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Bioinformatics tools for identification of pathogenic factors

Altino Branco Choupina[1,2]

[1]Instituto Politécnico de Bragança, Escola Superior Agrária de Bragança, Campus de Santa Apolónia, Apartado 1172, 5301-854 Bragança [2]Cimo - Centro de Investigação da Montanha, Campus de Santa Apolónia, Apartado 1172, 5301-854 Bragança, Portugal

The culture of the chestnut tree is extremely important in the northern region of Portugal, occupying a significant proportion of useful agricultural area. The annual average chestnut production in Portugal can reach 20 000 tons. New plantation areas have increased in the last few decades. However the ink disease caused by the oomycete Phytophthora cinnamomi has damage and killed many trees and up to now no concrete solutions have been offered to control the illness. As a consequence, the disease propagation in the orchards of chestnut trees has been causing severe productivity and yield breaks. In addition to the economical losses, the importance of sociological and landscape aspects for the region cannot be neglected.

The oomycetes form a phylogenetically distinct group of eukaryotic micro-organisms that includes some of the most notorious pathogens of plants. Among these, members of the genus Phytophthora cause enormous economic losses on crop species as well as environmental damage in natural ecosystems. Phytophthora cinnamomi is the most widely distributed Phytophthora species, with nearly 1000 host species. Although they have a filamentous growth habit oomycetes are distantly-related to fungi and possess distinct mechanisms for pathogenicity. Consequently fungicides rarely control them and the few anti-oomycete products are often overcome by resistant pathogen variants. There are no eradication methods available to combat those species.

Oomycetes species can manipulate biochemical and physiological processes in their host plants through a diverse array of virulence or avirulence molecules, known as effectors. In susceptible plants, these effectors promote infection by suppressing defense responses, enhancing susceptibility, or inducing disease symptoms. Alternatively, in resistant plants, effectors are recognized by the products of plant resistance genes, resulting in host cell death and effective defence responses known as the hypersensitive response (HR). We've identified and characterized some proteins involved in mechanisms of infection by Phytophthora cinnamomi: endo-1,3-beta-glucanase (complete cds), exo-glucanase (partial cds); glucanase inhibitor protein (GIP) (complete cds); necrosis-inducing Phytophthora protein 1 (NPP1) (complete cds), transglutaminase, under the projects Identification, characterization and role of molecular factors associated with the mechanisms of infection of Fagaceae species by Phytophthora cinnamomi, PTDC/AGR-AAM/67628/2006, funding by FCT; Combating by molecular methods to ink-disease of chestnut and other regional cultures, COMBATINTA/SP2.P11/02 - Interreg IIIA, funding by FEDER, among others.

Several technologies, such reverse transcriptase PCR, in vivo expression technology, and Bioinformatics tools have been used to study the expression of selected genes from fungi during infection. In this work we intend to integrate the necessary bioinformatics tools that were used in this investigation. These tools include the use of Databases and associated homology programs as Fasta and Clustal, and several programs for sequence analysis and design of experiments such PCR.