

Potentials and limits in the genomic uses of a 200 years old herbarium

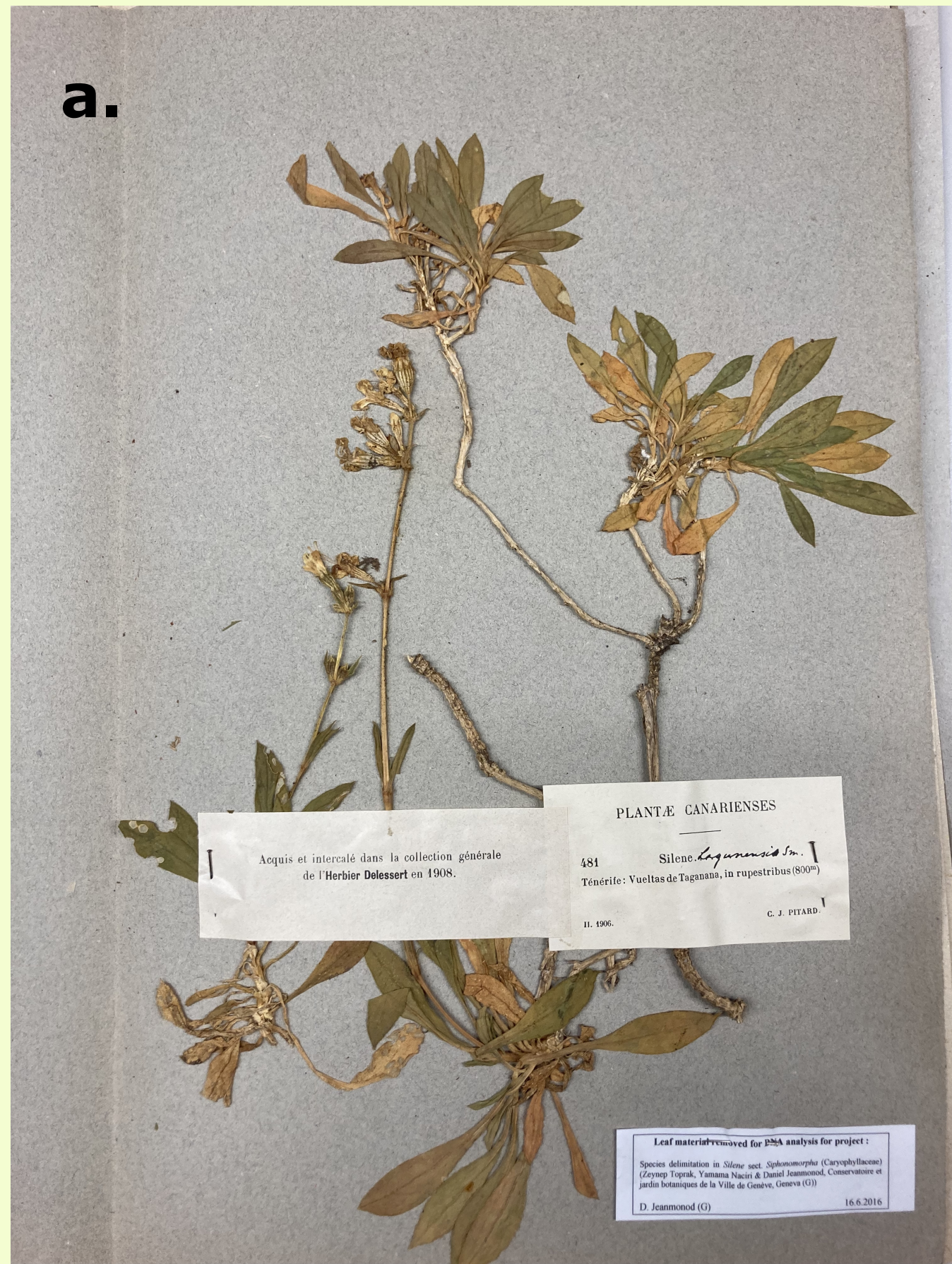


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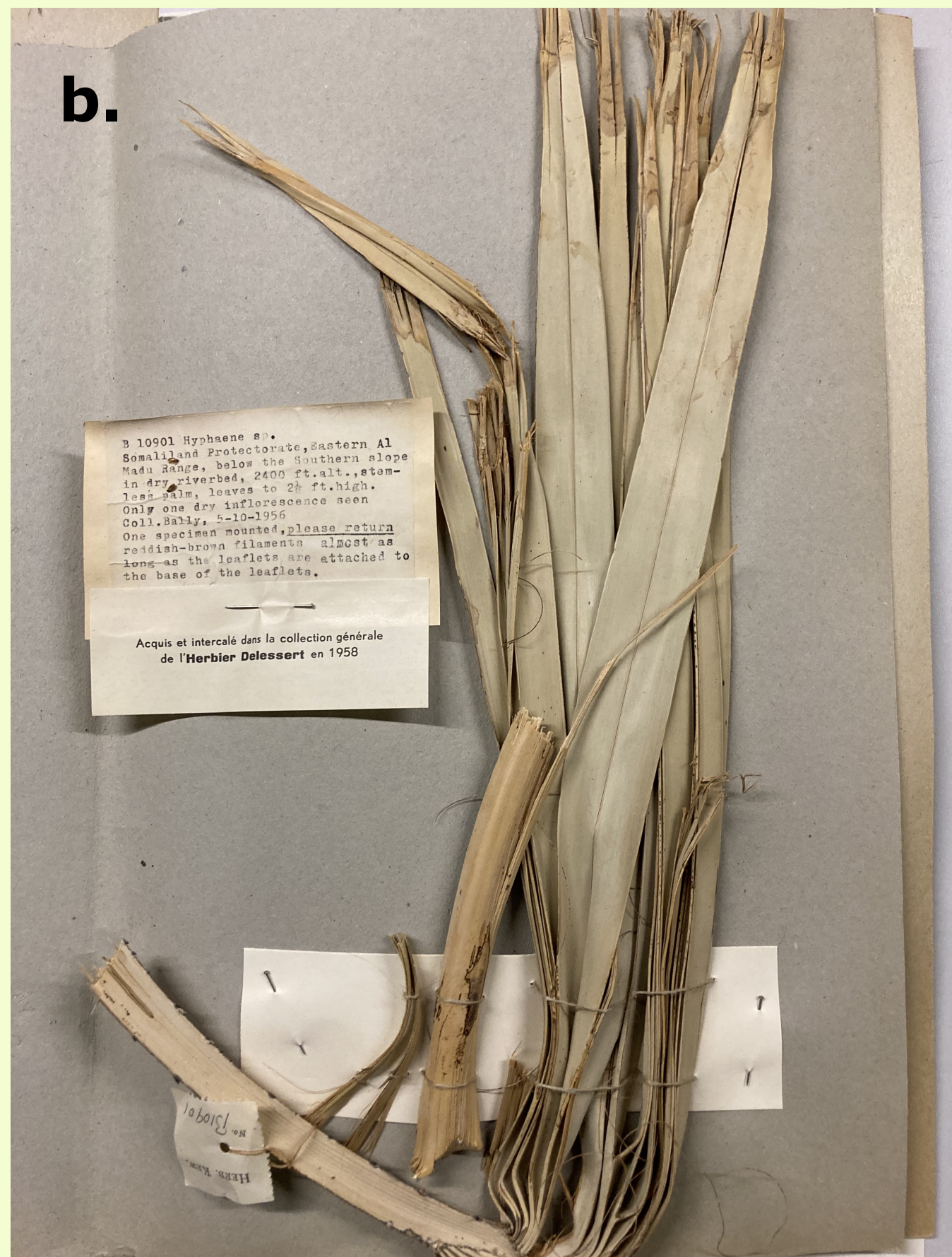


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Major herbaria, such as the one hosted by the botanical garden of Geneva have played a central role in the development of plant systematics over the last 200 years. Today, advances in high throughput sequencing technologies together with the development of specific and universal capture kit has considerably improved the use of herbaria as a source of genetic data, opening new avenues in the study of plant biodiversity.



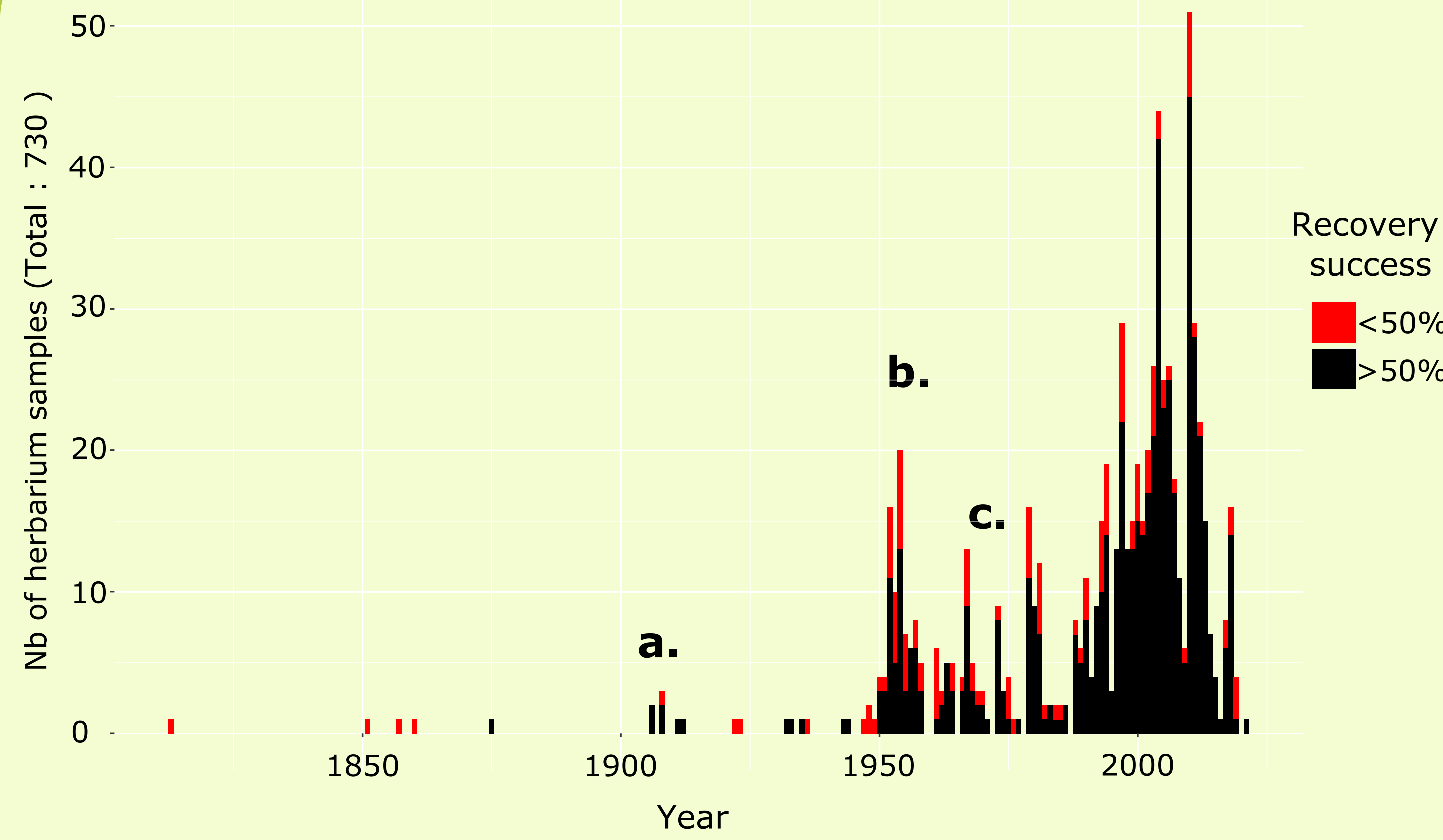
Silene lagunensis, collected in 1906 in the Canary Islands.



Hyphaene sp. collected in 1956 in Somalia, a region difficult to explore today but key to understand the diversification of this genus.

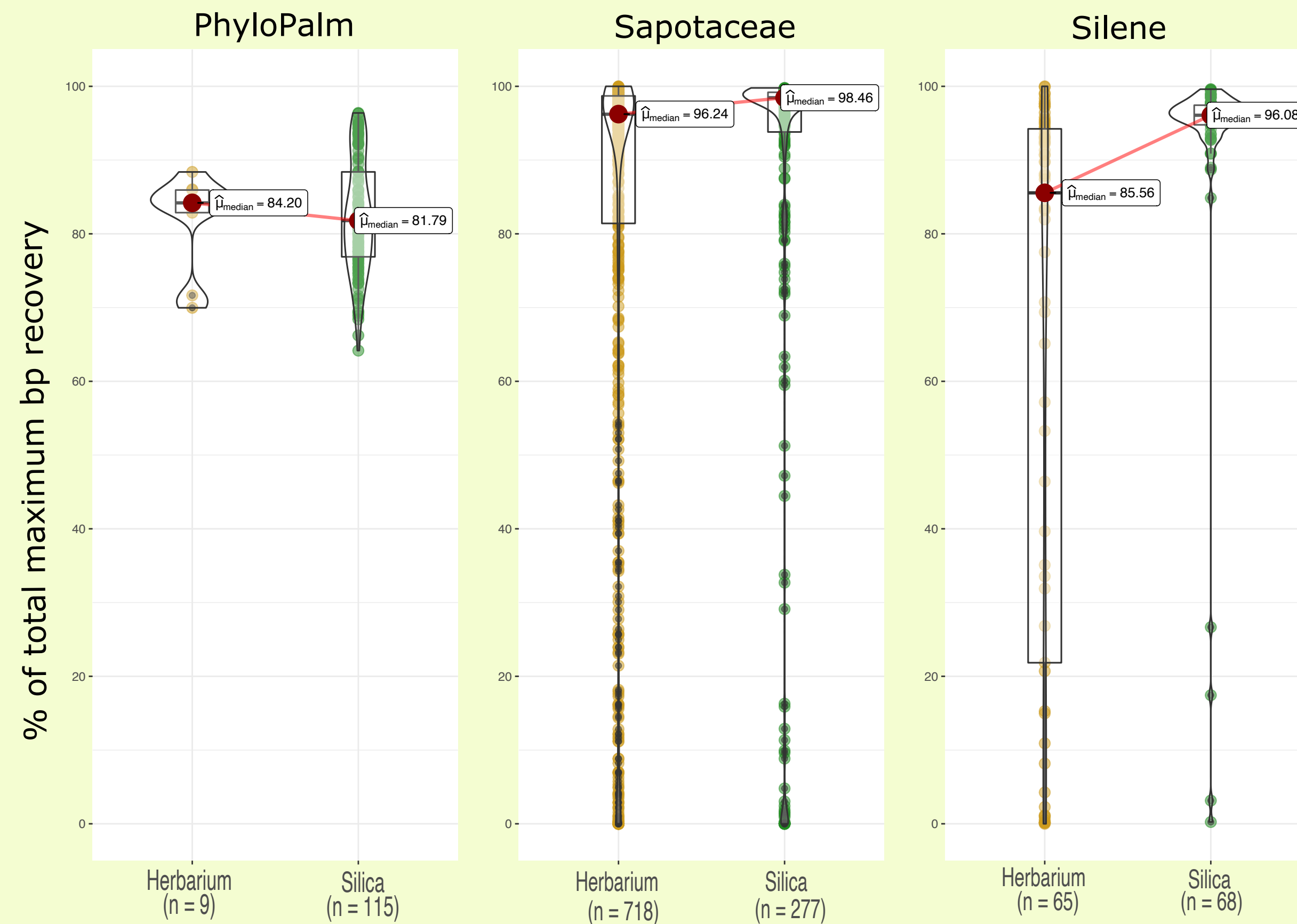


Capurodendron nanophyllum, the species with the smallest leaves in the Sapotaceae. Described in 2018 as already critically endangered due to deforestation¹.



Recovery success of high throughput sequencing according to the age of herbarium specimens

→ Herbarium specimens as old as 1875 can be used as a source of DNA for high throughput sequencing



Comparison of DNA sequencing success between herbarium and silica-dry material using three targeted capture kits : PhyloPalm² > 1'500'000 bp., Sapotaceae³, > 870'000 bp. and custom Silene kit > 650'000 bp.

→ On average, the amount of genomic data obtained from herbarium samples and silica-dry tissue are similar.

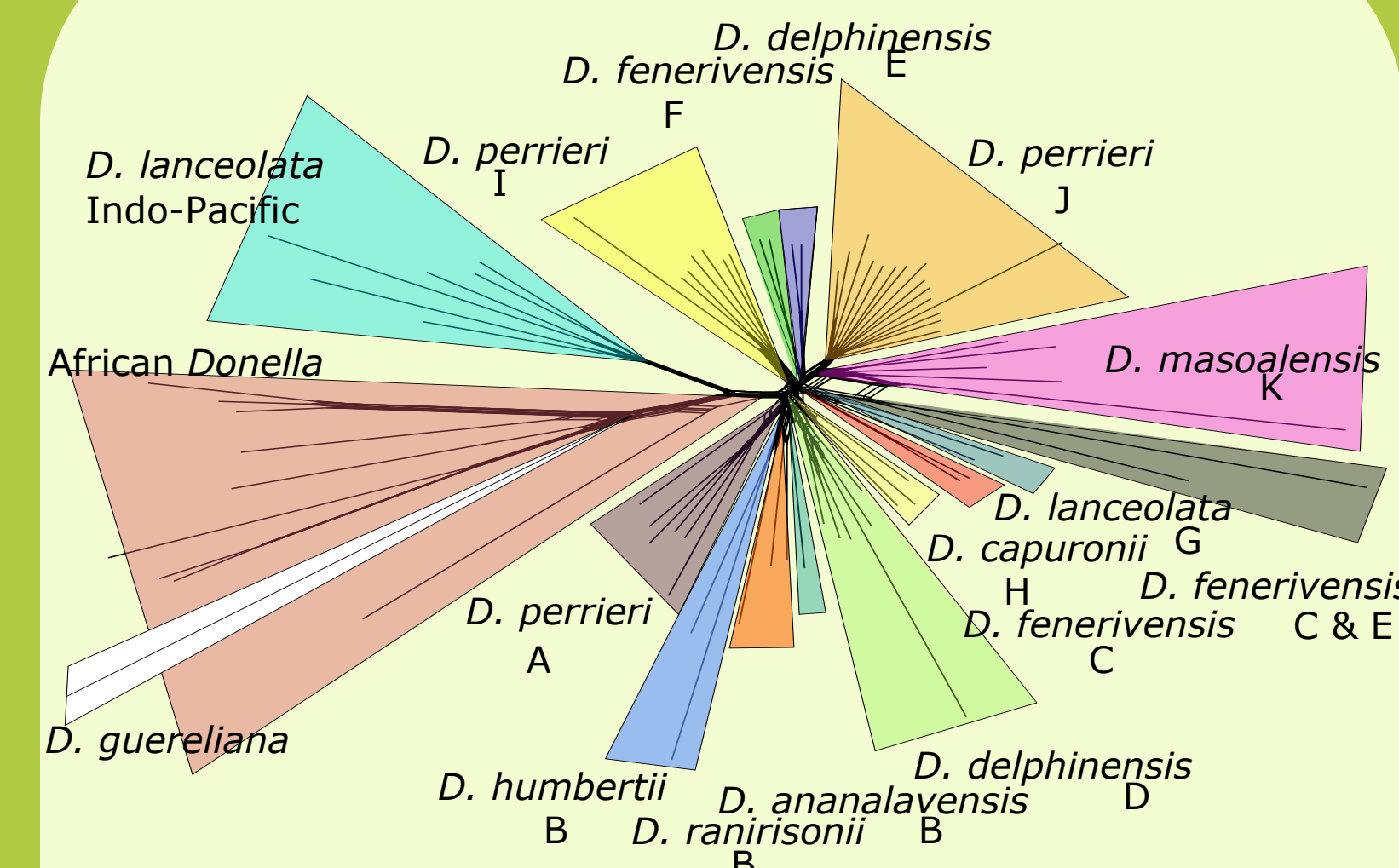
Our research projects using herbarium specimens from different taxonomical groups, ages and geographic origins shows that herbaria represent a promising source of genomic data allowing:

- 1) the reconstruction of phylogenetic relationships within lineages difficult to collect in the wild
- 2) the discovery of species new to science
- 3) the filling of taxonomical gaps in the plant tree of life by integrating historical referenced material and extinct species

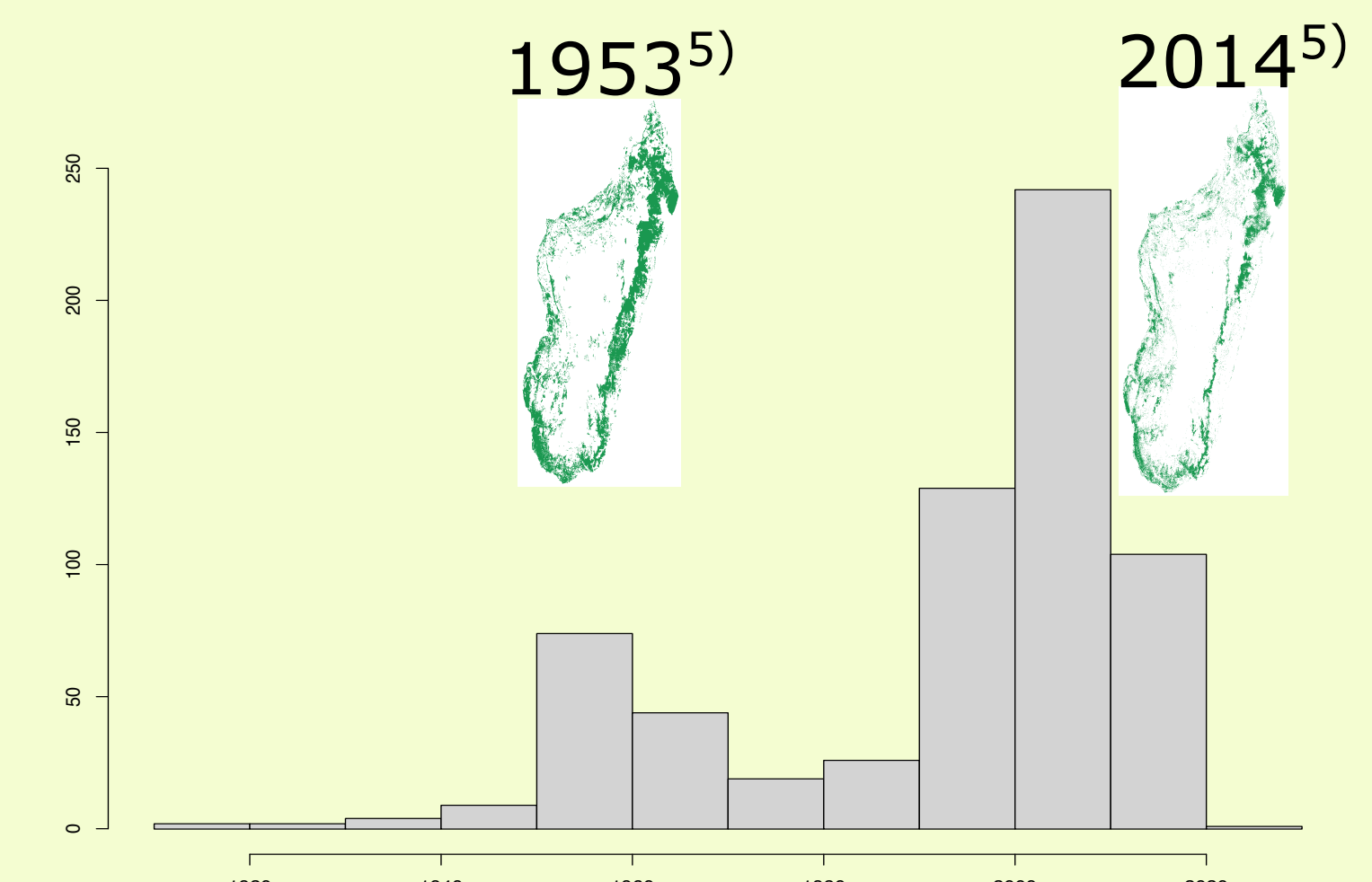
We foresee that the use of herbaria as source of genetic data will play a central role for the completion of the plant tree of life and the accurate quantification of plant diversity at all taxonomical levels.

However, the high quantity of DNA that is needed for high throughput sequencing and the destructive nature of the sampling request a wise selection of the samples to be sequenced.

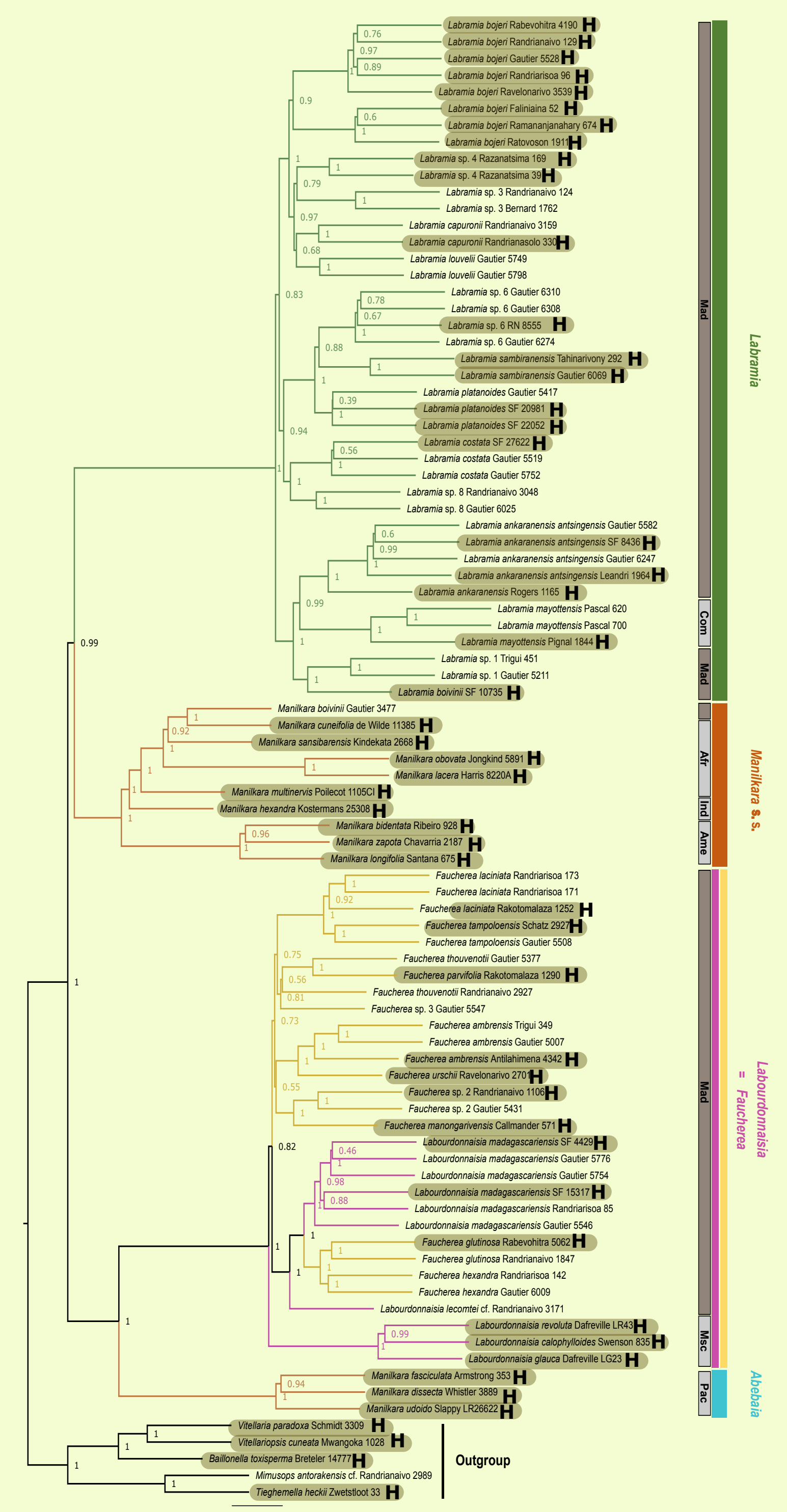
1) Gautier & Naciri (2018) Candollea 73: 127 2) Loiseau et al. (2019) Frontiers in Plant Science 10:864 3) Christe et al. (2021) Molecular Phylogenetic and Evolution 160 4) Kiedaisch 2022 Master thesis, Technical University of Munich, Germany 5) Vieilledent et al. (2018) Biological Conservation 222 6) Gautier et al. (2022) in The new natural history of Madagascar, Princeton University Press, NJ 7) Randriarisoa et al. (2022) Taxon (in press)



Species delimitation in Malagasy *Donella's* Sapotaceae as shown with phylogenetic network⁴. All DNA data used in this study derived from herbarium specimens.



Age distribution of herbarium samples used in Sapotaceae projects⁶. Specimens collected in the 50/60's in Madagascar hold information from regions now deforested. These collections were essential to understand the diversity of this family.



Generic circumscription within subtribe Manilkarinea (Sapotaceae)⁷. Herbarium specimens (highlighted) represent 64% of the samples