Abstract: Resistance to *X. fastidiosa* was evaluated in 10 six year old hybrids of crosses between Murcott tangor [*Citrus reticulata* Blanco x *Citrus sinensis* (L.) Osbeck] and Pera sweet orange [*Citrus sinensis* (L.) Osbeck] under field conditions. Healthy hybrids were grafted with buds collected from plants of Pera sweet orange infected with *X. fastidiosa*, forming a plant with two scions. We evaluated the symptoms of citrus variegated chlorosis (CVC), bacterial multiplication and differential gene expression in both scions. Hybrid scions had no symptoms, however three of them had bacteria detected by quantitative PCR (qPCR). Indeed, all scions that originated from buds collected from plants of Pera sweet orange infected with *X. fastidiosa* showed symptoms of CVC. We next monitored 13 defense-related genes by real-time quantitative PCR (qPCR). We suggest that some of these genes are involved with resistance of the hybrids to *X. fastidiosa*, since their expression was significantly higher in the resistant hybrid scions than in tolerant hybrids and scions originated from infected Pera sweet orange buds. Furthermore, we carried out Pearson's correlation analysis between gene expression, multiplication of bacteria and the presence of symptoms. Canonical correlation analysis revealed a relationship between the expression of these genes and hybrid scions, and also between scions that originated from infected buds and the presence of the bacteria and plant symptoms.

Bibliography

Coletta Filho, H.D.; Pereira, E.O.; Souza, A. A. De; Takita, M. A.; Cristofani-Yaly, m. & machado, m. A. Analysis of resistance to *Xylella fastidiosa* within a hybrid population of Pera sweet orange × Murcott tangor. Plant Pathology, v.56, 2007.

3.3 Conserved genetic defense response against *X. fastidiosa* subsp. *pauca* in olive and citrus

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Abstract: X*. fastidiosa* subsp. *pauca* causes diseases in citrus and olive plants. Fortunately, there are citrus species and olive varieties more tolerant to *X. fastidiosa* and therefore good genotypes to search for genetic sources of resistance. Following this approach, global gene expression analyses were recently achieved using *Citrus reticulata* cv. Ponkan and *Olea europaea* cv. Leccino allowing the identification of potential genes involved in plant defense response. Thus, the objective of this work was to identify key genes involved in common genetic defense responses that could be further explored to get resistant varieties. Overall we identified two main mechanisms for both plant species: i. Bacteria recognition and ii. Cell wall fortification. The former involve the expression of pattern-recognition receptors, which recognize pathogen molecular patterns and trigger cell defense responses. Some of these receptors belong to the LRR-XII group which contains cell surface immune receptors. The latter involves downregulation of genes in tolerant host such as expansin, pectate lyases and polygalacturonases, related with cell wall expansion and degradation. This suggests that in tolerant hosts, plant cell recognizes *X. fastidiosa* and reprograms the cell wall development to impair its colonization through the xylem vessels. Therefore these genes represent good candidates to be explored aiming their use in breeding and/or genetic engineering program.

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Bibliography

Giampetruzzi A., Morelli M., Saponari M., Loconsole G., Chiumenti M., Boscia D., Savino V.N., Martelli G.P. & Saldarelli P. 2016. Transcriptome profiling of two olive cultivars in response to infection by the CoDiRO strain of *Xylella fastidiosa* subsp. *pauca*. BMC Genomics 17:475.

Rodrigues C.M., De Souza A.A., Takita M.A., Kishi L.T. & Machado M.A. 2013. RNA-Seq analysis of *Citrus reticulata* in the early stages of *Xylella fastidiosa* infection reveals auxin-related genes as a defense response. BMC Genomics 14: 676.