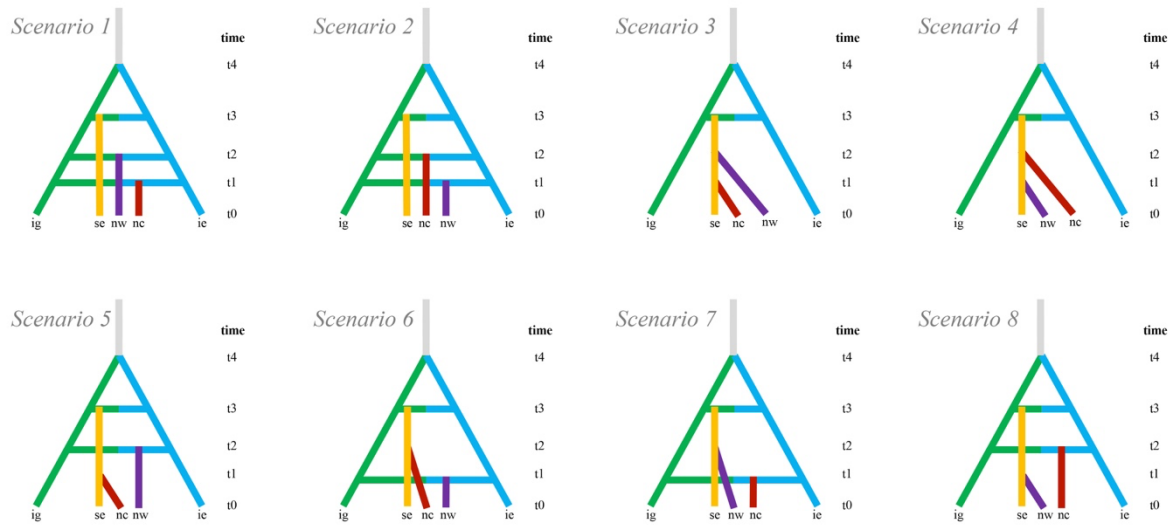


Supplementary material for:

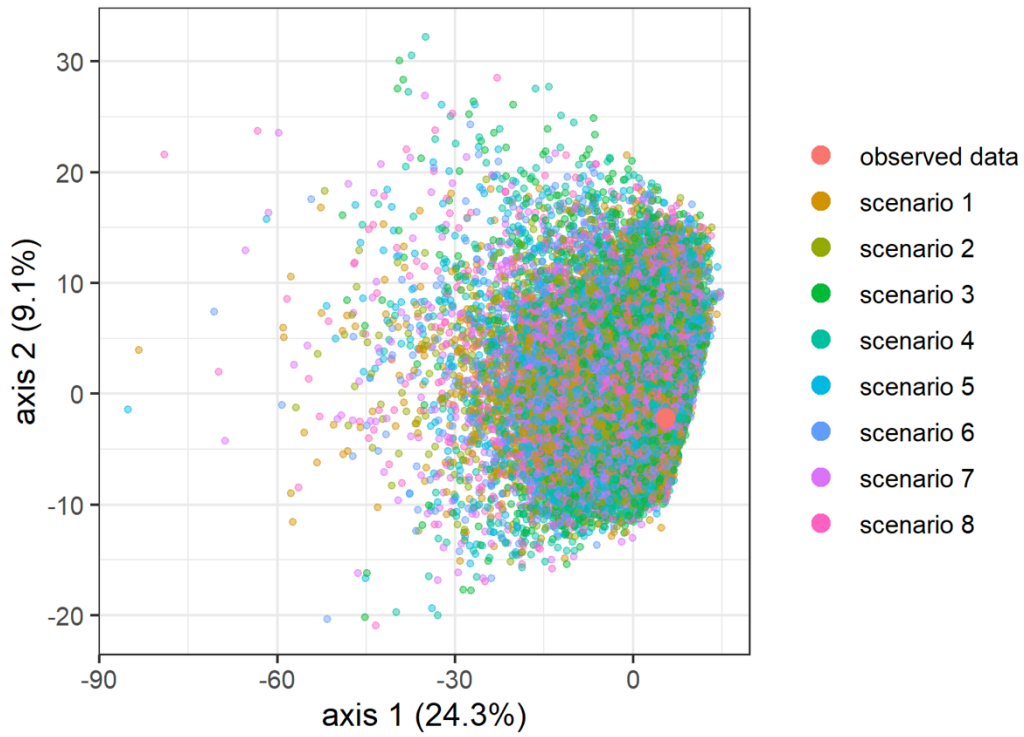
From divergence to contact: demographic history and genomic context shape introgression across independent damselfly hybrid zones

Table of contents:

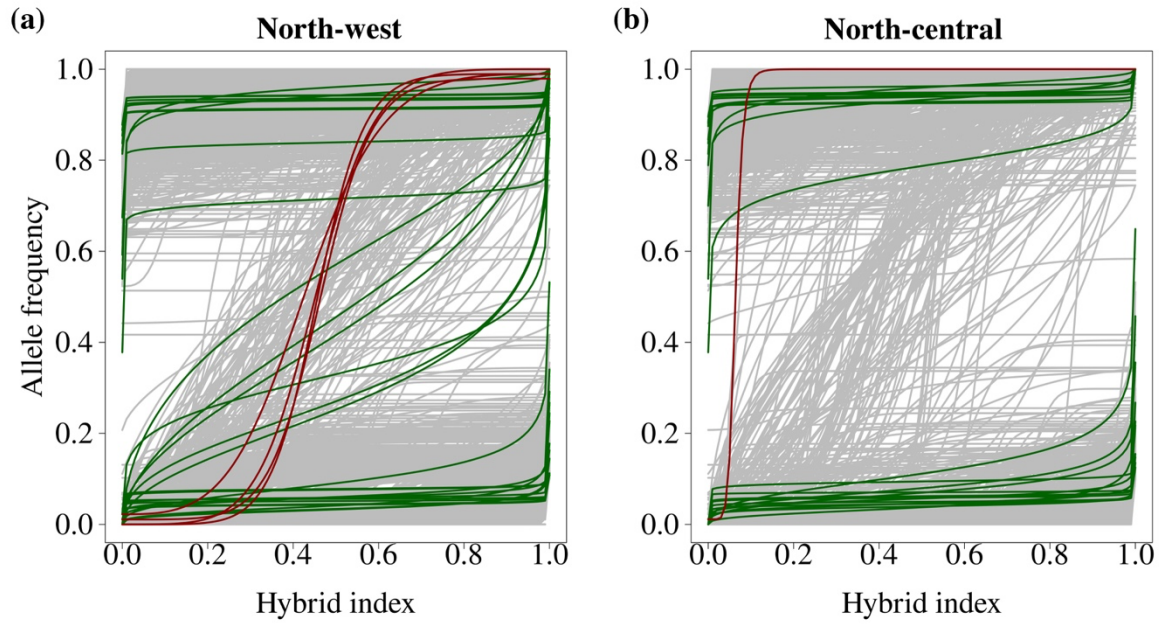
SuppFig. 1. Demographic scenarios tested using DIYABC-RF.....	2
SuppFig. 2. PCA model checking for DIYABC-RF analyses.....	3
SuppFig 3. Autosomal genomic clines in the NW and NC hybrid zones.....	4
SuppFig 4. Comparison of autosomal outlier SNPs between the NW and NC hybrid zones...	5
SuppFig 5. X-linked genomic clines in the NW and NC hybrid zones.....	6
SuppFig 6. Distribution of X-linked cline steepness and cline centre in the NW and NC hybrid zones.....	7
SuppTable 1. Sampling information for all populations.....	8
SuppTable 2. Gene Ontology terms associated with introgressed outlier SNPs.....	9



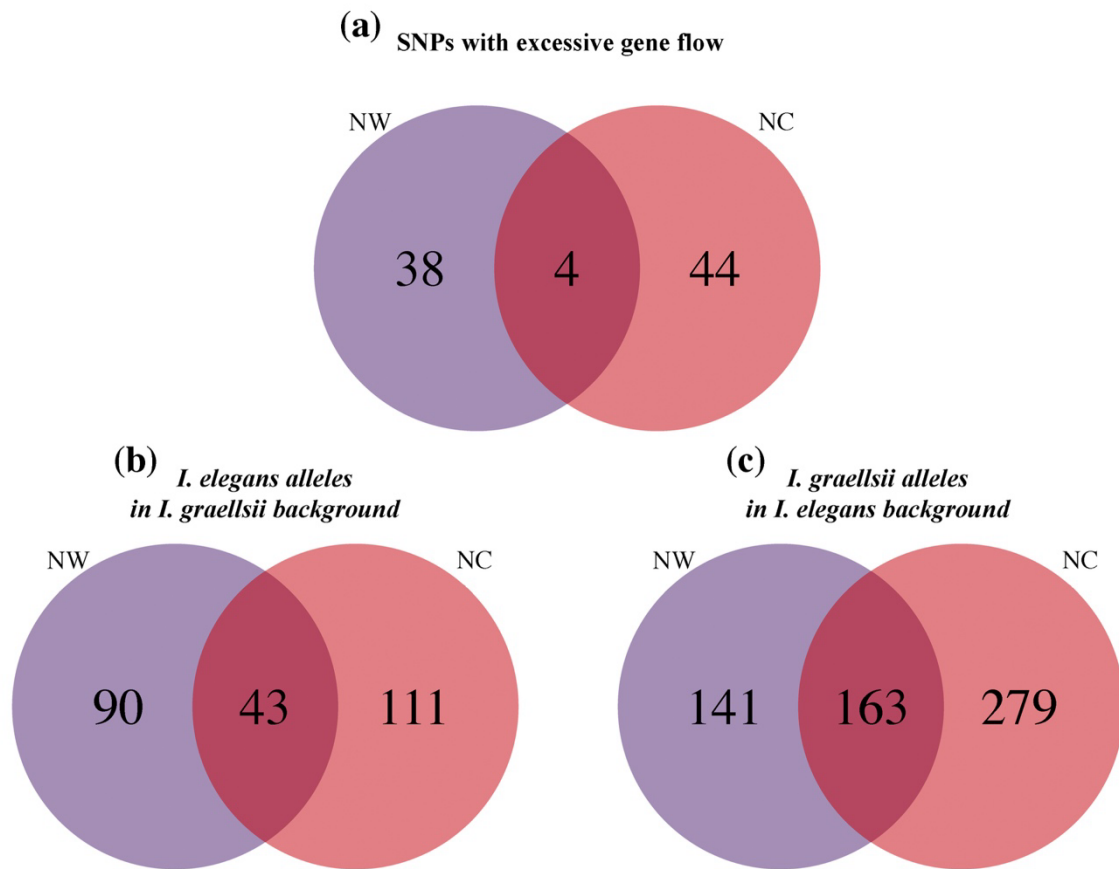
Supplementary Figure 1. Schematic overview of the eight alternative demographic scenarios tested using DIYABC-RF. Each scenario represents a different hypothesis about the timing and origin of the three hybrid zones, considering either independent admixture events or sequential formation driven by migration. Scenarios 1–2 represent independent origins of the NW, NC and SE hybrid zones, differing in the order of divergence. Scenarios 4–8 represent non-independent origins, where one zone arises from the split of another after divergence. In all scenarios, time points (t0–t4) indicate divergence or admixture events to the establishment of each hybrid zone. ig: *I. graellsii*, ie: *I. elegans*, nw: North-west hybrid zone, nc: North-central hybrid zone, se: South-east hybrid zone.



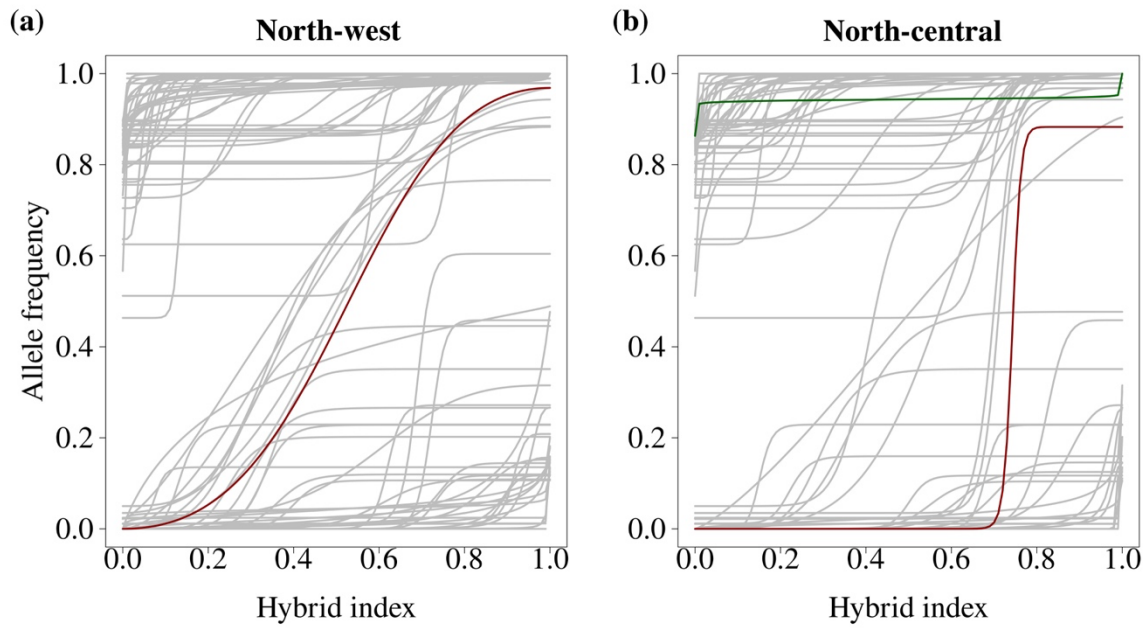
Supplementary Figure 2. Principal component analysis plot for model checking of the DIYABC-RF analysis derived from the simulated training datasets across the eight demographic scenarios. The observed dataset (red circle) falls well within the cloud of simulated points, indicating that the observed summary statistics are consistent with the prior parameter distributions and model space explored.



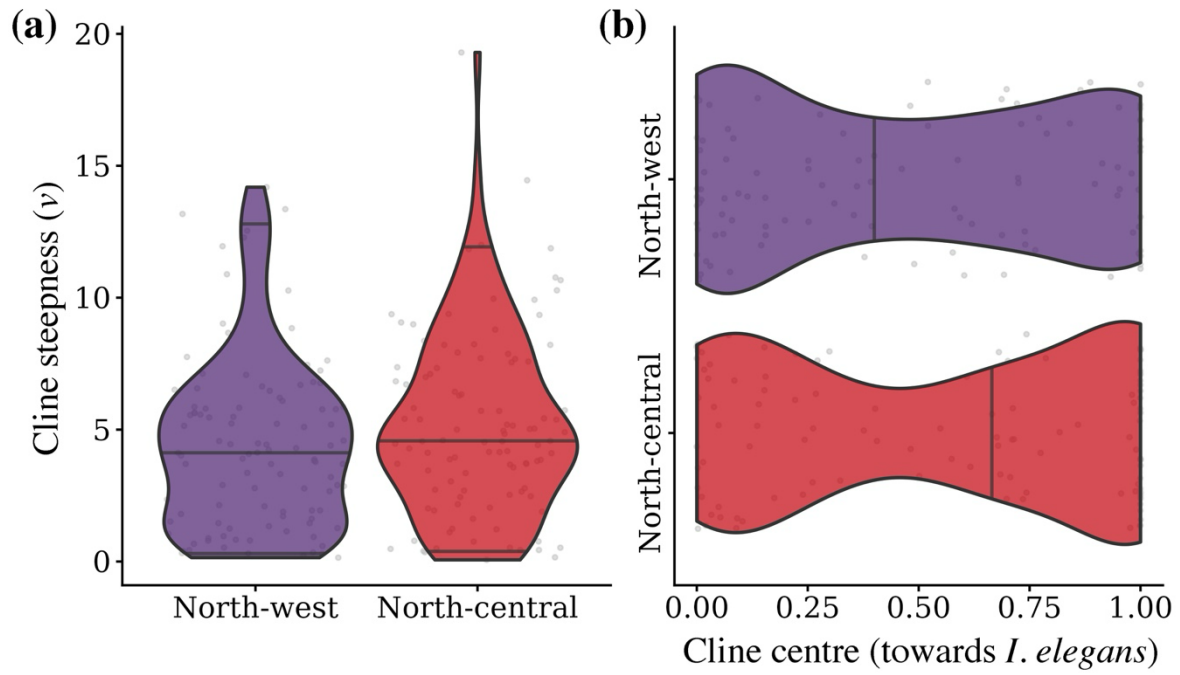
Supplementary Figure 3. Genomic clines estimated for autosomal SNP dataset across (a) NW and (b) NC hybrid zone. Clines are coloured according to their inferred introgression category, with loci showing neutral introgression rates (grey), excessive introgression (green), and restricted gene flow (red).



Supplementary Figure 4. Comparison of the autosomal outlier SNPs in NW (purple circle) and NC (red circle) hybrid zones. (a) Cline steepness outlier SNPs showing excessive introgression; (b) cline center outlier SNPs from *I. elegans* into the genomic background of *I. graellsii*; and (c) *vice versa*.



Supplementary Figure 5. Genomic clines estimated for X-linked SNP dataset across (a) NW and (b) NC hybrid zone. Clines are coloured according to their inferred introgression category, with loci showing neutral introgression rates (grey), excessive introgression (green), and restricted gene flow (red).



Supplementary Figure 6. Violin plots of cline steepness (a) and cline center (b) for the North-west and North-central hybrid zones for the X-linked SNPs dataset. Lines within each violin indicate the median and the 0.025 and 0.975 quantiles, and individual SNPs are shown in grey dots. Cline steepness reflects the strength of deviation from genome-wide neutral expectations of introgression, with higher values indicating steeper transitions across the admixture gradient. Cline center represents the position of allele frequency change along the hybrid index, indicating the direction of introgression between parental genomic backgrounds.

Supplementary Table 1. Sampling information for all populations included in the analyses. The region, locality name, geographic coordinates, sampling years, and the number of individuals retained in the full SNPs datasets are provided.

Region	Locality	Latitude	Longitude	Year	Full SNPs
Allopatric <i>I. graellsii</i>	Seyhouse, Algeria	36°28'27.03"N	07°22'27.03"E	2011	7
	Ribeira de Cobres, Portugal	37°39'49.25"N	07°57'48.10"W	2005	8
	Guadito, Spain	37°49'10.44"N	05°03'03.02"W	2008	10
	Salgados, Portugal	37°05'29.70"N	08°19'44.70"W	2015	21
North-west hybrid zone	Cachadas, Spain	42°27'12.19"N	08°50'55.37"W	2015	9
	Doniños, Spain	43°29'23.96"N	08°18'54.01"W	2014	10
	Laxe, Spain	43°12'46.82"N	08°59'38.35"W	2014	10
	Louro, Spain	42°45'28.08"N	09°05'44.90"W	2013	10
	Xuño, Spain	42°32'28.90"N	09°01'34.40"W	2014	10
North-central hybrid zone	Arreo, Spain	42°46'39.01"N	02°59'28.71"W	2008	10
	Cañas, Spain	42°29'0.09"N	02°24'17.14"W	2015	10
	Valpierre, Spain	42°27'11.00"N	02°51'48.00"W	2015	10
	Mateo, Spain	42°30'34.00"N	02°44'05.00"W	2015	10
	Perdiguero, Spain	42°17'18.78"N	01°58'50.55"W	2015	9
	Valbornedo, Spain	42°24'48.25"N	02°34'10.06"W	2015	10
	Villar, Spain	42°24'03.00"N	02°42'15.00"W	2015	9
South-east hybrid zone	Albufeira, Spain	39°57'0.00"N	04°14'59.99"E	2008	5
	Carraixet, Spain	39°30'06.41"N	0°19'30.44"W	2008	10
	Amposta, Spain	40°38'20.84"N	0°36'49.32"E	2008	1
	Marjal del Moro, Spain	39°37'49.57"N	0°16'17.14"W	2008	11
Allopatric <i>I. elegans</i>	Liverpool, UK	53°22'57.04"N	02°56'16.83"W	2008	6
	Marais D'Orx, France	43°35'58"N	01°23'30.00"W	2014	9
	Saint Cyprien, France	42°38'23.53"N	03°01'13.00"E	2015	10
	Vigueirat, France	43°37'46.87"N	04°40'45.24"E	2014	10
	Leuven, Belgium	50°51'49.83"N	04°47'54.65"E	2015	8
	Kaiserslautern, Germany	49°23'36.80"N	07°41'40.89"E	2008	4
Total					237

Supplementary Table 2. Gene Ontology (GO) terms of the Biological Process category assigned to protein sequences associated with introgressed outlier SNPs. For each term, the table reports the GO identifier, term name, associated protein sequences, the hybrid zone where the term was detected, and the direction of introgression.

GO ID	Name	Sequences associated	Hybrid zone	Direction
GO:0006182	cGMP biosynthetic process	XP_046393201.1	North-west	Bidirectional
GO:0006281	DNA repair	XP_046403763.1	North-central	Bidirectional
GO:0006289	nucleotide-excision repair	XP_046403763.1	North-central	Bidirectional
GO:0006357	regulation of transcription by RNA polymerase II	XP_046401584.1; XP_046403763.1	North-west; North-central	Bidirectional
GO:0006468	protein phosphorylation	XP_046385491.1; XP_046393201.1; XP_046386121.1	North-west	Bidirectional; <i>I. graellsii</i> allele in <i>I. elegans</i> genome
GO:0006508	proteolysis	XP_046392172.1	North-west	Bidirectional
GO:0006537	glutamate biosynthetic process	XP_046391907.1	North-central	<i>I. graellsii</i> allele in <i>I. elegans</i> genome
GO:0007165	signal transduction	XP_046392814.1	North-west	Bidirectional
GO:0007168	receptor guanylyl cyclase signaling pathway	XP_046393201.1	North-west	Bidirectional
GO:0007169	cell surface receptor protein tyrosine kinase signaling pathway	XP_046385491.1	North-west	Bidirectional
GO:0007275	multicellular organism development	XP_046385491.1	North-west	Bidirectional
GO:0008154	actin polymerization or depolymerization	XP_046402839.1	North-west	<i>I. graellsii</i> allele in <i>I. elegans</i> genome
GO:0009152	purine ribonucleotide biosynthetic process	XP_046399485.1	North-central	Bidirectional
GO:0009190	cyclic nucleotide biosynthetic process	XP_046393201.1	North-west	Bidirectional
GO:0010976	positive regulation of neuron projection development	XP_046385491.1	North-west	Bidirectional
GO:0015014	heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process	XP_046391929.1	North-central	<i>I. graellsii</i> allele in <i>I. elegans</i> genome
GO:0030036	actin cytoskeleton organization	XP_046386121.1	North-west	<i>I. graellsii</i> allele in <i>I. elegans</i> genome
GO:0030198	extracellular matrix organization	XP_046392172.1	North-west	Bidirectional
GO:0030239	myofibril assembly	XP_046402839.1	North-west	<i>I. graellsii</i> allele in <i>I. elegans</i> genome
GO:0031053	primary miRNA processing	XP_046385920.1	North-central	<i>I. graellsii</i> allele in <i>I. elegans</i> genome

GO:0033674	positive regulation of kinase activity	XP_046385491.1	North-west	Bidirectional
GO:0035556	intracellular signal transduction	XP_046393201.1	North-west	Bidirectional
GO:0044208	'de novo' AMP biosynthetic process	XP_046399485.1	North-central	Bidirectional
GO:0045737	positive regulation of cyclin-dependent protein serine/threonine kinase activity	XP_046403763.1	North-central	Bidirectional
GO:0045892	negative regulation of DNA-templated transcription	XP_046401584.1	North-west	Bidirectional
GO:0051014	actin filament severing	XP_046402839.1	North-west	<i>I. graellsii</i> allele in <i>I. elegans</i> genome
GO:0051016	barbed-end actin filament capping	XP_046402839.1	North-west	<i>I. graellsii</i> allele in <i>I. elegans</i> genome
GO:0051897	positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	XP_046385491.1	North-west	Bidirectional
GO:0055085	transmembrane transport	XP_046401563.1; XP_046403793.1; XP_046401563.1	North-west; North-central	Bidirectional; <i>I. graellsii</i> allele in <i>I. elegans</i> genome
GO:1990090	cellular response to nerve growth factor stimulus	XP_046385491.1	North-west	Bidirectional