SUNFLOWER DROUGHT: QTLs DISCOVERY IN SEMI CONTROLLED CONDITIONS

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ABSTRACT

Drought is defined as a period of soil water deficiency affecting plant growth and ultimately final yield. Sunflower (*Helianthus annuus)* is a specie known for its plasticity under drought conditions. The main objective of this study was to identify QTLs that explain variation in yield under drought conditions in comparison to the irrigated ones and flowering QTLs.

A mapping population of 240 lines was developed (Single Seed Descent) from two cultivated lines SY1 and SY2 contrasting by their phenotype under drought conditions. The 240 lines have been crossed with a single tester, producing 240 hybrids. The hybrids were grown in open field under semi-controlled conditions. Then, flowering date and yield measures were obtained and by using genetic resources, QTL detection was carried out independently for each of two conditions: water-stressed (WS) and well-watering (WW).

Four QTLs were detected for **yield** and **three QTLs** were detected for **flowering** on chromosomes **5, 11, 13, 16** and **17**. Both yield and flowering QTLs were differentiated according to the watering conditions. The next step of this work is to perform fine mapping and ultimately introduce these QTLs in a drought susceptible line to validated the efficacy of the QTLs to provide drought stress tolerance.

MATERIALS & METHODS

Population was developed from lines SY1 and SY2 which have complementary traits under drought [1][2]. **240 hybrids** have been produced using a **common tester** and were tested on well watering and water stressed conditions (4 repetitions on complete randomization design).

SY1 x SY2
↓
240 RILS x Tester
↓
240 hybrids

- **Well-watering** condition :
  Watering regularly, optimal development of plants
- **Water-stressed** condition :
  Watering was stoped 10 days before flowering, stress conditions

Studied variables : **yield** and **flowering date**

Graneros, Chile

Phenotyping drought tolerance : **Yield** : kg/plot (2 rows/plot & 20 plants/row) and **flowering date** : date of 50% plants bloom in the plot

RESULTS & DISCUSSION

Constitutive QTLs

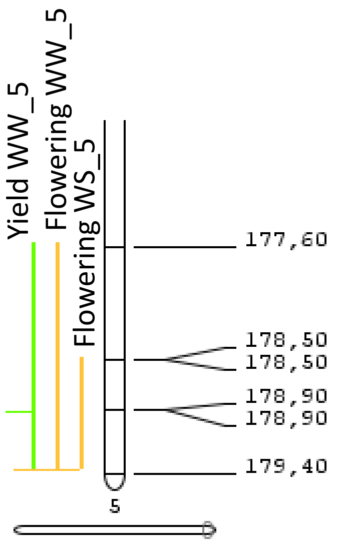

Figure 1 ***: QTLs detection on chromosome 5***

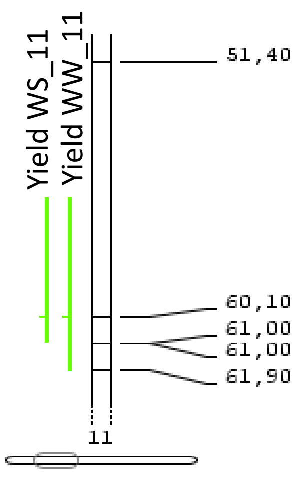

Figure 2 ***: QTLs detection on chromosome 11***

QTLs on chromosome 5 (flowering WS and flowering WW) and on chromosome 11 (yield WS and yield WW) are "constitutive", they are the same in well-watering and in water-stressed conditions [3] ***(Figures 1 and 2)***.

Adaptive QTLs on WS

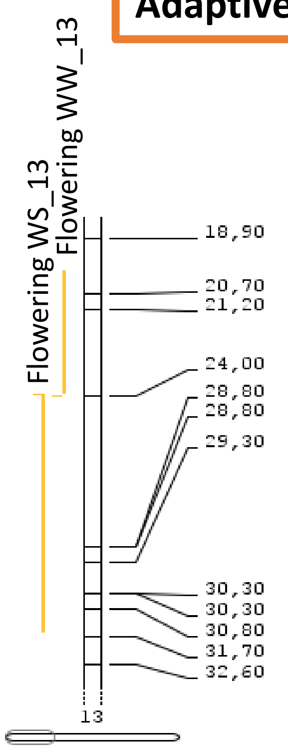

Figure 3 ***: QTLs detection on chromosome 13***

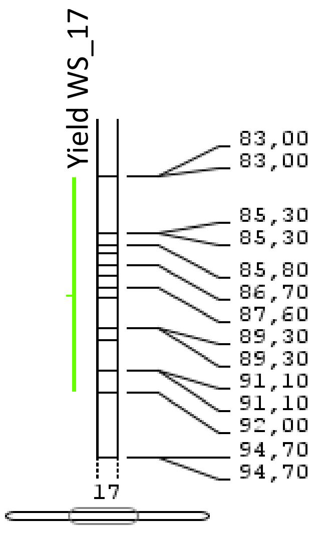

Figure 4 ***: QTLs detection on chromosome 17***

QTLs on chromosome 13 (flowering WS) and on chromosome 17 (yield WS) are "adaptive", they were detected only in water-stressed condition [4] (***Figures 3 and 4)***.

Adaptive QTLs on WW

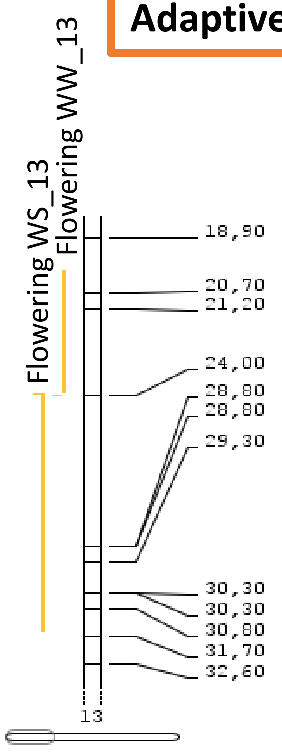

Figure 3 ***: QTLs detection on chromosome 13***

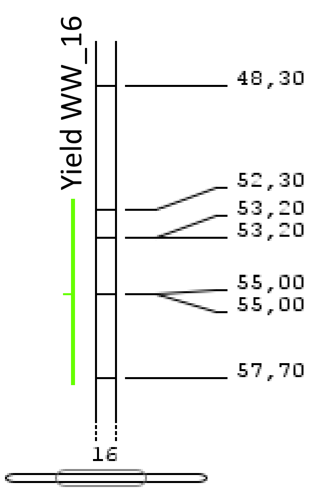

Figure 5 ***: QTLs detection on chromosome 16***

QTLs on chromosome 13 (flowering WW) and on chromosome 16 (yield WW) are "adaptive", they were detected only in well-watering condition (***Figures 3 and 5***).

Table 1 ***: QTLs detection on WW condition***

Trait	LG	LOD	Interval confiance (cM)
Yield WW_5	5	17,29	3,62
Flowering WW_5	5	30,7	1,81
Yield WW_11	11	4,32	6
Flowering WW_13	13	7,2	4
Yield WW_16	16	5,43	6

Table 2 ***: QTLs detection on WS condition***

Trait	LG	LOD	Interval confiance (cM)
Flowering WS_5	5	28,23	3,38
Yield WS_11	11	4,19	4,99
Flowering WS_13	13	6,35	7,72
Yield WS_17	17	4,12	9

All QTLs on chromosome 5 **(Figure 1)** have nearly same LOD and position **(Table 1 et 2)**. This maybe a unique QTL detected under different traits and conditions. It is the same case for QTLs on chromosome 11, it is probably a unique QTL **(Figure 2).**

FUTUR WORK

- QTLs validation by using new experiments in other environments.
- Determine QTLs biological functions by using sunflower physical mapping
- Reduce QTL zone by using fine mapping
- Improve breeding schema by introducing QTLs in sunflower pipeline

REFERENCES

[1] Henry, Camille. 2010. « Analyse de la variabilité génotypique des réponses au déficit hydrique du tournesol disponible au sein du matériel génétique de Syngenta. Evaluation de son impact potentiel sur l'amélioration de rendement en situation de déficit hydrique ». Montpellier, SupAgro.

[2] Radanielson, Ando Mariot. s. d. 2010 « Identification de nouveaux traits de sélection pour améliorer le rendement en conditions de déficit hydrique chez le tournesol Helianthus annuus L. ». Montpellier, SupAgro.

[3] Collins, Nicholas C., François Tardieu, et Roberto Tuberosa. 2008. « Quantitative Trait Loci and Crop Performance under Abiotic Stress: Where Do We Stand?: Table I. » *Plant Physiology* 147 (2): 469-86.

[4] Vargas, Mateo, Fred A. van Eeuwijk, Jose Crossa, et Jean-Marcel Ribaut. 2006. « Mapping QTLs and QTL x Environment Interaction for CIMMYT Maize Drought Stress Program Using Factorial Regression and Partial Least Squares Methods ». TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik 112(6)