

ORIGINAL ARTICLE

Speciation slowing down in widespread and long-living tree taxa: insights from the tropical timber tree genus *Milicia* (Moraceae)

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The long generation time and large effective size of widespread forest tree species can result in slow evolutionary rate and incomplete lineage sorting, complicating species delimitation. We addressed this issue with the African timber tree genus *Milicia* that comprises two morphologically similar and often confounded species: *M. excelsa*, widespread from West to East Africa, and *M. regia*, endemic to West Africa. We combined information from nuclear microsatellites (nSSRs), nuclear and plastid DNA sequences, and morphological systematics to identify significant evolutionary units and infer their evolutionary and biogeographical history. We detected five geographically coherent genetic clusters using nSSRs and three levels of genetic differentiation. First, one West African cluster matched perfectly with the morphospecies *M. regia* that formed a monophyletic clade at both DNA sequences. Second, a West African *M. excelsa* cluster formed a monophyletic group at plastid DNA and was more related to *M. regia* than to Central African *M. excelsa*, but shared many haplotypes with the latter at nuclear DNA. Third, three Central African clusters appeared little differentiated and shared most of their haplotypes. Although gene tree paraphyly could suggest a single species in *Milicia* following the phylogenetic species concept, the existence of mutual haplotypic exclusivity and nonadmixed genetic clusters in the contact area of the two taxa indicate strong reproductive isolation and, thus, two species following the biological species concept. Molecular dating of the first divergence events showed that speciation in *Milicia* is ancient (Tertiary), indicating that long-living tree taxa exhibiting genetic speciation may remain similar morphologically.

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INTRODUCTION

Angiosperm diversification was termed ‘abominable mystery’ by Charles Darwin because this is likely one of the most complex processes ever investigated by ecologists and biologists. This is because of the difficulty to understand the biogeographical history of specific populations as it depends on interactions between infinite variants of abiotic and biotic phenomena: geological events, climate changes and characteristics, life traits, gene flow between distant populations and sister taxa and so on (Davies *et al.*, 2004). Although most biologists thought that the use of modern tools in phylogenetic taxonomy and molecular ecology in conjunction with data from environmental sciences may provide more accurate insights for inference of biogeographical and evolutionary patterns, the existence of heterogeneous genomic divergence (differentiation across the genome can be highly variable) and the fact that differentiation and speciation are not always synonymous of morphological change

(producing cryptic species) can blur the outcomes (Bickford *et al.*, 2006; Nosil *et al.*, 2009).

Especially, addressing speciation in sister taxa is a real challenge complicated by debates on definition of species, as different approaches can reveal different patterns. Most definitions of species are derived from two concepts: (1) the biological species concept (BSC) that defines species as reproductively isolated groups of living organisms (Mayr, 1942), and (2) the phylogenetic species concept (PSC) that groups in a given species individuals forming a monophyletic group (or a clade), according to the monophyly version (De Queiroz, 2007). Because testing for reproductive isolation is difficult and PSC requires many (molecular) traits, historical taxonomy has mostly been based on the morphological similarity of individuals, and ideally the occurrence of multiple diagnostic qualitative traits to define species (Hey, 2006; Mallet, 2010). Nowadays, when multilocus genetic markers are available, large-scale

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population sampling and Bayesian clustering analyses allow identifying groups of individuals with a shared recent common ancestry, groups that have been reproductively isolated (historically at least) and can be thought as candidate units corresponding to the BSC. Moreover, when DNA sequences are available, they constitute ideal data to identify monophyletic groups of individuals that can be considered as evolutionary units corresponding to the PSC, although incomplete lineage sorting can blur the evidence. Whether historical taxonomic species delimitation converges with the BSC or the PSC has been rarely examined in African tree species (but see Koffi, 2010).

Although different approaches may lead to incongruent results because of reticulated evolution and incomplete lineage sorting, their integration in a pluralistic species concept can help make a consistent decision for taxonomic classification and conservation issues (Freeland *et al.*, 2011). Hence, species delimitation requires to integrate data from molecular phylogeny, classical taxonomy (morphology-based), ecology, historical and contemporaneous biogeography in a way that permits the reconstruction of the evolutionary history of the target taxon (see, for example, Datwyler and Weiblen, 2004; Odee *et al.*, 2012; Scotti-Saintagne *et al.*, 2012). We adopted a pluralistic approach to infer biogeographical history and delimit significant evolutionary units in the African genus *Milicia* Sim. Taxonomists recognize two sister tree species, *M. excelsa* (Welw.) C.C. Berg and *M. regia* (Chev.) C.C. Berg, both called Iroko in the wood trade. Iroko is one of the most important timber woods of Africa. At present, *M. regia* is viewed as a vulnerable taxon by IUCN (International Union for Conservation of Nature), whereas *M. excelsa*, a near-threatened species according to the same source, is considered threatened or endangered in some West and East African countries (Ebert, 2004; Ofori and Cobbinah, 2007).

Milicia belongs to the Moreae tribe that also contains *Morus*, the closest genus to *Milicia* (Zerega *et al.*, 2005; Nepal, 2012). The most recent common ancestor of *Milicia* and *Morus* was estimated between 41 and 72 million years ago (mya) (Zerega *et al.*, 2005). The Moreae have a Eurasian origin and may have primarily diversified during the Palaeocene and the Eocene. At the genus level, few genetic studies have been conducted in *Milicia*. Using the chloroplast intron *trnL* and the intergenic spacer *trnL-F*, Ofori *et al.* (2001) found no variation in populations collected from the Upper Guinea, the rainforest zone at the western part of the West Africa (Supplementary Figure S1). Ofori *et al.* (2003) tried to assess genetic differentiation between *Milicia* species via chloroplast markers, but their populations were assigned to species according to vegetation types because of difficulties in obtaining diagnostic morphological traits of the sampled individuals. Within *M. excelsa*, Dainou *et al.* (2010) demonstrated the existence of different gene pools in the Lower Guinea (the rainforest from the Atlantic Ocean until the western side of the Oubangui-Congo River; Supplementary Figure S1), despite extensive gene dispersal (Bizoux *et al.*, 2009), and suggested a relatively recent fragmentation during Pleistocene ice ages. Curiously, Dainou *et al.* (2010) also showed that West African *M. excelsa* populations from Benin in the Dahomey gap (the savannah interval separating the Upper Guinean and Lower Guinean forest blocks; Supplementary Figure S1) strongly diverged from Central African samples, despite the fact that *M. excelsa* presents a continuous range from West to Central Africa. This pattern questions whether *M. excelsa* individuals from Benin are more closely related to West African *M. regia* or to Central African *M. excelsa* populations. In fact, in contrast to the Lower Guinea, we have relatively little information about biogeographical patterns in the Upper Guinea or the Congolia (the humid forest zone eastwards from

the Oubangui-Congo River; Supplementary Figure S1; OJ Hardy, unpublished).

The present study aims to disentangle phylogenetic relationships between these sister species using an integrative approach that combines morphological and molecular data. For the present study, we collected samples from most of the distribution range of *Milicia* in Africa, from Senegal to Tanzania and Democratic Republic of the Congo. Our study represents the largest scale phylogeography study focused on tropical moist forests in Africa. Our investigations were motivated by the following questions: (1) In West Africa, are morphological and genetic markers congruent in delineating species boundary in *Milicia*? (2) At the scale of Africa, what are the significant evolutionary units within the *Milicia* species complex and which of them may represent different species? (3) What are the divergence times between evolutionary units and can they be related to the paleodynamics of African rainforests?

MATERIALS AND METHODS

Study taxa

Milicia is a tree up to 35–45 m tall and 1.5 m in diameter. The annual increment in diameter was estimated at 5.7 mm (Durrieu de Madron, 2003), and regular fruiting was observed on trees of at least 60 cm in diameter (Dainou *et al.*, 2012b). *M. regia* is only distributed in Upper Guinea mostly in the evergreen forests of West Africa, westwards of the Dahomey gap (Supplementary Figure S1). *M. excelsa* displays a larger geographic distribution from West to East Africa and can occur in a wide range of forest habitats, but is more abundant in semi-deciduous forests (Supplementary Figure S1). The range of the two taxa overlaps from the central part of Liberia to the East of Ghana. *M. excelsa* and *M. regia* are morphologically so similar that they are usually confused in the wood trade (ATIBT, 2010) and even by researchers and botanists (Chevalier, 1917; Schnell, 1946; Ofori *et al.*, 2003). Their woods do not present significant differences (White, 1966).

Very little information is available regarding the ecology of *M. regia* (Dainou *et al.*, 2012a). *M. excelsa* is a pioneer species with increasing population densities from evergreen forests to semi-deciduous forests (Nichols *et al.*, 1998). Both species are dioecious. *M. excelsa* is wind pollinated and its seeds are mostly dispersed by birds and the fruit-bat *Eidolon helvum* (Dainou *et al.*, 2012b). In West Africa, the two species flower and fruit at the same period from January to March (Berg, 1977; Nyong'o *et al.*, 1994).

Sampling and DNA extraction

Samples were obtained from 849 individuals in 17 countries. These included 550 individuals previously studied in Dainou *et al.* (2010) and sampled from the Lower Guinea and Benin (Dahomey gap) and 46 collected from herbarium collections at the National Botanical Garden of Belgium. During the sampling work, collaborators did not pay attention to the taxonomic identity of individuals. Whenever possible, samplers were asked to collect one entire leaf per individual especially for West African specimens in order to characterize leaf traits, but this was not always possible and many samples consist of a fragment of limb or cambium tissue. The morphological characterization of herbarium vouchers was conducted directly on specimens, as we could not collect entire leaf samples from herbarium collections. Fresh materials were silica-dried. DNA was extracted using the DNeasy Plant Mini kit (QIAGEN, Venlo, The Netherlands).

Genotyping and sequencing

Nuclear microsatellites (nSSRs) were genotyped on the whole sample through seven loci: Mex51, Mex63, Mex81, Mex95, Mex137, Mex163a and Mex202 (Ounsavi *et al.*, 2006). Amplification conditions were as reported in Bizoux *et al.* (2009). Genotyping was repeated until each individual is scored for at least six loci.

The amplification and polymorphism of nuclear DNA sequences (nDNA) were tested at 12 gene regions: *ADH*, *GScp*, *ADHc*, *Rn11*, *TPI 6rn/4rn*, *LF4 C11R*, *LF4 C14R*, *Agt1*, *App1*, *At103* (Li *et al.*, 2008), and *PEPC E1/E2* and *PEPC E2/E3* (J Duminil *et al.*, unpublished). Three of them successfully amplified,

Agt1, *Apg1* and *At103*, but only the latter was polymorphic and then selected for further analyses. For the plastid genome (pDNA), two intergenic regions, *psbA-trnH* and *trnC-ycf6*, were selected. The three nDNA and pDNA sequences were successfully amplified on fresh material but not on the herbarium vouchers in most cases. To overcome this problem, we defined new internal primers that amplified a significant proportion of herbarium samples. The new primer sequences were as follows: 5'-TTCTTGTTCTATCAGGAAGTTTGG and 3'-AATCCACTGCCTTGATCCAC (411 bp) for *psbA-trnH*, 5'-CCGACGGAGAAATCAATGA and 3'-TCTTTGTGTCGCCCTTCATT (496 bp) for *trnC-ycf6* and 5'-CCTGAAACACGATTTGAGAGG and 3'-AGAAGTGGTGRGAGGATGAG (342 bp) for *At103*. PCRs were performed in a thermal cycler PTC 200 (MJ-Research, Waltham, MA, USA). *psbA-trnH* was amplified in a total volume of 25 μ l with the Phusion polymerase (Finnzymes Espoo, Finland) following the manufacturer's protocol. PCR conditions for *trnC-ycf6* were as described in Dainou *et al.* (2010) and were also applied for *At103*. From the subsample of 260 individuals selected for sequencing, 195, 225 and 202 were successfully amplified for *psbA-trnH*, *trnC-ycf6* and *At103*, respectively, with 172 individuals common to the three fragments. In order to test whether *Milicia* forms a monophyletic group, we also included a sample from *Morus indica* in the sequencing processes.

Morphological characterization

In an exhaustive literature review of morphological traits that differentiate *M. regia* and *M. excelsa*, Dainou *et al.* (2012a) reported that there could be a slight difference in female flowers according to Aubréville (1959), whereas most botanists agree that 'in adult specimens the only differences can be found in the leaf venation and the indument' (Berg, 1977; pg 349). One qualitative and three quantitative leaf characters distinguish the adult specimens of the two species (Hawthorne and Jongkind, 2006). (1) Leaf lower surface is soft to touch (variable *Soft*) because of the presence of rounded areoles containing microscopic hairs in *M. excelsa* (*Soft* = 1), whereas this feature is absent in *M. regia* (*Soft* = 0). (2) The number of pairs of secondary veins (variable *N_veins*) should not exceed 11 in *M. regia*, whereas it ranges from 12 to 22 in *M. excelsa*. However, Berg (1977) and Hawthorne and Jongkind (2006) reported a few cases of *M. regia* leaves displaying up to 14 veins and *M. excelsa* leaves with only 10 veins. In such cases, the authors implicitly used only the character *Soft* to identify each species. (3) The length/width ratio of limb (variable *L/w_limb*) equals ~ 1.4 in *M. regia* and ~ 1.7 in *M. excelsa*. (4) The mean distance between two contiguous veins (variable *D_veins*) in *M. excelsa* is expected to be about half the value found in *M. regia* specimens (~ 1 cm).

We characterized these four traits on a subsample of 114 individuals with entire leaves that came from 11 countries of West and Central Africa. We performed a principal component analysis using STATISTICA 6.0 (StatSoft, 2004) considering the quantitative variables *L/w_limb*, *N_veins* and *D_veins*. The qualitative variable *Soft* was integrated in the principal component ordination using two different symbols to represent individuals with *Soft* = 0 or 1.

Identification of genetic clusters

Identification of the number of genetic clusters *K* was based on variation at nSSRs, using the Bayesian clustering algorithm implemented in TESS 2.3.1 (Chen *et al.*, 2007) without prior information of the morphological description. We applied the method as described in Dainou *et al.* (2010) with some slight differences. Only the admixture model was run with an interaction parameter $\psi = 0$, which means that no spatial information was included in the analysis. For each fixed value of the number of clusters (*K*_{max}) ranging from 2 to 10, we performed 10 runs with a burn-in of 20 000 for a total number of sweeps of 100 000. The best value of *K* was determined after plotting values of log-likelihood and deviance information criterion against *K*_{max}: for both approaches, the plateau starting point indicated the number of clusters *K* (Pritchard *et al.*, 2000 and François and Durand, 2010, respectively). We also applied the method in Evanno *et al.* (2005) to confirm the previous methods. The program CLUMPP (Jakobsson and Rosenberg, 2007) was then used to summarize the five most reliable simulations for the best *K*, and to estimate averaged cluster membership coefficients *q* for each individual. At this step, an individual was assigned to a given cluster whenever *q* > 0.5.

Phylogeography and phylogeny at pDNA and nDNA

The following analyses were performed on the subsample of 172 individuals sequenced at all pDNA and nDNA fragments. Two sets of haplotypes were defined based on variation at (1) *At103*, and (2) over the two plastid sequences *psbA-trnH/trnC-ycf6* (Supplementary Tables S1 and S2). Median joining networks were constructed with NETWORK 4.6 (Bandelt *et al.*, 1999).

Bayesian inferences of phylogenetic relationships were performed using BEAST 1.7.3 (Drummond and Rambaut, 2007). *M. indica* was used as outgroup. First, jMODELTEST 0.1.1 (Posada, 2008) indicated F81 and HKY as the likely substitution models for *psbA-trnH* / *trnC-ycf6* and *At103*, respectively, after likelihood ratio tests. Then, for each type of genomic sequence, BEAST was run and set up as follows: (1) for the model F81, the appropriate code was imported from BEAST webpage (http://beast.bio.ed.ac.uk/Substitution_model_code) and we modified the input file accordingly; (2) we assumed an uncorrelated lognormal relaxed molecular clock (in general, the uncorrelated relaxed clock models perform well even if the analyzing data are clocklike; Drummond *et al.*, 2006) and a Yule tree prior; (3) the tree root height was constrained with the age of the MRCA of *Milicia* and *Morus* (Zerega *et al.*, 2005), assuming a normal distribution with a mean of 56 mya and the s.d. of 9 mya (corresponding to 95% of the distribution lying between 41 and 71 mya); (4) the Markov Chain Monte Carlo was run independently five times for 50 million generations each, sampling 1 tree every 2000 generations. The output files of BEAST were checked with TRACER considering the effective sample size of > 100 and combined using LOGCOMBINER, both programs distributed with BEAST. TREEANNOTATOR 1.7.3 (also distributed with BEAST) was then used to select the maximum clade credibility tree (the tree with the highest sum of posterior probabilities on its internal nodes) with the height of nodes calculated as the mean height of all sampled trees for that clade. FIGTREE 1.3. (A Rambaut; <http://tree.bio.ed.ac.uk/software/figtree/>) was finally used to visualize the phylogenetic trees.

Diversity and differentiation parameters: detecting phylogeographic signal

The genetic clusters determined from nSSRs data were used as basis for computing diversity and differentiation parameters for each type of marker. Relative to the degree of genetic diversity, the following genetic diversity parameters were computed for each genetic cluster: *A*₀, total number of haplotypes (pDNA and nDNA) or alleles (nSSRs); *R*_S, haplotypic (pDNA and nDNA) or allelic richness (nSSRs); %*R*_{priv}, percentage of private haplotypes or alleles; and *H*_T and *V*_T, haplotypic diversity based on unordered and ordered haplotypes, respectively (after Pons and Petit, 1996). Differentiation at nSSRs between pairs of genetic clusters was computed using *F*_{ST} and tested with FSTAT 2.9.3.2 (Goudet, 1995). To check for a phylogeographic signal at nSSRs, we also computed *R*_{ST} that is based on allele size and expected to be larger than *F*_{ST} if mutations (under stepwise model) have contributed to differentiation (Hardy *et al.*, 2003). We also estimated differentiation between clusters and tested for a phylogeographic signal at pDNA and nDNA using *G*_{ST} (for unordered haplotypes) and *N*_{ST} (for ordered haplotypes) (Pons and Petit, 1996). Note that a genetic distance matrix between haplotypes was first inferred following the number of polymorphic characters that differed in state between each pair of haplotypes for pDNA and nDNA. In both cases, 10 000 permutations were performed. Unless specified, computations described above were carried out using SPAGEDI 1.3 (Hardy and Vekemans, 2002) except haplotypic and allelic richness computed using the rarefaction procedure implemented in HP-RARE 1.1 (Kalinowski, 2005). *R*_S and %*R*_{priv} were computed for subsamples of seven genes and 55 individuals at pDNA and nDNA sequences and nSSRs, respectively, taking into account the minimum size of the clusters for each type of markers.

RESULTS

Morphology-based species delimitation

The two first axes of the principal component analysis explained 93.05% of the total variance (Figure 1). The first axis, which was mainly determined by the variable *N_veins* (45.3% of contribution), split individuals in two groups, one containing samples from Central Africa, Benin and Nigeria presenting soft leaves (*Soft* = 1), and the

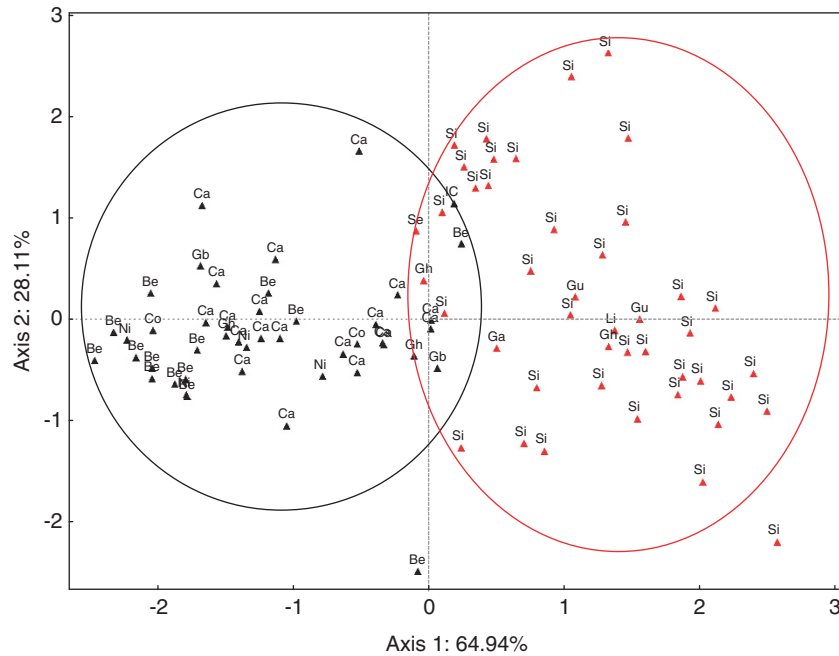


Figure 1 Principal component analysis (PCA) projection of *Milicia* individuals based on three leaf traits: *L/w_limb* (length/width ratio of limb), *N_veins* (number of secondary veins) and *D_veins* (distance between two contiguous veins). Black triangles represent samples with *Soft*=1, a character expected in *M. excelsa*, whereas red triangles are samples for which *Soft*=0, a characteristic of *M. regia*. Country codes: Be, Benin; Ca, Cameroon; Co, Republic of the Congo; Ga, Gambia; Gb, Gabon; Gh, Ghana; Gu, Guinea Bissau et Guinea-Conakry; IC, Ivory Coast; Li, Liberia; Ni, Nigeria; Se, Senegal; Si, Sierra Leone.

other one containing samples from Senegal to Sierra Leone and Ivory Coast, without hairs underneath the leaves (*Soft*=0), although there is a small overlap on the principal component analysis plane. As a consequence, the characters *N_veins*, *D_veins* and *L/w_limb* display significantly different mean values between individuals with *Soft*=0 and those with *Soft*=1 but their distributions overlap (Table 1). For example, four trees with *Soft*=0 presented 14–15 pairs of secondary veins that is unexpected in that group.

Thereafter, as there are no clear species-specific limits for the three quantitative traits, we will assign *M. excelsa* to individuals with *Soft*=1 and *M. regia* to individuals with *Soft*=0, as Berg (1977) and Hawthorne and Jongkind (2006) suggested. The character *Soft* allowed us to identify 335 specimens (135 from West Africa and 200 from Central Africa) because any small piece of leaf was enough for that. All individuals assigned to *M. regia* were distributed from Senegal to Ghana and never occurred in Central Africa. In West Africa, *M. excelsa* was found from Guinea-Conakry to Nigeria, making the overlap zone of the two species from Guinea-Conakry to Ghana (Supplementary Figure S1). *M. regia* mostly occurred in the evergreen forest zone, whereas *M. excelsa* was mostly present in semi-deciduous forests.

The nSSR genetic clusters and relationships with morphological designation

Log-likelihood and deviance information criterion methods (Pritchard *et al.*, 2000 and François and Durand, 2010, respectively) suggested $K=5$ as the number of clusters, whereas variation of ΔK (Evanno *et al.*, 2005) suggested two solutions: $K=2$ and $K=5$ (Supplementary Figure S2). The case of $K=2$ clusters may be explained by the existence of two sister species in our data set, as the method of Evanno *et al.* (2005) is known to detect the uppermost structure in situations of strong differentiation. It performs less well on situations of weak and moderate genetic differentiations (Waples

Table 1 Comparison of leaf traits between *Milicia excelsa* and *M. regia* specimens, identified from the presence (*Soft*=1) or absence (*Soft*=0) of hairs at the lower surface of leaf

Taxa	Mean value of <i>N_veins</i> (min–max)	Mean value of <i>D_veins</i> (cm) (min–max)	Mean ratio of <i>L/w_limb</i> (min–max)
<i>M. regia</i> (West Africa)	10.6 (8–15)	1.1 (0.7–1.6)	1.5 (1.0–2.4)
<i>M. excelsa</i> (West and Central Africa)	15.7 (12–22)	0.6 (0.3–1.2)	1.7 (1.2–2.4)

Abbreviations: *D_veins*, distance (cm) between two contiguous veins; *L/w_limb*, length/width ratio of limb; *N_veins*, number of secondary veins.
All differences are statistically significant (Student's *t*-test; $P<0.001$).

and Gaggiotti, 2006). Therefore, we have to consider $K=5$ clusters as the true number of clusters (K) in our data set. Cluster *K1* grouped together all morphology-based *M. regia* individuals (Figure 2). All West African *M. excelsa* individuals were grouped into *K2*. Clusters *K3*, *K4* and *K5* were constituted only of *M. excelsa* specimens from Central Africa. A proportion of 5.4% of the whole sample was not assigned to any cluster, with q never exceeding 0.50 in these cases. When assessing the degree of purity of each cluster through the proportion of admixed individuals for $q>0.8$, for example, *K1* was the purest (82%), followed by *K2* and *K3* (70%), *K4* (35%) and *K5* (22%) (Supplementary Figure S3). Clearly, most individuals assigned to *K4* or *K5* present a significant portion of their genome also assigned to another of the Central African clusters *K3*, *K4* and *K5* (Supplementary Figure S4).

One can also assess the hierarchy of clustering when considering the solutions of the clustering algorithm at lower K (Supplementary Figures S4 and S5). For $K=2$, West African samples (from Senegal to Benin, including all *M. regia* but also part of *M. excelsa*) were

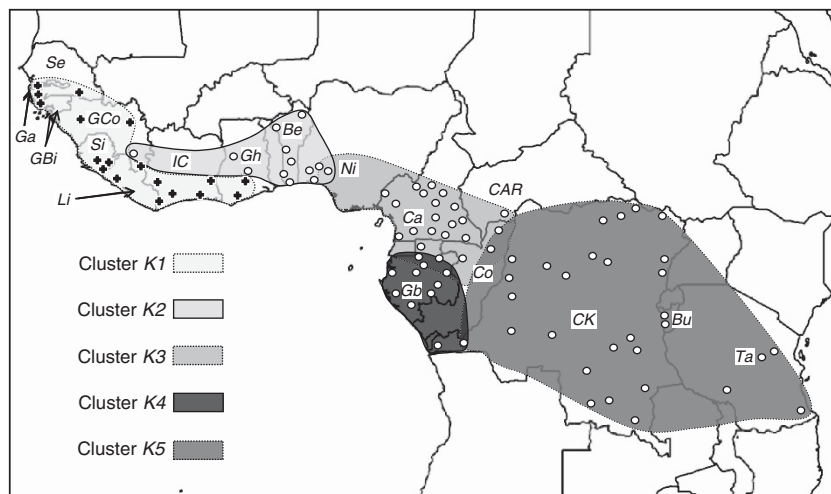


Figure 2 Spatial genetic structure of *Milicia* populations derived from Tess clustering algorithm for an optimal number $K=5$ clusters. Black crosses indicate morphology-based *M. regia* (group of) individuals, whereas the white circles stand for *M. excelsa*. Codes of the 17 sampled countries, from West to East: Se, Senegal; Ga, Gambia; GBi, Guinea Bissau; GCo, Guinea-Conakry; Si, Sierra Leone; IC, Ivory Coast; Gh, Ghana; Be, Benin; Ni, Nigeria; Ca, Cameroon; Co, Republic of the Congo; CK, Democratic Republic of the Congo; Bu, Burundi; Ta, Tanzania.

separated from the rest of the sampling (from Benin to Tanzania). The latter group was further subdivided at $K=3$ and $K=4$ (Supplementary Figures S4 and S5), but it was only when $K=5$ that all *M. regia* samples form a pure genetic cluster.

Degree of differentiation between the West African *M. excelsa* cluster K2 and the three clusters from Central Africa (K3 to K5; F_{ST} ranged from 0.121 to 0.163, R_{ST} from 0.103 to 0.201) were close or in the same range to values found at interspecific level (F_{ST} ranged from 0.147 to 0.255, R_{ST} from 0.171 to 0.308 between *M. excelsa*-K1 and any *M. excelsa* cluster K2 to K5), whereas differentiation was lower among Central African clusters (F_{ST} ranged from 0.087 to 0.158, R_{ST} from 0.027 to 0.099 between K3, K4 and K5; Table 2). Allele size permutation tests did not detect any phylogeographical signal at nSSR markers (Table 2).

Phylogeographic structure at pDNA and nDNA sequence variation

Whatever genome is considered, *M. regia* is well differentiated from *M. excelsa* populations as there is no shared haplotype and, when the trees are rooted, *M. regia* appears monophyletic (Figures 3a and b). At pDNA fragments, seven haplotypes were restricted to West Africa and, surprisingly, *M. excelsa* haplotypes in Central Africa belonged to a distinct lineage to the one of West African *M. excelsa*. When we excluded repetitive sequences (microsatellites) from the analysis, it turned out that only one mutation separates the unique haplotype of *M. regia* from the most frequent haplotype of *M. excelsa* in West Africa (Supplementary Figure S6A). Furthermore, at *psbA-trnH* only, excluding microsatellite sites led to a unique and common haplotype within West African populations, regardless of the taxon (Supplementary Figure S6B). A similar pattern of differentiation was observed at nDNA sequence (*M. regia* haplotypes forming one clade) except that West and Central African *M. excelsa* samples shared several haplotypes (Figure 3b). Nevertheless, differentiation indices between the West African cluster *M. excelsa*-K2 and the Central African clusters *M. excelsa*-K3 to K5 (G_{ST} ranged from 0.479 to 0.716 at pDNA and from 0.201 to 0.319 at nDNA) was nearly as high as between *M. excelsa*-K2 and *M. regia*-K1 ($G_{ST}=0.685$ at pDNA and 0.379 at nDNA), and much higher than between Central African clusters (G_{ST} ranged from 0.105 to 0.393 at pDNA and from 0.033 to

0.097 at nDNA) (Table 2). There was a significant phylogeographical signal ($N_{ST}>G_{ST}$) in the whole data set at both pDNA and nDNA, resulting from the interspecies comparison (Table 2). Within *M. excelsa*, a significant phylogeographic signal also occurred between the West African cluster K2 and the Central African *M. excelsa* clusters at pDNA but not at nDNA, whereas no signal of phylogeographical structure was found among Central African populations (Table 2).

When haplotypes at pDNA and nDNA, nSSR-based clusters and morphological assignments (based only on the character *Soft*) are compared, there is a strong congruence between all types of markers, for the subsample of 172 individuals common to them all (Table 3). All morphology-based *M. regia* individuals belonged to the lineage formed by pDNA haplotypes H9-H10-H11 and to the cluster K1. Similarly, *M. excelsa* in West Africa (K2 and far west of K3) was only represented in the lineage formed by pDNA H1-H2-H7-H8. At the cluster level, the pDNA haplotypes H1 and H8 were shared between clusters K2 and K3. However, the three individuals in cluster K3 with these haplotypes were located at the West of Nigeria, closer to Benin than to Cameroon. Therefore at the regional scale, there was no shared haplotype between West Africa and Central Africa for pDNA sequence. In contrast, nDNA sequences displayed shared haplotypes between West and Central Africa.

Variation of genetic diversity among regions and species

West African clusters displayed higher genetic diversity than those of Central Africa at nSSRs, with H_T varying from 0.600 to 0.683, whereas it was always <0.490 in Central Africa (Table 2). However, that trend was reversed at nDNA and pDNA sequences. Similarly, haplotypic richness looked higher in Central Africa, but the percentage of private alleles or haplotypes was threefold higher in West African clusters than in Central Africa, with the exception of cluster K5 for pDNA that presented an important proportion of endemic haplotypes (Table 2).

Phylogenetic relationships and timing of divergence

According to both pDNA and nDNA analyses, *M. regia* is monophyletic. In contrast, *M. excelsa* appears paraphyletic (Figure 4), at least at pDNA where West African populations of *M. excelsa* (cluster K2) form a well-supported clade (posterior probability of clade

Table 2 Genetic diversity and differentiation of nSSR clusters detected in *Milicia* for three types of markers: nSSRs, pDNA sequences and nDNA sequences

Type of marker	Region	Cluster at nSSRs	Taxon	Differentiation parameters					Diversity parameters					
				K1	K2	K3	K4	K5	N inds	A ₀	R _S	%R _{priv}	H _T	V _T
nSSRs	West Africa	K1	<i>M. regia</i>		0.195NS	0.308 NS	0.231 NS	0.171 NS	78	44	6.05	13.39	0.683	/
		K2	<i>M. excelsa</i>	0.147		0.185 NS	0.103 NS	0.201 NS	58	43	6.11	9.17	0.600	/
	Central Africa	K3	<i>M. excelsa</i>	0.196	0.121		0.027 NS	0.099 NS	416	45	5.12	1.76	0.486	/
		K4	<i>M. excelsa</i>	0.255	0.163	0.087		0.058 NS	149	37	4.45	0.22	0.477	/
		K5	<i>M. excelsa</i>	0.178	0.139	0.110	0.158		102	34	4.48	0.45	0.472	/
	<i>M. excelsa</i> samples (K2 to K5)				$F_{ST}=0.115$; $R_{ST}=0.085$ NS					725	54	/	/	0.585
All samples (both <i>M. excelsa</i> and <i>M. regia</i>)				$F_{ST}=0.139$; $R_{ST}=0.140$ NS					803	58	/	/	0.643	/
pDNA	West Africa	K1	<i>M. regia</i>		0.900 NS	0.832*	0.881 NS	0.869**	33	3	1.91	100.00	0.277	0.018
		K2	<i>M. excelsa</i>	0.685		0.901**	0.933*	0.916**	25	3	1.56	88.46	0.157	0.010
	Central Africa	K3	<i>M. excelsa</i>	0.696	0.716		0.075 NS	0.448 NS	75	7	2.33	15.88	0.404	0.052
		K4	<i>M. excelsa</i>	0.563	0.583	0.215		0.328 NS	31	3	2.21	10.41	0.529	0.036
		K5	<i>M. excelsa</i>	0.459	0.479	0.393	0.105		8	4	3.75	70.93	0.750	0.058
	<i>M. excelsa</i> samples (K2 to K5)				$G_{ST}=0.470$; $N_{ST}=0.817$ ***					139	12	/	/	0.868
All samples (both <i>M. excelsa</i> and <i>M. regia</i>)				$G_{ST}=0.540$; $N_{ST}=0.838$ ***					172	15	/	/	0.920	0.214
nDNA	West Africa	K1	<i>M. regia</i>		0.763**	0.646**	0.668**	0.667**	33	4	2.86	100.00	0.652	0.060
		K2	<i>M. excelsa</i>	0.378		0.264 NS	0.449 NS	0.284 NS	25	7	2.86	30.77	0.593	0.090
	Central Africa	K3	<i>M. excelsa</i>	0.276	0.201		0.067 NS	0.011 NS	75	7	4.00	10.50	0.796	0.124
		K4	<i>M. excelsa</i>	0.316	0.319	0.035		0.109 NS	31	7	3.50	20.00	0.715	0.105
		K5	<i>M. excelsa</i>	0.291	0.237	0.033	0.097		8	6	3.94	7.36	0.767	0.103
	<i>M. excelsa</i> samples (K2 to K5)				$G_{ST}=0.160$; $N_{ST}=0.220$ NS					139	12	/	/	0.855
All samples (both <i>M. excelsa</i> and <i>M. regia</i>)				$G_{ST}=0.228$; $N_{ST}=0.478$ ***					172	16	/	/	0.913	0.189

Abbreviations: A₀, number of alleles or haplotypes; H_T and V_T, gene diversity based on unordered and ordered alleles; nDNA, nuclear DNA; NS, not significant; nSSR, nuclear microsatellite; pDNA, plastid DNA; %R_{priv}, percentage of private haplotypes or alleles; R_S, haplotypic or allelic richness. In matrices of pairwise differentiation, G_{ST} (F_{ST} for nSSRs) and N_{ST} (R_{ST} for nSSRs) are given below and above the diagonals, respectively. Tests of phylogeographic signal (N_{ST} > N_{STperm} or R_{ST} > R_{STperm} for nSSRs) are indicated by NS (P > 0.05), *P < 0.05, **P < 0.001 and ***P < 0.001.

D = 0.99; Figure 4a) more closely related to *M. regia* than to Central African populations of *M. excelsa* (posterior probability support of the clade B = 0.94; Figure 4a). The nDNA phylogenetic tree does not display a *M. excelsa* clade restricted to West Africa, and although *M. excelsa* seems paraphyletic in the most likely tree (Figure 4b), there is no strong support (posterior probability of clade J < 0.50).

Molecular dating of the divergence of lineages in the genus *Milicia* was quite congruent in the two genomes used. The MRCA of *Milicia* was estimated at 31 and 32 mya (Middle Oligocene) with a wide confidence interval (12–55 mya; clades A and F; Figures 4a and b). Age should correspond to the maximum age of speciation in the genus *Milicia*. Most of the well-supported major clades within *Milicia* are dated between 16 and 24 mya (Late Oligocene to Early Miocene; clades B and E in Figure 4a, and clades G and K in Figure 4b). This includes the nDNA well-supported *M. regia* clade (K) dated at 16 mya. These results should be considered with caution as the confidence intervals were relatively wide because of the fact that we used a single calibration point provided with an important s.d.

DISCUSSION

The present work examined the pattern of genetic differentiation in the African timber tree genus *Milicia* that is threatened in several African countries because of overexploitation and habitat degradation. Our divergence date estimates showed that *Milicia* has a Tertiary origin. Despite the tenuous morphological differences between the two species classically recognized by taxonomists, all markers congruently supported the recognition of *M. regia* (forming one genetic cluster at nSSRs, and monophyletic groups at nDNA and pDNA sequences) that can be distinguished from *M. excelsa* by the absence of rounded areoles containing microscopic hairs. Differentiation within *M. excelsa* is more complex because (1) four genetic nSSR clusters were detected: one in West Africa well differentiated from three more related Central African clusters, (2) the West African pDNA clade of

M. excelsa is more related to *M. regia* than to Central African *M. excelsa* haplotypes, whereas many nDNA haplotypes are shared between West and Central Africa. Hence, West African populations of *M. excelsa* constitute a questionable group. Hereafter, we first discuss the implications of these results for species delimitation according to the species concepts, and then we question the origin of the differentiation pattern in relation to the history of African vegetation changes.

On phylogenetic relationships and interspecific mating

Under the PSC, a species must be a monophyletic group of organisms. Although DNA sequences show it is the case of *M. regia*, this does not apply for *M. excelsa*. The latter could be subdivided in two monophyletic groups according to pDNA but these groups are not supported by nDNA sequences. Hence, under strictly a PSC view, only one species could be recognized in *Milicia*, with two subspecies or varieties. Whereas phylogenetic analyses support only one species of *Milicia*, the other findings suggested a more cautious attitude. Three findings tended to confirm an important reproductive barrier between *Milicia* taxa, a key criterion for the BSC.

First, in West Africa where the two species cooccur, we detected a morphological differentiation for leaf traits. This argument could seem negligible as just leaf traits are used to distinguish the two species (see the next section of the discussion for the importance of using vegetative traits in species delimitation). We think that these slight leaf-trait differences are not insignificant in the case of *Milicia* for the following reasons. Morphological differentiation was congruent with interspecific genetic divergence. Moreover, assuming that *M. regia* leaf characters are simply signs of adaptation to evergreen forests would lead to expect such characters in Gabonese evergreen forests too, for example. This genus has likely a Tertiary origin and we should reasonably observe some individuals similar to the morphospecies *M. regia* in Central African evergreen forests.

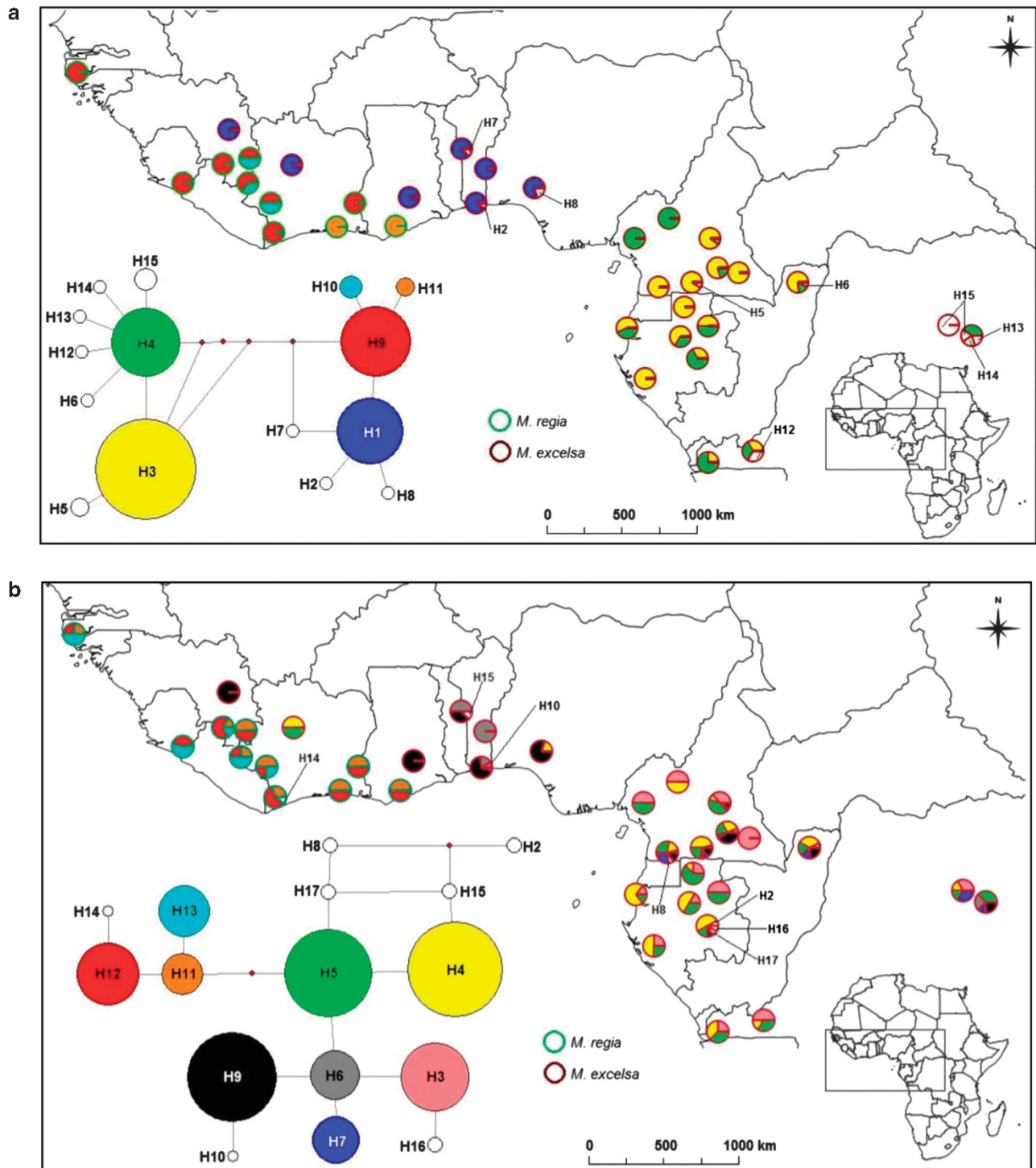


Figure 3 Geographical distribution of *psbA-trnH / trnC-ycf6* (a) and *At103* (b) haplotypes in *Milicia* and median joining networks. Repetitive sequences were included in these analyses.

That was not the case: Central African individuals in our sample, regardless of the vegetation type, had the same *M. excelsa* leaf traits as individuals from drier forest zones of West Africa (Dahomey gap).

A second argument that rejects the assumption of only one species in *Milicia* comes from the existence of mutual allelic exclusivity within this genus, in the sense of Doyle (1995) and Flot *et al.* (2010). This concept states that speciation can be assumed in paraphyletic

groups if they have no common allele (mutual exclusivity). Mutual exclusivity is reached in diverging groups generally before reciprocal allelic monophyly, and therefore it should be more suitable than monophyly for species delineation. Under that concept, we should accept two species in *Milicia* considering the cluster *K1* with respect to the others (Figure 5). Rosenberg (2003) showed that the time for a species (for example, *M. excelsa*) to become reciprocally monophyletic

Table 3 Concordance between the three types of genetic markers used and morphological identity in a subsample of 172 individuals of *Milicia excelsa* and *M. regia*

Clusters at nSSRs	Morphology-based designation		pDNA haplotypes	nDNA haplotypes
	<i>M. excelsa</i>	<i>M. regia</i>		
K1		3	H10	H11—H12—H13—H14
		2	H11	
		28	H9	
K2	23		H1	H3—H4—H5—H6—H9— H10—H15
	1		H2	
	1		H7	
K3	2		H1	H3—H4—H5—H6—H7—H8—H9
	1		H8	
	57		H3	
	11		H4	
	2		H5	
	1		H6	
K4	1		H16	H1—H3—H4—H5—H9— H16—H17
	18		H13	
	12		H3	
K5	1		H4	H3—H4—H5—H6—H7—H9
	1		H14	
	2		H15	
	4		H16	
			H4	

Abbreviations: nDNA, nuclear DNA; nSSR, nuclear microsatellite; pDNA, plastid DNA.

(99% of its loci) is $\sim 5.3N_e$ generations (N_e being the population size), assuming that its sister species is already monophyletic at all loci (for example, *M. regia*). If we assume that $N_e \approx 100\,000$ individuals (a minimum figure considering the distribution range and population densities; see, for example, Nichols *et al.*, 1998; Fétéké *et al.*, 2004) and a generation time of 100 years in *M. excelsa*, then it will take ~ 53 millions of years before monophyly would be expected at almost all loci. That estimate is much higher than the mean age of maximum divergence time in *Milicia*, so that the incomplete lineage sorting may be justified. Rejection of reciprocal monophyly for species identification is in line with the unified species concept of De Queiroz (2007) that defines hypothetical species as separately evolving metapopulation lineages, a lineage being a branch and several lineages forming a clade or a monophyletic group. From this point of view, any of the properties derived from other species concepts can be used as a line of evidence to confirm existence of different species, although it is necessary to have several lines of evidence to corroborate the hypothesis of distinct species.

Third, interspecific admixture seemed very scarce. Only four individuals presented jointly leaf characters of both species. In addition, using Bayesian approaches for identifying hybrid individuals as implemented in STRUCTURE (Pritchard *et al.*, 2000), TESS (Chen *et al.*, 2007) and NEWHYBRIDS (Anderson and Thompson, 2002), we found only three to six putative hybrids among 46 individuals sampled in the interspecific contact zone, from Guinea-Conakry to Ghana (K Dainou, unpublished results). However, this low hybrid proportion (6.5–13%) may be biased because the best hybrid zone for *Milicia* species should be located in the semi-deciduous forest region

of Ivory Coast and Ghana that was not sampled enough for the present study. Clearly, additional investigations are required to assess contemporaneous hybridization patterns in *Milicia* populations.

On the importance of morphological characters for species delimitation

Despite the limited number of distinctive characters in *Milicia*, it is worth remembering that scarcity of morphological differences does not mean absence of speciation. Of the animal studies, 23% revealed parphyly or polyphyly, suggesting a much common phenomenon than generally assumed (Funk and Omland, 2003). Investigating monophyly and species boundaries in higher plants is less common because of a more limited number of related studies and fewer attempts to combine morphological and genetic characterizations.

There are very few morphological characters that delimit *M. excelsa* from *M. regia*. Past assessment by taxonomists of the existence of two species on the basis of a few vegetative characters may look surprising. The evolution of vegetative characters is often thought to be related to adaptation to the growth environment, so that these characters are viewed as less reliable than floral traits for systematic studies (Ingrouille and Chase, 2004; Das *et al.*, 2007). However, floral traits may be less commonly used than assumed. Grant (1949) observed among 416 genera that although differences in floral traits were employed for classifying 37–40% of bird-, bee- and fly-pollinated plants, this proportion drops up to 4% for wind- and water-pollinated taxa. Plant species with generalist pollination systems are less subject to strong directional selection of floral traits (Johnson and Steiner, 2000), which may explain the absence of floral differentiation in *Milicia* species. In addition, Berg's 'correlation pleiades hypothesis' has received notable support from various studies (see, for example, Armbruster *et al.*, 1999; Meng *et al.*, 2008). This hypothesis predicted a stronger relationship between floral and vegetative traits in wind-pollinated and generalized flowers than in specialized flowers, because selective pressures affect jointly both categories of characters in the former (covariation is expected as flower components derived from leaves) whereas they are decoupled in the latter (in order to preserve the flower-pollinator fit, regardless of the environment characteristics). Thus, referring exclusively to vegetative traits for species delimitation in *Milicia*, a wind-pollinated genus, is quite justified.

Phylogeographical structuring: potential paleoenvironment influences

Diversification in gene genealogy can occur in a stable population, independently of environmental perturbations. However, time of coalescence is readily affected by fluctuating population sizes, natural selection and immigration (Freeland *et al.*, 2011).

Zerega *et al.* (2005) tracked back the biogeographical history and migration routes of most of genera known for Moraceae. They showed that Moraceae may have originated in Eurasia during the Mid-Cretaceous. The two collisions of the landmasses formed by Africa and India with Eurasia at ~ 60 and ~ 45 mya have created colonization routes for at least four tribes, including Moreae. That period coincided with the first main diversification phase of West African flora, from the Palaeocene to the Mid-Eocene (65–46 mya; Jacobs, 2004; Plana, 2004). All the northern part of the continent including the Sahara was covered by a mosaic of savannahs and forests. This period may be likely the timing of arrival of *Milicia* ancestor on the continent.

It is interesting to note that the mean ages of the two first divergence events in *Milicia* took place at the two first major environmental disturbances reported for the continent, after

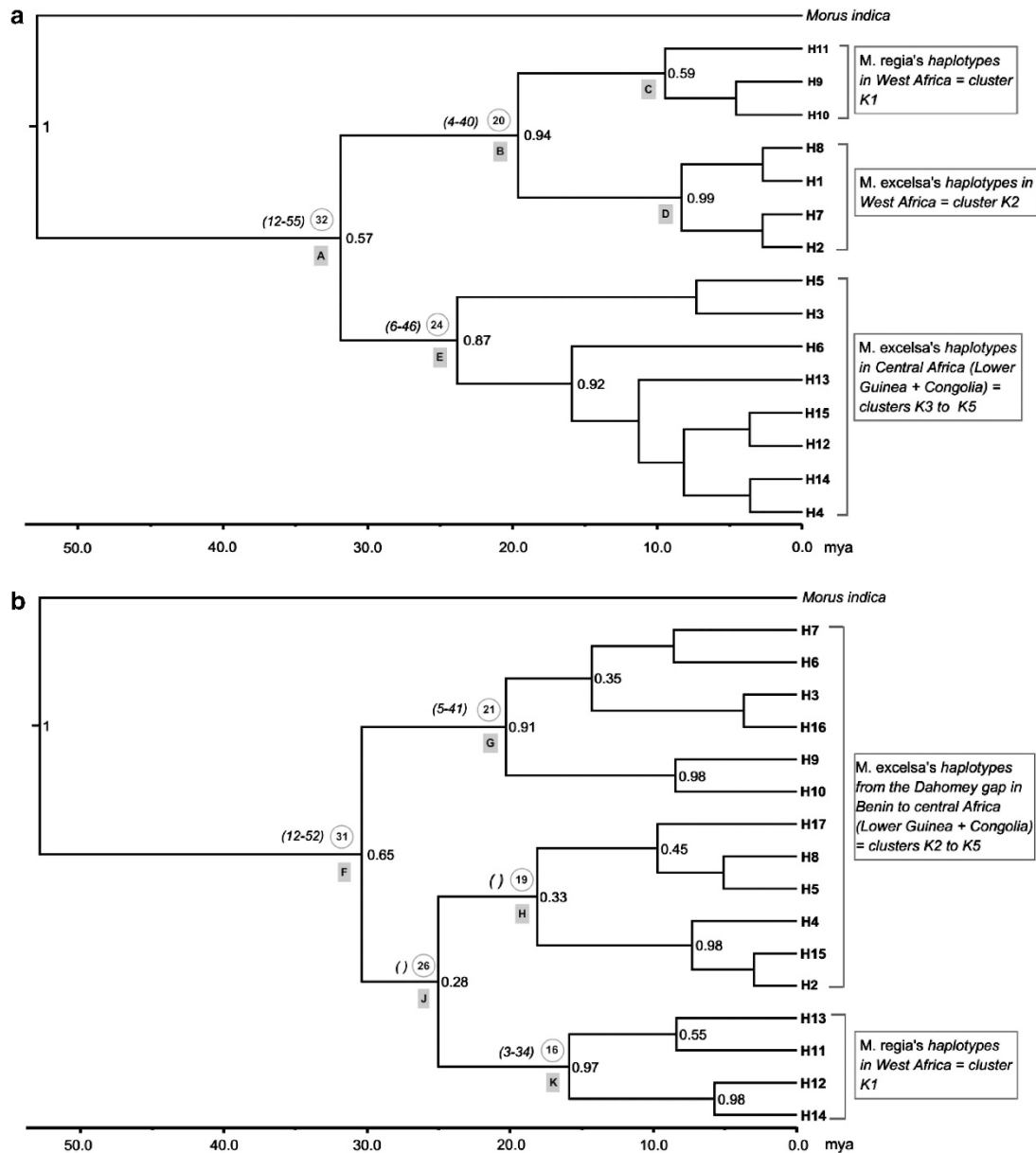


Figure 4 Phylogenetic trees in *Milicia* based on (a) pDNA (*psbA-trnH* and *trnC-ycf6* intergenic regions) and (b) nDNA (*At103* intron) regions. The tree root height was constrained with the age of the MRCA of *Milicia* and *Morus*: mean of 56 mya and s.d. of 9 mya (in millions of years ago (mya)) (Zerega *et al.*, 2005). Numbers at the right part of nodes are posterior probabilities (≤ 1). The scale bar at the bottom of each figure indicates time period. The estimated mean ages of selected clades are provided in circles along with their 95% highest posterior density (HPD) interval in brackets (empty brackets: no available HPD information as posterior probability was ≤ 0.50). Letters A to K are names used in the text for selected nodes.

establishment of West African flora at the Mid-Eocene. The start of speciation in *Milicia* was estimated at ~ 31 – 32 mya (mean ages of nodes A and F; Figure 4) that coincided with a sharp cooling period at the Late Eocene to the Early Oligocene (35–31 mya), leading to a major extinction in the hygrophilous African flora (Maley, 1996; Plana, 2004). The second major environmental perturbation occurred from the Early to the Mid-Miocene (23–15 mya): humid vegetation disappeared in the Sahara, the continent moved northwards, down positioning the Equator. The rainforest belt shifted southwards, and the Tethys Sea was closed (Maley, 1996; Jacobs, 2004). The highly supported nodes E, B, G and K in Figure 4 had mean ages included in that range. Obviously, these correlations are just hypotheses as our estimates of divergence times were not accurate enough.

At a regional scale, three clusters were detected in Central Africa. Unlike West Africa, there was no phylogeographical structure at any type of marker in Central Africa. In addition, the degree of differentiation is far lower within Central African clusters comparatively to values noted in West Africa or between West African clusters and those of Central Africa. Dainou *et al.* (2010) proposed that genetic clusters within Lower Guinea diverged more than 100 000 years ago, possibly during the ice age period lying from 160 000 to 130 000 years ago (Maley, 1996). The spatial organization of *M. excelsa* clusters in central Africa may result from the past forest fragmentation, possibly at ice ages. Clusters K3 and K4 centered on Cameroon and Gabon, respectively, may be expansions of the Atlantic coastal refuge zones that stretched from the southwestern part of

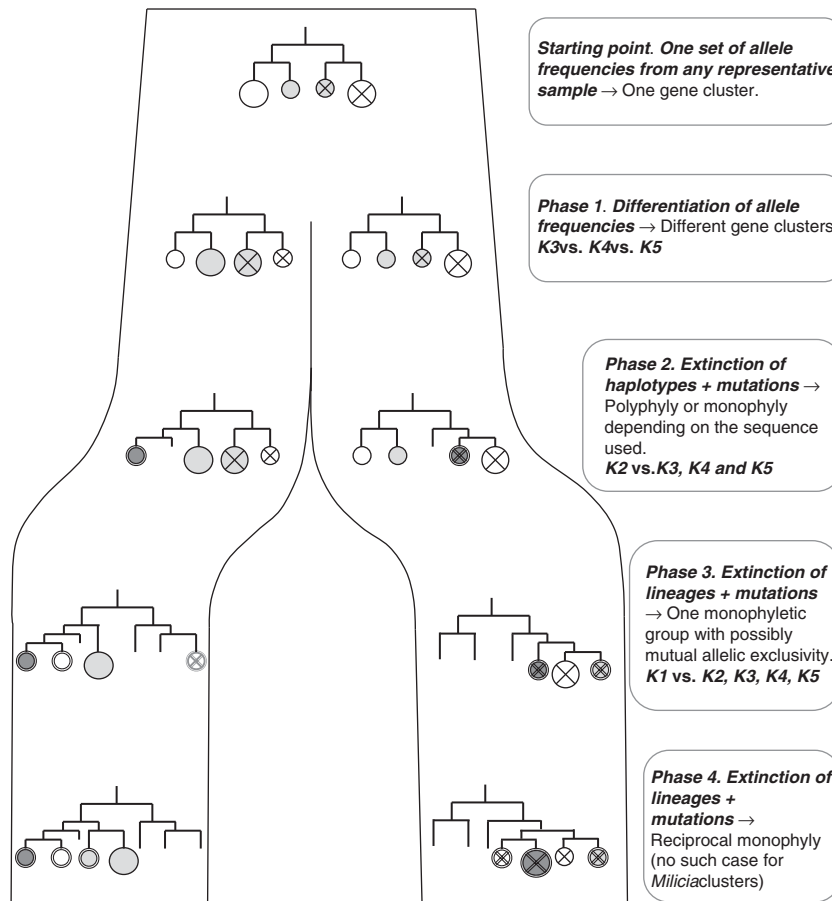


Figure 5 A schematic representation of lineage divergence and speciation that reflects the case of *Milicia*. The circles with cross inside represent a lineage, whereas the empty circles stand for another one. Different gray colors indicate different haplotypes within each lineage and circles are sized according to their relative frequency. Each *Milicia* cluster (*K1* to *K5*) is mentioned nearby the divergence phase it reaches with respect to the others. From the starting point to phase 1, the two diverging groups inherit the polymorphism of their ancestor and are distinguishable just by allele frequencies. $F_{ST}=0.1$ is obtained after $\sim Ne/5$ in the absence of homoplasy, Ne being the effective population size. If effective sizes are enough large, mutation will exert more influence than genetic drift on the time to reach phase 2. At this step, some sequences can reveal a monophyletic group, whereas others may show polyphyly. That is the case of the cluster *K2* with respect to *K3*, *K4* and *K5*. Much later, complete extinctions of lineages may occur leading, for example, to one clear monophyletic group and possibly mutual allelic exclusivity (phase 3): this is observed in *K1* with respect to the other genetic clusters. Reciprocal monophyly is reached at a later phase (phase 4), after $\sim 5Ne$ generations (Rosenberg, 2003): no pair of *Milicia* clusters displays such a situation.

Nigeria to the South of Democratic Republic of the Congo. The North–South divide nearby the Equator between these two clusters has been documented for other forest tree species (Duminil *et al.*, 2010; Debout *et al.*, 2011) and a significant floristic shift has recently been demonstrated at that latitude (Gonmadje, 2012). Cluster *K5* centered on the Democratic Republic of the Congo may represent populations spreading from inland forest refuges surrounding the Congo River. The larger extent of *K3* and *K5* comparatively to the Gabonese cluster *K4* may be related to the fact that they are located on more suitable zones for *M. excelsa* population dynamics (semi-deciduous forests).

In West Africa, making such link between genetic clusters and refuges is possible if we refer to the map in Anhuf *et al.* (2006) rather than the one proposed by Maley (1996). These authors diverged substantially in mapping the closest forest refuge of the East of the Dahomey gap. According to Maley (1996), a small, well-delimited refuge was established at the southern frontier of Ivory Coast and Ghana, whereas that refuge should have extended up to the extreme eastern boundaries of Ghana, thus partially located in the Dahomey

gap. Under the latter scenario, cluster *K2* could have extensively been developed eastwards from that refuge. However, phylogeographical signals within West African clusters denoted older isolations than those observed in Central Africa. Then, we should assume that the same places have acted as forest refuges since at least the Late Oligocene-Miocene after tropical forests were established on the continent (Jacobs, 2004; Plana, 2004). There is no proof of such an assumption for that period in West Africa, but elsewhere in East Africa the role of upland areas as refuges many millions years ago was demonstrated (Yemane *et al.*, 1987).

As *Milicia* populations in West Africa experienced severe exploitation pressures during past centuries, the lower degree of haplotypic richness in this region may be caused by rapid decrease of population density. The higher degree of allelic/haplotypic endemism in West Africa argues for the hypothesis assuming that West African flora may be substantially older than Central African vegetation (suggested in Vande Weghe (2003) and Jacobs (2004)). In the only two other genetic studies of rainforest tree species (*Irvingia gabonensis* and *Terminalia superba*) that have included both West and Central African

populations, diversity measures also showed that populations from the western African zones exhibit higher genetic diversity than those of the Lower Guinea and the Congolia (Vigneron, 1984; Lowe *et al.*, 2010). A phylogeographical study of *Khaya senegalensis*, a dry-forest tree species, also revealed that West African groups display higher levels of genetic diversity than those from Sudan and Uganda (Karan *et al.*, 2012).

CONCLUSIONS

The present study investigated the pattern of genetic differentiation in *Milicia*, based on nuclear microsatellites, plastid and nuclear sequences. Five genetic clusters were identified and their origin could be linked to past environmental disturbances. *Milicia* is a Tertiary genus with two cryptic species exhibiting incomplete lineage sorting. Existence of paraphyly in *Milicia* can be explained by the time required for isolated species to become reciprocally monophyletic, and this depends on effective population size and generation time that are likely very high in *Milicia* species. Mutual allelic exclusivity was observed and this tends to confirm the recognition of two species in that genus, despite very scarce morphological differences. Interspecific hybridization looks scarce at present, but this pattern requires further investigations.

DATA ARCHIVING

The *trnC-ycf6* and *psbA-trnH* plastid DNA sequences have been deposited in GenBank under the accession numbers KF719985–KF720330. The *At103* nuclear DNA sequences are available in GenBank under the accession numbers KJ129036–KJ129052. Nuclear microsatellites data have been deposited in DRYAD at <http://datadryad.org/resource/doi:10.5061/dryad.77j02>.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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