

Details of the Collaborative Activity

2020-21

Name of the Collaborating Institute: ICAR-Central Plantation Crops Research Institute Kasaragod, Kerala

Name of the Collaborating Department: Yenepoya Research Centre

Activities:

Faculty Visit

Dr. Keshava Prasad visited ICAR-CPCRI on 12th March 2018 to discuss potential collaborative projects

Joint Research and Publication

1. Rajesh MK, Gangurde SS, Pandey MK, Niral V, Sudha R, Jerard BA, Kadke GN, Sabana AA, Muralikrishna, KS, Samsudeen K, Karun A, **Prasad TSK**. Insights on genetic diversity, population structure and linkage disequilibrium in globally diverse coconut accessions using genotyping-by-sequencing. *OMICS: A Journal of Integrative Biology*. 2021.
2. Rajesha MK, Muralikrishnaa KS, Nair SS, Kumar, BK, Subrahmanya TM, Sonu KP, Subaharan K, Sweta H, **Prasad TSK**, Neeli C, Karunasagar I, Hebbara KB, Karun, Anitha. Facile coconut inflorescence sap mediated synthesis of silver nanoparticles and its diverse antimicrobial and cytotoxic properties. *Materials Science and Engineering*. 2020.111, 110834
3. Rajesh MK, Chowdappa, P, **Behera SK**, Kasaragod S, Gangaraj KP, Kotimoole CN, Nekrakalaya B, **Mohanty V**, Sampgod RB, Banerjee GB, Das AJ Niral V, Karun A, Gaikwad K, Singh NK, **Prasad TSK**. Assembly and annotation of the nuclear and organellar genomes of a dwarf coconut (Chowghat Green Dwarf) possessing enhanced disease resistance. *OMICS: A Journal of Integrative Biology*. 2020.24
4. Rajesh, MK, Gangaraj KP, Prabhudas SK, **Prasad TSK**. The complete chloroplast genome data of Areca catechu (Arecaceae). *Data in Brief*. 2020; 33, 106444.

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joint publication

ATTENDANCE CERTIFICATE

This is to certify that Dr. T. S. Keshava Prasad, Professor and Deputy Director Center for Systems Biology and Molecular Medicine, Yenepoya University, was the Chief Guest for the Workshop on NGS Data Analysis organized on 12.3.2018 at ICAR-CPCRI, Kasaragod. He has delivered the inaugural address during the Workshop. We also discussed several potential collaborative projects.

Place : Kasaragod

Date : 12.03.2018

M.K. Rajesh
12/3/18

(M.K. Rajesh)

Principal Scientist



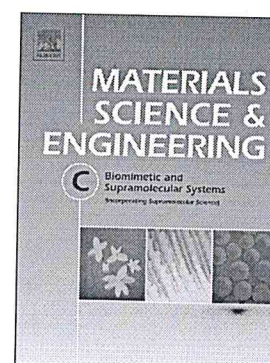
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Journal Pre-proof

Facile coconut inflorescence sap mediated synthesis of silver nanoparticles and its diverse antimicrobial and cytotoxic properties

M.K. Rajesh, K.S. Muralikrishna, Swapna S. Nair, B. Krishna Kumar, T.M. Subrahmanya, K.P. Sonu, K. Subaharan, H. Sweta, T.S. Keshava Prasad, Neeli Chandran, Indrani Karunasagar, K.B. Hebbar, Anitha Karun



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Facile coconut inflorescence sap mediated synthesis of silver nanoparticles and its diverse antimicrobial and cytotoxic properties

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Assembly and Annotation of the Nuclear and Organellar Genomes of a Dwarf Coconut (Chowghat Green Dwarf) Possessing Enhanced Disease Resistance

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Abstract

Coconut (*Cocos nucifera* L.), an important source of vegetable oil, nutraceuticals, functional foods, and housing materials, provides raw materials for a repertoire of industries engaged in the manufacture of cosmetics, soaps, detergents, paints, varnishes, and emulsifiers, among other products. The palm plays a vital role in maintaining and promoting the sustainability of farming systems of the fragile ecosystems of islands and coastal regions of the tropics. In this study, we present the genome of a dwarf coconut variety “Chowghat Green Dwarf” (CGD) from India, possessing enhanced resistance to root (wilt) disease. Utilizing short reads from the Illumina HiSeq 4000 platform and long reads from the Pacific Biosciences RSII platform, we have assembled the draft genome assembly of 1.93 Gb. The genome is distributed over 26,855 scaffolds, with ~81.56% of the assembled genome present in scaffolds of lengths longer than 50 kb. About 77.29% of the genome was composed of transposable elements and repeats. Gene prediction yielded 51,953 genes, which upon stringent filtering, based on Annotation Edit Distance, resulted in 13,707 genes, which coded for 11,181 proteins. Among these, we gathered transcript level evidence for a total of 6828 predicted genes based on the RNA-Seq data from different coconut tissues, since they presented assembled transcripts within the genome annotation coordinates. A total of 112 nucleotide-binding and leucine-rich repeat loci, belonging to six classes, were detected. We have also undertaken the assembly and annotation of the CGD chloroplast and mitochondrial genomes. The availability of the dwarf coconut genome shall prove invaluable for deducing the origin of dwarf coconut cultivars, dissection of genes controlling plant habit and fruit color, and accelerated breeding for improved agronomic traits.

Keywords: *Cocos nucifera*, dwarf cultivar, disease resistance, *de novo* assembly, organellar genomes, agri-genomics, nutrigenomics

Introduction

COCONUT (*COCOS NUCIFERA* L., $2n=32$) is a highly resilient pantropical palm that sustains the lives of millions of small and marginal indigenous farming communities, the majority of them residing in fragile ecosystems. One of the most useful trees in the world, almost every part of palm finds a use one way or other, befitting the sobriquet “Kalpavriksha”

(“Tree of life” in the Sanskrit language). Besides providing food, drink, and shelter, the palm also supplies a plethora of raw materials to several domestic and economic industries. In recent times, coconut is gaining popularity as a nutraceutical and functional food, with tender coconut water, virgin coconut oil, and inflorescence sap being harnessed toward a diversity of health products and preventive medicine applications (Asghar et al., 2020; Joshi et al., 2020; Reddy et al., 2018).

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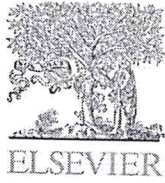
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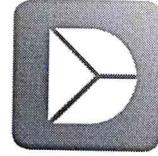
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Data Article

The complete chloroplast genome data of *Areca catechu* (Arecaceae)



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ABSTRACT

Areca is a genus comprising about 50 species endemic to the humid tropics. Arecanut (*Areca catechu* L.) is a commercially and economically important crop in South and South-east Asia. In addition to its contribution to the agricultural economies of countries where the crop is grown, arecanut holds an important place in the religious, cultural, and social milieu of the rural folks. The nuts have been used since time immemorial in traditional Indian (Unani and Ayurveda) and Chinese herbal systems of medicine for the treatment of various disorders like rheumatism, parasitic infection, diseases of gastrointestinal tracts, and depression. Here, we report the complete chloroplast (cp) genome sequence of arecanut. The cp genome of *A. catechu* was a typical circular DNA molecule with a size of 158,689 bp in length. The genome possessed a typical quadripartite structure composed of a pair of inverted repeats (IRa and IRb) of 27,137 bp separated by a large single-copy (LSC) region of 86,814 bp and a small single-copy (SSC) region of 17,601 bp and a GC content of 37.3%. The cp genome of arecanut encodes a set of 133 genes, comprising 88 protein-coding genes, 37 tRNA genes, and eight rRNA genes; among these, 21 contained introns. A total of 70 SSR loci were detected, the majority being in inter-genic regions.

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