

PROTEOME ANALYSIS OF RESISTANT AND SUSCEPTIBLE MAIZE RESPONSES TO SOUTHERN CORN RUST DISEASE

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Proteomics is not only a powerful molecular tool for describing complete proteomes at the organelle, cell, organ or tissue levels, but also for comparing proteomes affected by different physiological conditions, such as those resulting from the infection diseases. In the present study, in order to characterize responsive proteins and metabolic alterations in resistant and susceptible maize genotypes against *Puccinia polysora* infection, we had compared their proteome by 2D-electrophoresis and MALDI-TOF-TOF analysis. We had identified proteins down-regulated on both genotypes during infection process and one defense related protein (germin like) up-regulated 24 hours after infection only in the resistant genotype. The susceptible genotype shows down regulation on key enzymes from photosynthesis, acid citric cycle, glioxilate cycle and gluconeogenesis, six hours after infection. The resistant genotype shows a better control of its metabolism once fewer proteins are down-regulated. These data explain many agronomic parameters caused by this fungi disease like reduced grain production, premature desiccation, death of corn plant and give us new insights about the molecular mechanisms of maize resistance to southern corn rust disease.

Key word: maize defense response / southern corn rust disease