

Table S1. Comparative mitogenome features of 14 *Dendrobium* species

Species Name	Genome Size (bp)	GC Content	PCGs	tRNAs	rRNAs	Structure	Assembly Method	Platform	BioProject
<i>D. henanense</i>	807,551 bp	40.2% 46.2%	to 40	33	3	21 circular/ 3 linear	SPAdes v3.10.1	Nanopore + Illumina	PRJNA933365
<i>D. wilsonii</i>	763,005 bp	40.2% 46.2%	to 41	40	3	19 circular/ 3 linear	SPAdes v3.10.1	Nanopore + Illumina	PRJNA933365
<i>D. huoshanense</i>	650,957 bp	43.41%	37	28	3	20 circular	GetOrganelle version 1.7.5	Nanopore + Illumina	PRJNA735580
<i>D. moniliforme</i>	689,048 bp	43.56%	38	33	3	circular & linear 42	SOAPdenovo2	Nanopore + Illumina	PRJNA735580
<i>D. officinale</i>	625,267 bp	43.64%	37	23	3	21 circular	GetOrganelle version 1.7.5	Nanopore + Illumina	PRJNA1129803
<i>D. gratiosissimum</i>	420,538 bp	43.23%	38	28	3	circular & linear 41	SOAPdenovo2	second-generation + third-generation	PRJNA735580
<i>D. primulinum</i>	654,165 bp	43.09%	42	33	3	circular & linear 35	SOAPdenovo2	second-generation + third-generation	PRJNA735580
<i>D. aphyllum</i>	604,245 bp	43.21%	40	32	3	circular & linear 30	SOAPdenovo2	Second generation + third-generation	PRJNA735580
<i>D. nobile</i>	772,523 bp	43.44%	37	27	3	25 circular	GetOrganelle version 1.7.5	Nanopore + Illumina	PRJNA1129805
<i>D. loddigesii</i>	513,356 bp	43.41%	36	31	3	17 circular	NextPolish v1.3.1	second-generation + third-generation	PRJNA1113802
<i>D. lasianthera</i>	485,249 bp	44.70%	39	23	3	15 circular/ 5 linear	PMAT	HiFi	Pending
<i>D. tangerinum</i>	535,423 bp	43.80%	37	25	3	17 circular/ 3 linear	PMAT	HiFi	Pending
<i>D. huoshanense</i>	773,326 bp	44.30%	36	21	3	13 circular / 5 linear	SPAdes v3.15.2	Nanopore + Illumina	PRJNA1129804
<i>D. chrysotoxum</i>	568,767 bp	44.00%	36	22	3	17 circular	SPAdes v3.15.2	Nanopore + Illumina	PRJNA1194330

Note: Species analyzed in this study are shown in bold