

Authors: A. Dodonova*, D. Petrova*, E. Popova*, A. Minnegalieva, N. Zolotarev, K. Przesmycka, O. Lukasiewicz, J. Raubic, W. Babik, M. Konczal, M. Herdegen-Radwan, J. Radwan

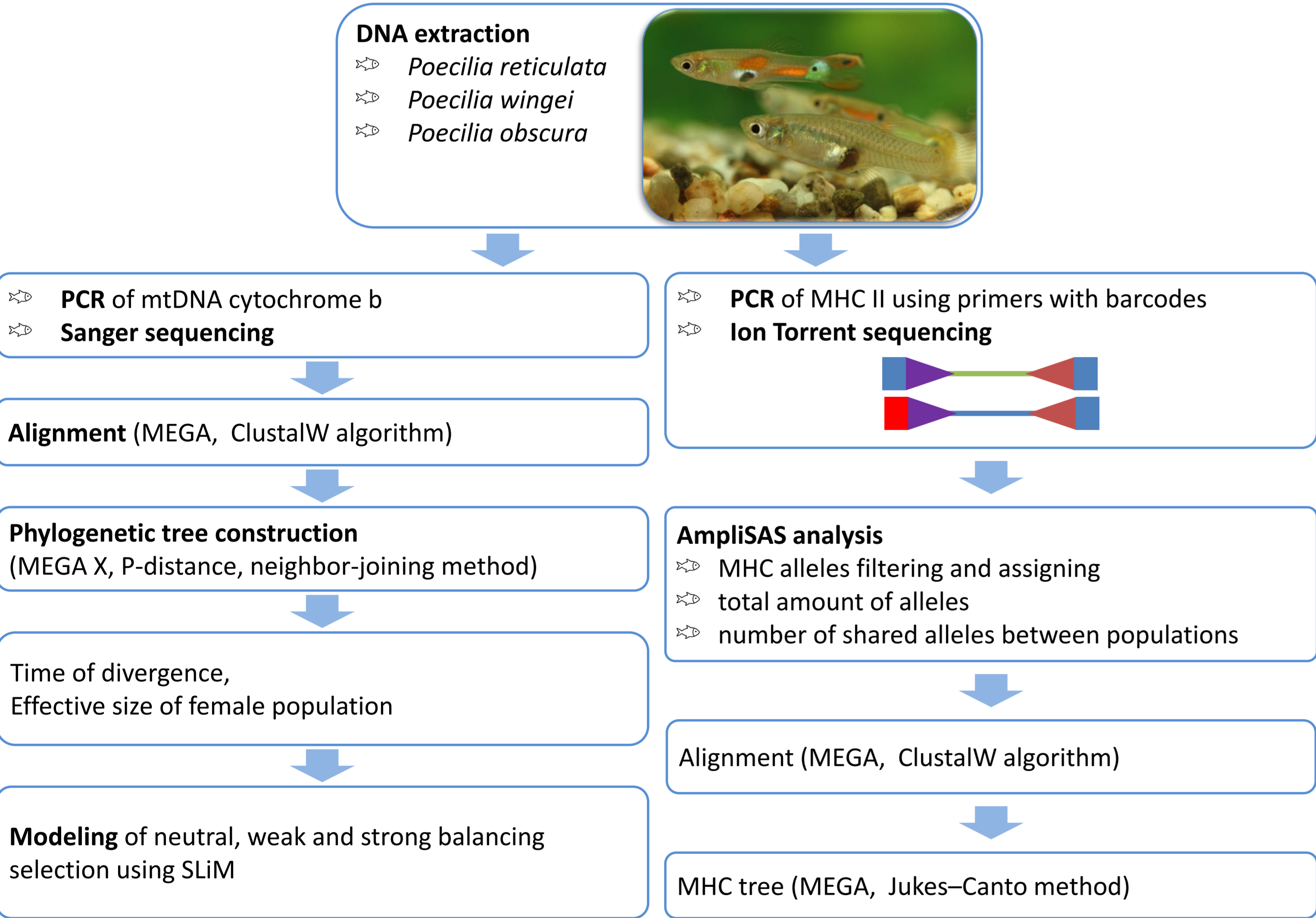
Introduction

- Co-evolution of parasites and hosts leads to the strong positive selection of Major Histocompatibility Complex (MHC) genes, because new alleles give their carriers advantage.
- Quick genetic fund changes in populations should result with decrease of numbers of shared alleles between them after the divergence. Despite this fact, we observe trans-species polymorphism – situation when some alleles are more similar between individuals in different species than within their population.
- The new hypothesis suggests that positive selection also supports introgression of MHC genes between hybridizing species. We want to test it by comparing shared alleles in different population of guppy, some of which was put into secondary contact by human.



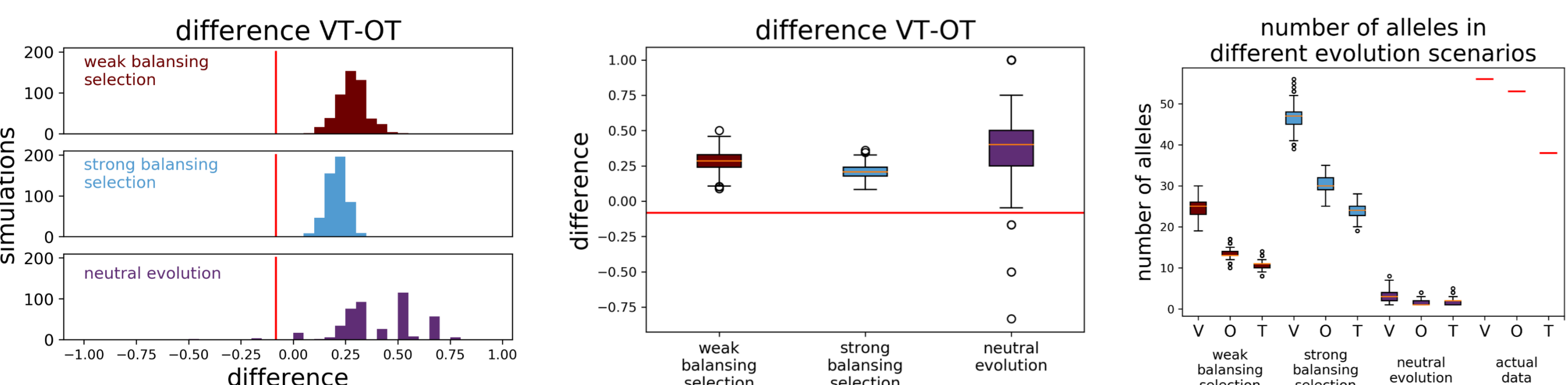
There are three different species presented on the map: *P. reticulata* (green), *P. wingei* (red) and *P. obscura* (blue). Despite overall genetic divergence, geographic proximity may allow for limited flow of MHC genes between *P. wingei* and *P. reticulata* in Venezuela, and *P. obscura* and *P. reticulata* on Trinidad. Gene flow is less likely between populations of *P. reticulata* which are separated by the sea.

Experiment and analysis setup



Simulation

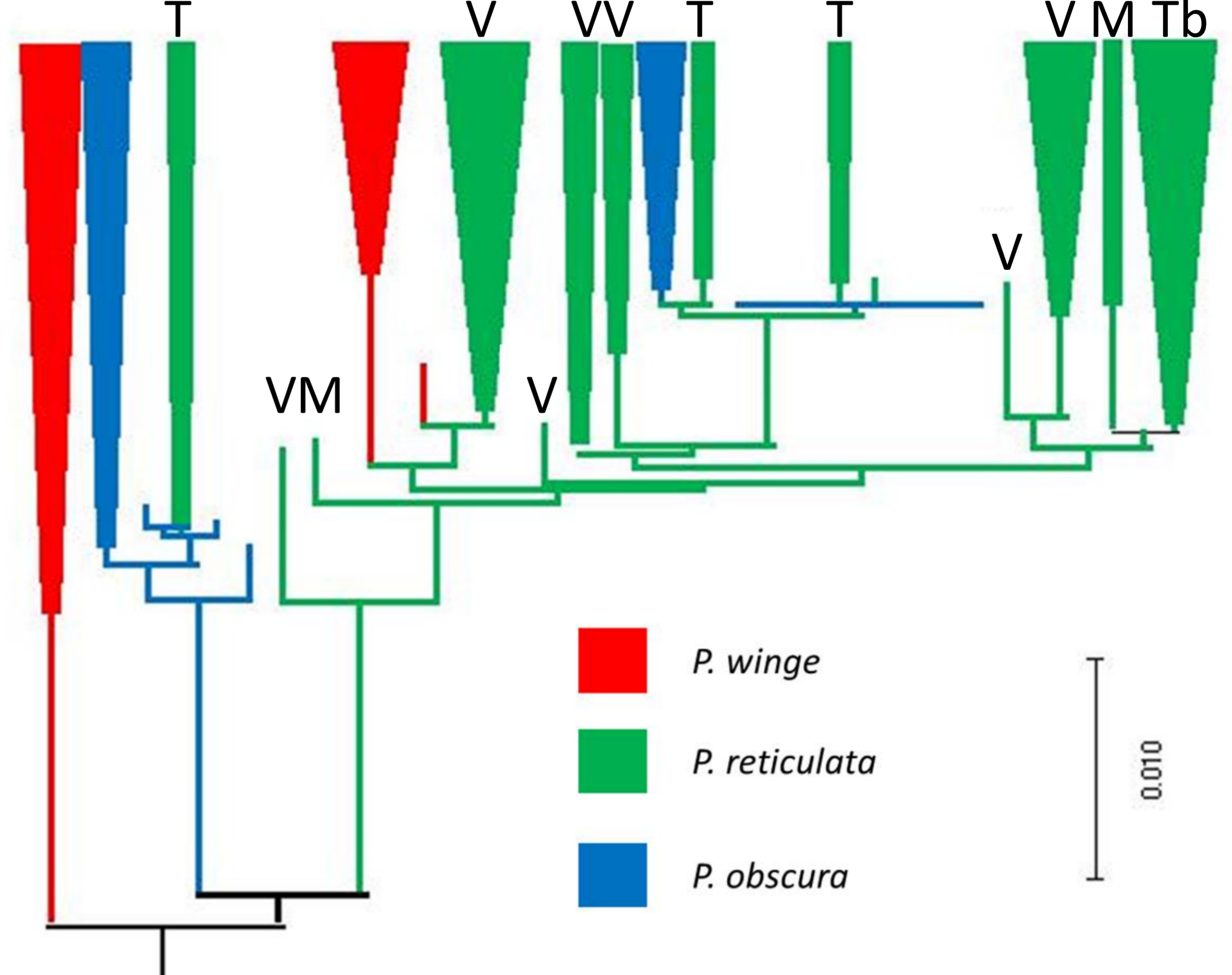
We simulated divergence of three groups from the original Venezuela population (V). *P. obscura* (O) separated 870k years ago and Trinidad population (T) of *P. reticulata* separated 220k years ago. We ran three simulations with difference scenarios: neutral evolution, strong and weak balancing selection. For initial settings we used estimated values based on real data including divergence time ($t = \frac{d}{2u}$) and effective population size ($N_{ef} = \pi 2u$). Mutation rate (u) estimated as 2% mutations per million years.



Distribution of differences in shared allele frequencies between closely related (VT) and more distant (OT) population for various evolution scenarios; thin red line represents actual data.

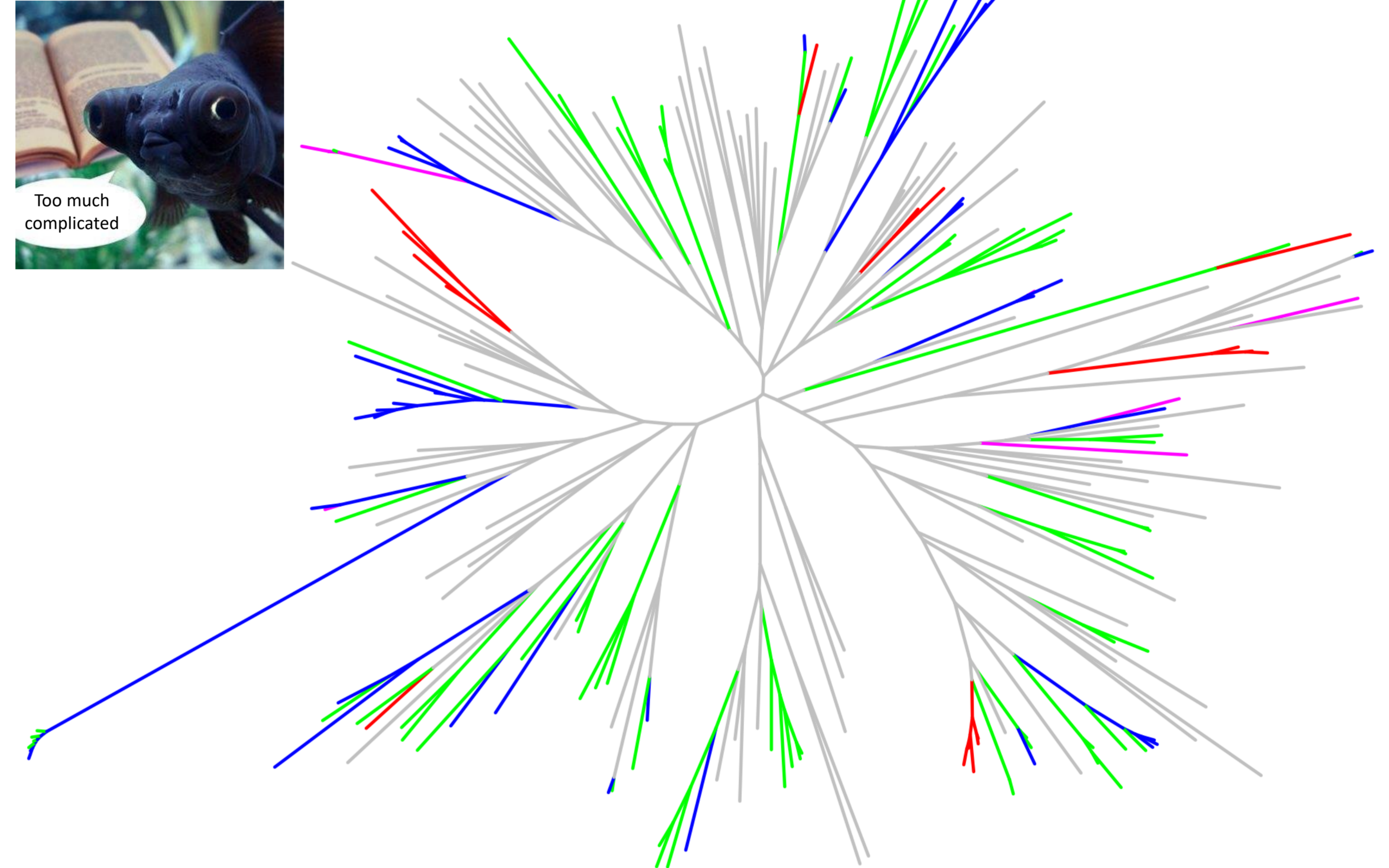
The number of alleles in three populations for each of the different evolution scenarios.

mtDNA phylogenetic tree



Phylogenetic tree of fragment of mitochondrial cytochrome B gene sequence (945 bp). Alleles belonging to different species have been color coded. Assuming the mutation rate of 2% per million years divergence between species can be dated at about 870k years and between *P. reticulata* population of different island at 220k years.

MHC phylogenetic tree



Phylogenetic tree of fragment of MHC II DAB gene sequence (II exon, 217 bp), alleles belonging to different species have been color coded only for clades with 70% or above bootstrap support. Example of trans-species polymorphism are indicated by pink.

Shared alleles between populations

	O-T	V-O	V-W	V-Tb	V-M	V-T	
All alleles	84	107	90	85	64	94	O – <i>P. obscura</i> W – <i>P. wingei</i>
Shared alleles	7	0	0	1	1	0	T – <i>P. reticulata</i> (Trinidad) Tb – <i>P. reticulata</i> (Tobago)
Frequency of shared alleles	0.083	0.000	0.000	0.012	0.016	0.000	V – <i>P. reticulata</i> (Venezuela) M – <i>P. reticulata</i> (Margarita)
	different species			<i>P. reticulata</i> specie			

This table represents that there are more shared alleles between *P. obscura* and *P. reticulata* inhabiting Trinidad island rather than between all *P. reticulata* species. Four of seven shared alleles comes from fish with different mtDNA.

Conclusions

- mtDNA tree showed larger divergence between putative species (*P. reticulata*, *P. obscura* and *P. wingei*) than between *P. reticulata* populations divided by the sea.
- The tree indicates old introgression of *P. reticulata* mtDNA to *P. wingei* and recent introgression between *P. reticulata* and *P. obscura*.
- More MHC alleles are shared between Trinidadian *P. reticulata* and *P. obscura* than between Venezuelan and Island populations of *P. reticulata*.
- Simulations showed that the pattern of MHC allele sharing can only be explained by introgression.
- MHC gene tree show patterns characteristic of trans-species polymorphism, including highly similar alleles between species in for which there is no evidence for introgression (*P. obscura* and *P. wingei*).
- Both introgression and balancing selection likely contributed to trans-species polymorphism in closely related *Poecilia* species.**