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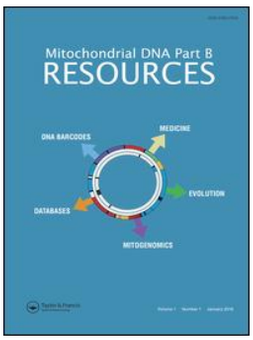

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MITOGENOME ANNOUNCEMENT

Complete plastome sequences of 14 African yam species (*Dioscorea* spp.)

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ABSTRACT

Complete plastomes of 14 African yam species were reconstructed from whole genome sequencing. These plastomes sizes varied from 151,908 to 155,155 bp. We predicted 130 genes, including 18 duplicated genes located in the two inverted regions. Phylogenetic analysis obtained using the maximum likelihood procedure revealed that each species was distinct with high support. This resource will be useful for phylogenetic and diversity analysis of *Dioscorea* species.

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Africa; chloroplast; *Dioscorea*; NGS; yam

The genus *Dioscorea* L. (Dioscoreaceae) plays a considerable role in tropical Africa because of its important staple crop *D. rotundata*, a vine cultivated for its starchy tuber. *Dioscorea* is a very species-rich and morphologically complex genus. Therefore, the taxonomy of this genus is difficult, as proven by the variation in the number of accepted species names (Caddick et al. 2002; Wilkin et al. 2005; Govaerts et al. 2017). Molecular phylogenetic analyses focusing on the genus are also poorly resolved (Terauchi et al. 1992; Ramser et al. 1997; Chaïr et al. 2005). Here we reconstructed complete plastomes of 14 West-African species.

Fourteen *Dioscorea* leaf samples, (*D. abyssinica*, *D. baya*, *D. bulbifera*, *D. burkilliana*, *D. cayenensis*, *D. dumetorum*, *D. hirtiflora*, *D. praehensilis*, *D. preussii*, *D. quartiniana*, *D. sagittifolia*, *D. sansibarensis*, *D. schimperiana,* and *D. togoensis*), were collected from WAG and G herbaria (Table 1). DNAs were extracted from dried leaves according to Scarcelli et al. (2006) and whole genome sequencing was performed as described in Mariac et al. (2014) on an Illumina MiSeq (Illumina, San Diego, CA). For each sample, the whole plastome was reconstructed using MITObim 1.7 (Hahn et al. 2013) as explained in Magwé-Tindo et al. (2018) with *D. rotundata* plastome as a reference (GenBank NC_024170.1). Annotations were recovered from the alignment of the target plastome to NC_024170.1 using Geneious Pro 4.8.5 with Mauve 2.2.0 plugin (Darling et al. 2010), then manually checked for start and stop codons (protein-coding genes) and by blasting the tRNA and rRNA sequences to GenBank nucleotide database (nr/nt, Altschul et al. 1990). Annotated plastomes were deposited into the GenBank database (Table 1).

Plastome lengths varied from 151,908 bp (*D. burkilliana*) to 155,155 bp (*D. baya*) and exhibited a typical quadripartite structure with a LSC (Large Single Copy) and a SSC (Short Single Copy) separated by two IR (Inverted Region). The mean GC content was 37% and varied from 31% within the SSC to 43% within the IR. The 14 species presented the same genetic structure as the reference (NC_024170.1): 130 genes corresponding to 84 protein-coding genes, 38 tRNA and 8 rRNA. Among these genes, 18 were duplicated in the IR: 6 protein-coding genes, 8 tRNA and 4 rRNA. The only exception was *D. quartiniana* which missed the *mat*K gene due to a mutation of the second codon into a stop codon. All species lost the *rps*16 gene.

A phylogenetic study was conducted using these 14 complete plastomes, with *D. rotundata* (NC_024170.1) as reference and *D. elephantipes* (NC_009601.1) as outgroup species. The 16 plastomes were aligned using MAFFT 7 (Katoh et al. 2002) and the alignment was cleaned using Gblocks 0.91b (Talavera and Castresana 2007). The phylogenetic tree was constructed using RAxML 8.2.9 (Stamatakis 2014) with 500 bootstraps. The phylogenetic tree obtained was well-resolved and revealed that each species was clearly distinct with strong support (Figure 1), except within the cultivated species complex.

Resources reconstructed here will help to understand the relationships between cultivated yams and their wild relatives and provide useful information for further taxonomic study.

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Table 1. Characterization of the samples used for sequencing.

Species	Herbarium voucher accession	Collection locality	Longitude	Latitude	Plastome GenBank ID
D. abyssinica	WAG.1781186	Cameroon	13.9	10.9	MG805602
D. baya	WAG.1781135	Cameroon	10.6	2.9	MG805603
D. bulbifera	WAG.1783436	Liberia	−8.6	6.3	MG805604
D. burkilliana	WAG.1783323	Cameroon	11.2	2.8	MG805605
D. cayenensis	WAG.1783287	Cameroon	11.5	3.9	MG805606
D. dumetorum	WAG.1943398	Gabon	10.7	−3.5	MG805607
D. hirtiflora	WAG.1783636	Senegal	−16.7	12.9	MG805608
D. praehensilis	G00420196	Côte d'Ivoire	−5.1	6.3	MG805609
D. preussii	WAG.1786123	Gabon	11.8	−0.1	MG805610
D. quartiniana	WAG.1786396	Malawi	35.5	−15.9	MG805611
D. sagittifolia	WAG.1786430	Cameroon	13.8	7	MG805612
D. sansibarensis	WAG.1786456	Gabon	11.6	−0.2	MG805613
D. schimperiana	WAG.1786876	Cameroon	11.5	3.9	MG805614
D. togoensis	WAG0283548	Togo	1.6	6.7	MG805615

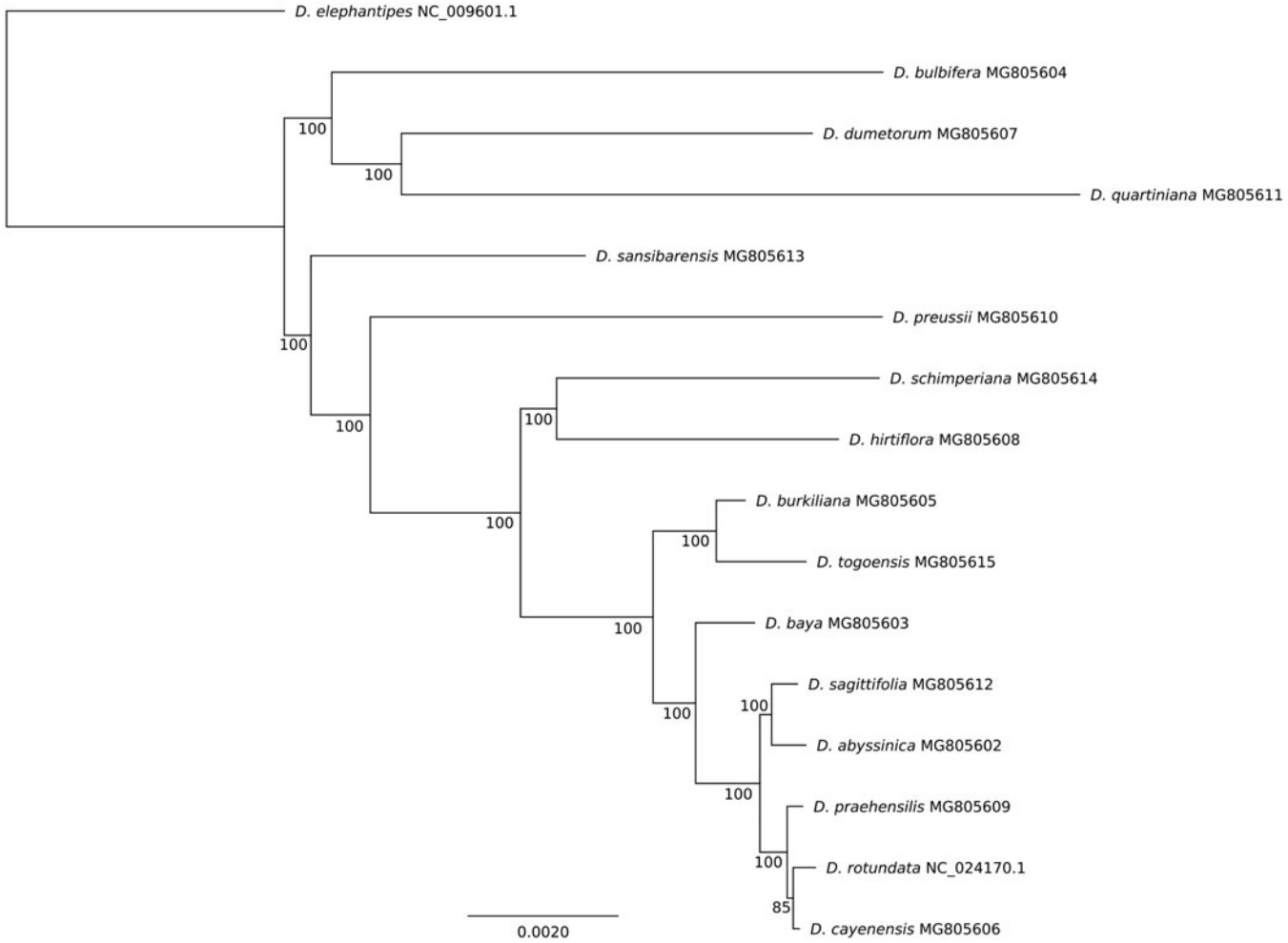

Figure 1. Phylogenetic tree of 16 African *Dioscorea* species constructed using maximum likelihood procedure and whole plastome sequences. *Dioscorea elephantipes* was included as outgroup species. Bootstrap values are indicated for each node. Each species is followed by its GenBank accession ID.

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Disclosure statement

No potential conflict of interest was reported by the authors.

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