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Poster Abstract - D.48

IDENTIFICATION OF RESISTANCE GENE TO *RALSTONIA SOLANACEARUM* IN POTATO

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Bacterial wilt of potatoes caused by *Ralstonia solanacearum*, which used to be a widespread disease in tropics and subtropics, has become a threat to potato production in temperate regions. It can affect more than 200 plant species among which tobacco, banana, tomato and potato. The diploid wild species *Solanum commersonii* has several desirable characteristics including cold tolerance and resistance to *R. solanacearum*. The bacteria enters plant roots via wounds or where secondary roots emerge, colonizes the root cortex, invades xylem vessels and rapidly spreads throughout the vascular system. During colonization of host plants, *R. solanacearum* produces a variety of extra cellular products that contribute to pathogenesis and cause disease symptoms. The aim of this study is to better understand the biochemical and molecular basis of plant-pathogen interactions in resistant/susceptible response.

Since in the compatible interaction polysaccharides of *R. solanacearum* play an important role for pathogenesis, isolation and partial purification of extracellular polysaccharide (EPS) from lyophilised culture filtrate and of lipopolysaccharide (LPS) from lyophilised cells of bacteria were carried out. The crude polysaccarides (EPS and LPS) and the filtered culture medium were tested to study whether they have a phytotoxic effects on plants. Preliminary analyses provided evidence of their phytotoxic effect. Other tests will be performed to investigate the chemical composition of phytotoxic compounds.

In order to identify differential genes expressed during the interaction between *R. solanacearum* and host plants, the cDNA-AFLP-TP technique was carried out on the resistant *Solanum commersonii* and the susceptible *Solanum tuberosum* cv Blondy. RNA was extracted from both genotypes 6, 24, 48 and 72 hours after inoculation. Up till now, 32 primer/enzyme combinations were tested and around 40 bands were observed for every combination. A clear uniformity of the samples at 6 and 24 hours after inoculation was found, whereas in the successive times, some polymorphisms induced after infection in both resistant and susceptible genotypes or only in one of them, were evidenced. The polymorphic fragments are being extracted from gels and subsequently, sequenced in order to define if they may represent genes involved in the interaction.

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