

CTV-INDUCED MODULATION OF THE *CITRUS* BARK PROTEOME –AND PHOSPHOPROTEOME – DURING COMPATIBLE AND INCOMPATIBLE INTERACTIONS

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Citrus tristeza virus (CTV) is the causal agent of various diseases with dramatic effects on citrus crops (*tristeza*, *stem pitting* and *seedling-yellow* syndromes). It causes the collapse and necrosis of sieve tubes and companion cells leading to the production of an excessive amount of non functional phloem, and the reduction of the root system. The tristeza disease occurs with wilt symptoms and leads to a complete decline of the susceptible plant in a few weeks. The propagation of *Citrus* spp. on tristeza-tolerant rootstocks is the only viable option to lower the incidence of this disease on citrus crops. Although CTV structure, genome organization and expression have been well characterized, little is known about the molecular mechanisms of this host-pathogen interaction, and the actual role of scion-rootstock interactions in the modulation of the response to CTV infection is still unknown. Global analysis of bark proteome and phosphoproteome has been carried out by means of 2DE in Tarocco Scirè sweet orange grafted either on sour orange or Carrizo citrange rootstocks (respectively susceptible and resistant to CTV), in infected and uninfected conditions. Three biological and technical replicates were performed for each experimental condition producing 36 2DE maps that were analyzed by the Progenesis SameSpots software (Nonlinear Dynamics, UK). 2DE analysis led to the identification of 125 protein spots differentially accumulated and 97 spots modulated by phosphorylation in the two scion-rootstocks combinations, in infected or uninfected conditions. Differentially accumulated spots were validated by statistical analysis and manually picked up from gels for trypsin digestion and LC/MS/MS analysis, leading to the identification of the protein patterns putatively associated to the resistance/susceptibility of citrus plants to the tristeza disease. The analysis of changes in protein phosphorylation patterns will highlight the possible role of this post-translational modification in the plant response to CTV infection, also providing further insight about scion-rootstock interaction in citrus.