONOMIA**  
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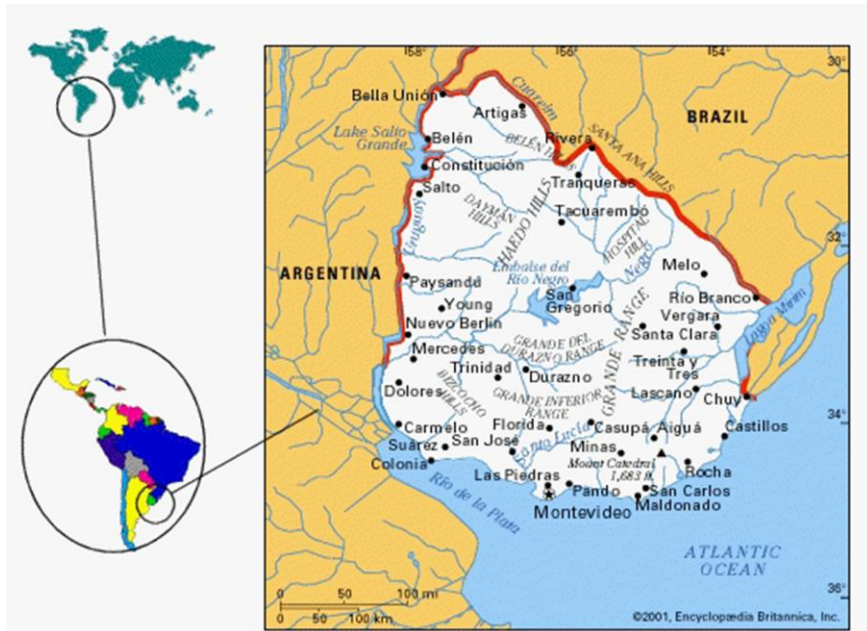


**Grupo CSIC UDELAR**  
*Estrés Abiótico en Plantas*

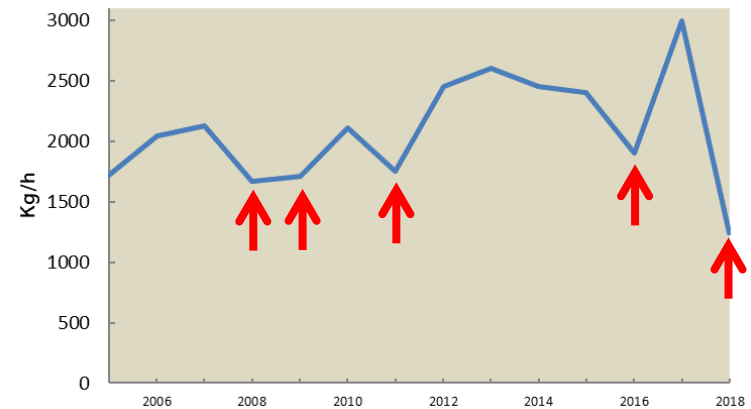
# A multi-approach for understanding the root growth under hydric deficiency

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Depto. Biología Vegetal  
Facultad de Agronomía  
Universidad de la República-URUGUAY

# Seasonal drought the main restriction on summer crops

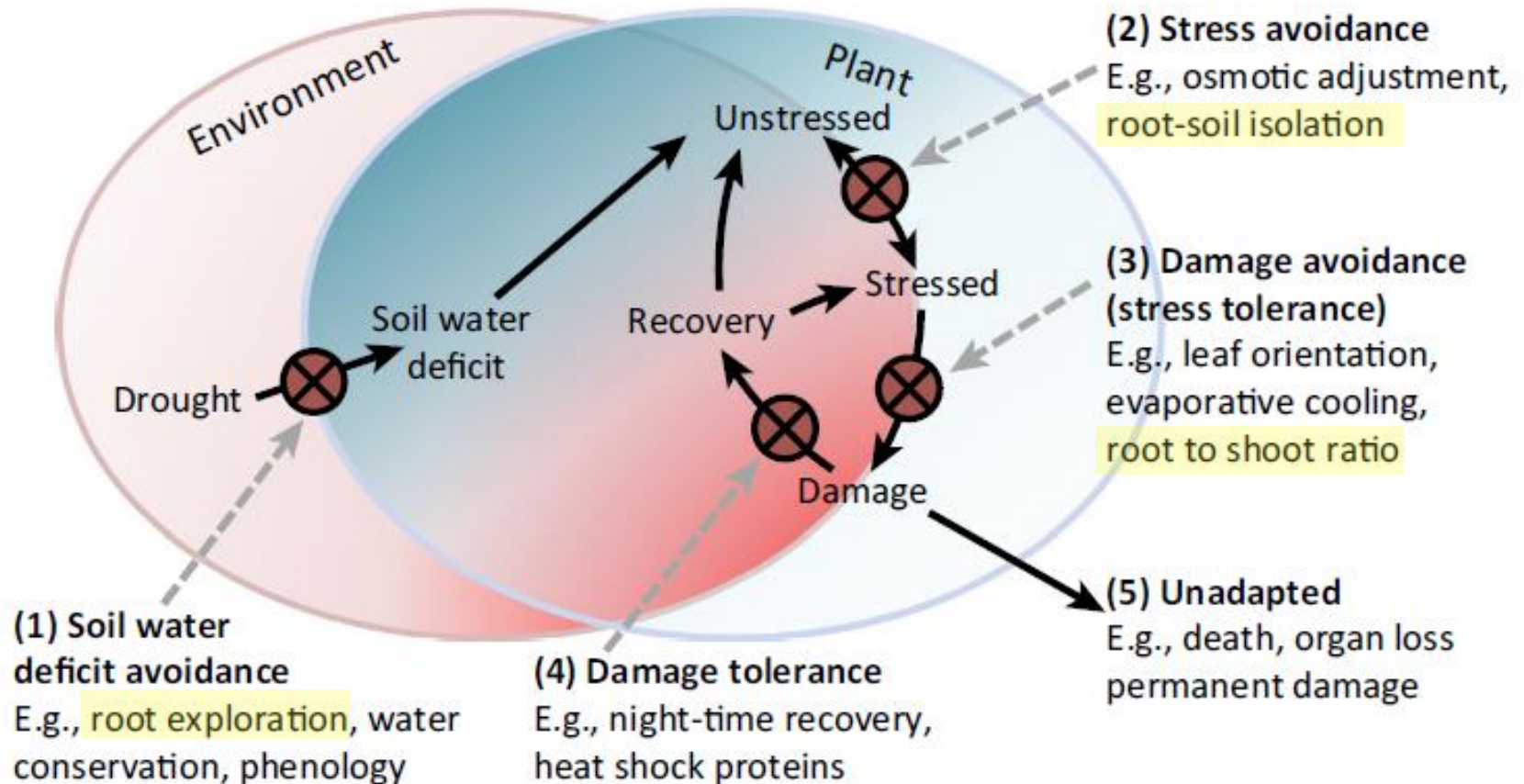


Impact of extreme weather events on soybean productivity of summer crop



Shallow soils with low water retention capacity determine the high risk of drought during the summer

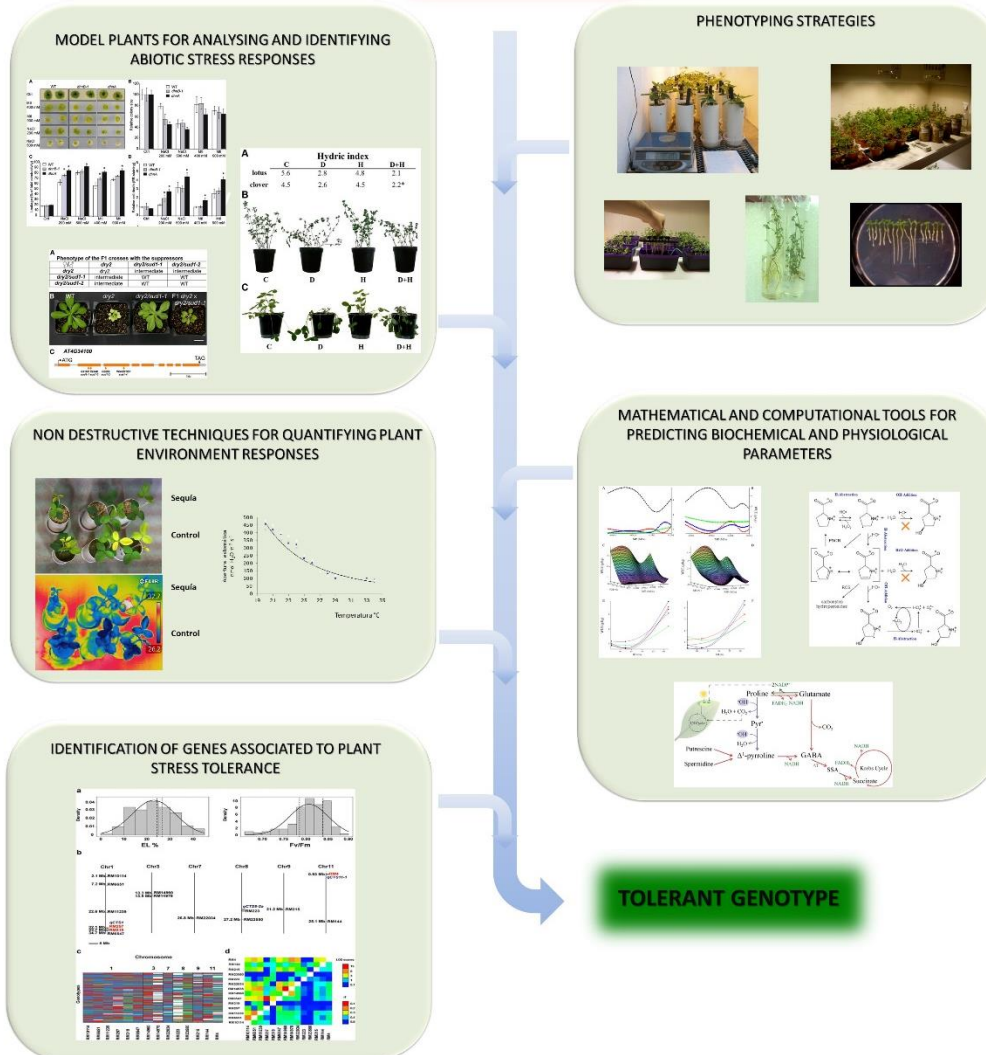
# Drought tolerance involve muligenic mechanism determining biochemical and physiological changes





# Work flow for a multi-approach strategy for plant drought responses analysis

**SENSIBLE GENOTYPE**

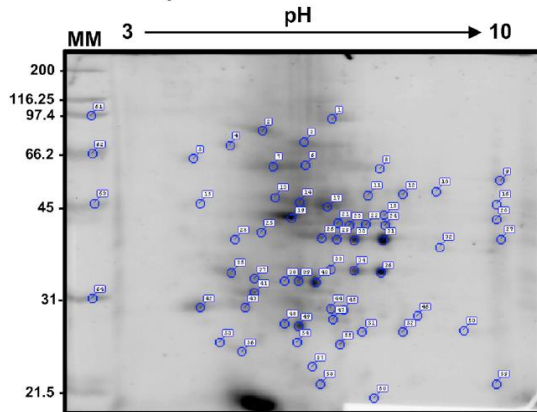


*Lotus* spp. is an important legume component of pastures in livestock systems

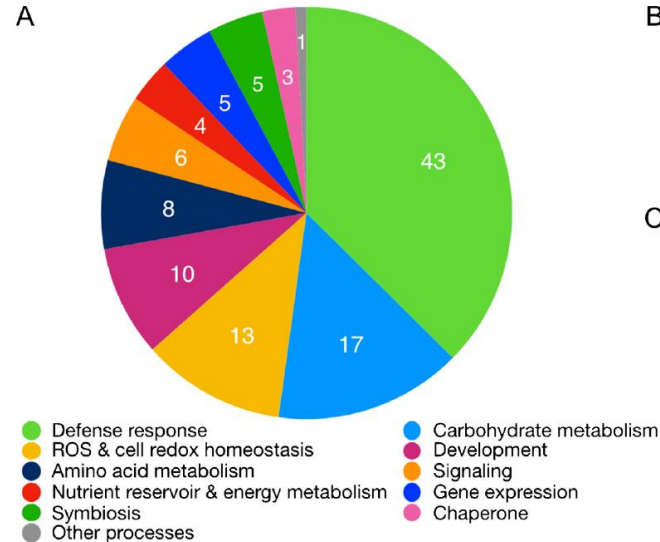


# Proteomic analysis of *L. japonicus* roots under stress conditions identify specific changes in response to drought

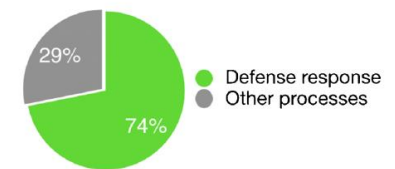
A. 2 D electrophoresis



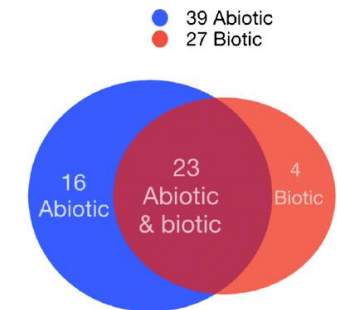
A



B



C

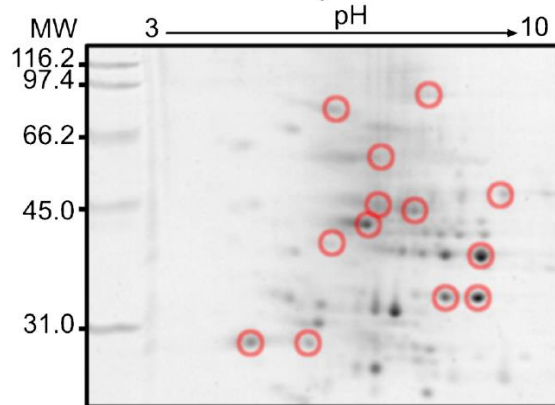


## GSNO content

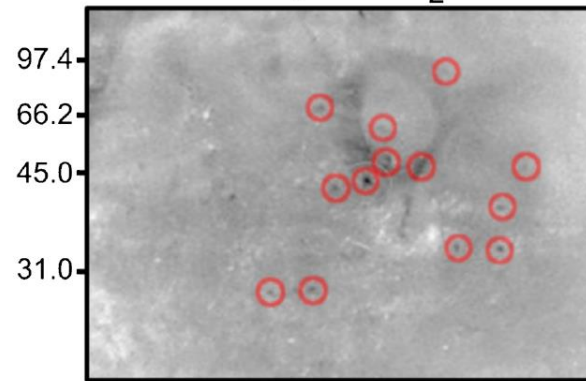
|       | Roots            |                   | Leaves           |                  |
|-------|------------------|-------------------|------------------|------------------|
|       | C                | D                 | C                | D                |
| Means | 6.1 <sup>a</sup> | 3.4 <sup>ab</sup> | 0.8 <sup>b</sup> | 1.1 <sup>b</sup> |
| SD    | 2.7              | 0.2               | 1.4              | 0.3              |

# Specific protein nitration under drought stress could control root adaptation response

**A. SYPRO ruby stain**



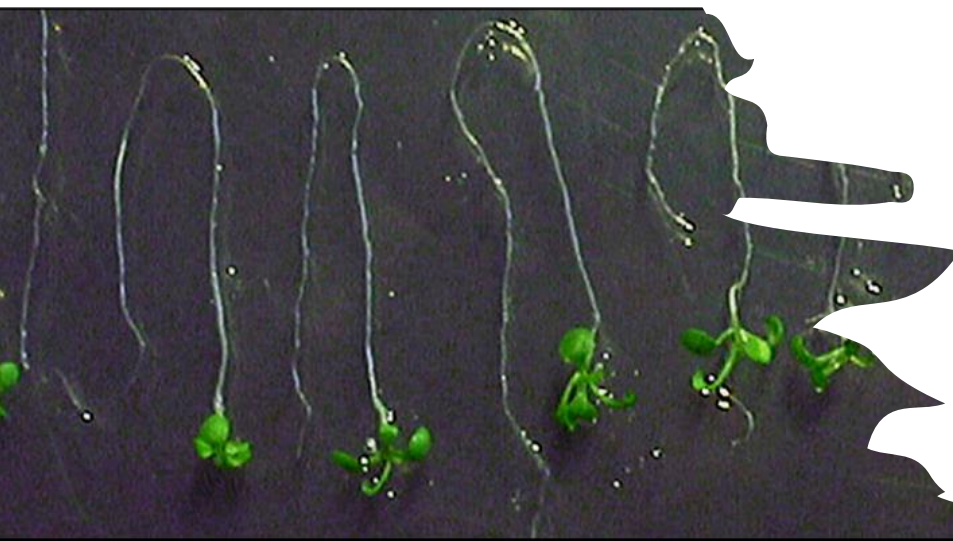
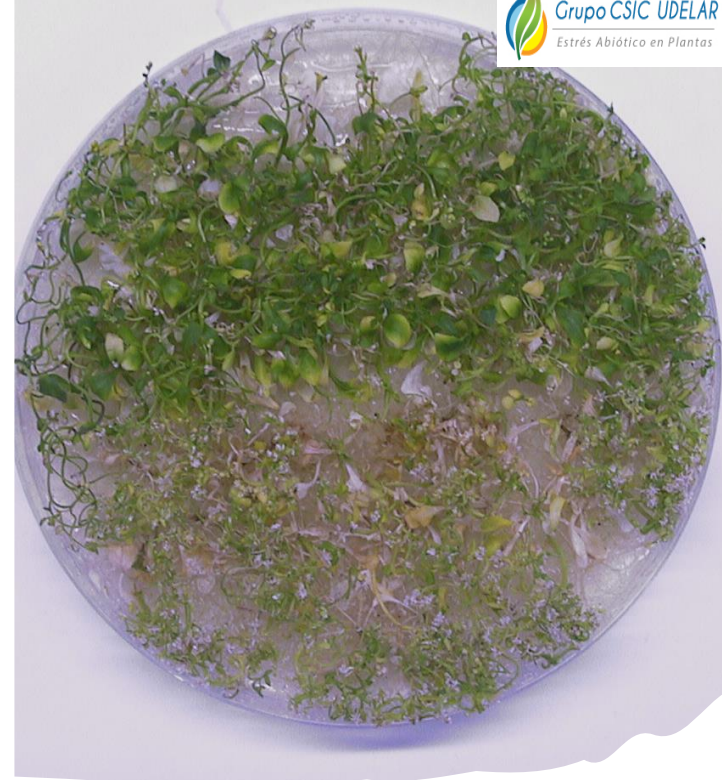
**B. WB anti Tyr-NO<sub>2</sub>**



| Spot | Proteins   | Tyr | Predicted position of nitrated Tyr(s) | Lj ID                            |
|------|--|-----|---------------------------------------|----------------------------------|
| 1    | Methionine synthase                                | 9   | 4, 203                                | Lj0g3v0222539.1                  |
| 2    | HeatShock Protein 70-family                        | 15  | 314,408,423,801                       | Lj1g3v4550110.1, Lj3g3v3188570.1 |
| 6    | Adenosyl-homocysteinase                            | 9   | 222,254,263                           | Lj6g3v0270780.1                  |
| 12   | Peroxidase   | 6   | UN                                    | Lj5g3v1925220.1                  |
| 14   | Alcohol dehydrogenase 1                            | 8   | 53                                    | Lj1g3v0913280.1                  |
| 17   | Alcohol dehydrogenase ADH1 Lj                      | 8   | 53                                    | Lj1g3v0913270.1                  |
| 19   | Glutamine synthetase cytosolic Lj                  | 18  | 73                                    | Lj6g3v1887790.1                  |
| 25   | Fructokinase 4                                     | 7   | 147,174                               | Lj3g3v0381590.1                  |
| 31   | 1,3-beta-D-glucanase                               | 6   | 62                                    | Lj0g3v0213009.1                  |
| 34   | Chitinase  | 6   | UN                                    | Lj0g3v0247049.1                  |
| 36   | Endochitinase                                      | 16  | UN                                    | Lj0g3v0247049.1                  |
| 42   | Pre-mRNA splicing factor domain-containing protein | 15  | 72                                    | Lj0g3v0100099.1, Lj0g3v0011739.1 |
| 43   | L-type lectin-domain containing receptor kinase    | 1   | 168                                   | Lj6g3v1693730.1                  |



**Santiago Signorelli**  
 UdelaR Uruguay

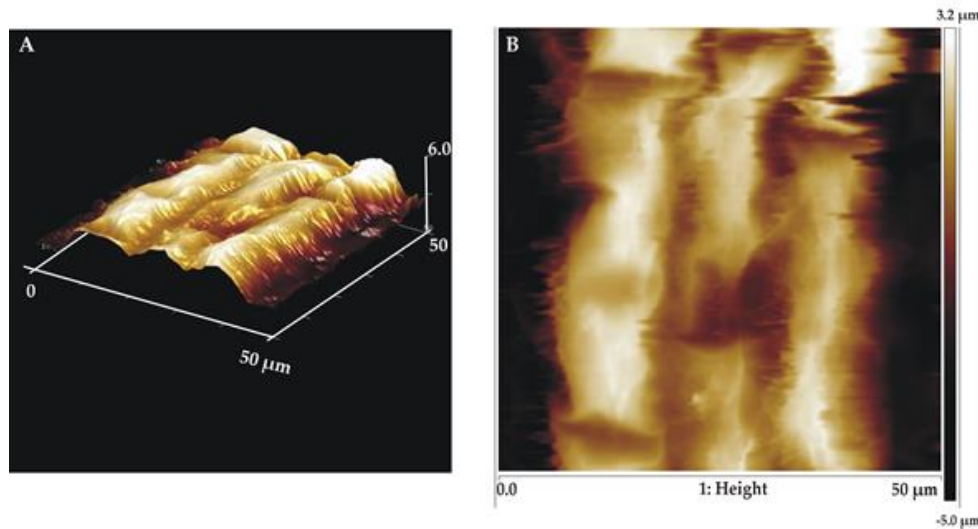


Arabidopsis is a friendly model for plant drought responses studies



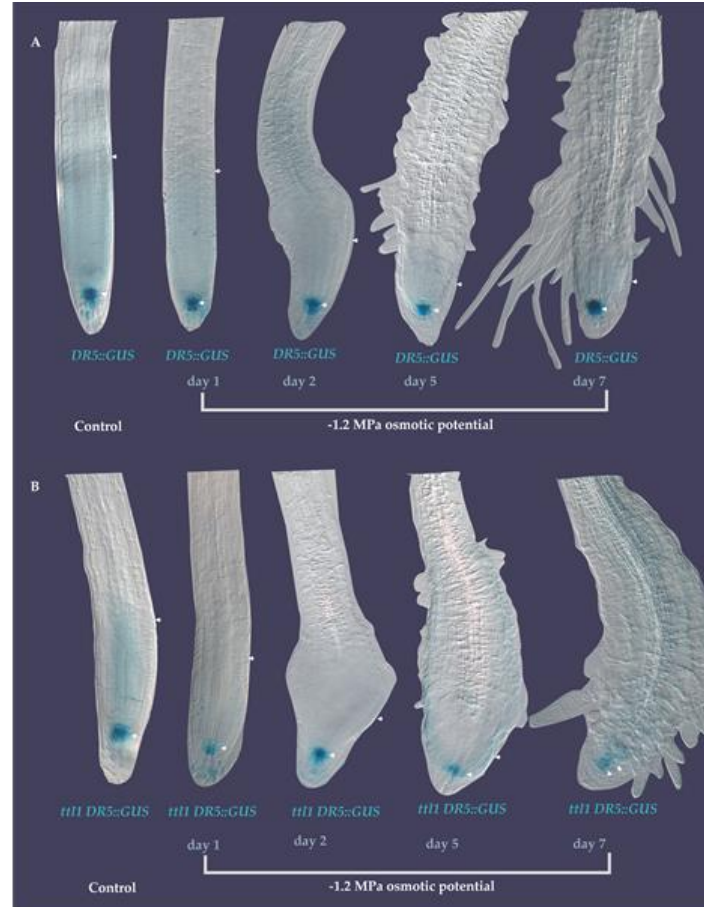


# Atomic force microscopy imaging of the surface of the root elongation zone cells reveal a cell wall of the *ttl1* mutant less rigid



| Control                   | Y (kPa)         | N    | Error |
|---------------------------|-----------------|------|-------|
| Col-0                     | 88.12 ± 2.79 a  | 201  | 0.19  |
| <i>ttl1</i>               | 16.08 ± 6.87 b  | 1184 | 0.19  |
| Osmotic Stress (-1.2 MPa) | Y (kPa)         | N    | Error |
| Col-0                     | 164.98 ± 2.66 a | 263  | 0.16  |
| <i>ttl1</i>               | 29.71 ± 13.9 b  | 324  | 0.77  |

# Hormonal homeostasis is altered in the mutant affecting cell wall dynamic



Mariana Sotelo-Silvera  
UdelaR Uruguay

# Public-private initiative for promoting crop biotechnology in Uruguay



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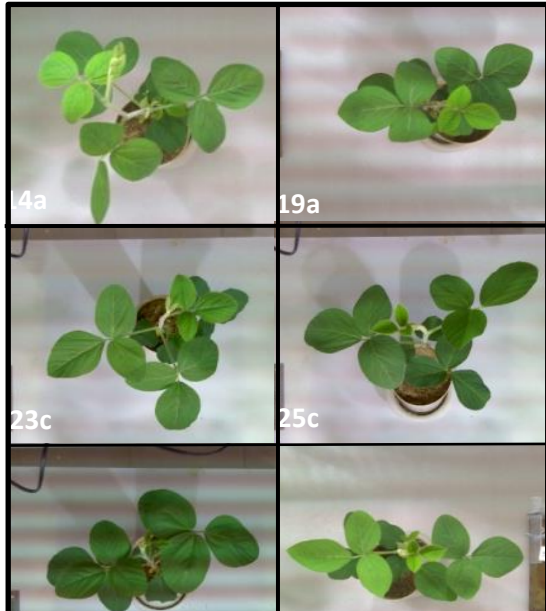




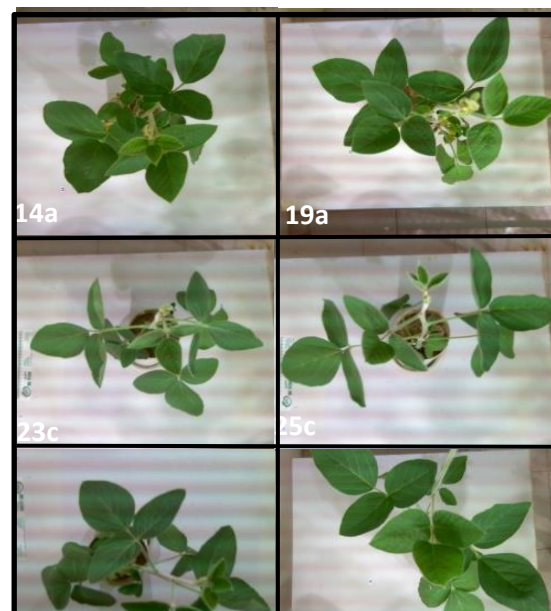
Could we speed up the soybean breeding for a complex trait as drought tolerance ?

Is it possible to identify markers (phenotypic or genotypic) with strong association to drought tolerance ?





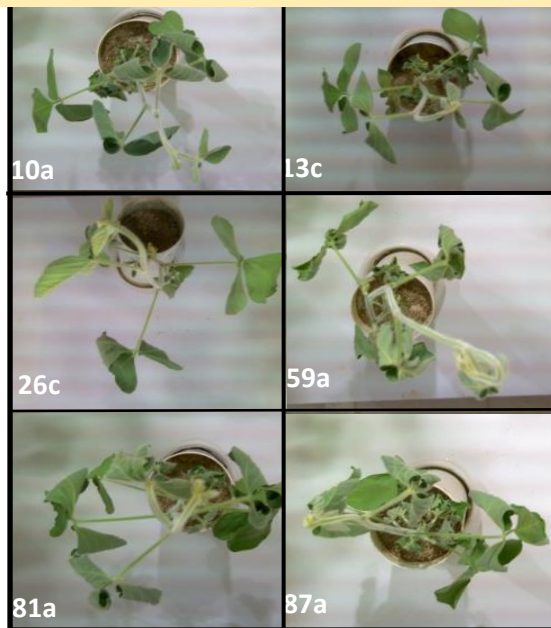
“Slow-wilting”  
phenotypes



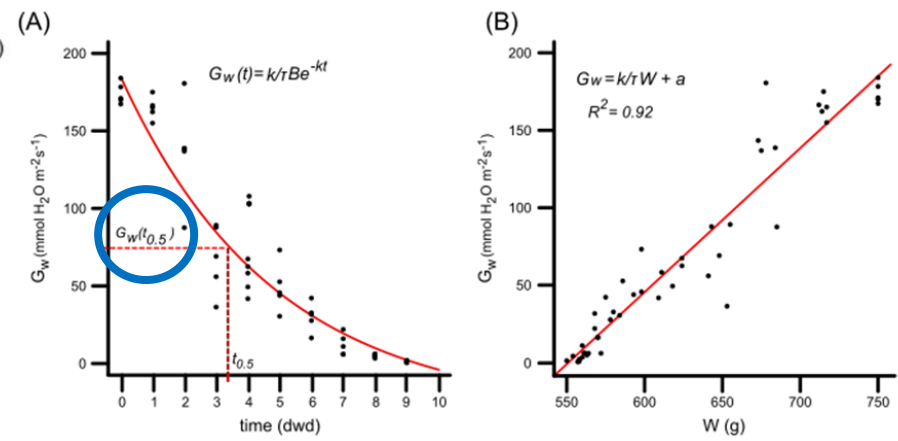
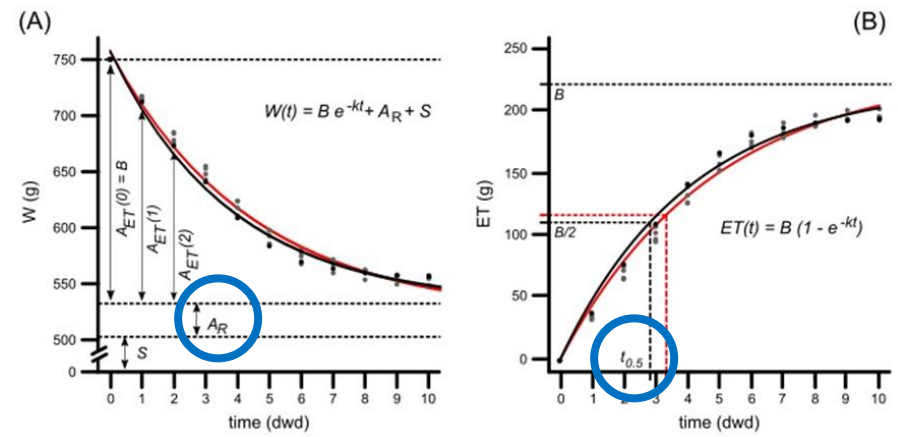
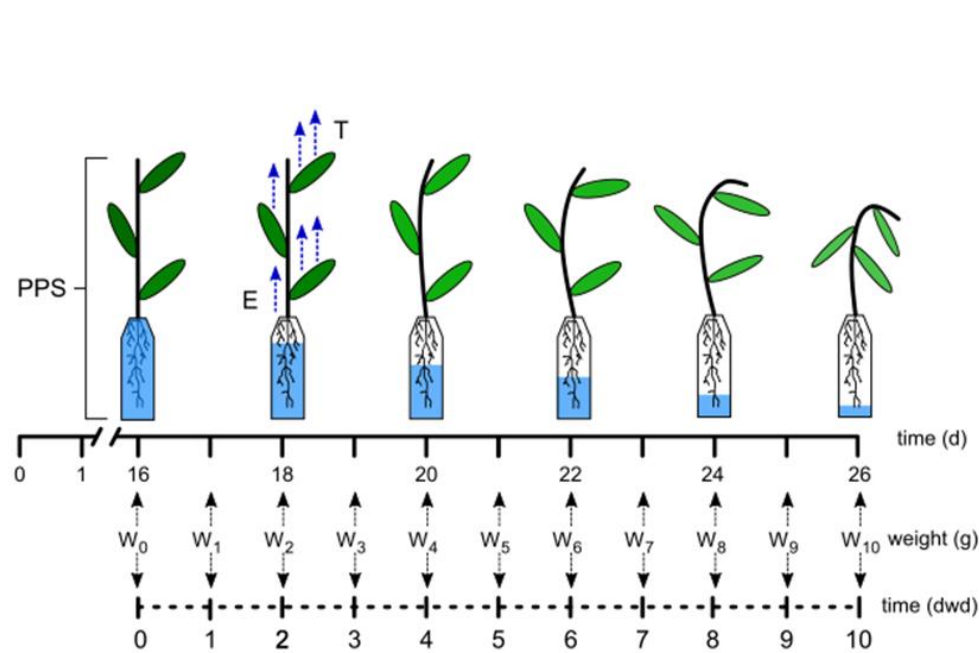
A set of 200 soybean genotypes were grouped depending on the kinetic changes in physiological parameters



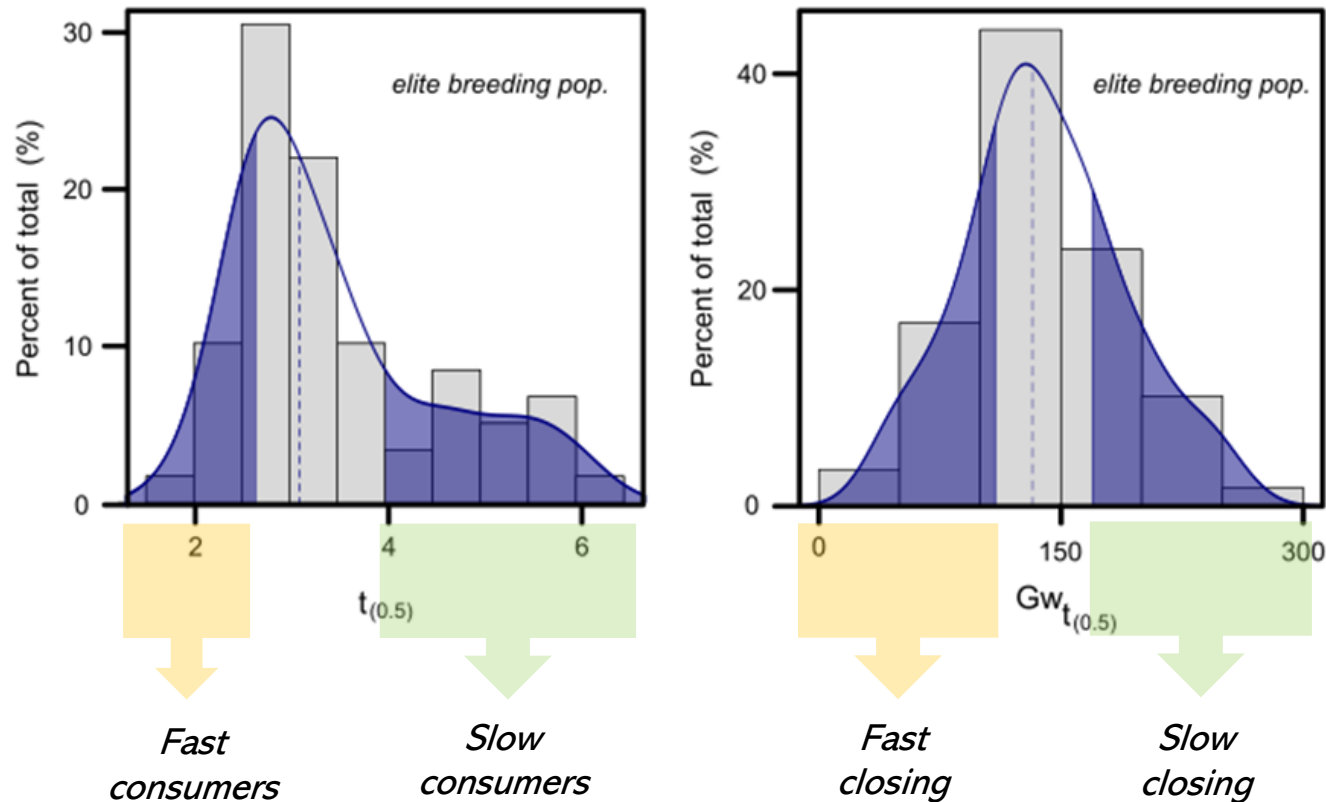
“Fast-wilting”  
phenotypes



# Responses of genotypes to drought can be explained by a mathematical modelling of water consume curve



## Grouping of genotypes based on parameters of water consume and stomatal response

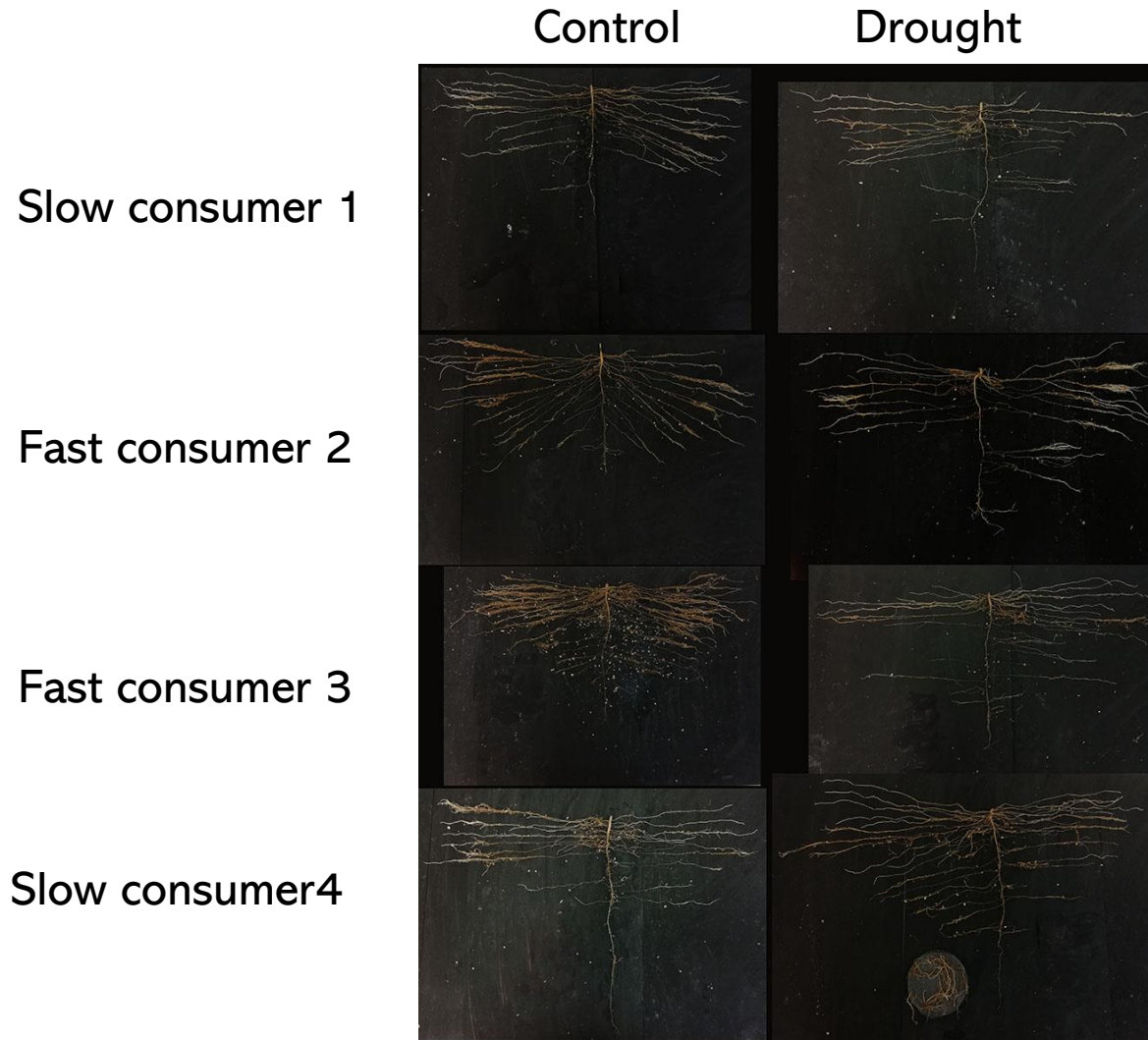


In more than 90 % of genotypes  $t_{0.5}$  and  $GW_{t_{0.5}}$  are closely related.

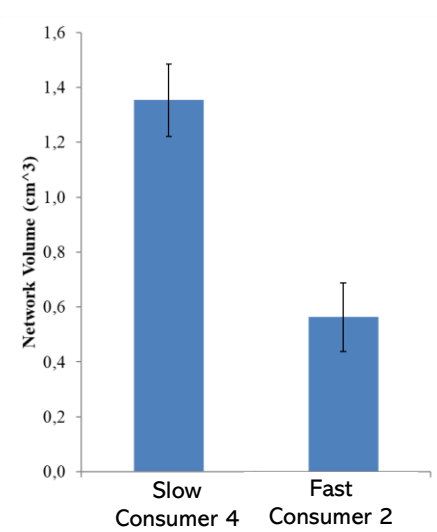
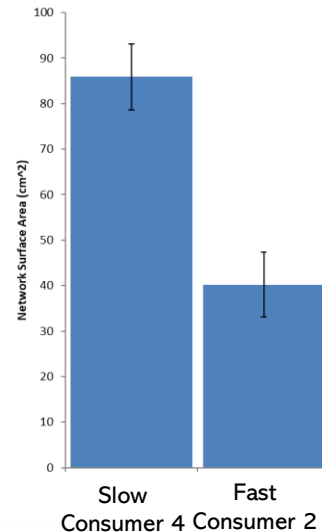
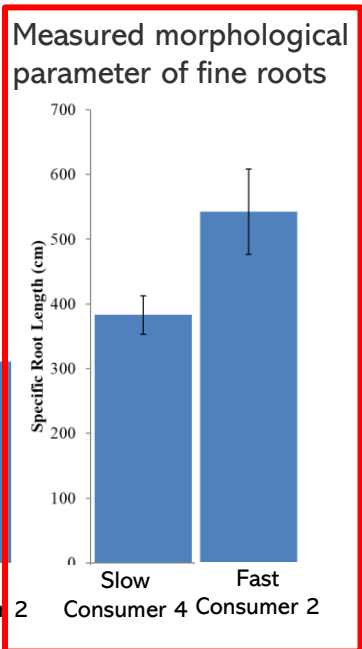
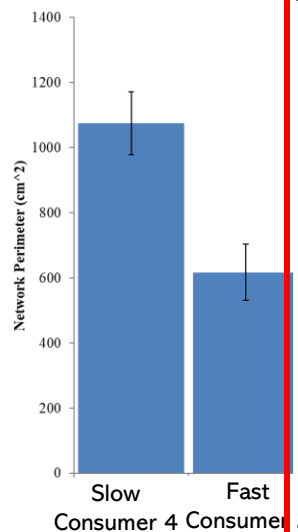
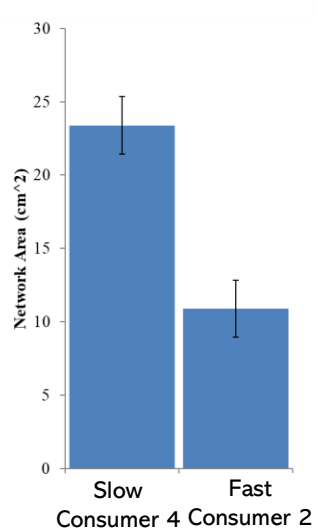
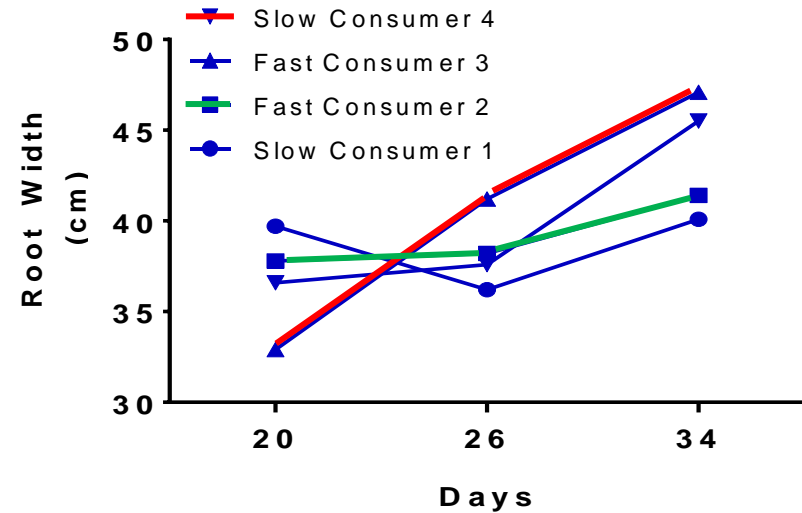
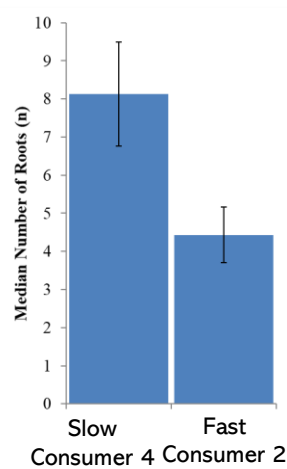
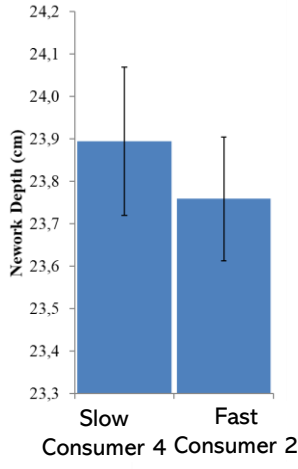
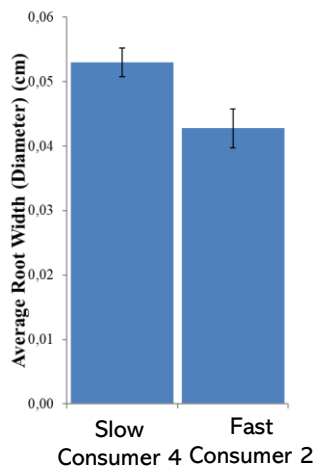
However in some genotypes water consume kinetic is not explained by shoot parameters (stomatal response, shoot area, etc.)



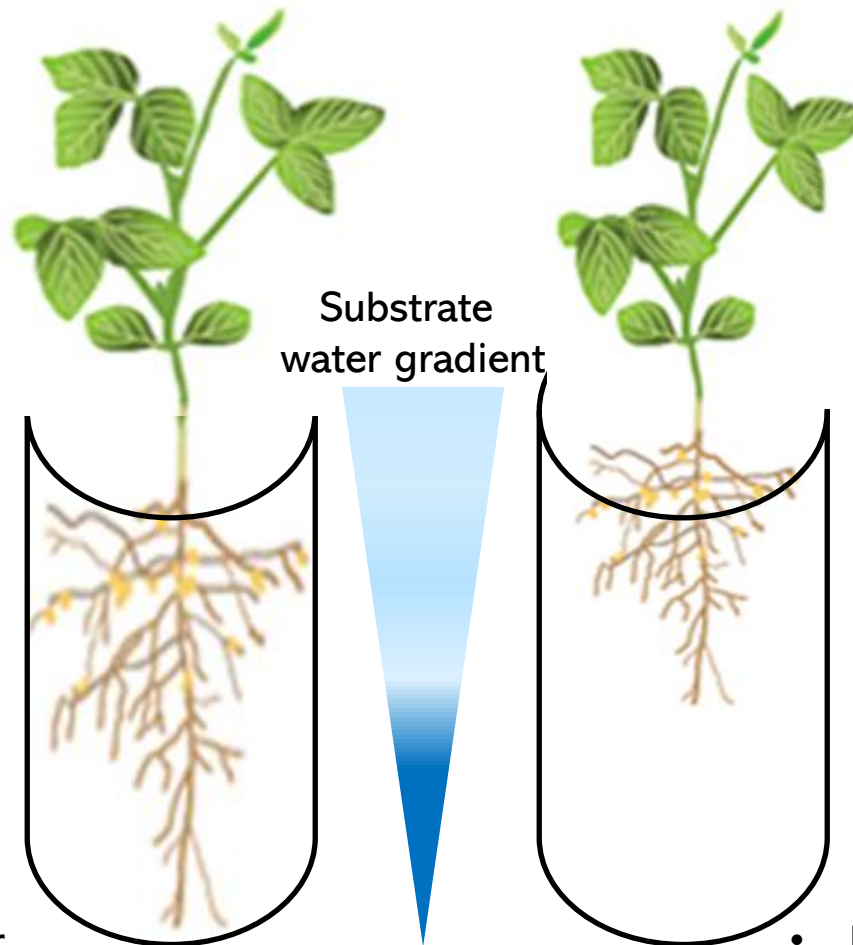
# Roots characterization provide information for understanding the *outlayer* genotypes behavior under water restriction



# GIA root analysis of contrasting genotypes under well watered conditions



# Differential root adaptation to water restriction determine water consume rate in contrasting genotypes



Esteban Casaretto  
UdelaR Uruguay



Gastón Quero  
UdelaR Uruguay



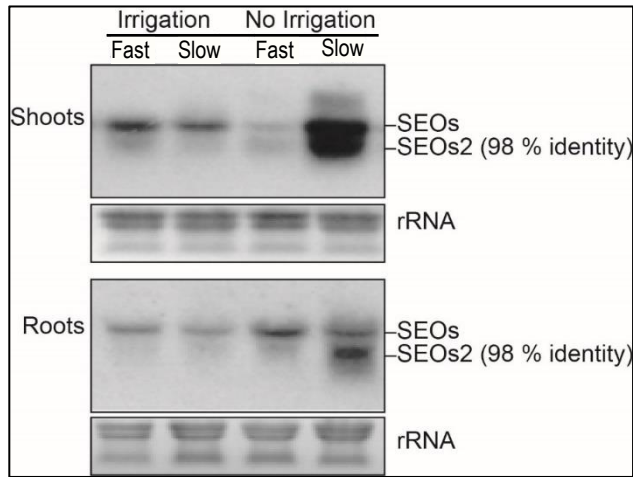
Sebastian Simondi  
Universidad Nacional de  
Cuyo  
Argentina

- Slow consumer
- High stomatal conductance
- Low remanent water

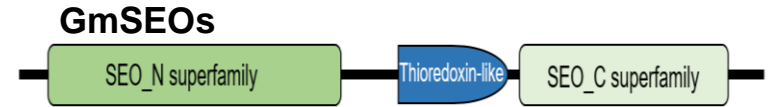
- Fast consumer
- Low stomatal conductance
- High remanent water

# *GmSEOs* (*G*lycine *m*ax *S*ieve *E*lement *O*cclusion *s*) identified in a slow consumer genotypes is involved in abiotic stress tolerance

*GmSEOs* is differentially upregulated in response to water deficit in a slow consumer soybean cultivar.

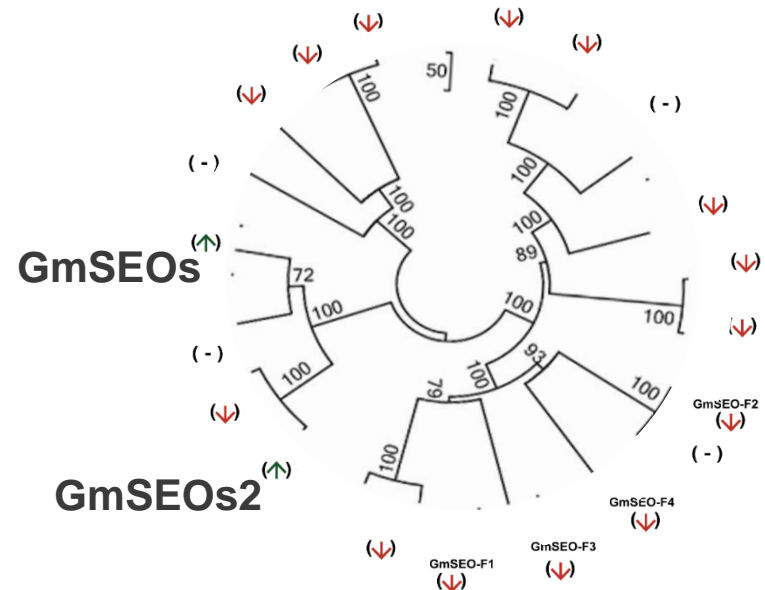


**Proposed function under investigation:** regulation of: vascular tissue development/ root growth/ translocation/ senescence.



*GmSEOs* is a member of a multigenic gene family encoding phloem proteins which accumulate during sieve element differentiation.

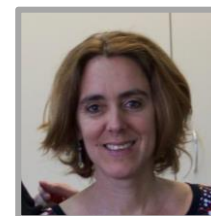
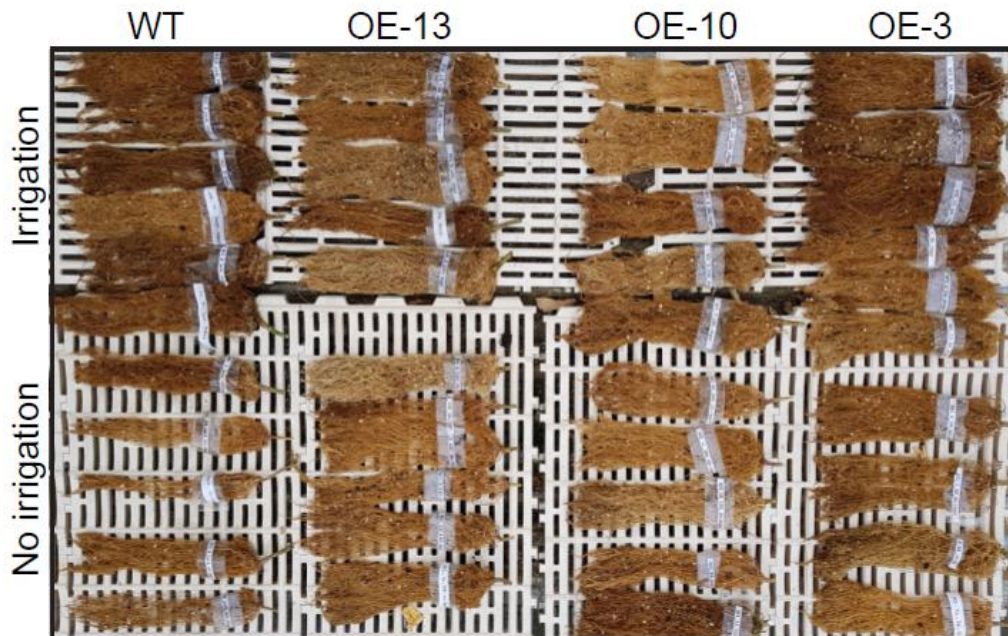
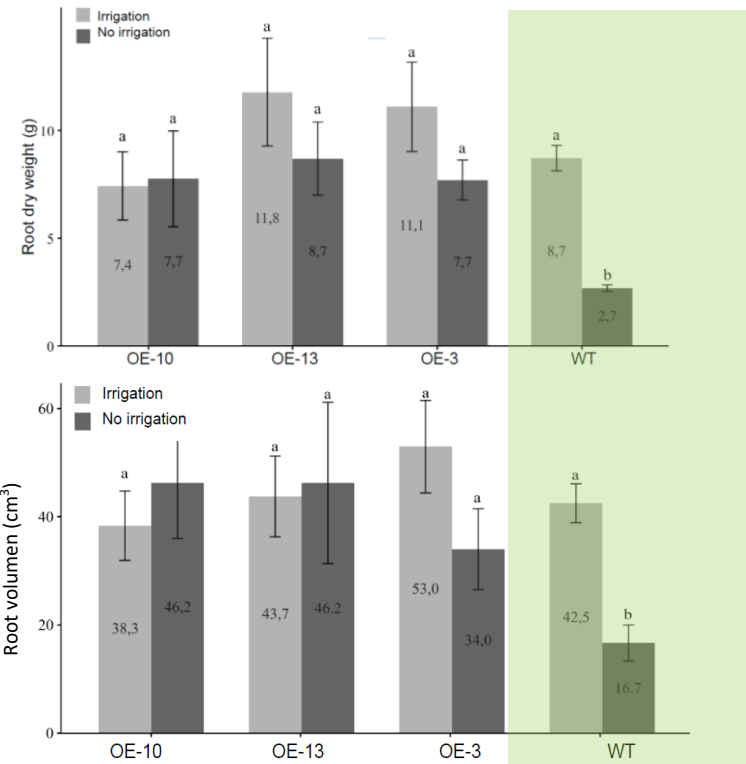
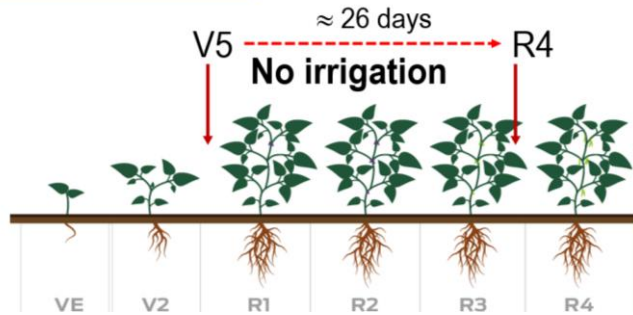
## The soybean *SEO* gene family



↑ Upregulated by water deficit ↓ Downregulated by water deficit

# Homologous constitutive expression of SEO confer root growth adaptation under drought condition

## VEGETATIVE ASSAY

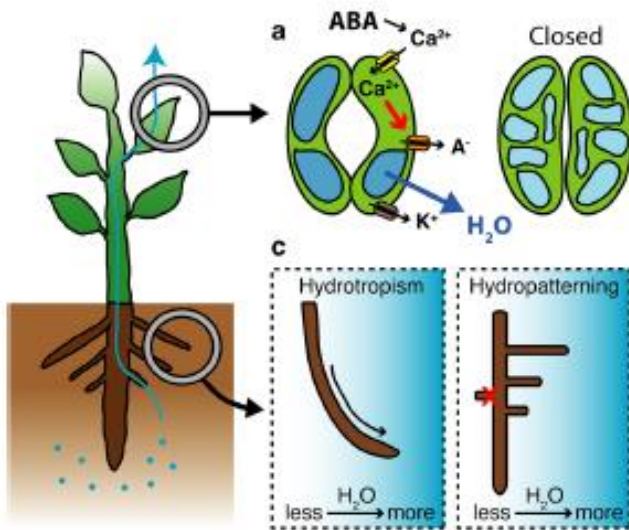


Sabina Vidal  
Udelar Uruguay

# RNAseq showed cell wall dynamic changes associated with responses genotype dependent

| Gene  | "Slow consumer" genotype |                 | "Fast consumer" genotype |                 |
|---|--------------------------|-----------------|--------------------------|-----------------|
|   | Control                  | Drought         | Control                  | Drought         |
| Pectin lyase-like superfamily protein                       | <b>2,192577</b>          | 1,108976        | <b>-2,7459</b>           | <b>-3,62903</b> |
| Pectin lyase-like superfamily protein                       | <b>3,842031</b>          | -1,36622        | <b>3,664448</b>          | <b>-2,9977</b>  |
| Pectin lyase-like superfamily protein                       | -1,02251                 | <b>2,082256</b> | -1,17901                 | -1,75844        |
| Pectin lyase-like superfamily protein                       | 1,402364                 | <b>2,707498</b> | <b>-2,28893</b>          | -1,25282        |
| Pectin lyase-like superfamily protein                       | -1,11635                 | <b>3,536709</b> | 1,44179                  | 1,349715        |
| Pectin methylesterase 31                                    | -1,03542                 | <b>2,831388</b> | -1,00091                 | 1,886135        |
| Pectinacetylerase family protein                            | -1,2763                  | <b>2,011844</b> | -1,5324                  | -1,52435        |
| Plant invertase/pectin methylesterase inhibitor superfamily | -1,6596                  | <b>-4,05132</b> | <b>-2,35084</b>          | -1,4039         |
| Wall associated kinase 3                                    | -1,04087                 | <b>-2,36497</b> | 1,446811                 | <b>-2,26623</b> |
| Wall associated kinase 3                                    | 1,139773                 | <b>-3,59044</b> | 1,779121                 | -1,59144        |
| Wall associated kinase 5                                    | -1,48518                 | <b>-2,48876</b> | -1,39717                 | -1,02946        |
| Wall-associated kinase family protein                       | 1,492177                 | <b>-3,34143</b> | <b>2,229683</b>          | <b>-2,0239</b>  |
| Xyloglucan endotransglucosylase/hydrolase 28                | 1,969525                 | <b>2,133212</b> | <b>2,319366</b>          | -1,40107        |
| Xyloglucan endotransglucosylase/hydrolase 16                | <b>-2,20407</b>          | <b>3,595355</b> | -1,15113                 | 1,237413        |
| cellulose synthase 1  | -1,92923                 | <b>-2,20433</b> | <b>-2,19626</b>          | -1,36881        |
| Cellulose synthase 1  | -1,86164                 | <b>-2,19446</b> | -1,86585                 | -1,0854         |
| Cellulose synthase A4                                       | <b>-6,75294</b>          | <b>3,060695</b> | <b>-5,23456</b>          | 1,659179        |
| Cellulose synthase A4                                       | <b>-7,19104</b>          | <b>2,383764</b> | <b>-5,01077</b>          | 1,52199         |
| Cellulose synthase family protein                           | <b>-6,822</b>            | <b>2,437408</b> | <b>-5,17519</b>          | 1,471333        |
| Cellulose synthase family protein                           | <b>-6,33174</b>          | <b>2,594023</b> | <b>-5,4938</b>           | 1,660726        |
| Cellulose synthase like G1                                  | 1,95238                  | <b>2,6244</b>   | 1,023708                 | <b>5,89779</b>  |

# Hydric balance contribute to drought tolerance by root and stomatal functionality



Future task:

Search of genetic component with simultaneously relevance on stomata and root functionality under osmotic stress conditions

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in plants J. Scharwies, J. Dinneny



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THANK  
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