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***Wolbachia* infection in arthropods: Detection and assessment of genetic variation**

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Wolbachia cause inherited intracellular infections in many invertebrates. *Wolbachia* has the ability to override chromosomal sex determination, induce parthenogenesis, selectively kill males and also generate cytoplasmic incompatibility. These bacteria have important evolutionary implications and also useful in pest and disease control. Surveys show that these bacteria are present in over 16% of insect species. In this study, screenings of *Wolbachia* infection in arthropods was done along with identification of *Wolbachial* strains. 10 different insect species from diverse insect orders were used in the study. Universal primers were used to amplify 16SrDNA gene fragment in the bacterium. Variation of infection among the individuals of same insect types and those of different insect types were observed. After identification of infected individual strains of *Wolbachia* present were also identified using the 16S strain A and 16S strain B specific amplification. Then 16SrDNA was sequenced and compared to estimate genetic diversity in the *Wolbachial* haplotypes in different orders of insects. *Wolbachia* were detected in 6 insect species and most of them belonged to *Wolbachial* Strain A. Variation among *Wolbachia* haplotypes in the diverse insects orders studied was found to be very low.

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Morphological and molecular characterization of Kuttiyadi ecotype of coconut (*Cocos nucifera* L.)

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The major coconut growing state in the country is Kerala, where the most popular variety grown by the farmers is West Coast Tall (WCT), which occupies over 95 percent of the area under coconut. The long history of cultivation along the length and breadth of Kerala state has resulted in the development of many ecotypes of WCT. The present work aims to carry out morphological and molecular characterization of Kuttiyadi ecotype growing in hilly midland region of Kerala and comparison of its similarity/diversity with West Coast Tall (WCT) cultivar with the help of vegetative reproductive, fruit component characters and microsatellite markers. Materials selected were WCT population growing in coastal region at CPCRI, Kasaragod [12.31°N latitude and 74.51°E longitude and at an altitude ranged from 15-17 meter above mean sea level] and Kuttiyadi ecotype of WCT growing in midland region in Kozhikode District [11.41°N latitude and 75°E longitude and at an altitude of 80-350m above]. Geographically, these two locations showed wide range of variations. Morphological, palm, reproductive and fruit characters, of WCT and Kuttiyadi also showed variations. The characters plant height, girth at the base of the stem and

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