Mangrove plants using deoxyribonucleic acid barcodes for enhancing biodiversity and conservation

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Abstract	a:2:{i:0;s:3550:"BACKGROUND AND OBJECTIVES: Mangrove forests in North Sumatra and Aceh are concentrated on the east coast of Sumatra Island. Mangrove habitats are highly productive, diversified, and ecologically and commercially significant ecosystems. However, they are vulnerable to both anthropogenic and natural hazards. The identification of coastal ecosystem species, such as mangrove and coastal forests, is very important in conserving and using the biodiversity of coastal ecosystems, which appears to be hindered by a lack of taxonomic and molecular expertise. This study aimed to address the lack of reference deoxyribonucleic acid barcodes from mangroves in North Sumatra and Aceh and assess the effectiveness of four deoxyribonucleic acid barcoding methods in terms of primer universality, successful identification rate, barcoding gap and species-tree inference, and then phylogenetic tree construction. METHODS: This study focused on selecting the main regions where mangroves are predominantly distributed in the provinces of North Sumatra and Aceh: Percut Sei Tuan and Deli Serdang mangrove areas, Pulau Sembilan and Lubuk Kertang of Langkat mangrove areas in North Sumatra, and Langsa mangrove areas in Aceh. The genomic deoxyribonucleic acid of mangrove plants was isolated from fresh leaf material using the Geneaid genomic deoxyribonucleic acid mini kit. Based on the guidance provided by the International Union for Biological Barcoding with four molecular sequences, deoxyribonucleic acid barcodes were chosen for amplification: chloroplast ribulose 1,5-bisphosphate carboxylase/oxygenase, maturase-K, transfer ribonucleic acid for histidine-photosystem II reaction center protein A, and nuclear genome internal transcribed spacer. The Tamura 3-parameter + Gamma method in molecular evolutionary genetics analysis X software was used to measure and describe the genetic distances between different species and within the same species. The construction of phylogenetic trees was carried out using the molecular evolutionary genetics analysis X from ribulose 1,5-bisphosphate carboxylase/ oxygenase, transfer ribonucleic acid for histidine-photosystem II reaction center protein A, Internal transcribed spacer, and maturase-K barcodes based on the bootstrap analysis conducted using 100 permutations. FINDINGS: This study showed that the primers ribulose 1,5-bisphosphate carboxylase/oxygenase, transfer ribonucleic acid for histidine-photosystem II reaction center protein A, internal transcribed spacer, and maturase-K had the highest success rates during amplification, which could be strong barcodes for enhancing taxonomic clarification and gaining insights into phylogenetic relationships. The primers ribulose 1,5-bisphosphate carboxylase/oxygenase, transfer ribonucleic acid for histidine-photosystem II reaction center protein A, internal transcribed spacer, and maturase-K had the highest success rates during amplification. The success rate for the ribulose 1,5-bisphosphate carboxylase/oxygenase gene was the highest (90% percent), followed by (86 percent), transfer ribonucleic acid for histidine-photosystem II react percent ion center protein Ainternal transcribed spacer (75 percent), and maturase-K (57 Percent). The significant differences were as follows: inter- and intraspecific genetic distance (probability (p) <0.001), maturase-K (probability = 0.0001), combination maturase-K + photosystem II reaction center protein A (probability = 0.0008), maturase-K + ribulose 1,5-bisphosphate carboxylase/oxygenase (probability = 0.";i:1;s:933:"0008), maturase-K + internal transcribed spacer (probability = 0.0003), ribulose 1,5-bisphosphate protein A + internal transcribed spacer (probability = 7.051e-05), and three combined markers maturase-K + photosystem II reaction center protein A + internal transcribed spacer (probability = 0.0007). It is noteworthy that the maturase-K barcode could construct the clustering and differentiate the mangrove species based on family and not from sites. The ribulose 1,5-bisphosphate carboxylase/oxygenase barcode showed that members of aureum), and Scyphiphora hydrophyllaceae from Rubiaceae existed in one branch. CONCLUSION: This study provided a reference database both molecularly and taxonomically to strengthen biodiversity assessment and monitor mangrove forests. This database can be used to clarify the results of deoxyribonucleic acid barcodes for morphological and biochemical identification in the eastern coast of Sumatra.";}
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