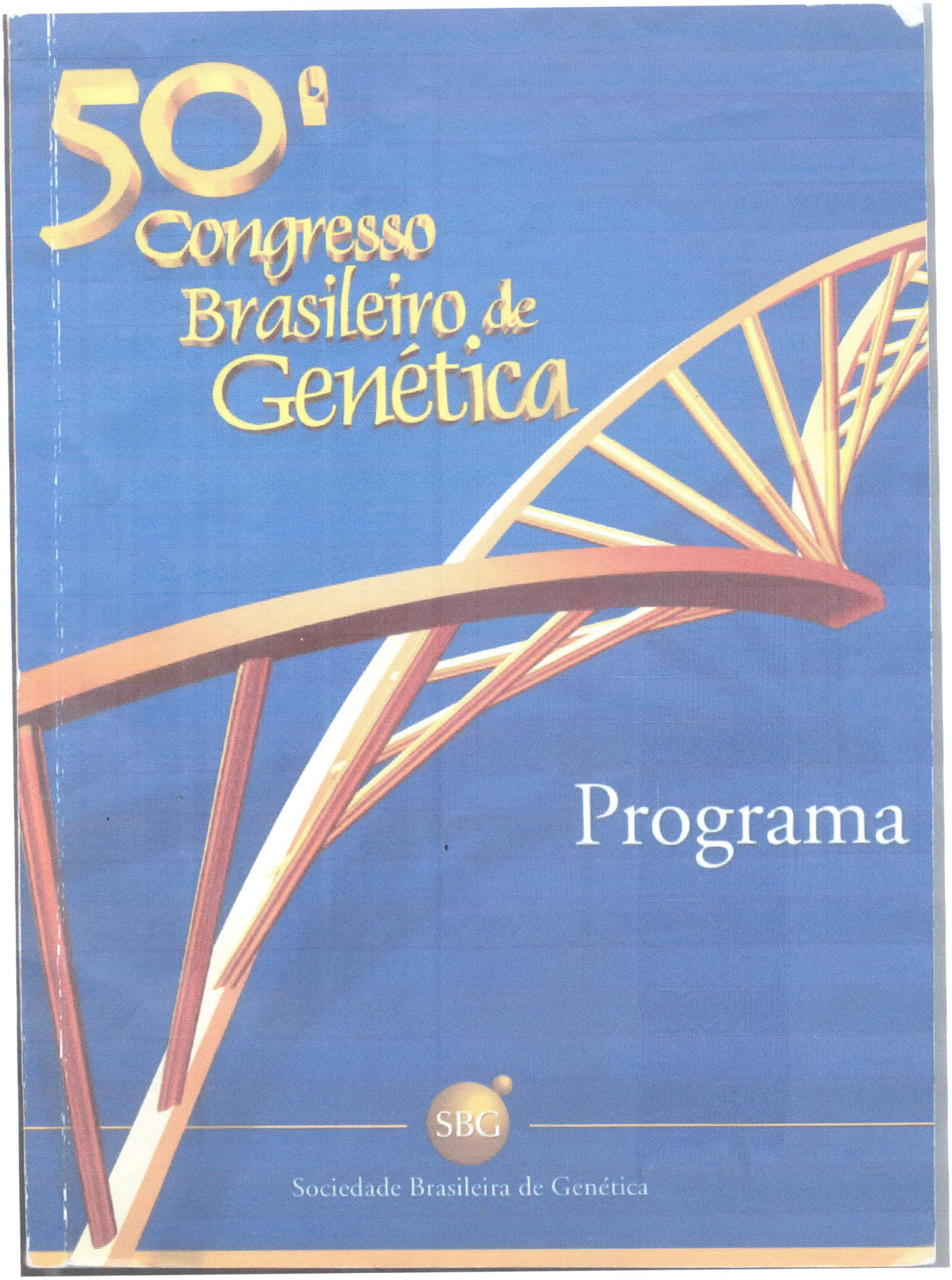
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ANALYSIS OF RESISTANCE GENE ANALOGS IN *MUSA ACUMINATA* CV CALCUTTA 4

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Commercial banana varieties (*Musa* spp.) are cultivated in over 120 countries, generating an annual global production of around 100 million tons. Brazil represents the second largest producer, with a production area of 500 thousand hectares and an annual production of six million tons. In 1998, the fungal pathogen *Mycosphaerella fijiensis*, causal organism of black leaf streak disease, which causes premature fruit ripening, necrotic leaf surfaces lesions, leading to leaf area decomposition and yield losses of up to 50%, was reported for the first time in Brazil in the Amazon region. Subsequently, the pathogen has spread over seven states in the north of the country.

Specific recognition of plant pathogens, leading to programmed cell death, is controlled by resistance genes (R-genes). A number of R-gene subfamilies frequently possess conserved NBS (nucleotide binding site) and LRR (leucine rich repeat) domains. The objectives of this study are to identify sources of resistance in *Musa acuminata* cv Calcutta 4, through the analysis of resistance gene analogs (RGAs) using degenerate primers designed from highly conserved amino acid domains (NBS and LRR), and later via full length sequencing of positive BAC clones.

Specific PCR amplified products of expected size from genomic DNA targeting P-loop, and GLPL amino acid motifs within the NBS domain. A second set of degenerate primers, designed from conserved amino acid motifs within non - Tir type NBS (P-loop, kinase 2, RNBS, GLPL) and LRR domains from monocot protein databases, also resulted in PCR products of expected size. Following sequencing of cloned PCR products, vector masking, quality trimming, and generation of sequence clusters, BlastX analysis with a non-redundant NCBI protein database, showed homologies to resistance genes and RGAs, from *M. acuminata*, *Oryza sativa*, *Elaeis guineensis*, *Solanum tuberosum*, *Theobroma cacao*, and *Arabidopsis thaliana*. All RGAs will subsequently be characterized via reverse northern blots in order to determine whether they represent gene regions, and candidate sequences will be labelled for use as probes against a *M. acuminata* cv Calcutta 4 BAC library.

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