

## Caribbean Pine Questions:

### Biogeography

Is this pattern of dispersal unique to Caribbean *Pinus*, or is dispersal from Central America common for Caribbean Basin fauna and flora? The authors noted there is no reason to believe an origin from North America. Are there any cases of dispersal from Florida to the Caribbean, or is dispersal more likely to occur from the Caribbean to Florida?

Do these species of *Pinus* disperse their seeds at the time of Hurricanes or other major weather systems? How does this affect the direction of seed dispersal? Does this, coupled with the seeds of some Pine species, pre-dispose them to multiple, long distance dispersals?

Is *Pinus occidentalis* still extant on the Haitian side of Hispaniola? If so, how might the addition of those populations to the study have affected the relationship of *P. occidentalis* and *Pinus cubensis* in the Minimum spanning network?

### Hybridization

Are there any reports of hybrids between the four species of Caribbean *Pinus*?

Assuming that the interchange of plastid clusters was mediated by seeds (and also assuming that at least the populations involved weren't monospecific so there are mixed populations of *P. caribea* var *caribea* and *P. caribea* var *hondurensis*), now that these two varieties got closer it would be expected to find they are breeding, as this is apparently not happening (no shared plastids between varieties), are we really talking about varieties? or proper reproductively isolated species?

### Methodology

I find somewhat confusing (or contradictory?) the discussion about the small cluster of plastid of *Pinus caribea* var *caribea* in the population of *P. caribea* var. *hondurensis* (and viceversa), the authors say it could be explained by seed dispersal rather than pollen transfer, but wouldn't it mean that the populations weren't monospecific as they claimed in materials and methods?

What are some of the pros and cons of using haplotype networks? Are they better suited for population-level analyses than are 'traditional' phylogenetic analyses?

How does the mismatch distribution analysis work? I did not understand what they are comparing (e.g. what are assumptions of the simulated distribution, which are the alternatives to sudden expansion model?)

The authors says they cannot use a stepwise mutation model in BAPS (pg 232) for finding geographical structure of genetic variation. What does it mean? Would it have large effects in the results?

The authors use gene flow to explain why some haplotypes of var. *caribaea* are more closely related to var. *hondurensis* than to the rest of var. *caribaea*. Are there alternate explanations for this observation? Also, the authors indicate three "ancestral" haplotypes in Figure 3 (indicated by the squares) - is there any geographical signal associated with these or any other explanation for why these three haplotypes would be the most connected?