A comparison of 25 complete chloroplast genomes sheds light on differential energy requirements between sister mangrove species Kandelia obovata and Kandelia candel geographically separated by the South China Sea

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Abstract

In 2003, Kandelia obovata was identified as a new mangrove species differentiated from Kandelia candel. However, little is known about their chloroplast (cp) genome differences and their possible ecological significance. In this study, 25 whole cp genomes, with seven samples of K. candel from Malaysia, Thailand, and Bangladesh and 18 samples of K. obovata from China, were sequenced for comparison. The cp genomes of both species encoded 128 genes, namely 83 protein-coding genes, 37 tRNA genes, and eight rRNA genes, but the cp genome size of K. obovata was ˜2 kb larger than that of K. candle due to the presence of more and longer repeat sequences. Of these, tandem repeats and simple sequence repeats exhibited great differences. Principal component analysis based on indels, and phylogenetic tree analyses constructed with homologous protein genes from the single-copy genes, as well as 38 homologous pair genes among 13 mangrove species, gave strong support to the separation of the two species within the Kandelia genus. Homologous genes ndhD and atpA showed intraspecific consistency and interspecific differences. Molecular dynamics simulations of their corresponding proteins, NAD(P)H dehydrogenase chain 4 (NDH-D) and ATP synthase subunit alpha (ATP-A), predicted them to be significantly different in the functions of photosynthetic electron transport and ATP generation in the two species. These results suggest that the energy requirement was a pivotal factor in their adaptation to differential environments geographically separated by the South China Sea. Our results also provide clues for future research on their physiological and molecular adaptation mechanisms to light and temperature.

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