GWAS of tomato response to water deficit: focus on major fruit quality traits

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Context

- Water scarcity is a crucial constraint for agriculture productivity.
- **Water deficit** can improve **tomato flavour** by concentrating the **major taste compounds** in the fruit, but the right balance must be found **to limit yield loss**. [1]
- There is a **high genetic variability** for response to water deficit in cultivated tomato (*S. lycopersicum*), in particular in **small fruited accessions** (*S. l. cerasiforme*). [2]

Objectives

Using small fruited accessions, we aimed to (1) characterize the pattern of **genotype by watering regime interactions** at the **phenotypic** & **genotypic levels,** and (2) identify the **major loci and genes** involved in tomato fruit quality variation under water deficit.

Materials & Methods

- **141 highly diverse small fruited accessions,** among which **4 were fully re-sequenced** [5]
- **Greenhouse** experiment with **two watering conditions**
  - well watered: WW
  - water deficit: WD = 40% WW
- **11 fruit traits**: fruit number, fresh weight (FW), dry matter (DMW), soluble sugar (SSC), ascorbic acid (VitC), glucose, fructose, pH, malic & citric acid content
- **6,501 SNP** genotyped over the genome (SOLCAP array)
- **Genome Wide Association (GWA):**
  - multi loci mixed model: **MLMM** [3] (highly polygenic traits)
  - multi trait mixed model: **MTMM** [4] (G x W tests)
- Publicly available **expression data** (tomato genome consortium)

Results

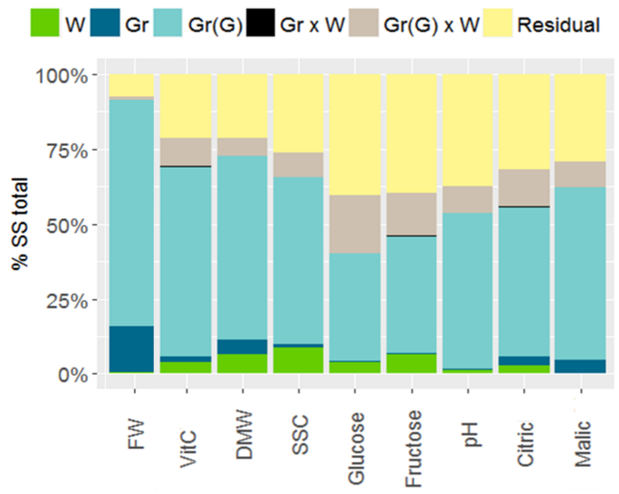

Fig 1 | Variance partitioning

← The trait variations resulted from **large genotypic** effects and **medium genotype by watering regime interaction** effects.
(W = watering, Gr = genetic group, G = genotype)

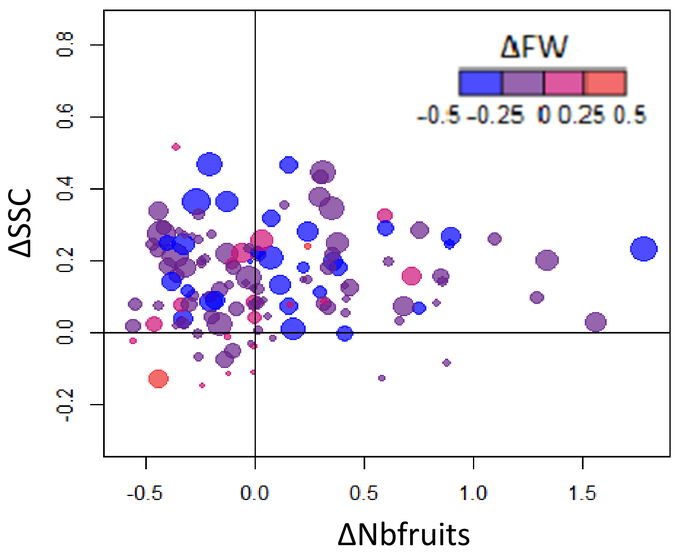

Fig 2 | Fruit quality & Yield variations
Δ = (WD-WW)/WW

↑ **Fifty accessions** (with small to medium fruit size) had **both improved fruit SCC and maintained fruit number** under WD.

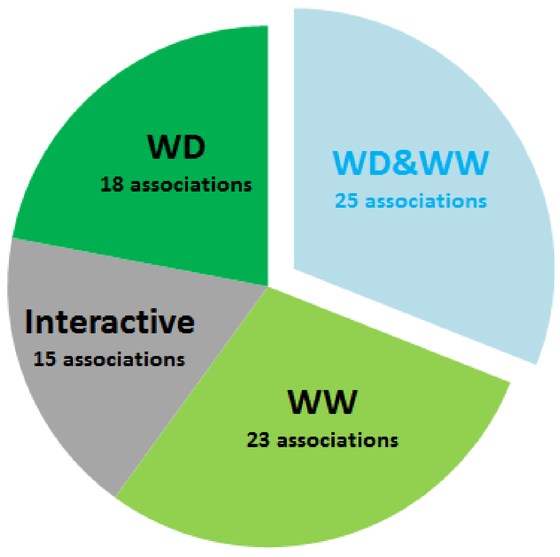

Fig 3 | Marker-trait associations according to their type

↑ A total of **81 associations** were identified, **51% were specific** to one condition (**WD** or **WW**) and **18% were interactive** with the watering regime.

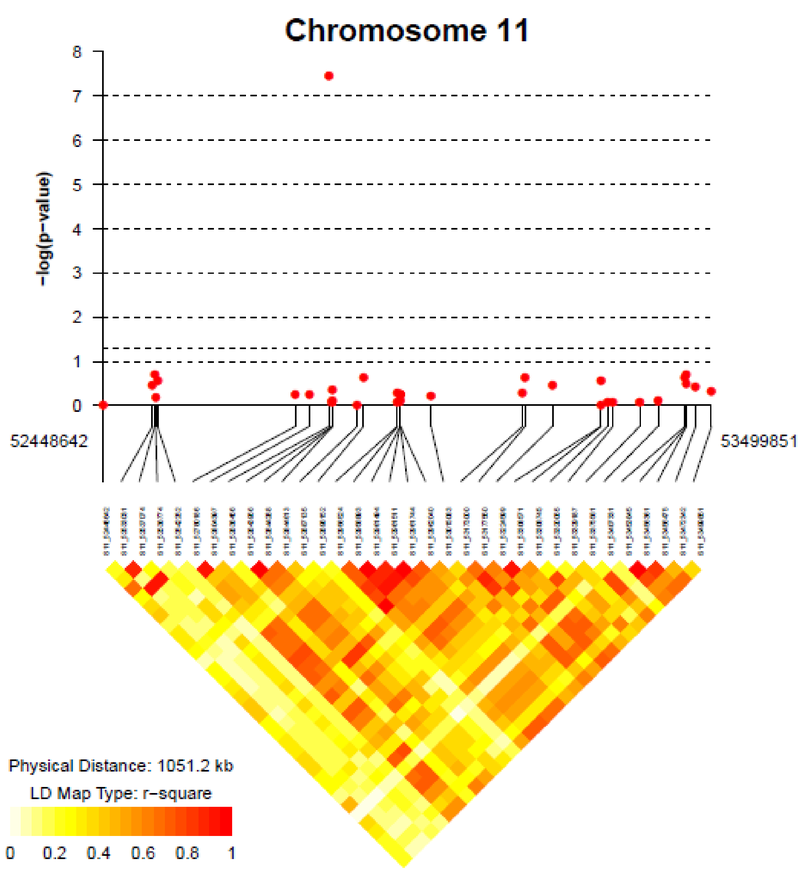

Fig 4 | Manhattan plot & LD heatmap

↑ An association was detected on chr11 for **Fructose under WD**, including in its linkage disequilibrium block **5 genes**, all **expressed in tomato fruit**. Among these genes, one encodes a '**Neutral Invertase**' with a **non-synonymous variants** between the 4 re-sequenced accessions of the GWA collection.

Take home messages

- ✓ Tomato **quality** could be **improved** under deficit irrigation **while maintaining yield**.
- ✓ The underlying genetic architecture relies on **numerous loci** with **small effects** and **varies with water availability**.
- ✓ **Genes** related to **sugar metabolism** were identified under some associations and could control the variations observed.

Funding

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References

[1] Ripoll et al. 2014
[2] Albert et al. 2016
[3] Korte et al. 2013
[4] Segura et al. 2012
[5] Causse et al. 2013

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