From museums to genomics: old herbarium specimens shed light on a C3 to C4 transition



ollections of specimens held by natural history museums are invaluable material for biodiversity inventory and evolutionary studies, with specimens accumulated over 300 years readily available for sampling. Unfortunately, most museum specimens yield low-quality DNA. Recent advances in sequencing technologies, so called next-generation sequencing, are revolutionizing phylogenetic investigations at a deep level.



Muséum national d'Histoire naturelle, Paris (France), Collection : Plantes vasculaires (P), Spécimen P02260115

Ground: Spécimen P00446293.



Here, the Illumina technology (HiSeq) was used on herbarium specimens of Sartidia (subfamily Aristidoideae, Poaceae), a small African-Malagasy grass lineage (six species) characteristic of wooded savannas, which is the C_3 sister group of *Stipagrostis*, an important C_4 genus from Africa and SW Asia. Complete chloroplast and nuclear ribosomal sequences were assembled for two Sartidia species, one of which (S. perrieri) is only known from a single specimen collected in Madagascar 100 years ago. Partial sequences of a few single-copy genes encoding phosphoenolpyruvate carboxylases (ppc) and malic enzymes (nadpme) were also assembled. Based on these data, the phylogenetic position of Malagasy Sartidia in the subfamily Aristidoideae was investigated and the biogeographical history of this genus was analysed with full species sampling. The evolutionary history of two genes for C₄ photosynthesis (ppc-aL1b and *nadpme-IV*) in the group was also investigated. The gene encoding the C₄ phosphoenolpyruvate caroxylase of *Stipagrostis* is absent from *S. dewinteri* suggesting that it is not essential in C₃ members of the group, which might have favoured its recruitment into a new metabolic pathway. Altogether, the inclusion of historical museum specimens in phylogenomic analyses of biodiversity opens new avenues for evolutionary studies.

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G. Besnard, P.-A. Christin, P.-J. G. Malé, E. Lhuillier, C. Lauzeral, E. Coissac and M. S. Vorontsova