

Genomics of the *Crinipellis perniciosa*-*Theobroma cacao* pathosystem (witches' broom).

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Theobroma cacao is the solely source of chocolate used in the confectionary industry. Brazil was one of the major producing countries until 1989, when the hemibiotrophic fungus *C. perniciosa*, the causal agent of the witches' broom disease, was accidentally introduced in Bahia, the major producing region in Brazil. As a result, the production dropped almost 75%, from 400,000 tons/year to 100,000, in the 90's. The social and environmental consequences were enormous, with degradation of the Atlantic Forest fragments associated with the cacao. Several efforts (resistant genotypes, pruning) were introduced in an attempt to overcome this situation, but none of them was totally effective. Understanding this, a genome program was launched in 2000, supported by the State of Bahia and subsequently by CNPq. A comprehensive model for the disease was drawn largely based on the finding of specific genes and experimentation related to them. The process starts when monokaryotic spores germinate in meristems, penetrating the tissues occupying the intercellular space (biotrophic phase). We found that the infection induces the accumulation of calcium oxalate crystals, which are abundant in susceptible plants. The oxalate degradation releases hydrogen peroxide, that, together with several substances, like theobromine, caffeine and alkaloids, might compose the initial plant defense strategy. We found a fungus alternative oxidase which expression could be responsible for resistance to peroxide. Within the plant, the peroxidation of auxins could lead to hormonal imbalance explaining the hypertrophic green broom. The green broom turns dry in a well-defined PCD process induced by the pathogen. Simultaneously, the fungus becomes necrotrophic. An identified necrosis inducing protein may be crucial for this change, accelerating necrosis, immobilizing nutrients at the infected tissues. The last step is the basidiocarp formation, which starts after environmental and biochemical signals possible involving light receptors found in the *C. perniciosa* genome. The knowledge obtained with the program is allowing us to design strategies to cope the disease.