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Complete sequencing of the largest peanut disease resistance gene clusters

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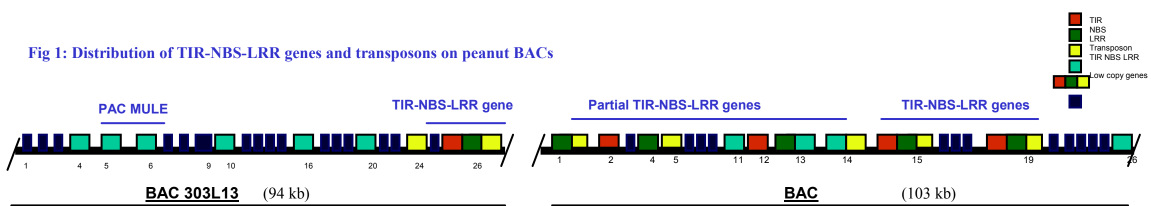
Introduction

The cultivated peanut has a large and complex genome. At present limited information is available about the disease resistance genes and their location in peanut genome. The main objectives of the present study were to explore the largest cluster of NBS-LRR disease resistance gene-like sequences in the peanut genome and to assess evolutionary relationships both among the peanut sequences and with similar sequences from other taxa.

Results

To investigating the genomic organization of resistance gene-related sequences, we isolated and characterized BACs containing NBS-LRR sequences by using overgo probes. For sequencing, we selected two BACs which showing strong hybridization signals with all the R gene specific probes. Sequencing of these two BACs yielded 197,802 bp. Annotation of the BACs 303L13 and 205D04 identified twelve tandemly arrayed NBS-LRR gene homologs or partial R genes (Figure 1).

Fig 1: Distribution of TIR-NBS-LRR genes and transposons on peanut BACs



To understand the evolution of the NBS-LRR genes in the sequenced region, we performed phylogenetic analyses using the NB domain of each gene with the previously identified genes from peanut and other related legumes. Phylogenetic analysis indicated that peanut NBS-LRR genes share a high degree of homology to three genes viz *Phaseolus* gene CMR1 (ABH07384), *Medicago* TIR (AC149204.1) and *Lens* disease resistance protein (AJ516091.1). CMR1 is a viral resistance gene from common bean that functions across plant families. High homology of peanut NBS LRR sequences to CMR1 indicated that these sequences might also be involved in conferrering resistance to viral diseases in peanut (Figure 2).

Our second objective was to investigate the level and structure of synteny between the legume models (primarily soybean, *Medicago*) and peanut. To determine the origin of the differences in sequence content between Peanut and other legumes, we compared their gene contents with the homologous region from *Medicago and* Soybean and aligned BAC contigs based on positions of conserved low-copy genes. Our comparison of peanut BAC clones reveals that Medicago, soybean and peanut display limited micro-collinearity in this 197,802 bp of genomic sequences. The comparison of peanut with soybean and *Medicago* enabled us to infer whether differences represented losses or insertions.

Our results suggested that the peanut R genes share ancestral relationship with related legumes and are present in the region which may be responsible for providing resistance to important diseases in peanut. These studies also revealed exceptions to conserved synteny, including gene duplication, and insertions/deletions. Phylogenetic analysis and organization of the NBS-LRR gene clusters provided new insights about comparative genome organization and evolution of peanut and other legumes.

Figure 2: Genetic relationships of peanut NBS-LRR genes with other legumes