

Supporting information

Table S1. List of localities, coordinates and numbers of individuals sampled for each species.

Table S2. Genbank accession number for each markers and species.

Figure S1. Distribution of plastid DNA haplotypes of *Afrostryax kamerunensis*.

Figure S2. Distribution of plastid DNA haplotypes of *Scorodophloeus zenkeri*.

Figure S3. Distribution of plastid DNA haplotypes of *Afrostryax lepidophyllus*.

Figure S4. Distribution of plastid DNA haplotypes of *Greenwayodendron suaveolens* subsp. *suaveolens* var. *suaveolens*.

Figure S5. Distribution of plastid DNA haplotypes of *Erythrophleum suaveolens*.

Figure S6. Distribution of plastid DNA haplotypes of *Santiria trimera*.

Figure S7. Distribution of plastid DNA haplotypes of *Milicia excelsa*.

Figure S8. Distribution of plastid DNA haplotypes of *Symphonia globulifera*.

Figure S9. Genetic distinctiveness of each tree species within each locality (for localities with at least 2 species sampled) in Atlantic Central Africa. Distinctiveness above or below average is based on standardized differentiation S_{ij} computed for each species among populations.

Each barplot represents, respectively, from left to right distinctiveness values for *S. trimera*, *E. suaveolens*, *G. suaveolens*, *A. kamerunensis*, *A. lepidophyllus*, *S. zenkeri*, *S. globulifera* and *M. excelsa*.

Table S1. List of localities, coordinates and numbers of individuals sampled for each species.

Sp1: *Afrostryrax kamerunensis*, Sp2: *Afrostryrax lepidophyllus* Sp3: *Erythrophleum suaveolens*, Sp4: *Greenwayodendron suaveolens*, Sp5: *Milicia excelsa*, Sp6: *Santiria trimera*, Sp7: *Scorodophloeus zenkeri*, Sp8: *Symphonia globulifera*.

	Latitude	Longitude	Sp1	Sp2	Sp3	Sp4	Sp5	Sp6	Sp7	Sp8
1	-3.283	11.118	0	0	2	14	0	0	5	0
2	-2.682	10.463	1	0	4	16	0	14	5	4
3	-1.828	12.247	0	10	0	6	2	0	10	0
4	-1.417	10.427	0	7	2	6	0	0	5	0
5	-1.343	12.725	2	2	0	3	0	0	5	0
6	4.510	14.027	0	5	17	13	12	0	0	0
7	-1.126	12.060	0	1	0	6	0	0	6	0
8	-0.717	11.195	12	20	3	8	0	23	7	0
9	-0.858	12.963	0	6	7	0	13	0	13	0
10	-0.155	12.543	0	16	8	9	0	4	18	0
11	-0.091	10.760	0	3	0	1	0	0	7	0
12	0.461	12.487	0	5	5	9	2	17	16	1
13	4.161	11.438	0	0	1	1	0	0	0	0
14	0.404	11.225	1	11	3	7	0	7	15	0
15	0.454	10.190	12	5	1	24	0	10	8	3
16	2.665	10.869	0	5	0	15	13	20	6	2
17	3.389	10.339	4	3	0	5	0	16	13	10
18	1.143	13.169	0	9	1	14	2	19	14	1
19	3.977	9.267	2	1	0	0	0	0	0	1
20	-1.890	10.128	10	1	3	7	2	1	0	0
21	1.641	12.038	0	1	3	1	5	0	0	0
22	-0.919	9.957	0	0	1	1	0	3	0	0
23	4.898	9.276	0	6	0	4	3	23	0	13
24	5.146	11.786	0	0	6	7	6	0	0	0
25	3.381	14.080	0	12	26	2	25	5	0	2
26	-1.403	11.177	11	17	2	13	0	16	4	2
27	3.885	17.902	0	8	8	9	2	12	0	0
28	-2.454	16.597	0	1	0	2	0	0	0	3
29	2.810	12.904	0	8	12	19	11	24	6	4
30	-0.360	11.420	1	0	0	0	3	0	0	0
31	2.506	15.409	0	2	8	3	0	10	0	3
32	-3.655	11.161	0	4	0	8	0	0	3	0
33	0.980	11.328	0	3	0	5	1	0	3	0

34	-0.130	11.340	0	1	0	0	0	0	0	0
35	2.285	9.947	0	0	0	12	0	8	0	0
36	2.244	13.945	0	0	0	4	0	0	0	0
37	0.574	9.335	0	0	0	3	9	0	0	6
38	-1.860	13.870	0	0	0	1	0	0	0	1
39	-1.618	11.765	0	0	0	2	0	0	0	0
40	-0.261	9.732	0	0	0	2	1	8	0	0
41	-2.666	11.252	0	2	0	5	2	2	5	2
42	-2.934	10.537	0	0	0	0	0	0	1	0
43	4.558	10.472	0	0	0	0	0	4	1	0
44	1.600	10.100	0	0	0	0	0	2	1	0
45	-1.914	10.742	0	0	0	0	0	4	1	0
46	-1.119	17.914	0	0	0	0	0	0	0	1
47	-2.392	9.628	0	0	0	0	0	0	0	1
48	0.326	9.330	0	0	0	0	0	0	0	6
49	0.745	16.652	0	0	25	0	0	0	0	0
50	2.763	17.261	0	0	5	0	13	0	0	0

Table S2. Genbank accession numbers

Taxon	Haplotype	Marker	Accession number
<i>A.kamerunensis</i>	H3	<i>trnC-petN1R</i>	KJ442716
<i>A.kamerunensis</i>	H5	<i>trnC-petN1R</i>	KJ442705
<i>A.kamerunensis</i>	H6	<i>trnC-petN1R</i>	KJ442730
<i>A.kamerunensis</i>	H8	<i>trnC-petN1R</i>	KJ442709
<i>A.kamerunensis</i>	H10	<i>trnC-petN1R</i>	KJ442718
<i>A.kamerunensis</i>	H11	<i>trnC-petN1R</i>	KJ442729
<i>A.kamerunensis</i>	H12	<i>trnC-petN1R</i>	KJ442720
<i>A.kamerunensis</i>	H21	<i>trnC-petN1R</i>	KJ442703
<i>A.lepidophyllus</i>	H1	<i>trnC-petN1R</i>	KJ442707
<i>A.lepidophyllus</i>	H2	<i>trnC-petN1R</i>	KJ442727
<i>A.lepidophyllus</i>	H4	<i>trnC-petN1R</i>	KJ442710
<i>A.lepidophyllus</i>	H7	<i>trnC-petN1R</i>	KJ442735
<i>A.lepidophyllus</i>	H9	<i>trnC-petN1R</i>	KJ442719
<i>A.lepidophyllus</i>	H13	<i>trnC-petN1R</i>	KJ442725
<i>A.lepidophyllus</i>	H14	<i>trnC-petN1R</i>	KJ442713
<i>A.lepidophyllus</i>	H15	<i>trnC-petN1R</i>	KJ442700
<i>A.lepidophyllus</i>	H16	<i>trnC-petN1R</i>	KJ442732
<i>A.lepidophyllus</i>	H18	<i>trnC-petN1R</i>	KJ442723
<i>A.lepidophyllus</i>	H19	<i>trnC-petN1R</i>	KJ442733
<i>A.lepidophyllus</i>	H20	<i>trnC-petN1R</i>	KJ442697
<i>G.suaveolens</i>	H4	<i>trnC-petN1R</i>	KJ442728
<i>G.suaveolens</i>	H6	<i>trnC-petN1R</i>	KJ442722
<i>G.suaveolens</i>	H8	<i>trnC-petN1R</i>	GU121914
<i>G.suaveolens</i>	H9	<i>trnC-petN1R</i>	GU121910
<i>G.suaveolens</i>	H10	<i>trnC-petN1R</i>	GU121909
<i>G.suaveolens</i>	H11	<i>trnC-petN1R</i>	GU121911
<i>G.suaveolens</i>	H12	<i>trnC-petN1R</i>	KJ442711
<i>G.suaveolens</i>	H13	<i>trnC-petN1R</i>	GU121917
<i>G.suaveolens</i>	H14	<i>trnC-petN1R</i>	KJ442699
<i>G.suaveolens</i>	H15	<i>trnC-petN1R</i>	GU121915
<i>G.suaveolens</i>	H16	<i>trnC-petN1R</i>	GU121912
<i>G.suaveolens</i>	H17	<i>trnC-petN1R</i>	GU121913
<i>G.suaveolens</i>	H18	<i>trnC-petN1R</i>	KJ442701
<i>G.suaveolens</i>	H19	<i>trnC-petN1R</i>	GU121916
<i>G.suaveolens</i>	H20	<i>trnC-petN1R</i>	GU121918
<i>G.suaveolens</i>	H21	<i>trnC-petN1R</i>	KJ442715
<i>S.zenkeri</i>	H1	<i>trnC-petN1R</i>	KJ442724
<i>S.zenkeri</i>	H2	<i>trnC-petN1R</i>	KJ442714
<i>S.zenkeri</i>	H3	<i>trnC-petN1R</i>	KJ442704
<i>S.zenkeri</i>	H4	<i>trnC-petN1R</i>	KJ442702
<i>S.zenkeri</i>	H5	<i>trnC-petN1R</i>	KJ442712
<i>S.zenkeri</i>	H6	<i>trnC-petN1R</i>	KJ442717
<i>S.zenkeri</i>	H7	<i>trnC-petN1R</i>	KJ442696
<i>S.zenkeri</i>	H8	<i>trnC-petN1R</i>	KJ442731
<i>S.zenkeri</i>	H9	<i>trnC-petN1R</i>	KJ442695
<i>S.zenkeri</i>	H10	<i>trnC-petN1R</i>	KJ442721

<i>S.zenkeri</i>	H11	<i>trnC-petN1R</i>	KJ442736
<i>S.zenkeri</i>	H12	<i>trnC-petN1R</i>	KJ442708
<i>S.zenkeri</i>	H13	<i>trnC-petN1R</i>	KJ442706
<i>S.zenkeri</i>	H14	<i>trnC-petN1R</i>	KJ442694
<i>S.zenkeri</i>	H15	<i>trnC-petN1R</i>	KJ442698
<i>S.zenkeri</i>	H16	<i>trnC-petN1R</i>	KJ442734
<i>S.zenkeri</i>	H17	<i>trnC-petN1R</i>	KJ442726
<i>E.suaveolens</i>	H16	<i>trnC-petN1R</i>	JX840204
<i>E.suaveolens</i>	H17	<i>trnC-petN1R</i>	JX840195
<i>E.suaveolens</i>	H18	<i>trnC-petN1R</i>	JX840205.1
<i>E.suaveolens</i>	H19	<i>trnC-petN1R</i>	JX840206
<i>E.suaveolens</i>	H20	<i>trnC-petN1R</i>	JX840209
<i>E.suaveolens</i>	H21	<i>trnC-petN1R</i>	JX840196
<i>E.suaveolens</i>	H22	<i>trnC-petN1R</i>	JX840197.1
<i>E.suaveolens</i>	H23	<i>trnC-petN1R</i>	JX840198
<i>E.suaveolens</i>	H24	<i>trnC-petN1R</i>	JX840199
<i>E.suaveolens</i>	H25	<i>trnC-petN1R</i>	JX840208
<i>E.suaveolens</i>	H26	<i>trnC-petN1R</i>	JX840194
<i>E.suaveolens</i>	H27	<i>trnC-petN1R</i>	JX840200
<i>E.suaveolens</i>	H28	<i>trnC-petN1R</i>	JX840207
<i>E.suaveolens</i>	H30	<i>trnC-petN1R</i>	JX840202
<i>S.trimera</i>	H1-H2-H3-H4	<i>rbcl</i>	FN796551
<i>S.trimera</i>	H1	<i>rpl26-infA-rps8</i>	FN796568
<i>S.trimera</i>	H2-H5	<i>rpl26-infA-rps8</i>	FN796569
<i>S.trimera</i>	H3	<i>rpl26-infA-rps8</i>	FN796570
<i>S.trimera</i>	H4	<i>rpl26-infA-rps8</i>	FN796571
<i>S.trimera</i>	H6	<i>rpl26-infA-rps8</i>	FN796572
<i>S.globulifera</i>	H2	<i>trnC-petN1R</i>	KF487898
<i>S.globulifera</i>	H3	<i>trnC-petN1R</i>	KF487913
<i>S.globulifera</i>	H4	<i>trnC-petN1R</i>	KF487931
<i>S.globulifera</i>	H5	<i>trnC-petN1R</i>	KF488049
<i>S.globulifera</i>	H6	<i>trnC-petN1R</i>	KF487914
<i>S.globulifera</i>	H8	<i>trnC-petN1R</i>	KF487922
<i>S.globulifera</i>	H9	<i>trnC-petN1R</i>	KF487936
<i>S.globulifera</i>	H10	<i>trnC-petN1R</i>	KF487934
<i>S.globulifera</i>	H11	<i>trnC-petN1R</i>	KF487894
<i>S.globulifera</i>	H12	<i>trnC-petN1R</i>	KF487900
<i>S.globulifera</i>	H13	<i>trnC-petN1R</i>	KF487912
<i>S.globulifera</i>	H14	<i>trnC-petN1R</i>	KF488056
<i>S.globulifera</i>	H15	<i>trnC-petN1R</i>	KF488043
<i>S.globulifera</i>	H16	<i>trnC-petN1R</i>	KF488042
<i>S.globulifera</i>	H17	<i>trnC-petN1R</i>	KF487939
<i>S.globulifera</i>	H18	<i>trnC-petN1R</i>	KF488055
<i>S.globulifera</i>	H19	<i>trnC-petN1R</i>	KF487941
<i>S.globulifera</i>	H20	<i>trnC-petN1R</i>	KF487924
<i>S.globulifera</i>	H21	<i>trnC-petN1R</i>	KF487902
<i>S.globulifera</i>	H22	<i>trnC-petN1R</i>	KF487895
<i>S.globulifera</i>	H23	<i>trnC-petN1R</i>	KF487907
<i>S.globulifera</i>	H24	<i>trnC-petN1R</i>	KF488047
<i>M.excelsa</i>	H1-H2	<i>trnC-petN1R</i>	HM543892.1

<i>M. excelsa</i>	H4-H5-H7	<i>trnC-petN1R</i>	HM543884.1
<i>M. excelsa</i>	H8	<i>trnC-petN1R</i>	HM543888.1
<i>M. excelsa</i>	H1	<i>psbA-trnH</i>	HM543948.1
<i>M. excelsa</i>	H2-H7	<i>psbA-trnH</i>	HM543949.1
<i>M. excelsa</i>	H4	<i>psbA-trnH</i>	HM543969.1
<i>M. excelsa</i>	H5-H8	<i>psbA-trnH</i>	HM544018.1

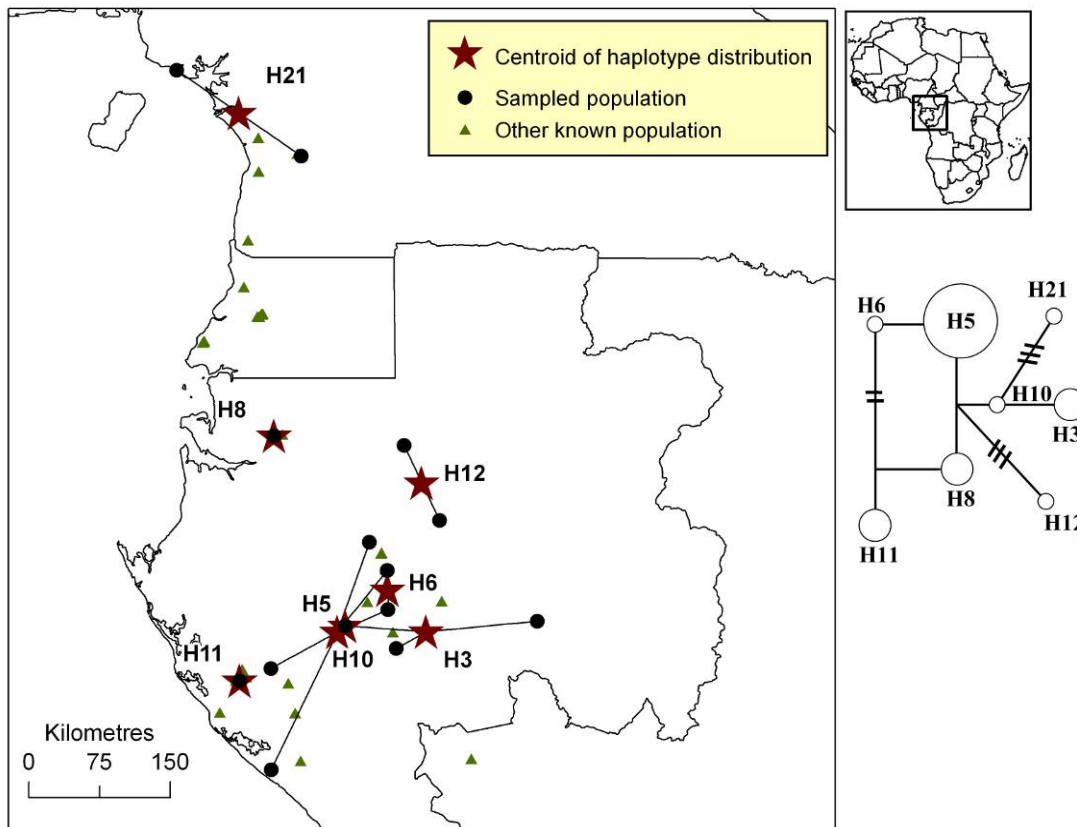


Figure S1. Distribution of pDNA haplotypes of *Afrostyrax kamerunensis* in Atlantic Central Africa. All populations that host a given haplotype are linked to the centroid of the haplotype's distribution (star). The phylogenetic network is based on one pDNA region (*trnC-PetNIR* inter-genic spacer). A simple link between haplotypes indicates one mutation event. Links with bars indicate more than one mutation event.

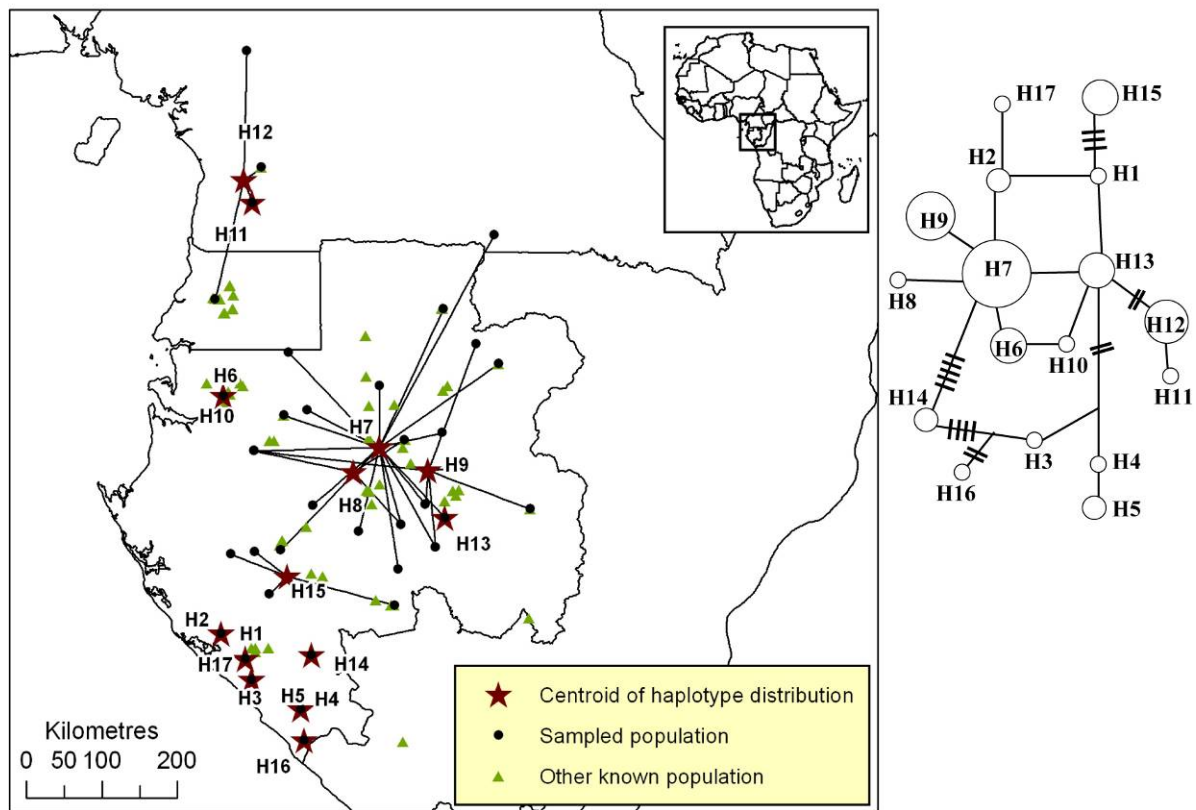


Figure S2. Distribution of pDNA haplotypes of *Scorodophloeus zenkeri* in Atlantic Central Africa. All populations that host a given haplotype are linked to the centroid of the haplotype's distribution (star). The phylogenetic network is based on one pDNA region (*trnC-PetNIR* inter-genic spacer). A simple link between haplotypes indicates one mutation event. Links with bars indicate more than one mutation event.

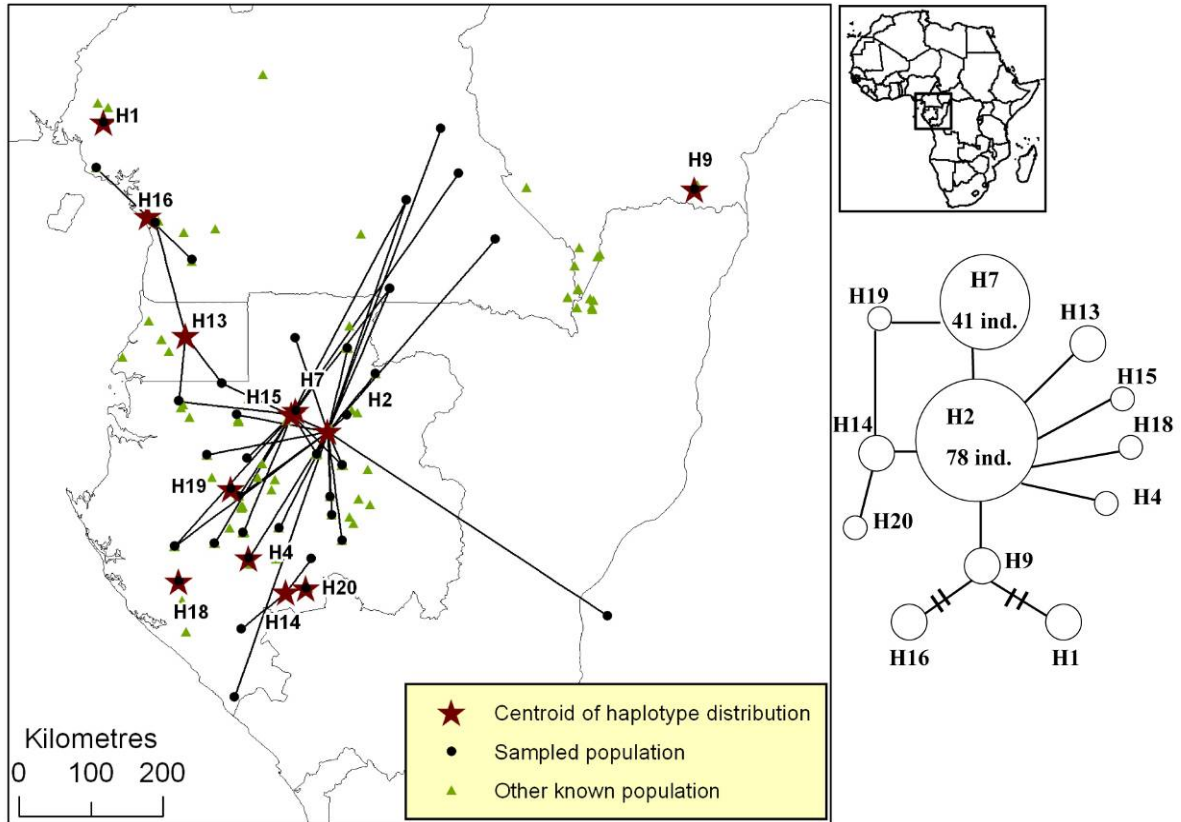


Figure S3. Distribution of pDNA haplotypes of *Afrostyrax lepidophyllus* in Atlantic Central Africa. All populations that host a given haplotype are linked to the centroid of the haplotype's distribution (star). The phylogenetic network is based on one pDNA region (*trnC-PetNIR* inter-genic spacer). A simple link between haplotypes indicates one mutation event. Links with bars indicate more than one mutation event.

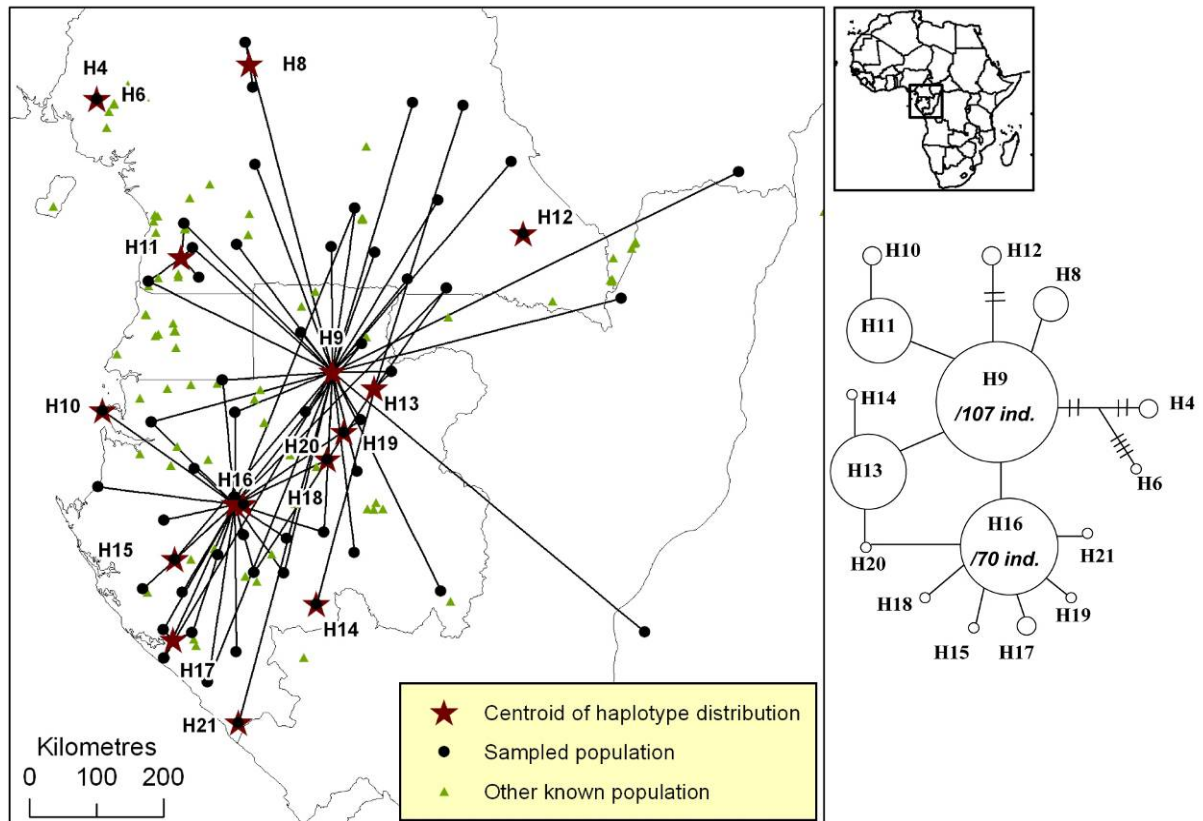


Figure S4. Distribution of pDNA haplotypes of *Greenwayodendron suaveolens* subsp. *suaveolens* var. *suaveolens* in Atlantic Central Africa. All populations that host a given haplotype are linked to the centroid of the haplotype's distribution (star). The phylogenetic network is based on one pDNA region (*trnC-PetN1R* inter-genic spacer). A simple link between haplotypes indicates one mutation event. Links with bars indicate more than one mutation event.

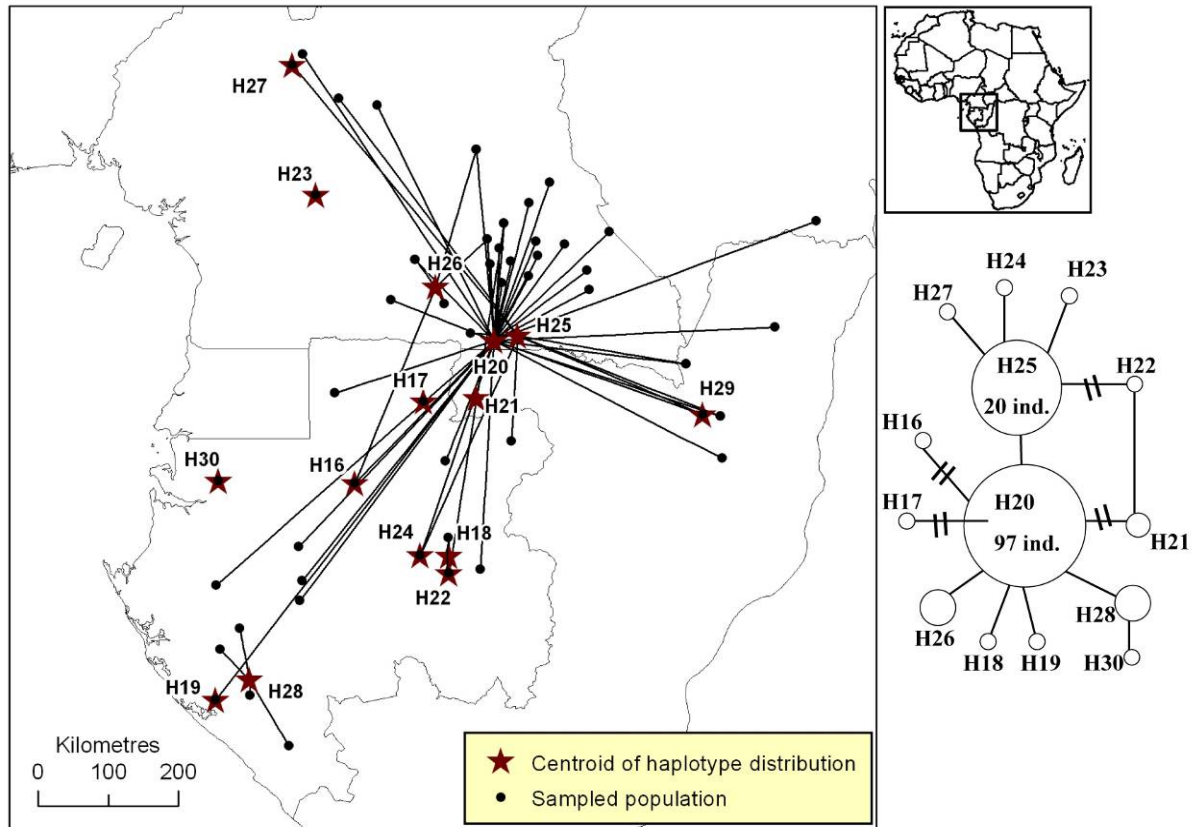


Figure S5. Distribution of pDNA haplotypes of *Erythrophleum suaveolens* in Atlantic Central Africa. All populations that host a given haplotype are linked to the centroid of the haplotype's distribution (star). The phylogenetic network is based on one pDNA region (*trnC-PetNIR* inter-genic spacer). A simple link between haplotypes indicates one mutation event. Links with bars indicate more than one mutation event.

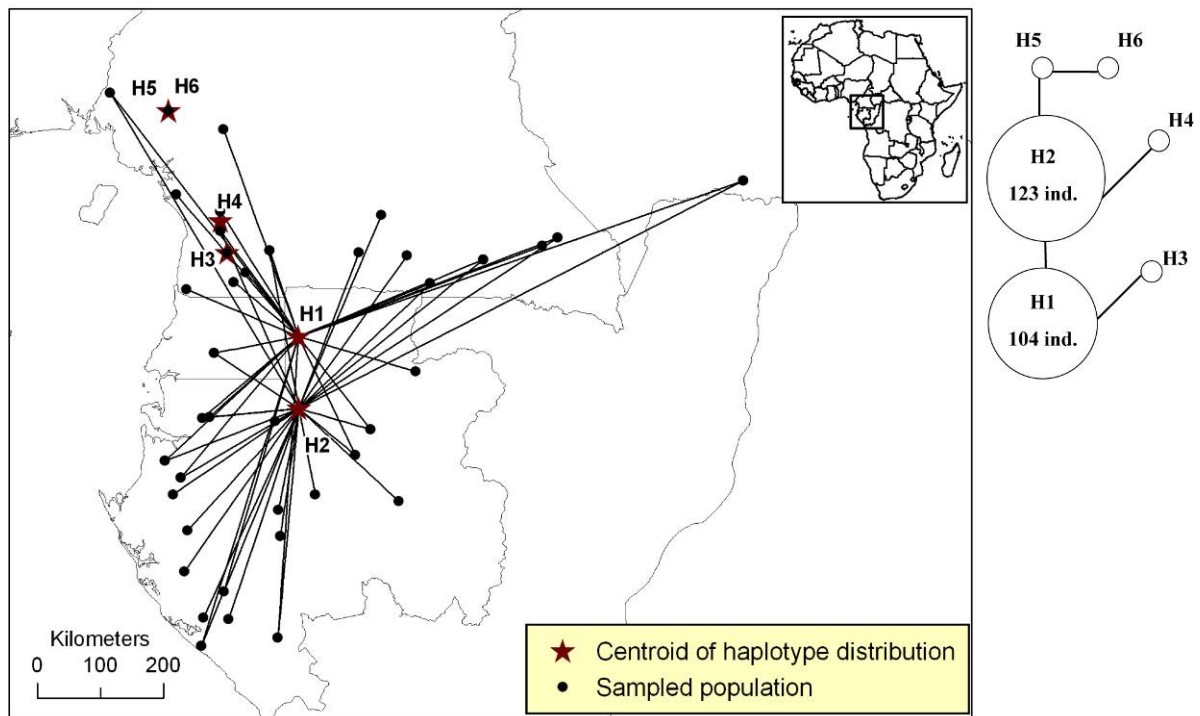


Figure S6. Distribution of pDNA haplotypes of *Santiria trimera* in Atlantic Central Africa. All populations that host a given haplotype are linked to the centroid of the haplotype's distribution (star). The phylogenetic network is based on two pDNA regions (*rpl26-infA-rps8* and part of the *rbcL* gene). Link between haplotypes indicate one mutation event.

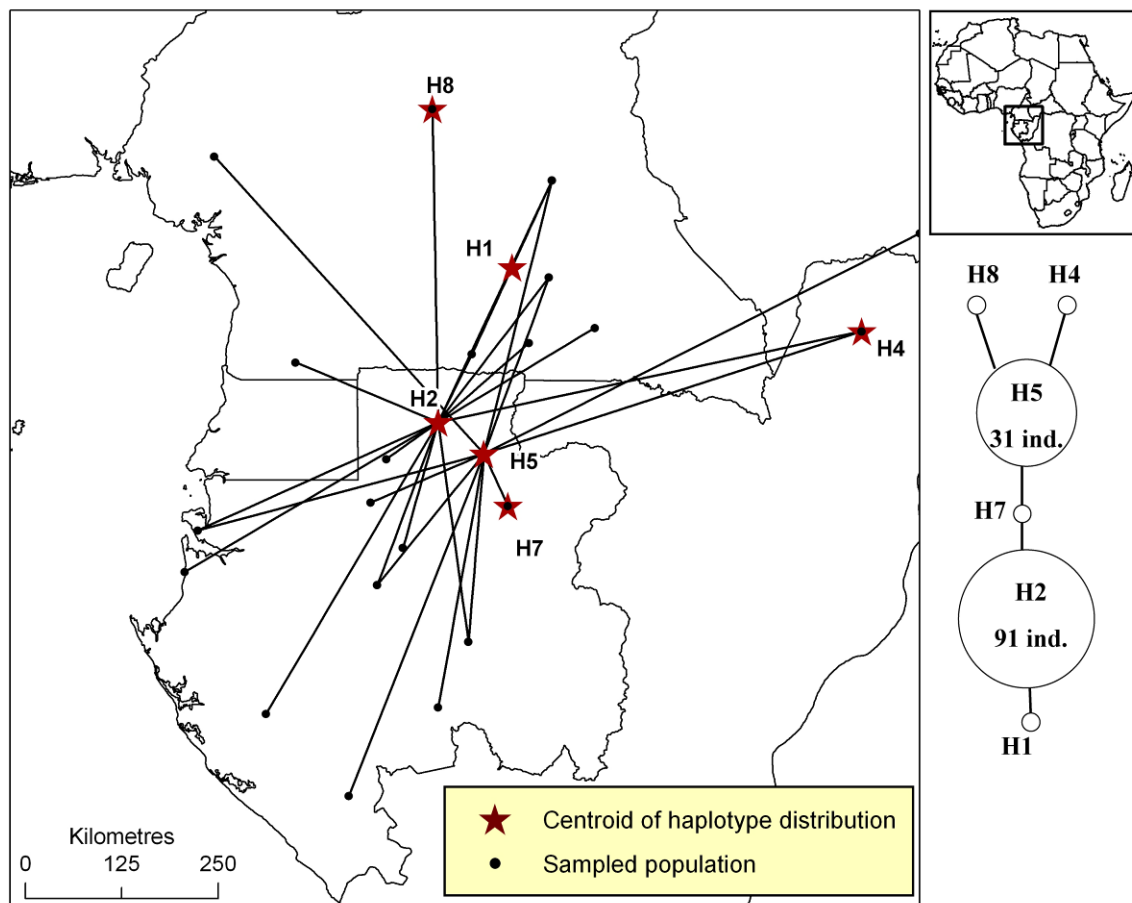


Figure S7. Distribution of pDNA haplotypes of *Milicia excelsa* in Atlantic Central Africa. All populations that host a given haplotype are linked to the centroid of the haplotype's distribution (star). The phylogenetic network is based on two pDNA regions (*trnC-PetN1R* and *psbA-trnH* inter-genic spacers). Link between haplotypes indicate one mutation event.

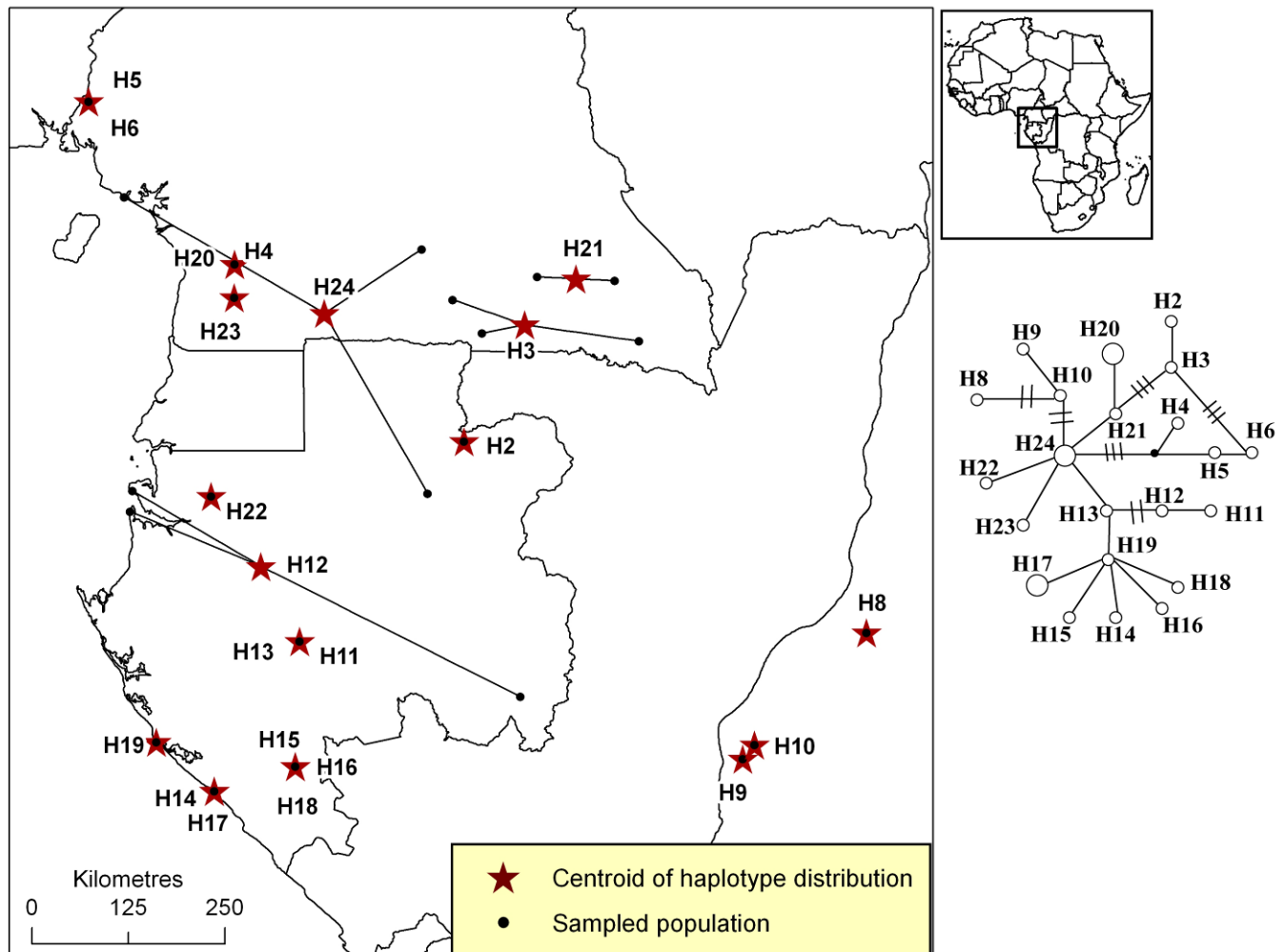


Figure S8. Distribution of pDNA haplotypes of *Symphonia globulifera* in Atlantic Central Africa. All populations that host a given haplotype are linked to the centroid of the haplotype's distribution (star). The phylogenetic network is based on one pDNA region (*trnC-PetNIR* inter-genic spacer). A simple link between haplotypes indicates one mutation event. Links with bars indicate more than one mutation event.

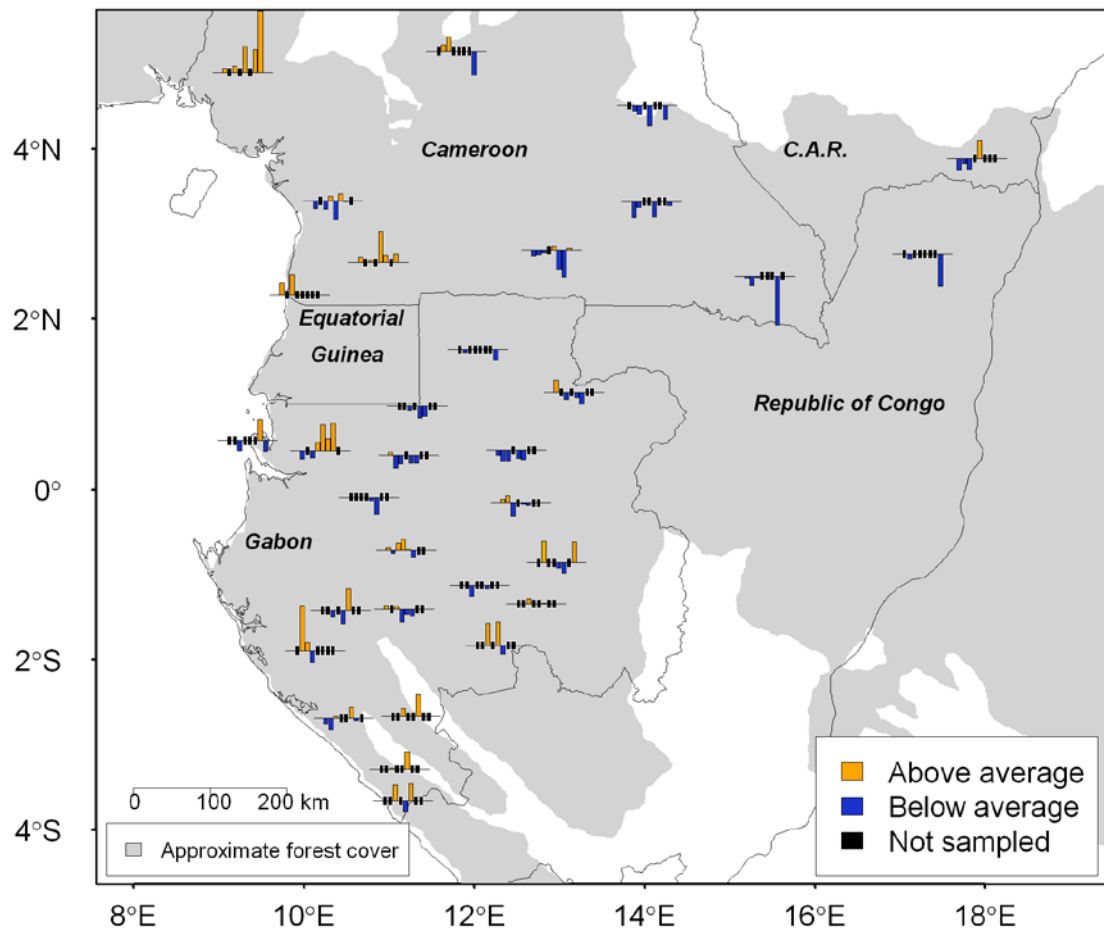


Figure S9. Genetic distinctiveness of each tree species within each locality (for localities with at least 2 species sampled) in Atlantic Central Africa. Distinctiveness above or below average is based on standardized differentiation S_{ij} computed for each species among populations. Each barplot represents, respectively, from left to right distinctiveness values for *S. trimera*, *E. suaveolens*, *G. suaveolens*, *A. kamerunensis*, *A. lepidophyllus*, *S. zenkeri*, *S. globulifera* and *M. excelsa*.