

USE OF A PCR BASED APPROACH TO IDENTIFY NUCLEOTIDE BINDING SITES OF RESISTANCE GENES IN *oryza* GERMPLASM

P. GUIMARÃES¹; D.BERTIOLI.(david@cenargen.embrapa.br)¹;

S.LEAL-BERTIOLI¹; M.E. FERREIRA¹

¹Embrapa Recursos Genéticos e Biotecnologia

The majority of genes conferring gene-for-gene resistance that have been isolated from plants belong either to a class encoding a stretch of leucine rich repeats (LRRs) and a putative nucleotide binding site (NBS) or to a class that encodes an LRR domain but no NBS. To date, PCR primers based on short stretches of amino acids conserved among NBS resistance proteins have been used to amplify resistance gene analogs from different species such as soybean, maize, potato and lettuce. In the present work, this approach was used to search for these sequences in both, wild (*O. glumaepatula*) and cultivated (*O. sativa*) *Oryza* germplasm. Crosses between *O. glumaepatula* X *O. sativa* have been used for mapping and introgression of productive and resistance characteristics in breeding programs. Both species produced PCR products which consisted of a mixture containing NBS regions of around 500bp. These amplicons were sequenced and their homology to resistance genes previously described confirmed through BLAST analysis. These resistance gene analogs will be used as DNA markers through a PCR or RFLP approach to evaluate their relation to already mapped resistance loci in these species, to aid in the isolation of resistance genes.

Key words: PCR, RFLP, genetic variability