SEARCHING FOR NUCLEOTIDE BINDING SITES OF RESISTANCE GENES IN WILD *ARACHIS* GERMPLASM

D.BERTIOLI (david@cenargen.embrapa.br); S.LEAL-BERTIOLI; J.F.M.VALLS and P.GUIMARÃES

Embrapa Recursos Genéticos e Biotecnologia

Perhaps the most economically important use of wild germplasm has been the integration of resistance genes (R genes) into cultivated varieties by plant breeding. Resistant crop varieties are an efficient, cost-effective and environmentally-friendly method of pest control. Although the successes of plant breeding have been enormous, it is limited by sexual incompatibility and the complexity of the breeding process. This could be overcome by the use of genetic engineering to introduce R genes into cultivated species considering that plant transformation using some cloned resistance genes have shown that R-genes remain functional when transferred between species. In this work, we used a PCR based approach to search for conserved regions in R genes in wild accessions of *Arachis* spp., especially the N-terminal nucleotide binding site (NBS). The products of PCR using this approach consisted of complex mixtures containing NBS regions, all of about 500bp. These products were cloned and sequenced, and showed high nucleotide homology to known functional R genes, therefore, they can be referred to as R gene analogues (RGAs). The clones sequenced could be grouped into seven different classes, with more than 95% homology within the same class and less than 70% homology between classes. Members of the same class occur in different *Arachis* species. Presently we are also screening a number of accessions in the section *Arachis* from the germplasm bank in Embrapa for resistance against root-knot nematodes. Accessions resistant and susceptible to these nematodes will be used to develop segregating populations which will be used to map these RGAs. We plan to extend this work to other sections and other pests and pathogens.

Key words: *Arachis*, resistance genes, nucleotide binding sites.