

# SPECIES DELIMITATION AND DIVERSIFICATION IN THE WIDESPREAD AFRICAN TREE GENUS, *MILICIA* (MORACEAE)

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## Why *Milicia*?

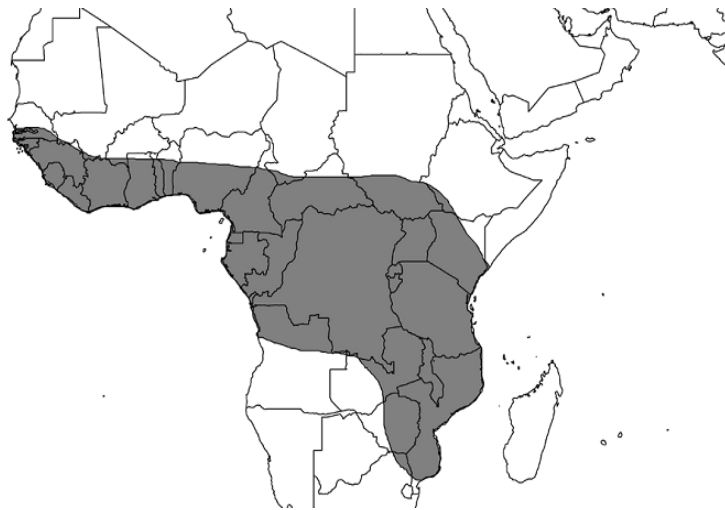
- An overexploited timber tree
- Endangered in several countries
- Lack of ecological information for specific management plans
- Wind-pollinated
- Animal seed-dispersed





*Two species have been described although botanists have questioned that statement*

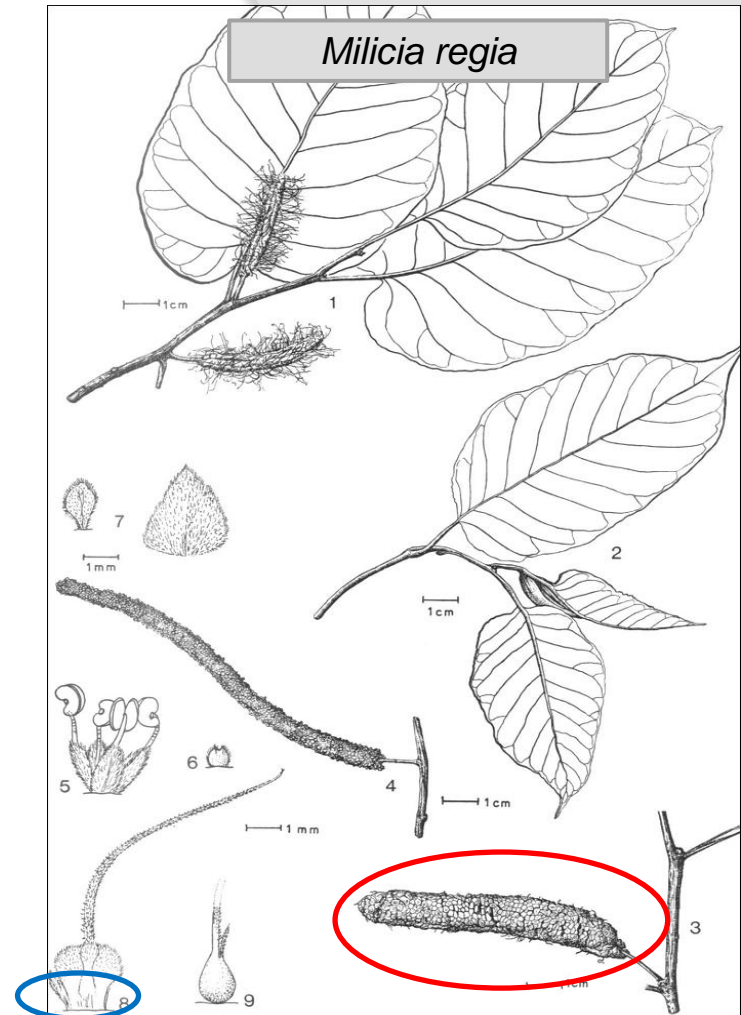
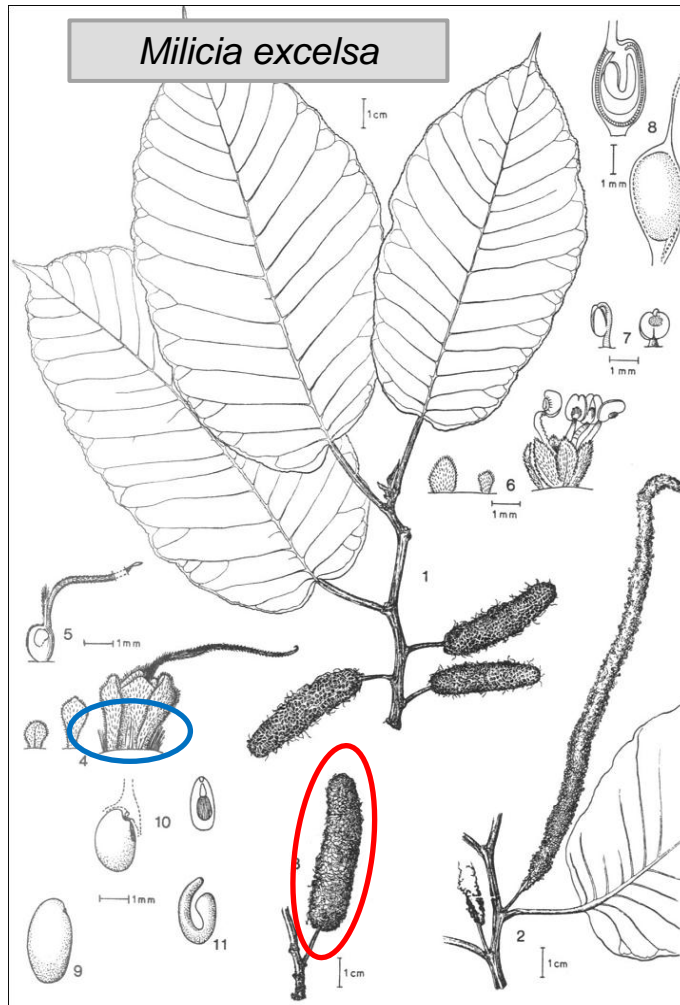
1. *Milicia regia*: potentially more adapted to West African evergreen forests.  
« **Vulnerable** » (IUCN redlist)
2. *Milicia excelsa*: widespread with higher population densities in semi-deciduous forests



*M. excelsa*

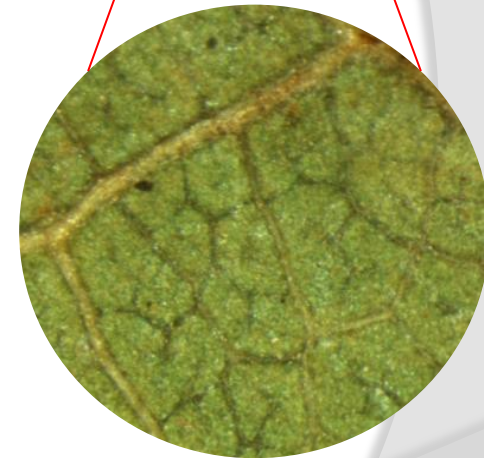
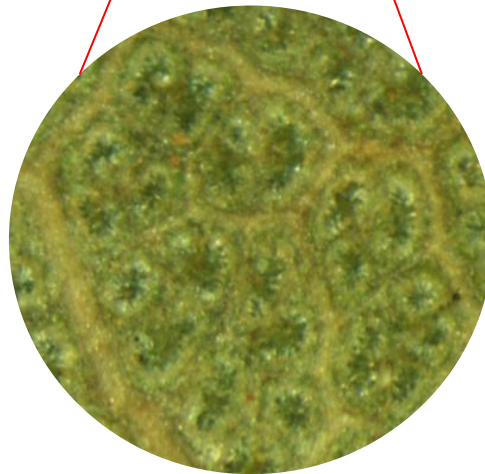


*M. regia*

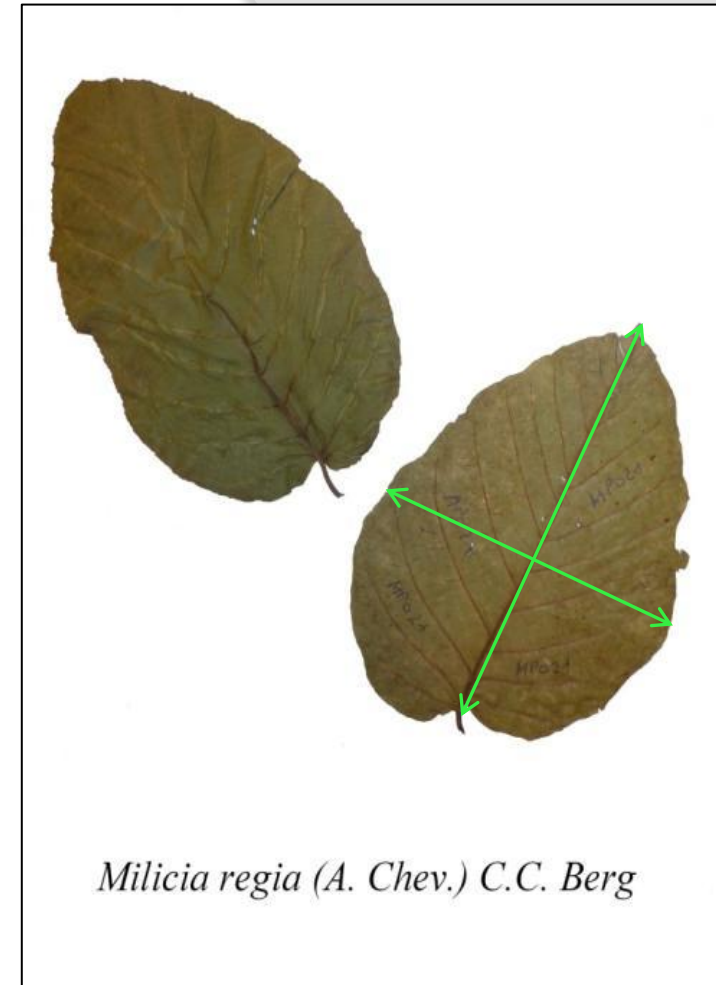


Possibly differences in two reproductive traits (?)

Reproductive periods are the same for both morphospecies



Lower surface of leaf is soft in only *M. excelsa*

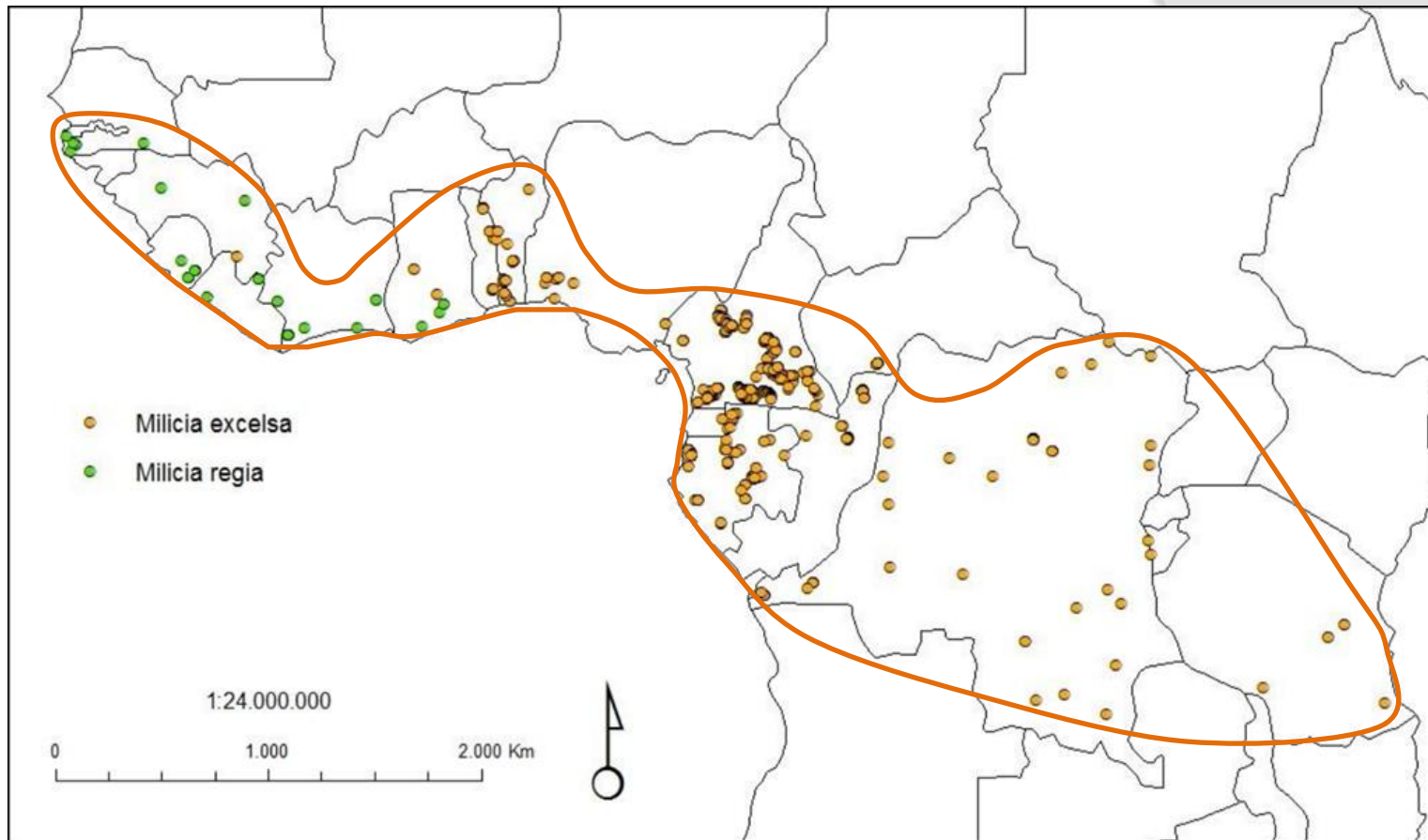


- Number of secondary veins
- Ratio « length / width »
- Distance between two contiguous veins



1. Are the qualitative and quantitative traits congruent to distinguish two morphological units?
2. What is the degree of congruence between morphological- and genetic-based species delimitation?
3. Is there any evidence of contemporaneous hybridization?
4. Finally, what is the evolutionary history of this genus?

Sampling more than 1,000 individuals over the range of *Milicia*

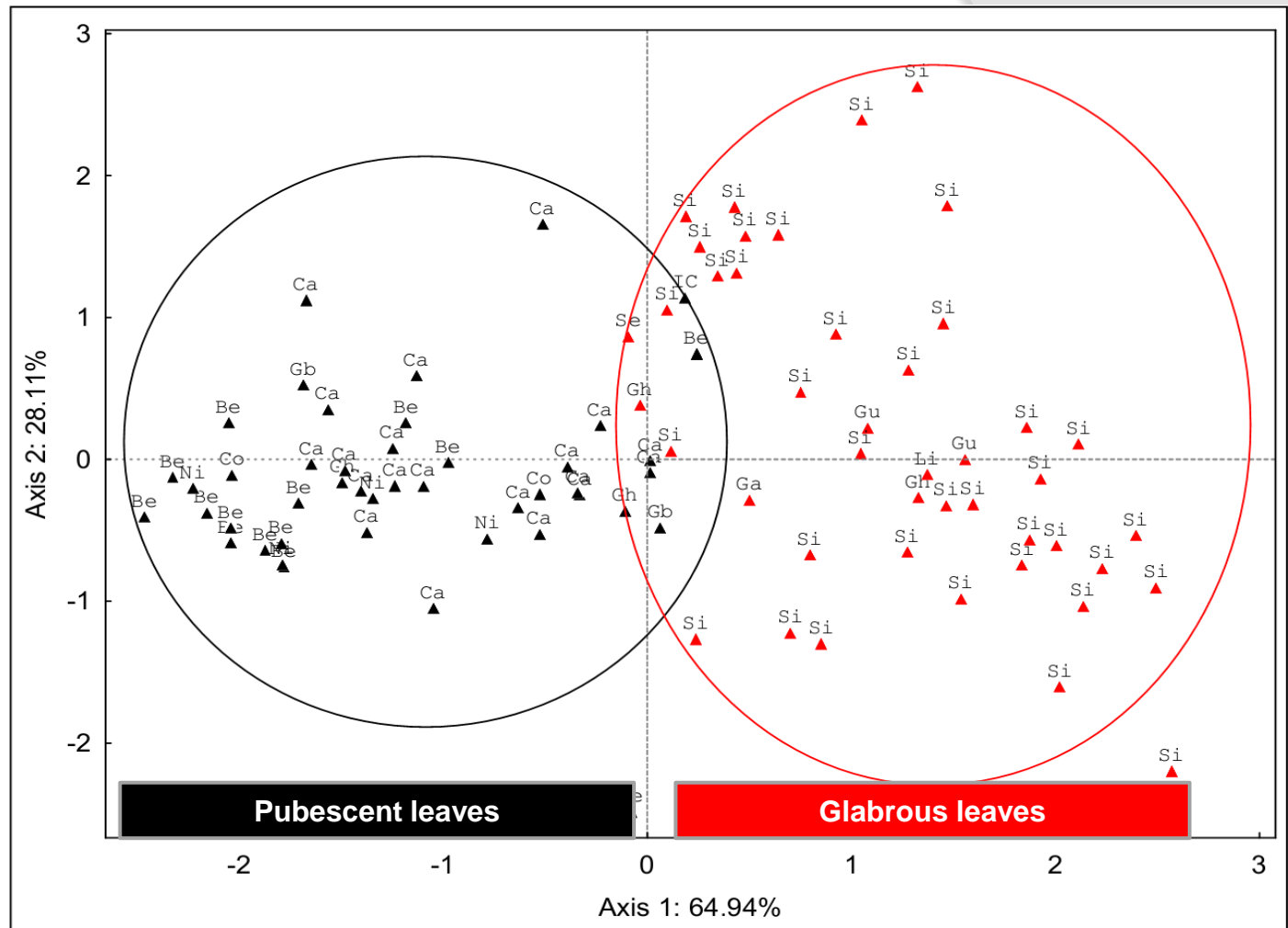




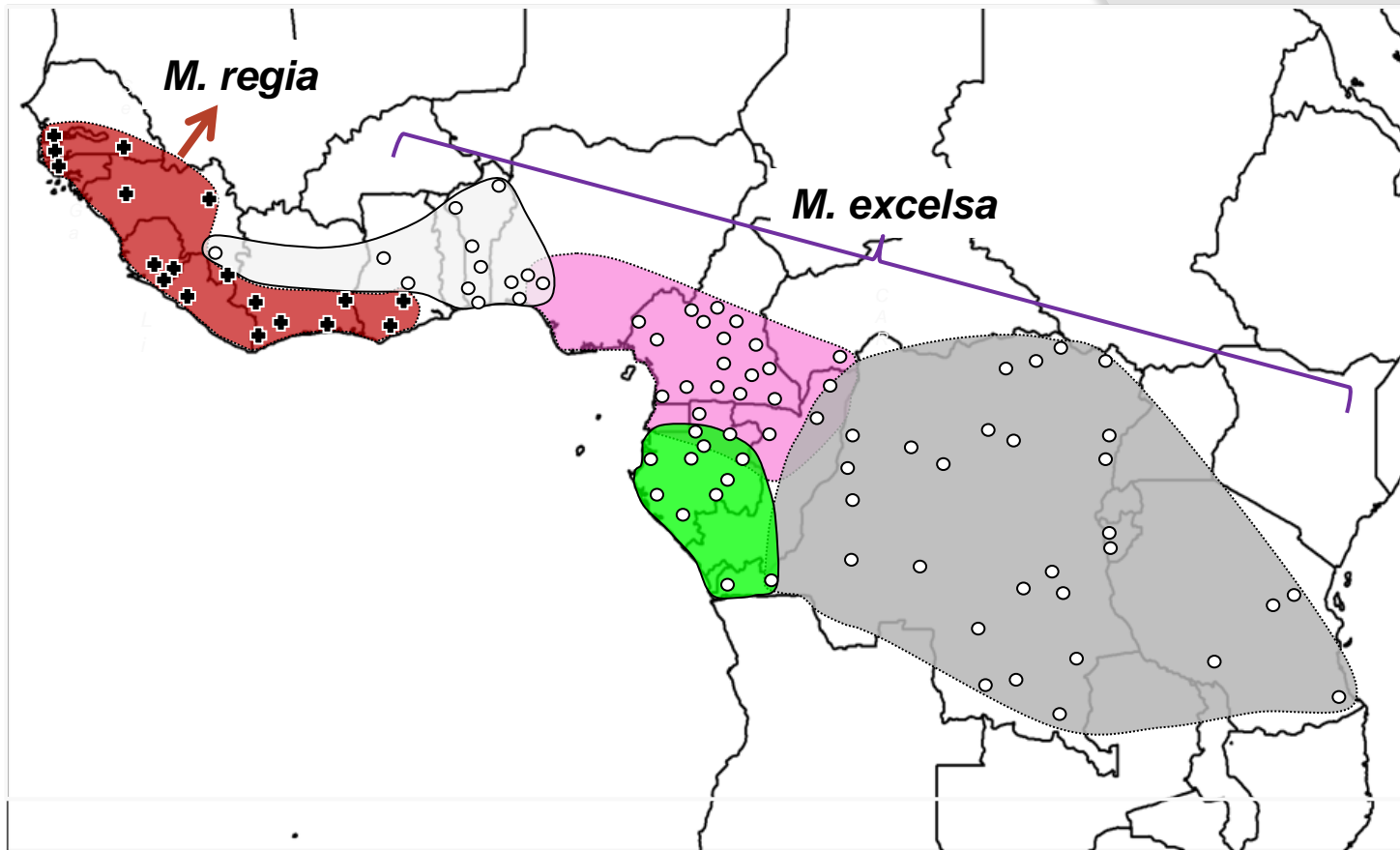


Investigation	Methods	Sub-sample used (individuals)
<i>Morphological characterization</i>	Analysis of leaf traits (PCA)	114
<i>Identification of genetic clusters</i>	7 nuclear SSR markers	850
<i>Phylogenetic reconstruction</i>	1 nuclear gene, <i>At103</i>	172
	2 plastid sequences, <i>trnC-ycf6</i> and <i>psbA-trnH</i>	
<i>Dating of divergence times</i>	Based on both nDNA and pDNA	172

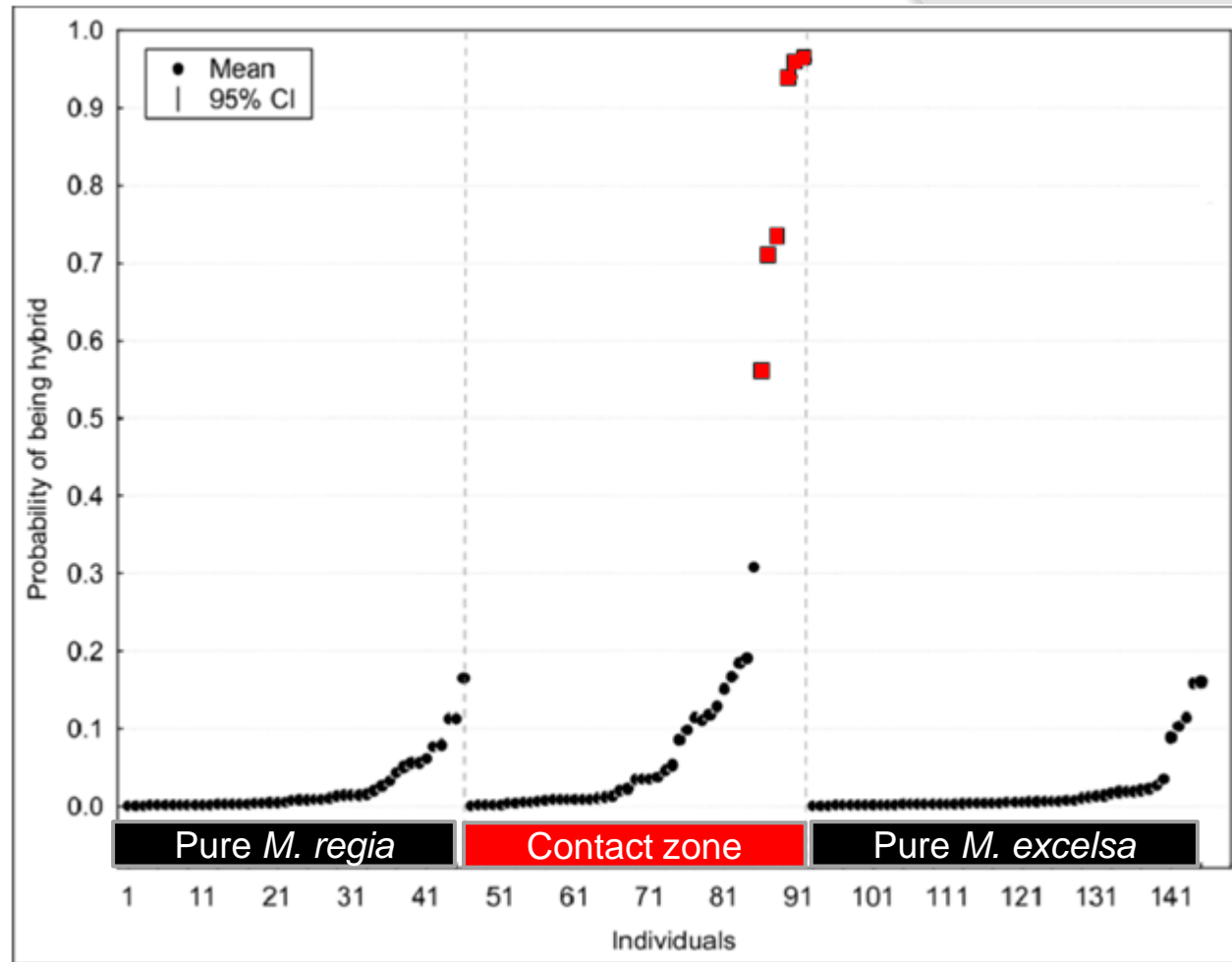
## PCA results based on the 3 quantitative leaf traits



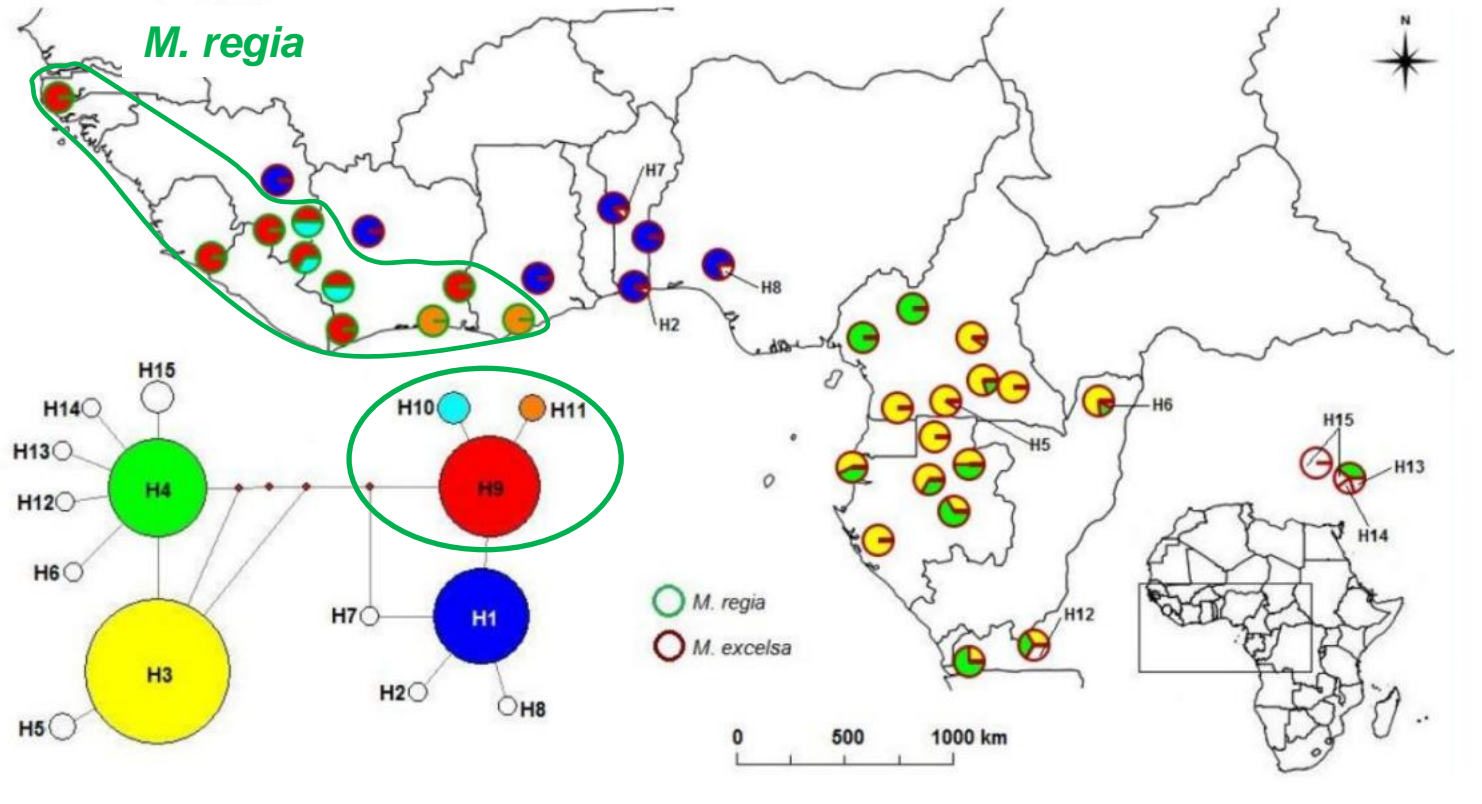
Good congruence between the quantitative and qualitative leaf characters



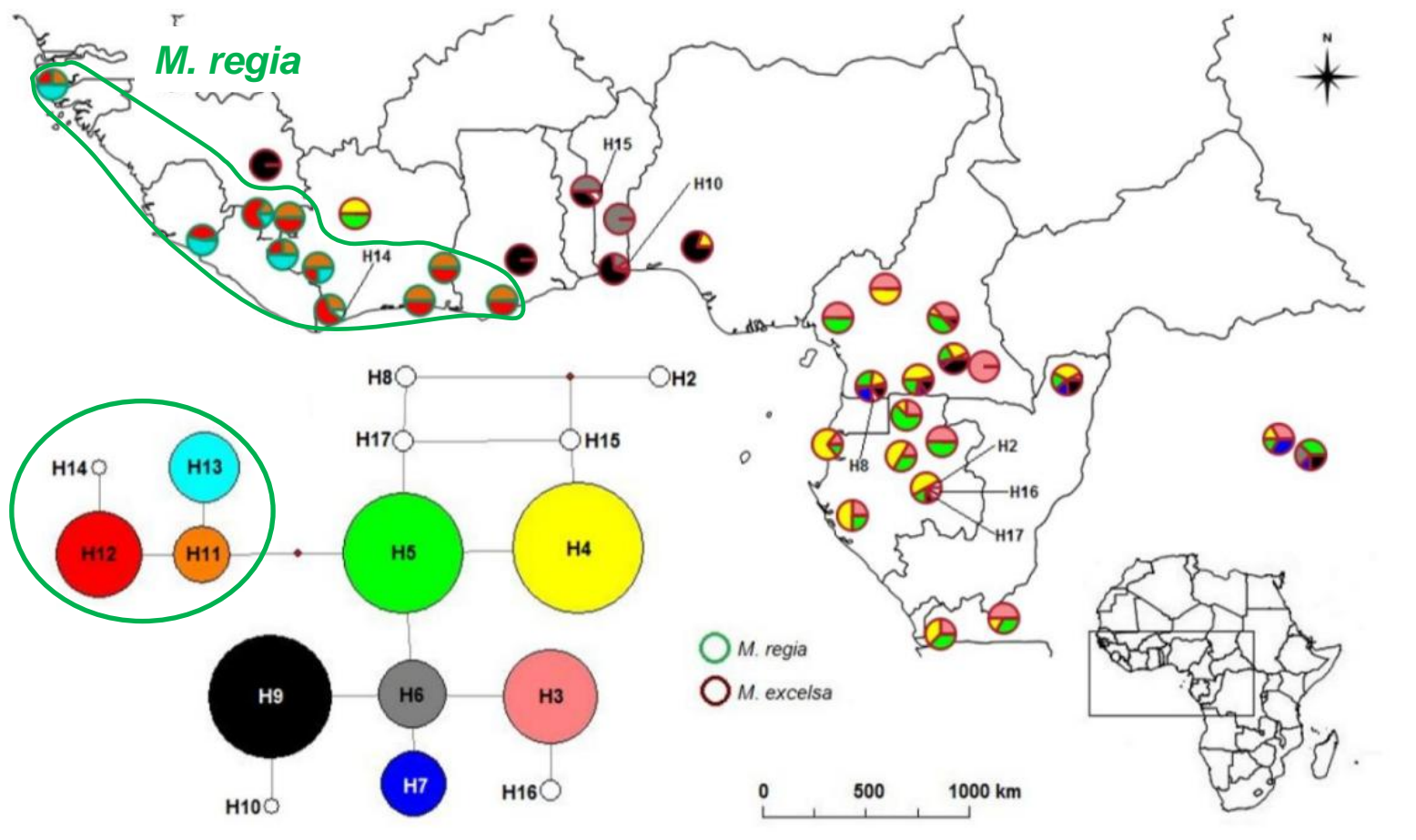
5 genetic clusters were detected, with a perfect separation of individuals of the two morpho-species (TESS, Chen *et al.* 2007)



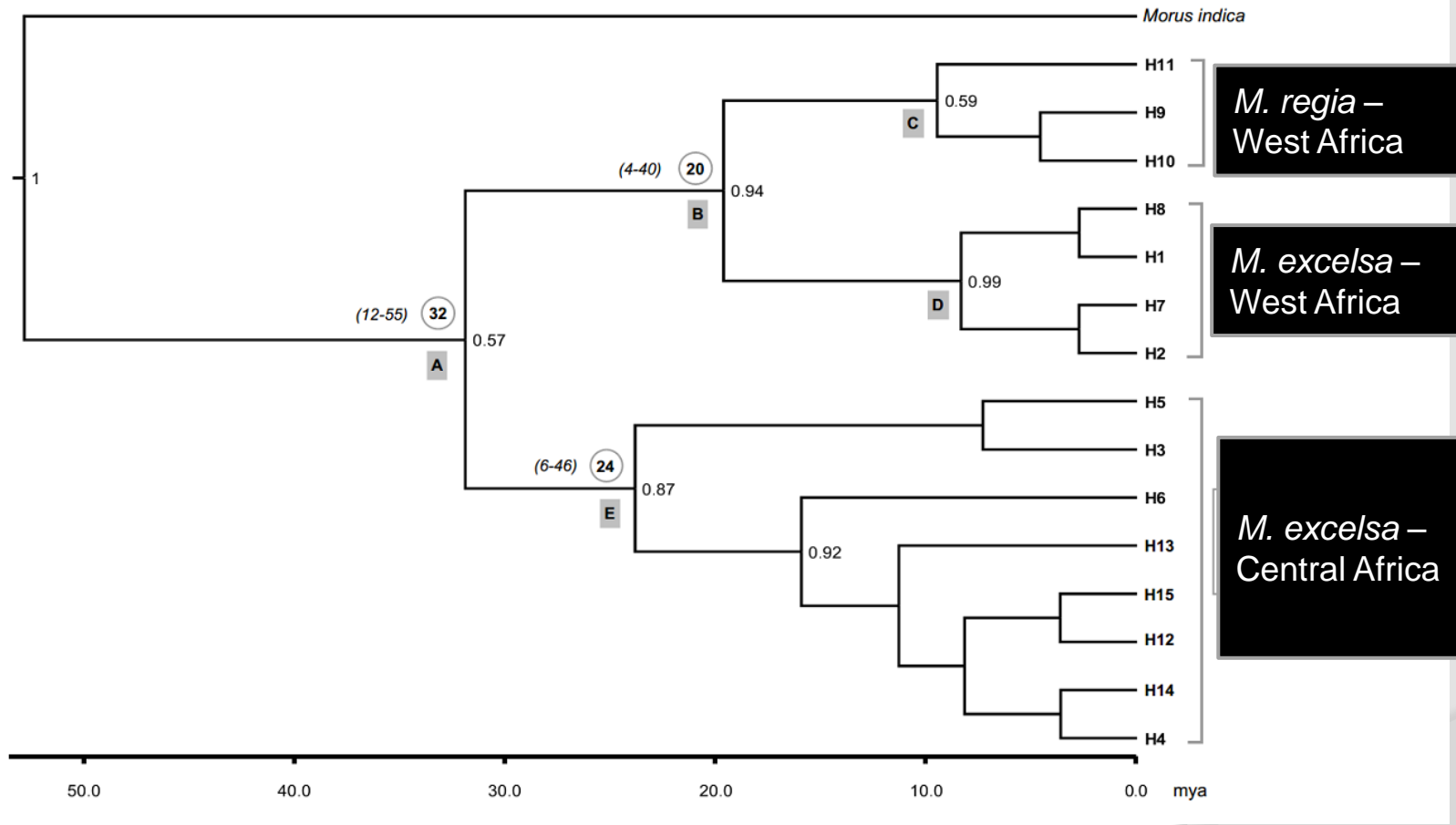
Other Bayesian algorithms confirmed scarcity of interspecific hybrids in the contact zone: 6 to 12% (STRUCTURE, Pritchard *et al.* 2000; NEWHYBRIDS, Anderson & Thompson 2002)



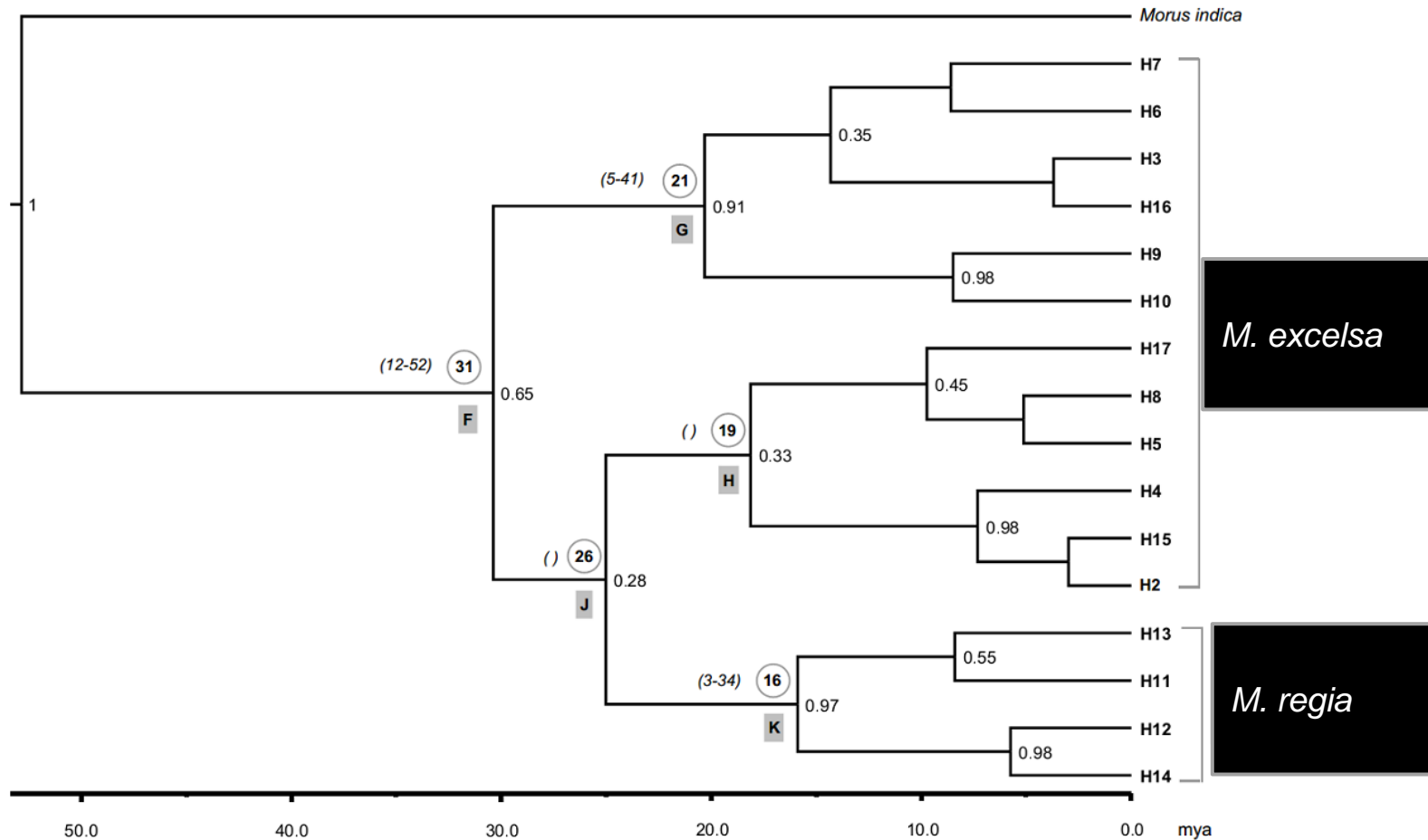
Median joining network from the pDNA sequences (NETWORK, Bandelt *et al.* 1999)



Median joining network from the nDNA sequences (NETWORK, Bandelt *et al.* 1999)



pDNA tree and divergence times (BEAST, Drummond and Rambaut 2007)



nDNA tree and divergence times (BEAST, Drummond and Rambaut 2007) : *M. regia* is monophyletic but not *M. excelsa*





Clusters at nuSSRs	Morphological-based designation		cpDNA haplotypes	nuDNA 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		H4	
K5	1		H14	H3 – H4 – H5 – H6 – H7 – H9
	1		H15	
	2		H16	
	4		H4	



## Thus...

- *Milicia* has a Tertiary origin
- According to the BSC, two species may be confirmed
- According to the PSC, we could suggest one species... but
  - There is « haplotype exclusivity » (Doyle 1995 and Flot *et al.* 2010)
  - Time to become reciprocally monophyletic is  $\approx 5.3 N$  generations (Rosenberg 2003)
    - If  $N = 100,000$  and generation time = 100 years, it would take about 53 millions of years before reciprocal monophyly
  - Paraphyly is much more common than assumed (e.g., 23% of animal taxa are paraphyletic; Funk & Omland 2003)

**Lack of reciprocal monophyly between reproductively isolated species may be common in long-lived plants that display large effective population sizes**

*Thanks for your attention*

