

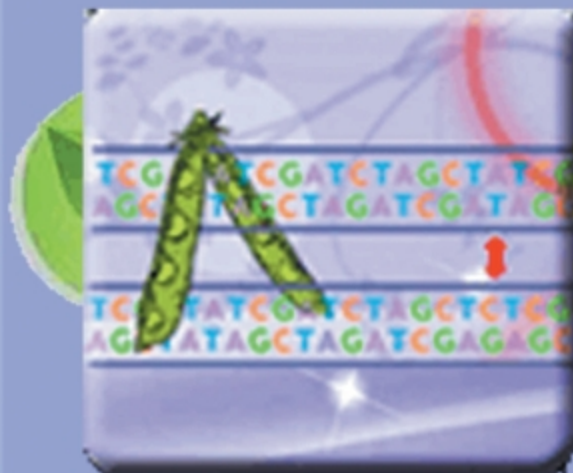


VISCEA

Vienna International Science
Conferences and Events Association

International Conference

Plant Genetics & Breeding Technologies III



Programme and Abstracts

Vienna, Austria
July 12-13, 2018

Construction of a Genetic Map for Cucumber and Mapping of PSL Gene and QTL for Angular Leaf Spot Resistance

Renata Słomnicka, Helena Olczak-Woltman, Aleksandra Korzeniewska, Katarzyna Niemirowicz-Szczytt, Grzegorz Bartoszewski

Department of Plant Genetics, Breeding and Biotechnology, Faculty of Horticulture Biotechnology and Landscape Architecture, Warsaw University of Life Sciences, Warsaw, Poland. Correspondence to: renata_slomnicka@sggw.pl

One of the most common cucumber (*Cucumis sativus* L.) diseases is angular leaf spot (ALS) caused by *Pseudomonas syringae* pv. *lachrymans*. Increased occurrence of this disease in cucumber open-field production has been observed over the last years. ALS symptoms may vary depending on the bacteria virulence, cucumber cultivar, and environmental conditions. The aim of this study was to construct advanced cucumber genetic map to map *psl* gene and quantitative trait loci (QTL) controlling ALS severity. RILs mapping population was developed from a narrow cross of cucumber line Gy14 carrying *psl* resistance gene and susceptible line B10. Parental lines and RILs were tested under growth chamber conditions for ALS symptoms. Genetic map was constructed based on SSR and DArTseq genome-wide genotyping. The *psl* gene was mapped on cucumber chromosome 5. To identify QTL for ALS resistance several approaches were tested and multiple-QTL model was used. Two QTL related to ALS severity were identified also on chromosome 5. Moreover, *psl* gene was placed within major QTL *psl5.1*. Constructed map could be useful in cucumber breeding programs and provides new insights into the angular leaf spot resistance in cucumber.