



The complexity of symbiotic interactions influences the ecological amplitude of the host

Lucie Vančurová¹, Lucia Muggia², Ondřej Peksa³, Tereza Řídká¹, Pavel Škaloud¹

¹Charles University in Prague, Faculty of Science, Department of Botany, Czech Republic

²University of Trieste, Department of Life Sciences, via Giorgieri 10, 34127 Trieste, Italy

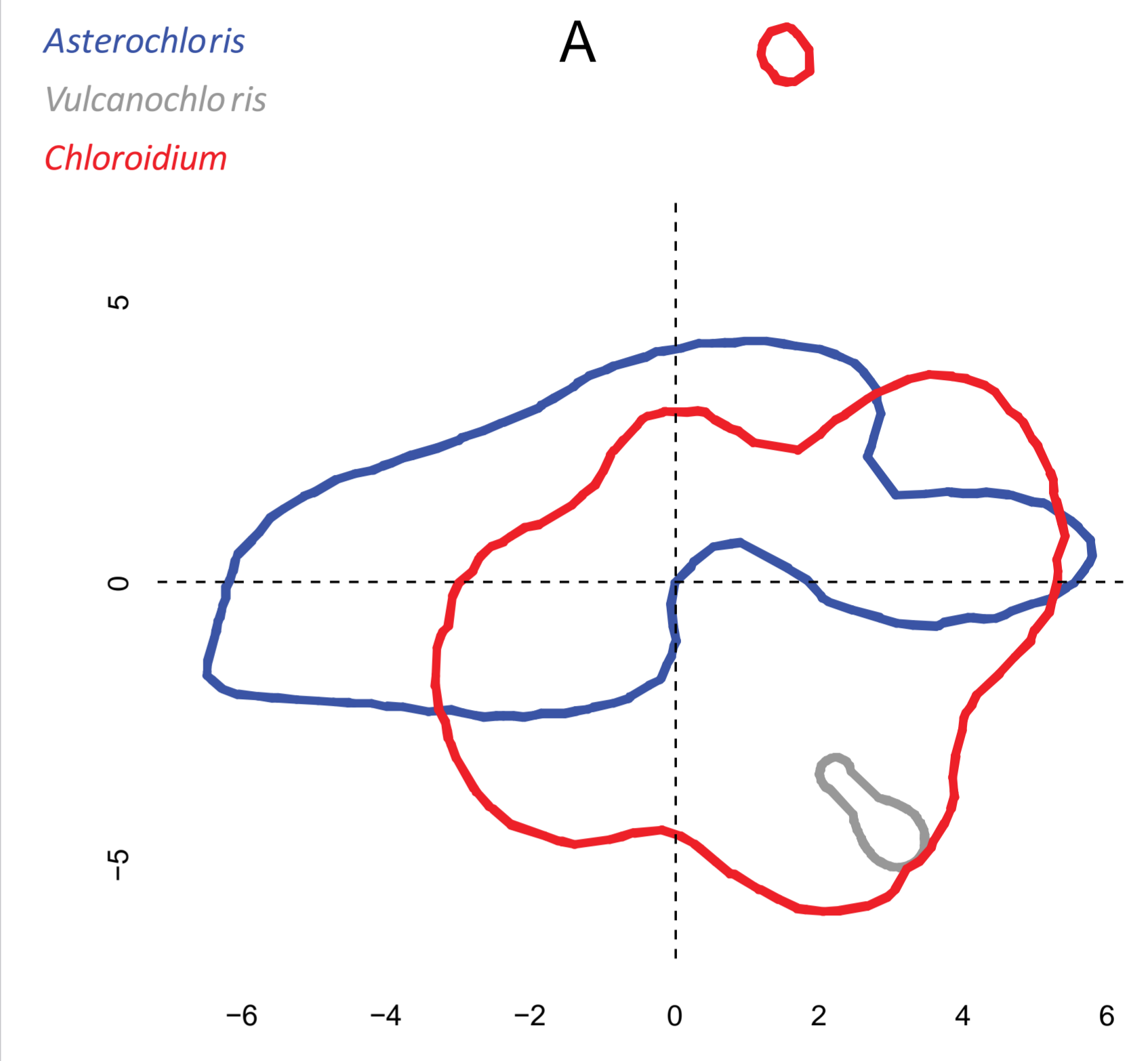
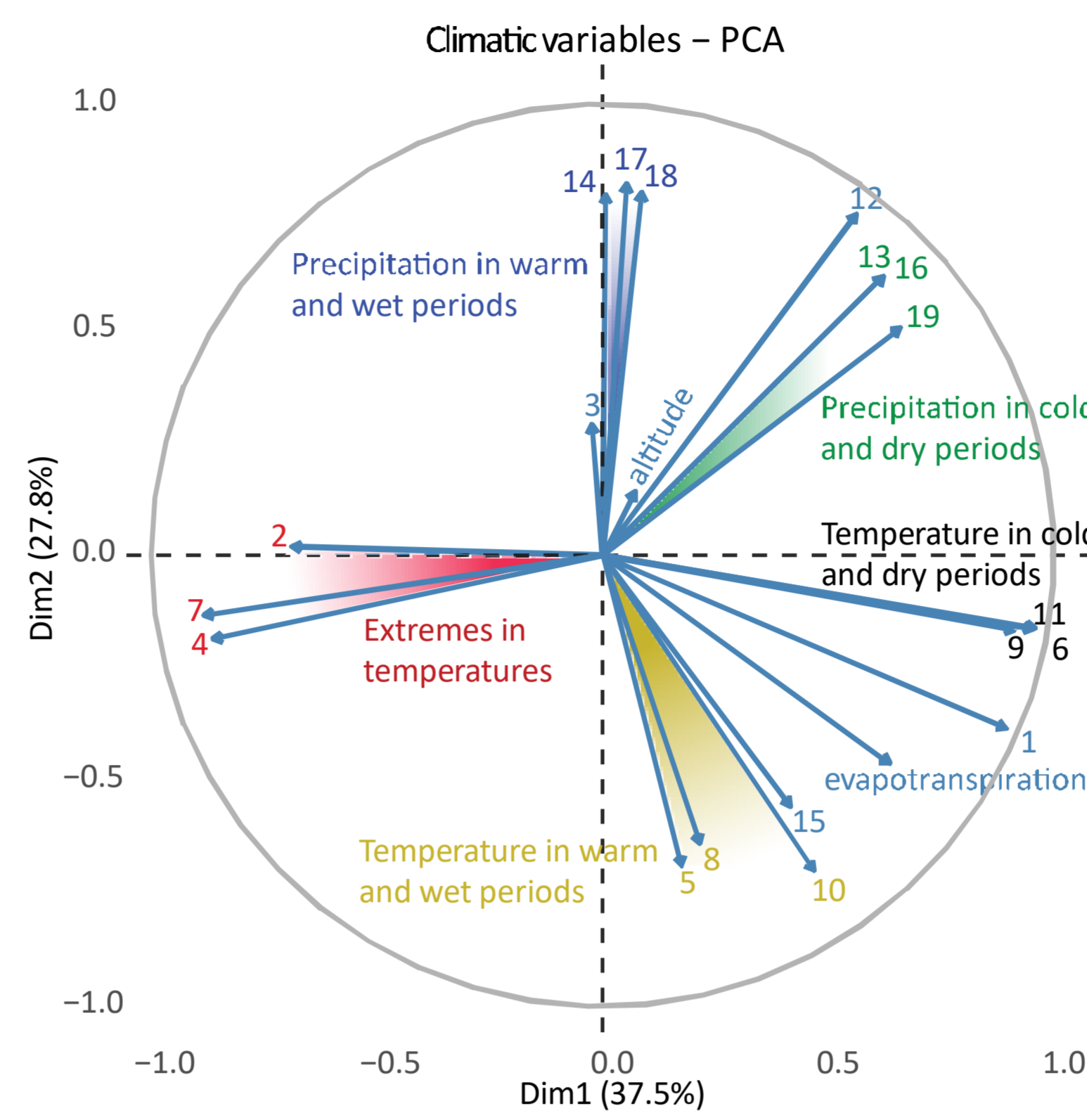
³The West Bohemian Museum in Pilsen, Kopeckého sady 2, 301 00 Plzeň, Czech Republic



Model organism

Lichen-forming fungal genus *Stereocaulon* occurs in very diverse environments from polar areas [1] to tropics [2], in a wide range of altitude, frequently on toxic substrata, tolerates submersion [3] as well as aridity.

Climatic niches

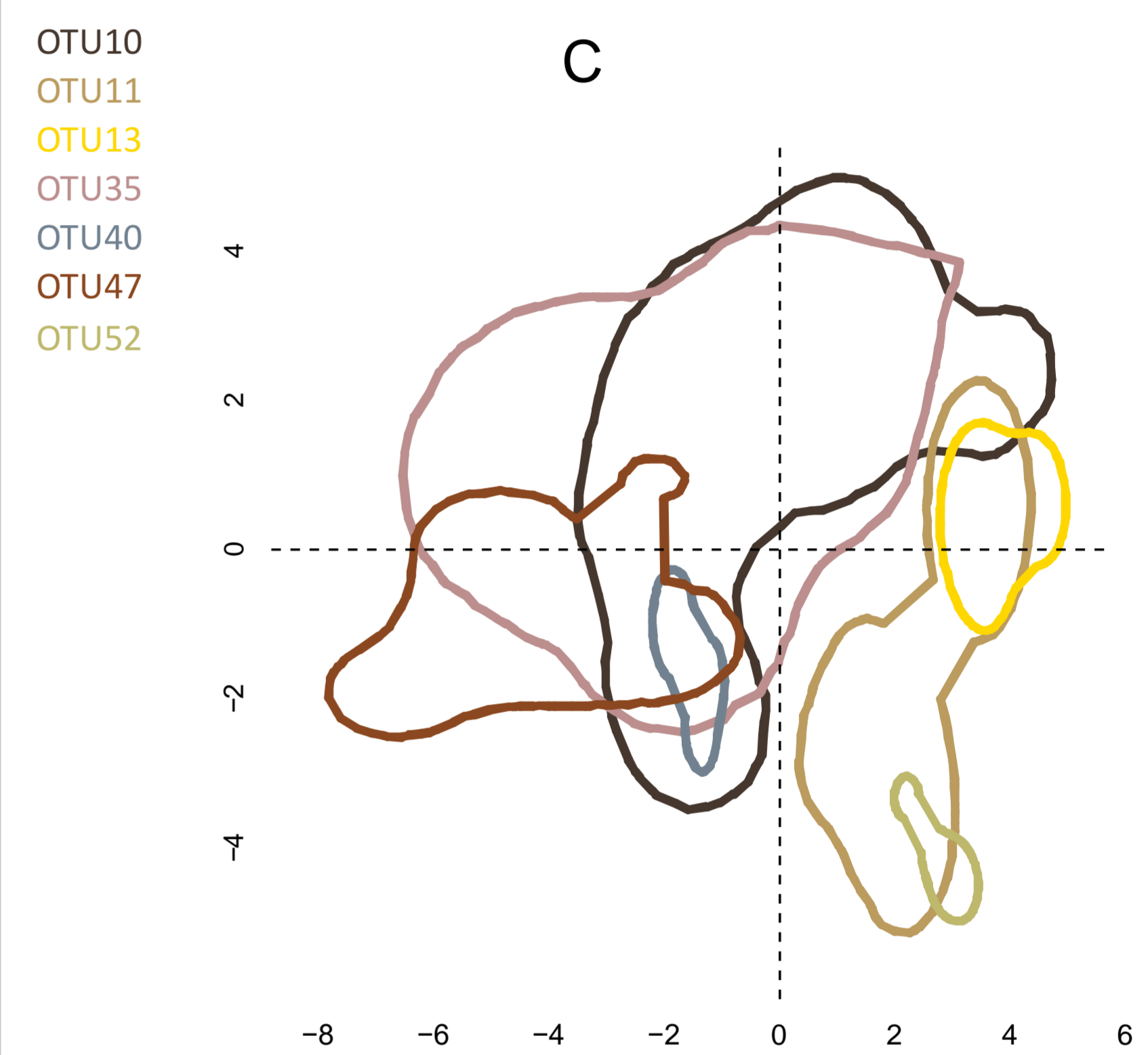
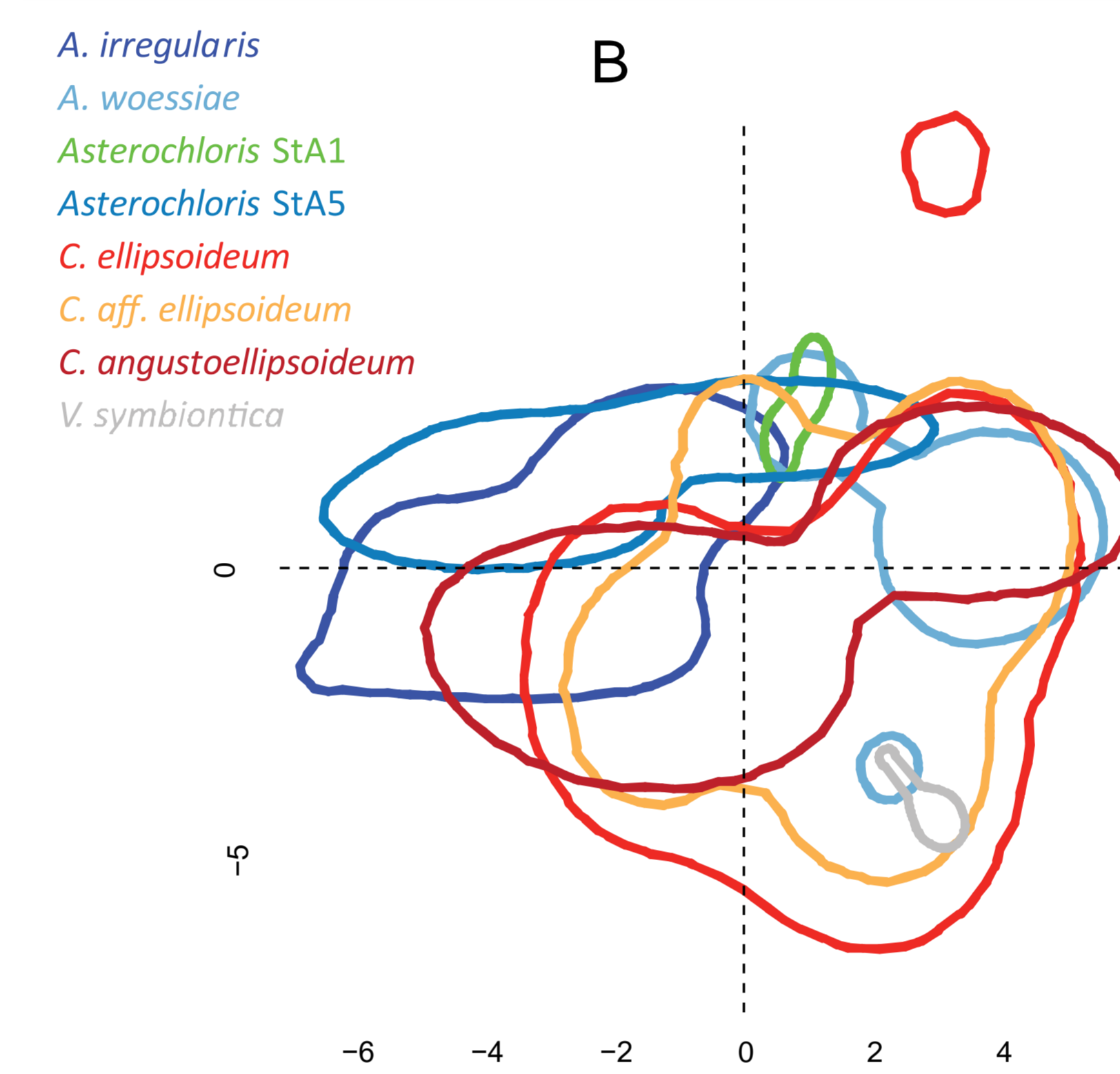


What is the diversity of phycobionts associated with the lichen-forming genus *Stereocaulon*?

Do phycobionts and mycobionts exhibit reciprocal specificity/selectivity and how does this affect the width of their climatic niches?

Diversity of phycobionts

The diversity of predominant phycobionts is exceptional: the three trebouxioid genera, *Asterochloris*, *Chloroidium* and *Vulcanochloris*, and several dozens of their species.



Specificity and selectivity

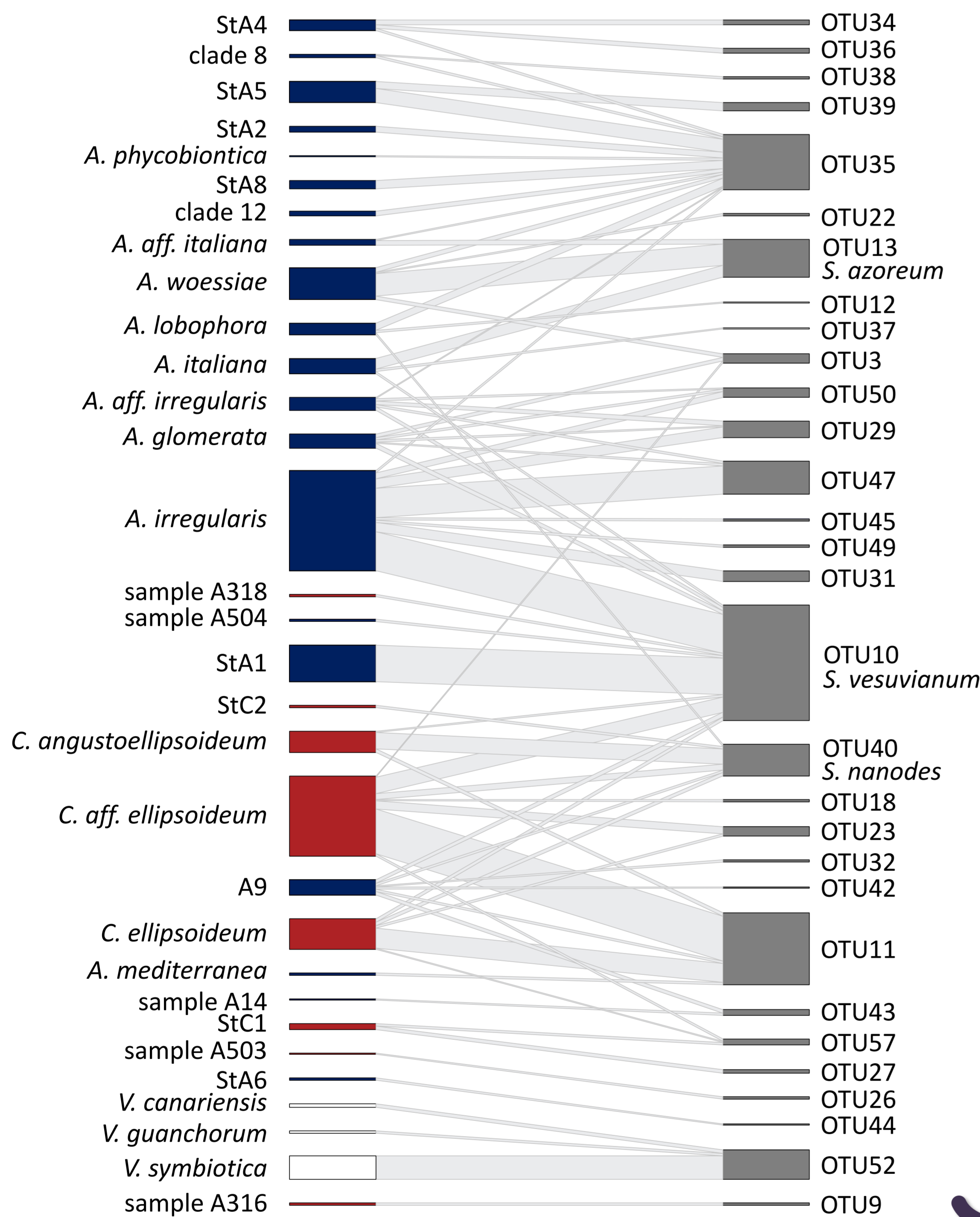


Fig. 1. Interaction network structure between phycobiont species-level lineages and mycobiont species-level lineages in the genus *Stereocaulon*. The width of the links is proportional to the number of specimens forming the association. The *Asterochloris* lineages in blue, *Chloroidium* in red, *Vulcanochloris* in white, mycobiont in grey.

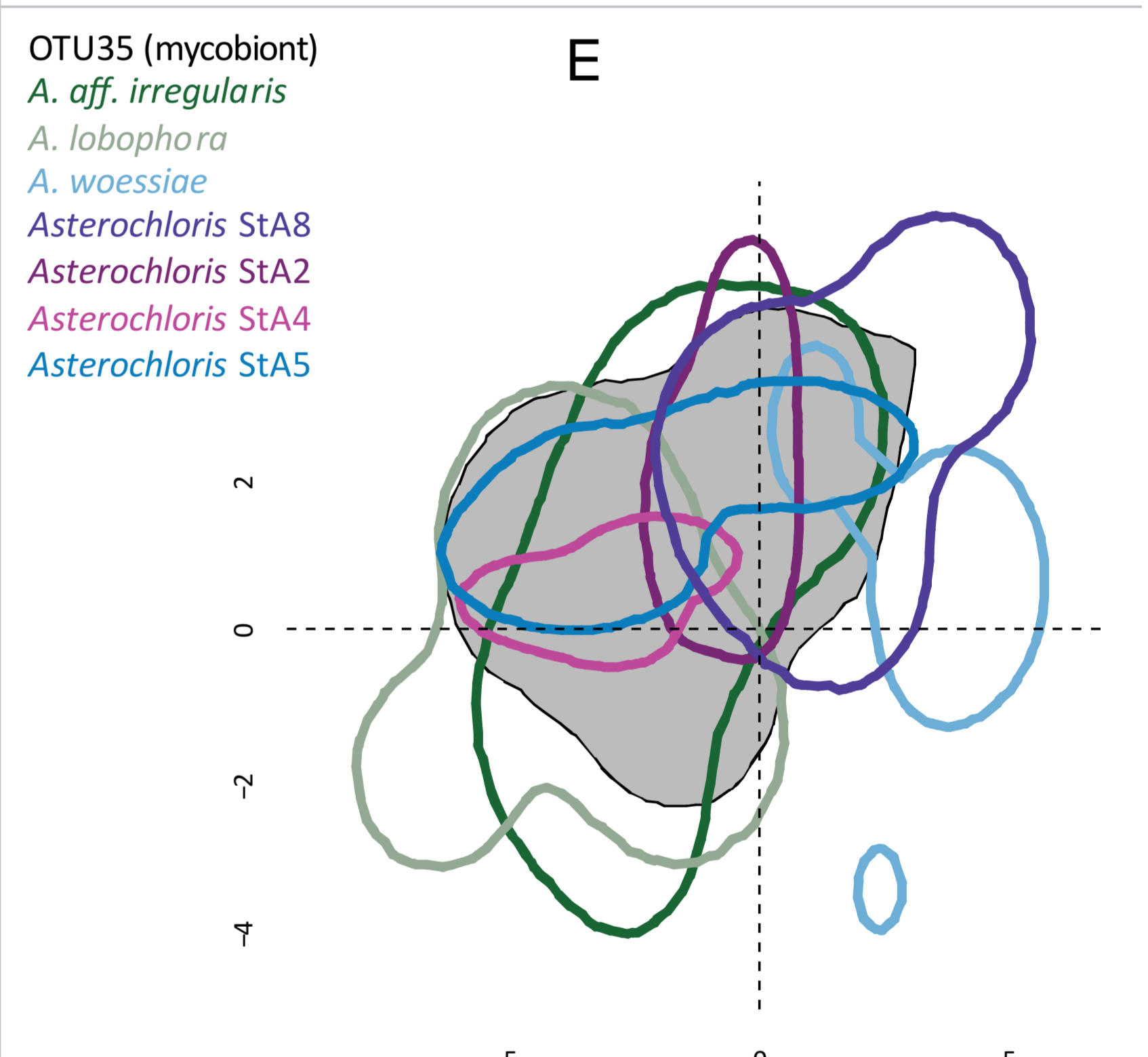
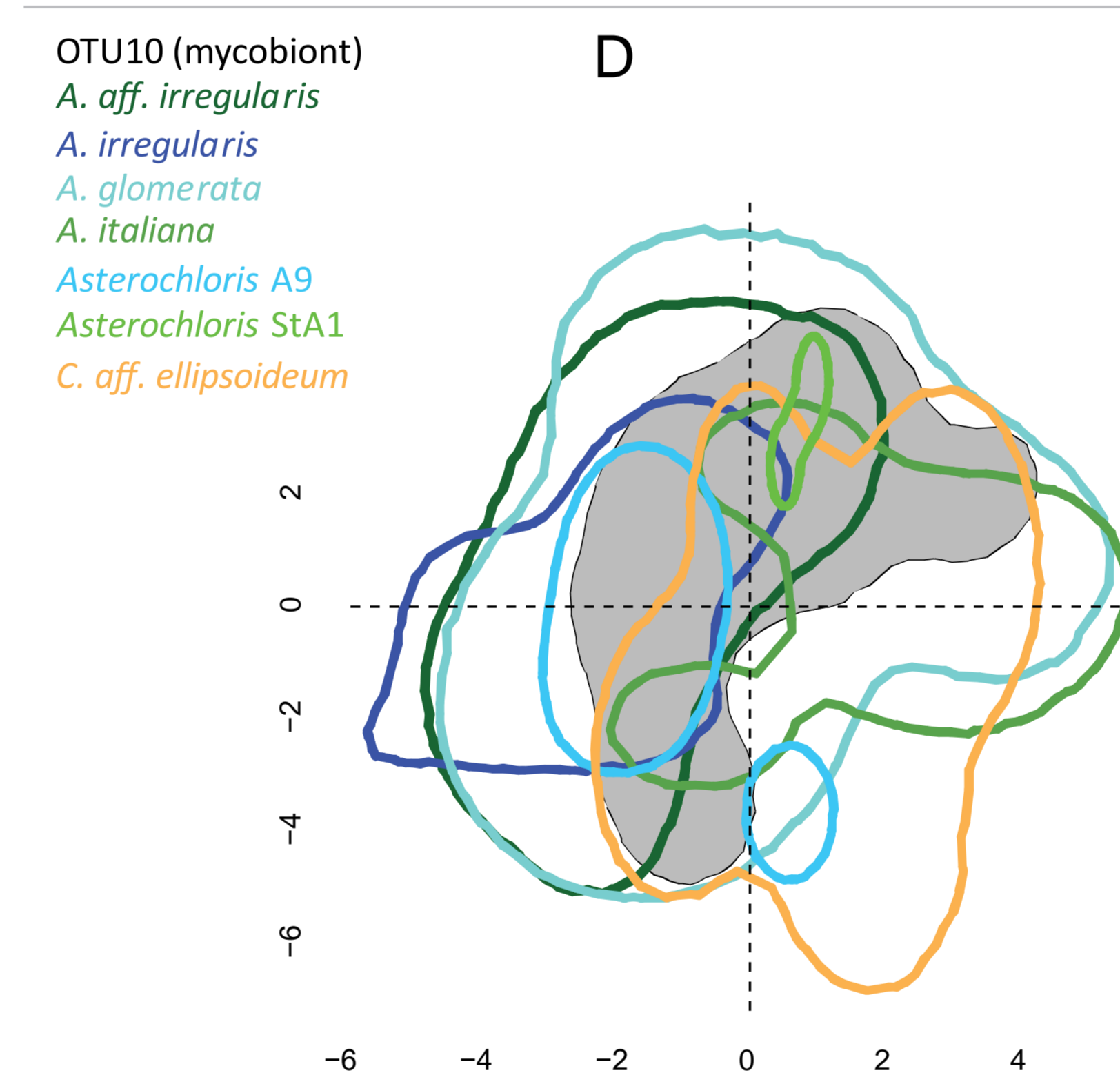
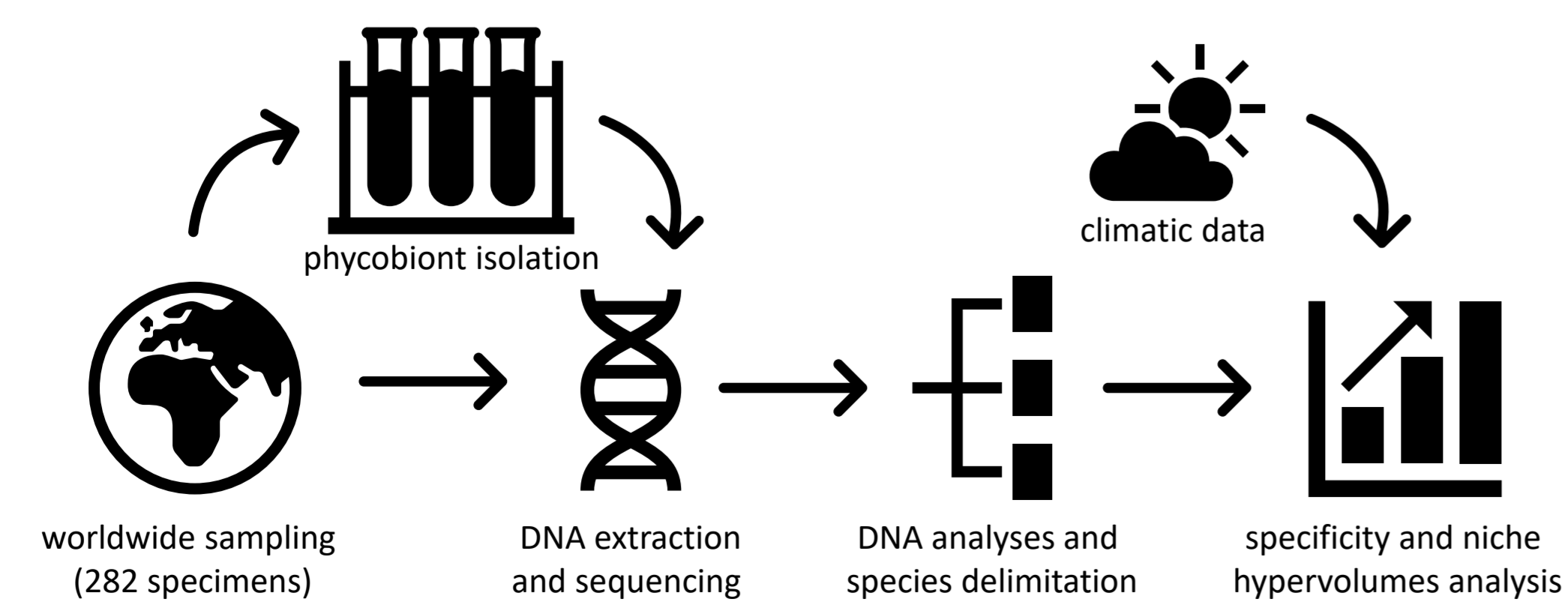


Fig. 2. Climatic niche hypervolumes for (a) algal genera *Asterochloris*, *Vulcanochloris* and *Chloroidium*, (b) eight most abundant algal species-level lineages (phycobionts), (c) seven most abundant fungal species-level lineages (mycobionts), (d) fungal OTU10 (grey filled) with its seven most abundant (of total 11) associating phycobionts, (e) fungal OTU35 (grey filled) with its seven most abundant (of total 12) associating phycobionts based on climatic PC1–PC2 axes (explaining 65% of variation). Climatic variables: 1 = annual mean temperature, 2 = mean diurnal range, 3 = isothermality, 4 = temperature seasonality, 5 = max temp. of warmest month, 6 = min temp. of coldest month, 7 = temp. annual range, 8 = mean temp. of wettest quarter, 9 = mean temp. of driest quarter, 10 = mean temp. of warmest quarter, 11 = mean temp. of coldest quarter, 12 = annual precipitation, 13 = prec. of wettest month, 14 = prec. of driest month, 15 = prec. seasonality, 16 = prec. of wettest quarter, 17 = prec. of driest quarter, 18 = prec. of warmest quarter, 19 = prec. of coldest quarter [4]

Species-level lineages, which accept more symbiotic partners, have wider climatic niches

Material and methods



This study was published in *Mol. Ecol.*, vol. 27, no. 14, pp. 3016–3033, 2018. See the paper for more details.



References: [1] C. Seo, J. H. Sohn, S. M. Park, J. H. Yim, H. K. Lee, and H. Oh, *J. Nat. Prod.*, vol. 71, no. 4, pp. 710–2, Apr. 2008.; [2] F. Ismed, F. Lohézic-Le Dévéhat, O. Delalande, S. Sinbandhit, A. Bakhtiar, and J. Boustie, *Fitoterapia*, vol. 83, no. 8, pp. 1693–8, Dec. 2012.; [3] A. Sadowsky, A. Hussner, and S. Ott, *Nov. Hedwigia*, vol. 94, no. 3, pp. 323–334, May 2012.; [4] D. N. Karger et al., *Sci. Data*, vol. 4, p. 170122, Sep. 2017.

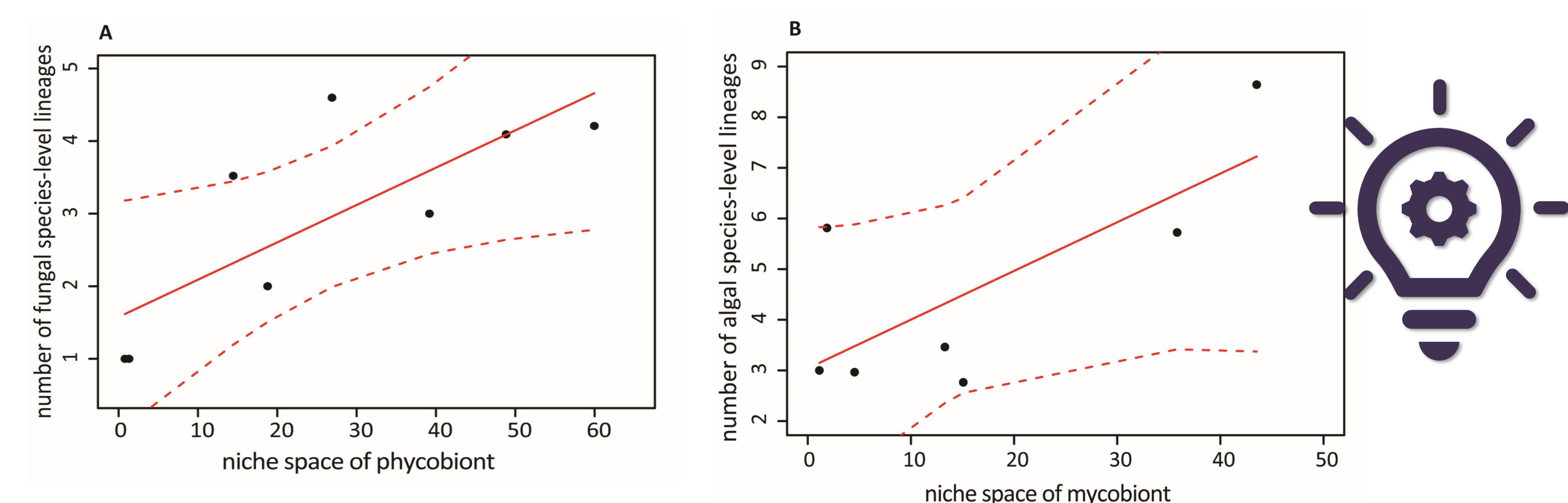


Fig. 3. (a) Bayesian linear regression of algal niche space (hypervolume) as a predictor of the number of accepted species-level fungal lineages. (b) Bayesian linear regression of fungal niche space (hypervolume) as a predictor of the number of accepted species-level algal lineages. Dashed lines show the 95% CRI around the regression line.

Acknowledgements: We are grateful to everyone who helped us during this study, especially Magdalena Oset for identifying some *Stereocaulon* specimens, J. Vančurová, J. Vondrák, J. Malíček, J. Steinová, S. Werth, D. Svoboda, Z. Palice, F. Bouda, W. Obermayer, D. Trauber, V. Kalníková, V. Fanta, K. Vančura, L. Vančura, J. Pilátová and O. Koukol for collecting material and/or help with fieldwork, and L. Flašková, B. Klug and S. Kraker for help with molecular work. Martin Grube is thanked for hosting LV in the lab. This study was supported by the grant no. GP13-39185P from the Czech Science Foundation and the Primus Research Programme of Charles University no. SCI/13. Part of the laboratory work was conducted during the cooperation with the Karl-Franzen University Graz during the OEAD 2010-2011 project action entitled "Symbiotic selection arenas in lichens."