

Diversity and Phylogenetic Placement of Seven *Inocybe* (Inocybaceae, Fungi) from Benin

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Abstract : Climate change and human actions cause the extinction of wild mushrooms. In Benin, the diversity of fungi is large and may still contain species new to science but the inventory effort remains low and focuses on particularly edible species (*Russula*, *Lactarius*, *Lactifluus*, and also *Amanita*). In addition, inventories have started recently and some groups of fungi are not sufficiently sampled, however, the degradation of fungal habitat continues to increase and some species are already disappearing. (Yorou and De Kesel, 2011), however, the degradation of fungi habitat continues to increase and some species may disappear without being known. This genus (*Inocybe*) overlooked has a worldwide distribution and includes more than 700 species with many undiscovered or poorly known species worldwide and particularly in tropical Africa. It is therefore important to orient the inventory to other genera or important families such as *Inocybe* (Fungi, Agaricales) in order to highlight their diversity and also to know their phylogenetic positions with a combined approach of gene regions. This study aims to evaluate the species richness and phylogenetic position of *Inocybe* species and affiliated taxa in West Africa. Thus, in North Benin, we visited the Forest Reserve of Ouémé Supérieur, the Okpara forest and the Alibori Supérieur Forest Reserve. In the center, we targeted the Forest Reserve of Toui-Kilibo. The surveys have been carried during the raining season in the study area meaning from June to October. A total of 24 taxa were collected, photographed and described. The DNA was extracted, the Polymerase Chain Reaction was carried out using primers (ITS1-F, ITS4-B) for Internal transcribed spacer (ITS), (LROR, LWRB, LR7, LR5) for nuclear ribosomal (LSU), (RPB2-f5F, RPB2-b6F, RPB2-b6R2, RPB2-b7R) for RNA polymerase II gene (RPB2) and sequenced. The ITS sequences of the 24 collections of Inocybaceae were edited in Staden and all the sequences were aligned and edited with Aliview v1.17. The sequences were examined by eye for sufficient similarity to be considered the same species. 13 different species were present in the collections. In addition, sequences similar to the ITS sequences of the thirteen final species were searched using BLAST. The nLSU and RPB2 markers for these species have been inserted in a complete alignment, where species from all major Inocybaceae clades as well as from all continents except Antarctica are present. Our new sequences for nLSU and RPB2 have been manually aligned in this dataset. Phylogenetic analysis was performed using the RAxML v7.2.6 maximum likelihood software. Bootstrap replications have been set to 100 and no partitioning of the dataset has been performed. The resulting tree was viewed and edited with FigTree v1.4.3. The preliminary tree resulting from the analysis of maximum likelihood shows us that these species coming from Benin are much diversified and are distributed in four different clades (*Inosperma*, *Inocybe*, *Mallocybe* and *Pseudosperma*) on the seven clades of Inocybaceae but the phylogeny position of 7 is currently known. This study marks the diversity of *Inocybe* in Benin and the investigations will continue and a protection plan will be developed in the coming years.

Keywords : Benin, diversity, *Inocybe*, phylogeny placement

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