

BIOGEOGRAPHY AND EVOLUTION OF THE ATACAMA GENUS *CRISTARIA* (MALVACEAE)

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The Atacama Desert, located on the western side of the Andes in northern Chile, harbours a range of endemic species adapted to hyperarid conditions. Vegetation is largely restricted to coastal fog oases and the Andean foothills, which are separated by a largely vegetation-free zone. Diversifications have been shown to be surprisingly recent in some Atacama clades, which is at odds with the extremely long history of aridity documented for this region. Here, we report the results of a molecular dating analysis of the Atacama genus *Cristaria* (Malvaceae) and its East Andean sister genus *Lecanophora* based on plastid sequence data.



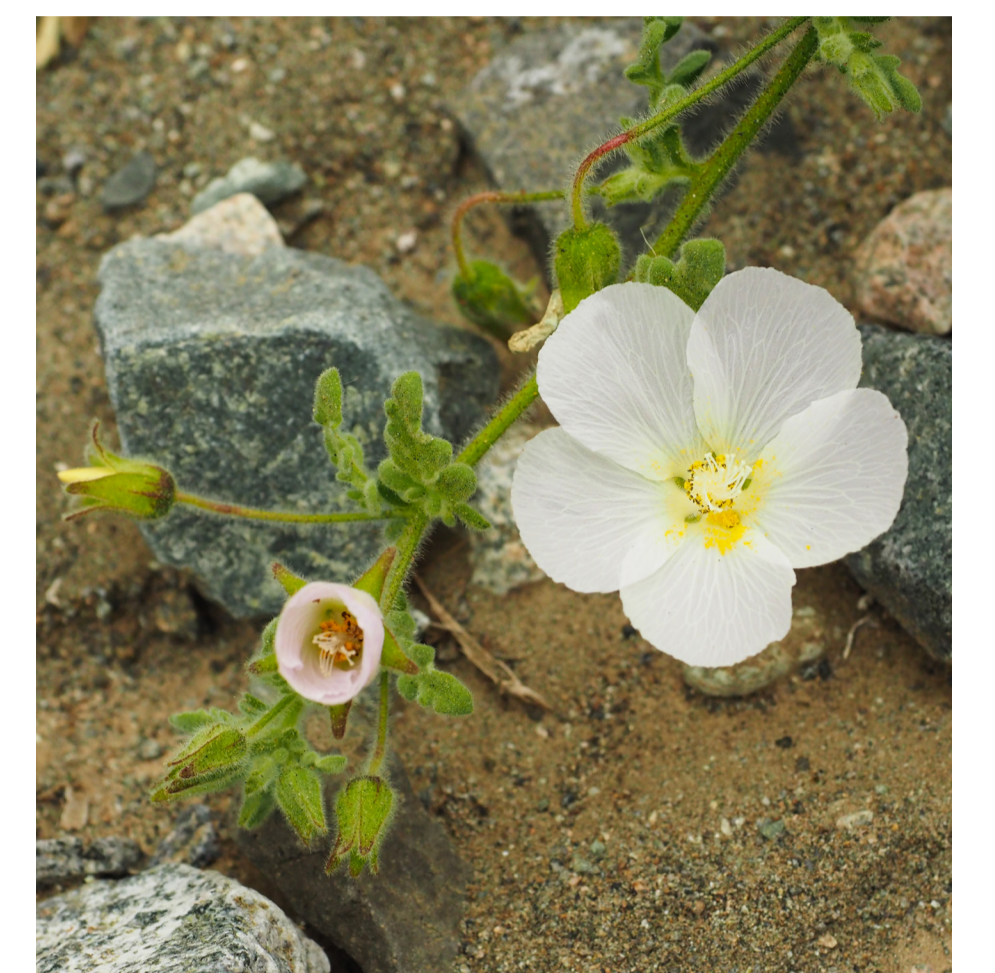
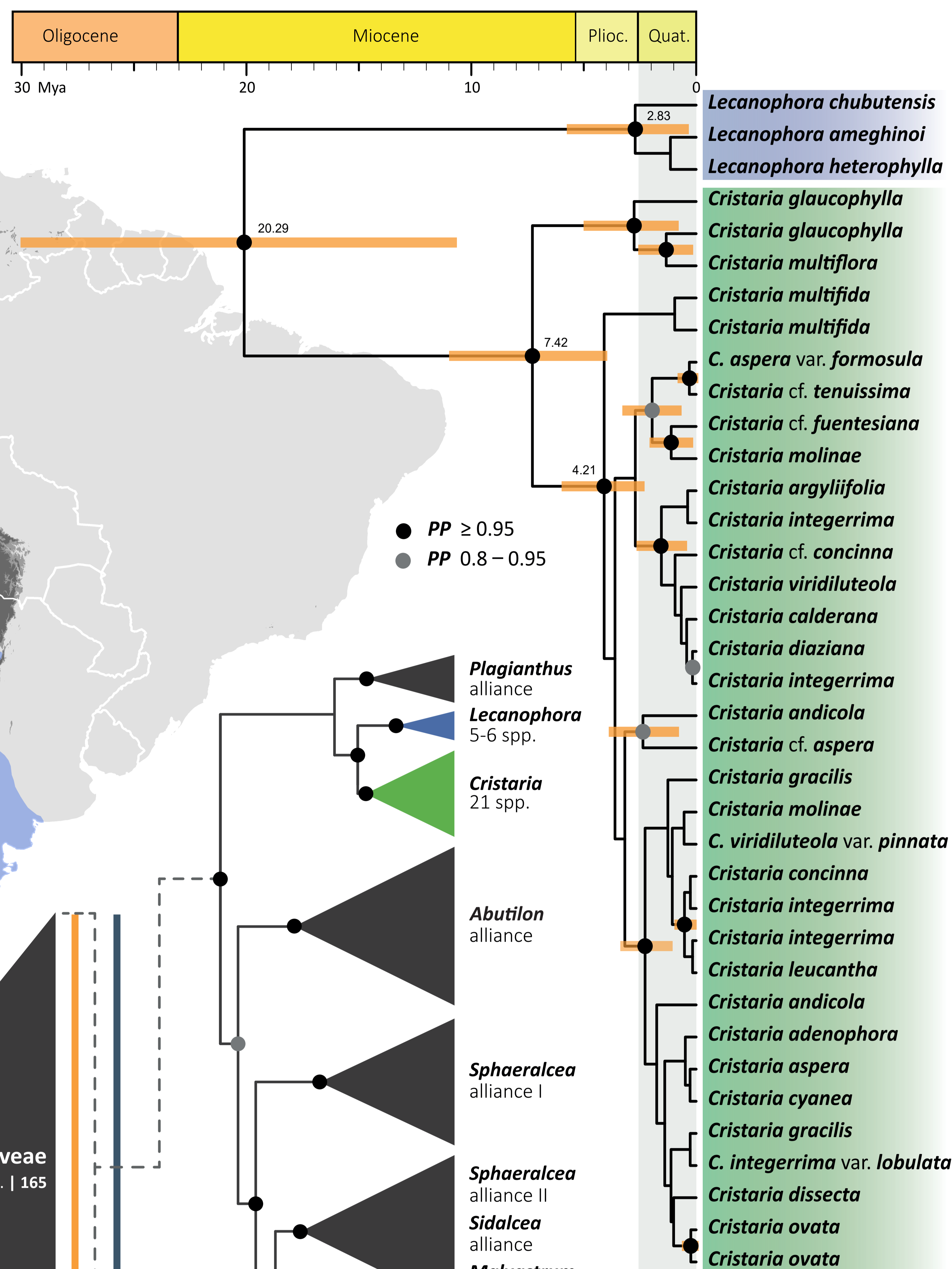
Atacama Desert near Taltal

Conclusion

Divergence times of *Cristaria* suggest that the split from *Lecanophora* predates the major phase of the Central Andean uplift, but do not discard an East-West vicariance scenario. Diversification of *Cristaria* in the Atacama Desert appears to coincide with the onset of hyperaridity since the late Miocene. The sister relationship with the Western Pacific *Plagianthus* alliance – although only weakly supported – indicates a possible vicariance scenario between South America and Oceania.

Project context

In the context of a large-scale project on landscape and biotic evolution of hyperarid environments, we investigate the origin and diversification of the Atacama Desert flora. We are conducting additional phylogenetic and dating analyses in the species-rich genera *Atriplex* (Amaranthaceae) and *Cryptantha* (Boraginaceae) as well as the subfamily Larreoideae (Zygophyllaceae), making use of Sanger and Genotype-by-Sequencing approaches. Furthermore, we aim to measure gene flow between populations of four widely distributed plant taxa in the Atacama Desert.



Cristaria leucantha



Cristaria andicola



Cristaria dissecta



Cristaria integerrima

Tab. 1 | List of crown fossils used for the BEAST2 analysis. Placing of the fossils is indicated by green dots in the backbone phylogeny of the Malvoideae.

Fossil taxon	Age [Mya]	Clade	Reference
<i>Hibiscoxylon nyloticum</i>	88 – 66	Core Malvoideae	Kräusel (1939) <i>Abh. Bay. Akad. der Wis.</i>
<i>Malvaciphyllum macondicus</i>	60 – 58	Eumalvoideae	Carvalho et al. (2011) <i>Am. J. Bot.</i>
<i>Malvacearumpollis</i> sp.	37 – 30	Malveae	MacPhail & Truswell (1989) <i>BMR J. Aust. Geol. Geop.</i>
<i>Echiperiporites estelae</i>	45 – 34	Hibisceae	Germeraad et al. (1968) <i>Rev. Palaeobot. Palyno.</i>

Methods

We used a molecular data set of three plastid markers (*ndhF*, *trnK/matK* and *rp16*)², complemented with sequences from 50 samples of Malveae from our own field collections. Taxon sampling comprises 19 of the 21 accepted species (90 %) across the range of the genus. We ran a Bayesian node dating approach with four fossil calibrations (table 1) using BEAST2³. Additionally, we tested the fossilized-birth-death (FBD) process model with 18 fossils^{1,2,4}.

Results

The phylogenetic analysis with 333 samples across Malvoideae confirms the monophyly of *Cristaria* and the sister relation to *Lecanophora*. Southern Atacama and Peruvian coastal species are consecutive sister to the main Atacama radiation. The FBD approach revealed surprisingly high age estimations along the phylogeny. The analysis with four fossils gave good support and are in line with the majority of published data.

References

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