

## Answer to the reviewer.

Reviewer:

### **PLACEMENT TAXONOMY (?) OF *Syzygium boerlagei* (Merr.) Govaerts (MYRTACEAE) CONFIRMED WITH ATPB-RBCL INTERGENIC SPACER**

Widodo P, Chikmawati,T. and Kusuma,Y.W.C

Answer:

Our title is: PLACEMENT of *Syzygium boerlagei* ..... because previously it was UNPLACED. The word PLACEMENT is normal in taxonomy. Currently there are many unplaced names that should be placed in a better taxa. So we prefer to keep the title as it was.

Reviewer

Both samples of *Eugenia* are clearly characterised by (1) substitution of C to T at position of 143 and followed by insertion TAC from position of 144-146 ; (2) substitution of T to C at 359 and followed by insertion of ATTGCC from 360-365. However, *E. pyriformis* and *E. uniflora* are distinctly marked by deletion from position of 762 to 776. Molecularly, there are still other differences between *Eugenia* and *Syzygium*, but these are not significant.

Note

**Commented [E1]:** These figures are not found in the table.

**Commented [E2]:** not iin the table?

**Commented [E3]:** not in the table?

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**Commented [E6]:** PLEASE CHECK ALL THE FIGURES/NUMBERS mentioned in the texts. These should synchronize with those in the tables.

**Comment [E6]:** PLEASE CHECK ALL THE FIGURES/NUMBERS mentioned in the texts. These should synchronize with those in the tables.

Answer

This paragraph is a result of the observation on the following very large table of alignment which should not be inserted in the paper.

Input data matrix:

```
1111111111222222222233333333334444444444555555555666
Taxon/Node      1234567890123456789012345678901234567890123456789012
-----
E boerlagei     AATTTTTT-GCGAAA-TTGTGCGAA-TCCAAAAAAAATG-TTCGATAGCAAGTTGATCGGTTA
E pyriformis    GATTTTTTTGCGAAA-TTGTGCGAATCCAAAAAAAATGGTTCGATAGCAAGTTGATCGGTTA
E uniflora      GAATTTTTTGCAGAAAATGTCGAATCCAAAAAAAATG-TTCGATAGCAAGTTGATCGGTTA
S aqueum        AATTTTTT-GCGAAA-TTGTGCGAA-TCCAAAAAAAATG-TTCGATAGCAAGTTGATCGGTTA
S aromaticum    TGTTTTTTTGCAGAAA-TTGTGCGAA-TCCAAAAAAAATG-TTCGATAGCAAGTTGATCGGTTA
```

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S astronioides  AAATTTTTCGCGAAA-TTGTCGAA-TCCAAAAAAATG-TTCGATAGCAAGTTGATCGGTTA
S cumini       AATTTTTCGCGAAA-TTGTCGAA-TCCAAAAAAATG-TTCGATAGCAAGTTGATCGGTTA
S lineatum     AATCTTTT-GCGAAA--TTGTCGAA-TCCAAAAAAATG-TTCGATAGCAAGTTGATCGGTTA
S littorale    AATTTTTCGCGAAA-TTGTCGAATCCA-AAAAAAATG-TTCGATAGCAAGTTGATCGGTTA
S malaccense   AATTTTTCGCGAAA-TTGTCGAA-TCCAAAAAAATG-TTCGATAGCAAGTTGATCGGTTA
S polyanthum   AATTTTTCGCGAAA-TTGTCGAA-TCCAAAAAAATG-TTCGATAGCAAGTTGATCGGTTA
S polycephalum AATTTTTCGCGAAAATTGTCGAATCTATAAAAAATG-TTCGATAGCAAGTTGATCGGTTA
S samarangense AATTTTTCGCGAAAATTGTCGAA-TCCAAAAAAATG-TTCGATAGCAAGTTGATCGGTTA

```

Figure 1. Alignment of nucleotide sequences of *atpB-rbcl* spacer of the chloroplast DNA of *Syzygium* and *Eugenia*.

AUTHORS Widodo, P. Sr., Chikmawati, T. III and Kusuma, Y. W. C. IV.

**TITLE** Placement of *Syzygium boerlagei* (Merr.) Govaerts (Myrtaceae)  
Confirmed with *atpB-rbcl* Intergenic Spacer

**JOURNAL** BIOTROPIA (2018) In press

JOURNAL Submitted (20-DEC-2017) Biology, Fakultas Biologi Unsoed, Jl dr  
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GenBank Submissions grp 6329030

gb-admin@ncbi.nlm.nih.gov

Attachments 12:16 AM (10 hours ago)

to me, pudjiwi

Dear Widodo:

We have received the following 7 sequence submission(s) from you:

BankIt2070719 : (7)

Complete feature annotation has not been included for some or all of the sequence(s) you have submitted.

A. Please resubmit your sequence(s) with relevant features such as:

- coding regions (CDS features), partial or complete, including nucleotide spans and reading frame. Using this information, our software will add the amino acid translations for you.
- structural RNAs such as rRNAs, tRNAs, misc\_RNAs, with nucleotide spans
- features which may describe your sequence, such as repeat\_regions, UTRs, promoters with nucleotide spans

If we do not hear from you by Jan 4, 2018, all of your submission(s) will be deleted from the processing queue.

We have appended a list of a few common methods for adding features to records. We cannot accept annotation in text format, you must resubmit.

B. If you are unsure how to add the annotation, please contact GenBank Users Services at: [info@ncbi.nlm.nih.gov](mailto:info@ncbi.nlm.nih.gov) and include this message with your request.

C. If you are unable to determine the feature annotation, please provide a biological reason for the lack of annotation. Alternatively, you may choose to unverify your records and the following comment will be added:

COMMENT GenBank staff is unable to verify sequence and/or annotation provided by the submitter.

The commented record(s) will indicate that the data are unverified and your sequence(s) will not be included in NCBI BLAST databases.

For more information about annotating your submission, please see:

<https://www.ncbi.nlm.nih.gov/books/NBK53711/>

Please analyze your data prior to resubmission. In order to avoid delays in receiving your accession numbers, ensure that your submission does not have:

- internal stop codons or reading frame shifts in any coding regions
- sequences less than 200 bp
- sequences containing vector contamination
- untrimmed low-quality sequencing read ends

In addition, include:

- unique identifying information for each sample, such as strain isolate, clone, specimen voucher or laboratory identifier
- properly fielded source information using the correct source modifiers

Details about adding identifiers and other source information are attached.

Send your reply to: [gb-admin@ncbi.nlm.nih.gov](mailto:gb-admin@ncbi.nlm.nih.gov) and your resubmitted sequence(s) through Bankit.

#### ORIGIN

```
1 aatttttgc gaaattgtcg aatccaaaaa aaatgttcga tagcaagttg atcggttaat
61 tcaataagaa atgtaatta gcactcgatt tcattgttac catccaaccg aatccaattc
```

121 cattttgttt acttattcaa ttcaatgag tgaattctca agtcaacca acctatntt  
181 taaaatatca agtgggatga ataaaaattc ttgaggcttg agaaaagtcc ttaattgat  
241 ttgtctatca ttataaaca ataaactcca taattatcta tggaattcga acctgaactc  
301 tatttacaat tccattatnt ttatctcctt tttttttct ttttcagca ggccttcta  
361 tgcctagtct attctttttt ttataccta taccctttct ttttaattgg atacaaattc  
421 ctctatntt cacatctagg atttcatat acaacataga tcaactgtcaa gaggtaaatt  
481 ctattatnt caatatgata ttttgattca aaaaaaagtg agggattcca aatttcaaaa  
541 acaagaattg ggttgcgcca tacatatgaa agagtataca ataattgatgt attttgcgaa  
601 tcaaatacca tggataata aaagaacctat tatgattagt tgataatatt cgttgatgat  
661 ttttgaaag aatttcttgt gaaagcttcc attaactccg aatttctgtc gagtagacct  
721 tgttggttg ataatctta attcatgagt ttagggagg gacttatgtc accacaaaca  
781 gagactaaag caagtgttg attc

//

LOCUS Seq7 794 bp DNA linear PLN 13-DEC-2017  
DEFINITION [Syzygium polyanthum (Wight) Walp.] Voucher Widodo 139 in PUNS  
atpB-rbcl.

ACCESSION

VERSION

KEYWORDS .

SOURCE chloroplast *Eugenia pyriformis*

ORGANISM *Eugenia pyriformis*

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;  
Pentapetalae; rosids; malvids; Myrtales; Myrtaceae; Myrtoideae;  
Myrteae; *Eugenia* group; *Eugenia*.

REFERENCE 1 (bases 1 to 794)

AUTHORS Widodo, P. Sr., Chikmawati, T. III and Kusuma, Y. W. C. IV.

TITLE Placement of *Syzygium boerlagei* (Merr.) Govaerts (Myrtaceae)

Confirmed with atpB-rbcl Intergenic Spacer

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REFERENCE 2 (bases 1 to 794)