

Genetic Basis of Resistance in *Eucalyptus* spp. Pathosystems

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Eucalyptus is the most widely planted hardwood crop in worldwide tropical and subtropical regions because of its high growth rate, coppicing capacity, broad adaptability and multipurpose wood properties. Until the 1970s, the *Eucalyptus* plantations in Brazil were practically disease-free. However, plantations have continued to expand into warmer and more humid areas that are more favorable to pathogen infection. Furthermore, the use of high-yielding genotypes with unknown disease resistance, the implementation of clonal forestry, and the introduction of new management techniques have favored the emergence of disease epidemics in recent decades. Presently, prominent diseases such as rust (*Puccinia psidii*), ceratocystis wilt (*Ceratocystis fimbriata*), and canker (*Chrysoporthe cubensis*) are the most damaging diseases in *Eucalyptus* plantations. During recent years, we have conducted a series of inoculation experiments with controlled-crossed progenies to better understand the genetic basis of resistance for the prominent *Eucalyptus* pathosystems.

Resistance to rust occurs naturally in many *Eucalyptus* species and it is predominantly expressed by a hypersensitive reaction (HR). In 2003, we identified and mapped the first rust-resistance major locus (*Ppr-1*) in a controlled-pollinated family of *E. grandis*. The locus *Ppr-1* was positioned on the reference genetic map for *Eucalyptus* on the linkage group 3. Additionally, its position was validated by association genetics in one related and two unrelated background families. These results are consistent with the hypothesis that *Ppr-1* controls a large proportion of the variation for rust resistance in *E. grandis*. In recent studies, analyses of several inter-specific families, displaying different segregation patterns for rust resistance, provided additional evidence that the genetic control of rust resistance in *Eucalyptus* is more complex and includes quantitative resistance traits.

In other disease screening tests, estimates of resistance heritability to ceratocystis wilt were based on data from 10 inoculation experiments with hybrid families derived from crosses of *E. grandis* × *E. urophylla* genotypes. The statistical analyses indicated high genetic variability for resistance to ceratocystis wilt in both species. Estimates of individual narrow (50%) and broad (59%) sense heritability suggest a high degree of additive genetic control and low allelic dominance influencing the trait. High genetic variation among and within families appeared associated with contributions to high heritability and genetic gains for resistance to ceratocystis wilt.

For the *C. cubensis-eucalyptus* pathosystem, we evaluated resistance in *E. grandis* and *E. urophylla* parents, as well as in individuals from their crossed progenies. Six-month-old plants were inoculated, and xylem and bark lesions were measured at 8 months post-inoculation. The results demonstrated that xylem lesions should be used for selection of resistant clones. The phenotypic analyses indicated the existence of a high genetic variability for resistance in both species. Individual narrow and broad sense heritability estimates were 17% and 81%, respectively, suggesting that canker resistance is a quantitative trait and highly dependent on dominance and epistasis.

Studies have also been conducted to understand the genetic structure of the pathogen populations to provide a controlled basis for selecting resistant genotypes.