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Development and use of single nucleotide polymorphism markers for candidate resistance genes in wild peanuts (*Arachis* spp)

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ABSTRACT. The cultivated peanut (*Arachis hypogaea* L.) is an allotetraploid of recent origin, with an AABB genome and low genetic diversity. Perhaps because of its limited genetic diversity, this species lacks resistance to a number of important pests and diseases. In contrast, wild species of *Arachis* are genetically diverse and are rich sources of disease resistance genes. Consequently, a study of wild peanut relatives is attractive from two points of view: to help understand peanut genetics and to characterize wild alleles that could confer disease resistance. With this in mind, a diploid population from a cross between two wild peanut relatives was developed, in order to make a dense genetic map that could serve as a reference for peanut genetics and in order to characterize the regions of the *Arachis* genome that code for disease resistance. We tested two methods for developing and genotyping single nucleotide polymorphisms in candidate genes for disease resistance; one is based on single-base primer extension methods and the other is based on amplification refractory mutation system-polymerase chain reaction. We found single-base pair extension to be an efficient method, suitable for high-throughput, single-nucleotide polymorphism mapping; it allowed us to locate five candidate genes for resistance on our genetic map.

Key words: Single nucleotide polymorphisms; Molecular markers; *Arabidopsis* disease resistance genes; *Arachis*; Genetic mapping