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A LARGE-SCALE ANALYSIS OF RESISTANCE GENE ANALOGS (RGAs) ENCODING NBS DOMAINS IN THE GENUS *Elaeis* / Análise em larga escala de análogos de gene de resistência (RGAs) codificadores de domínios NBS no gênero *Elaeis*. M. de L. SANTOS¹; G.S. COSTA ALVES²; M.G. COTTA²; F.C.A. FONSECA²; R.C. TOGAWA³; M.M. do CARMO COSTA³; A.A. ALVES⁴; R.N.G. MILLER²; M.T. SOUZA Jr⁴. ¹Programa de Pós-Graduação em Biotecnologia Vegetal, UFLA, Lavras, Brasil / ²Departamento de Biologia Celular, UnB, Brasília, Brasil / ³Embrapa Recursos Genéticos e Biotecnologia, Brasília, Brasil / ⁴Embrapa Agroenergia, Brasília, Brasil. E-mail: manojel.souza@embrapa.br

Oil palm (*Elaeis guineensis*) is responsible for the majority of the world's vegetable oil supply, with application in cosmetic, pharmaceutical, food and biofuel industries. The susceptibility of this crop to a number of diseases represents a considerable constraint to production. The introgression of resistance genes into elite genotypes is an important measure for integrated control and mitigation of disease losses. The most abundant resistance genes identified in plants encode intracellular receptor proteins with nucleotide binding (NBS) and leucine-rich repeat (LRR) domains. NBS-LRR proteins play an important role in the recognition of pathogen effectors and initiating the defense response. In view of the exposed problem, the aim of this study was to identify and characterize NBS-LRR genes present in the genome sequences of *E. guineensis* and the closely related species *E. oleifera*. Hidden Markov Model (HMM) profiles were employed for identification of genes encoding proteins containing NBS-LRR structural elements. A HMM amino acid profile resulted in the identification of 220 NBS-LRR gene sequences in *E. guineensis*, 20 more than previously reported. A developed nucleotide HMM profile also enabled identification of 36 NBS-LRR family genes with continuous ORFs within the *E. oleifera* genome. These shared structural domains protein homologues for *E. guineensis*, *Phoenix dactylifera*, *Glycine max* and *Arabidopsis thaliana*. Phylogenetic analysis of sequences identified in *Elaeis* spp., together with reference sequences from *A. thaliana* (dicotyledonous) and *Brachypodium distachyon* (monocotyledonous), enabled classification of the *Elaeis* spp. sequences into seven distinct groups. This study represents the first large-scale analysis of the diversity of this gene family in *Elaeis* spp.

Key words: *E. guineensis*; *E. oleifera*; Biotic stress; NBS-LRRs.