

Utilization of microsatellite markers in rubber tree for genetic diversity analysis and genetic mapping of agronomic traits.

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418 microsatellite markers already developed on rubber tree by CIRAD geneticists (*Seguin et al 2008*)

Most of them from enriched libraries

Dinucleotides: majority of AG/CT, some AC/GT

Non coding regions of genomic DNA

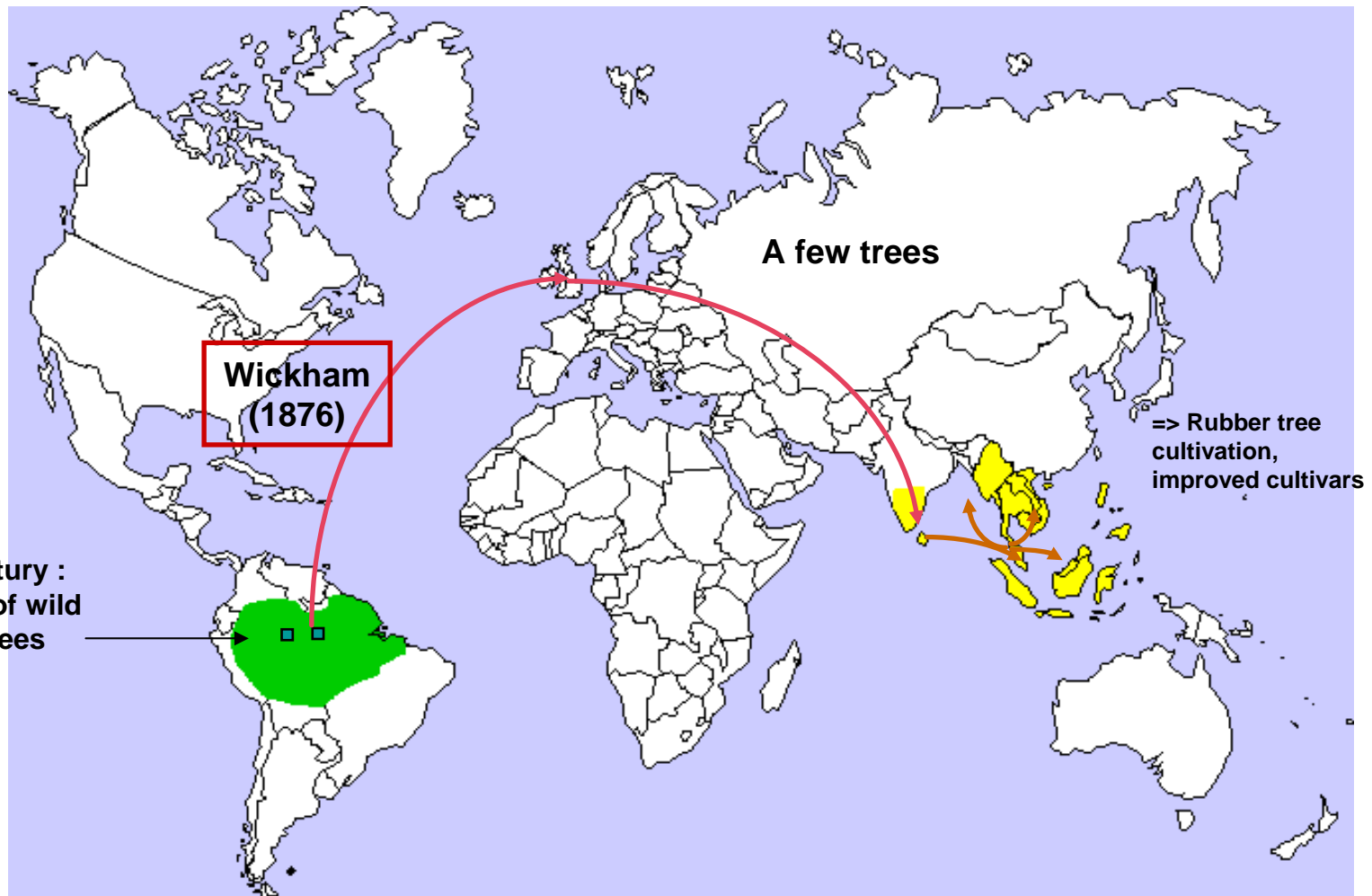
365 polymorphic microsatellite markers



Two examples of their use in rubber tree genetics studies

- ✓ Genetic diversity
- ✓ Linkage mapping

Analysis of genetic diversity among wild
Amazonian rubber tree populations



19th century :
tapping of wild
rubber trees

● Area of origin

● Main area of
breeding (1877-)

Rubber tree : a trans-domestication





Hevea brasiliensis (Willd. ex Adr. de Juss.) Muell.-Arg.

(Priyadarshan & Gonçalves, 2003)

Genetic diversity of wild rubber tree populations

Sample under study comes from an *ex situ* collection located in French Guiana

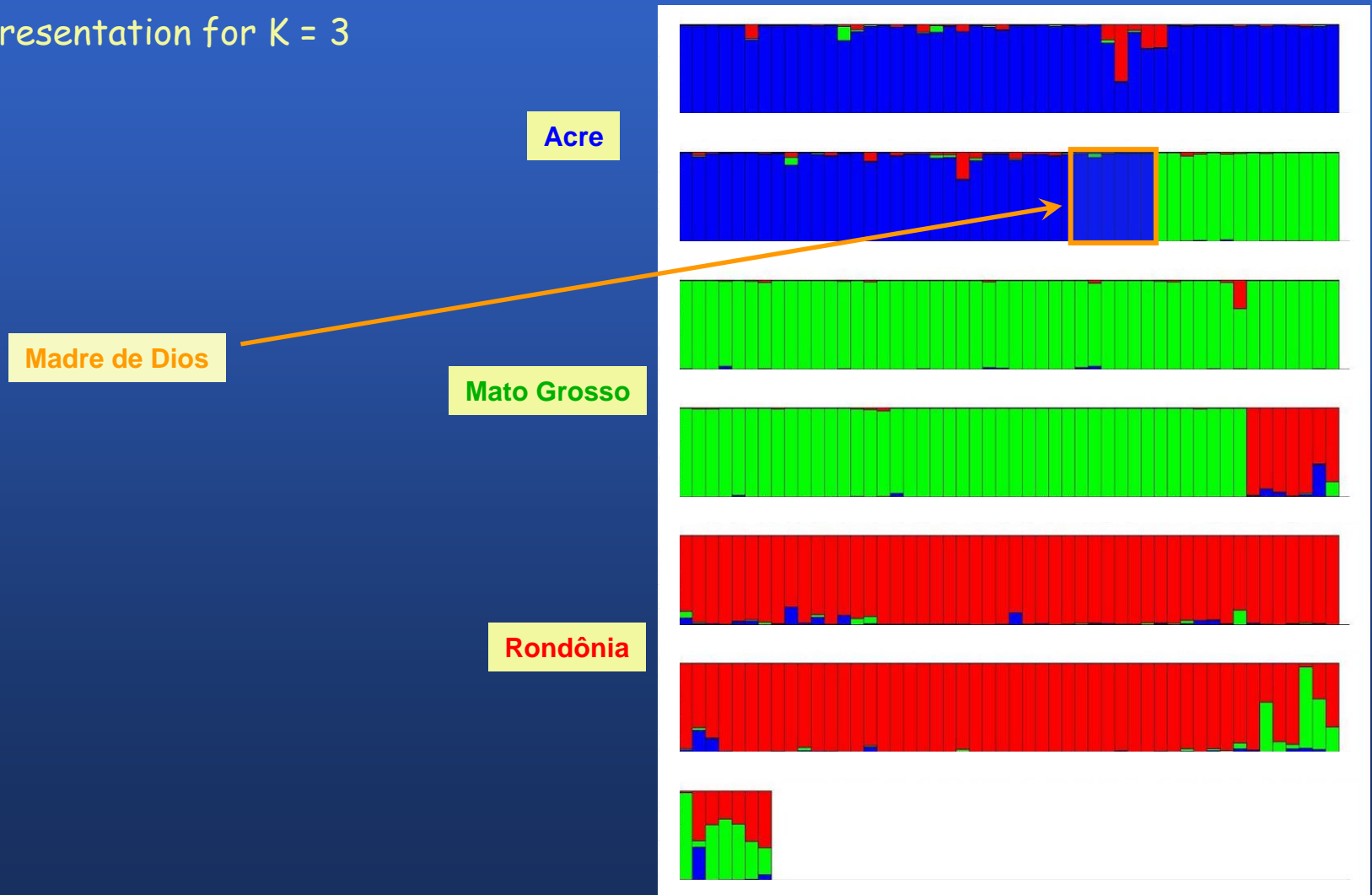
Initial survey	Area of origin	Number of locations	Number of genotypes
Peruvian Minist. Agric.(1948)	Madre de Dios (Peru)	1	6
EMBRAPA/IRCA (1974)	Acre (Brazil)	2	8
	Rondônia (Brazil)	2	7
IRRDB (1981)	Acre (Brazil)	5	72
	Mato Grosso (Brazil)	4	108
	Rondônia (Brazil)	7	106
<i>Total number of clones in sample:</i>			307

15 microsatellite markers, each on a different linkage group

Genetic diversity of wild rubber tree populations

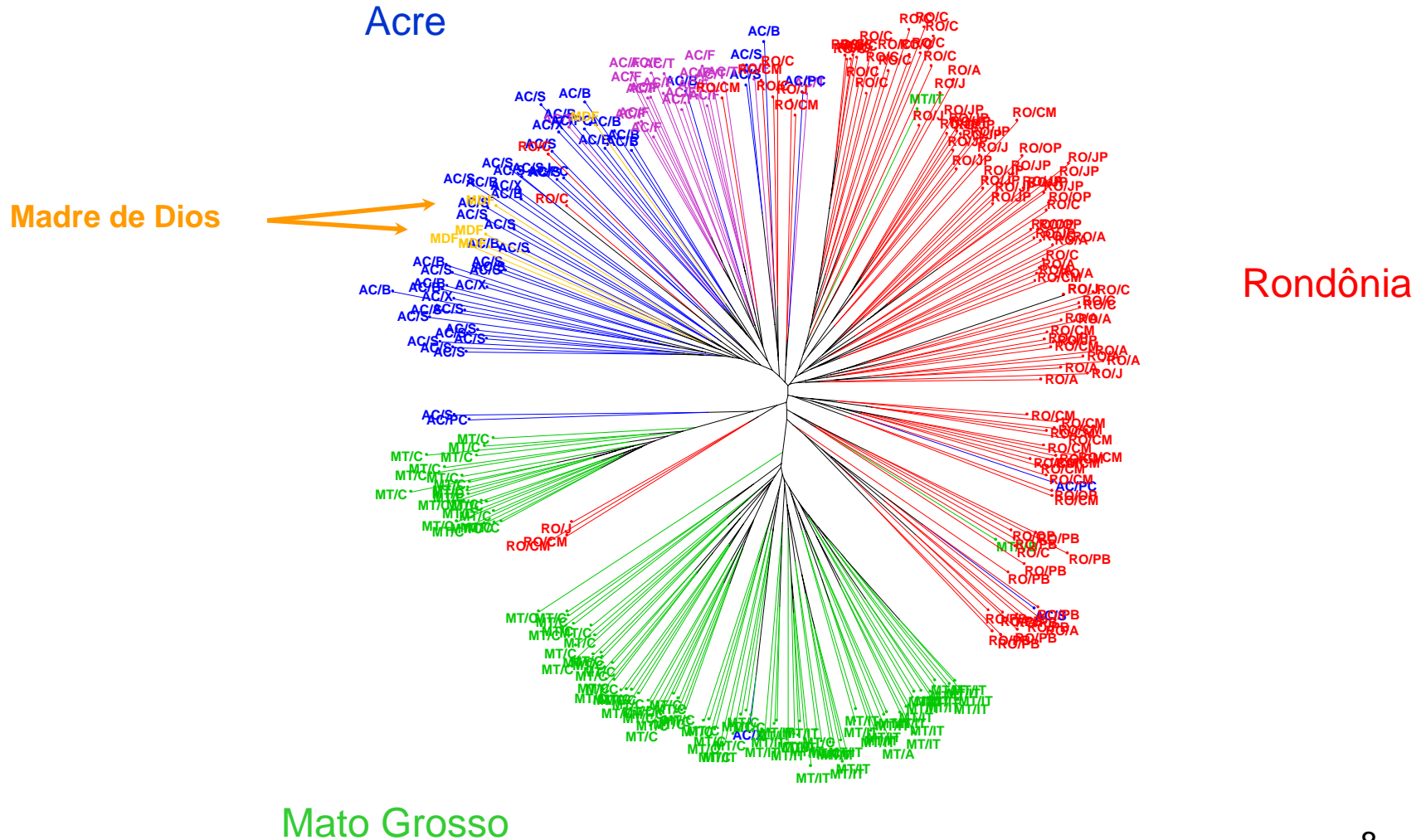
Structure software: a clustering algorithm to infer the structure of populations

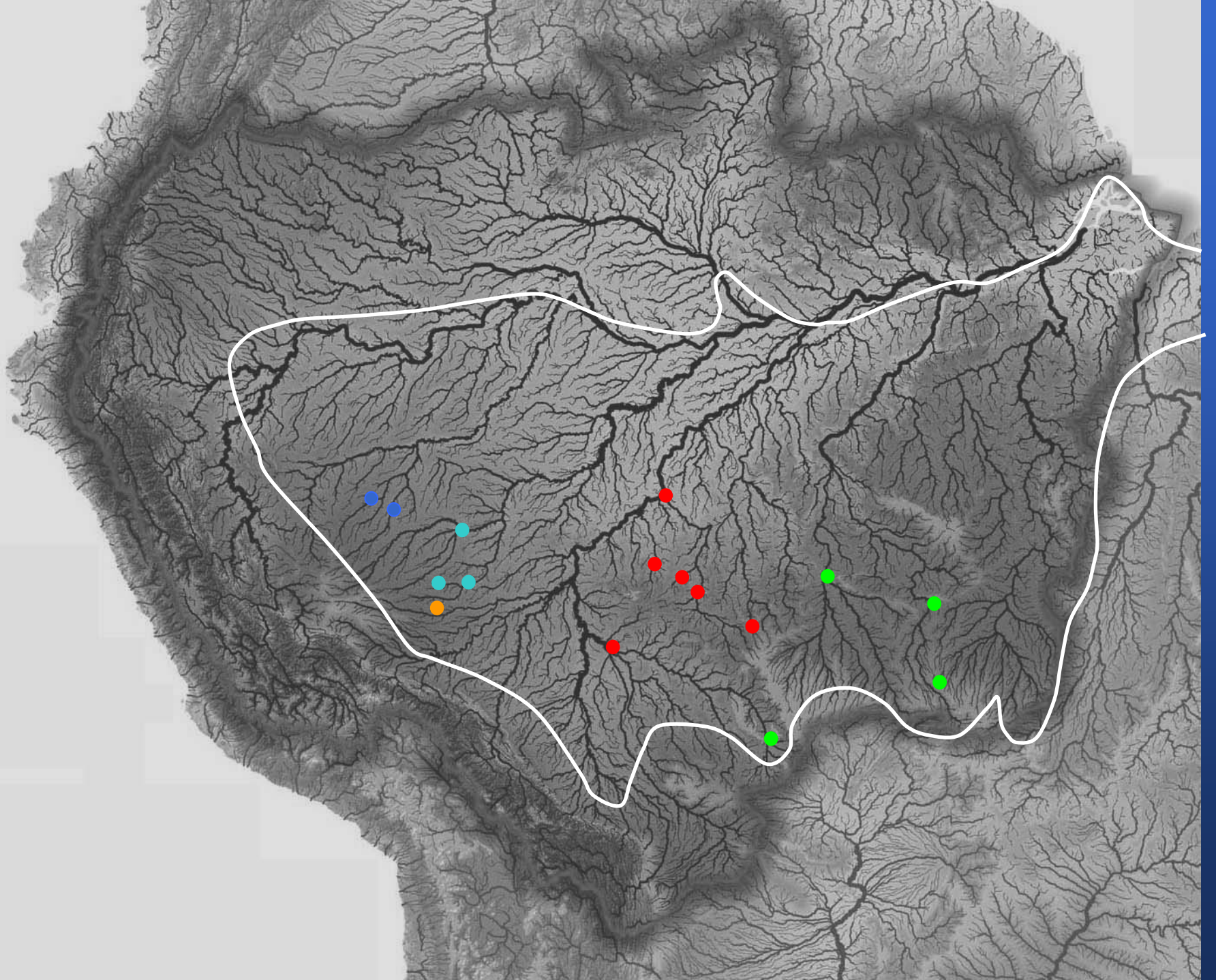
Best representation for $K = 3$ clusters

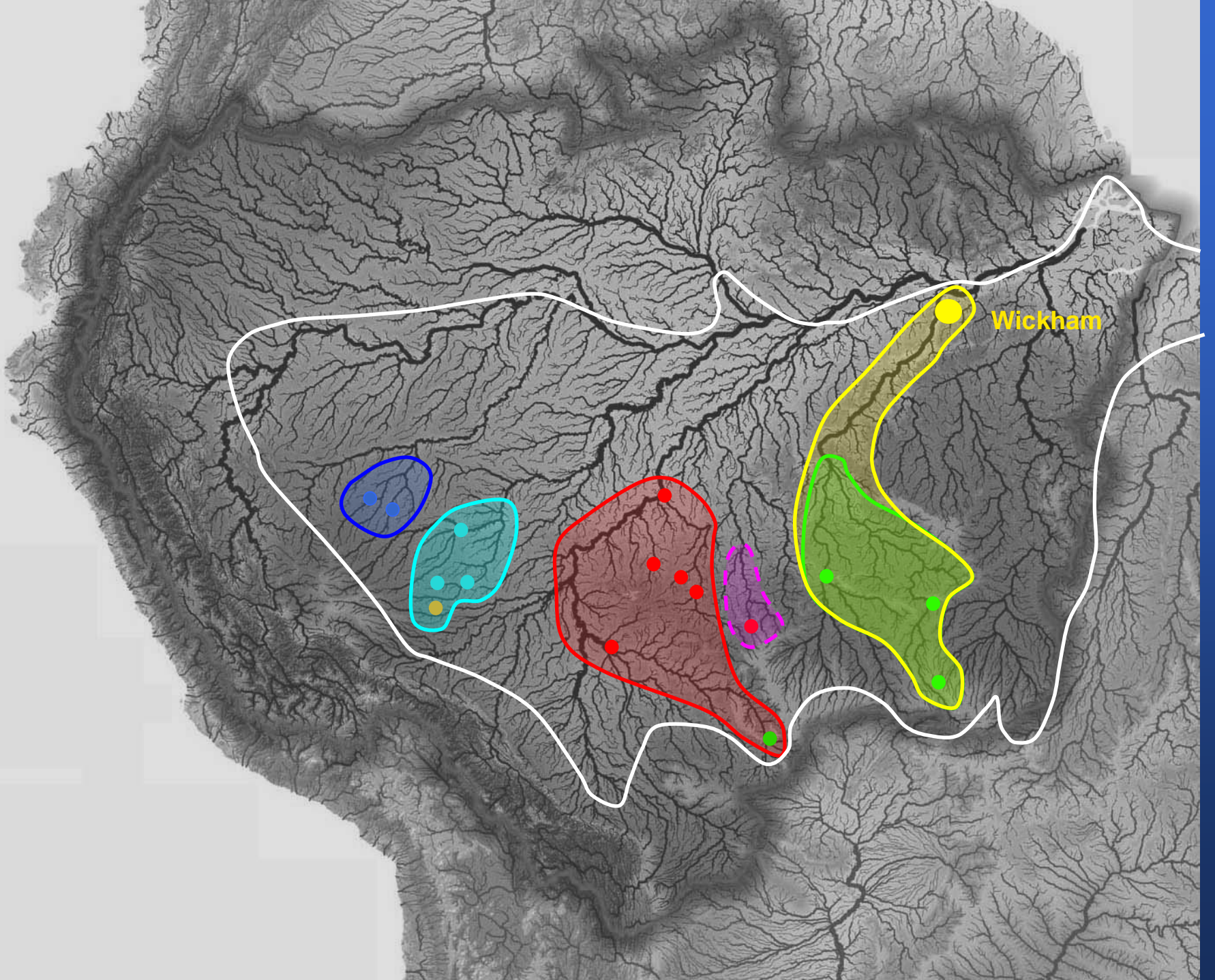


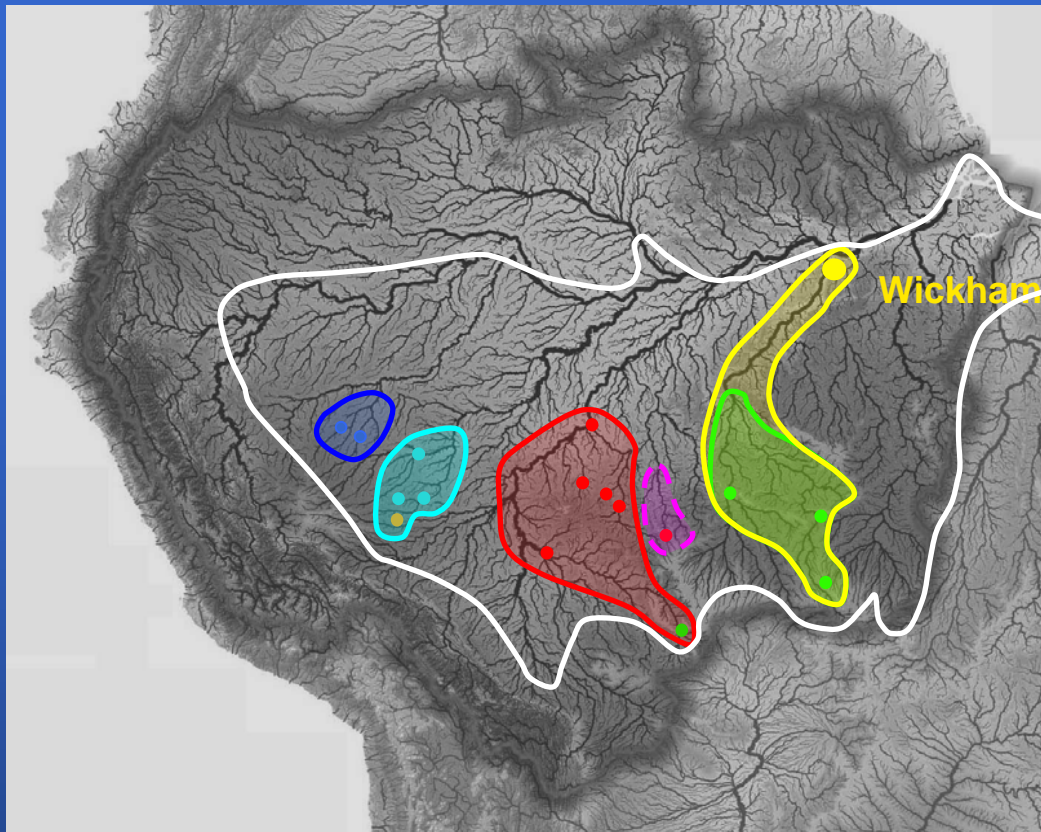
Genetic diversity of wild rubber tree populations

Darwin software: construction of a dissimilarity measure to draw Neighbor-Joining trees









- Hydrographical network and isolation by distance
- Some populations may not exist any more
- Necessity of additional surveys
- Highly polymorphic markers (21.7 alleles/locus)
- Not suitable for association genetics studies

Genetic linkage mapping for the detection of quantitative trait loci

Three progeny populations already mapped at Cirad

- PB260 × FX3899
 - Detection of loci for SALB resistance
(Lespinasse et al 2000a; Lespinasse et al 2000b; Le Guen et al 2003; Le Guen et al 2007)
- RRIM600 × PB217
 - Detection of QTLs for growth and latex production
(Prapan et al 2006; Rattanawong et al 2008)
- PB260 × MDF180
 - Identification of loci for durable resistance to SALB

South American Leaf Blight due to *Microcyclus ulei*

Asiatic clones highly susceptible



MDF180 is a resistant cultivar:

High level of partial resistance
Durable resistance

(Le Guen et al 2008)



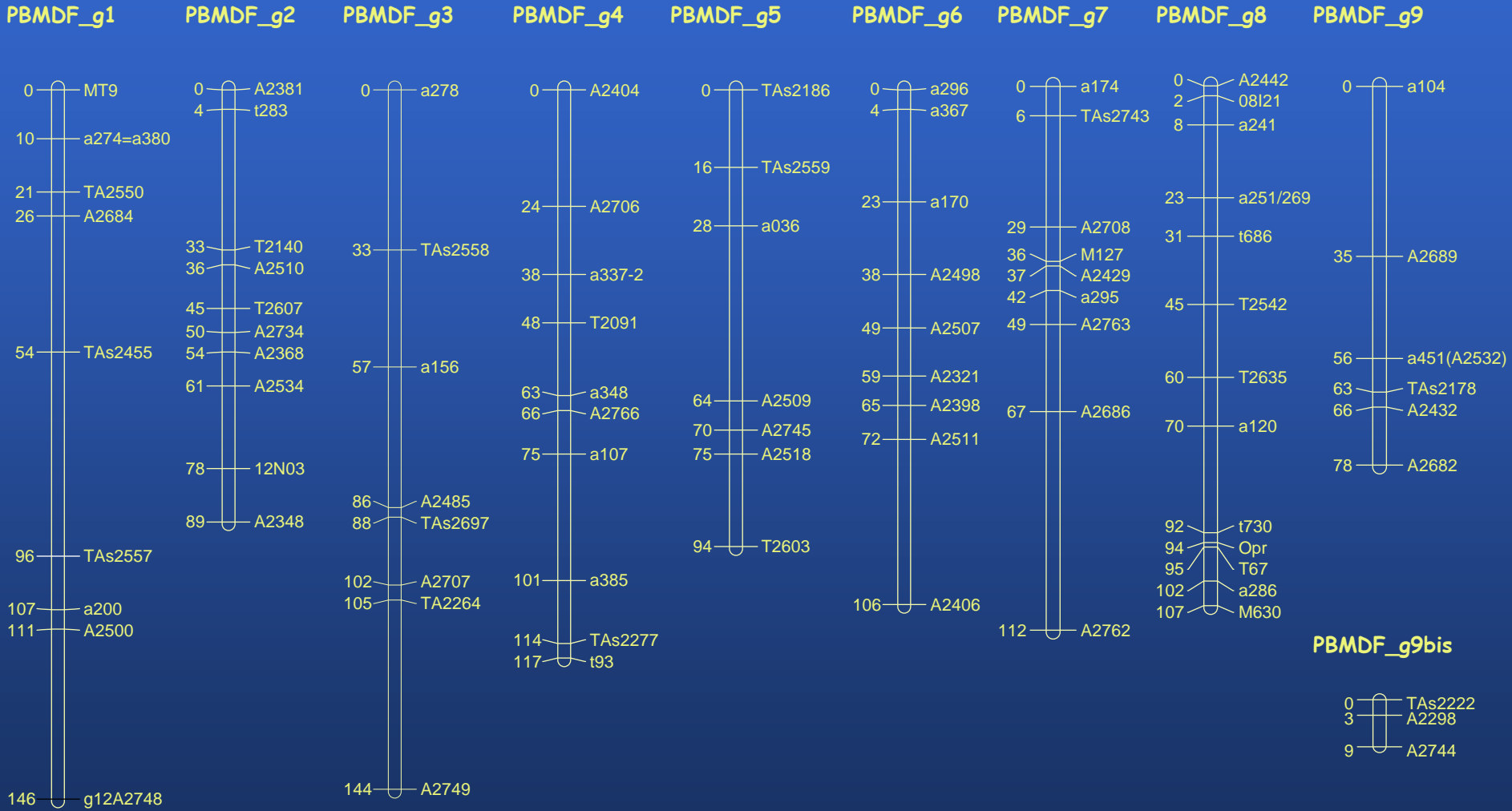
298 clones from PB260 x MDF180 cross were genotyped with 177 microsatellites

Disease observation under controlled conditions and in the field

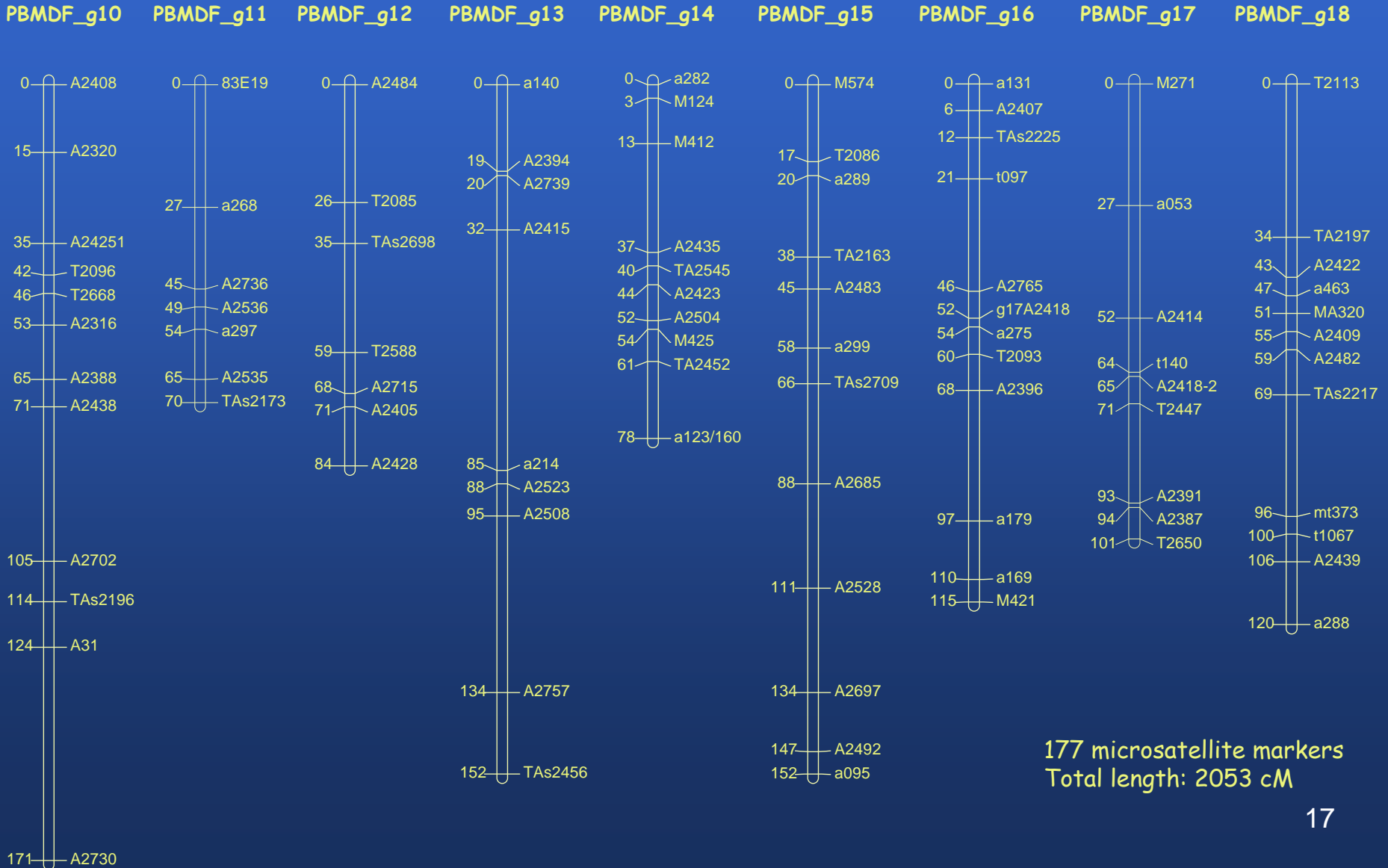
Construction of a linkage map (JoinMap)

Location of markers linked to the expression of resistance (MapQTL)

Genetic linkage map of PB260 x MDF180 (JoinMap 3.0)

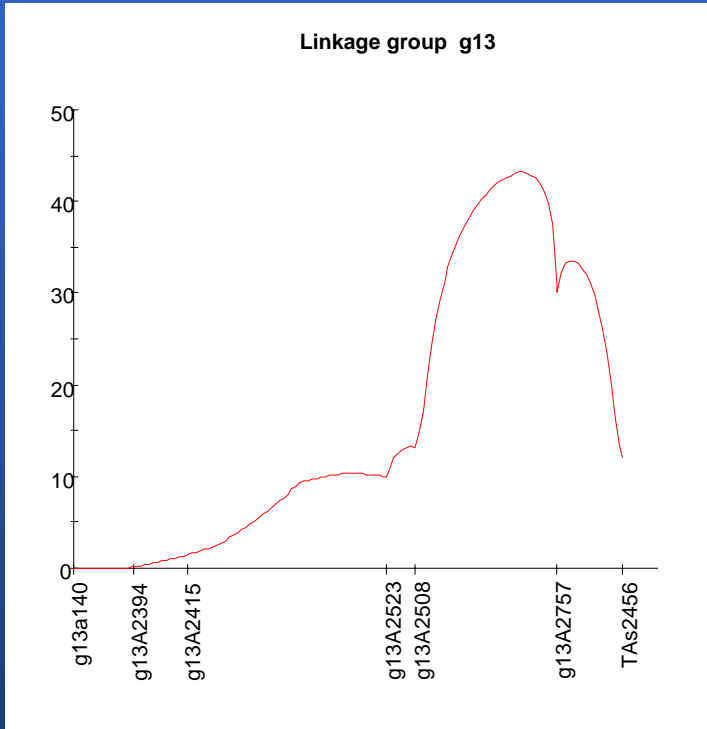


Genetic linkage map of PB260 x MDF180 (JoinMap 3.0)

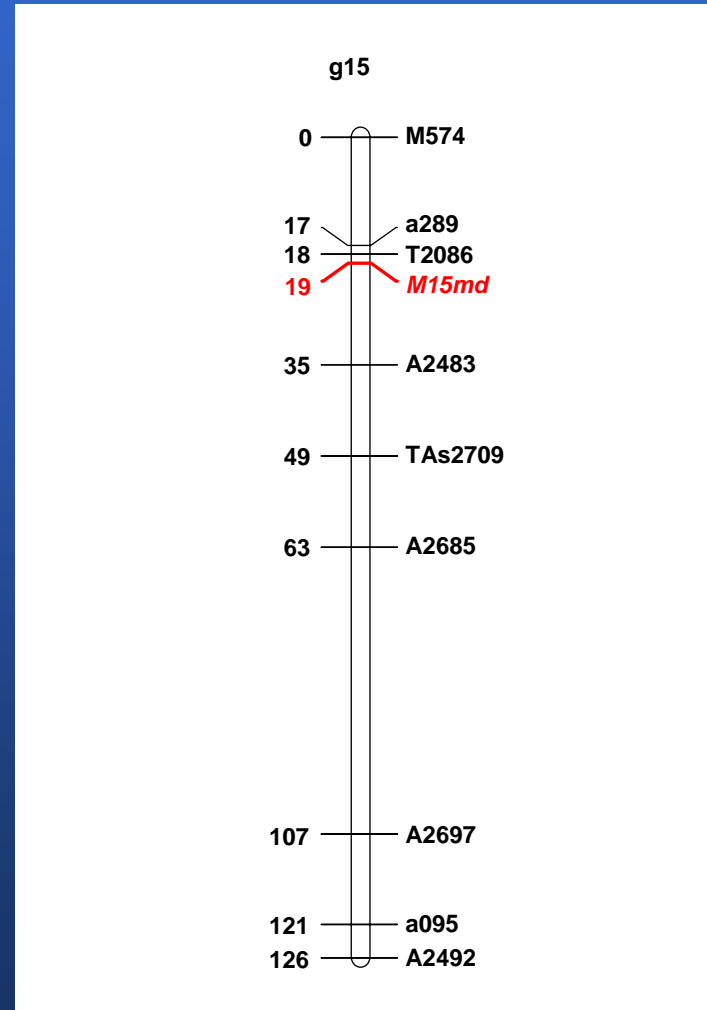


177 microsatellite markers
Total length: 2053 cM

Lod score value for an important resistance QTL on linkage group 13



Location of the major resistance gene M15md on linkage group 15



Four minor QTLs were also detected on other linkage groups

Microsatellite-based linkage map allowed identification of a major gene and QTLs for SALB resistance

However there are some large gaps in the linkage map

There is a need of additional locus-specific markers for Marker Assisted Selection

Conclusion

- Advantages of microsatellite markers in non-coding DNA:
Well adapted to diversity analysis and genetic mapping:
Neutrality, locus specificity, multi-allelism, co-dominant segregation pattern, ease of use

- Drawbacks:

Multi-allelism is a flaw for linkage disequilibrium assessment
Their number is not sufficient for precise QTL location

- Sequencing rubber tree (either whole genome, or expressed genes or BACs) would be very useful for geneticists to:

- ✓ Identify new and less variable microsatellite markers
- ✓ Identify SNPs (the most useful type of marker for association genetics studies)
- ✓ Combine « candidate gene » and « QTL detection » approaches

References

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