Characterization of Expressed Resistance Gene Analogs (RGAs) from Peanut (Arachis hypogaea L.) Expressed Sequence Tags (ESTs).

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Cultivated peanut (Arachis hypogaea L.) is one of the most important food legume crops grown worldwide, and is a major source for edible oil and protein. However, due to low genetic variation, peanut is very vulnerable to a variety of pathogens, such as early leaf spot, late leaf spot, rust and Tomato spotted wilt virus (TSWV). In recent years, the peanut research community has developed and deposited a large number of ESTs (225,264 ESTs by 11-11-2011) in GenBank. These data offer good opportunities to identify functional genes and to develop molecular markers. In the present study, we used the protein sequences of the 54 known R-genes to screen peanut EST database and identified 995 ESTs targeting different classes of known R genes. Among the 995 ESTs, 559 (56%) were from ten cultivated peanut cultivars and 436 (44%) were from three wild peanut genotypes. After assembly, 401 unigenes were developed and considered as peanut expressed RGAs. These expressed RGAs consisted of 75, 196, 89, 27, and 14 RGAs representing for NBS-LRR, protein kinase (PK), LRR-PK/TM, toxin reductase, and other domain encoding R genes, respectively. A total of 33 SSRs were identified from 28 peanut expressed RGAs and one SSR (RGA121) was found polymorphic in two mapping populations. Genotypic data were generated on one of these mapping population possessing 353 recombinant inbred lines (RILs) derived from SunOleic 97R and NC94022, and mapped on linkage group 01 along with the putative qtswv2 (Qin et al. 2012. TAG).