Barcoding of Bromeliaceae (Poales)

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Background
The angiosperm family Bromeliaceae comprises 3912 species (Butcher & Gouda 2017: http://botu07.bio.uu.nl/bcg/taxonList.php), almost all of them restricted to the Neotropics (a single species is native to West Africa). The family is characterized by exceptionally high morphological and ecological diversity as well as a very low DNA sequence variability. Most of the species are monocarpic, propagating vegetatively with lateral shoots. In several genera, plants are vegetatively very similar, which makes determination of bromeliads difficult (fig. 2). Especially in Botanic Gardens this is a problem, when plants are cultivated several years before flowering. Barcoding is a very promising approach to provide fast and cheap determination of bromeliads, however, the observed low genetic variability causes specific problems.

Results
In the course of a project (Evo-BoGa) funded by the German Federal Ministry of Education and Research (BMBF) to improve access and scientific use of living collections, a number of DNA markers was tested for their suitability for barcoding (nuclear: agt1, ETS, phyC; plastid: matK, ycf1, trnL-F, psbA-trnH).

The highly variable nuclear marker agt1 was identified as suitable barcode marker for identification.

Significance
The barcoding approach will improve the availability of bromeliad collections in Botanic Gardens.

Outlook
At present, app. 400 species of subfamily Bromelioideae have been barcoded, app. further 500 species will be sequenced in the course of the project. A special web-portal for Bromeliaceae will be provided based on the BrassiBase database (URL: https://brassibase.cos.uni-heidelberg.de).

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