Identification of Avirulence Genes, Co- Structural Analysis and Detection of *Phytophthora infestans* Causing Late Blight of Potato

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Abstract—*New markers targeting avirulence genes of Phytophthora infestans were developed for rapid identification and detection of* Phytophthora infestans, *the causal agent of late blight of potato and tomato using PCR. Primers were developed for targeted avirulence genes (Avr1, Avr2, Avr3, Avr4, Avr blb1 and Avr bl) resulted in consistent amplification products .All newly developed primer pairs were specific for* P. infestans *and does not amplify with other* Phytophthora *species. In silico structure analysis including physicochemical characterization, secondary and tertiary structure analysis of all avirulence genes was done using different software. Physico-chemical characterization interprets properties such as pI, EC, AI, GRAVY and instability index and provides data about these proteins and their properties. Prediction of motifs was done by MEME for functional characterization. Three dimensional structures for these proteins were not available as yet at PDB. Therefore, homology models for avirulence proteins were developed. The modelling of the three dimensional structure of these proteins were done by Swiss model and pocket sites in the protein were identified by Metapocket. PROCHECK was used to appraise the steriochemical properties of protein and result revealed that most of the residues were in the favoured region which is required for good quality model. This is the first report on the use of Avirulence gene as a molecular diagnostics in Phytophthora infestans and the prediction of 3D structure of Avr genes that could be used to predict the molecular function and interaction of the Avr gens to the host during pathogenesis.*