

Identification of resistance gene analogs in cabbage by PCR-SSCP analysis

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The class of R-genes encoding a Nucleotide Binding Site (NBS) and/or a Leucine Rich Repeat (LRR) region is responsible for a mechanism of resistance to pathogens in many crops. The use of degenerate primers designed on the conserved domains would be a fast technique for the identification of candidate R-genes. The Resistance Gene Analogs (RGAs) of the NBS-LRR class from the genomic DNA of cabbage will be isolated using degenerate primers. PCR-generated

fragments arising from a multi-gene family will be cloned into a plasmid vector. Followed by the fingerprinting using SSCP-analysis of the inserts in order to find out unique clones before sequencing. Specific-RGAs will be characterised by conformational polymorphism (SSCP analysis) in a panel of cabbage genotypes carrying different levels of resistance. The expression of R-genes in the presence or absence of Black rot pathogen will also be taken up in the present study.