Reviewer’s report

Title: Should DNA sequence be incorporated with other taxonomical data for routine identifying of plant species?

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Reviewer: Arunrat Chaveerach

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Actually, they are so many species in many genera and families can not be used barcode regions for identification as of they are short sequences and from some partial gene sequences. The efficient regions frequently trend to be non-coding regions such as trnH-psbA spacer, ITS, this is the first problem. the second, DNA extraction from finished products is the second problem. The single sequence of nuclear genome contains ITS region, not much copies as chloroplast DNA. The DNA barcode fragments frequently different sizes in the genera, families, may be in the same family. With many reasons, I think, the ms Topic should be changed.

Please edit trnH-psbA to trnH-psbA spacer region.

ITS region for identical species Clinacanthus nutans and Clinacanthus siamensis is not new information as of The Plant Lists of Kew and Missouri Botanical gardens insisted that Clinacanthus nutans is the accepted name, Clinacanthus siamensis is the synonym, but just only supported data. However, which one is the species each as of they are the same.

If the author use the topic as Acanthaceae, the controls required have many more species studying of the family in Thailand. Because of a little variation in the barcode short sequence of each species in a genus can be occurred in the plant growing in varied areas as in different growth factors.

The conclusions should be covered to the scope of the investigated plants, not quoted all the family.

The authors can change for the scope of the investigated plants instead of extensively studied species of Acanthaceae, because of a small number of each studied genus and above mentioned reasons.

These are my opinions.

Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

Yes
Does the work include the necessary controls?
If not, please specify which controls are required in your comments to the authors.

No

Are the conclusions drawn adequately supported by the data shown?
If not, please explain in your comments to the authors.

No

Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?
If an additional statistical review is recommended, please specify what aspects require further assessment in your comments to the editors.

I am able to assess the statistics

Quality of written English
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Not suitable for publication unless extensively edited

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