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109. A summary of National Survey and Compliance Testing for *Phytophthora ramorum* by NPGBL -- 2005-2006. Zeller, K. A., Twieg, E. N., Picton, D. D., Negi, S. S., Owens, K. J., DeVries, R. M., and Levy, L. Phytopathology 97(7)Suppl:S129. 2007.

A summary of National Survey and Compliance Testing for *Phytophthora ramorum* by NPGBL – 2005–2006

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Routine diagnoses of samples provided as part of operational testing for *Phytophthora ramorum* (PR), causal agent of Phytophthora blight and of Sudden Oak Death, during 2005 and 2006 have utilized a combination of validated conventional and Real-time PCR diagnostics. Over this period, we have used 3 PCR assays to test >3100 sample DNAs from 43 states, and from >55 plant genera. In both years the most commonly submitted samples were from *Rhododendron* (excluding Azalea), and were also the most often diagnosed as positive for PR. Other host genera frequently diagnosed as positive for PR included *Camellia, Kalmia, Pieris* and *Viburnum.* Samples from other hosts were rarely submitted for testing, or were rarely or never diagnosed as positive. PR positive samples were not evenly distributed across the USA. Greater than 90% of all PCR positives were received from sites in CA, OR or WA. Other positive diagnoses were rare, broadly distributed among states, and could be traced to known sources. Our data suggest that PPQ efforts since 2004 to restrict movement and establishment of PR have been generally effective, but that vigilance needs to be maintained in order to confirm that the quarantine strategies in place maintain effectiveness.

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Fire blight, caused by *E. amylovora*, is a particularly devastating bacterial disease of apples and pears. Early studies in elucidating the molecular basis for pathogenesis have identified an essential virulence system - the *hrp* type III secretion system (*hrp*-T3SS) in *E. amylovora* which delivers effector proteins into host plants. Subtractive hybridization and genome sequence have revealed two novel T3SS PAIs (*Erwinia-p*athogenicity *i*slands, EPI1 and EPI2). The two PAIs are closely related to each other, have a significantly lower %G+C content (38.4 and 43.4% mol G+C, respectively, compared to 53.5% mol G+C content in the whole genome), and phylogenetically related to the tsetse fly endosymbiont *Sodalis glossinidius* SSR-1 and to human pathogens *Salmonella* SPI-1 and *Yersinia* Ysa T3SS-PAIs. In order to study the function, regulation and substrate specificity of EPI1 and EPI2, a PCR-based novel gene deletion approach was employed to generate whole island deletion mutants. Pathogenicity assay with immature pear fruit and apple seedlings showed that EPI1 and EPI2 are not involved in virulence in plants. These results indicated that both EPI1 and EPI2 are acquired by *E. amylovora* through horizontal gene transfer and may function during interaction with insect vectors. Future studies are needed to elucidate the role of EPI1 and EPI2 during interaction with insect vectors.