

## MICROSATELLITE DEVELOPMENT FOR THE GENUS *GUIBOURTIA* (FABACEAE, CAESALPINIOIDEAE) REVEALS DIPLOID AND POLYPLOID SPECIES<sup>1</sup>

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- *Premise of the study:* Nuclear microsatellites (nSSRs) were designed for *Guibourtia tessmannii* (Fabaceae, Caesalpinioideae), a highly exploited African timber tree, to study population genetic structure and gene flow.
- *Methods and Results:* We developed 16 polymorphic nSSRs from a genomic library tested in three populations of *G. tessmannii* and two populations of *G. coleosperma*. These nSSRs display three to 14 alleles per locus (mean 8.94) in *G. tessmannii*. Cross-amplification tests in nine congeneric species demonstrated that the genus *Guibourtia* contains diploid and polyploid species. Flow cytometry results combined with nSSR profiles suggest that *G. tessmannii* is octoploid.
- *Conclusions:* nSSRs revealed that African *Guibourtia* species include both diploid and polyploid species. These markers will provide information on the mating system, patterns of gene flow, and genetic structure of African *Guibourtia* species.

**Key words:** Fabaceae; flow cytometry; *Guibourtia*; microsatellites; next-generation sequencing; polyploidy.

The African tree *Guibourtia tessmannii* (Harms) J. Léonard (Fabaceae, Caesalpinioideae) is a hermaphrodite rainforest species distributed from Cameroon to Gabon (Fougère-Danezan et al., 2007; Tosso et al., 2015). Known as “bubinga” or “kevazingo,” it has high commercial and social value but is under significant threat due to illegal logging. The genus *Guibourtia* Benn. includes 13 African species distributed from Senegal to Mozambique in forest or savannah habitats. The genus was divided by Léonard (1949) into three main subgenera: (i) *Pseudocopaiva*: *G. tessmannii*, *G. pellegriniana* J. Léonard, *G. coleosperma* (Benth.) J. Léonard, *G. leonensis* J. Léonard; (ii) *Guibourtia*: *G. carrissoana* (M. A. Exell) J. Léonard, *G. copallifera* Benn., *G. demeusei* (Harms) J. Léonard, *G. sousae* J. Léonard; and (iii) *Gorskia*: *G. arnoldiana* (De Wild. & T. Durand) J. Léonard, *G. conjugata* (Bolle) J. Léonard, *G. dinklagei* (Harms) J. Léonard, *G. ehie* (A. Chev.) J. Léonard, *G. schliebenii* (Harms) J. Léonard. We developed polymorphic microsatellite

markers for *G. tessmannii* and tested them on nine African congeneric species to verify species delimitation and document population genetic structure and gene flow patterns. Because microsatellite typing suggested that some species were polyploid, we used flow cytometry to compare the ploidy levels of two related species for which appropriate fresh material was available.

### METHODS AND RESULTS

**Microsatellite development**—We extracted total DNA from 30 mg of dry leaf of *G. tessmannii* (FT0001; Appendix 1) using a cetyltrimethylammonium bromide (CTAB) method (Fu et al., 2005). We prepared a nonenriched DNA genomic library, following Mariac et al. (2014), and generated 150-bp-long paired-end reads on an Illumina MiSeq platform (San Diego, California, USA). We assembled the resulting 78,279 reads by pair with PANDaseq (Masella et al., 2012). Using the software QDD (Megléczy et al., 2014), we detected 2483 microsatellite loci. Of these, 149 had at least eight repeats and flanking regions appropriate to define pairs of PCR primers. We developed primers for 48 loci with at least eight di-, tri-, or tetranucleotide repeats and primer regions at least 20 bp distant from the microsatellite region. We added one of four possible linkers (Q1–Q4; Micheneau et al., 2011) to the 5′ end of the forward primer of each locus to label PCR products with fluorochromes FAM, NED, VIC, and PET (Table 1).

We tested 48 primer pairs using two samples of *G. tessmannii* (FT0002 and FT0003; Appendix 1). PCR reactions (total volume of 15 μL) used 1.5 μL of buffer (10×), 0.6 μL MgCl<sub>2</sub> (25 mM), 0.45 μL dNTPs (10 mM each), 0.3 μL of each primer (0.2 μM), 0.08 μL TopTaq DNA Polymerase (5 U/μL; QIAGEN, Venlo, The Netherlands), 1.5 μL of Coral Load, 1 μL of template DNA (of ca. 10–50 ng/μL), and 9.27 μL of water. PCR conditions were: 94°C (4 min); 30 cycles of 94°C (30 s), 55°C (45 s), and 72°C (1 min); and a final extension at 72°C (10 min). We visualized PCR products stained with SYBR Safe (Invitrogen, Merelbeke, Belgium) on a 1% agarose gel. Forty-two loci amplified consistently.

We assessed polymorphism on seven *G. tessmannii* individuals from Cameroon and Gabon (Appendix 1). We used fluorescent labeling by PCR amplification in

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TABLE 1. Characterization of 16 polymorphic and one monomorphic nuclear microsatellite loci isolated from *Guibourtia tessmannii*.

Primers <sup>a,b</sup>	Primer sequences (5'–3')	Labeled primer <sup>c</sup>	Repeat motif	Allele range size (bp)	GenBank accession no.
R12-Seq10*	F: AGGACTTAAGAATGGTGTATGCAA R: TTTGGCTTCCCTCTCTTCT	Q1-6-FAM	(AT) <sub>10</sub>	150–200	KX086193
R12-Seq15*	F: CCTGATTGGAGTTACACCACC R: AGGACAAGCTTGAGCGACAT	Q1-6-FAM	(AG) <sub>13</sub>	98–124	KX086194
R12-Seq21*	F: TTTCATTCAACAACCGCA R: CTGACACACAACACAGCCA	Q2-NED	(ATA) <sub>11</sub>	176–218	KX086197
R12-Seq35*	F: GACACTCCTCAGGTGGTTTCA R: GAGGTTAGATTCCAACATGTGC	Q3-VIC	(AAT) <sub>20</sub>	123–165	KX086204
R12-Seq29*	F: CCAAATTGCAGACGATGAAA R: AATTCGGACTTGAAGTTGCAG	Q3-VIC	(TCT) <sub>11</sub>	205–247	KX086201
R12-Seq08**	F: AACATGCATACCTTAACCGCAA R: TTTCATCAACACTTATCCTTGG	Q4-PET	(TTTC) <sub>9</sub>	148–172	KX086191
R12-Seq06**	F: ATCTCCGCTGTACTGCGT R: AATCAAGCCTCCGTAAAGCA	Q1-6-FAM	(GA) <sub>8</sub>	187–203	KX086190
R12-Seq26**	F: CACAATACATGAGCTGAAGAAACATGA R: CACGAGAAAGGGAGGAAATG	Q2-NED	(TCT) <sub>13</sub>	153–186	KX086200
R12-Seq34**	F: GACTCCTCAGGTGGTTTCA R: GAGGTTAGATTCCAACATGTGC	Q3-VIC	(TAT) <sub>13</sub>	150–186	KX086203
R12-Seq16**	F: CCCATAATCAGCCTACAAACC R: CAGATGAGGTAGACATTGTGGG	Q2-NED	(AG) <sub>11</sub>	226–262	KX086195
R12-Seq09***	F: ACCTACGTTTGTGATTATGAATGG R: TTTGGGTGATCTTTATGCTTTC	Q1-6-FAM	(GA) <sub>8</sub>	166–196	KX086192
R12-Seq20***	F: AAATCCGGAGGAGGAAAGA R: CTGACTCTGGCTTGACCCAT	Q2-NED	(AG) <sub>8</sub>	194–218	KX086196
R12-Seq22***	F: TTATGATGCGTGTCCCAA R: GAATGAATGCAGGGAGGAC	Q2-NED	(TA) <sub>21</sub>	157–177	KX086198
R12-Seq01****	F: CCTCATCATACAATTCAAGTGC R: GATGCCATGACTCTGGCTAAA	Q1-6-FAM	(AT) <sub>20</sub>	201–241	KX086189
R12-Seq25****	F: CATAGACTTGGAGGGAGCCA R: TTGCTTCCCTGTATCTTTAACAATTT	Q2-NED	(GA) <sub>9</sub>	174–196	KX086199
R12-Seq31****	F: ATTCCTATCAGATGAACAGATTATCA R: AGCTTGTGCAAAATGGATTG	Q3-VIC	(AT) <sub>8</sub>	221–245	KX086202
R12-Seq43**	F: GGCAGAATTTCCAGAAGCAA R: ACACAACCTTCTTTCCTGC	Q4-PET	(TA) <sub>23</sub>	143	KX086205

<sup>a</sup> \* = Multiplex Mix 1, \*\* = Mix 2, \*\*\* = Mix 3, \*\*\*\* = Mix 4.

<sup>b</sup> Optimal annealing temperature was 60°C for all loci.

<sup>c</sup> Q1 = TGTAACGACGGCCAGT (Schuelke, 2000); Q2 = TAGGAGTGCAGCAAGCAT; Q3 = CACTGCTTAGAGCGATGC; Q4 = CTAGTTATTGCTCAGCGGT (Q2–Q4, after Culley et al., 2008).

a total volume of 15 µL, combining 0.15 µL of the reverse and 0.1 µL of the forward (0.2 µM for both) microsatellite primers, 0.15 µL of Q1–Q4 labeled primers (0.2 µM each), 3 µL of Type-it Microsatellite PCR Kit (QIAGEN), H<sub>2</sub>O, and 1 µL of DNA. PCR conditions were: 5-min initial denaturation at 95°C; followed by 30 cycles of (95°C for 30 s, 60°C for 90 s, 72°C for 1 min) and 10 cycles of (95°C for 30s, 55°C for 45 s, 72°C for 60 s, 72°C for 1 min); and a final elongation step at 60°C for 30 min. We mixed 1.1 µL of each PCR product with 12 µL of Hi-Di Formamide (Life Technologies, Carlsbad, California, USA) and 0.3 µL of MapMarker 500 labeled with DY-632 (Eurogentec, Seraing, Belgium). The preparation was genotyped on an ABI3730 sequencer (Applied Biosystems, Lennik, The Netherlands).

After excluding loci that did not amplify consistently or were unreadable, we combined 16 polymorphic loci (one locus [R12-Seq43] was monomorphic) in four multiplexed reactions (Table 1) using Multiplex Manager 1.0 software (Holleley and Geerts, 2009). Preliminary population genetic analyses were performed on three populations of *G. tessmannii* (35–58 individuals per population; Table 2 and Appendix 1). Multiplexed PCRs were as above except that 3 µL of the 5× Q-solution of the Type-it Microsatellite PCR Kit was added. The individuals of *G. tessmannii* studied revealed a high degree of polymorphism, with more than two alleles per individual, suggesting a polyploid genome (Table 2).

**Microsatellite marker data analysis in *G. tessmannii* and *G. coleosperma***—The three populations of *G. tessmannii* (Table 2 and Appendix 1) had three to 14 alleles per locus (mean 8.94 alleles per locus, Table 2). Single-locus genotypes had one to eight alleles (2.35 ± 0.94 alleles per locus) and no fixed heterozygosity, suggesting an autopolyploid.

For *G. coleosperma*, the diploid species in which cross-amplification was the most successful (see below), we considered two populations (Table 2). For each of the 10 amplifiable loci, we calculated allele size range, number of alleles (A)

per locus, observed ( $H_o$ ) and expected ( $H_e$ ) heterozygosity, inbreeding coefficient ( $F$ ), and null allele frequency ( $r$ ) with INEst 1.0 (Chybicki and Burczyk, 2009). Deviation from Hardy–Weinberg equilibrium (HWE) was tested for each locus with SPAGeDi (Hardy and Vekemans, 2002). Loci exhibited one to 14 alleles (mean 4.5) with  $H_o$  (mean ± SE) of 0.28 ± 0.09 and  $H_e$  of 0.41 ± 0.11 for the Democratic Republic of Congo (DRC) population and one to 10 alleles (mean 3.67) with  $H_o$  of 0.17 ± 0.05 and  $H_e$  of 0.36 ± 0.10 for the Namibia population. Significant deviation from HWE was observed in at least one population for four primer pairs. Loci R12-Seq20 and R12-Seq22 for the DRC population exhibited a significant deficit of heterozygotes due to the presence of null alleles (Table 2).

**Flow cytometry**—We used flow cytometry to confirm the ploidy level of *G. tessmannii* and compare its genome size with *G. coleosperma*. We used fresh material from seeds collected in central Gabon (*G. tessmannii*) and northern Namibia (*G. coleosperma*) (Appendix 1). From 1 cm<sup>2</sup> pieces of fresh leaves, we obtained suspensions of leaf cell nuclei by chopping them in a buffer solution using the CyStain UV Precise P Kit (Partec GmbH, Münster, Germany) with DAPI (4',6-diamidino-2-phenylindole, diacetate). We ran samples with Ploidy Analyser equipment (Partec GmbH). We used tomato as an internal standard (*Solanum lycopersicum* L. “Montfavet 63-5” [2C = 1.99 pg, 40.0% GC; Marie and Brown, 1993]). Under the assumption that the GC content of our samples and the standard were similar, the genome size of *G. coleosperma* ranged from 3.20 to 3.70 pg ( $N = 3$ ) and *G. tessmannii* from 11.87 to 15.78 pg ( $N = 3$ ). Although these estimates should be considered with caution in the absence of information on the GC content, the genome size of *G. tessmannii* is nearly four times larger than that of *G. coleosperma*. Because the latter species displays microsatellite profiles typical of diploids, the flow cytometry results confirm that *G. tessmannii* is an octoploid species.

TABLE 2. Results of initial primer screening of 17 nuclear microsatellite loci developed in *Guibourtia tessmannii* (three populations) and 10 that cross-amplified in *G. coleosperma* (two populations).

Locus	<i>G. tessmannii</i> (octoploid)						<i>G. coleosperma</i> (diploid)										
	Gabon (Makokou; N = 35)		Gabon (Bambidie; N = 58)		Cameroon (Ma'an; N = 38)		DRC (Dilolo; N = 20)			Namibia (Rundu; N = 13)							
	A	A <sub>range</sub>	A <sub>ind</sub>	A <sub>range</sub>	A	A <sub>range</sub>	A <sub>ind</sub>	A	H <sub>e</sub>	F <sub>a</sub>	r	N	A	H <sub>e</sub>	F <sub>a</sub>	r	
R12-Seq15	4	1-3	1.13	1-3	11	1-3	1.5	6	0.11	0.26	0.31	20	4	0.11	0.26	0.31	0.09 ± 0.08
R12-Seq10	14	1-5	2.34	1-4	18	1-6	2.13	20	0.67	0.91	0.23	18	14	0.67	0.91	0.23	0.07 ± 0.05
R12-Seq35	6	1-4	1.85	1-5	13	1-3	2.69	8	0.5	0.71	0.12	20	4	0.5	0.71	0.12	0.06 ± 0.05
R12-Seq08	6	1-4	2.45	1-3	5	1-3	1.28	5	0	0.09	1*	20	2	0	0.09	1*	0.11 ± 0.09
R12-Seq26	7	1-5	2.56	1-4	11	1-4	1.91	9	0.67	0.67	—	20	1	—	—	—	0.12 ± 0.09
R12-Seq34	7	1-6	4.48	1-4	5	1-4	2	5	0.5	0.39	—	20	7	0.67	0.67	—	0.05 ± 0.04
R12-Seq16	14	1-8	5.38	1-6	12	2-8	4.72	13	0.5	0.39	-0.07	20	3	0.5	0.39	-0.07	0.05 ± 0.04
R12-Seq09	10	1-5	2.95	1-2	16	2-6	3.55	12	0.06	0.11	0.49	19	2	0.06	0.11	0.49	0.29 ± 0.09
R12-Seq20	9	1-5	2.63	1-3	5	1-3	1.51	2	0	0.3	1**	20	3	0	0.3	1**	0.20 ± 0.36
R12-Seq22	3	1-3	1.42	1-3	9	1-3	1.22	4	0.34	0.77	0.49***	20	6	0.34	0.77	0.49***	0.16 ± 0.07
R12-Seq01	11	1-6	2.83	1-4	14	1-7	2.98	17	—	—	—	—	—	—	—	—	—
R12-Seq25	7	1-4	2.03	1-4	7	1-4	2.25	7	—	—	—	—	—	—	—	—	—
R12-Seq31	13	1-5	2.31	1-4	10	1-4	2.26	7	—	—	—	—	—	—	—	—	—
R12-Seq21	10	1-4	2.44	1-3	12	1-3	2.07	11	—	—	—	—	—	—	—	—	—
R12-Seq29	6	1-4	2.16	1-4	4	1-3	1.76	10	—	—	—	—	—	—	—	—	—
R12-Seq06	5	1-3	2.03	1-4	5	1-3	2.14	5	—	—	—	—	—	—	—	—	—
R12-Seq43	1	1	1	1	1	1	1	1	—	—	—	—	—	—	—	—	—

Note: — = not applicable; A = number of alleles; A<sub>ind</sub> = mean number of alleles per individual; A<sub>range</sub> = range of number of alleles per individual; DRC = Democratic Republic of Congo; F = fixation index; H<sub>e</sub> = expected heterozygosity; H<sub>o</sub> = observed heterozygosity; N = number of individuals sampled; r = null allele frequency.  
\*Significance of deviation from Hardy-Weinberg equilibrium: \*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001.

**Cross-amplification in congeneric species and ploidy determination—**  
Among the 17 loci selected from *G. tessmannii*, a majority successfully amplified in two other species from the subgenus *Pseudocopaiva* (Table 3). Less than six loci amplified in the other species, most of which belong to other subgenera (Table 3). In *G. pellegriniana*, all loci were polymorphic and the genotypes showed up to eight alleles per individual and locus, suggesting an octoploid genome. By contrast, in the other species individuals did not display more than two alleles per locus, suggesting diploid genomes.

CONCLUSIONS

We developed 16 polymorphic microsatellite markers in *G. tessmannii* that amplified to varying degrees in nine congeneric species. The microsatellites and flow cytometry results showed for the first time that the genus *Guibourtia* includes diploid and polyploid species. These markers will be useful to assess the mating system and genetic structure of *Guibourtia* species.

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TABLE 3. Results of cross-amplification (allele size ranges) of microsatellite loci isolated from *Guibourtia tessmannii* and tested in nine additional taxa.

Species	Subg. <i>Pseudocopaiva</i>			Subg. <i>Guibourtia</i>			Subg. <i>Gorskia</i>		
	<i>G. pellegriniana</i> (N = 14)	<i>G. leonensis</i> (N = 3)	<i>G. coleosperma</i> (N = 33)	<i>G. carrisoana</i> (N = 2)	<i>G. copallifera</i> (N = 7)	<i>G. demousei</i> (N = 9)	<i>G. arnoldiana</i> (N = 2)	<i>G. ehie</i> (N = 20)	<i>G. dinklagei</i> (N = 1)
R12-Seq10	156–170	148–150	148–186	—	—	—	—	—	—
R12-Seq15	108–124	—	108–122	—	—	—	—	—	—
R12-Seq21	182–212	—	—	—	—	—	—	—	—
R12-Seq35	129–159	141–150	136–154	—	—	—	—	—	—
R12-Seq29	199–223	—	—	—	—	217	—	—	—
R12-Seq08	136–168	—	152–156	142–148	—	—	—	136–208	—
R12-Seq06	194–198	194	—	—	—	—	—	—	—
R12-Seq26	156–180	158–160	158*	—	—	158	—	138–198	—
R12-Seq34	150–174	150	150–160	150	—	—	—	150–174	154
R12-Seq16	226–250	202	224–266	236	226	228–252	232	232–252	—
R12-Seq09	200	—	168–170	—	—	—	—	—	—
R12-Seq20	205	—	203–223	—	203–205	203–207	—	—	—
R12-Seq22	169–173	—	168–172	—	164–172	162–166	—	—	—
R12-Seq01	205–231	—	—	—	—	—	—	—	—
R12-Seq25	180–190	—	—	—	—	—	—	180–192	—
R12-Seq31	221–231	—	—	—	—	—	—	—	—
R12-Seq43	143*	143*	—	—	—	—	—	143*	—

\*Monomorphic locus.

APPENDIX 1. Voucher and locality information for the samples used in this study.<sup>a</sup>

Species	n	Voucher no.	Country	Latitude	Longitude
<i>Guibourtia tessmannii</i> (Harms) J. Léonard <sup>b</sup>	1	FT0001	Gabon	1.4286	11.5886
<i>Guibourtia tessmannii</i> <sup>c</sup>	3	FT0002, FT0635–FT0636	Cameroon	2.2236	10.3793
<i>Guibourtia tessmannii</i> <sup>c</sup>	4	FT0003, FT0800–FT0802	Gabon	–0.3802	12.5649
<i>Guibourtia tessmannii</i> <sup>d</sup>	35	FT0540–FT0545, FT0572–FT0600	Gabon	0.36	13.10
<i>Guibourtia tessmannii</i> <sup>d</sup>	58	FT0800–FT0849, FT0851–FT0856, FT0900–FT0902	Gabon	0.76	12.9
<i>Guibourtia tessmannii</i> <sup>d</sup>	38	FT0605–FT0636, OH4675, OH4679, OH4682, OH4683, OH4684, OH4685	Cameroon	2.37	10.63
<i>Guibourtia pellegriniana</i> J. Léonard <sup>d</sup>	14	FT0641–FT0654	Gabon	–2.53	9.77
<i>Guibourtia coleosperma</i> (Benth.) J. Léonard <sup>d</sup>	20	FT0698–FT0717	DRC	–10.48	22.45
<i>Guibourtia coleosperma</i> <sup>d</sup>	13	FT0021–FT0024, FT0028–FT0031, FT0722–FT0726	Namibia	–18.05	19.62
<i>Guibourtia leonensis</i> J. Léonard <sup>d</sup>	3	BR0000013186371 <sup>f</sup> , BR0000013186401 <sup>f</sup> , BR0000013186388 <sup>f</sup>	Liberia	7.66	–10.02
<i>Guibourtia demousei</i> (Harms) J. Léonard <sup>d</sup>	9	FT0873–FT0879, OH3245, BR0000009459977 <sup>f</sup>	DRC	–0.88	18.12
<i>Guibourtia ehie</i> (A. Chev.) J. Léonard <sup>d</sup>	10	FT0335–FT0344	Ivory Coast	6.28	–3.68
<i>Guibourtia ehie</i> <sup>d</sup>	10	FT0163–FT0172	Ghana	7.02	–2.05
<i>Guibourtia carrisoana</i> (M. A. Exell) J. Léonard <sup>d</sup>	2	BR0000013186210 <sup>f</sup> , BR0000013186418 <sup>f</sup>	Angola	–8.83	13.25
<i>Guibourtia copallifera</i> Benn. <sup>d</sup>	7	FT0880–FT0886	Burkina-Faso	9.95	–4.67
<i>Guibourtia arnoldiana</i> (De Wild. & T. Durand) J. Léonard <sup>d</sup>	2	FT0638, GID2040	Gabon	–3.4098	11.4185
<i>Guibourtia dinklagei</i> (Harms) J. Léonard <sup>d</sup>	1	BR0000013186265 <sup>f</sup>	Liberia	6.23084	–9.81249
<i>Guibourtia tessmannii</i> <sup>e</sup>	3	FT0007, FT006, FT008	Gabon	–0.42	12.58
<i>Guibourtia coleosperma</i> <sup>e</sup>	3	FT0020, FT0024, FT0028	Namibia	–17.99	24.09

Note: DRC = Democratic Republic of Congo; n = number of individuals.

<sup>a</sup> Vouchers are deposited at the Herbarium of the Université Libre de Bruxelles, Belgium (BRLU), silica gel collection of Dr. Olivier Hardy.

<sup>b</sup> Individual used for DNA bank.

<sup>c</sup> Individual used for tests of amplification and polymorphism.

<sup>d</sup> Individuals used for cross-amplification.

<sup>e</sup> Individuals used for flow cytometry (code for the mother tree).

<sup>f</sup> Codes of specimens from which samples were collected in Botanic Garden Meise (BR), Belgium.