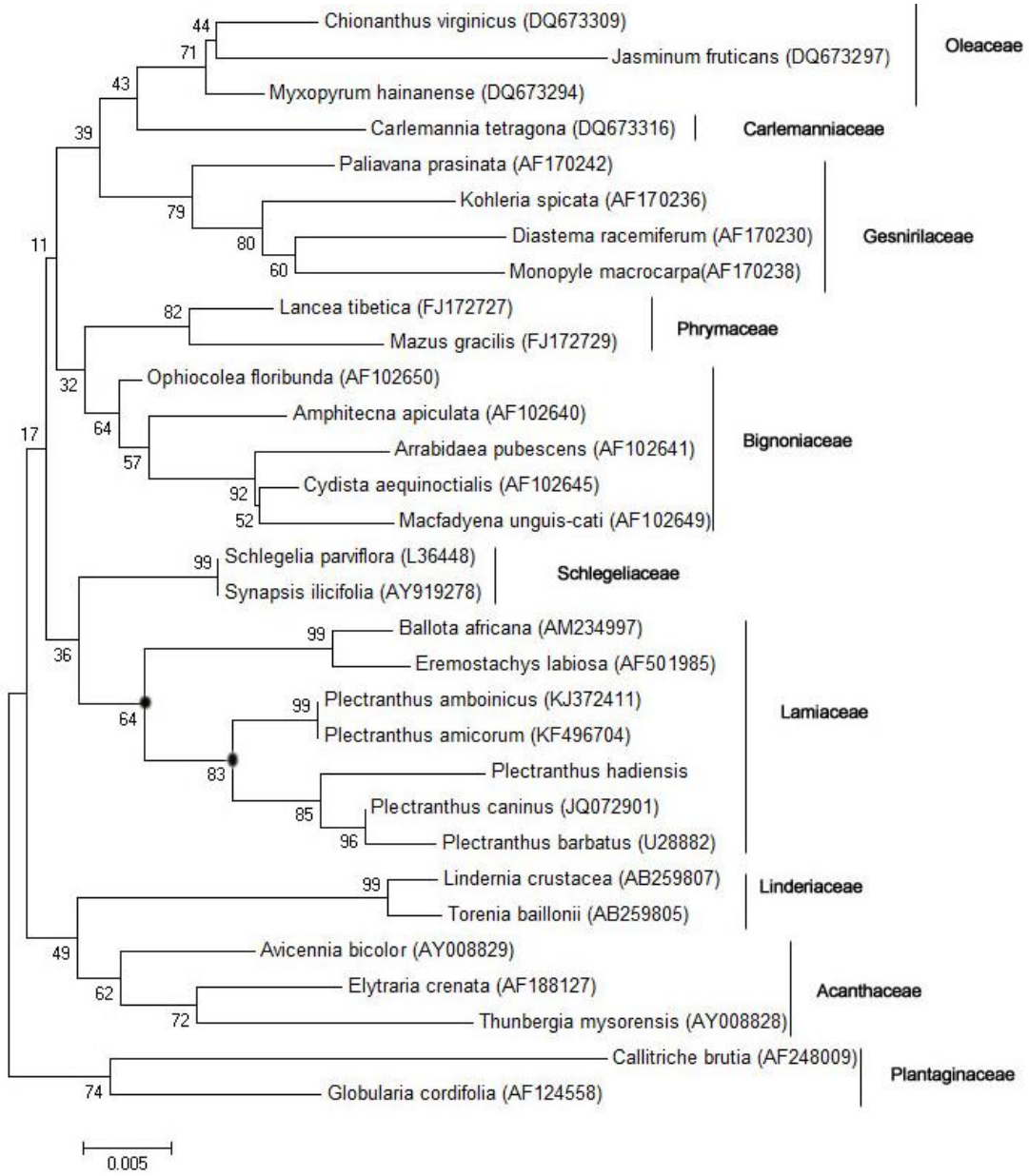

Figure 2: The NJ Tree constructed from the *rbc*L sequences of the order Lamiales based on the K-2-P distances. Bootstrap analysis (1000 replicates) was conducted to estimate the statistical supports of the topology of the consensus tree. The bootstrap percentages are shown at the branches. GenBank accession numbers are in parentheses.

According to Kress and Erickson (2008a) a nucleotide sequence must satisfy three criteria to be practical as a DNA barcode such as the sequence should contain a sufficient variation to discriminate between species, consist of flanking sites to develop universal PCR primers and have a short sequence length to facilitate current capabilities of DNA extraction and amplification. As the *rbc*L region was successfully amplified and sequenced placing the species in the correct family and genus and showed considerable interspecific divergence, this region can be considered as a suitable barcode to discriminate *P. hadiensis* from some other species of the same genus.

To find out the best barcode region to identify *P. hadiensis* from other *Plectranthus* spp. *psb*A-*trn*H and *mat*K also should be compared using the same approach once the sequences are available. Further, DNA barcoding should also be carried out for the commercial *P. hadiensis* herbal preparations to find the most effective and accurate DNA barcodes for the species identification after processing the plant.

4. Conclusion

Optimized DNA isolation protocol and PCR protocol can be used for successful amplification of barcode regions of metabolite rich *P. hadiensis.* Comparison of *rbc*L sequence of *P. hadiensis* with reference *rbc*L sequences of other *Plectranthus* spp. identified single nucleotide polymorphism. Additionally, *rbc*L region placed the species in the correct family and genus showing a considerable interspecific divergence.

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