

Identification of QTLs for *Fom* race 1.2 resistance using a genotyping by sequencing approach

Ramon Botet^{1,2}, Ana Garcés-Claver¹, José Ma^a Álvarez¹

¹Agrifood Research and Technology Centre (CITA). Avda. Montañana, 930. 50059, Zaragoza, Spain.

²Laboratory of Genetics, Wageningen University and Research (WUR), P.O. Box 16, 6700 AA, Wageningen, The Netherlands

Corresponding author. E-mail: agarc@cita-aragon.es. Tfno: +34976716560. Fax: +34976716335

Fusarium wilt of melon (*Cucumis melon* L.), caused by *Fusarium oxysporum* Schlecht. f. sp. *melonis* Snyder & Hans. (*Fom*) is an important disease spread worldwide. Race 1.2, subdivided into pathotype 1.2y (Yellow) and 1.2w (Wilt), overcomes all resistance genes described and could become a serious threat to this crop cultivation. The development of cultivars exhibiting enhanced resistance to *Fom* race 1.2 is an important objective of breeding programs.

Partial resistance to *Fom* race 1.2 was studied using a recombinant inbred line (RIL) population derived from a cross between cv. 'Piel de Sapo', a highly valuable cultivar, and 'BG-5384', a partially resistant line. Artificial inoculations were performed with a yellow strain and a wilt one and two environments, growth chamber and greenhouse. Genotyping was carried out by using genotyping-by-sequencing approach. Genotypic data for 2625 single nucleotide polymorphism (SNP) markers on twelve chromosomes were used for the association analysis, revealing polygenic control with 10 different small effect QTLs. Those showed to be environment specific, probably due to a high RIL – environment interaction, and pathotype specific in most cases. These results match with previously reported research. Further work will be made on fine-mapping regions of interest and determining the molecular basis of such a complex resistance.

Key words: disease resistance, genotyping by sequencing, melon, RILs, QTLs.