

numbers of fully opened leaves on the crown were significant higher in Kuttiyadi compared to WCT. Length of leaflet was significantly higher in WCT compared to Kuttiyadi. The length of inflorescence was significantly higher in Kuttiyadi compared to WCT. Length of spikelets, number of spikelets, number of female flowers and number of nuts/year were significantly higher in WCT compared to Kuttiyadi. fruit weight, fruit length, fruit breadth, fruit circumference (polar and equatorial), husk thickness, husk weight, nut weight, nut breadth, nut circumference (polar and equatorial), shell weight endosperm thickness, cavity diameter on the polar region, cavity volume and copra weight were significantly higher in WCT compared to Kuttiyadi. The characters of husk percentage, cavity diameter of nut in the equatorial region and oil percentage in copra were significantly higher in Kuttiyadi compared to WCT. Fifteen SSR primers specific to coconut were checked for amplification in 36 palms (20 palms for Kuttiyadi and 16 palms for WCT) accessions. The similarity index based on DICE's coefficient, obtained after pair wise comparison of Kuttiyadi and WCT samples revealed that the percentage similarity varied from the coefficient range 0.20 to 0.97 between the WCT and Kuttiyadi palms. UPGMA clustering clearly distinguished the two populations with WCT and Kuttiyadi forming separate clusters. Morphological and molecular characters studied here helped to distinguish Kuttiyadi as a separate population different from WCT.

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### **LTTRPred: A tool for prediction of transcriptional regulator of pyoluteorin pathway in *Pseudomonas* species using SVM-based approach**

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Plant growth promoting *Pseudomonas* spp. produce an antifungal compound called pyoluteorin (Plt) that suppress plant diseases caused by fungi. The pathway specific regulator PltR, a typical LysR-type transcriptional regulator (LTTR), is responsible for the transcriptional activation of the Plt biosynthetic operon. The LTTR family represents one of the largest classes of bacterial transcriptional regulatory proteins. A large numbers of LTTRs possess function as global transcriptional activators or repressors of unlinked genes or operons involved in metabolism, quinoline signal, virulence etc. The proposed method, LTTRPred, is an useful tool developed for identifying and predicting the LTTR, which is responsible for the activation of Plt transcription regulators, in whole genomes of various *Pseudomonas* spp. LTTRPred was developed using support vector machine (SVM) based on the composition of amino acid and amino acid pairs. Modules were first developed using traditional amino acid, dipeptide (n+1) and hybrid amino acid composition and an overall accuracy of 98%, 100% and 98% respectively was achieved. The performance of the tool was tested using various datasets of LTTR genes from different

*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.