Mr. J.I. Márquez-Corro

Universidad Pablo de Olavide

Ctra. de Utrera, km 1

ES-41013, Sevilla

Spain

Email: jimarcorr@gmail.com

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Dear Editor-in-Chief,

We would very much appreciate if you could consider the enclosed manuscript entitled "**Inferring Hypothesis-based Transitions in Clade-specific Models of Chromosome Number Evolution along Phylogenies**" for publication in **Molecular Phylogenetics and evolution**.

The enclosed manuscript is not under consideration for publication in another journal or book, its submission for publication has been approved by all relevant authors and institutions, and all persons entitled to authorship have been so named. All authors have seen and agreed to the submitted version of the manuscript.

We contrast a null hypothesis of a single mode of chromosome number evolution against a number of alternative complex scenarios with multiple models of chromosome evolution. The chosen scenarios are based on previously detected diversification bursts. We have chosen as study group the sedges. The family Cyperaceae is the tenth most species-rich angiosperm family and chromosomal mutations (dysploidy and polyploidy) have been suggested to have key role in the diversification process.

We provide new insights into the study of chromosome number evolution. In this study we show an innovative approach to compare single versus complex scenarios of chromosome evolution along the phylogeny. Specifically, we have revealed a complex scenario in Cyperaceae, including different models of chromosome evolution with regards of previously reported diversification rates shifts. In addition, we also provide new insights into relationship between shifts in diversification rates and chromosome number transitions, which is still poorly understood.

This study combines the newest and most comprehensive phylogeny of the family Cyperaceae -including more than a thousand species- with a first-time implemented approach in the study of chromosome evolution. In particular, we aimed to evaluate transitions in the mode of chromosome evolution in different lineages with shifts in diversification rates. With the use of this new approach, our study shows how chromosome number evolves differently in three high species-rich lineages of Cyperaceae. Moreover, this study leads to further questions about how chromosome evolution diversity is related with diversification.

We consider our study falls within the aims and scope of Molecular Phylogenetics and Evolution and could be of general interest to its readers. In this study, we use a new approach to address consequential questions in karyotype evolution.

Thank you very much in advance

Sincerely yours,

J.I. Márquez-Corro and co-authors

Report:

- Original research article

- Full text (introduction, materials and methods, results, discussion and acknowledgements, author contributions) = 3,867 words

- 70 references aprox.

- 2 Tables

- 2 Figures

- Supporting Information: 6 materials