

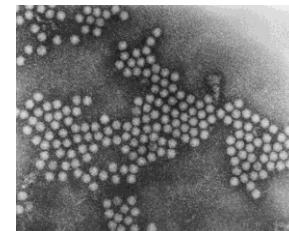
Genotypic diversity of the aphids from the *Melanaphis sacchari* group

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Pest status of *Melanaphis sacchari*

- *Melanaphis sacchari* is one of the vectors of the Sugarcane Yellow leaf disease (Schenk & Lehrer 2000)
 - Causal agent = the Sugarcane yellow leaf virus (SCYLV), Luteoviridae family, Polerovirus genus
 - in Reunion (Rassaby et al. 2003, 2004)
 - Field transmission -> 25% incidence in 4 months after planting of virus-free plants -> more than 40% in R1
 - Field survey: 98% incidence on R575, 16-94% on R570, 21-92% on R579
 - Up to 37% yield loss on susceptible cultivar (R575), 0% on tolerant cv. (R570)
- *Ms* is also a major pest of sorghum -> direct damages (Singh et al. 2004)



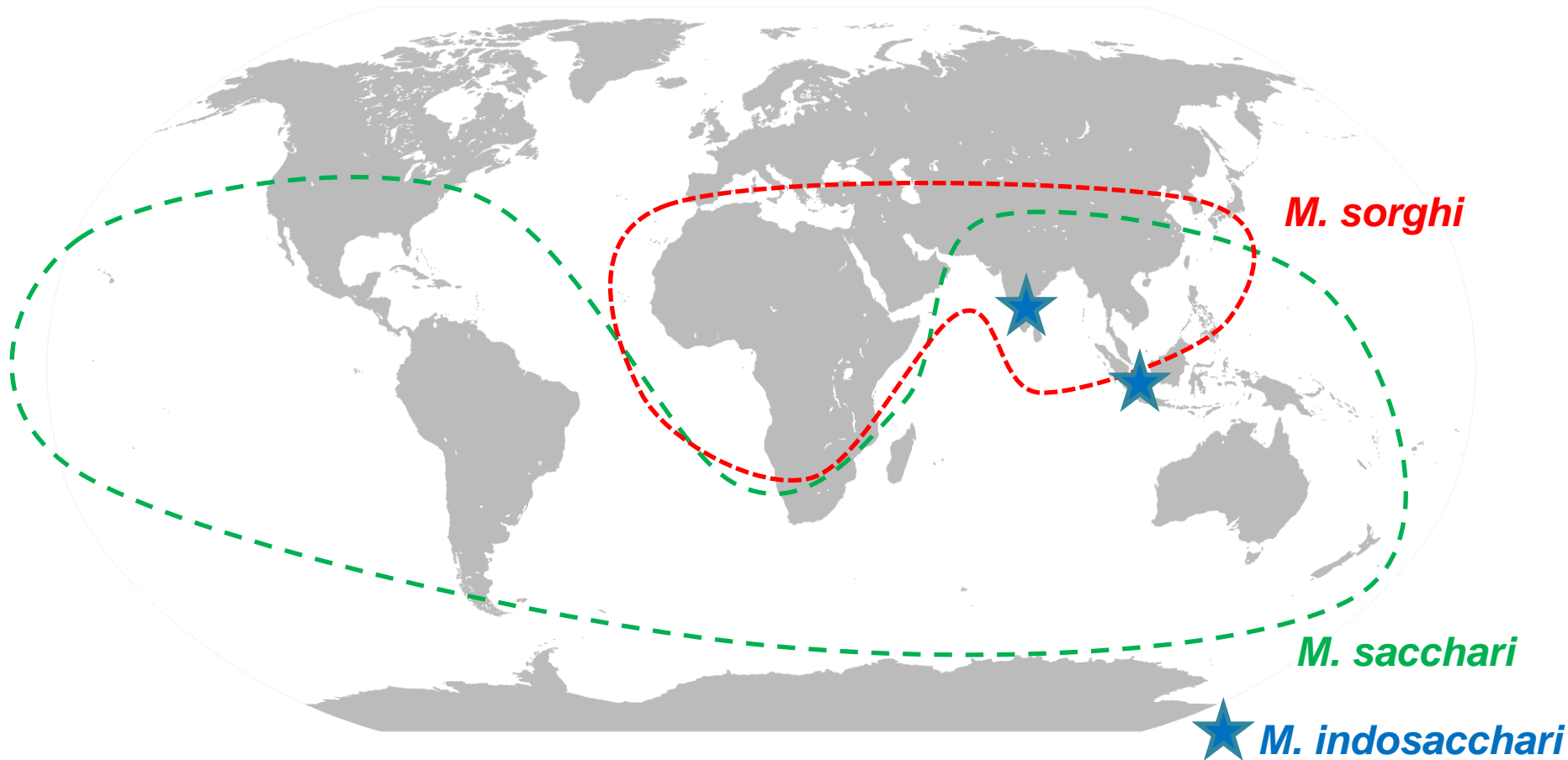
Melanaphis spp.

- Homoptera, Aphididae, Aphidinae, Aphidini, Rhopalosiphina
- Around 20 species, most of them from Asia
- 3 species on sugarcane (Blackman & Eastop, 2006)
 - *M. sacchari* (Zehnter)
 - *M. sorghi* (Theobald)
 - *M. indosacchari* (David)
- *sacchari* and *sorghi* also present on sorghum
- Mainly anholocyclic (clonal reproduction), but holocycle signaled in East Asia



(A. Frank)

Distribution



(from Blackman & Eastop, 2006)

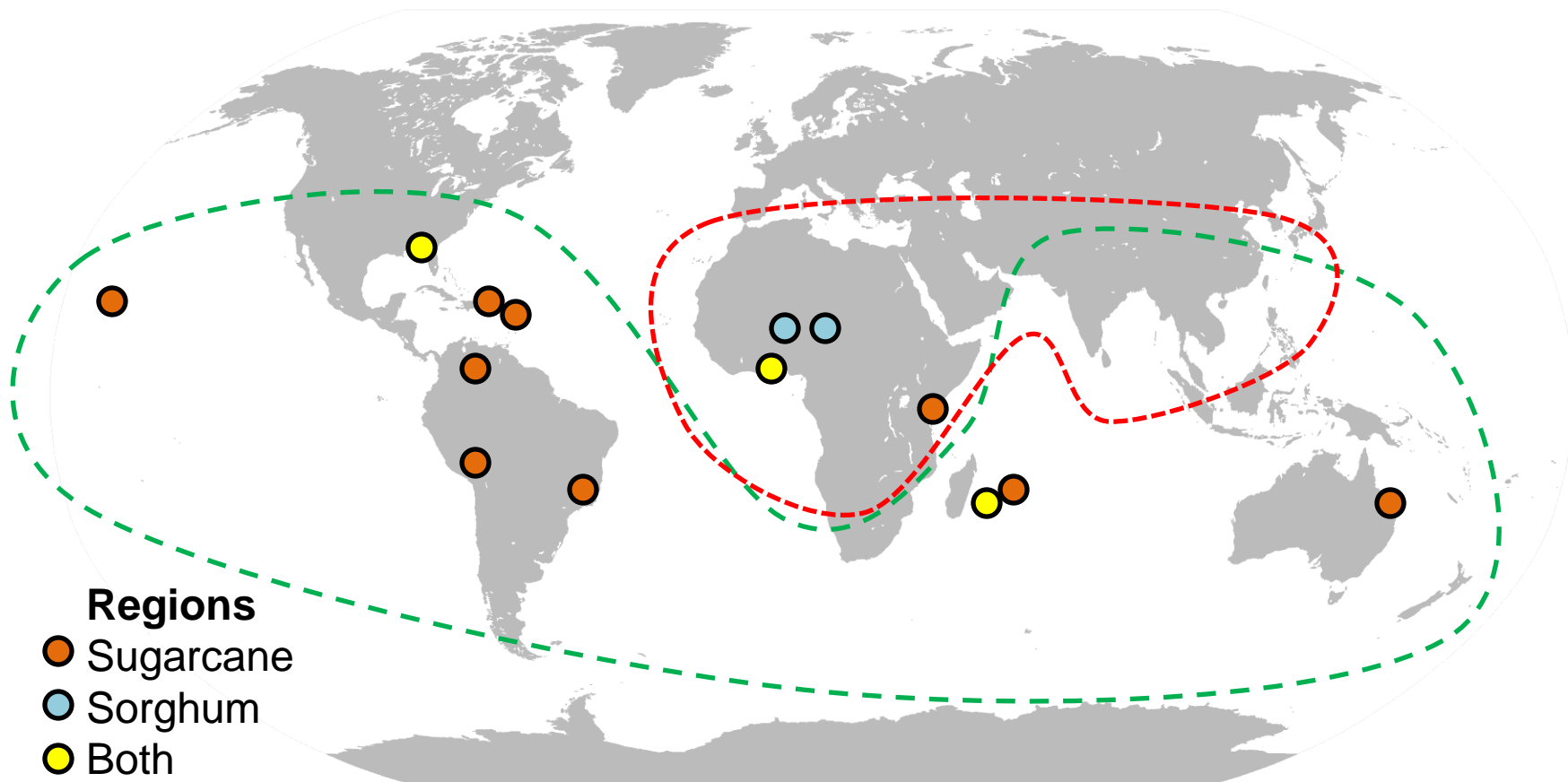
Objectives

- Genetic diversity of aphids may influence
 - Varietal resistance:
 - Specificity of plant R gene – aphid interaction (Dogimont et al. 2010)
 - Virus epidemiology
 - Genetic variability of the ability to virus transmission (Burrows et al. 2006)
- Objectives :
 - Clarify the taxonomic status of the two main forms *sorghii* and *saccharii*
 - Evaluation of the worldwide genetic diversity and structuring of populations

Methods

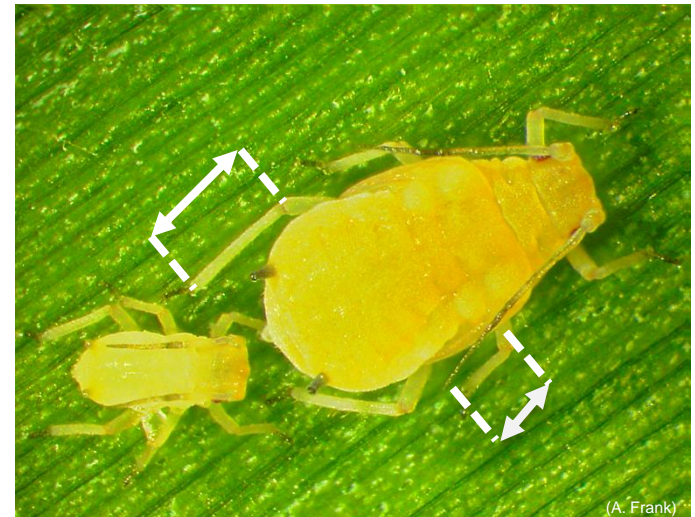
- 52 samples from 42 localities from 14 regions
 - 1,288 individuals

Distribution of samples



Methods

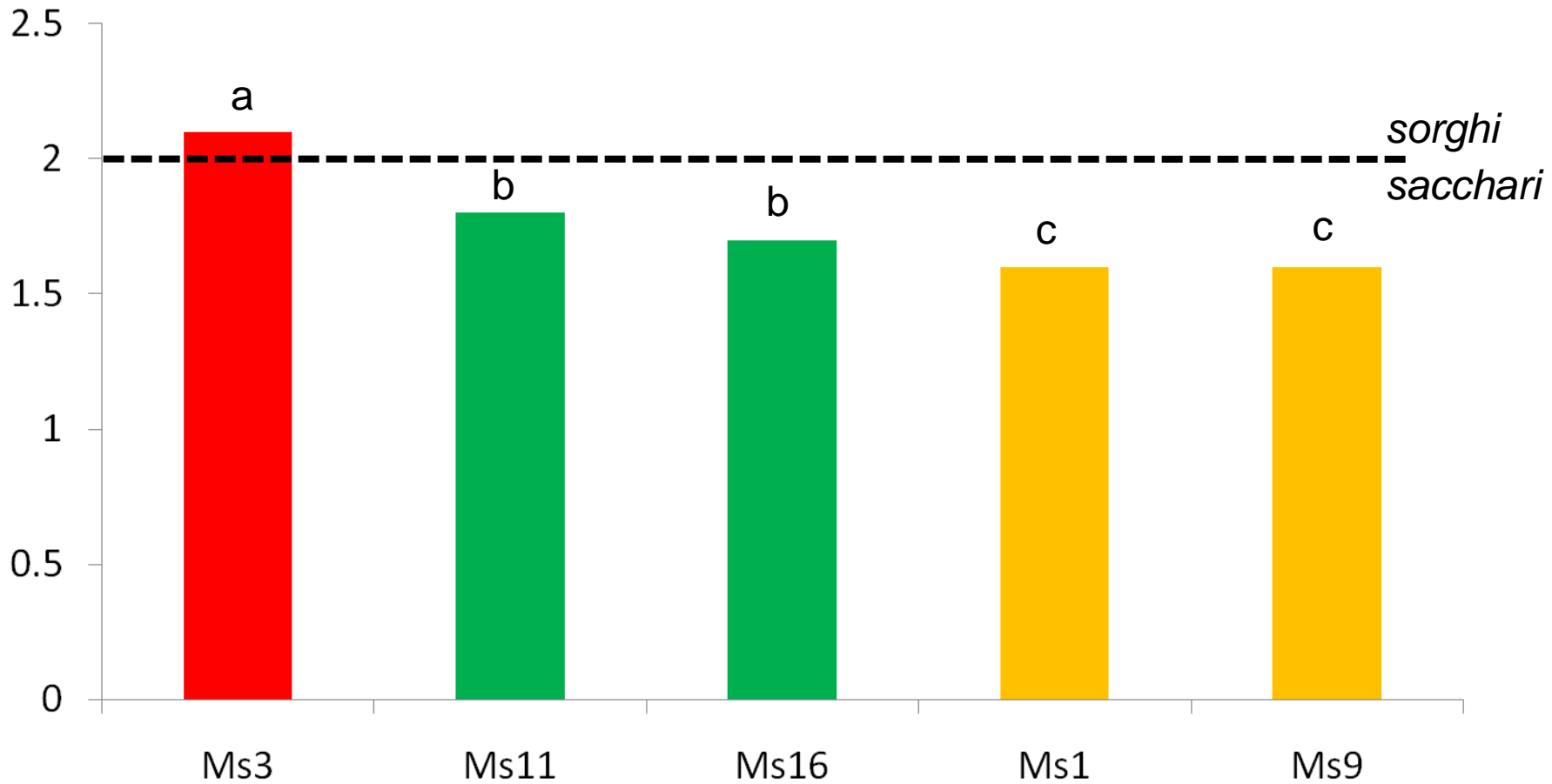
- 52 samples from 42 localities from 14 regions
 - 1,288 individuals
- Taxonomy
 - Morphometric study
 - Length of antennal terminal process vs. length of hind tibia (Blackman & Eastop 2006 key)
 - 211 individuals
 - CO1 sequence
 - 33 individuals



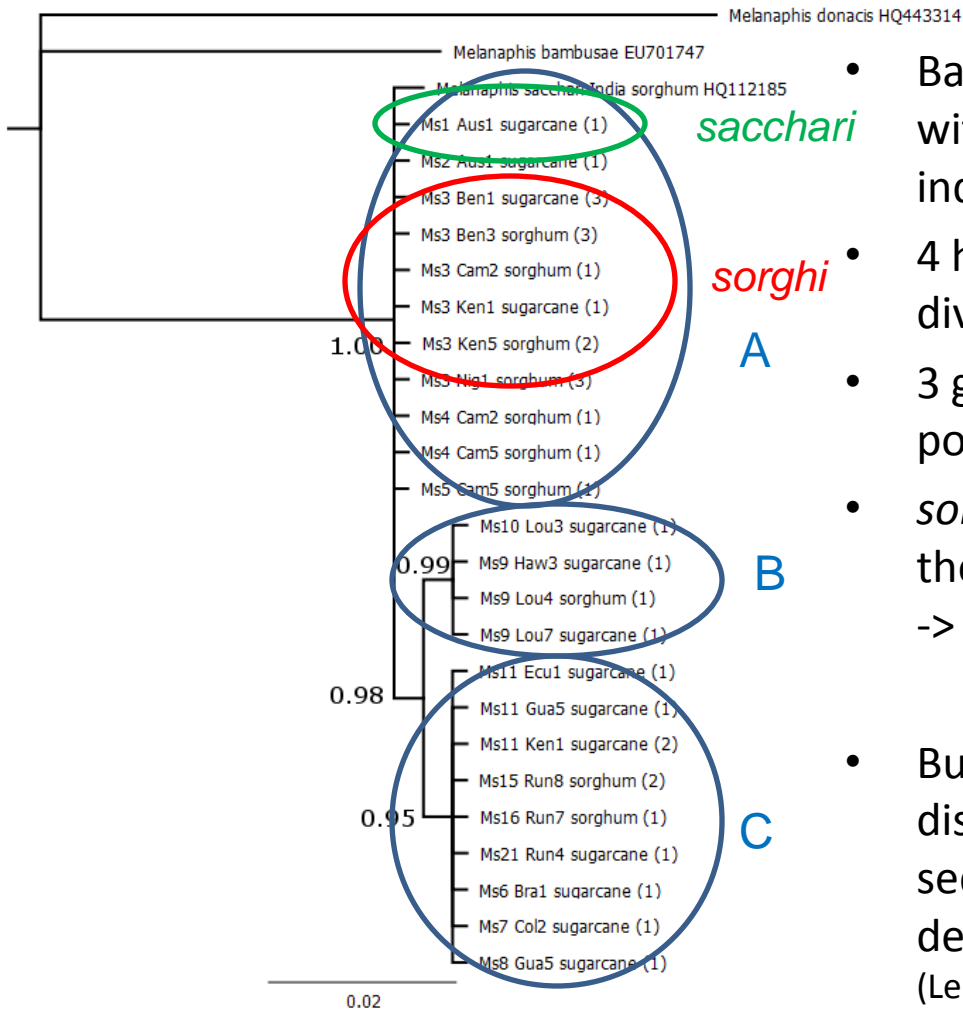
Methods

- 52 samples from 42 localities from 13 regions
- Taxonomy
 - Morphometric study
 - Barcoding with CO1 gene sequence
- Genetic diversity and pop. structure -> microsatellites
 - 10 SSR loci (Fartek et al. 2010 Mol. Ecol. Res.)
 - Capillary sequencer

Tibia / LPT ratio



CO1 sequences



- Bayesian phylogenetic tree constructed with 658 bp sequence of CO1 from 33 individuals
- 4 haplotypes, max. sequence divergence = 0.46%
- 3 groups supported by high bayesian post. proba
- *sorghum* and *sacchari* individuals share the same haplotype
-> same species ?
- But several cases of failure to distinguish aphid species using COI sequences have recently been demonstrated in the Aphididae family (Lee et al. Mol Ecol Res 2011)

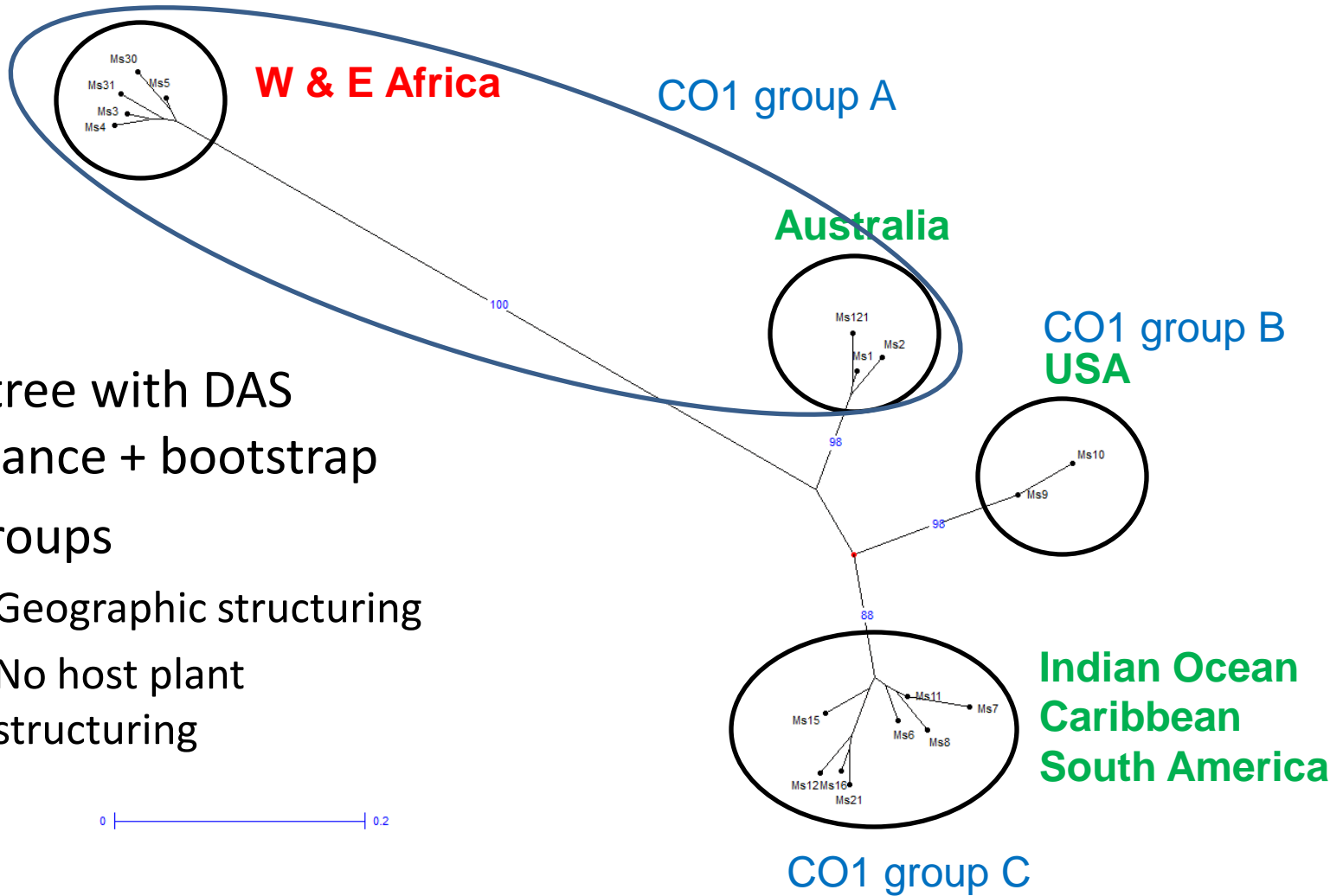
Microsatellites

- Analysis of allele frequencies:
 - all samples differed significantly from Hardy Weinberg equilibrium
 - Heterozygote excess
 - linkage disequilibrium among most of loci pairs
- -> consistant with clonal reproduction

Microsatellites

- Low genetic diversity
 - 18 Multilocus Genotypes (MLG)
 - 4 MLGs represent 87% of individuals
 - 10 geographic regions with 1-2 MLGs
- Most regions comprise
 - a main MLG
 - and few others derived from the main one by stepwise mutations or private allele at 1-2 loci

Microsatellites

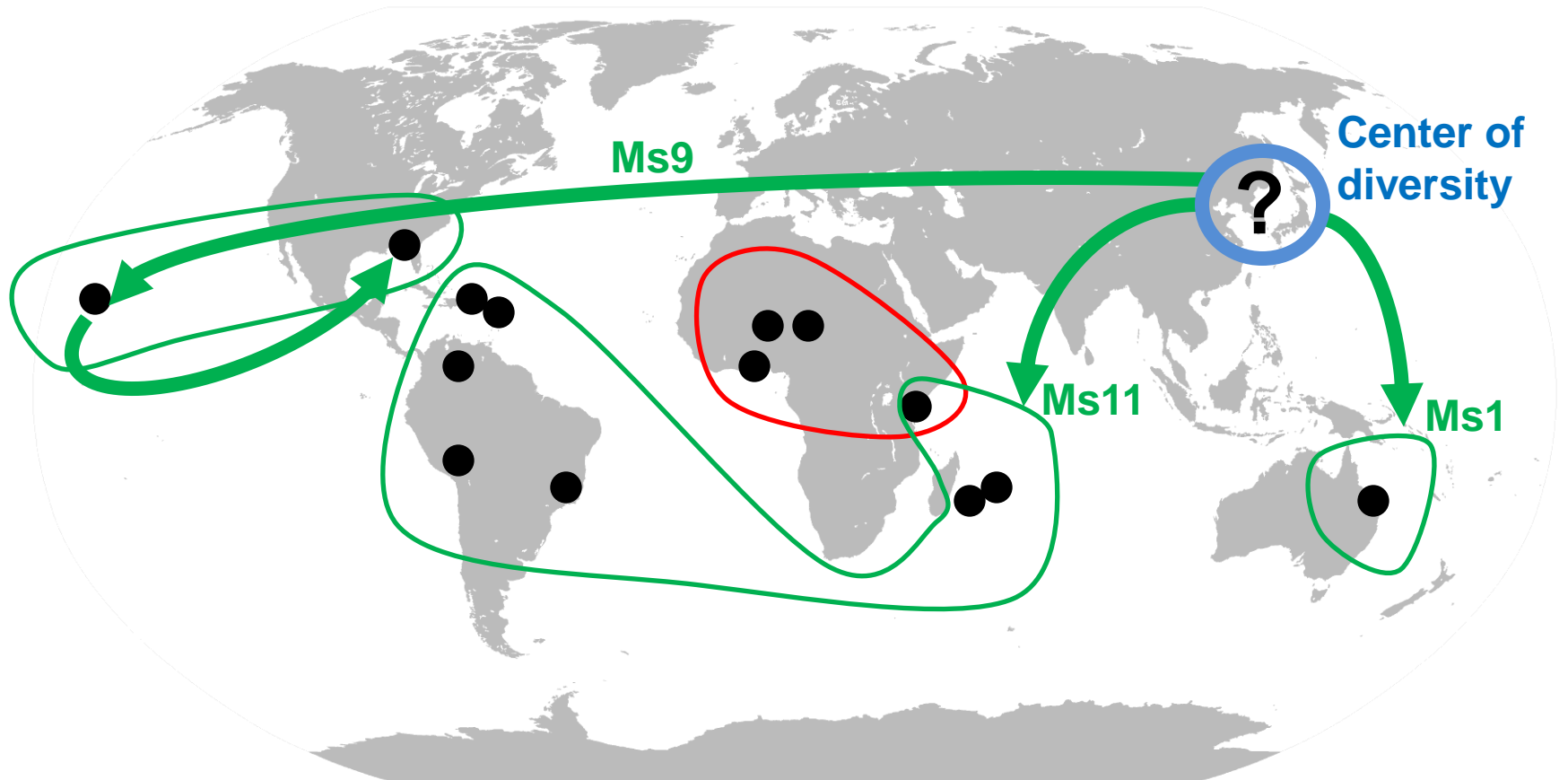


- NJ tree with DAS distance + bootstrap
- 4 groups
 - Geographic structuring
 - No host plant structuring

Conclusions

- Two taxa *sorghii* and *sacchari*
 - taxonomic status still unclear -> species, subspecies, forms ...
 - Relevance when considering clonal organisms ?
 - other groups (USA & Australia) ?
 - Need further morphometric studies
- Clonal reproduction
- Low genetic diversity
- No structuring by host plant
- Strong geographical structuring in *sacchari*
 - Invasive *sacchari* 'superclones' (Vorburger et al. 2003)
 - Highly successful genotype with wide geographical and ecological distribution area with no or few genetic diversity

Possible routes of invasion of *sacchari* 'superclones'



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