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RH: Phylogeography in *Jehlius cirratus*

Large-scale gene flow in the barnacle *Jehlius cirratus* and contrasts with other broadly-distributed taxa along the Chilean coast

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Abstract

We evaluate the population genetic structure of the intertidal barnacle *Jehlius cirratus* across a broad portion of its geographic distribution using data from the mitochondrial cytochrome oxidase I (COI) gene region. Despite sampling diversity from over 3000km of the linear range of this species, there is only slight regional structure indicated, with overall Φ_{CT} of 0.036 ($p<0.001$) yet no support for isolation by distance. While these results suggest greater structure than previous studies of *J. cirratus* had indicated, the pattern of diversity is still far more subtle than in other similarly-distributed species with similar larval and life history traits. We compare these data and results with recent findings in four other intertidal species that have planktotrophic larvae. There are no clear patterns among these taxa that can be associated with intertidal depth or other known life history traits.

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Introduction

A persistent question in marine biogeography and population biology involves the interaction of species life history, geographic range, and trait or genealogical diversity within that range. In some cases, genealogical diversity or "structure" (Wares 2016) *within* a species is informative of mechanisms that act to limit other species' distributional ranges (Dawson 2001; Wares 2002; Wares *et al.* 2001). Of course, these studies often find that organisms with limited larval or juvenile dispersal have greater amounts of structure and less extensive ranges, but there are often exceptions (Marko 2004). It is the variation among species, and the exceptions to the "rules", that offer continued opportunity to understand marine diversity.

Early approaches to comparative phylogeography (Dawson 2001; Wares 2002; Wares & Cunningham 2001) focused primarily on regions of co-diversification of intraspecific lineages, e.g. the regions across which species were likely to exhibit structure. Subsequently, Marko (2004) noted that even when species had apparently identical life history and dispersal mechanisms, the distribution of a species across habitats (e.g. intertidal height) could influence their persistence in distinct glacial refugia. However, certainly to understand these associations more taxa should be compared, and Kelly and Palumbi (2010) made explicit comparisons of diversity and population divergence for 50 species along the Pacific coast of North America to suggest that species high in the intertidal were perhaps more likely to exhibit spatial genetic structure than those at lower depths.

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53 The particular spatial structure of the species represented in Kelly and Palumbi
54 (2010) varies; however, there is often concordance of population structure among
55 species (Pelc *et al.* 2009; Small & Wares 2010) on this coast. Other regions that have
56 been similarly explored – for example, the NW Atlantic coast – have fewer instances
57 of strong population structure aside from regions that are also biogeographic
58 transitions (Altman *et al.* 2013; Díaz-Ferguson *et al.* 2009). Another such example of
59 this concordance of genetic diversity with biogeography was recently published by
60 Haye et al. (2014), looking at species with short-dispersing larval forms around the
61 well-characterized biogeographic transition near 30°S latitude along the coast of
62 Chile. Again, the structure of diversity within species was informative to the
63 mechanisms – including shifts in upwelling intensity and nutrient availability
64 (Navarrete *et al.* 2005) – that may limit the distribution of other taxa.

65

66 Evaluating broad-scale diversity structure on the Chilean coast is of key interest as
67 there are so many oceanographic and biogeographic comparisons to be made
68 between this well-studied coastline and the well-studied Pacific coast of North
69 America (Navarrete *et al.* 2008). However, until recently there were few data
70 available for species that spanned most of the length of the Chilean coastline. This
71 scale is of interest because it spans *two* major biogeographic transitions – the region
72 around 30°S noted above, as well as a notable biogeographic transition near 42°S
73 (Thiel *et al.* 2007).

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Some of the first such work at this spatial scale was done in the direct-developing gastropod *Acanthina monodon* (Sanchez *et al.* 2011) and another gastropod *Concholepas concholepas* (Cardenas et al. 2009). In *Acanthina*, which has low dispersal potential among locations, strong concordance of intraspecific diversity with the 30°S biogeographic boundary was found, but association with the 42° boundary was less clear. Nevertheless, statistically significant genetic structure and shifts in phenotypic diversity are associated with this region. The gastropod *Concholepas concholepas*, on the other hand, has high potential for pelagic larval dispersal, is similarly distributed along the coast of Chile, but exhibits no significant genetic structure at all (Cardenas *et al.* 2009). These contrasts are wholly in line with predictions based on larval life history.

Recently, large data sets have become available for other commonly encountered taxa in the Chilean intertidal. Microsatellite data were analyzed in the mussel *Perumytilus purpuratus* (Guiñez *et al.* 2016), which both spawns gametes and has a long-lived planktotrophic larva, and this ecosystem engineer exhibited significant structure with two main lineages (separated at approximately 40°S) and isolation by distance within each lineage. Similarly, Ewers-Saucedo et al. (2016) explored genetic variation in the high intertidal barnacle *Notochthamalus scabrosus*, with nauplius larvae that have high pelagic larval dispersal potential, and found two primary lineages that mirror the dominant biogeographical pattern of Chile: in the northern Peruvian region only one lineage is found, while both are found in the Intermediate Area that represents the overlap of the Peruvian and Magellanic

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98 regions, and only the southern lineage is found south of 42°S. Another barnacle, the
99 edible *picoroco* (*Austromegabalanus psittacus*) exhibits only slight structure along
100 most of the Chilean coast (Pappalardo *et al.* 2016), but nevertheless the structure is
101 statistically significant and seems to be associated with the northern (30°S)
102 biogeographic transition.
103
104 To these data we add one more layer: Zakas et al. (2009) had explored
105 mitochondrial sequence population structure in the high intertidal barnacle *Jehlius*
106 *cirratus*, a species that is biologically and ecologically very similar to
107 *Notochthamalus* but found slightly higher in the intertidal (Lamb *et al.* 2014; Shinen
108 & Navarrete 2010, 2014). Zakas et al. (2009) found that unlike *Notochthamalus*,
109 there was very little apparent genetic structure in *J. cirratus*. However, that analysis
110 comprised only a small section of the Chilean coast, from ~28-34°S. Here, we
111 expand the sampling of *J. cirratus* to include diversity from ~3500km of coastline,
112 including most of the known distribution (Häussermann & Försterra 2009). As
113 chthamalid barnacles have a propensity to harbor cryptic genetic diversity (Dando
114 & Southward 1981; Meyers *et al.* 2013; Tsang *et al.* 2008; Wares *et al.* 2009; Zardus
115 & Hadfield 2005), we specifically look for any phylogeographic structure that may
116 add to our understanding of coastal biodiversity in Chile. We then more directly
117 compare the whole-coast data described above for the ecological implications of the
118 population structure identified within and among taxa.
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Methods

Specimens of *J. cirratus* were collected from the intertidal in 2004-2013 under permits indicated in (Ewers-Saucedo *et al.* 2016). Sequences of cytochrome oxidase I (n=153) from Zakas et al (2009) were used in this study (Genbank GU126073 – GU126226); additional sequences (n=187) were generated from subsequent samples collected in 2011-2013 using PCR methods as in Zakas et al. (2009). Samples were mostly collected in central Chile (Figure 1, Table 1), but this additional effort also added substantially to information from northern Chile and northern Patagonia.

After quality control and alignment of sequence data using CodonCode Aligner v6.0.2 (CodonCode Corporation), data were formatted for analysis using Arlequin v3.5.2.2. (Excoffier *et al.* 2005) to identify population structure. Pairwise Φ_{ST} was calculated for all sites and compared to a matrix of pairwise geographic distance for signal of isolation by distance (Wright 1943); this was done both with haplotypic data as well as nucleotide data under a K2P distance model. Additionally, an exact test of differentiation was calculated for all pairs of populations. Analysis of molecular variance (AMOVA) was performed to identify maximal structure along the coast as in (Dupanloup *et al.* 2002) and Zakas et al (2009), using an iterative approach for K contiguous spatial groups, increasing K if there were significant patterns of Φ_{SC} within the determined regional groups. Following the results of AMOVA, a haplotype network was generated using PopArt (http://popart.otago.ac.nz). Haplotypes were coded by sample location and by regions separated

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by the iterative AMOVA results that maximize Φ_{CT} to visually identify components of diversity associated with each regional group. Population diversity was also assessed at each sampled location; nucleotide diversity (π) and haplotype diversity (H) are estimated at each location using Arlequin.

Results

New sequences are archived in Genbank under accession numbers KX014910 - KX015034. Site-specific diversity is presented in Table 1; pairwise values of Φ_{ST} are presented in Table 2. Only a single sequence was recovered from the northernmost collection site of Arica, so this sequence was included in the Antofagasta sample (results identical when excluded) for statistical purposes. Values of Φ_{ST} are very low and in general not statistically significant (Table 2); the only exceptional locations are Guanaqueros (30°S) and Pichilemu (34°S), each of which tend to exhibit higher differentiation from a broader set of other locations. No population pairs are significantly different under an exact test. Testing these results for a pattern of genetic isolation by distance was not significant (p 0.245).

Although only slight structure is exhibited along the Chilean coast in *J. cirratus* (Φ_{ST} of -0.019, $p \sim 1$), there is statistical regional structure detectable with the increased power of sampling at that scale. Our implementation of spatial AMOVA (Zakas et al. 2009) recovered two contrasts for K=2 regions in which $\Phi_{CT} > 0.035$ and $p<0.01$, though similar results are found if the separation among regions is near to either of these locations (Table 3). These local maxima in Φ_{CT} separate Guanaqueros (30°S) and sites to the north from all locations to the south; and Pichilemu (44°S) and all

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sites to the south from all locations to the north. No significant Φ_{SC} is exhibited in these comparisons. If K=3 groups are chosen using these same delineations, Φ_{CT} is comparable (0.03661, p <0.001).

From these results, a haplotype network (minimum spanning tree) is presented in Figure 2; "northern" diversity (from Guanaqueros northward), "southern" diversity (including Pichilemu and southward sites), and "central" diversity (locations in between), for visualization.

Discussion

As noted in Zakas et al. (2009) there is only slight population structure in *J. cirratus*. Previous efforts had also noted that using alternate statistics such as Hudson's (Hudson 2000) Snn also recovered no signal of structure or pattern of isolation by distance (Wares 2014). Here, we do identify statistically significant structure that is roughly associated with the 30°S biogeographic transition between the Peruvian and "Intermediate" zones, and there may also be structure further south – but not associated with the boundary at 42°S. Overall, the statistical significance indicated – given that pairwise statistical support was not consistent between permutational tests of Φ_{ST} and pairwise exact tests of population differentiation – suggests little actual spatial variation but sufficient sampling to identify the differential representation of regional samples in the 2 dominant haplotypes found (Figure 2).

Excluding the direct developer *A. monodon* from further consideration, the studies reviewed earlier and current study include 5 intertidal species with high larval

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187 dispersal potential that are distributed and analyzed along the length of the Chilean
188 coast. Unfortunately, there is no clear pattern associated with intertidal depth; the
189 species with no or slight population genetic structure (*J. cirratus*, this study; *A.*
190 *psittacus*, Pappalardo *et al.* 2016; *C. concholepas*, Cardénas *et al.* 2009) are in the
191 highest reaches of the intertidal (*J. cirratus*) and the low intertidal (*A. psittacus* and
192 *C. concholepas*). The two species that exhibit significant structure, each with two
193 primary lineages and evidence for isolation by distance within each lineage, are in
194 the high-to-middle intertidal (*N. scabrosus*, Ewers-Saucedo *et al.* 2016; *P.*
195 *purpuratus*, Guiñez *et al.* 2016).
196
197 Clearly a sample of only 5 taxa is insufficient for statistical consideration. However,
198 what we can indicate is that all 3 barnacles (*A. psittacus*, *J. cirratus*, and *N. scabrosus*)
199 have at least some signal associated with the 30-32° oceanographic transition in
200 upwelling (Lagos *et al.* 2005; Navarrete *et al.* 2005); however the two molluscs, the
201 mussel *P. purpuratus* and abalone *C. concholepas* do not. The association of genetic
202 structure with the southern biogeographic boundary near 42°S (Thiel *et al.* 2007) is
203 far more varied; other taxa with shorter distributional ranges that span this
204 biogeographic transition, such as the mussel *Mytilus chilensis*, show little spatial
205 structure at mitochondrial or other putatively neutral markers (L. Besch and
206 Bockrath, unpublished; Areneda *et al.* (2016)) but can be distinguished among
207 different coastal environments by outlier markers (Araneda *et al.* 2016) and
208 expression profiling (Núñez-Acuña *et al.* 2012). Ewers-Saucedo *et al.* (2016) note
209 that environmental transitions and current-mediated larval dispersal in this region,

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where trans-oceanic currents are separated as they reach the continental margin (Acha *et al.* 2004), are likely to transport regionally-differentiated diversity along a broad swath of this coastline. Thus, identifying concordant intraspecific diversity patterns among taxa may require a different analytical approach that is model-driven as in Ewers-Saucedo *et al*. (2016).

There is an expanding interest in exploration of genetic diversity within and among regional populations of intertidal species along the coast of Chile (see Haye et al. 2014 for a recent synthesis). Such data are being used to explore the underlying causes of biogeographic transition (Cardenas *et al.* 2009; Ewers-Saucedo *et al.* 2016; Zakas *et al.* 2009), to inform management and aquacultural concerns (Haye & Munoz-Herrera 2013; Núñez-Acuña *et al.* 2012; Pappalardo *et al.* 2016), and better understand how the dynamics of a coastal ocean influence local diversity (Aiken & Navarrete 2014; Broitman *et al.* 2001; Navarrete *et al.* 2005). For example, even with variation among the data and taxa evaluated here, there is a concordance between the genetic transitions exhibited in these taxa and regions of strong upwelling along coastal Chile (Navarrete *et al.* 2005).

What remains unsatisfying is our ability to predict – based on what we know of life history, ecology, and other parameters of a given taxon – which species are likely to exhibit structure across a certain region. Haydon et al. (1994) first noted the problem of both stochastic and deterministic contributions to biogeography and overall population structure. Certainly some 'significant' phylogeographic structure may simply represent the interaction of genealogical processes and modest

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limitations on gene flow (Irwin 2002). However, the most direct contrast of the taxa included here involves the barnacles *N. scabrosus* and *J. cirratus*, which are ecologically nearly indistinguishable (Lamb *et al.* 2014; Shinen & Navarrete 2010, 2014) with little known distinction in larval life history. In fact, though *N. scabrosus* exhibits significant phylogeographic structure (Ewers-Saucedo *et al.* 2016), the larvae of *N. scabrosus* appear to require longer times in the plankton and longer times for cyprid metamorphosis than *J. cirratus* (Venegas *et al.* 2000). Whether the cause for this contrast in population structure is ecological, physiological, or simply fortune remains unclear.

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Table 1 Collection sites, number of individuals per sampling site (n) and summary statistics of genetic variability for *Jehlius cirratus*.

Site (South Latitude)	sampled	haplotypes	haplotype diversity	nucleotide diversity (π)
Antofagasta/Arica (18.49°)	31	27	0.978±0.020	0.012±0.009
Huasco (28.46°)	41	25	0.945±0.022	0.009±0.003
Temblador (29.40°)	21	16	0.948±0.040	0.009±0.006
Guanaqueros (30.20°)	24	18	0.942±0.040	0.011±0.006
Punta Talca (30.95°)	23	14	0.893±0.052	0.008±0.004
Los Molles (32.25°)	28	23	0.971±0.024	0.011±0.007
Monte Mar (32.95°)	28	24	0.987±0.014	0.011±0.006
El Quisco (33.45°)	29	25	0.988±0.013	0.010±0.006
Las Cruces (33.49°)	17	16	0.993±0.023	0.012±0.006
Matanzas (33.95°)	24	20	0.975±0.024	0.011±0.006
Pichilemu (34.42°)	32	24	0.958±0.025	0.010±0.008
Niebla (39.85°)	25	17	0.957±0.024	0.014±0.008
Añihue (43.85°)	8	7	0.964±0.077	0.016±0.009
Isla Madre de Dios (50.42°)	7	3	0.667±0.160	0.009±0.004

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Table 2 Pairwise Φ_{ST} values among sites (indicated as header) for mitochondrial COI sequence data in *J. cirratus*. Statistically significant (p<0.01) comparisons are bolded and in blue.

Antofagasta	Huasco	Temblador	Guanaqueros	Punta Talca	Los Molles	Monte Mar	El Quisco	Las Cruces	Matanzas	Pichilemu	Niebla	Añihue
-0.10721												
-0.02397	-0.10075											
-0.06007	0.00344	-0.09836										
-0.00797	-0.07271	0.01272	-0.01539									
-0.01641	-0.09486	-0.01873	-0.07157	0.00493								
-0.07084	0.01909	-0.06296	**0.05349**	-0.0808	-0.03693							
-0.17547	-0.01582	-0.18666	0.02576	-0.1819	-0.15953	-0.03391						
-0.00509	-0.06798	0.00201	-0.02185	-0.02005	0.01097	-0.08597	-0.16477					
-0.07137	0.01015	-0.05613	**0.04841**	-0.0811	-0.04482	-0.0131	-0.02592	-0.07314				
0.06509	0.01927	**0.10959**	**0.10642**	0.01976	**0.085**	-0.01377	-0.10077	**0.04336**	-0.02223			
-0.03313	-0.0885	0.01678	-0.04187	-0.04029	-0.02781	-0.09641	-0.21442	-0.03887	-0.10159	-0.01699		
-0.01175	0.02556	-0.00176	0.07232	-0.03869	0.00933	-0.03799	-0.02988	-0.04939	0.00464	0.02127	-0.05271	
-0.0777	0.01877	-0.04544	0.08615	-0.11043	-0.08512	0.04286	-0.00793	-0.07119	0.03113	-0.09806	-0.13056	0.04426

Table 3 Iterative AMOVA for K=2 regions of sequence diversity. Site is listed as dividing *that location and all sites to the north* from all locations to the south. The northernmost 2 sites (Arica, Antofagasta) were pooled for analysis as were the southernmost 2 sites (Añihue, Madre de Dios). Strongest values of Φ_{CT} (by magnitude and p-value) indicated in bold. Similar value of Φ_{CT} (0.0366, p<0.001) is obtained with K=3 and the regions separated as in Figure 2.

Site	Φ_{CT}	**p-value**
Huasco	0.01406	0.16
Temblador	0.01977	0.11
Guanaqueros	**0.03679**	**<0.001**
Punta Talca	0.02623	0.03
Los Molles	0.03215	<0.01
Monte Mar	0.02998	0.01
El Quisco	0.02896	<0.01
Las Cruces	0.03463	<0.01
Matanzas	**0.03615**	**<0.005**
Pichilemu	0.00076	0.55
Valdivia	0.00635	0.64

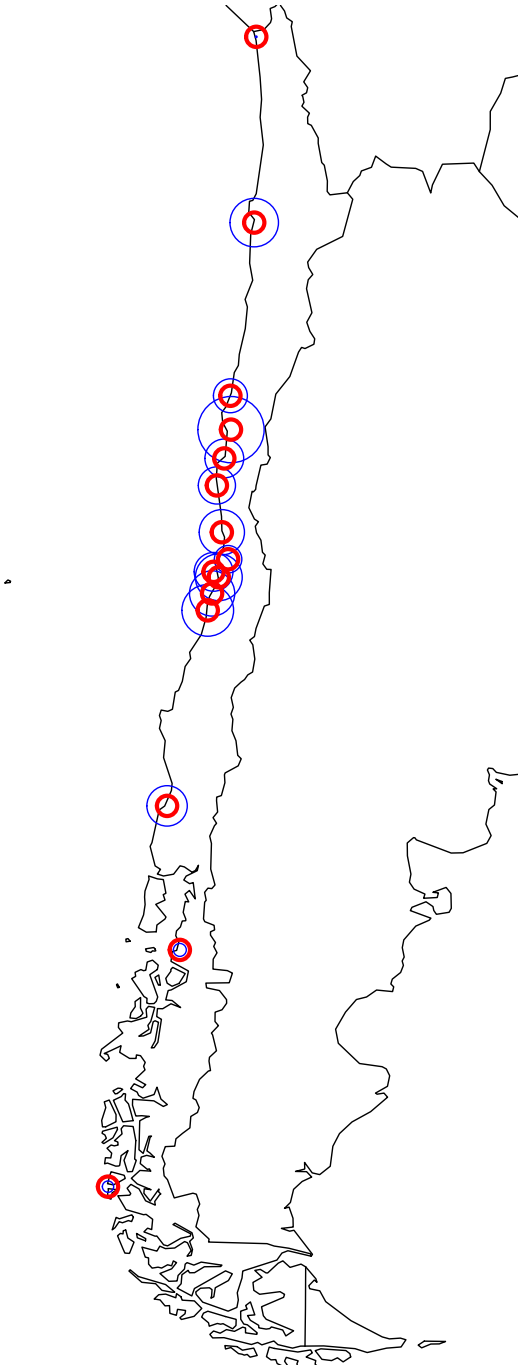

Figure 1. Sample locations (bold circles) and log sample size (thin circles) indicate sampling of *J. cirratus* along the Chilean coast. Additional information in Table 1.

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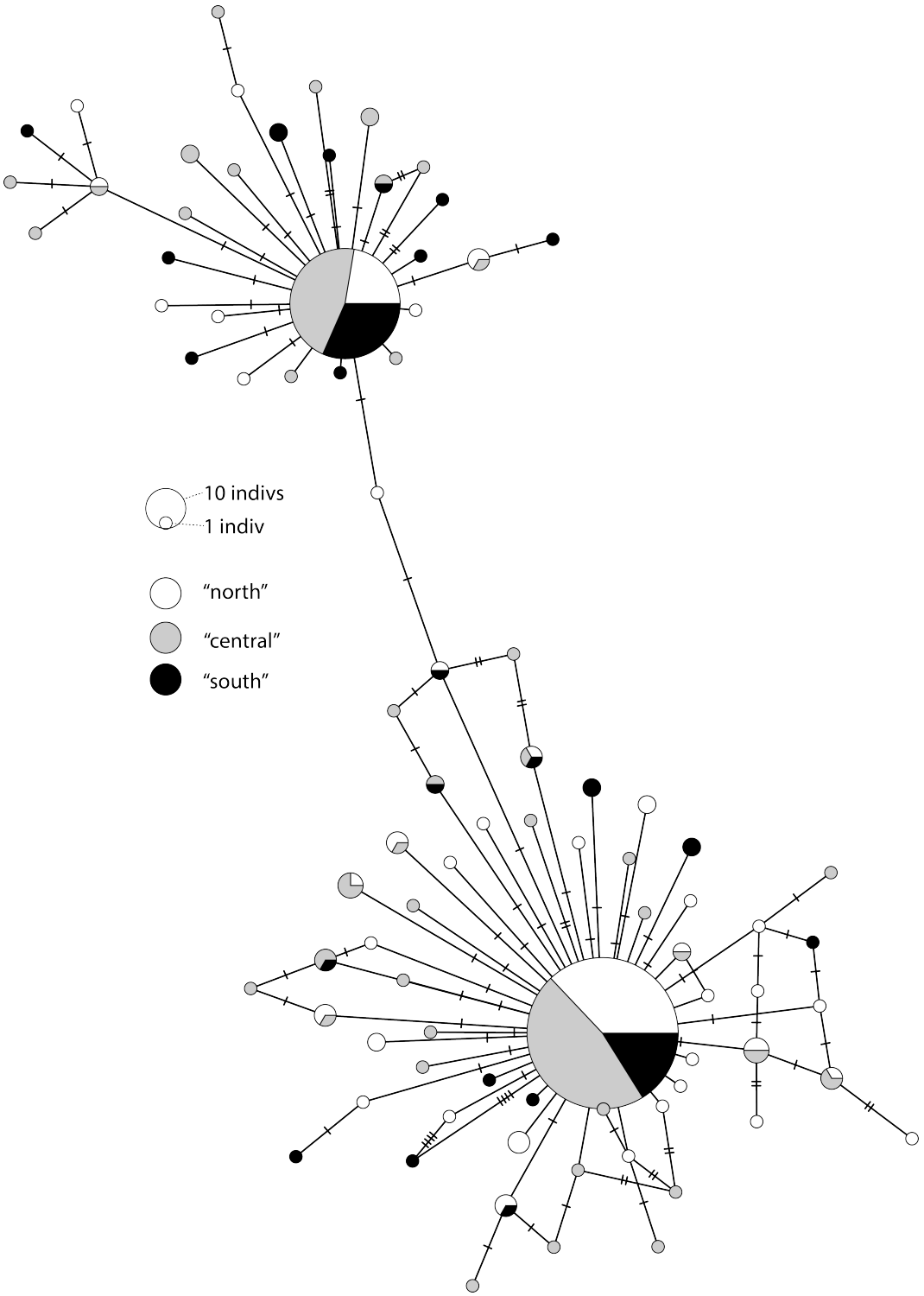

Figure 2. Minimum-spanning tree of mitochondrial COI diversity in *J. cirratus*. Regional designations are generated from maximal Φ_{CT} values along the coast.

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