

sequences against grape protein databases translated from the available grape EST databases in NCBI. Three up-regulated proteins, thaumatin-like protein, heat shock protein STI (stress-induced protein) and lipoxygenase were identified in resistant genotype only. The level of differential expression sharply increased for thaumatin-like protein as the disease progressed. In contrast, a putative GTP-binding protein was down-regulated in susceptible genotype only. In addition, a putative ripening-regulated protein, superoxide dismutase [Cu-Zn], enolase, and three heat shock protein 17.9 kDa, 18.6 kDa and protein 26 were found higher expression in resistant genotype in compared with the proteins in susceptible genotype. Our findings indicate that the differentially expressed proteins in response to *Xf* infection are genotype, tissue types and developmental stages dependent. The characterization of the roles among these candidate proteins is in progress. Revealing molecular mechanisms and biological functions of these proteins will help improve crop performance against PD.

Molecular characterization of *Fusarium oxysporum* isolates from koa (*Acacia koa*) in Hawaii

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Acacia koa (koa) is a very important native tree in Hawaii. However, many koa forests and plantations suffer from serious wilt and dieback. The major causal agent of the disease was previously shown to be *Fusarium oxysporum* (FO). Genetic diversity of 129 FO isolates from Hawaiian koa plants were evaluated for DNA polymorphism using amplified fragment length polymorphism (AFLP) markers. Four FO isolates from conifer seedlings and one (Fo47) used as biological control agent were also included for comparison. A total of 420 informative AFLP markers were scored among the isolates using eight *EcoRI-MseI* primer combinations. Cluster analysis showed that 113 of the isolates formed six major clades and the other 21 isolates were clustered into smaller clades or outliers. Correlations were not found between AFLP clades and isolate locations or host origins. Some isolates collected from different islands or different sources (rhizosphere soil, healthy and diseased tissues, seedlings and seeds) were clustered into the same AFLP clades. Our results suggest that migration of FO populations might have occurred recently among different islands. Pathogenicity testing of isolates will be used to reveal potential relationships between virulence and molecular groupings.

Diverse virulence and fitness functions are regulated by VsrAD in *Ralstonia solanacearum*

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Ralstonia solanacearum, which causes bacterial wilt disease of many crop plants, depends on quantitative virulence factors that are controlled by a complex regulatory network. The VsrA/D two-component regulator was