



The SBE meeting 2021's Book of Abstracts

Edited by the SBE meeting 2021's organizing committee

June, 2021

DOI: [10.5281/zenodo.4904236](https://doi.org/10.5281/zenodo.4904236)

II Virtual Meeting of Systematics, Biogeography, and Evolution: The Research of Biodiversity and the Diversity of Researchers

www.sbemeeting.com

June 19–23, 2021

Time Zone: UTC-4



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About

The I Meeting of Systematics, Biogeography, and Evolution (SBE) occurred from July 28 to July 30, 2020. The theme of the first meeting was *A Joint Effort in the Coronavirtual Era* (see <https://sbemeeting.weebly.com/>).

This abstracts book contains the abstracts of the second SBE meeting, from June 19 to 23, 2021. Our 2021's theme is *The Research of Biodiversity and the Diversity of Researchers*. Although the themes changed, our primary purposes remained the same.

First, to provide a high-quality international scientific meeting on systematics, biogeography, and evolution.

Second, to make the event accessible to people that could have difficulty attending other international scientific events due to financial constraints or the COVID-19 pandemic.

Third, to promote diversity and gender equality in science, technology, agronomy, mathematics, and medicine (STEAMM).

Come celebrate the richness of variety!

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Sponsors, Supporters, and Collaborators

The SBE Meeting 2021 is made possible thanks to our sponsors, supporters and collaborators.

Different poster awards were offered by:

- Asociación Paleontológica Argentina (APA, www.apaleontologica.org.ar/)
- Asociación Hepetológica Argentina (AHA, <http://aha.org.ar>)
- BIO+ Ciência (biomaisciencia.com)
- Transmitting Science (www.transmittingscience.com)

We thank the University of North Carolina at Charlotte (UNC Charlotte) for making the webinars on Zoom possible without costs for the participants.



Mar Chiquita district had at least three independent introduction routes. Furthermore, the route of contagion through aerosols would not be the main spread route of the virus among cattle herds. Alternatively, due to the low correlation between geographic and genetic distances, a virus dispersal of the virus by non-replicating vectors is proposed, for example, by machinery, water, and human transport.

Phylogeny of the species of the genus *Celtis* (Cannabaceae) of southern South America: morphological and molecular evidence

June 22
12:00 PM
Session 7

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The genus *Celtis* (Cannabaceae) comprises around 70 temperate to tropical woody species, commonly known as hackberries. In southern South America it is represented by around ten taxa (all belonging to the subgenus *Mertensia* Planch.) restricted to the Domain of Neotropical Seasonally Dry Forests, and the subtropical Chaco and Espinal biogeographical regions. The latter species present significant inter- and intraspecific morphological variability and similarity that has generated widespread taxonomic confusions. This work aimed was to study the phylogeny of some species of the genus *Celtis*, with morphological characters and DNA sequences combined, as well as the main morphological features to improve taxonomic circumscriptions. Twenty-nine specimens representing seven taxa of *Celtis* and five outgroup accessions were included. Twenty vegetative and reproductive morphological characters were selected based on previous works. The nuclear FA16180b marker was amplified and sequenced. The sequences were aligned using Mega 6.06, through ClustalW v1.8. The data were analyzed under the parsimony optimality criterion using the program TNT. This group of *Celtis* species resulted as monophyletic, although there is no clear resolution between these taxa. Nevertheless, six species of southern South America *Celtis* are recognized. As regards *C. pallida* (with its two varieties), a polytomy of specimens was observed; however, it differentiates clearly from the rest of the species. Meanwhile, *C. tala*, *C. chichape* and *C. clauseniana* do not form a clade but are visibly separated from the rest of the species. A defined clade formed by *C. serratissima* and *C. spinosissima* differentiates from the rest. The characters that have the greater correspondence with the formed groups were: growth habit, type of spines, type of styles, type of foliar margin, indument of the foliar veins and, pyrene ornamentation. Except for the hygrophilous *C. chichape*, the other five species are confined to well-defined biogeographical regions, thus coinciding with its distribution in the phylogenetic tree.
