ABSTRACT

Molecular Characterization of Wood Ear Mushrooms (Auricularia Sp.) from Kakamega Forest in Western Kenya

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Mushrooms of the genus Auricularia, generally termed wood ear mushrooms are in high demand in Western Kenya due to their numerous medicinal and nutritional properties. Interventions to characterize and conserve the native wood ear mushrooms are necessary to mitigate possible extinction of this valuable bio-resource. Currently, the species richness and bio-geographical relatedness of the Kenyan native wood ears is not fully elucidated. This study used molecular sequence analysis of the internal transcribed spacer (ITS) and the 28S nuclear ribosomal large subunit (nLSU) genes in species delimitation of six strains of wood ear mushrooms native to Kakamega Forest. Phylogeny of both the ITS and nLSU gene regions showed that three strains clustered with Auricularia delicata while the other three strains clustered with Auricularia polytricha at bootstrap support values of above 97%. An intragenomic dichotomy appeared to occur in the Auricularia delicata strains based on the genetic distance of the nLSU gene sequences. The wood ear mushrooms identified from the Kakamega Forest strains were Auricularia delicata and Auricularia polytricha and not Auricularia auricula as previously reported. This rich biodiversity needs further exploration to widen the nutritional and medicinal base of the rural populace who depend on the mushrooms through conservation, cultivation and commercialization activities.

KEY WORDS: Molecular characterization, Wood ear mushrooms, Auricularia sp., Kakamega Forest, Western Kenya, Genetic diversity, DNA sequencing, Phylogenetic analysis, Fungal taxonomy, Ecological niche

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