

Transcriptomic profile analysis of the pre-disposition geminiviral infection in Capsicum chinense BG-3821

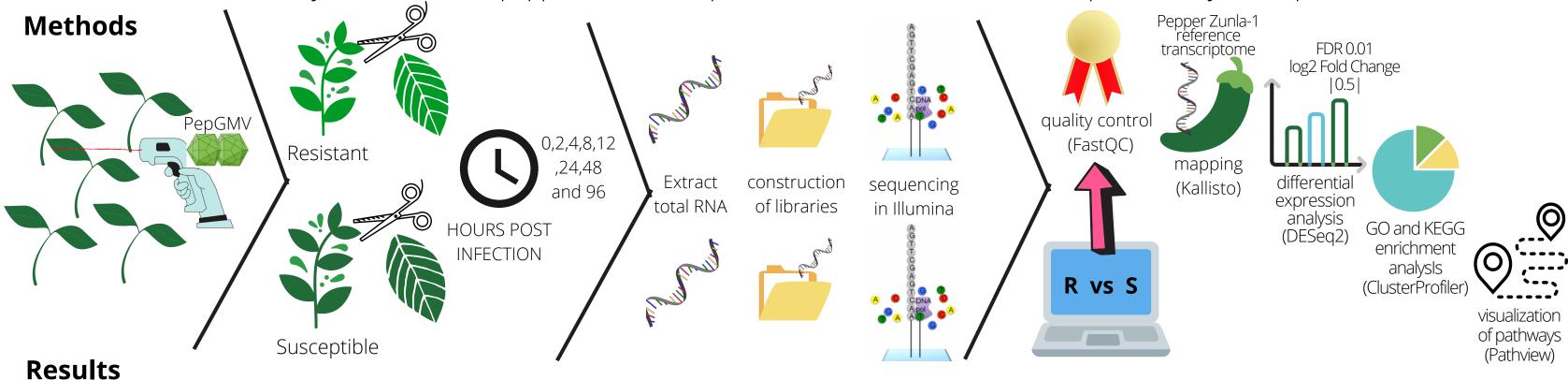
Mónica de Jesús Rodríguez-González 1, José Luis Pablo-Rodríguez 1, Diana L. Trejo Saavedra 1, Octavio Martínez-de la Vega 2, Rafael F. Rivera-Bustamante 1.

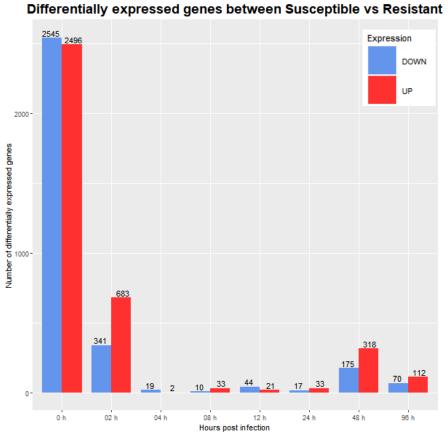
- 1. Unidad Irapuato, Departamento de Ingeniería Genética, Centro de Investigación y de Estudios Avanzados (Cinvestav) del IPN, Km. 9.6 Libramiento Norte, C.P. 36821, Irapuato, Guanajuato, México.
- 2. Laboratorio Nacional de Genómica para la Biodiversidad (Langebio), Cinvestav, Campus Guanajuato, Apartado Postal 629, C.P. 36500, Irapuato, Guanajuato, México.

Corresponding author e-mail address: monica.de.rodriguez@cinvestav.mx

Introduction

Geminiviruses are part of an important family of plant viruses that infect a wide variety of crops worldwide. In Mexico the geminivirus PepGMV has emerged as an important problem in pepper, tomatoes, and other crops. PepGMV is spread widely throughout the country and is transmitted by whiteflies, a vector present in tropical and subtropical climates. Mexico is the main producer of habanero pepper worldwide; this species of pepper is grown mainly in the Southeast of Mexico, a region that also favours whiteflies populations. The habanero pepper accession BG-3821 has demonstrated a resistant mechanism to PepGMV and mixed infections with other geminivirus, this mechanism was characterized by early activation of defence mechanisms, including restriction of viral movement from the areas where the mechanical infection was carried out. This study aimed to elucidate the mechanisms by which habanero pepper can resist PepGMV infections, therefore, a transcriptomic analysis was performed.





between Susceptible vs Resistant habanero pepper plants.

Differential expression analysis indicated that resistant and susceptible plants were very different by time 0 hours preinfection (hpi), displaying more genes differentially expressed between both phenotypes (5041 DEGs), as shown in Figure 1. We analysed the GO terms and KEGG pathway by enrichment analyses, to interpret the differences between both plants that occur even before infection. From all the enriched routes at time O hpi, one with the greatest presence is the biosynthesis of jasmonic acid, which has been reported as an important route to start a signalling cascade route where several products of this pathway work as a signal (1). In addition, jasmonates, such as methyl jasmonate (MeJA), have been reported in Capsicum Figure 1. Bar plot of differentially expressed genes anuumm as an inducer of PR-proteins (2).

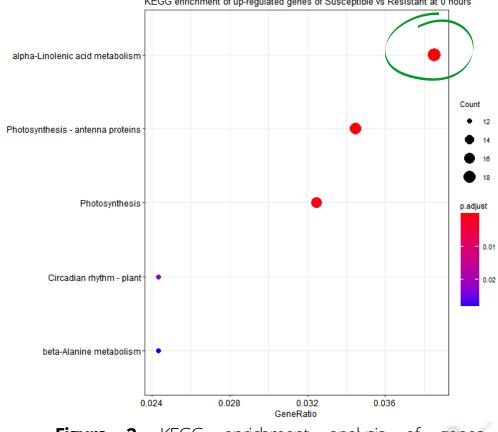


Figure 2. KEGG enrichment analysis of overexpressed at time 0 hpi.

Conclusions

It is suggested that resistant habanero pepper plants could present an overexpression of the JA biosynthesis pathway, as (3) mentioned for resistant maize plants, research is now continuing focused on transcription factors related to JA biosynthesis.

References

- 1.Sabater-Jara, A. B., Almagro, L., Belchí-Navarro, S., Ferrer, M. A., Barceló, A. R., & Pedreño, M. A. (2010). Induction of sesquiterpenes, phytoesterols and extracellular pathogenesis-related proteins in elicited cell cultures of Capsicum annuum. Journal of plant physiology, 167(15), 1273–1281. https://doi.org/10.1016/j.jplph.2010.04.015
- 2. Zhang, L., Zhang, F., Melotto, M., Yao, J., & He, S. Y. (2017). Jasmonate signaling and manipulation by pathogens and insects. Journal of experimental botany, 68(6), 1371–1385. https://doi.org/10.1093/jxb/erw478
- 3. Shivaji, R., Camas, A., Ankala, A. et al. Plants on Constant Alert: Elevated Levels of Jasmonic Acid and Jasmonate-Induced Transcripts in Caterpillar-Resistant Maize. J Chem Ecol 36, 179–191 (2010). https://doi.org/10.1007/s10886-010-9752-z







