



# Consorcio para la Conservación de Magnolias del Neotrópico



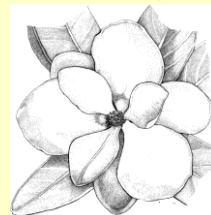
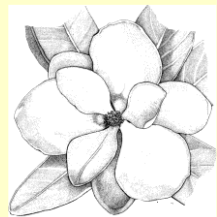
## Genetic and ecological divergence of species of the *Magnolia pacifica* A.Vázquez complex in western Mexico

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**Universidad de Guadalajara**

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Mexico

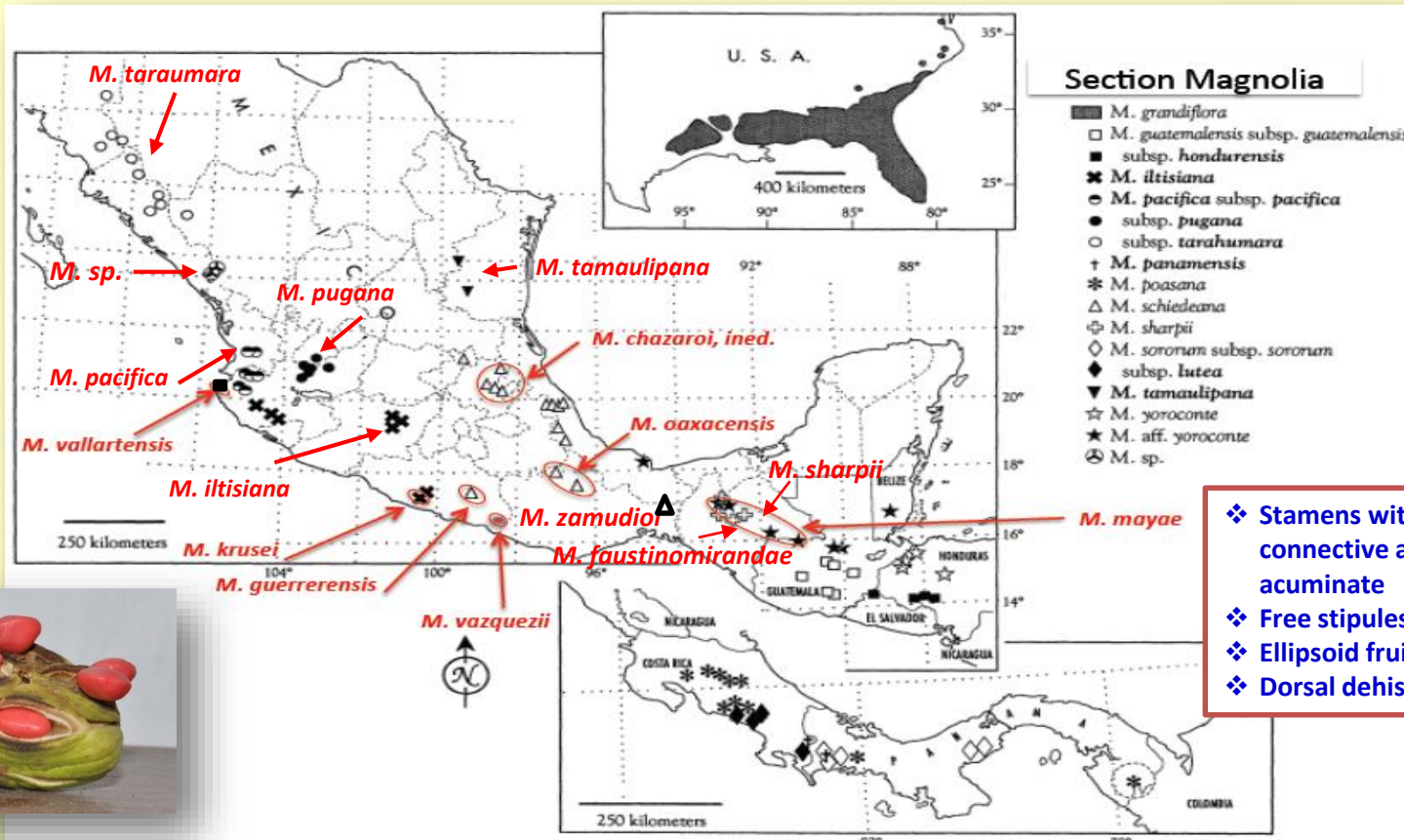
July 8th – 14th, 2019



# Genus *Magnolia* L., Section *Magnolia* in México y Central America



In Mexico, there are *ca.* 40 species of the Magnoliaceae family  
19 species belong to Section *Magnolia*



- ❖ Stamens with short connective apex acute or acuminate
- ❖ Free stipules
- ❖ Ellipsoid fruit
- ❖ Dorsal dehiscence



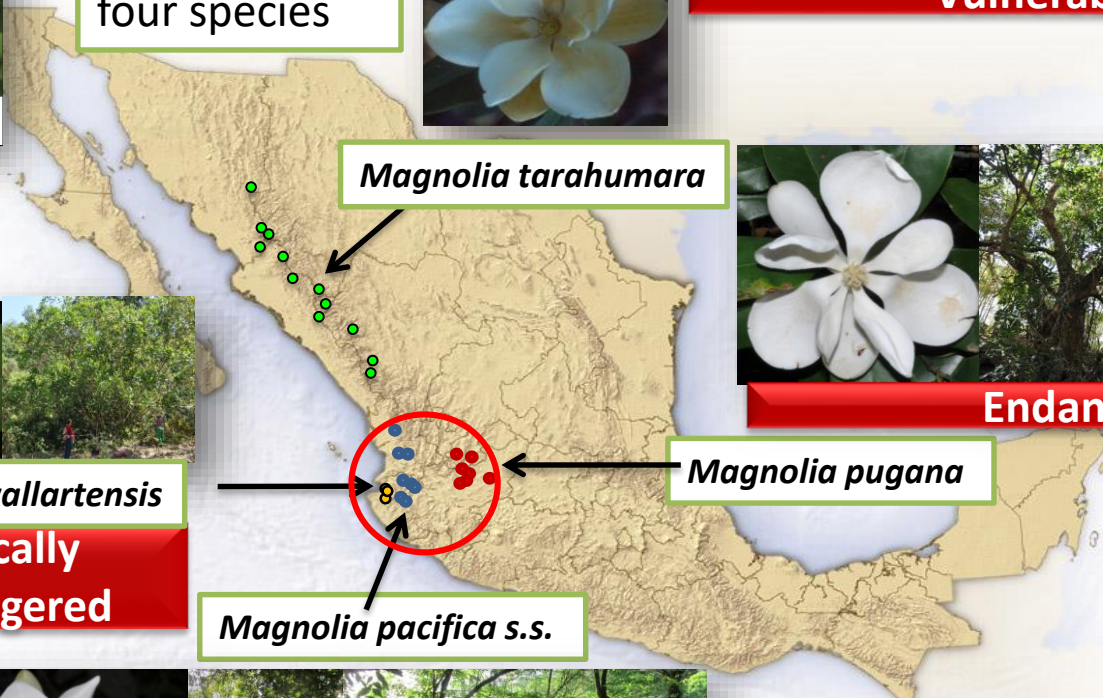


# *Magnolia pacifica* A.Vázquez species complex in SW Mexico

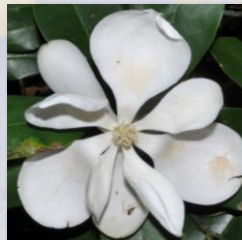
Composed by  
four species



**Vulnerable**



*Magnolia tarahumara*



**Endangered**



*Magnolia pugana*



*Magnolia vallartensis*

**Critically  
Endangered**

*Magnolia pacifica s.s.*



**Endangered**

Because species are the  
fundamental units of  
evolutionary biology their  
delimitation is an essential  
task of current systematics



*Magnolia vallartensis*



*Magnolia pacifica s.s.*



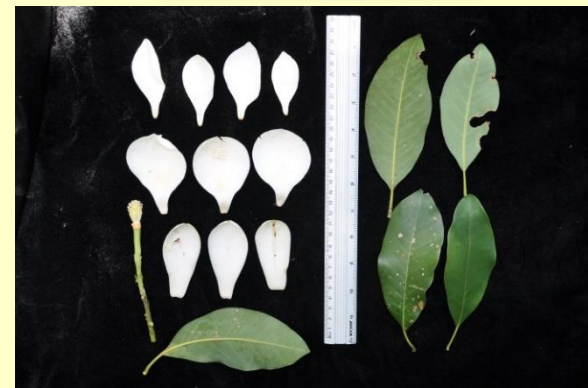
*Magnolia pugana*



**Carpels 14-19**



**Carpels 18-25**



**Carpels 25-35**



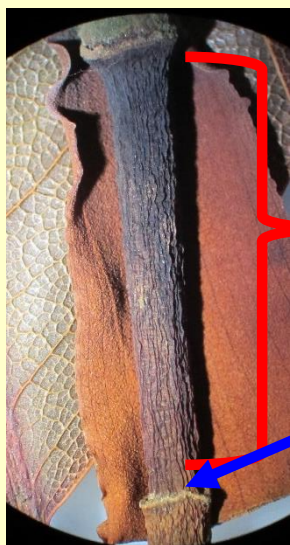


Peduncle indumentum

*M. vallartensis*

*M. pacifica s.s.*

*M. pugana*

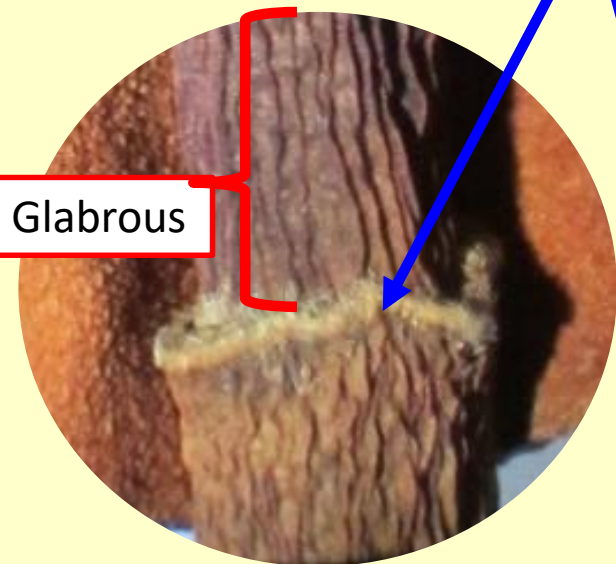


Glabrous

Pubescent



Essentially  
Glabrous



Glabrous



*M. Muñiz-Castro 1312*

*J. Curiel 69*

*Iltis 29722 (Isotype)*

# Taxonomy complexes



***Cycas segmentifida* complex**



***Magnolia pacifica* complex**

Species identification can be troublesome  
when taxa are closely related

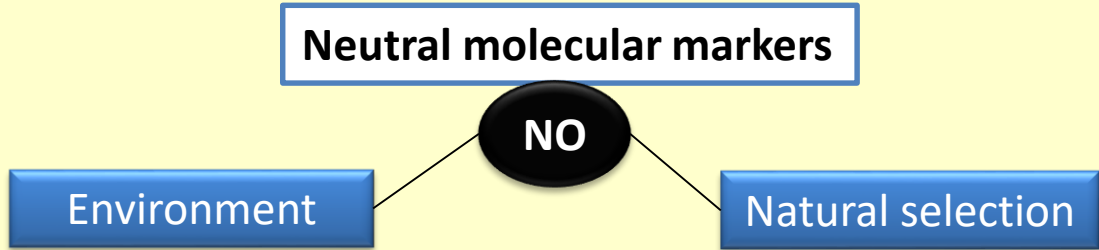
**Population  
genetics approach**

**Defining boundaries  
between species complexes**

For reliable identification, it is necessary to validate both  
morphological and molecular markers.

# Molecular markers

The development of **neutral single locus molecular markers** has the advantage of **infer recent events of speciation** helping to understand delimitation of species



## ISSR (Inter Simple Sequence Repeats)

The ISSR allows observing the variation in inter-microsatellite regions of the genome.



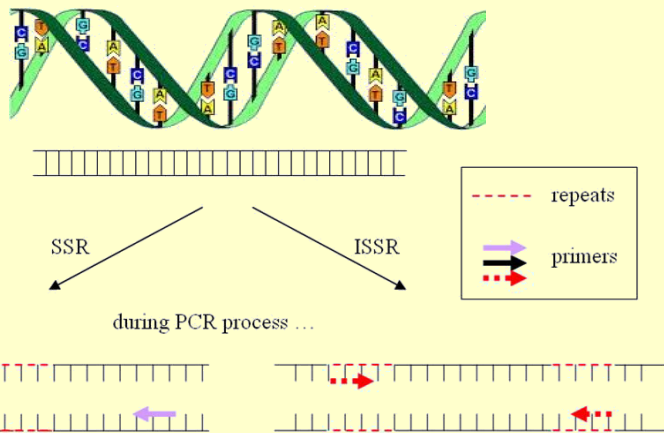
### Advantages

- High genetic variability (polimorphism)
- Small DNA concentrations
- Fast and easy to get
- Eficients
- Low cost

### Disadvantages

- Fragment homology
- Dominant marker. Assumes HW equilibrium

The last ones sorted out by statistical corrections





# Objectives

1. Analyze species boundaries and genetic relationships within the *M. pacifica* complex under a population genetics approach.
2. Evaluate ecological divergence of the three species by using ecological niche models

***M. vallartensis***



***M. pacifica s.s.***



***M. pugana***

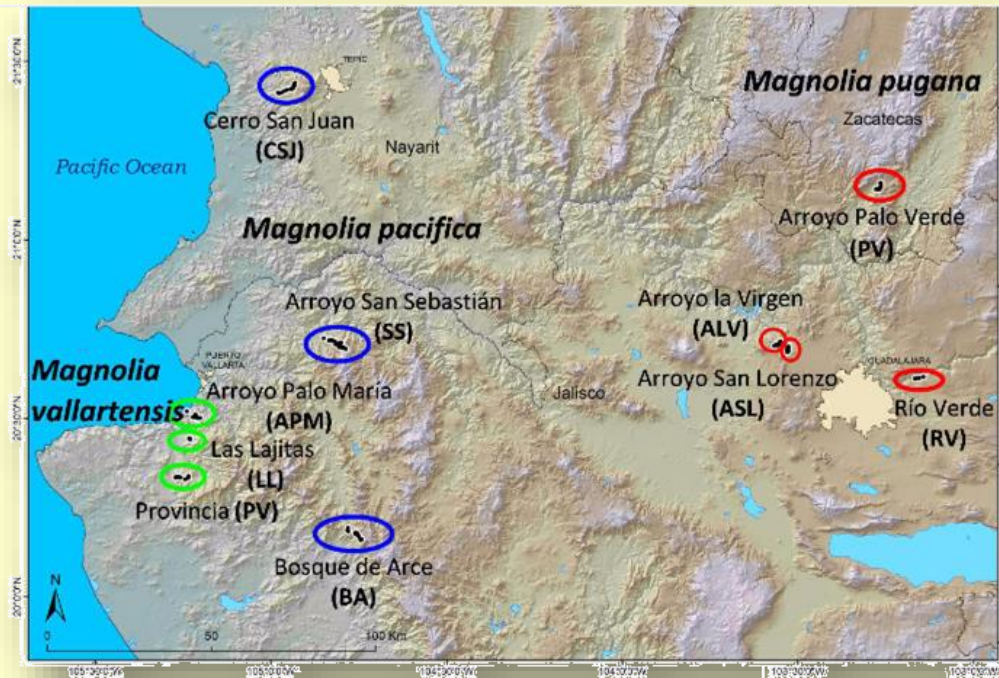




# Materials and methods

1

Sample collection

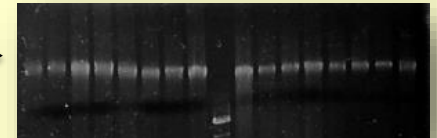


*M. vallartensis* ○  
*M. pacifica s.s.* ○  
*M. pugana* ○

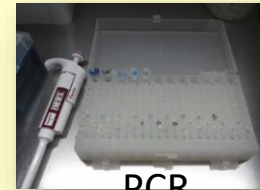
2

Sample Processing

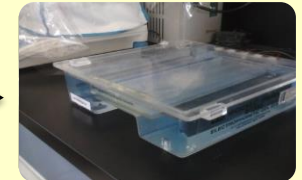
DNA extraction (Cota-Sánchez CTAB method)



Amplification of ISSR markers

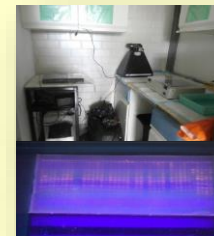


PCR



Electrophoresis

810-814-834-836-855-857

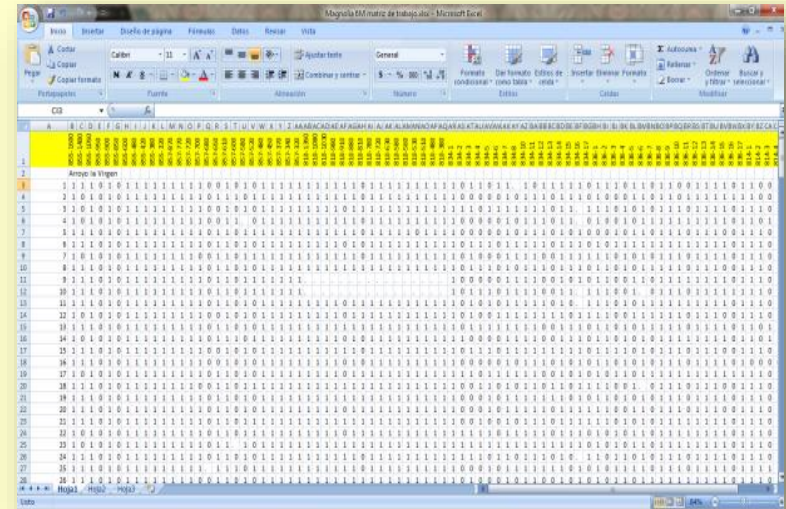
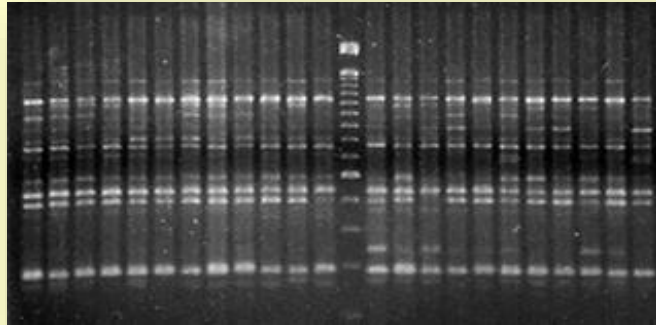


Gels Photo-documentation

## Binary matrix

3

## Data Analysis

A screenshot of a Microsoft Excel spreadsheet. The spreadsheet contains a large grid of binary data (0s and 1s) organized into columns and rows. The columns are labeled with letters A through Z, and the rows are numbered. The data appears to be a binary matrix representing genetic information.

## Genetic structure

Bayesian clustering to detect number of clusters **STRUCTURE 2.3.4**

UPGMA Nei's genetic distances **TFPGA 1.3**

Genetic similarity between localities **Exact Test for Population Differentiation TFPGA**

Distribution of the genetic variance for groups **AMOVA GenALEx 6.5**

## Genetic diversity

PB(%), I,  $H_E$ , HS, HT, **POPGENE 1.31**

## Genetic differentiation

Jost's D and  $G''_{ST}$  corrected standardized fixation index **GenoDive  $\beta$  2.0**



# Ecological niche modelling

## Modelado de nichos ecológicos y distribuciones geográficas

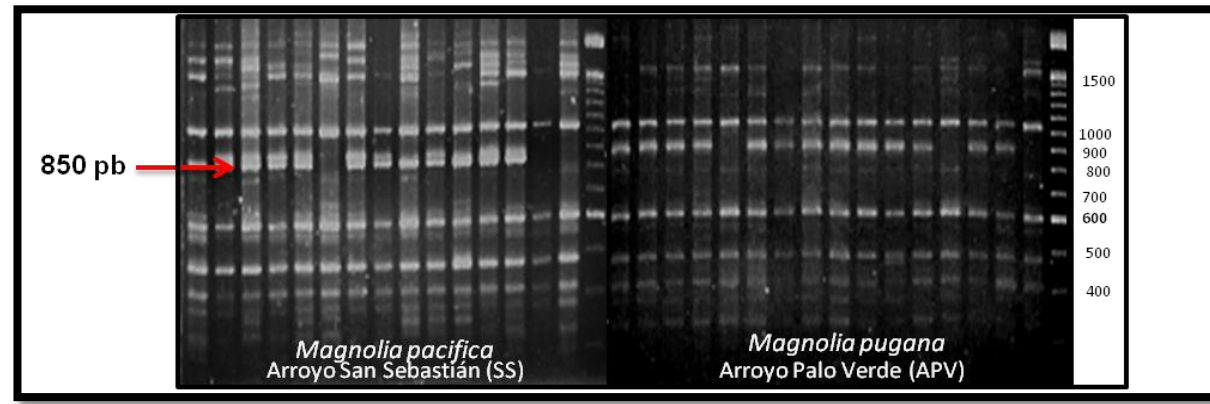
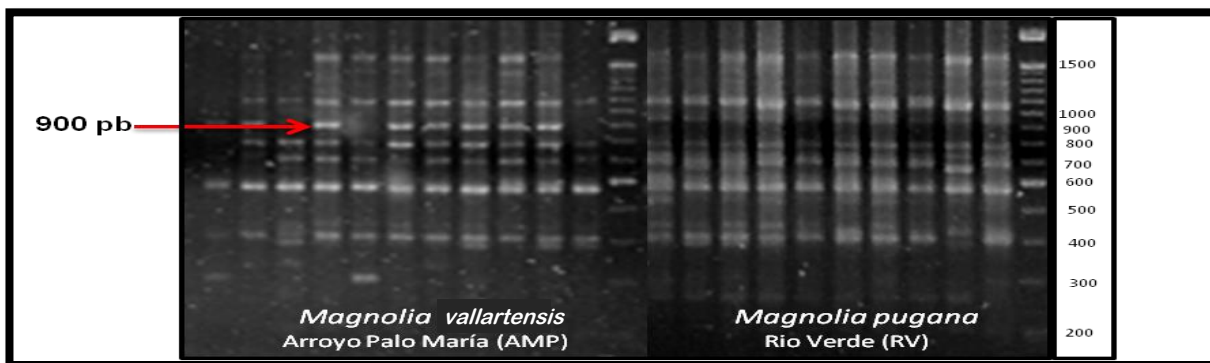


- MAXENT**
- CROSS-VALIDATION**
- 10 REPLICATES**
- 500 ITERATIONS**
- 1000 BACKGROUND POINTS**

---19 bioclimatic layers WorldClim V. 2.0  
 (Fick & Hijmans, 2017)  
 ---M. Pugana 39 records  
 M. Pacifica 49 & M. vallartensis 22

Potential Geographic Distribution

# Results



• 76 fragments

• 41 loci polymorphic

• Size 290 to 1650 pb

• Two exclusive fragments  
for *M. pacifica* s.s. and  
*M. vallartensis*

ISSR usually produce a high number of private bands (loci)

(Maltagliati et al. 2006, Casu et al. 2009)

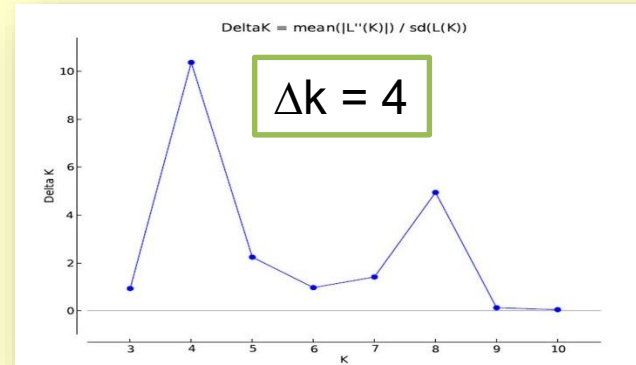
*M. pugana*, the most divergent species of *M. pacifica* complex



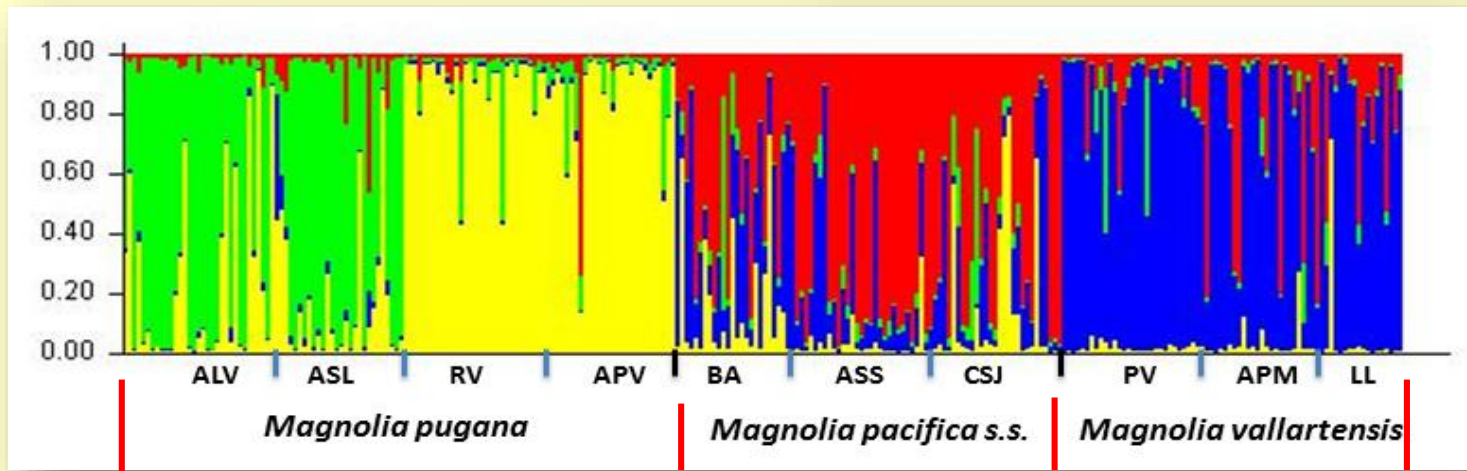


# Genetic Structure

Estimated genetic clustering STRUCTURE 2.3.4



Genetic component



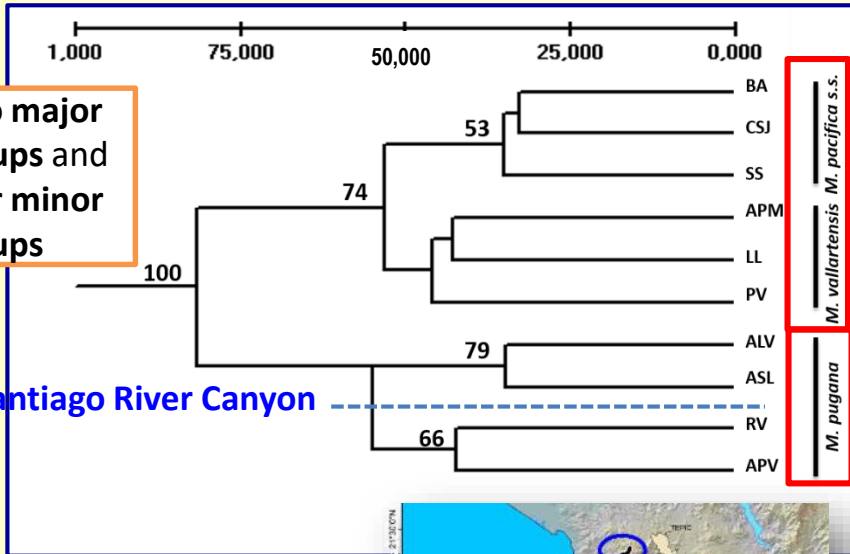
Four genetic groups

Two panmictic subpopulations of one species: *M. pugana*

Two taxa: *M. pacifica s.s* and *M. vallartensis*

# Genetic relationships

UPGMA dendrogram based on Nei's genetic distances  
Bootstrap (%) at each node (1000 replicates)

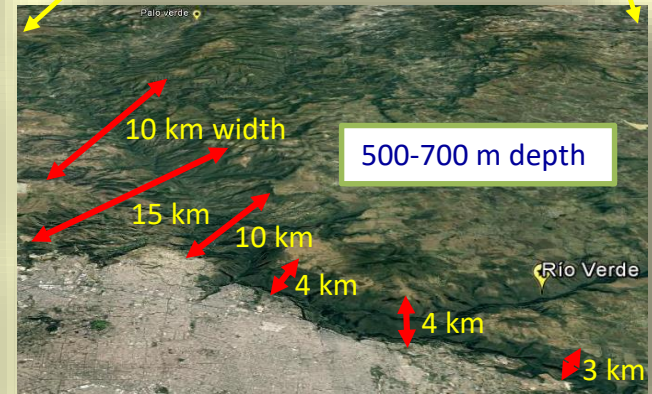
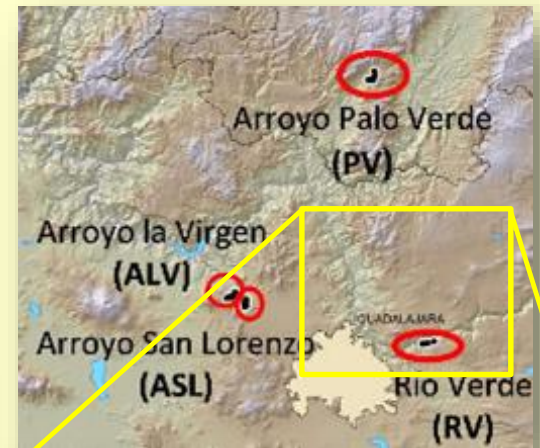
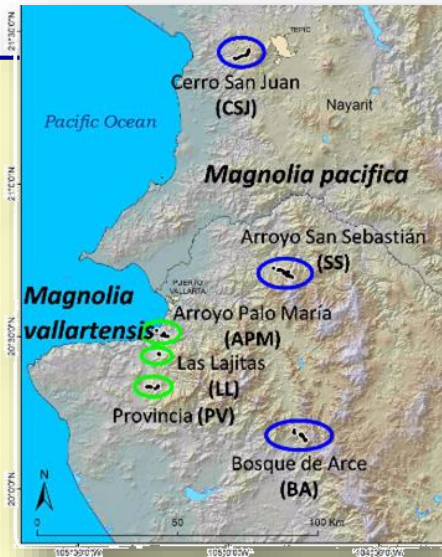


Two major groups and four minor groups

Santiago River Canyon

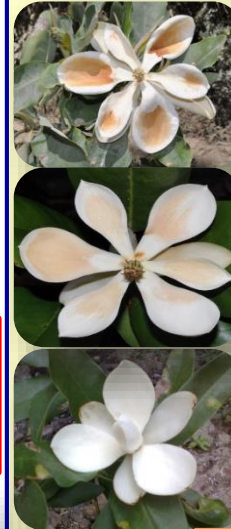
*M. vallartensis* in the same major group of *M. pacifica* s.s.

Current process of parapatric divergence from *M. pacifica* s.s.



Two allopatric subpopulations of *M. pugana* separated by a physiographical barrier:

Santiago River Canyon





# Pairwise genetic differentiation among *M. pacifica* complex localities



Nei's unbiased genetic distance

Species	<i>Magnolia pugana</i>				<i>Magnolia pacifica s.s.</i>			<i>Magnolia vallartensis</i>		
	Locality	ALV	ASL	RV	APV	BA	ASS	ASJ	PV	APM
ALV	-	<b>0.032</b>	0.052	0.05	0.069	0.07	0.066	0.099	0.08	0.097
ASL	0.144	-	0.054	0.051	0.055	0.06	0.05	0.077	0.072	0.079
RV	0	0.001	-	<b>0.039</b>	0.07	0.074	0.073	0.11	0.088	0.112
APV	0.013	0.006	0.079	-	0.057	0.069	0.06	0.098	0.088	0.097
BA	0	0	0	0.002	-	<b>0.031</b>	<b>0.03</b>	0.058	<b>0.049</b>	<b>0.042</b>
ASS	0	0.002	0	0	0.52	-	<b>0.032</b>	0.065	<b>0.045</b>	<b>0.042</b>
ASJ	0	0	0	0	0.703	0.312	-	0.056	<b>0.04</b>	<b>0.042</b>
PV	0	0	0	0	<b>0.052</b>	<b>0.06</b>	<b>0.05</b>	-	<b>0.043</b>	<b>0.039</b>
APM	0	0	0	0	0.21	0.062	0.162	0.55	-	<b>0.038</b>
LL	0	0	0	0	0.475	0.06	0.119	0.976	0.36	-

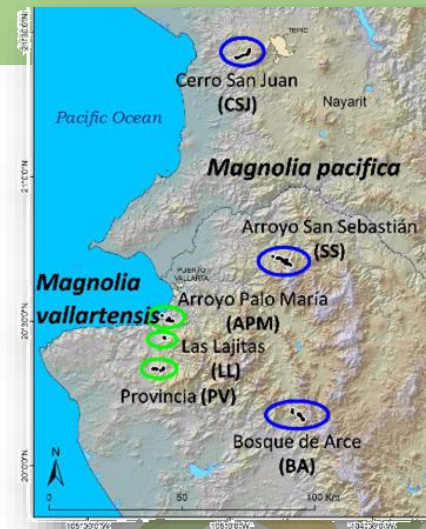
Exact test of differentiation probability

Nei's unbiased (1978) distance

Close genetic relationships among localities are presented in red bold

There are not differentiation of most of *M. pacifica* localities with *M. vallartensis* ones

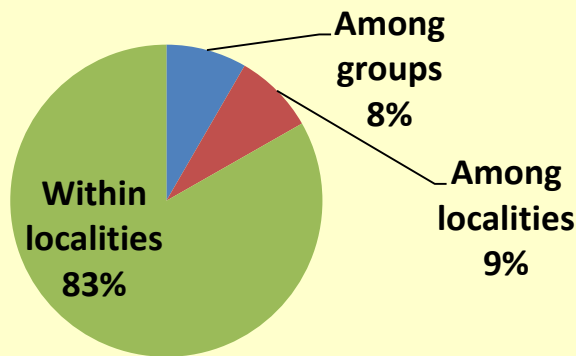
Among the *M. vallartensis* localities, Provincia (PV) the most differentiated from the *M. pacifica s.s.* group



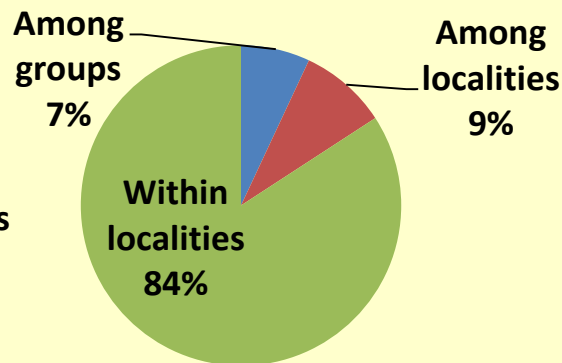
# Genetic Structure

## Molecular variance analysis (AMOVA) for taxonomical/Bayesian analysis groups and species of the *Magnolia pacifica* complex

Variation source	Percentage of variation %					
	Groups		Species			
	Taxonomic (3)	Bayesian analysis (4)	<i>M. pugana</i>	<i>M. pacifica</i> s.s.	<i>M. vallartensis</i>	<i>M. coriacea</i> (Zhao et al. 2012)
Among groups	8	7				
Among localities/groups	9	9	12	7	7	23
Within localities/all localities	83	84	88	93	93	77
$\Phi_{ST}$ p(rand>= data)	0.168 0.001	0.158 0.001	0.118 0.001	0.070 0.001	0.070 0.001	0.070 0.001



3 taxonomic groups



4 Bayesian groups

- ❖ The population genetic approach assumes a **higher genetic structure between species than within species** (Drummond & Hamilton 2007). It supports the current **taxonomical status of three species**.
- ❖ *M. pacifica* complex spp. has **moderate to low genetic structure**
- ❖ **Lower  $\Phi_{ST}$**  than perennial (0.25), cross-pollinated (0.27) and widely distributed plant species (0.34) (Nybom 2004)



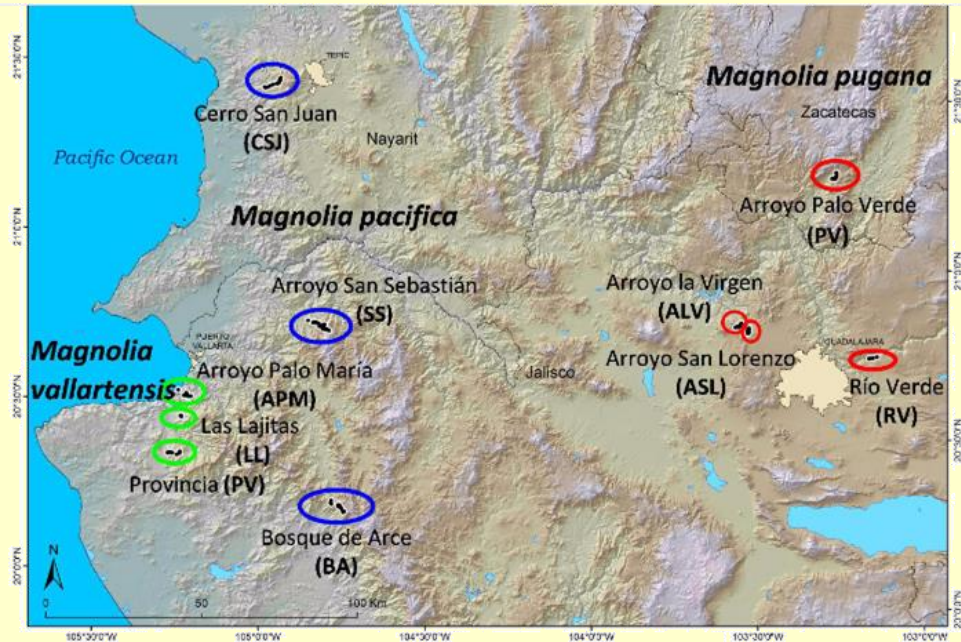
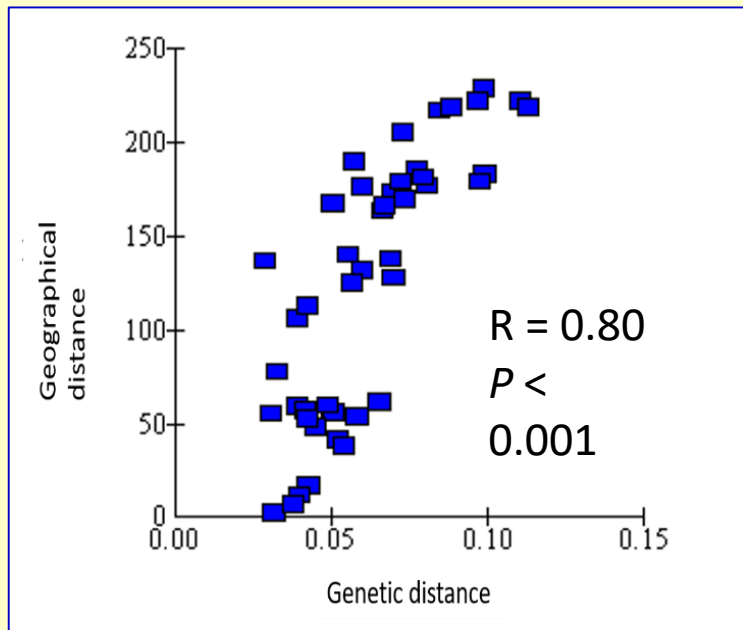
# Genetic diversity and differentiation parameters in species of the *Magnolia pacifica* complex

Species	Locality	P(%)	I	H <sub>E</sub>	H <sub>T</sub>	H <sub>S</sub>	G'' <sub>ST</sub>	D (Jost)
<i>M. pugana</i>	ALV	38	0.208	0.138				
	ASL	39	0.23	0.14				
	RV	38	0.218	0.121				
	APV	38	0.227	0.136				
<i>M. pugana</i>		51	0.268(0.288)		0.158(0.023)	0.134 (0.020)	0.178(0.030)	0.028(0.007)
<i>M. pacifica</i> s.s.	BA	47	0.28	0.178				
	ASS	38	0.209	0.14				
	ASJ	41	0.233	0.159				
	<i>M. pacifica</i> s.s.		51	0.272(0.286)		0.175(0.025)	0.159(0.023)	0.105(0.026)
<i>M. vallartensis</i>	PV	39	0.244	0.159				
	APM	39	0.241	0.147				
	LL	39	0.236	0.152				
<i>M. vallartensis</i>		46	0.275(0.310)		0.171(0.024)	0.153(0.022)	0.124(0.027)	0.021(0.006)
<b>Total</b>		<b>64</b>	<b>0.309(0.285)</b>		<b>0.178(0.023)</b>	<b>0.147(0.20)</b>	<b>0.222(0.039)</b>	<b>0.040(0.009)</b>

P polymorphism, I Shannon index, H<sub>E</sub> expected heterozygosity, H<sub>T</sub> total heterozygosity, H<sub>S</sub> intrapopulation heterozygosity, G''<sub>ST</sub> corrected and standardized fixation index, D Jost's differentiation index, standard deviation in parentheses

- ❖ G''<sub>ST</sub> produce higher values than G<sub>ST</sub> (0.12, 0.06, 0.07), these latter are lower than *M. coriacea* (G<sub>ST</sub>=0.187) (Zhao et al. 2012).
- ❖ *M. pacifica* complex Shannon Diversity (I=0.31) was lower than *M. sharpii* (0.56) and *M. schiedeana* (0.50) (Newton et al. 2008).
- ❖ *M. pugana* is the more endangered species, because their low genetic diversity (I=0.27), higher population differentiation and isolation, so they need more protection priority.

# Mantel test



Significant positive correlation between genetic and geographical distance:  
A process of **isolation by distance (IBD)**

# RESULTS

## SPECIES POTENTIAL

### GEOGRAPHIC DISTRIBUTION

### MODELS

#### POTENTIAL DISTRIBUTION AREAS



*M. pugana*



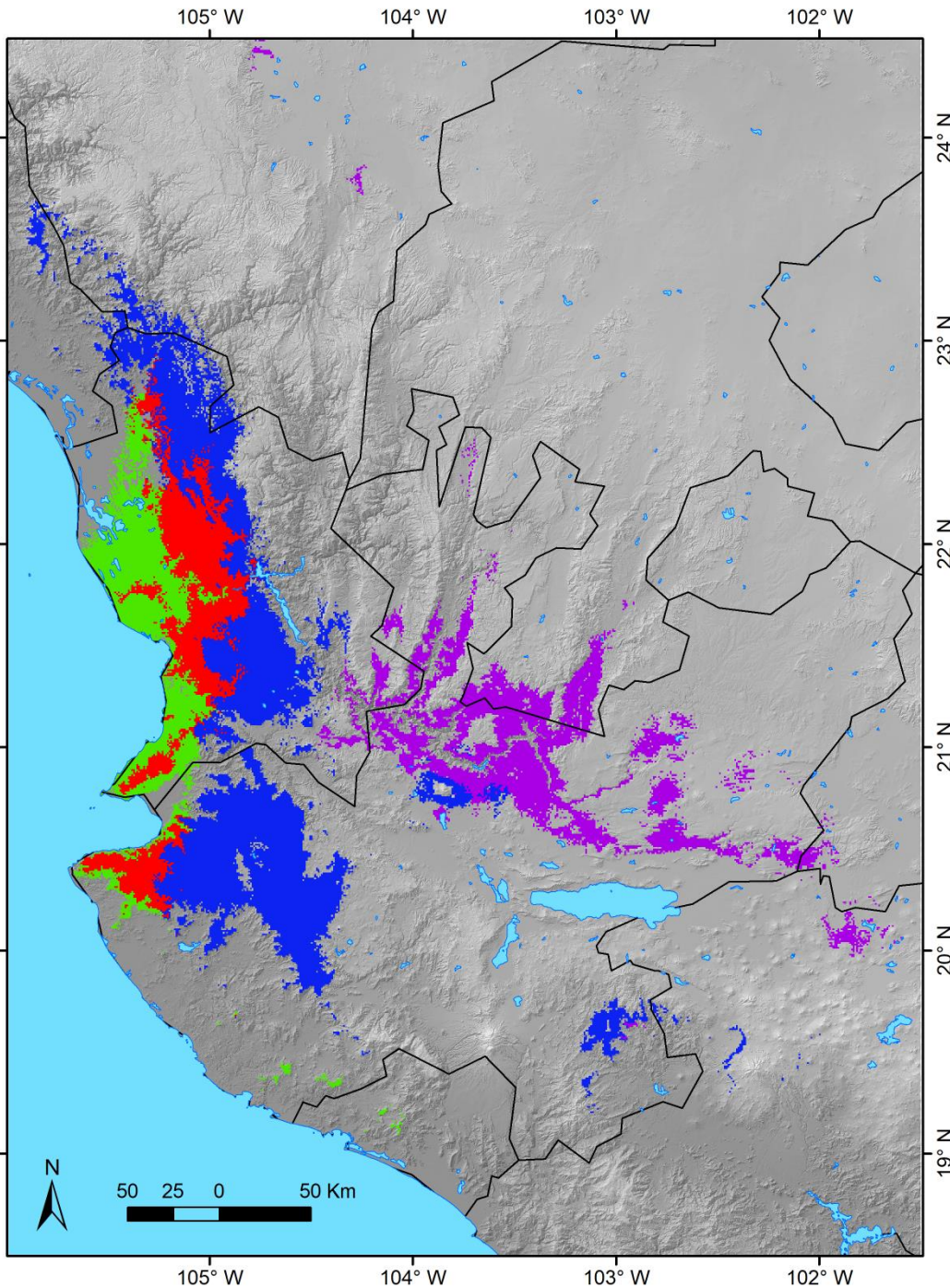
*M. pacifica*



*M. vallartensis*



Overlap area for *M. pacifica* and *M. vallartensis*

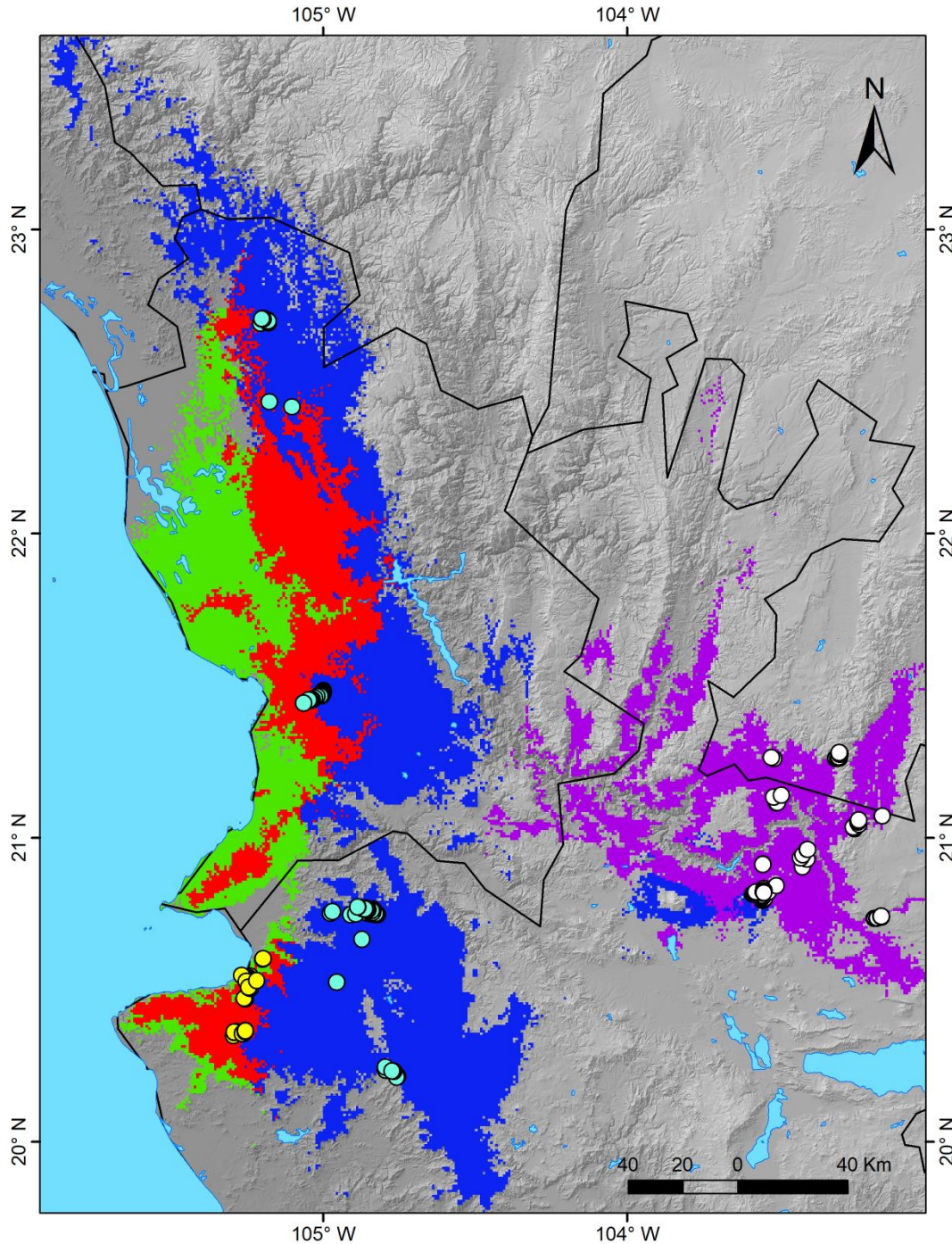
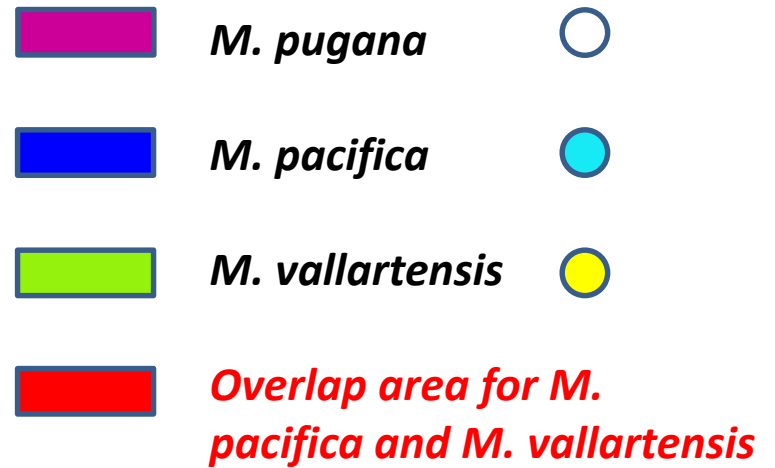




# RESULTS

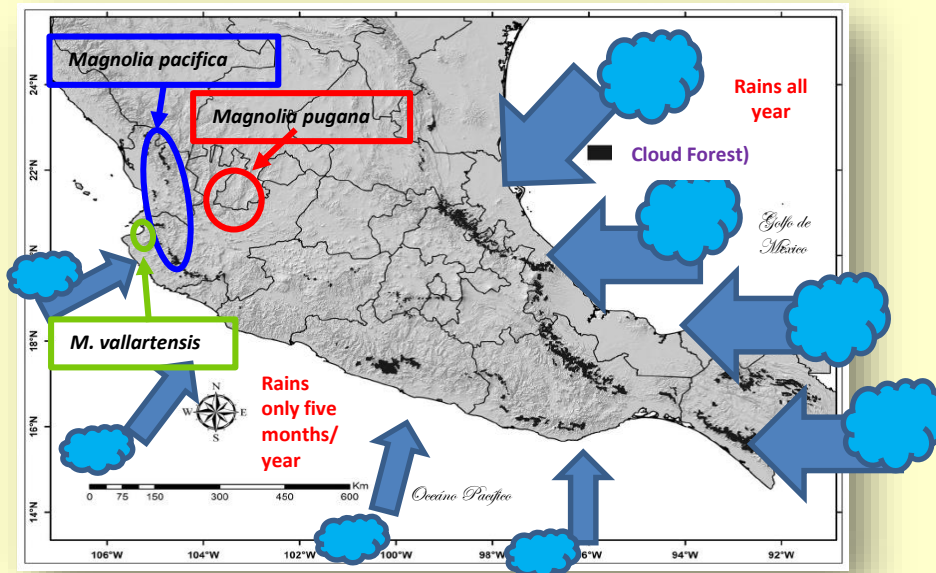
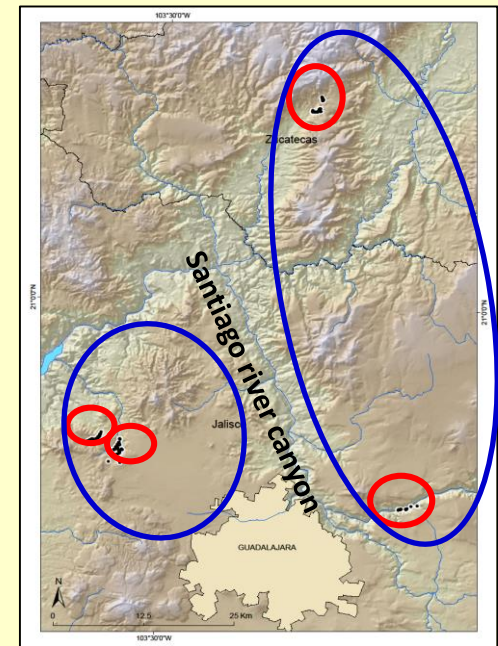
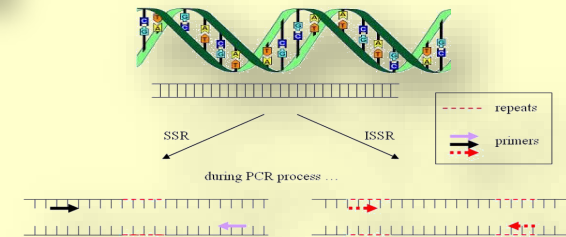
## SPECIES GEOGRAPHIC DISTRIBUTION MODELS

### POTENTIAL DISTRIBUTION AREAS



# Conclusions

1. ISSR markers are a useful and complementary tool **helping to species delimitation in taxonomy complexes of closely related species.**
2. **Two major genetic groups** in the *Magnolia pacifica* complex in SW Mexico:
  1. *M. vallartensis* and *M. pacifica* s.s. form a group and are in current process of **parapatric and ecological divergence.**
  2. A second group: **two allopatric panmictic subpopulations of *M. pugana*** separated by **Santiago Canyon partial barrier.**





# Conclusions

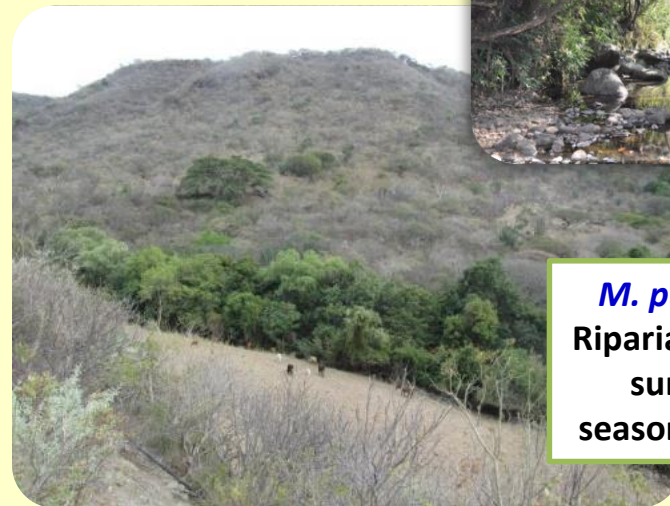
3. The current taxonomical status (three species) is supported by **the higher genetic structure between these species than within species**,
4. but the ISSR genetic differentiation between *M. vallartensis* and *M. pacifica* s.s. subpop. is not significant.
5. The four genetic groups deserves especific conservation efforts, **but *M. pugana* ones are imore endangered**, because their lower genetic diversity and higher isolation, **so they need more protection priority**.



*M. pacifica* s.s. and  
*M. vallartensis* habitat  
Cloud forest



*M. pugana* habitat  
Riparian gallery forest  
surrounded by  
seasonally dry forest





# CONCLUSIONS

6. The results for the differentiation of ecological niches and areas of potential geographical distribution **support the results of genetic divergence.**
7. The ecological niche and the geographical distribution of *M. pugana* **are completely separated from the other two species.**
8. **The potential geographical distribution of *M. pacifica* and *M. vallartensis*, although different in their greater proportion, present a partial overlap.** The foregoing indicates an ecological divergence not very far between these two species.

Thanks !!!



PRO-SNI  
P3E



**promEP**

PROMEP/103.5/12/3418

