

Haplotypes of “*Candidatus Liberibacter europaeus*” also separate by geography and plant/insect host species

Version 2 has a few minor sentence rewordings to clarify and read better. The specific sequences aligned and analysed are noted. The main change is to format it to a more easily and coherently readable form.

The Nelson et al 2011 paper describing haplotypes of a related *Liberibacter* species suffered similar comments as this one but has subsequently been cited 35 times. In particular, biological differences are now being noted between the haplotypes beyond the obvious geographic range and host (insect/plant) species.

This is intended to be the final version and I have no intention of submitting elsewhere.

Version 1 was submitted to PeerJ but rejected, reviewer comments follow as per PeerJ requirements for revision of PrePrints.

Reviewer Comments

Reviewer 1 (Anonymous)

Basic reporting

In my opinion the paper does not include any relevant information to validate a scientific publication. The author just shows the analyses of some sequences from unknown number of bacterial strains which looks like were not even obtained in this work but found in the databases. The results are shown in an unique table which is not even well presented or discussed.

Introduction is short and does not include sufficient information about *Liberibacter* species as well as disease description and in my opinion does not justify the really small work presented.

I have similar criticism on the material and method section, just a few sentences on the sequence analysis!! The reader does not know if where the sequences come from, how many strains?, origin? Strain identification? Not information at all!

Result and Discussion section, again, no much information is shown and for sure not enough for scientific paper

Experimental design

No experimental design at all and no clear which is the real objective of the work

Validity of the findings

In my opinion just to identify variability in a ribosomal region among undetermined number of isolates of *Liberibacter* is not enough to justify a scientific publication but the start point for future research

Reviewer 2 (Anonymous)

Basic reporting

Not enough novel material or analysis.

Experimental design

See below

Validity of the findings

Findings based in a very small sample of sequences.

Comments for the author

For this study the author focuses on studying ‘*Candidatus Liberibacter europaeus*’ (Leu), a bacterium that seems to be associated with diseases in Scotch broom, and was found also associated with pear. The author screened the NCBI database and retrieved 9 DNA sequences of 16S or 16-23S samples attributed to Leu. Then the author compared to the close relative ‘*Candidatus Liberibacter americanus*’ (Lam) in search for SNPs, and in particular looking for differences between Leu from New Zealand and Leu from Italy. He found that Leu-NZ shares 10 SNPs with Lam, but those are not shared between Leu-IT and Lam. So he defines two haplotypes among Leu. This is an interesting observation, but it feels like preliminary data that needs further investigation. There are several problems with this research:

- 1) As the author acknowledges (Ln. 37), only 2 laboratories have contributed the 9 sequences he is using. This can lead to major biases.
- 2) There is not novel data presented here.
- 3) Comparisons with other *Ca. Liberibacter* spp. may be useful (*asiaticus*, *americanus*, *crescens*)
- 4) Support for using Lam as a comparisons needs to be explained better
- 5) The writing needs to be revised, multiple sentences were not clear. In particular it needs to be better described the knowledge on Leu as a pathogen, or as an endophyte.

Reviewer 3 (Anonymous)

Basic reporting

The manuscript report a 16S and 16-23S sequences of *Candidatus Liberibacter europaeus* of Italian and New Zealand isolates showing great difference among both. Interesting, no difference was observed between Leu (Italy) and *Liberibacter americanus* from Brazil. About this interesting found the author only did a speculation that "the biogeographic inference derived from molecular dating and plate

tectonics, indicating a historical geographic link some millions of years old separating Lam in the Americas and Leu in central Europe". Why none report was done about Leu in Brazil, yet?

Experimental design

The experimental procedure used for the author is poorly describe witch is consequence of few dataset used for.

Validity of the findings

The dataset used in this paper are results of sequencing of 16S and 16-23S genomic regions of Leu and also from GenBank access. The main subjection is the few sequences were used and no statistic analysis (a simple phylogram, for instance) was done. As consequence a superficial discussion was done with deeper speculations like present in the lines 45 - 47.

Comments for the author

The manuscript should be submitted as a communication once a poor dataset was used with no statistic analysis.