

Genome of salt-secreting mangrove species identified

Findings will help develop drought, salt-tolerant food crops

SPECIAL CORRESPONDENT
CUDDALORE

A group of researchers from the Department of Genetic Engineering, SRM Institute of Science and Technology, Chennai; Centre for Advanced Studies in Marine Biology, Faculty of Marine Sciences, Annamalai University; and the Institute of Life Sciences, Bhubaneswar, have identified a reference-grade whole genome sequence of a highly salt-tolerant and salt-secreting mangrove species, *Avicennia marina*.

Mangroves are important resources for the coastal region and are of great ecological and economic value. They form a link between marine and terrestrial ecosystems, protect shorelines, and provide habitat for a diverse array of terrestrial organisms.

The team of researchers sequenced nearly 99% of the genome of the species and aligned them to 31 chromosomes of the species. The findings have been published in the latest issue of *Nature Communications Biology*.

The study was supported by the Department of Biotechnology, Government of



Natural asset: Mangroves are important resources of great ecological and economic value. ■ SPECIAL ARRANGEMENT

India. This will play a key role in developing drought and salt-tolerant food crops for the 7,500 km-long Indian coastline.

According to Ayyaru Gopalakrishnan, assistant professor, Faculty of Marine Sciences, Annamalai University, "*Avicennia marina* constitutes a major part of the mangrove forests of India. It is a salt-secreting and extraordinarily salt-tolerant mangrove species that grows optimally in 75% seawater and tolerates more than 250% seawater."

"It is a rare plant species, which can excrete 40% of the salt through the salt glands in the leaves, besides its extraordinary capacity to exclude salt entry to the roots."

First author of this study

Purushothaman Natarajan noted that they had employed the latest genome sequencing and assembling technologies and identified 31,477 protein-coding genes, consisting of 3,246 salinity-responsive genes and characterized 614 of them for salinity tolerance genes.

This particular study is important because global agriculture productivity is being affected chronically due to the unavailability of water and salinisation of arable land, which account for about 40% of the total cultivable area.

"We are in the process of developing searchable data to make the mangrove genome data available to the world research community," said senior author of this study Dr. Parani Madasamy.