

Genetic engineering applied to the development of plants resistant to viruses and fungi**Francisco JL Aragão¹, Faria JC², Dias BBA¹, Ribeiro SG¹, Tinico ML¹, Cunha WG¹, Cruz ARR¹.**¹Embrapa Recursos Genéticos e Biotecnologia, Brasília, DF, Brazil; ²Embrapa Arroz e Feijão, Santo Antônio de Goiás, GO, Brazil. E-mail: aragao@cenargen.embrapa.br

Plant genetic engineering has promised researchers improved flexibility with regard to the introduction of new traits into cultivated crops. A variety of approaches has been applied to produce pathogen-resistant transgenic plants, some of which have proven to be remarkably successful, especially for virus, nematode, and more recently for fungal resistance. Since the first reports of CMV-resistant transgenic plants, many strategies have been utilized to achieve virus-resistant plants (VRP), mainly involving expression of the coat protein (CP) genes, transdominance and post-transcriptional gene silencing (PTGS). In order to obtain common bean plants resistant to the Bean golden mosaic virus we transformed plants with the viral genes *Rep-TrAP-REn* and *BCI* cloned in antisense orientation and two transgenic lines presented delayed and attenuated viral symptoms. Using the strategy

of transdominance, transgenic bean lines (expressing a mutated *rep* gene) revealed resistance to the virus. More recently, the concept of using RNAi construct to silence the *ACI* viral gene has been explored to generate highly resistant transgenic common bean plants. A similar strategy has been used to achieve Geminivirus-resistant tomatoes. Regarding fungal resistance, we have developed strategies to express some antimicrobial genes, mainly those coding for small peptides, to obtain *Sclerotinia*-tolerant lettuce and soybean lines. Studies on the behavior of transgenic plants under field conditions have been conducted. Biotechnological tools complement those from classical breeding and have the potential to accelerate the generation of new varieties containing genes from agronomic traits, which are difficult to be found in the primary or secondary gene pool.

MESA REDONDA 4-A**Aplicações de microscopia no estudo da interação planta-patógeno**

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Applications of electron microscopy to plant pathology: emphasis on plant-pathogen interactions**Richard J. Zeyen.** Department of Plant Pathology, University of Minnesota, Saint Paul, Minnesota, USA. E-mail: richz@umn.edu

Human beings are visually oriented. Nearly 90% of the information a normal human takes in comes in the form of visual images. Human learning and understanding require visualization. Microscopes aid this learning requirement by making objects "visible" to us that our eyes cannot see. Indeed, we would know little or nothing about the microbial world were it not for various types of microscopes. Limitations of the resolving power of light microscopy spurred the invention and utilization of electron microscopy, so that we might "see" even smaller objects. Today electron microscopes are essential tools for plant pathologists. The images from these instruments make it possible for us to visualize plant-pathogen interactions. Images from various types of microscopes (correlative microscopy) when joined with results from biochemistry, genomics and molecular biology experiments, add great depth and comprehension to our understanding of plant-pathogen interactions.

An example for correlative microscopy**The Powdery Mildew Disease of Cereal Crops**

Powdery mildew disease of cereal crops is one of the most wide spread and damaging of cereal diseases. The development of the causal agent, *Blumeria graminis* (an epidermal penetrating, biotrophic fungus,) and corresponding cereal plant epidermal cell responses have been studied using light microscopy for more than 100 years. Modern studies of *B. graminis* and cereal plant epidermal cell interactions use correlative microscopy. In these studies various tissue preparation protocols and types of light, scanning electron and transmission electron microscopy are correlated with biochemical, molecular and molecular genetic data to give a comprehensive and deep understanding of this plant-pathogen interaction.