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UM GENE NLR DO GUANDU É CAPAZ DE CONFERIR RESISTÊNCIA À FERRUGEM DA SOJA ASIÁTICA NA SOJA / A NLR gene from pigeonpea is able to confer resistance to Asian soybean rust in soybean.

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Asian soybean rust (ASR) caused by the obligate biotrophic fungus *Phakopsora pachyrhizi* is one of the most economically important soybean diseases. In the field, *P. pachyrhizi* infects leaf tissue from a broad range of leguminous plants (at least 31 species in 17 genera). Currently, no commercially grown soybean (*Glycine max*) cultivars are available that are fully resistant to *P. pachyrhizi*. Therefore, fungicide applications are the only method available to control the disease. Resistance to *P. pachyrhizi* in soybeans is rare; USDA evaluated the entire USA germplasm collection and found that less than 5% was resistant or partially resistant against *P. pachyrhizi*. We postulated that Asian soybean rust resistance (*R*) genes can be mapped and cloned from other legume species, and subsequently transferred to soybean to provide resistance to *P. pachyrhizi* via heterologous expression. We identified the major resistance gene in *Cajanus cajan* against *P. pachyrhizi* via a map-based approach and named it *CcRpp1* (*Cajanus cajan* Resistance against *Phakopsora pachyrhizi*). We used next-generation sequencing technology to identify the required closed linked markers. Synteny between *G. max* and *C. cajan* cultivar resistant accession G119-99 in the region of dCAPS140555 marker revealed a tight linkage with the *CC-NB-LRR* gene (*Glyma12g01420*) on chromosome 12 in *G. max*. To identify the presence of *NLR* genes in the *CcRpp1* mapping interval, two overlapping BAC clones were pooled out from the *R* gene locus and it was identified four highly homologous *NB-LRR* gene paralogs (*NB-1* to *-4*), subsequently confirmed by Southern blotting. High level of variation at the *CcRpp1* locus was observed when comparing the NBLRR CDS sequences between four different *C. cajan* accessions. G119-99 transcriptome reads were aligned back to the *CcRpp1* physical interval showing that only *NB-2* had RNASeq reads aligned to it, suggesting that *NB-2* is the only gene that has a basal expression in G119-99. Plant transformation constructs containing the four individual *NB-LRR* genes were driven by the *G. max* SUBI-1 promoter. These constructs were introduced into soybean by biolistic transformation. When challenged with *P. pachyrhizi* (isolates G05 and MS08), no differential phenotypes were observed for *NB-1*, *NB-3* or *NB-4*, even though they were all expressed. In conclusion, *NB-2* (*CcRpp1*) is the *R* gene conferring resistance against *P. pachyrhizi* and successfully provides full efficacy against *P. pachyrhizi* in soybean. Our findings show that legume species related to soybean such as pigeonpea, cowpea, common bean and others could provide a valuable and diverse pool of resistance traits for crop improvement.

Key words: *Cajanus cajan*; *Glycine max*; *Phakopsora pachyrhizi*; *R* gene; *NB-LRR* gene.

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