

Capturing and managing genetic diversity in *ex situ* collections of threatened tropical trees: a case study in *Karomia gigas*

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Although *ex situ* collections of threatened plants are most useful when they contain as much genetic variation as possible, the conservation and maintenance of genetic diversity in collections are often poorly known. Here, we present a case study using population genomic analyses of an *ex situ* collection of *Karomia gigas*, a critically endangered tropical tree from Tanzania. Only ~43 individuals remain in two wild populations, and *ex situ* collections containing 34 individuals were established in two sites from wild-collected seed. The study aimed to understand how much diversity is represented in the collection, analyse the parentage of *ex situ* individuals, and identify efficient strategies to capture and maintain genetic diversity both *in situ* and *ex situ*. We genotyped all known individuals, compared genetic diversity in wild populations and *ex situ* collections, and conducted parentage analysis of the collections. Only 32.6% of the wild individuals are represented *ex situ* and many *ex situ* individuals were the product of selfing by one wild individual. Population genomic analyses provided important insights into the conservation of genetic diversity in *K. gigas*, identifying gaps and inefficiencies, but also highlighting strategies to conserve genetic diversity *ex situ*. The results highlight how population genomic analyses provide essential information to ensure that collections effectively and efficiently conserve genetic diversity in threatened tropical trees.