Molecular Phylogeny of Some Moss Taxa and Its Implications for Identification

Thesis

Submitted In Fulfillment of the Requirements for the Degree of Doctor of Philosophy of Science in Botany

(Bryology)

By

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Declaration

This thesis has not been previously submitted for any degree at this or any other university.

The references in the text will show specifically the extent to which I have availed myself of the work of other authors.

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Dedication

All thanks to Allah

I dedicate this work

To my beloved great Dad, my kind Mum, my Husband Khaled, my sweet little girl Fayrouz, my lovely boy Noor El-Din and my brothers Amr and Mohamed.

Yours

Sahar Ibrahim EL-Sakaty

بسم الله الرحمن الرحيم

﴿وما أوتيتم من العلم إلا قليلا ﴾

صدق الله العظيم

سورة الاسراء/ اية ٨٥

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List of Abbreviations

bp	:base pair
BS	:BootStrap
CAIA	:Cairo – Ain Shams
IRs	:Inverted Repeats
ISSRs	:inter-simple sequence repeats
LSC	:Large Single copy
MCL	:Maximum Composite Likelihood
ML	:Maximum Likelihood
NCBI	:National Center for Biotechnology information
nm	:nano meter
nt	:nucleotide
ORF	: Open Reading Frame
PCR	: Polymerase Chain Reaction
rDNA	: ribosomal DeoxyriboNucleic Acid
nrDNA	:nuclear ribosomal DeoxyriboNucleic Acid
RFLPs	: Restriction Fragment Length Polymorphism
rpm	:round per minute
rRNA	: ribosomal RiboNucleic Acid
SSC	:Small Single Copy

ABSTRACT

Abstract

In this study, Forty six herbarium samples and one freshly collected sample were selected for morphological reinvestigation to confirm their identification. DNA was extracted and purified for PCR reaction; 17 samples were positive for both *rbcL* and ITS regions in addition to eight samples were positive for *rbcL* region only. DNA sequencing analysis shows that 20 samples gave high quality for *rbcL* region, 13 for partial ITS and three for ITS1 regions with high quality sequences which were used in the Phylogenetic analysis. All 20 sequences of *rbcL* and three out of 16 ITS sequences were submitted to GenBank as a new record for mosses and the others 13 sequences of ITS regions were already identified on GenBank. Phylogenetic analysis was performed using these two loci by Maximum Likihood method using the obtained model of evolution. Two samples were omitted from final phylogenetic analysis because of conflicting data. The identification of *Tortella nitida* and *Didymodon vinealis* was proved by Phylogenetic analysis. The identification of 14 mosses was confirmed on the generic level but disapproved and therefore corrected specific level. Names of five samples were changed on both generic and specific level. Phylogenetic analysis revealed that our concept of morphological variation inside the same species must be wider.