



**ESTIMATING GENETIC
EROSION USING THE
EXAMPLE OF *PICEA
CHIHUAHUANA*
MARTINEZ**

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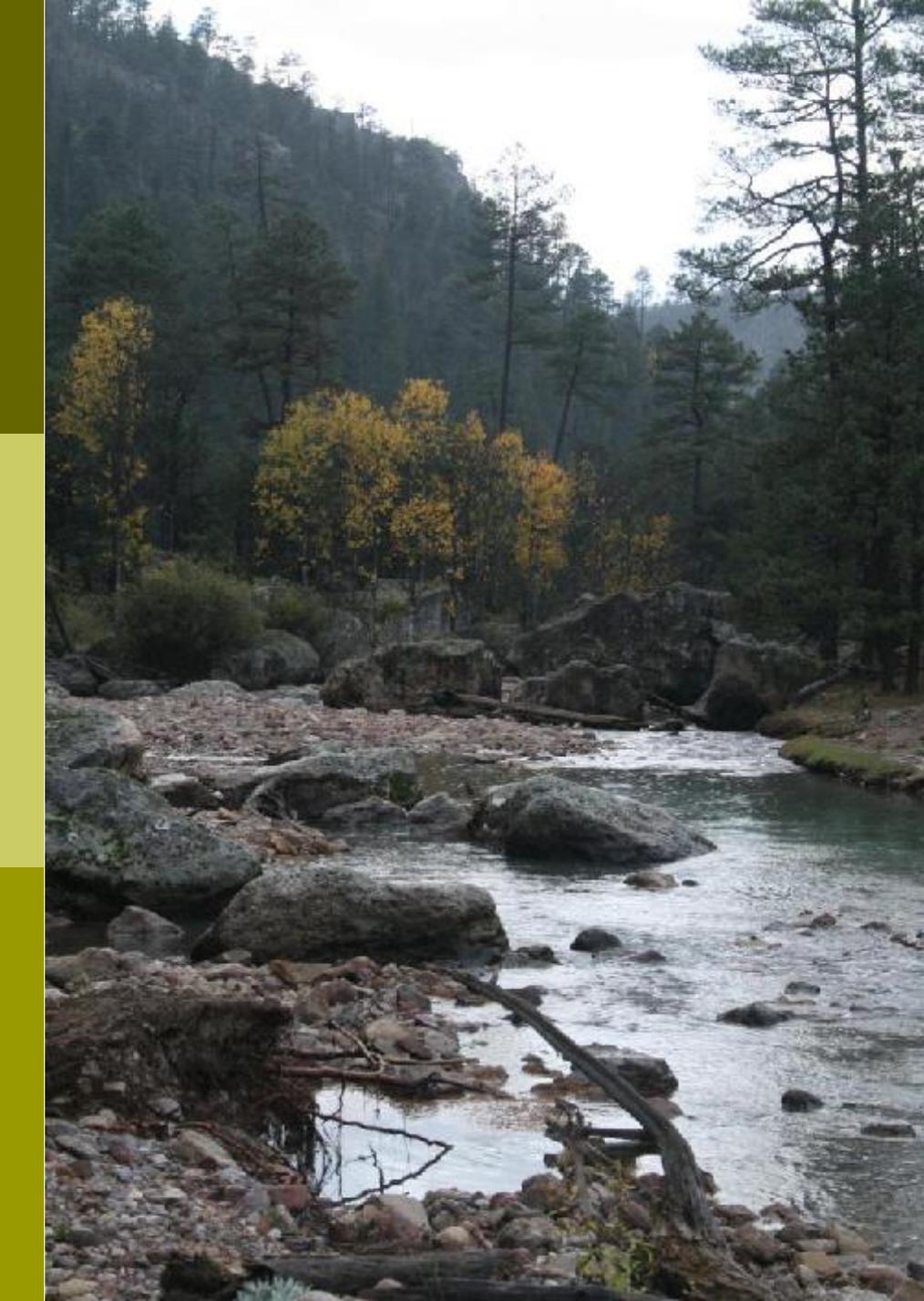
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Introduction (1)

- Genetic erosion can be detrimental to
 - the short-term viability of individuals and populations,
 - the evolutionary potential of populations and species, and
 - the direct use of genetic resources (Brown et al. 1997).
- Therefore, various international and inter-governmental organizations and networks have recognized the need to assess and monitor plant genetic erosion in order to reverse this tendency (Diulgheroff 2006).
- But a literature review has shown that there are, unexpectedly, only few studies on assessing this important process in forest tree communities.



Introduction (2)

- ❑ **Genetic erosion** can be viewed as the
 - 1) loss of genetic diversity, in a particular location and over a particular period of time,
 - 2) including the loss of individual genes, and
 - 3) the loss of particular combinations of genes such as
 - 4) those manifested in landraces or varieties.
- ❑ It is thus a function of change of genetic diversity over time (FAO/IPGRI, 2002).
- ❑ This definition does not specify whether genetic erosion is caused by adaptation (selection), genetic drift or inbreeding.

Introduction (3)

- In relation to estimating potential genetic erosion, the endemic and rare tree species *Picea chihuahuana* Martinez, so known as Chihuahua spruce or prickly spruce, is an excellent research subject.
- It occurs in about 39 often isolated relict populations between altitudes of 2,155 and 2,990m in the Sierra Madre Occidental in the states of Durango and Chihuahua, Mexico.
- The population size varies from 21 to 5546 individuals including trees, saplings and seedlings.



Introduction (4)

- Thus, according to our previous definition, genetic erosion has proceeded in the species as a whole since the last glacial period.
- However, the question remains open whether genetic erosion took or takes place in single isolated populations recently (within a tree age).
- Therefore, in this study we tested five populations of *Picea chihuahuana* M. in Durango State, Mexico, for genetic erosion comparing genetic diversity among diameter at breast height (DBH) classes as a surrogate variable for time.

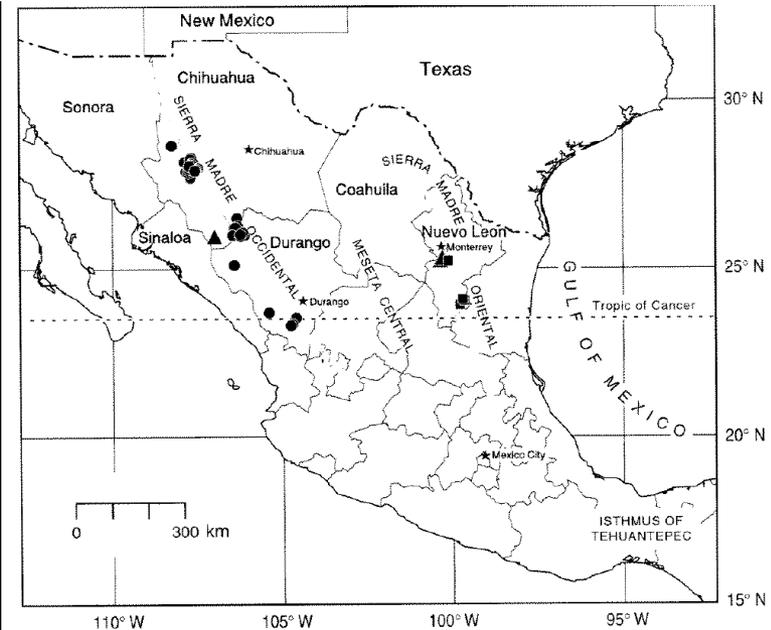
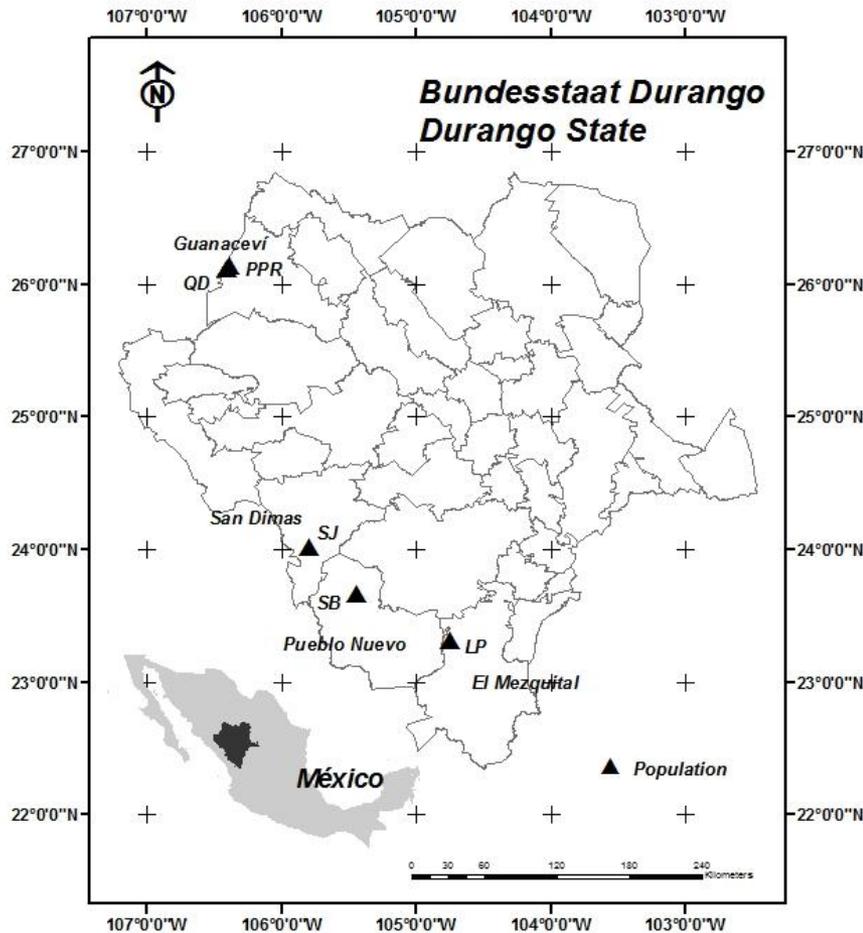


Fig. 1: Locations of Chihuahua spruce (●) (Ledig et al. 2000)

Study sites and populations studied



- Branches were collected separately from 254 randomly chosen individuals of *Picea chihuahuana* M. distributed in the five populations (Fig. 2).
- Additionally, the diameter at breast height (*DBH*) for trees and saplings and the diameter at ground level for seedlings were assessed for every studied individual, along with other variables.

Fig. 2. Map of the five locations of the studied populations of *Picea chihuahuana* M. in the State of Durango, Mexico.

Methods (1)

- DNA data from frozen needles were obtained by amplified fragment length polymorphism (*AFLP*) technology.
- The genotype diversity in every *DBH* class and at each gene locus was quantified by the measure total population differentiation or differentiation within populations (collectives) (δ_T) (Gregorius 1987).



$$\delta_T = \frac{N}{N-1} \left(1 - \sum_i p_i^2 \right)$$

Methods (2)

- In order to test the possibility that a positive trend between diameter classes (d_c) and observed degrees of δ_T per d_c is produced solely by random events rather than directed forces (e.g. genetic erosion), at each gene locus (L),
 - a two-sided permutation test was performed
 - for the observed degrees of covariation (C) (Gregorius et al. 2007).

$$C := \frac{\sum_{i < j} (X_i - X_j) \cdot (Y_i - Y_j)}{\sum_{i < j} |(X_i - X_j) \cdot (Y_i - Y_j)|}$$

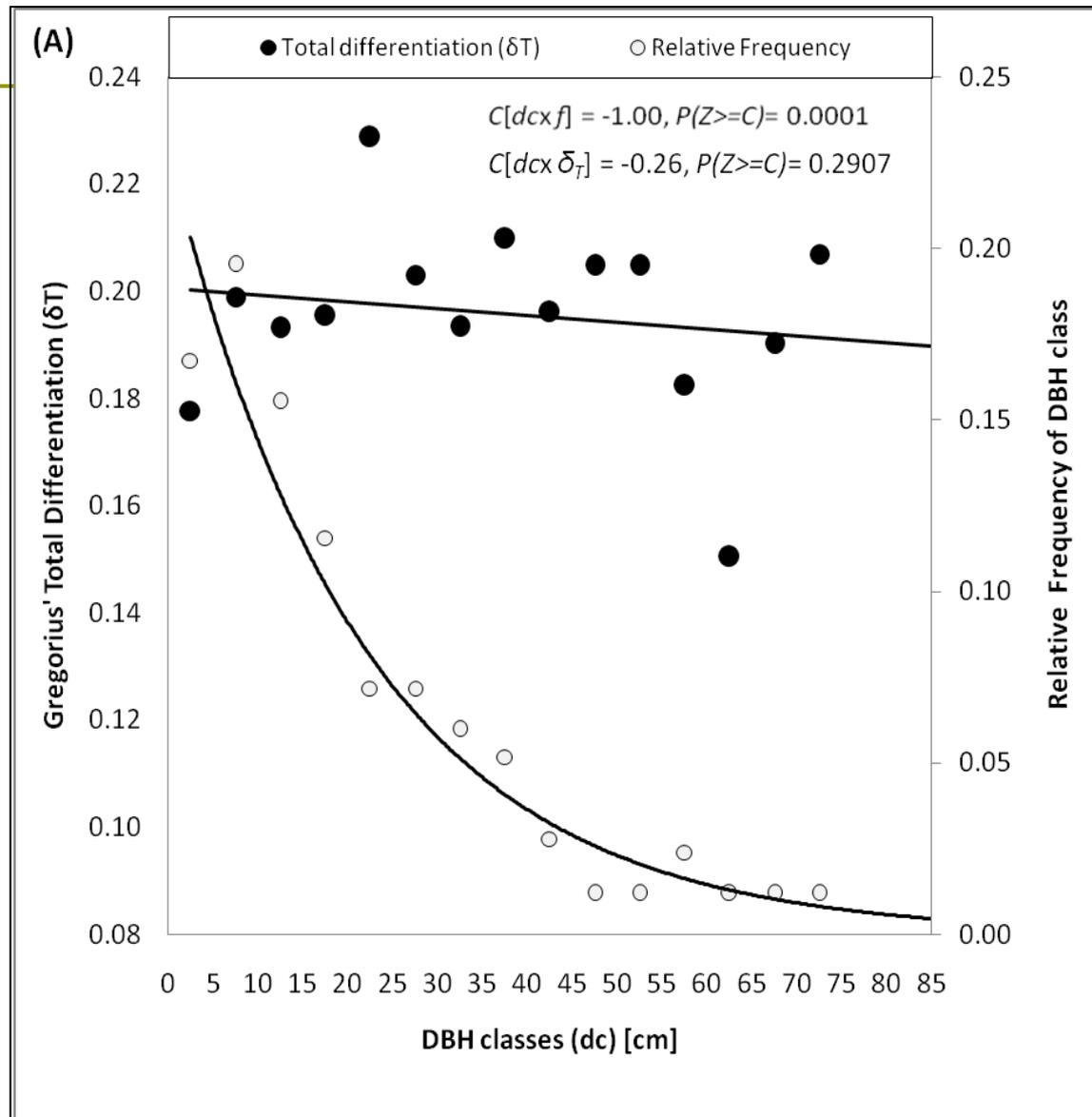
Results (1)

- (1) The *AFLP* primer combination resulted in 319 polymorphic bands of 75-500 base pairs across all 254 individuals.
- (2) The mean total genetic differentiation is positively correlated with the population size ($C[\delta_T \times N] = 1.00$; $P(Z \geq C) = 0.017$).
- (3) Positive $C[d_c \times \delta_{T,L}]$ and, thus, genetic erosion were only detected in two larger populations at 2.8% of *AFLP* loci and in at 0.6% of loci.

Results (2)

(4) On the analysis lumping individuals across the five populations, there were not statistically significant C at the 319 loci (Fig. 3).

Fig. 3. Relationships between DBH classes and mean δ_T , across all populations and for observed relative diameter distribution.



Results (3)

(5) Only C between d_c and mean δ_T among all loci was significant positive in population *San Jose de Causas* (SJ) (Fig. 4).

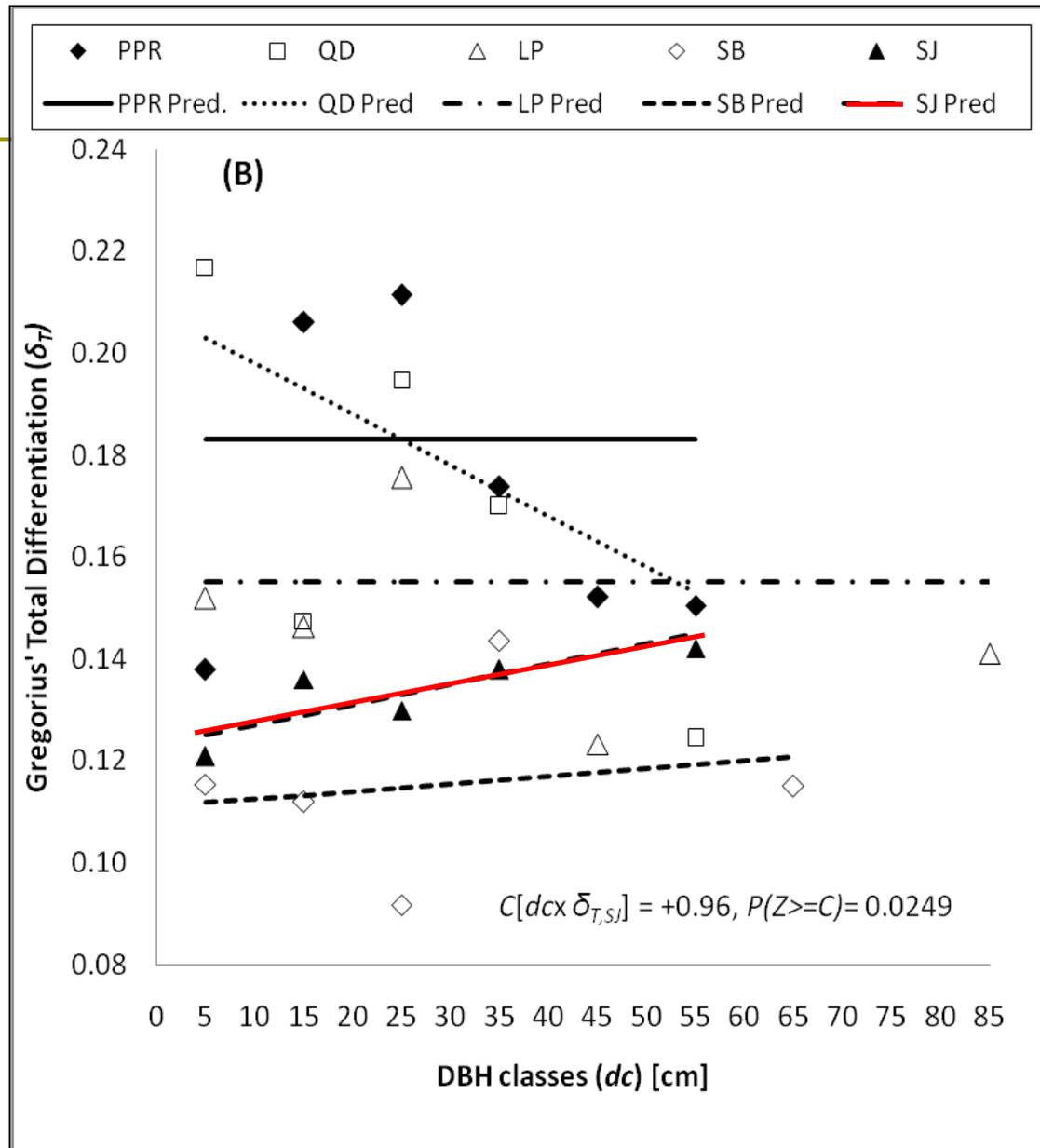


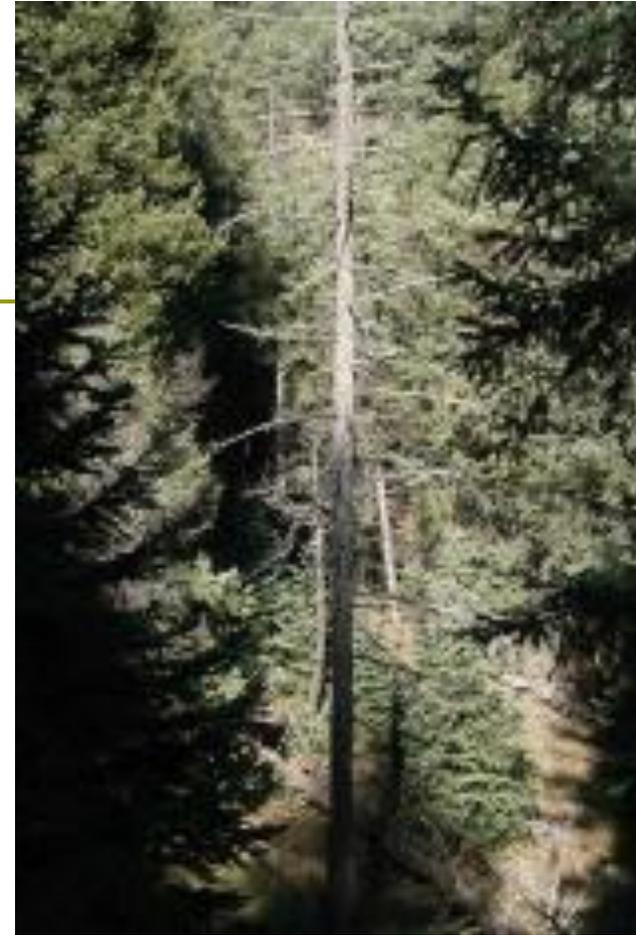
Fig. 4. Relationships between DBH classes and mean δ_T for each population.

Discussion (1)

- ❑ This study presents a user-friendly method estimating genotype erosion.
- ❑ If genetic diversity at a set of *AFLP* loci reflects diversity in the genome as a whole,
 - genetic erosion per se is not the reason for the relictual status of Chihuahua Spruce,
 - excluding the very small populations like San José de Causas (*SJ*).
- ❑ Probably, *SJ* with about 120 trees but only an effective population size of 45 has fallen below the level of a minimum viable population size.

Discussion (2)

- It is important to note that the trend of genetic erosion can be reversed if pollen and/or seedlings originated from seeds (collected) from old trees (containing larger genetic variation than younger individuals) are reintroduced in the original populations or to different populations.
- The predicted reduction and eventual disappearance of a suitable climatic habitat for *P. chihuana* due to climatic change (Ledig et al. 2010) imposes an additional risk of extinction.



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Thank you for your attention!