

Pseudomonas spp. and compared with other gene predicting tools. This tool can be used for the functional annotation of the microbial genome data providing insights into genome evolution and identifying different strains containing LTR genes.

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Amplification and sequencing of partial-length disease resistant gene homologues coding NBS LRR-type proteins in coconut

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The coconut palm is highly susceptible to diseases caused by different organisms. Replanting with resistant/tolerant varieties is the best way to manage the diseases. Considering the long life cycle of coconut, selection of resistant varieties through conventional breeding methods will be time consuming and laborious. A possible strategy to reduce the risk of resistance breakdown and to achieve durable resistance could be the combination of different major and minor resistance genes in a single cultivar so that, to be able to infect the plant, the pathogen has to simultaneously circumvent several resistance mechanisms. It is therefore important to identify sources of resistance within the genome of these palms, conferred by new and still unknown major resistance genes, or by genes conferring quantitative or partial resistance against pathogens. Therefore, obtaining a collection of Resistance Gene Analogues (RGAs) sequences could be an effective strategy to identify genomic regions linked to disease resistance in coconut. Considerable conservation at the DNA/protein level in R-genes has led to the development of novel PCR based molecular approaches to isolate putative resistant gene analogues (RGAs) from new plant source with considerable ease. We have successfully used one such approach to amplify putative RGA from coconut with specific primer pairs designed from conserved disease resistant motifs like P-LOOP and GLPL and kinase region of NBS-LRR domain of date palm (*Phoenix dactylifera*), the genome of which has been completely sequenced. The amplified sequence (~2211 bp) was cloned and sequenced using a primer walking strategy and characterized by BLAST homology searches, which showed that the sequence from coconut had high identity to the disease resistant-like genes (NBS-LRR) of oil palm (*Elaeis guineensis*), *Oryza sativa*, *Musa acuminata* and like other members of monocots. By using a comparative genomics tool mVISTA, the alignment of the isolated coconut RGA could be predicted from other species with clear annotations. The high degree of similarity between coconut, oil palm and date palm sequences suggest an ancestral relationship in the evolution of RGAs in palms.