

# Abstract submission

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### 1. Title of manuscript \*

Global hotspots of plant phylogenetic diversity

### 2. Authors and affiliations \*

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4. Article type (for details see here under Article types: <https://tinyurl.com/ms5wkd3m> and <https://tinyurl.com/56w4p4d7>) \*

Full paper

5. Which journal (*New Phytologist* or *Plants, People, Planet*) do you prefer for your contribution? \*

☒ *New Phytologist*

☐ *Plants, People, Planet*

## 6. Do you agree to also be considered for the alternative journal if your first preference isn't possible? \*

☒ Yes

☐ No

7. Data details – specifically indicate how RBG Kew's World Checklist of Vascular Plants (<https://tinyurl.com/33fe6um9>) will be used in the study, and indicate which other data will be used. \*

The WCVF will be used as the taxonomic backbone and source of geographic distribution data, i.e. to quantify the presence/absence of phylogenetic branches across all of the world's "botanical countries". To this end, the WCVF will be combined with a new global phylogeny of seed plants (Sun et al. in prep), and a dated phylogeny resulting from the Plant and Fungal Trees of Life (PAFTOL) project at the Royal Botanic Gardens, Kew (Carruthers, Zuntini et al. in prep.). Measures of long-term climate stability (e.g. Miocene climate anomalies), present environment (climate, soils), topography, geographic isolation etc. will be included as potential drivers of phylogenetic diversity/endemism. Measures of threat,

8. Main research questions / hypotheses your contribution will address (max. 100 words) \*

We hypothesise areas of high phylogenetic diversity and endemism to differ significantly from areas of high species diversity and endemism, due to different underlying drivers such as long-term geographic isolation and environmental stability. We thus expect that hotspots (sensu Myers et al. 2000, Nature) of phylogenetic diversity will only partly overlap with the widely used hotspots of species diversity. Species-based hotspots that are caused by high neoendemism (recent, rapid radiations) will not be hotspots of phylogenetic diversity. Meanwhile, areas of disproportionately high phylogenetic diversity and paleoendemism, if

9. What is the scientific novelty of this research? (max. 100 words) \*

Although protecting evolutionary history is a widely appreciated conservation target, there is no global understanding of where this evolutionary history is found in plants and why, and where it is most threatened. Importantly, it remains unknown which historical and ecological factors shape the global distribution of evolutionary history in plants. This study will tackle these issues by testing specific hypotheses on the determinants of phylogenetic diversity and its overlap with anthropogenic threat globally. We will both explore what drives the distribution of plant evolutionary history, and highlight regions that are hotspots of global

10. What is the geographical scope of the study? \*

Global

11. What is the taxonomic scope / sampling of the study? \*

All species of seed plants

12. Analyses – briefly describe the statistical analyses used to address the main research questions / hypotheses (max. 100 words) \*

We will calculate phylogenetic diversity (PD) and phylogenetic endemism (PE) in all of the world's botanical countries, and test the relationships of PD and PE to putative historical, geographic and environmental drivers (see "Data") using spatial regression. We will quantify past and projected future anthropogenic threats for the botanical countries using variables including human footprint, deforestation, climate change etc. We will identify hotspots as (clusters of) botanical countries combining high PD/PE with high threat levels, and compare these to species-based hotspots. Analyses will be conducted at different phylogenetic depths

13. If your proposal is very similar to those of another submitted contribution, would you be willing to discuss with the other author(s) to explore a collaboration or discuss how to minimise overlap (and can we contact you in that case about this)? \*

Yes

14. Abstract (max. 300 words) \*

Protecting unique evolutionary history is a widely acknowledged conservation priority that can only be implemented efficiently once we understand the relation between unique evolutionary history and anthropogenic threat. For seed plants (Spermatophyta), this knowledge is lacking at a global scale. Here we will analyse the distribution of phylogenetic diversity (PD) and phylogenetic endemism (PE) globally and across all species of seed plants, combining the World Checklist of Vascular Plants (WCVP) with a new comprehensive all-evidence phylogenetic tree of spermatophyta. We hypothesise that the distribution of PD and PE, especially at deep phylogenetic levels, differs significantly and predictably from the distribution of species diversity and endemism, respectively, due to different underlying mechanistic drivers. We will test putative drivers using macroecological models, i.e. by relating patterns of PD and PE at different phylogenetic depths to measures of geohistory and environment. We will then identify regions that maximise PD/PE and anthropogenic threat (human footprint, deforestation, climate change etc.). These will be defined as the "hotspots" of plant phylogenetic diversity. We will compare these hotspots to hotspots based on species richness and endemism (both based on literature and the WCVP) and discuss the conservation implications of the observed differences. We expect that some species-based hotspots, especially those resulting from an abundance of recent rapid radiations, will not be hotspots of plant phylogenetic diversity, while areas not previously recognised as

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