DRIVERS OF REPRODUCTIVE ISOLATION IN WALL LIZARDS INFERRED FROM COMPARATIVE ANALYSIS OF CONTACT ZONES

Guilherme Caeiro-Dias[1,2], Alan Brelsford[3], Antigoni Kaliontzopoulou[1], Miguel A. Carretero[1], Pierre-André Crochet[4] , Catarina Pinho[1,*]

[1]CIBIO/InBIO, Research Center in Biodiversity and Genetic Resources, University of Porto, Portugal; [2]Porto University of Sciences, Portugal; [3]Evolution, Ecology, and Organismal Biology Department, University of California Riverside, USA; [4]CEFE, CNRS, Univ Montpellier, Univ Paul Valéry Montpellier 3, EPHE, IRD.

***catarina@cibio.up.pt**

01 INTRODUCTION

We typically think of speciation as a process correlated to divergence time: as time progresses, diverging taxa should experience increasing restrictions to gene exchange. However, other aspects (i.e. ecological or phenotypic divergence for example) may also act as important engines of reproductive isolation (RI).

Stuyding multiple contact zones between closely-related taxa may help disentangle which factors are more important in driving RI.

Here we present preliminary results comparing contact zones in wall lizards.

02 MODEL SYSTEM

Wall lizards *Podarcis* spp. from the Iberian Peninsula and North Africa are a cryptic species complex with a mosaic of distributions establishing many different contact zones.

Figure 1. A male *P. bocagei*. Credits: G. Caeiro-Dias.

03 METHODS

We sampled 9 contact zones between different pairs of wall lizard species.

Multilocus genotypes were characterized using RADseq data.

RI was measured as the average maximum assignment probability across individuals in the contact zone, estimated with software STRUCTURE [1].

Mantel tests were used to evaluate correlations of RI to different predictors:

.nuclear DNA (Dxy based on ~13Kb of nuclear sequence loci, unpublished data; **nuc-Dxy**)

.mitochondrial DNA (Dxy based on ~2.2Kb of mtDNA sequence [2]; **mt-Dxy**)

.body size (euclidean distances on species mean snout-vent length [3]; **ed-svl**)

morphology (squared Mahalanobis distance on size-adjusted biometric variables [3]; **d2-biom**)

.ecological niche (ecological niche model overlap based on climatic variables [4]; **enm-D**)

.distribution overlap (Jacquard similarity index [4], **dist-JSI**)

.preferred temperatures (squared Mahalanobis distance between species [5-7], **d2-TP**)

.evaporative water loss (squared Mahalanobis distance between species [5-7], **d2-EWL**)

04 RESULTS & DISCUSSION

Most contact zones are highly bimodal, yet levels of admixture vary depending on the pair.

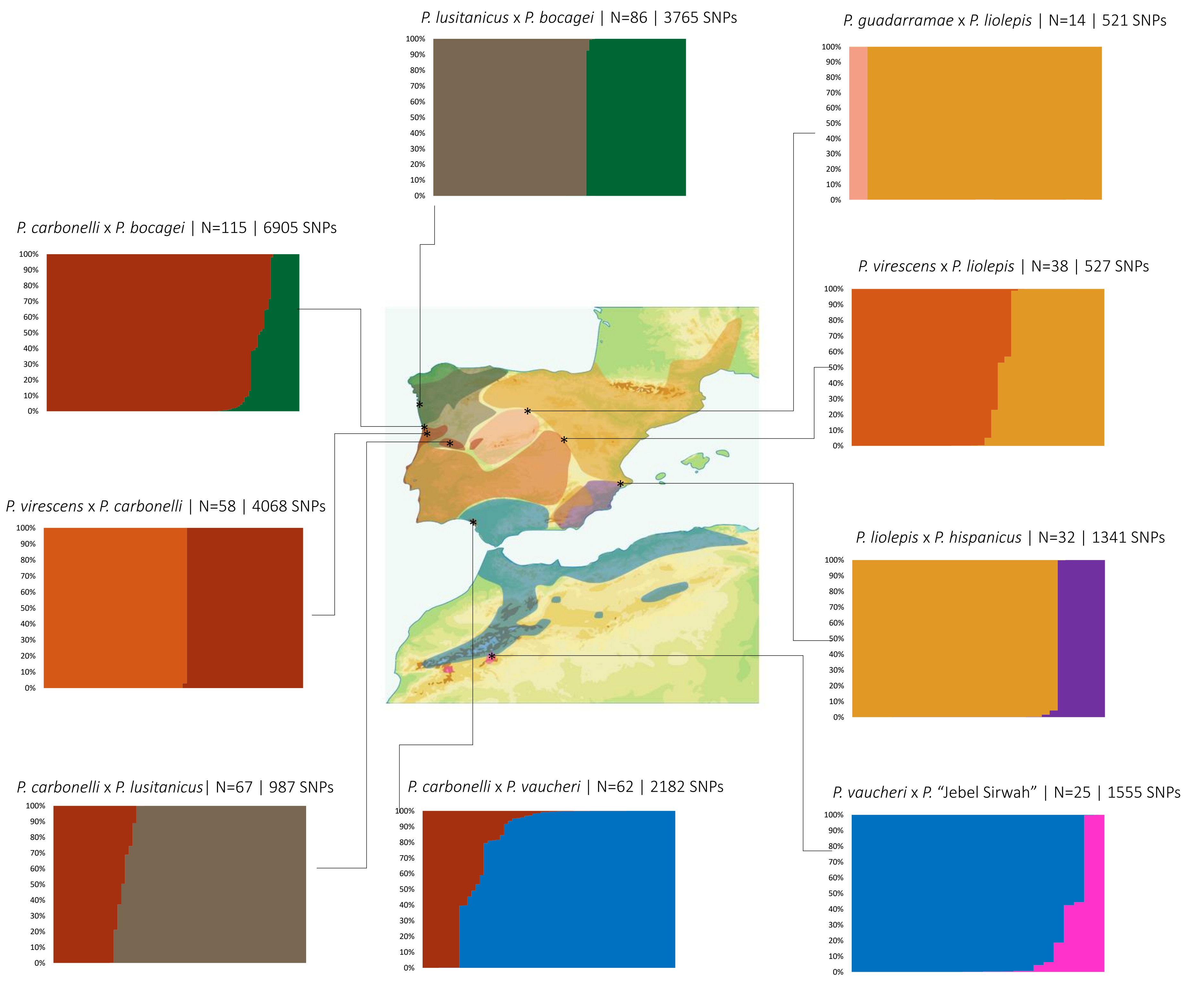

Figure 2. Distribution of species of the *Podarcis hispanicus* species complex, location of the contact zones analysed and genetic profile of each contact zone.

Remarkably, there is no correlation between genome divergence (either nuclear or mitochondrial) and levels of gene exchange, unlike the trend in other taxa. Our preliminary results suggest that differences in **hydric physiology** (water loss) and to a lesser extent **morphology** may be related to restrictions to gene flow and suggest that aspects other than genome divergence may be important in determining RI in this system.

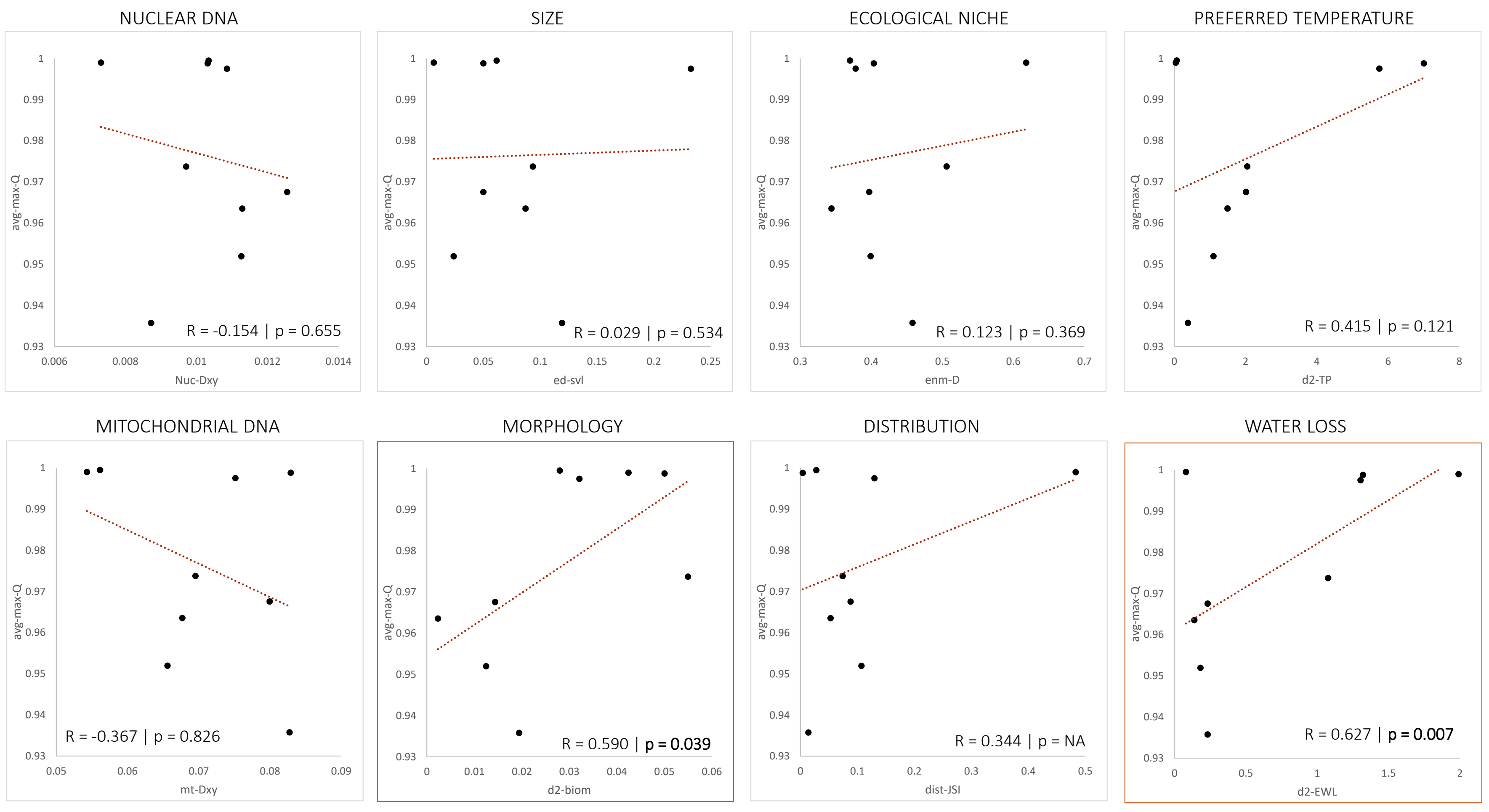

Figure 3. Relationships between different predictors and restrictions to gene flow, measured as the average maximum assignment probability (avg-max-Q) in each contact zone. Significance was assessed using Mantel tests. Significant correlations are highlighted, although none remains significant after correction for multiple tests.

REFERENCES

[1] Pritchard JK et al. (2000) *Genetics* 155:945-959;
[2] Kaliontzopoulou A et al. (2011) *Biol J Linn Soc* 103: 779-800;
[3] Kaliontzopoulou A *et al.* (2012) *Zool J Linn Soc* 164: 173-193.
[4] Caeiro-Dias G *et al.* (2018) *J Zool Syst Evol Res* 00:1-14.
[5] Ferreira CC *et al.* (2016) *PeerJ 4:e2017*
[6] Carneiro D *et al.* (2015) *Salamandra* 51:335-344
[7] García-Muñoz E, Carretero MA (2013) *Acta Herpetologica* 8:123 – 128.

ACKNOWLEDGEMENTS

The authors thank everyone who participated in sampling campaigns.
Funding references: SFRH/BD/89750/2012 (to GCD), IF/00641/2014/CP1256/CT0008 (to AK), IF/01597/2014/CP1256/CT0009 (to CP), all from Fundação para a Ciência e a Tecnoogia, and project NORTE-01-0145-FEDER-000007 (to MAC). This project was cofinanced by FCT projects PTDC/BIA-BEC/101256/2008 and PTDC/BIA-BEC/102179/2008 and by 02/SAICT/2017 projects 030288 (Norte2020) and 28014 (Portugal2020).