A high-throughput image analysis method for assessing pepper quantitative resistance to Cucumber mosaic virus

Judith Hirsch, Marion Szadkowski, Sylvain Piry, Christelle Lacroix, Louis McLeod, Benoît Moury, Véronique Lefebvre

To cite this version:

Judith Hirsch, Marion Szadkowski, Sylvain Piry, Christelle Lacroix, Louis McLeod, et al.. A high-throughput image analysis method for assessing pepper quantitative resistance to Cucumber mosaic virus. 15. International symposium of plant virus epidemiology, Jun 2022, Madrid, Spain. , 2022. hal-03689913

HAL Id: hal-03689913
https://hal.inrae.fr/hal-03689913v1

Submitted on 7 Jun 2022

A high-throughput image analysis method for assessing pepper quantitative resistance to Cucumber mosaic virus

J. Hirsch[1], M. Szadkowski[1], S. Piry[1,2], C. Lacroix[1], L. McLeod[3], B. Moury[1], and V. Lefebvre[3]

[1]Pathologie Végétale, INRAE, 84140 Montfavet, France; [2]CBGP, INRAE, CIRAD, IRD, Institut Agro, Univ. Montpellier, Montpellier, France; [3]INRAE, GAFL, F-84140 Montfavet, France.

(judith.hirsch@inrae.fr) *S6-P5*

Cucumber mosaic virus (CMV) is an economically important virus in pepper cultures worldwide. In the absence of curative methods, growing resistant cultivars is one of the main means of controlling plant viruses. Moreover, quantitative resistance is likely to be more durable than major gene resistance for controlling CMV in pepper. To gain insight into the genetic basis of quantitative resistance to CMV, we have explored natural variation in the response of pepper to CMV in order to perform a genome-wide association study (GWAS), focusing on the initial steps of infection in the inoculated leaves. A subset of 56 INRAE accessions belonging to the 423 accessions from the pepper core-collection of the G2P-SOL project (http://www.g2p-sol.eu/) were assessed for resistance to the N strain of CMV, which induces necrotic local lesions on mechanically-inoculated leaves. The percentage of leaf surface covered by local lesions was measured as a quantitative estimate of disease severity. A phenotyping method based on automated analysis of scanned leaf images was developed. Measurement of the leaf surface was automated using ImageJ software and was associated with accession code, plant number and leaf number using datamatrices and a dedicated R script. An analysis process using deep learning was set up to automatically detect lesions and estimate the total surface of lesions. Pepper plants infected by CMV showed a quantitative response, with pepper accessions displaying a continuum of resistance levels, from highly susceptible to highly resistant. The automated data acquisition and deep-learning pipelines make it possible to scale up the phenotyping process and analyze a much larger panel of accessions, as required in GWAS. By combining the phenotypic data reported here with the high-density genotypic dataset obtained on the G2P-SOL pepper core-collection, a GWAS will be conducted to identify Quantitative Trait Loci and candidate genes underlying early resistance to CMV.