Waking up from a taxonomic nightmare – tracing the evolutionary history of *Tecticornia* Hook.f.

Zerdoner Calasan A[a], Shepherd KA[b], Kadereit G[a]

[a]Faculty of Biology: Princess Therese von Bayern Chair of Systematics, Biodiversity and Evolution of Plants, Ludwig Maximilian University of Munich (LMU), Menzinger Str. 67, 80638 Munich, Germany
[b]Western Australian Herbarium (PERTH), Biodiversity and Conservation Science, Department of Biodiversity, Conservation and Attractions, Locked Bag 104, Bentley Delivery Centre, Western Australia 6983, Australia

A.Zerdoner@lmu.de

Samphires (*Tecticornia* Hook.f. and *Salicornia* L.; Salicornioideae, Amaranthaceae/Chenopodiaceae) form dominant vegetation communities in estuarine and inland saline habitats across Australia. Despite their prevalence these plants are often overlooked, as to many they represent a taxonomic nightmare due to a lack of obvious morphological diagnostic features and high ecological plasticity. An absence of basic understanding of these species' biology is also due to their low genetic diversity, presence of polyploids, hybrids and potential apomicts. Despite increasing threats through land development, climate change, and increased mining activity, conservation plans to mitigate the habitat loss of this integral part of Australian flora are often missing. While there are presently only three *Salicornia* species known to be native to Australia, *Tecticornia* comprises a recalcitrant group of about 70 endemic species including many undescribed taxa. With an aim to improve our understanding of this group and infer the evolutionary history of *Tecticornia*, we utilised a target sequencing approach using an Angiosperms353 bait set as part of the national Bioplatforms Genomics for Australian Plants project, as well as custom bait set designed based on available transcriptomes of Salicornioideae. While the Angiosperms353 data showed limited resolution, the custom baits target accuracy increased dramatically (80-90% of the desired regions vs 10-20%) producing a well-supported topology. These results point towards a monophyletic *Tecticornia* with *Salicornia* being its sister. Preadapted to xeric and saline conditions, the last common ancestor of *Tecticornia* likely arrived at the Australian coastline via long-distance dispersal from the Mediterranean and the western Irano-Turanian floristic regions in the second half of the Miocene. During this epoch, decreased precipitation, eustatic sea level decline and retreat of continental water bodies promoted the aridification of Australian interior, and thus preadapted floral elements were able to rapidly diversify in the absence of competition. Accustomed to coastal shores, *Tecticornia* probably benefited from the Pliocene mesic pulse as well, during which inland Australian lakes saw a temporary expansion due to tectonic damming of several river systems. We gained new insights into the complex evolutionary history of this floral element and confirmed the 'littoral connection' hypothesis. Our comparative bait analysis uncovers further advantages of HybSeq and offers guidelines to disentangle sources of gene tree discordance among such recalcitrant study systems. Our data thus provides a framework to support future work on the taxonomy and conservation of this challenging group and offers potential guidelines for disentangling evolutionary histories of other problematic plant groups.