Variable genomic patterns of hybridization in two independent hybrid zones of damselflies

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Abstract

Hybrid zones with multiple independent contact regions between the same species allow to determine the relative importance of intrinsic and extrinsic factors in the evolution of hybrid zones and thus, parallelism in hybridization outcomes. In this study, we take advantage of two hybrid regions between the damselfly species Ischnura elegans and I. graellsii in Spain to measure: i) the extent of parallelism across geographic hybridization replicates, and what factors (intrinsic and extrinsic) drive that variation; and ii) if hybridization has an impact on the ability of species to expand their ranges. RAD sequencing was used to generate 5,702 SNPs to quantify population diversity and population differentiation, and a subset of 381 species-specific SNPs to analyze genotypic composition (individual ancestry and the proportion of individuals in different hybrid classes Our individual ancestry results showed on-going hybridization and introgression with different admixture-class distributions between hybrid regions and between populations explained by i) species proportions, ii) time elapsed since colonization, and iii) asymmetric and reinforced prezygotic barriers and Batson Dobzhansky and Müller (BDM) hybrid incompatibilities, and indicated a role of hybridization as a facilitator of species range expansions. Our study highlights the value of studying complex hybrid zones to gain insights into microevolutionary processes.

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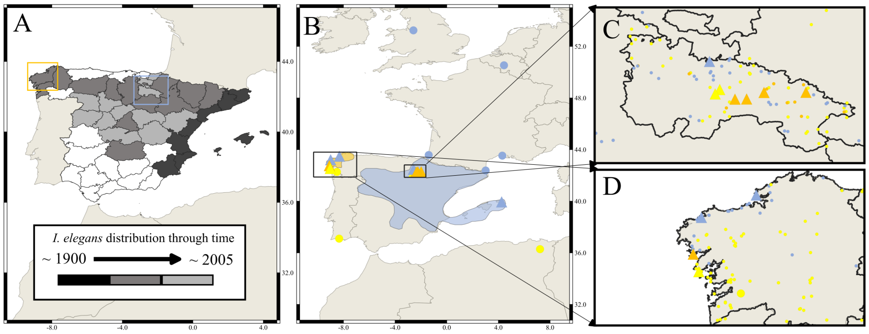
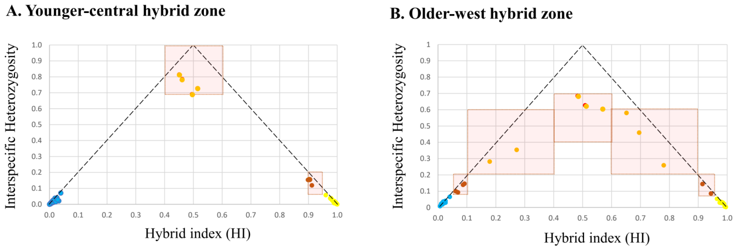
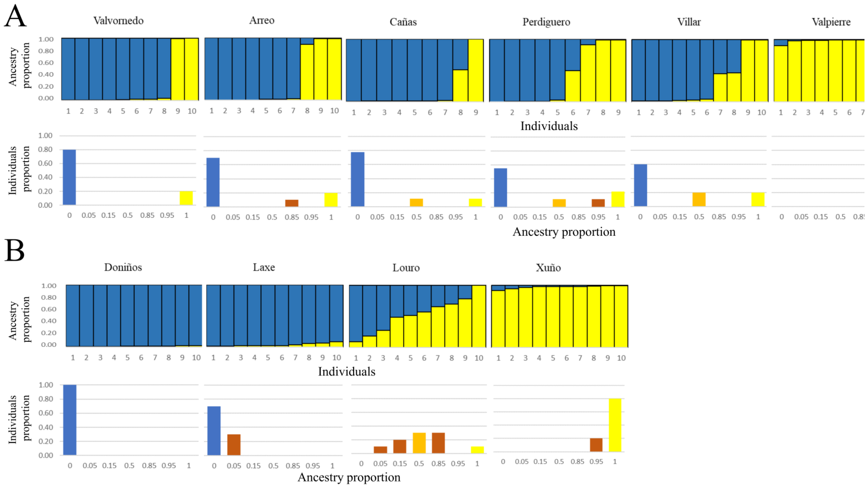
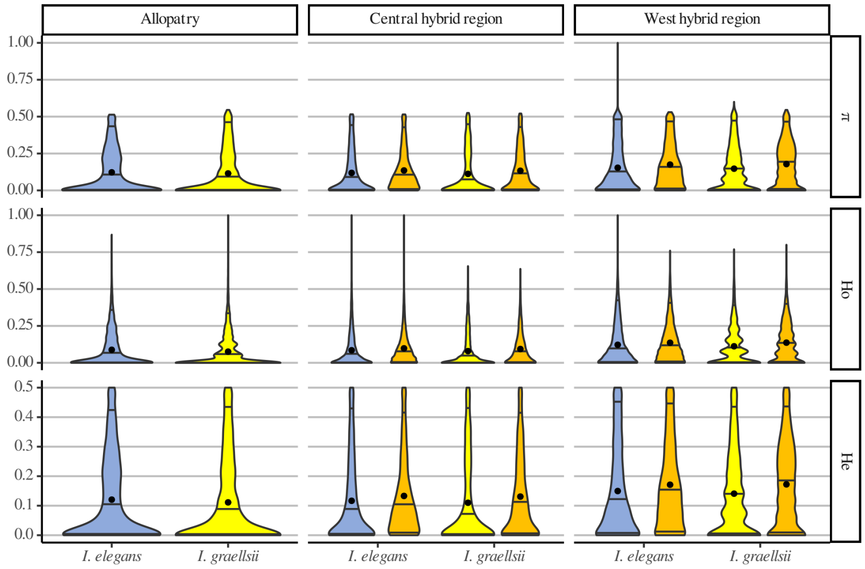

A
B
C
D
I. elegans distribution through time
~ 1900
~ 2005
44.0
40.0
36.0
32.0
52.0
48.0
-8.0
-4.0
0.0
4.0
8.0


A. Younger-central hybrid zone
B. Older-west hybrid zone
Interspecific Heterozygosity
Hybrid index (HI)
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0


A
Valvornedo
Arreo
Cañas
Perdiguero
Villar
Valpierre
Ancestry proportion
Individuals
Individuals proportion
Ancestry proportion
B
Doniños
Laxe
Louro
Xuño
Ancestry proportion
Individuals
Individuals proportion
Ancestry proportion
0
0.05
0.15
0.5
0.85
0.95
1


Allopatry
Central hybrid region
West hybrid region
π
Ho
He
1.00
0.75
0.50
0.25
0.00
0.5
0.4
0.3
0.2
0.1
0.0
I. elegans
I. graellsii