

OPTIMIZATION AND IDENTIFICATION OF SSR PRIMERS ASSOCIATED WITH POWDERY MILDEW RESISTANCE IN MELON

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Abstract:

In Brazil, melon production is concentrated in the Northeast (95.8%), a region lacking resources and opportunities. Currently, it represents the second in the export items of Rio Grande do Norte, with 63 thousand tons sent to other countries in the first half of 2022, having a great participation in the region's economy, generating jobs and opportunities. Some fungal diseases are very limiting in Brazil production, especially powdery mildew (*Podosphaera xanthii*). The management of this disease is difficult, as there are no registered fungicides to control this pathogen in melon. An alternative is genetic resistance, a type of control that is safer for the environment and the consumer. In this sense, SSR (Simple Sequence Repeats) molecular markers have been widely used as an efficient tool in disease resistance studies. Thus, the objective of this work was to identify SSR molecular markers associated with powdery mildew resistance in two melon lines, susceptible (female parent - Vdrantais) and resistant (male parent - PI 414723) from the melon genetic improvement program at Embrapa Vegetables. The SSR loci were amplified through PCR reactions (Polymerase Chain Reaction) and the fragments were separated by electrophoresis in a 5% polyacrylamide gel. Initially, 244 SSR primers developed by the plant genetics laboratory of EMBRAPA Genetic Resources and Biotechnology were tested on the two genotypes used. Of these, 115 did not amplify, 68 were polymorphic and 61 did not differ between genotypes (monomorphic), representing 47%, 28% and 25% of the tested primers, respectively. Thus, the studied loci showed a low level of polymorphism between the contrasting strains, requiring greater genomic coverage, with the aim of identifying more loci associated with powdery mildew resistance to perform the genetic mapping.

Palavras-chave: Melon; SSR; resistance; powdery mildew;

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