



Population structure of guppies in north-eastern Venezuela, the area of putative incipient speciation

Magdalena Herdegen¹, Heather J. Alexander², Wiesław Babik¹, Jesús Mavárez^{3,4}, Felix Breden⁵ and Jacek Radwan⁶

¹ Institute of Environmental Sciences, Jagiellonian University, Gronostajowa 7, 30-387, Krakow, Poland
² Bamfield Marine Sciences Centre, University of Victoria, Bamfield, British Columbia, V0R 1B0, Canada
³ Centro de Ecología, Instituto Venezolano de Investigaciones Científicas, Apartado 20632, Caracas 1020-A Venezuela;
⁴ Laboratoire d'Ecologie Alpine, UMR 5553 CNRS-Université Joseph Fourier, BP 53 2233 Rue de la Piscine, 38041 Grenoble, France 11
⁵ Department of Biological Sciences, Simon Fraser University, Burnaby, British Columbia V5A 1S6, Canada
⁶ Institute of Environmental Biology, Faculty of Biology, Adam Mickiewicz University, Umultowska 89, 61-614 Poznan, Poland

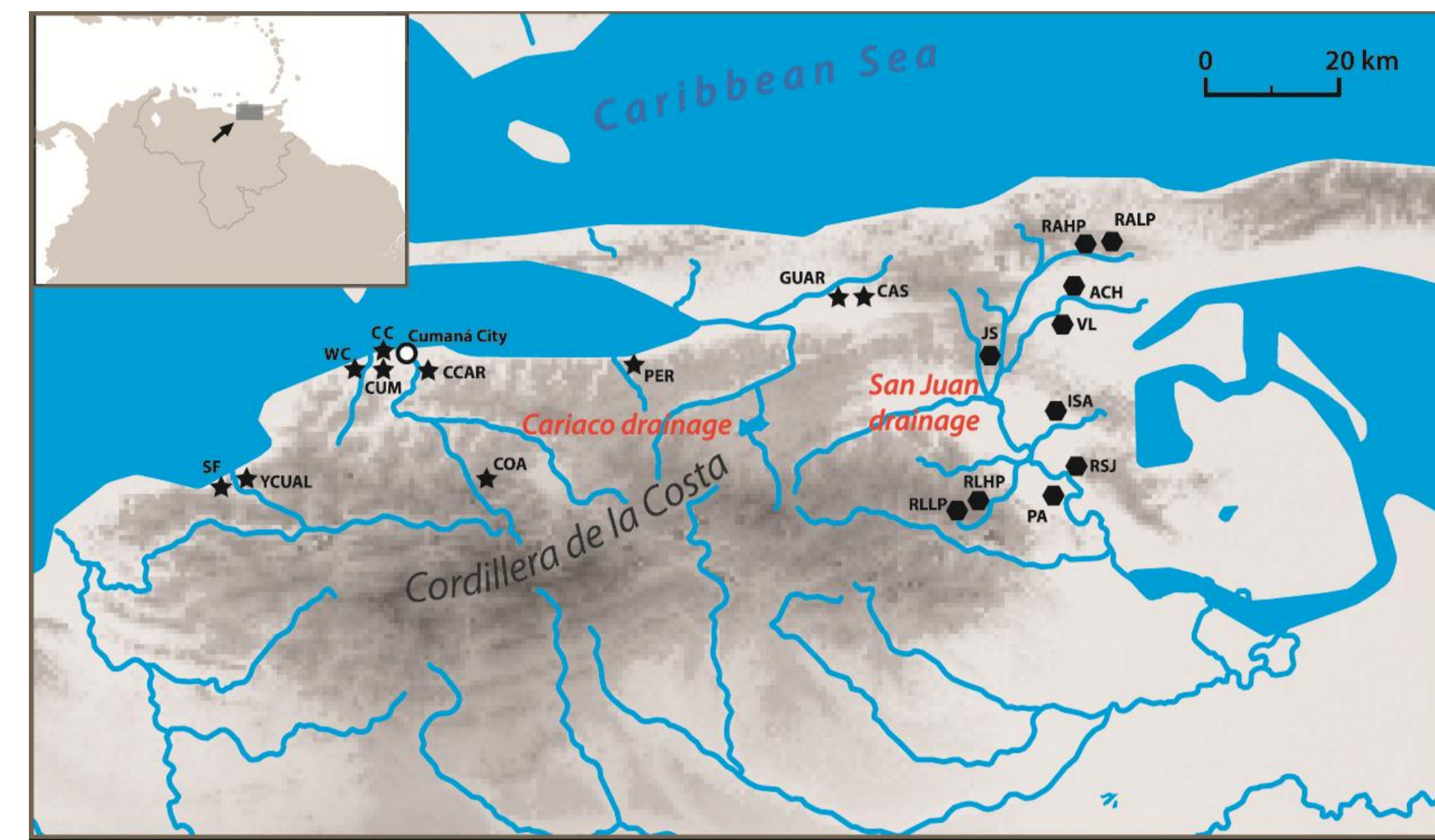


Fig. 1. Sampling sites in northern Venezuela. Locations within the Cariaco drainage are marked with stars, within the San Juan drainage locations with hexagons.

Introduction and aim of the study:

Geographic barriers and divergent selection on sexual traits are among factors facilitating genetic and reproductive isolation, which in turn may lead to speciation. The guppy from the Cumaná region (within the Cariaco drainage, see map) of eastern Venezuela has been previously described as a case of incipient speciation driven by sexual selection (Alexander and Breden 2006), significantly differentiated in sexual colouration and body shape from the typical common guppy, *Poecilia reticulata*, occurring widely in northern Venezuela, including the south-eastern side of Cordillera de la Costa (San Juan drainage, see map).

The main goal of this study was to quantify genetic and phenotypic differentiation among populations in the Cariaco and San Juan drainages, to understand the degree of divergence and putative isolation mechanisms between those two groups of populations.



Fig. 2A) Cumaná type guppy (from Cariaco drainage)



Fig. 2B) typical common guppy (from San Juan drainage)

Methods:

- samples: 10 populations from Cariaco and 10 populations from San Juan drainages (see map)
- markers: mitochondrial DNA - cytochrome *b* (504 individuals); 15 microsatellite loci (519 individuals)
- body shape and sexually selected colour patterns: number of black crescents, presence/absence of a double sword on the caudal fin, tail orange area and the thickness of the caudal peduncle (shown to differ between Cumaná and common guppy, Alexander and Breden 2004)

1. Multidimensional scaling of genetic distances showed that Cariaco and San Juan drainage populations generally cluster separately.

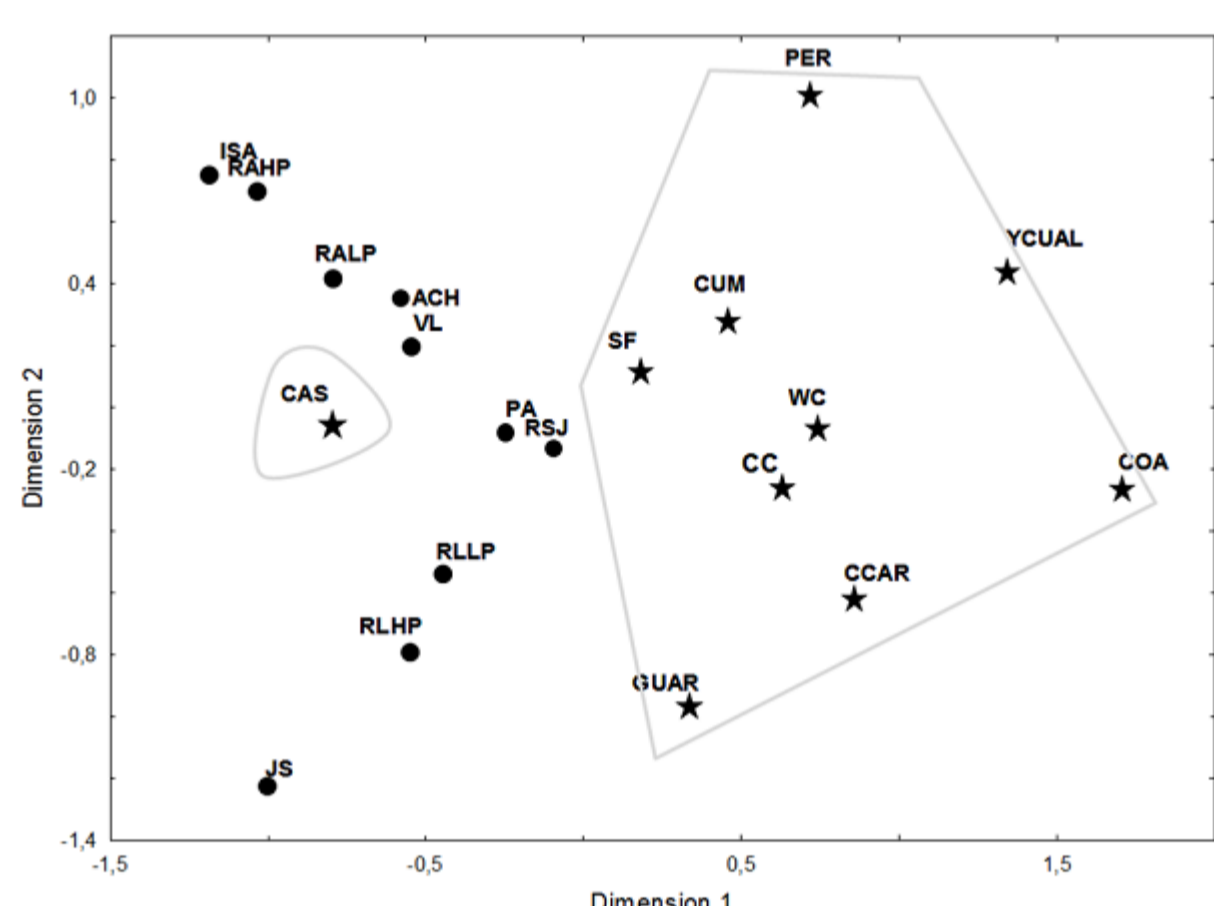


Fig. 3. Multidimensional scaling. Two-dimensional scaling of the matrix of pairwise F_{ST} values between all sampled populations based on microsatellite frequencies; Cariaco drainage populations are enclosed in grey lines.

2. The most likely number of genetic clusters identified in STRUCTURE analysis was 8.

When $K=2$ was enforced, populations from Cariaco and San Juan drainages fell into separate clusters, but populations GUAR, CAS and SF located near the border of the regions, showed admixture of San Juan alleles.

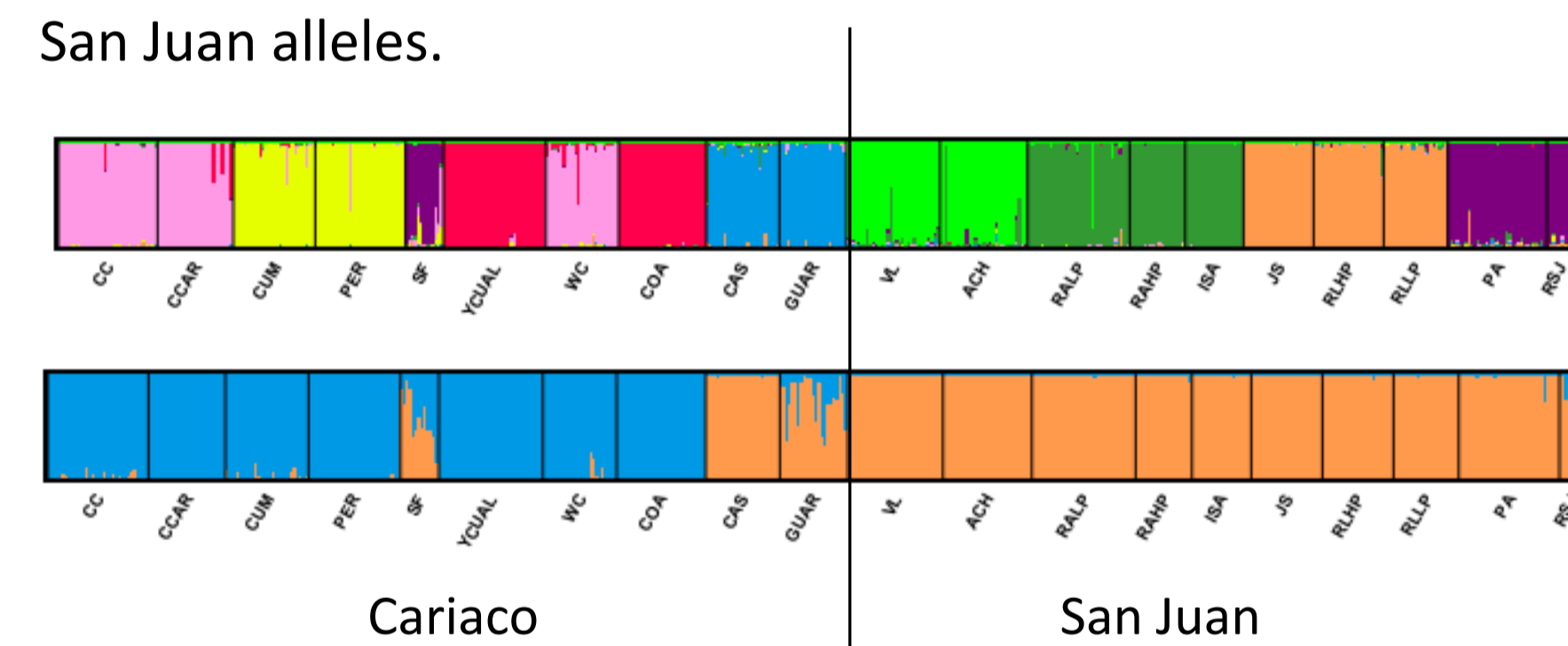


Fig. 4. STRUCTURE analysis based on 15 microsatellite loci. Results for A) $K=8$, B) $K=2$.

3. Analysis of molecular variance showed a considerable differentiation between Cariaco and San Juan drainage guppies, although most variance was explained on population level.

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation
Among groups	1	316.721	0.48905 Va	7.83
Among populations within groups	18	1063.020	1.05555 Vb	16.89
Within populations	1018	4789.035	4.70436 Vc	75.28
Total	1037	6168.776	6.24896	

Fig. 5. ANOVA results, with groups defined as the Cariaco and San Juan drainage guppies

4. The 69 identified mitochondrial cytochrome *b* haplotypes cluster into two major lineages corresponding to Cariaco and San Juan drainages. The San Juan lineage harbours a well-supported Cariaco sub-lineage suggesting an old introgression event.

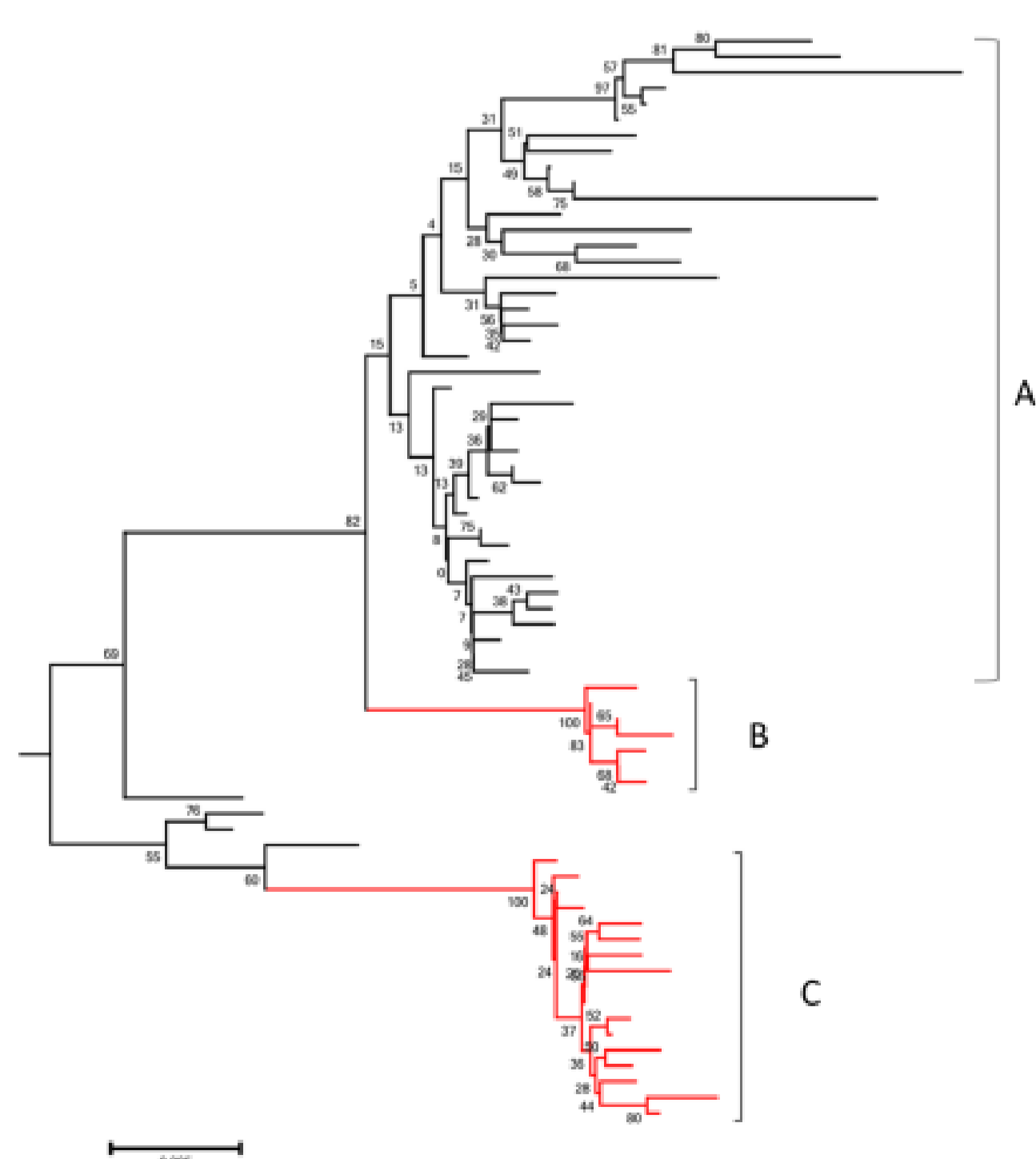


Fig. 6. Mitochondrial neighbour-joining tree. The tree shows the relationships between 69 *P. reticulata* haplotypes; A) haplotypes of guppies from San Juan drainage B and C) haplotypes of guppies from Cariaco drainage; *P. latipinna* was used as the out-group.

5. Among the four phenotypic traits analysed only the mean number of black crescents differed significantly between Cariaco and San Juan guppies ($P=0.0057$, Mann-Whitney test). However, within a group of genetically homogenous populations from the Cumaná region (pink cluster in Fig. 2A; red frames in Fig. 6), CC and WC showed typical Cumaná guppy characteristics, while CCAR represented a common guppy morphotype.

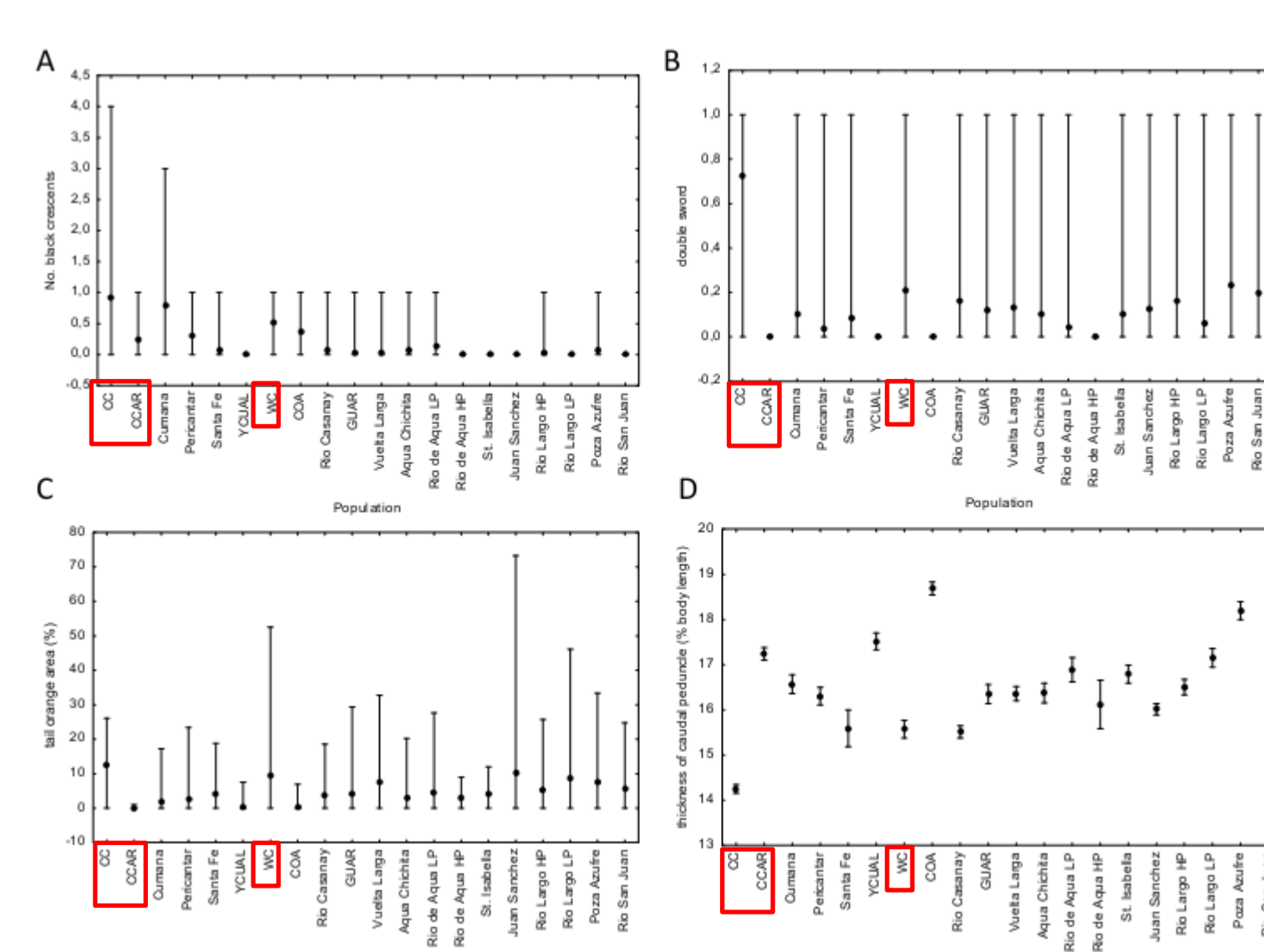


Fig. 7. Phenotypic traits of the sampled populations. (A) mean number of black crescents, (B) mean number of double swords, (C) mean relative orange area on the caudal fin, (D) mean relative thickness of caudal peduncle; error bars represent minimum and maximum values for A, B and C, and standard error for D.

Conclusions:

- significant genetic differentiation between guppy in Cariaco and San Juan drainages
- introgression from San Juan drainage guppies into the Cariaco drainage causing erosion of genetic differentiation of the guppies in the Cariaco region
- little phenotypic differentiation between regions, but a group of typical Cumana guppies resists phenotypic homogenisation with genetically similar guppies from the same region, suggesting a possible role of mate preferences in maintaining differences in sexually selected traits
- minor role of the geographic barrier of Cordillera de la Costa in strengthening the incomplete pre-zygotic reproductive barrier between Cumaná and common guppy relative to the influence of limited gene flow between streams within drainages