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Title

PHYLOGEOGRAPHY OF A CANOPY-FORMING KELP, *EISENIA BICYCLIS* (LAMINARIALES, PHAEOPHYCEAE), BASED ON A GENOME-WIDE SEQUENCING ANALYSIS [1]

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PHYLOGEOGRAPHY OF *E. BICYCLIS*

ABSTRACT

Analyses of phylogeographic patterns and genetic diversity provide fundamental information for the management and conservation of species. However, little is published about these patterns in Japanese kelp species. In this study, we conducted phylogeographic analyses of a canopy-forming kelp, *Eisenia bicyclis*, based on genome-wide SNPs identified by ddRAD-seq. We obtained 1,299 SNPs for 76 samples from nine localities across the distribution. STRUCTURE, NeighborNet, and discriminant analysis of principal components consistently showed high genetic differentiation among the Eastern Pacific, Central Pacific, and Sea of Japan coastal regions. Relatively strong gene flow was detected only within populations in the Eastern Pacific and in the Sea of Japan. Genetic diversity and genetic uniqueness were high in the Central Pacific and low in the Sea of Japan. These results suggest that there were at least three independent refugia corresponding to the three regions during the Last Glacial Maximum (LGM). Furthermore, relatively larger populations in the Central Pacific and smaller populations in the Sea of Japan have been maintained in the demographic history from before the LGM to the present. These phylogeographic histories were supported by an Approximate Bayesian Computation analysis. From a conservation genetics perspective, the loss of southern populations in the Central Pacific would greatly reduce the total genetic diversity of the species. Southern populations in the Sea of Japan, which have relatively low genetic diversity, may be highly vulnerable to environmental change, such as heat waves and increased feeding. Therefore, careful monitoring and conservation are needed in the two regions.

Key index words:

Arthrothamnaceae, ddRAD-seq, Demography, Genetic diversity, Genetic structure, Kelp forest, Phylogeography

Abbreviations:

ABC, Approximate Bayesian Computation; BIC, Bayesian information criterion; CI, confidence interval; CTAB, cetyltrimethylammonium bromide; DA, discriminant analysis; DAPC, discriminant analysis of principal components; ddRAD-seq, double digest RAD-seq; LGM, Last Glacial Maximum; PCA, principal component analysis; RAD-seq, restriction site-associated DNA sequencing; SNPs, single nucleotide polymorphisms; SS, summary statistics; SST, surface seawater temperature

INTRODUCTION

Kelp forests are key components of coastal rocky ecosystems in temperate to boreal zones by providing food, habitat, and shelter for various organisms (North 1971, Steneck et al. 2002, Graham 2004, Steneck and Johnson 2014). They also serve as a significant carbon sink to mitigate global warming (Chung et al. 2013, Krause-Jensen and Duarte 2016). However, kelp forests have been declining in various parts of the world (Krumhansl et al. 2016, Wernberg et al. 2019), including Japan (Fujita 2010), due to the dominance of sea urchins (Filbee-dexter and Scheibling 2014, Ling et al. 2015), overbrowsing by herbivores (Gianni et al. 2017, Zarco-Perello et al. 2017), and recent climate change (e.g., Wernberg et al. 2016, Bennet and Catton 2019, Tanaka et al. 2020). Although effective re-forestation techniques have been developed to restore kelp forests (e.g., Ling et al. 2010, Westermeier et al. 2014, Fredriksen et al. 2020), their implementation should consider intraspecific genetic diversity and genetic structure (Moritz 2002, Hoban et al. 2020). Furthermore, recent studies have reported that populations with high genetic diversity tend to show high resilience against heatwaves in kelp populations (Wernberg et al. 2018) and against disturbance by grazing geese in seagrass populations (Hughes and Stachowicz 2004). Restoration that incorporated genetic structure and diversity was demonstrated in a canopy-forming brown alga by Wood et al. (2020). The mechanism by which genetic diversity positively affects the resilience is entirely unclear, but it is likely to be one of the important factors in management of kelp forest. Thus, understanding genetic diversity and genetic structure in each kelp species will provide fundamental information for the management and conservation of kelp forests.

Phylogeographic analyses are a powerful tool to reveal genetic diversity, genetic

structures, demographic histories, and future demographic shifts (Avise 2000). Microsatellite markers and/or organellar markers are frequently employed in studies of brown algae (reviewed in Hu et al. 2016). However, these markers are limited in number, ranging from one to a dozen loci, and the resolution of the genetic structure is poor, especially in the case of species with complex demographic histories. Alternatively, genome-wide SNP information, including hundreds to thousands of loci, provides a robust and clear basis for estimating demographic histories (reviewed in Edwards et al. 2015). The recent development of RAD-seq enabled low-cost high-throughput SNP genotyping, even in non-model organisms (Miller et al. 2007). Subsequently, ddRAD-seq, which uses two restriction enzymes with rare and frequent cutting, enabled precise, repeatable size selection and more stable shared region recovery across samples compared with RAD-seq (Kai et al. 2014). In fact, the recent employment of the ddRAD-seq method for phylogeographic studies of brown algae has revealed much clearer demographic histories than those obtained with previous markers (Guzinski et al. 2018, Kobayashi et al. 2018, LeCam et al. 2020).

Eisenia bicyclis (Kjellman) Setchell is a palm-like kelp and a representative component of kelp forests in Japan (Maegawa 1990, Terada et al. 2020). This kelp occurs in the lower intertidal zone to subtidal zone at depths shallower than 10 m (Maegawa 1990, Sakanishi et al. 2018), with a geologically disconnected distribution on the Pacific coast of central to eastern Honshu and the Sea of Japan coast of north-western Honshu, northern Kyushu, and Ulleungdo island in Korea (Fig. 1) (Kawai et al. 2020). The optimal growth temperature for this kelp ranges from 10 to 20 ºC (Ohta 1988, Kurashima et al. 1996, Baba 2010). Upper survival temperature is 29 ˚C (reviewed in Baba 2021), though the tolerance varies among localities (Ohtake et al

126 2020) and temperatures as low as 5 ºC are tolerated, with growth rates only dropping to
127 80% when compared to optimal temperatures, under adequate light intensity
128 (Kurashima et al. 1996). Further, a success in restoration (Yotsui and Maesako 1993)
129 and afforestation (Taniguchi and Agatsuma 2001, Taniguchi et al. 2001) of *E. bicyclis*
130 bed were reported. As described above, ecophysiological properties of this kelp have
131 been well-documented in efforts to conserve kelp forests. However, phylogeographic
132 and conservation genetic studies of the species have not yet been conducted and,
133 accordingly, the genetic structure and genetic diversity are still unknown. Further, the
134 demographic histories enable us to estimate future shifts in the distribution, as
135 mentioned above. The purpose of the present study was to reveal the genetic structure,
136 genetic diversity, and demographic history of the kelp using SNP markers based on
137 ddRAD-seq.
138
139 MATERIALS & METHODS
140 *Sampling and ddRAD-seq library construction*
141 Eighty-eight thalli were collected from nine localities covering the southern and
142 northern limits of the two disconnected distributions (Fig. 1, Table S1). The individuals
143 were collected at least 1 m apart to avoid the sampling of close relatives. The samples
144 were preserved at -30 °C until DNA extraction. Total genomic DNA was extracted using
145 the CTAB method as described by Doyle and Doyle (1990). A ddRAD library was
146 prepared with the *EcoR*I and *Bgl*II enzymes following a previously described protocol
147 (Peterson et al. 2012) with slight modifications, as described in Kobayashi et al. (2018).
148 The library was sequenced to generate 151 bp paired-end reads in one lane of HiSeq X
149 Ten (Illumina, San Diego, CA, USA) by a DNA sequencing service (Macrogen Japan

150 Corp., Tokyo, Japan).

151

152 *SNP calling*

153 From the paired-end reads, only the first reads (R1) were used for subsequent analyses
154 for the following two reasons: 1) the quality of the R2 reads was relatively poor; 2)
155 there was no clear advantage in using adjacent SNP sites for population genetics
156 analyses. From the raw data, trimming was carried out using Trim Galore
157 (https://github.com/FelixKrueger/TrimGalore/). This is a wrapper script to automate
158 quality and adapter trimming as well as quality control; it runs Cutadapt and FastQC
159 internally. In this tool, we used Cutadapt 1.18 (Martin 2011) and FastQC v.0.11.8
160 (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/). The trimming process
161 included three steps. First, all raw reads from all samples were trimmed with a quality
162 threshold of 30, minimum length of 80, and auto-detection of the adapter set. However,
163 with this first trimming alone, many adapter sequences were detected by FastQC as
164 overexpressed. Therefore, a second trimming step was performed with quality 30 and
165 minimum length 100, specifying the adapter sequences detected by each FastQC check
166 for each sample individually. Finally, the first 100 bp sequences were extracted from the
167 5'-end of the reads to obtain a uniform read length.

168 Stacks 1.48 (Catchen et al. 2011) was used to process the trimmed ddRAD-seq reads
169 with the following parameter settings: minimum number of identical reads required to
170 create a stack (m = 3), nucleotide mismatches between loci within a single individual
171 (M = 2), and mismatches between loci when building the catalogue (n = 4). The SNP
172 genotype for each individual was exported with a minimum stack depth of 5 and a
173 maximum observed heterozygosity cutoff of 0.6. Only the first SNP in each catalogue

174 was retrieved to exclude highly linked SNPs from the dataset. This filtering was carried
175 out using the 'populations' command in Stacks. The exported SNPs were filtered using
176 TASSEL 5.2.66 (Bradbury et al. 2007) with the following conditions: loci with a minor
177 allele frequency < 0.01, loci with a missing individual rate > 0.6, and individuals with a
178 missing locus rate > 0.4. During these filtering procedures, 12 individuals were filtered
179 out due to low genotyping rates. Furthermore, 177 SNPs were detected as outliers with
180 an FDR threshold of 0.05 using R v.3.6.3 (R Core Team 2020) with the package
181 PCAdapt (Duforet-Frebourg et al. 2014) and removed. In this outlier detection, $K = 1$
182 was used because the first principal component explained most of the variance. The
183 outlier SNPs may have adaptive information. Unfortunately, in the present study, we
184 decided not to use the outliers for further analysis. Outliers detected when using a small
185 number of environmentally and genetically different populations would be less reliable.
186 The remaining neutral SNPs are a good dataset that accurately shows the trend of
187 genetic differentiation across the genome, and it was used for the subsequent analysis.
188
189 *Genetic diversity*
190 As genetic diversity parameters, the number of different alleles per locus (N_A), number
191 of effective alleles per locus (N_E), number of private alleles (N_P), Shannon's information
192 index (I), observed heterozygosity (H_O), expected heterozygosity (H_E), unbiased
193 expected heterozygosity (uH_E), and inbreeding coefficient (F_{IS}) were calculated for each
194 population using GenAlEx v.6.501 (Peakall and Smouse 2012). Allelic richness (AR)
195 after rarefaction to the smallest sample size of N = 7 was calculated using the diveRsity
196 package (Keenan et al. 2013) in R v.3.6.3 (R core team 2020).
197 The contributions of each population to allelic diversity (Caballero et al. 2010) in

198 total (A_T), within populations (A_S), and between populations (D_A) were estimated using
199 Metapop2 (López-Cortegano et al. 2019). Because allelic diversity relies on the
200 calculation of allelic richness and the dissimilarity of alleles across subpopulations
201 rather than on gene diversity (López-Cortegano et al. 2019), it is appropriate in this
202 case, in which different alleles are expected to be distributed across regions.
203
204 *Genetic structure*
205 Genetic structure was inferred using model- and distance-based methods. In the model-
206 based method, a Bayesian analysis under the admixture F model for correlated allele
207 frequencies (Falush et al. 2003) was conducted using STRUCTURE v.2.3.4 (Pritchard
208 et al. 2000). Clusters (K) from K = 1 to 10 were estimated with a burn-in of 100,000
209 followed by 100,000 Markov chain Monte Carlo repetitions, without a priori population
210 assignment of individuals. Twenty independent runs were performed for each K value.
211 Then, the meaningful number of genetic clusters (K) was determined based on a
212 combination of the mean Ln probability of the data (LnP(K)) (Pritchard et al. 2000) and
213 the second-order rate of change in the log probability of the data (ΔK) (Evanno et al.
214 2005). The ΔK values were calculated using STRUCTURE HARVESTER v.0.6.94
215 (Earl and von Holdt 2012). For each cluster, H_E and F_{ST} values were calculated using
216 STRUCTURE to estimate genetic diversity and genetic drift from a common ancestral
217 population, respectively. The F_{ST} values in STRUCTURE are analogous to traditional
218 F_{ST} values between a cluster and a common ancestral population; see the user manual
219 for STRUCTURE (Pritchard et al. 2010).
220 In the distance-based analysis, we used DAPC, a multivariate method based on
221 sequential K means clustering and model selection that does not assume any genetic

222 model (Jombart et al. 2010), implemented in the adegenet 2.0.1 package (Jombart and
223 Ahmed 2011) in R v.3.2.3. (R core team 2020). This method uses a PCA prior to the DA
224 to infer genetic groups. The best-fit *K* cluster value was selected based on BIC
225 following the tutorial (Jombart and Collins 2015). A NeighborNet phylogenetic network
226 (Bryant and Moulton 2004) was inferred using SplitsTree v.4.14.2 (Huson and Bryant
227 2006) based on the genetic distance matrix among individuals calculated using TASSEL
228 5.2.66 (Bradbury et al. 2007). Furthermore, Jost's *D* was calculated for each population
229 pair using GenAlEx v.6.501.

230 The direction and magnitude of gene flow among populations were estimated using
231 the divMigrate function in the diveRsity package (Keenan et al. 2013) in R v.4.0.2 (R
232 core team 2020). This program produces a migration network graph with relative values
233 for gene flow among populations scaled to 1 at the largest magnitude estimated. Nei's
234 G_{ST} was used as a measure of genetic differentiation. For the direction of gene flow
235 between each population pair, the CIs were calculated by 1,000 bootstrap replicates, and
236 overlap between the 95% CIs was evaluated.

237

238 *Population demographic history*

239 ABC methods implemented in DIYABC v.2.1 (Cornuet et al. 2014) were employed to
240 infer the most likely demographic history of *E. bicyclis*. According to the above genetic
241 structure assessments, Pp 4 was excluded owing to its highly mixed genetic cluster
242 pattern. The remaining eight populations were classified into three regional population
243 groups: Sea of Japan populations (Pop1: Ps 1–4), Eastern Pacific populations (Pop2: Pp
244 1–3), and Central Pacific population (Pop3: Pp 5). Completely missing loci within each
245 population, as well as loci with minor allele frequencies < 0.01, were removed from the

original SNP dataset used for other population genetic analyses to meet the software requirements.

In this ABC analysis, any population demographic scenarios are examinable. However, since the validity is only inferred for a set of chosen scenarios, it is necessary to test a wide number of possibilities to conduct a reliable analysis. Considering the current distribution of this species, ocean currents, and the genetic structure detected above, we first conducted preliminary ABC analyses with various scenarios. Based on the preliminary ABC analyses, six demographic scenarios which include wide possibilities were designed (Fig. 2). Scenarios 1 and 2 assume that Pop3 is the ancestor, and differ in the order of divergence of the remaining two regional populations (Pop1 and Pop2). Scenario 3 assumes that Pop1 is ancestral and that the distribution expanded geographically from the Pop1. Scenario 4 assumes that Pop2 is the ancestor and that the distribution expanded in the opposite direction to that in scenario 3. In Scenario 5, Pop1 and Pop2 initially diverged across the Japanese archipelago, and then Pop3 was created by secondary contact and hybridization. Finally, in scenario 6, all three regional population groups diverged simultaneously, probably from an ancestral population that had spread throughout the area around the Japanese archipelago. In developing these scenarios, we did not account for the expansion of Pop1 or Pop2 through the Tsugaru Strait (between Hokkaido and Honshu). This expansion is nearly impossible in terms of ocean current flow and was not supported by our preliminary analyses. In these scenarios, t# indicates time scale measured in generations (t1, t2, and t3), and N1–3 and Na correspond to the effective population sizes for Pop1, Pop2, Pop3, and the ancestral population, respectively. Scenario 5 included an admixture event wherein the admixture rate ‘ra’ and ‘1-ra’ represent the genetic contribution of each ancestral population. In

this case, if ‘ra’ is close to 0, Pop3 mainly diverged from Pop2. Conversely, if ‘ra’ is close to 1, Pop3 mainly diverged from Pop1. Therefore, scenario 5 covers a wide range of possibilities. In scenario 6, a demographic event had occurred at a single point in t3; thus t1 and t2 have no meaning.

The parameter settings are listed in Table S2. We employed SS of genetic diversity and Nei’s distances for each population and each pair of populations, respectively. For both statistics, the proportion of zero values, variance of non-zero values, and mean of complete distribution were employed, for 18 SS in total. We simulated 1,000,000 datasets for each of the scenarios. To identify the most likely scenario, we compared the posterior probabilities of scenarios using both direct and logistic approaches. In the direct approach, the posterior probabilities of scenarios were estimated using the 500 simulated data closest to the observed data. A logistic regression with linear discriminant analysis on SS was applied for the logistic approach to estimate the posterior probabilities using 1% of simulated data showing the greatest similarity to the observed data. Confidence in the scenario choice was assessed using the DIYABC function ‘evaluate the confidence in scenario choice’ with logistic regression to estimate type I (false positives) and type II (false negative) errors with ‘linear discriminant analysis on SS’. Type I error is the probability of rejecting a scenario even though it is the true scenario, and type II error is the probability of selecting a scenario even though it is not the true scenario. To evaluate the error rates, we computed 1,000 datasets under all scenarios. We also used the option ‘model checking’ with PCA using DIYABC to assess the goodness of fit of the most likely scenario. This option can be used to evaluate the consistency of the observed data with the posterior predictive distribution of the model for the best scenario.

294

295 RESULTS

296 *General ddRAD-seq results*

297 We obtained 200,080,717 pairs of raw DNA sequences with an average of 2,273,645 ±
298 53,612 (mean ± SE) per sample. All raw ddRAD-seq reads were submitted to the DDBJ
299 Sequence Read Archive under accession number DRA012247–55 (Table S1). Following
300 the base call quality- and sequence length-based filtering and adapter trimming of the
301 R1 reads (see Materials and Methods), 53,368,014 reads (620,558 ± 51,504 per sample)
302 of 100 bp were obtained. After a Stacks analysis and subsequent SNP filtering, the final
303 dataset comprised 1,299 unlinked SNP loci for 76 *E. bicyclis* samples (Table S1). The
304 mean (min–max) genotyping rate for each individual was 78.6% (40.9–95.8%).

305

306 *Genetic diversity*

307 The estimated values for genetic diversity parameters and the fixation index are shown
308 in Table 1. Genetic diversity was higher in populations on the Pacific coast (Pp 1–5: *AR*
309 = 1.199, 1.078–1.325; *I* = 0.189, 0.104–0.259; and uH_E= 0.140, 0.08–0.200; mean, min–
310 max) than in populations in the Sea of Japan (Ps 1–4: *AR* = 0.947, 0.937–0.967; *I* =
311 0.024, 0.017–0.039; and uH_E = 0.017, 0.012–0.027). Among the Pacific coast
312 populations, genetic diversity was highest at the southern edge (Pp 5: Shimoda,
313 Shizuoka Prefecture) and lowest at the northern edge (Pp 1: Minami-sanriku, Miyagi
314 Prefecture). Diversity was consistently low in the Sea of Japan populations. N_p, a
315 measure of genetic uniqueness in each population, was also higher in populations on the
316 Pacific coast (N_P = 0.069, 0.005–0.189) than in those in the Sea of Japan (N_P = 0.012,
317 0.009–0.021). The fixation index was low and often negative in the Sea of Japan

318 populations but high and always positive in the Pacific Ocean populations (Table 1).
319 The contribution to allelic diversity (A_S, D_A, and A_T) was negative in all Sea of Japan
320 populations (Fig. 3). By contrast, except for D_A in Pp 1, all contributions were positive
321 in Pacific populations, with the highest values obtained for Pp 5 (Fig. 3).
322
323 *Genetic structure*
324 In the STRUCTURE analysis, the log-likelihood value LnP(K) increased gradually from
325 K = 1 to 4, and ΔK was highest for K = 2 and 3 (Fig. S1). Accordingly, we showed
326 results of K= 2 to 4 in Figure 1a. The results of 20 independent runs within K = 2, 3, and
327 4 were similar and stable, so that we evaluated the results with the highest log-
328 likelihood value among 20 runs for each K. The ΔK value was highest at K = 2, and the
329 genetic clusters clearly separated the populations in the Sea of Japan (Ps 1–4) and on the
330 Pacific coast (Pp 1–5). In the Central Pacific coast populations (Pp 4 and Pp 5), the Sea
331 of Japan cluster (yellow, gray in black and white version) was mixed with the Pacific
332 coast cluster (blue, off white in black and white version) at a relatively low frequency
333 (Fig. 1a, b). Low genetic diversity (H_E) and high genetic drift (F_{ST}) were detected in the
334 Sea of Japan cluster, whereas the opposite results were obtained for the Pacific coast
335 cluster (Fig. 1b). The ΔK value was second highest at K = 3, with a new genetic cluster
336 involving populations on the southern edge of the Pacific coast (Pp 5), in addition to the
337 clusters found at K = 2 associated with the Sea of Japan (Ps 1–4) and the Eastern Pacific
338 coast (Pp 1–3). For Pp 4, the assignment probabilities to the three clusters were mixed
339 (Fig. 1b). Similar to the results for K = 2, relatively low H_E and high F_{ST} values were
340 detected in the Sea of Japan cluster. Furthermore, Pp 4 and Pp 5 were assigned to
341 different clusters when K = 4 (Fig. 1a).

342 In the DAPC analysis, we retained 10 PCs, accounting for 68.97% of the total
343 variance. The BIC values indicated four to seven genetic clusters. At $K = 4$, individuals
344 were classified into four regional groups: Sea of Japan coast (Ps 1–4), Eastern Pacific
345 coast (Pp 1–3), Central Pacific coast (right five individuals from Pp 5 in Fig. 1a), and
346 Central Pacific coast (Pp 4 and rest of two individuals from Pp 5 in Fig. 1a; Fig. 4). The
347 individuals assigned to the last group corresponded to the individuals assigned to mixed
348 clusters at $K = 3$ and light green (light gray in black and white version) cluster at $K = 4$
349 in the STRUCTURE analysis (Fig. 1a). When the number of genetic clusters was five to
350 seven, the clusters were further divided based on four clusters (Fig. S2). Therefore, we
351 selected the result at $K = 4$.
352 The NeighborNet analysis showed four genetic clades: Sea of Japan populations (Ps
353 1–4), Eastern Pacific populations (Pp 1–3), and Central Pacific (Pp 4 and Pp 5) (Fig. 5).
354 Pp 4 was geographically located between Pp 5 and the Eastern Pacific populations (Pp
355 1, 2, and 3), and was genetically intermediate to these populations in the NeighborNet
356 analysis.
357 In the analysis of genetic differentiation (Jost's *D*) among all population pairs, while
358 inter-population differentiation within the Sea of Japan area was low for all population
359 pairs, levels of differentiation within the Pacific Ocean area were high (Fig. 6). In
360 particular, the Eastern Pacific population (Pp 1–3) and the southern edge of Central
361 Pacific population (Pp 5) showed high genetic differentiation (Jost's $D = 0.257–0.355$).
362 Gene flow estimates are shown in Fig. 7. Relatively high levels of gene flow were
363 mainly detected between populations within the Pacific coast (Pp 1–3) and the Sea of
364 Japan coast (Ps 1–4) (Fig. 7). Conversely, no substantial gene flow was detected
365 between the two coastal regions, except for weak gene flow from Ps 1 to Pp 5. Weak

366 gene flow into the Central Pacific populations (Pp 4 and Pp 5) from the Eastern Pacific
367 populations (Pp 1, 2, and 3) was detected. Bootstrap simulations showed significant
368 directional gene flow in the direction of influx from the surrounding populations (Ps 1
369 and 4) into Ps 2 in the Sea of Japan. Significant directional gene flow was also detected
370 in Ps 3 to Ps 2, although the magnitude of gene flow (0.29) was lower than our setting
371 of the threshold (0.30).
372
373 *Inference of population demographic history*
374 After additional SNP filtering, a dataset containing 1,002 SNP loci for 68 individuals
375 from eight populations was used for this DIYABC analysis. Among the six scenarios
376 (Fig. 2), the posterior probability was higher for scenario 6 (direct approach: 0.4400
377 with 0.0049–0.8751 of 95% CI, logistic approach: 0.9955 with 0.9942–0.9967 of 95%
378 CI) than for scenario 1 (0.1420, 95% CI: 0.0000–0.4480 and 0.0000, 95% CI: 0.0000–
379 0.0000), scenario 2 (0.2860. 95% CI: 0.0000–0.6821 and 0.0041, 95% CI: 0.0029–
380 0.0053), scenario 3 (0.0100. 95% CI: 0.0000–0.0972 and 0.0000, 95% CI: 0.0000–
381 0.0000), scenario 4 (0.1220. 95% CI: 0.0000–0.4089 and 0.0004, 95% CI: 0.0003–
382 0.0005), and scenario 5 (0.0000. 95% CI: 0.0000–0.0000 and 0.0000, 95% CI: 0.0000–
383 0.0000). As a result of model checking for scenario 6, the observed data were highly
384 similar to the simulated data in a PCA (Fig. S3). The probability of a type I error for
385 scenario 6 was p = 0.2391. The type II errors for scenario 6 under scenarios 1, 2, 3, and
386 4 were p = 0.2078, p = 0.1753, p = 0.2857, and p = 0.1947, respectively. For scenario 6,
387 the original mode values of t1, t2, and t3 were 373 (95% CI: 375–38,300), 34,900 (95%
388 CI: 5,580–51,100), and 45,900 (95% CI: 24,600–60,000) generations, respectively
389 (Table S3). The original modes of the effective population sizes N1, N2, N3, and Na

390 were 9,730 (95% CI: 4,570–14,100), 36,300 (95% CI: 22,800–45,100), 45,900 (95%
391 CI: 18,400–49,500), and 146,000 (95% CI =129,000–150,000), respectively (Table S3).
392 The generation time for *E. bicyclis* is roughly 3–6 years based on an ecological study
393 (Taniguchi and Kito 1988, Kawamata 2012). Using this estimate, the meaningful
394 divergence time in scenario 6 (t3) was converted to 137,700–275,400 years ago.
395

396 DISCUSSION

397 In the present study, we revealed the genetic structure of a canopy-forming kelp, *E.*
398 *bicyclis*, using 1,299 genome-wide SNP loci. According to simulation studies (Haasl et
399 al. 2011, Nazareno et al. 2017) and other recent phylogeographic studies using ddRAD-
400 seq (Lu et al. 2020, Yoichi et al. 2021), the number of SNP markers and the sample size
401 within populations in the present study would be sufficient for the phylogeographic
402 analyses. By a combination of STRUCTURE, DAPC, and NeighborNet analyses, we
403 detected four genetic groups distributed on the Eastern Pacific coast (Pp 1–3), Central
404 Pacific coast (Pp 4), Central Pacific coast (Pp 5), and Sea of Japan coast (Ps 1–4).
405 However, based on a STRUCTURE analysis assuming $K = 3$, Jost's D values, and
406 relative gene flow, Pp 4 was in a transition zone between the groups on the Eastern
407 Pacific coast (Pp 1–3) and Central Pacific coast (Pp 5), indicating that Pp 4 is a hybrid
408 population. Therefore, this kelp is likely composed of three genetically distinct groups
409 distributed on the Sea of Japan coast (Ps 1–4), Eastern Pacific coast (Pp 1–3), and
410 Central Pacific coast (Pp 5). Similar to results of previous phylogeographic studies of
411 brown algae in Japan (Uwai et al. 2006, Uwai 2010, Horiuchi et al. 2017, Kobayashi et
412 al. 2018), the genetic boundary between the Eastern Pacific population and Central
413 Pacific population of this kelp was identified as the area from the southern Tohoku to

Kanto regions.

The three genetic groups that distribute in different geographic regions suggested that a distinct refugium existed in each of the three regions during LGM. Each of them would have become the origin of the current three genetic groups, respectively. High, intermediate, and low genetic diversity were detected in the Central Pacific, Eastern Pacific, and Sea of Japan, respectively. These different patterns of genetic diversity indicate heterogeneity in the demographic history of the three groups. Additionally, the DIYABC analysis suggested the simultaneous split of the three groups in the greater ancestral period (137,700–275,400 years ago), before the LGM. After divergence, large, medium, and small effective population sizes were detected in the Central Pacific, Eastern Pacific, and Sea of Japan, respectively. This pattern corresponds to the pattern of genetic diversity described above. Thus, the three clusters were presumably influenced differently by past geographic and climatic events.

Low genetic diversity and small effective population sizes were detected in *E. bicyclis* in the Sea of Japan. These results suggest that the Sea of Japan populations underwent severe bottlenecks in the past (e.g., during the LGM). Therefore, the present wide distribution along the Sea of Japan coast probably formed after the LGM by a rapid range expansion from refugia along the coast, supported by the high genetic homogeneity in the Sea of Japan populations. A recent range expansion has also been reported in *Cystoseira tamariscifolia* (Hudson) Papenfuss in northern Europe (Bermejo et al. 2018) and *Laminaria digitata* (Hudson) J.V. Lamouroux in the Northeast Atlantic (Neiva et al. 2020). During the LGM, in addition to cold water temperatures similar to current temperatures in the northern Sea of Japan of 46–48°N, low salinity (26–29‰) has been reported in the southern region of the Sea of Japan (Oba and Tanimura 2012).

Although studies of salinity tolerance are lacking in *E. bicyclis* and a few even in the other kelp species, in general, kelp species can grow the salinity range of 26–29‰ (Bartsch et al. 2008). Water temperature in the past 5 years ranged from 6 to 21ºC in the northernmost region of this kelp distribution (available here: https://www.suigi.pref.iwate.jp/teichi, recorded in the depth of 3 m), and between 4 to 21 ºC in the northern Sea of Japan 46-48 ºN (available here: https://www.jma-net.go.jp/sapporo/kaiyou/engan/engan.html, recorded at surface). Given this kelp can survive ~ 5 ˚C (Kurashima et al. 1996), *E. bicyclis* could survive in the lower temperature of the northern Sea of Japan 46-48 ºN. Accordingly, this kelp species has the potential to survive in a wide area on the Sea of Japan coast, even during the LGM, from this physiological perspective. Therefore, abiotic factors other than temperature and salinity probably limited the distribution of *E. bicyclis* to refugia during the LGM. For example, the kelp prefers strong light intensity, thereby limiting it to shallow water, usually < 10 m in depth (Maegawa et al. 1988, Kurashima et al. 1996). It is possible that photosynthetically active radiation could be a limiting factor in the past distribution of this kelp, as the kelp is currently absent in coastal areas with heavy snowfall (i.e., frequently cloudy in the winter) in the Sea of Japan from Fukui Prefecture to Hokkaido. In contrast to *E. bicyclis*, the Sea of Japan populations of *Sargassum thunbergii* (Mertens ex Roth) Kuntze, an intertidal-dominant brown alga, show high genetic diversity and large effective population sizes, suggesting their stable persistence in this area (Kobayashi et al. 2018). More studies are needed to reveal the macroalgal distribution in the Sea of Japan during the LGM.

The highest genetic diversity was detected in a *E. bicyclis* population at the southern edge of the Pacific coast. In Japan, the highest genetic diversity was found in southern

462 populations in various species of brown algae, including *Sargassum fusiforme* (Harvey)
463 Setchell (Horiuchi et al. 2017) and *S. thunbergii* (Kobayashi et al. 2018), and in a red
464 alga, *Gelidium elegans* Kützing (Chimura et al. 2020). A similar pattern has been
465 reported for brown algae distributing European coasts, at localities considered to be
466 refugia during the LGM (Assis et al. 2014, 2016, Neiva et al. 2014, Bermejo et al. 2018,
467 Neiva et al. 2020, Schoenrock et al. 2020). Accordingly, the southern edge population of
468 *E. bicyclis* was probably maintained for a long time before the LGM. Given the
469 difference in genetic diversity between the Eastern and Central Pacific coasts, the
470 population size of *E. bicyclis* during the LGM was likely smaller on the Eastern Pacific
471 coast, as supported by the DIYABC.

472 Currently, many kelp forests are threatened by ocean warming (Kumagai et al. 2018,
473 Wernberg et al. 2019). Especially on temperate coasts, tropicalization increases kelp
474 consumption by herbivorous fish, and the decline or disappearance of kelps has been
475 found in various transition zones between temperate and tropical areas (Vergés et al.
476 2016, Zarco-Perello et al. 2017). In Japan, SST has risen by +1.16°C over the last 100
477 years (Japan Meteorological Agency:
478 https://www.data.jma.go.jp/gmd/kaiyou/english/long_term_sst_japan/sea_surface_temp
479 erature_around_japan.html). Declines in distribution within next 2-3 decades were
480 predicted for most kelp species in Japan (Kumagai et al. 2018, Sudo et al. 2020). As to
481 *E. bicyclis*, it has been predicted that southern central Pacific and southern Sea of Japan
482 population are highly vulnerable to heat stress and herbivorous feeding in 2009-2035
483 (Kumagai et al. 2018). Indeed, a long-term monitoring in northwestern Kyushu revealed
484 that losses of ecklonian kelp forests were driven by high temperature in summer,
485 subsequent feeding by herbivorous fish in autumn, and small number of recruitments

(Kiyomoto et al. 2021). Several studies have revealed the importance of potential deep sea refugia for temperate kelp against the global warming (Graham et al. 2007, Assis et al. 2016). However, *E. bicyclis* prefers a strong light intensity (Maegawa et al. 1988, Kurashima et al. 1996) and is therefore found in shallow water, usually at depths of < 10 m (Maegawa 1990, Sakanishi et al. 2018). Thus, deep sea refugia would be unavailable for this kelp.

E. bicyclis conservation efforts need to consider the genetic structure and genetic diversity revealed in the present study. The decline of *E. bicyclis* beds on the southern edge of the Pacific coast has recently been found at a long-term monitoring site (Biodiversity Center of Japan, Ministry of the Environment, Government of Japan 2020; http://www.biodic.go.jp/moni1000/index.html, Terada et al. 2020). In the present study, the southern populations in the Central Pacific (Pp 4 and Pp 5) contributed substantially to the total genetic diversity of this species. Therefore, the loss of Central Pacific populations (Pp 4 and Pp 5) would drastically decrease total genetic diversity within this kelp. Especially for our southern edge population, Pp 5, which showed the highest genetic diversity and the highest genetic uniqueness (Table 1), is only 3 km from this monitoring site and may be declining as well. Pp 5 also showed the highest F_{IS} values (Table 1), suggesting high level of inbreeding, probably as a result of the population decline. Similar to this kelp, high F_{IS} values in declining populations have been reported in *Saccorhiza polyschides* (Lightfoot) Batters (Assis et al. 2013). Inbreeding depression is frequently observed in animals and land plants (Frankham et al. 2002). It has not been a major concern in macroalgae but should be considered, in addition to genetic diversity and uniqueness. However, in a laminarialean kelp *Postelsia palmaeformis* Ruprecht, selfing did not reduce the fitness of the offspring (Barner et al. 2011), and further, in

small populations, the demographic processes had an affect greater than genetic diversity (Wootton and Pfister 2013). On the other hand, temporary drastic losses of *E. bicyclis* beds have been observed in the southern part of the Sea of Japan due to heat wave occurred in 2013 (Yatsuya 2014, Yoshida 2016). As revealed in the present study, all Sea of Japan populations have low genetic diversity, indicating that they may be vulnerable to environmental changes, such as climate change and feeding increases. Therefore, these populations need to be monitored for potentially rapid changes in response to environmental changes. Because the Sea of Japan populations formed a unique genetic cluster distinct from the Eastern and Central Pacific populations, their conservation is essential as well. Furthermore, future losses of southern populations in both the Central Pacific and Sea of Japan due to increased kelp consumption by herbivorous fish are predicted (Kumagai et al. 2018). Immediate conservation actions on the Central Pacific coast and southern Sea of Japan coast are needed to maintain *E. bicyclis* beds based on current genetic diversity levels. In addition, generally, a greater understanding of the effects of inbreeding and the loss of genetic diversity is needed across kelp species.

CONCLUSION

We revealed the genetic structure of a canopy-forming kelp, *E. bicyclis*, using genome-wide SNP loci in the present study. Three genetically distinct groups were detected in the Eastern Pacific, Central Pacific, and Sea of Japan. The estimated divergence time of these three groups was before the last glacial period. They likely survived for a long time after divergence in each region. The Central Pacific populations have high genetic diversity and uniqueness. The southern population in the Sea of Japan may be

vulnerable to environmental change due to its low genetic diversity. The conservation of *E. bicyclis* populations in these two areas is an urgent issue. The demonstrated effectiveness of reforestation of brown algae, inclusive of genetic considerations (Wood et al. 2020), emphasizes that phylogeographic studies like the present study, which can provide us fundamental genetic basis, have become more important. Phylogeographic studies on various canopy-forming brown algae are needed to effectively promote the conservation of macroalgal forests.

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947 **Table 1.** Genetic diversity of *Eisenia bicyclis* populations collected in the present study

Population code	N	N_A	N_E	N_P	*AR* [7]	*I*	H_O	H_E	uH_E	F_{IS}
Ps 1	9	1.030	1.013	0.009	0.939	0.019	0.017	0.013	0.013	-0.274
Ps 2	9	1.079	1.037	0.021	0.967	0.039	0.025	0.025	0.027	0.011
Ps 3	8	1.028	1.014	0.008	0.937	0.017	0.015	0.011	0.012	-0.182
Ps 4	8	1.039	1.024	0.010	0.945	0.022	0.02	0.014	0.016	-0.293
Pp 1	7	1.156	1.088	0.005	1.078	0.104	0.063	0.070	0.080	0.070
Pp 2	10	1.348	1.194	0.013	1.164	0.177	0.080	0.117	0.127	0.281
Pp 3	10	1.332	1.174	0.037	1.157	0.167	0.089	0.109	0.117	0.166
Pp 4	8	1.447	1.255	0.104	1.271	0.240	0.127	0.159	0.178	0.184
Pp 5	7	1.443	1.286	0.189	1.325	0.259	0.077	0.175	0.200	0.522
Mean	8.4	1.211	1.120	0.044	1.087	0.116	0.057	0.077	0.086	0.233

948 *N* = No. of specimens, N_A = No. of different alleles, N_E = No. of effective alleles, N_P = No. of private alleles, AR = Allelic richness (the
949 number in square brackets is the rarefaction size corresponding to the smallest sample size in the present study), *I* = Shannon's
950 information index, H_O = Observed heterozygosity, H_E = Expected heterozygosity, uH_E = Unbiased expected heterozygosity, F_{IS} =

fixation index.

952 FIGURE LEGENDS

953

954 **Fig. 1.** Distribution of *Eisenia bicyclis* (gray area), localities of collection sites (star),
955 and genetic clustering based on a STRUCTURE analysis setting $K = 2$, $K = 3$, and $K =$
956 4. Each vertical bar shows the assignment probability for individuals (a). Pie charts in
957 the map indicate the frequency of each cluster in the population (b).

958

959 **Fig. 2.** Six scenarios for the demographic histories of *Eisenia bicyclis* obtained using
960 DIYABC v.2.1. t# represents the time scale measured in the number of generations. N1–
961 3 and Na correspond to effective population sizes for Pop 1, Pop 2, Pop 3, and the
962 ancestral population. The most likely scenario is shown by a double underline.

963

964 **Fig. 3.** Contributions of nine *Eisenia bicyclis* populations to overall genetic diversity
965 and diversity within and between populations on the basis of allelic diversity.

966

967 **Fig. 4.** Discriminant analysis of principal components at $K = 4$ for the *Eisenia bicyclis*
968 samples in the present study. Asterisks indicate individuals from Pp 5 within the Central
969 Pacific cluster (Pp 4 and Pp 5).

970

971 **Fig. 5.** NeighborNet inferred using 76 samples from nine *Eisenia bicyclis* populations.
972 Instead of sample IDs, population codes are indicated on the tips of branches.

973

974 **Fig. 6.** Pairwise genetic differentiation values (Jost's *D*) for all population pairs. The
975 black-to-white gradient corresponds to the change from higher to lower values.

Fig. 7. Direction and relative magnitudes of gene flow among the nine *Eisenia bicyclis* populations. Relative gene flow estimates of < 0.30 are not shown. Asterisks (*) show significant directional gene flow based on 1,000 bootstrap replicates.

SUPPLEMENTARY FIGURES AND TABLES

Fig. S1. Delta *K* values (a) and LnP (*K*) (b) in each *K* cluster in a STRUCTURE analysis.

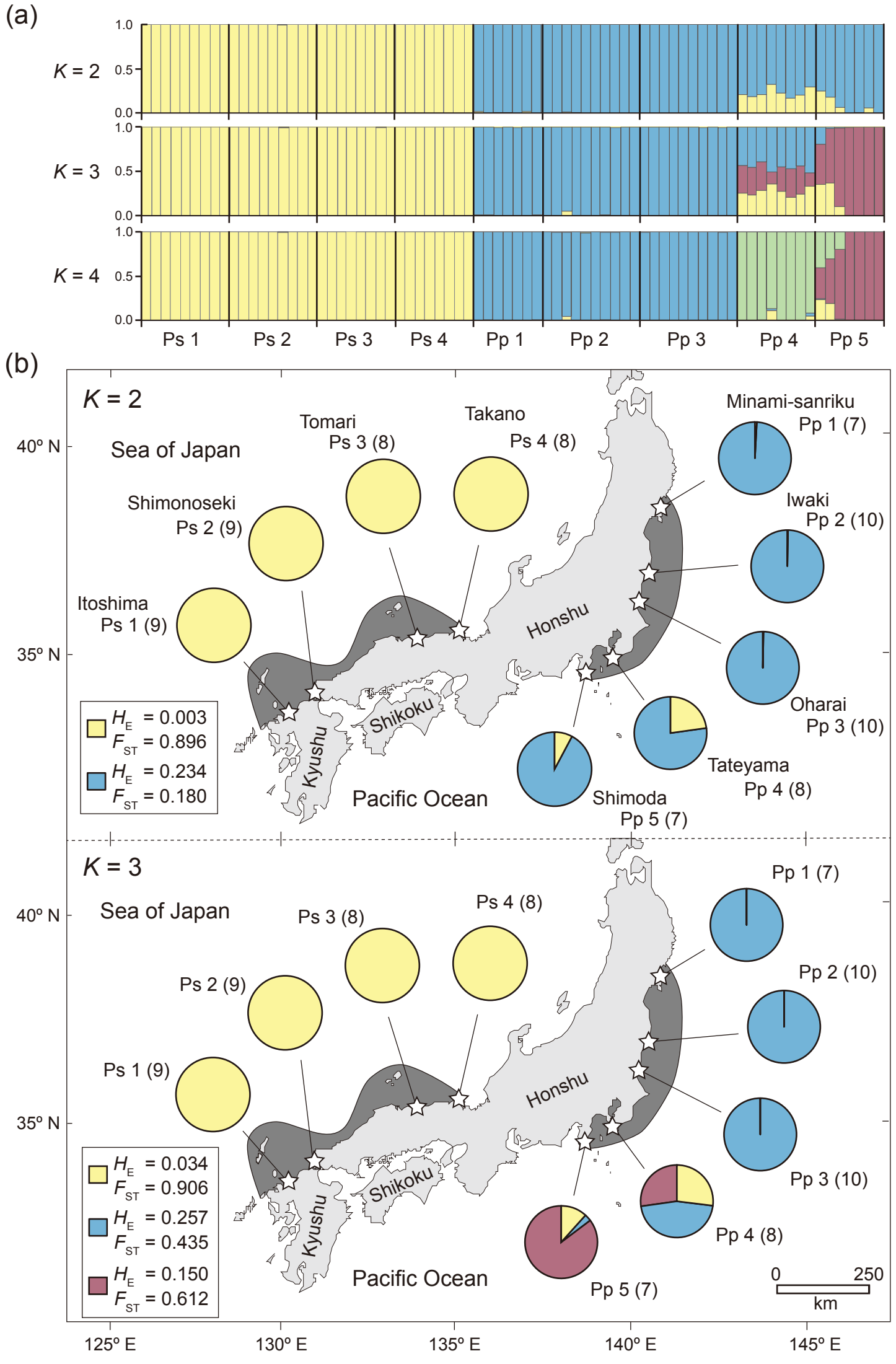
Fig. S2. BIC values for each value of *K* (a). Discriminant analysis of principal components for *K* = 5 (b), *K* = 6 (c), and *K* = 7 (d) based on *Eisenia bicyclis* collected in the present study.

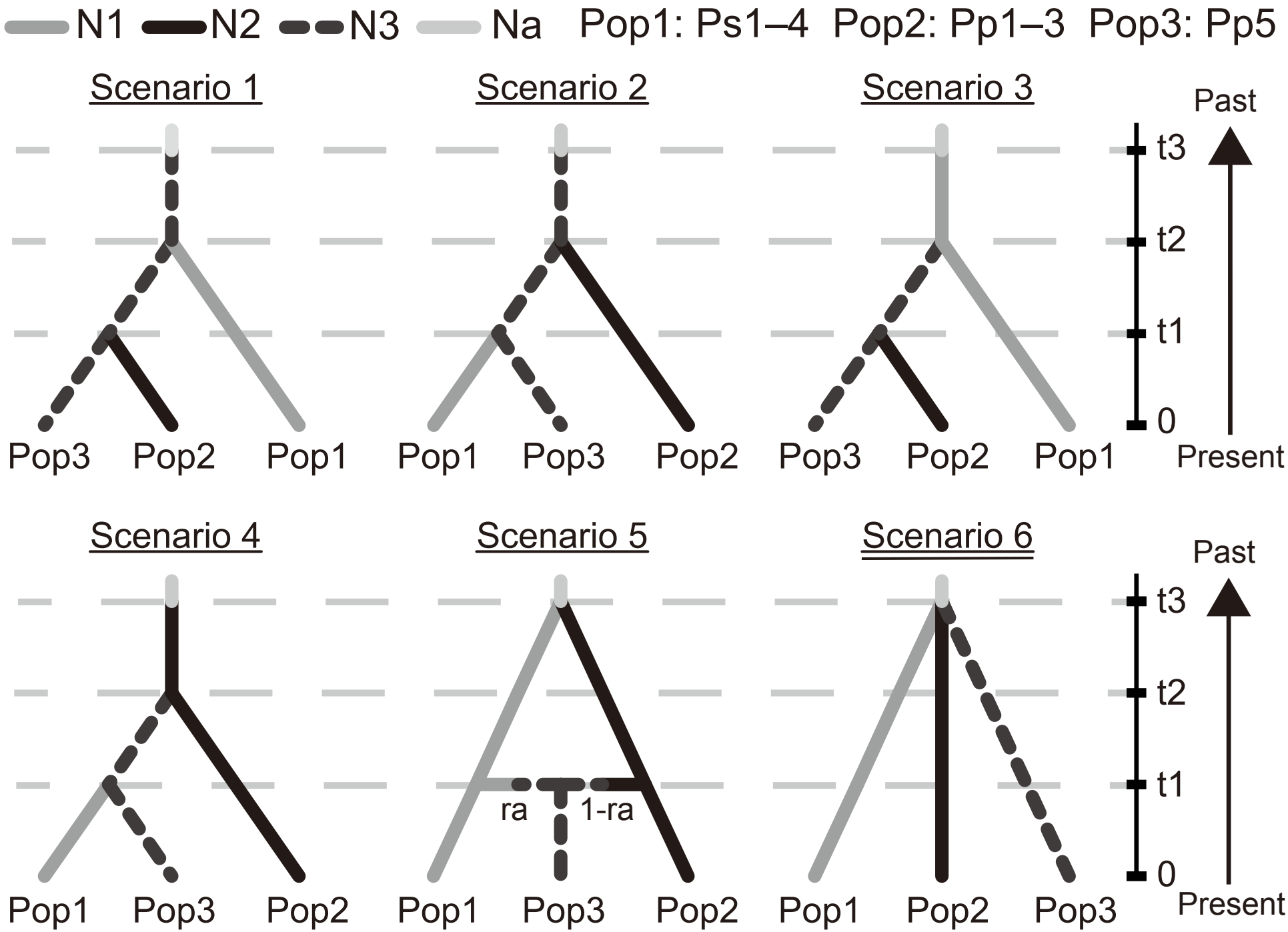
Fig. S3. PCA of SS for the best-supported scenario 6 based on 1,000 simulations in the DIYABC analysis.

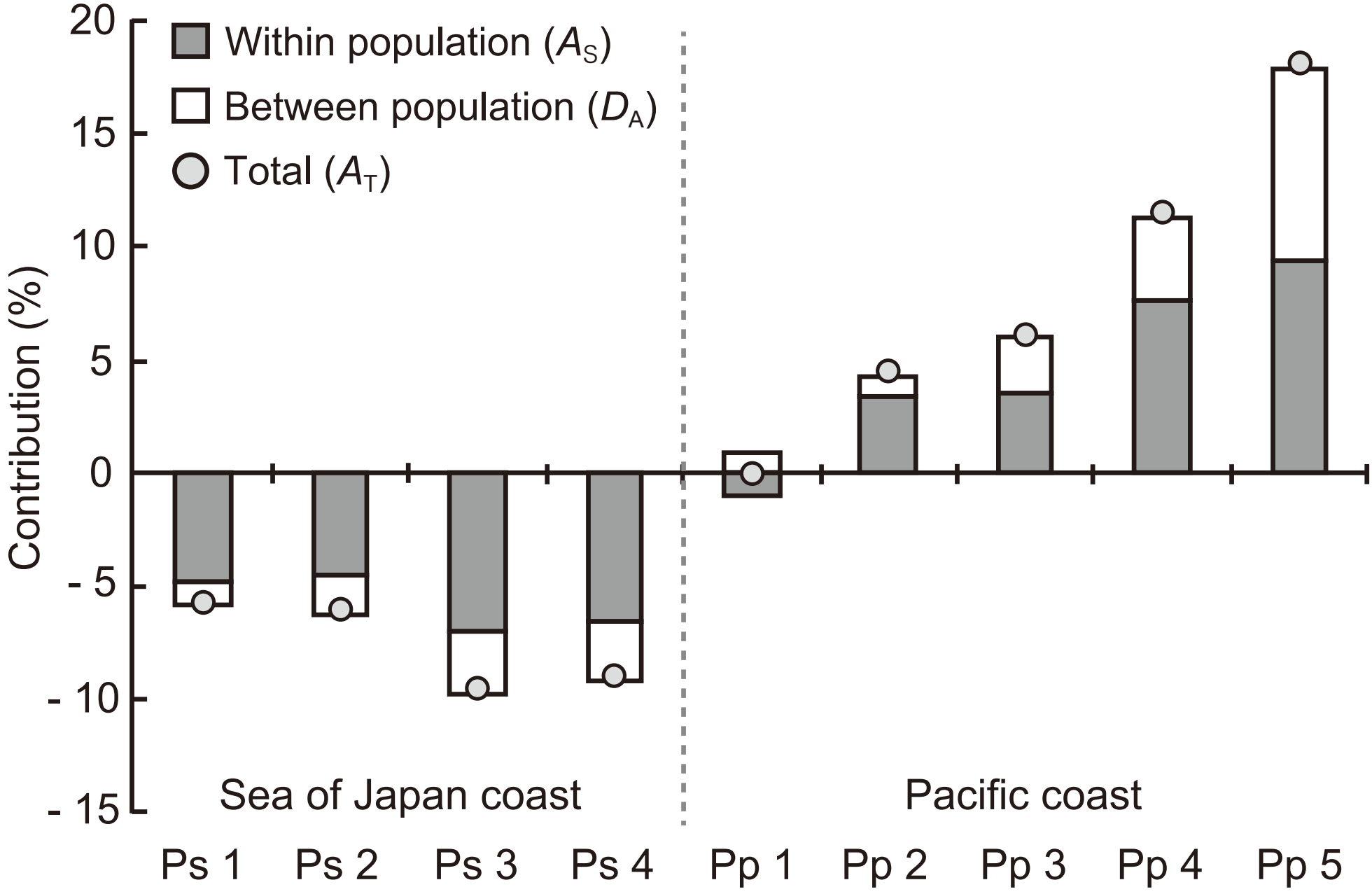
Table S1. Sample information includes the population code, locality, number of samples collected, and final dataset for analysis

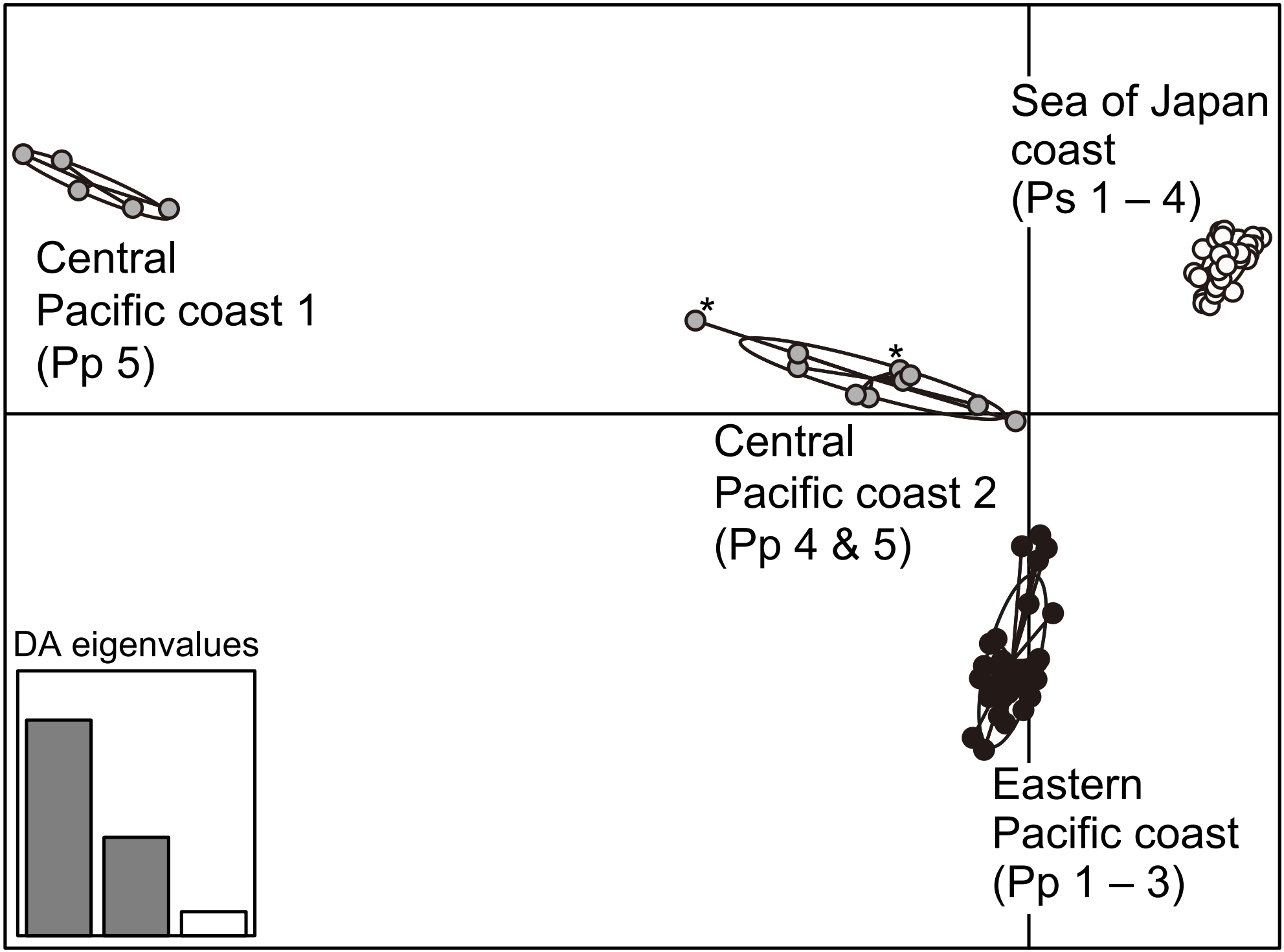
Table S2. Prior distributions of the parameters used in DIYABC

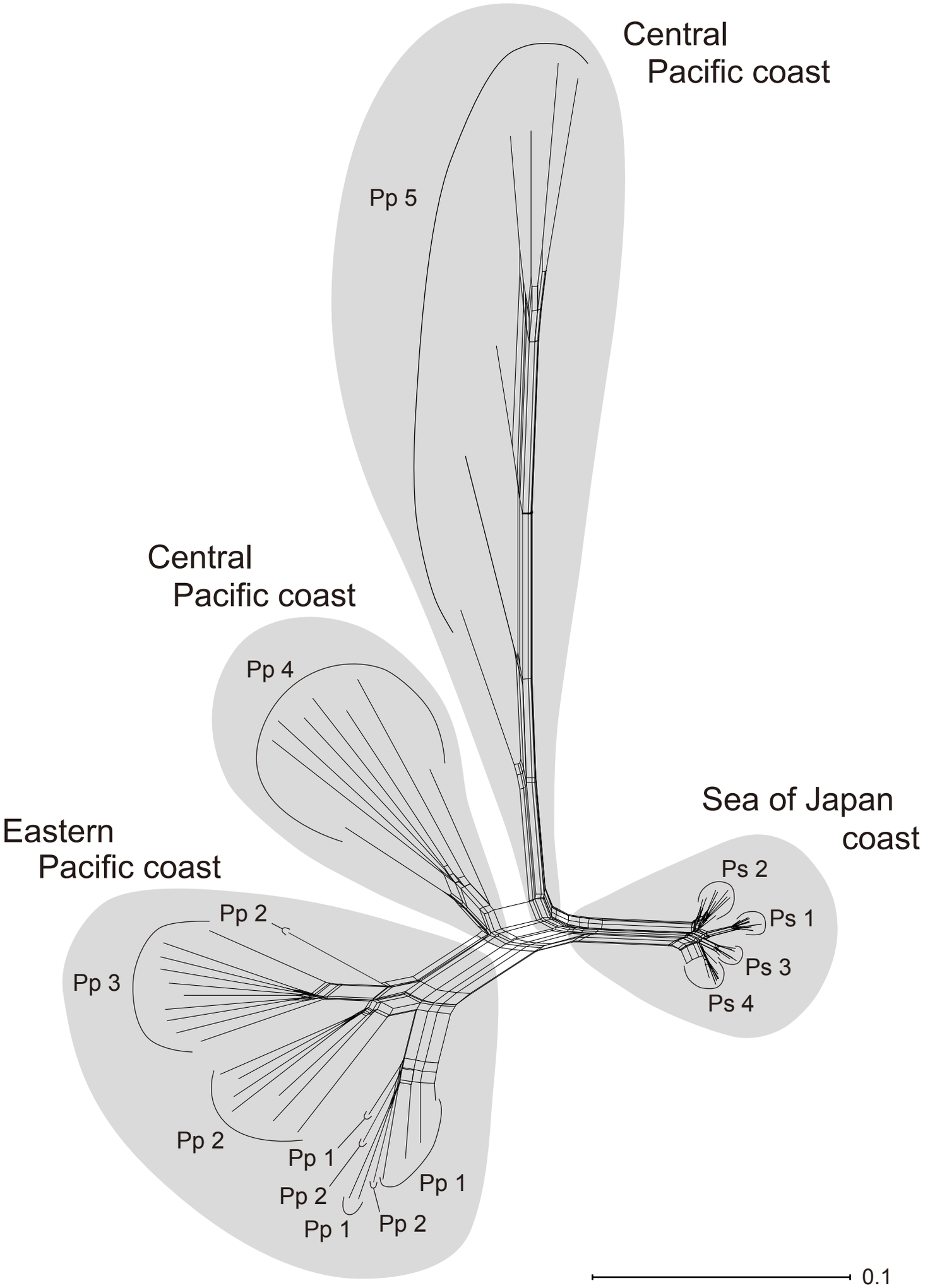
Table S3. Original demographic parameters estimated by DIYABC in scenario 6


(a)
K = 2
K = 3
K = 4
1.0
0.5
0.0
Ps 1
Ps 2
Ps 3
Ps 4
Pp 1
Pp 2
Pp 3
Pp 4
Pp 5
(b)
K = 2
Sea of Japan
Tomari
Ps 3 (8)
Takano
Ps 4 (8)
Minami-sanriku
Pp 1 (7)
Shimonoseki
Ps 2 (9)
Iwaki
Pp 2 (10)
Itoshima
Ps 1 (9)
Honshu
Shikoku
Kyushu
Oharai
Pp 3 (10)
Tateyama
Pp 4 (8)
Shimoda
Pp 5 (7)
Pacific Ocean
H_E = 0.003
F_{ST} = 0.896
H_E = 0.234
F_{ST} = 0.180
K = 3
Sea of Japan
Ps 3 (8)
Ps 4 (8)
Pp 1 (7)
Ps 2 (9)
Pp 2 (10)
Ps 1 (9)
Honshu
Shikoku
Kyushu
Pp 3 (10)
Pp 4 (8)
Pp 5 (7)
Pacific Ocean
H_E = 0.034
F_{ST} = 0.906
H_E = 0.257
F_{ST} = 0.435
H_E = 0.150
F_{ST} = 0.612
0
250
km
40° N
35° N
125° E
130° E
135° E
140° E
145° E


N1
N2
N3
Na
Pop1: Ps1–4
Pop2: Pp1–3
Pop3: Pp5
Scenario 1
Scenario 2
Scenario 3
Scenario 4
Scenario 5
Scenario 6
Past
Present
t3
t2
t1
0
Pop3
Pop2
Pop1
ra
1-ra


Within population (A_S)
Between population (D_A)
Total (A_T)
Contribution (%)
20
15
10
5
0
- 5
- 10
- 15
Sea of Japan coast
Pacific coast
Ps 1
Ps 2
Ps 3
Ps 4
Pp 1
Pp 2
Pp 3
Pp 4
Pp 5


Sea of Japan
coast
(Ps 1 – 4)
Central
Pacific coast 1
(Pp 5)
*
*
Central
Pacific coast 2
(Pp 4 & 5)
DA eigenvalues
Eastern
Pacific coast
(Pp 1 – 3)


Central
Pacific coast
Pp 5
Central
Pacific coast
Pp 4
Sea of Japan
coast
Eastern
Pacific coast
Ps 2
Ps 1
Ps 3
Ps 4
Pp 2
Pp 3
Pp 2
Pp 1
Pp 2
Pp 1
Pp 1
Pp 2
0.1

	Ps 1	Ps 2	Ps 3	Ps 4	Pp 1	Pp 2	Pp 3	Pp 4
Sea of Japan coast								
Ps 2	0.064							
Ps 3	0.059	0.038						
Ps 4	0.052	0.035	0.035					
Eastern Pacific coast								
Pp 1	0.332	0.244	0.284	0.255				
Pp 2	0.265	0.194	0.217	0.193	0.044			
Pp 3	0.247	0.211	0.220	0.209	0.161	0.069		
Central Pacific coast								
Pp 4	0.253	0.192	0.222	0.180	0.144	0.121	0.185	
Pp 5	0.417	0.319	0.372	0.336	0.257	0.268	0.355	0.192

Sea of Japan coast: Ps 1, Ps 2, Ps 3, Ps 4

Eastern Pacific coast: Pp 1, Pp 2, Pp 3

Central Pacific coast: Pp 4

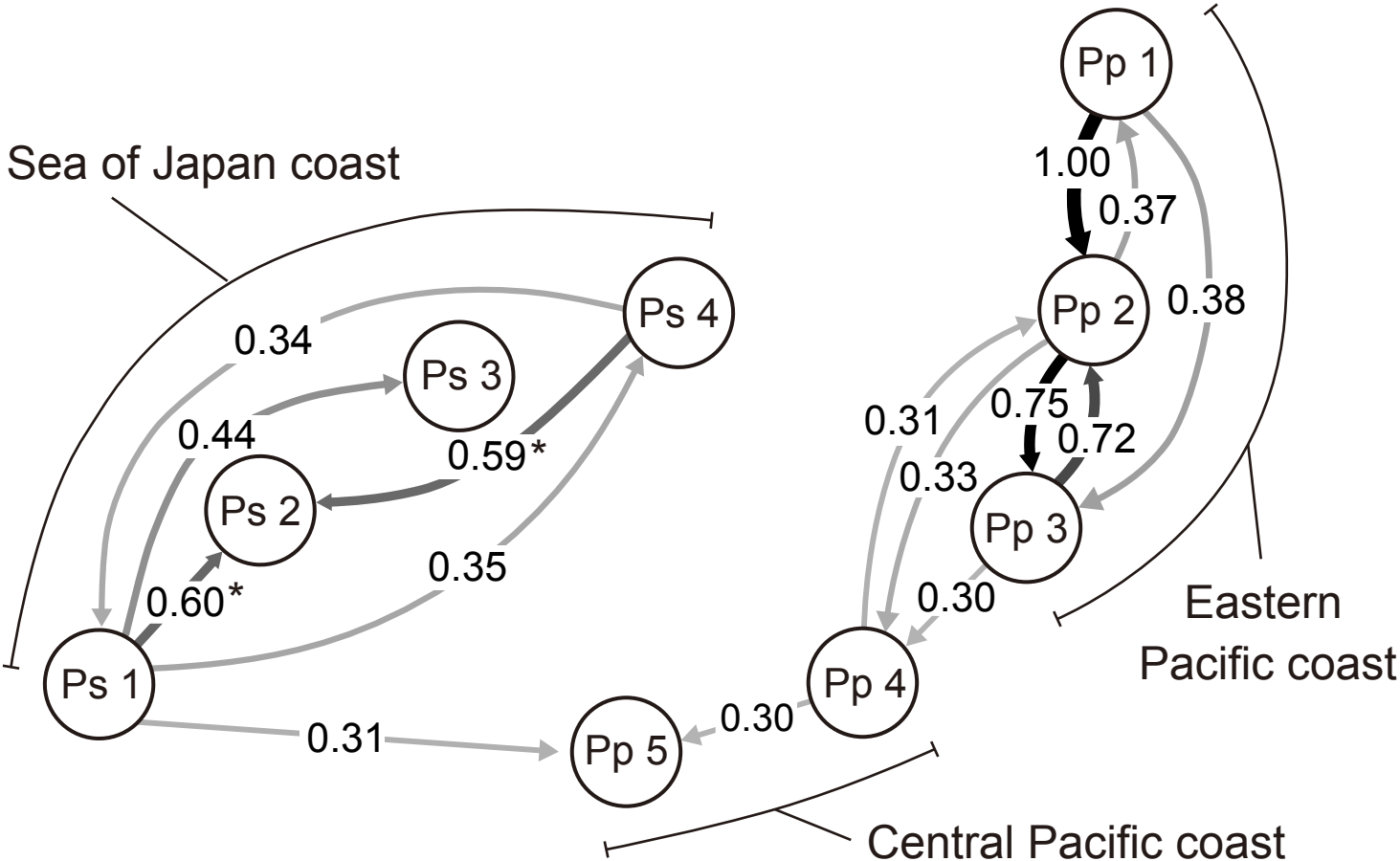

Sea of Japan coast
Ps 1
Ps 2
Ps 3
Ps 4
0.34
0.44
0.59*
0.60*
0.35
0.31
Pp 1
Pp 2
Pp 3
Pp 4
Pp 5
1.00
0.37
0.38
0.31
0.75
0.72
0.33
0.30
0.30
Eastern
Pacific coast
Central Pacific coast

Table S1. Samples information showing population code, locality, number of samples collected, and final dataset for analysis.

Population code	Locality	Coordinate	Date	No. of individuals	No. of individuals after the SNP calling	Population classification for DIYABC analysis	Accession no. of raw data of ddRad-seq
Ps 1	Itoshima, Fukuoka	33˚63’21 N 130˚18’17 E	November, 6–7, 2018 September, 13, 2019	10	9	POP 1	DRA012247
Ps 2	Shimonoseki, Yamagushi	34˚15’44 N 130˚89’76 E	June, 25, 2019	10	9	POP 1	DRA012248
Ps 3	Tomari, Tottori	35˚51’84 N 133˚94’87 E	June, 13, 2019	10	8	POP 1	DRA012249
Ps 4	Takano Kyoto,	35˚74’47 N 135˚11’10 E	June, 13, 2019	8	8	POP 1	DRA012250

Pp 1	Minami-sannrikucho, Miyagi	38˚38’42 N 141˚28’33 E	June, 19, 2019	10	7	POP 2	DRA012251
Pp 2	Iwaki, Fukushima,	36˚99’66 N 140˚98’11 E	May, 17, 2019	10	10	POP 2	DRA012252
Pp 3	Oharai, Ibaraki	36˚31’89 N 140˚59’30 E	May, 23, 2019	10	10	POP 2	DRA012253
Pp 4	Tateyama Chiba	34˚97’94 N 139˚82’20 E	June, 6, 2019	10	8	—	DRA012254
Pp 5	Shimoda, Shizuoka	34˚65’24 N 138˚96’47 E	June, 18, 2019	10	7	POP 3	DRA012255
Total				88	76		

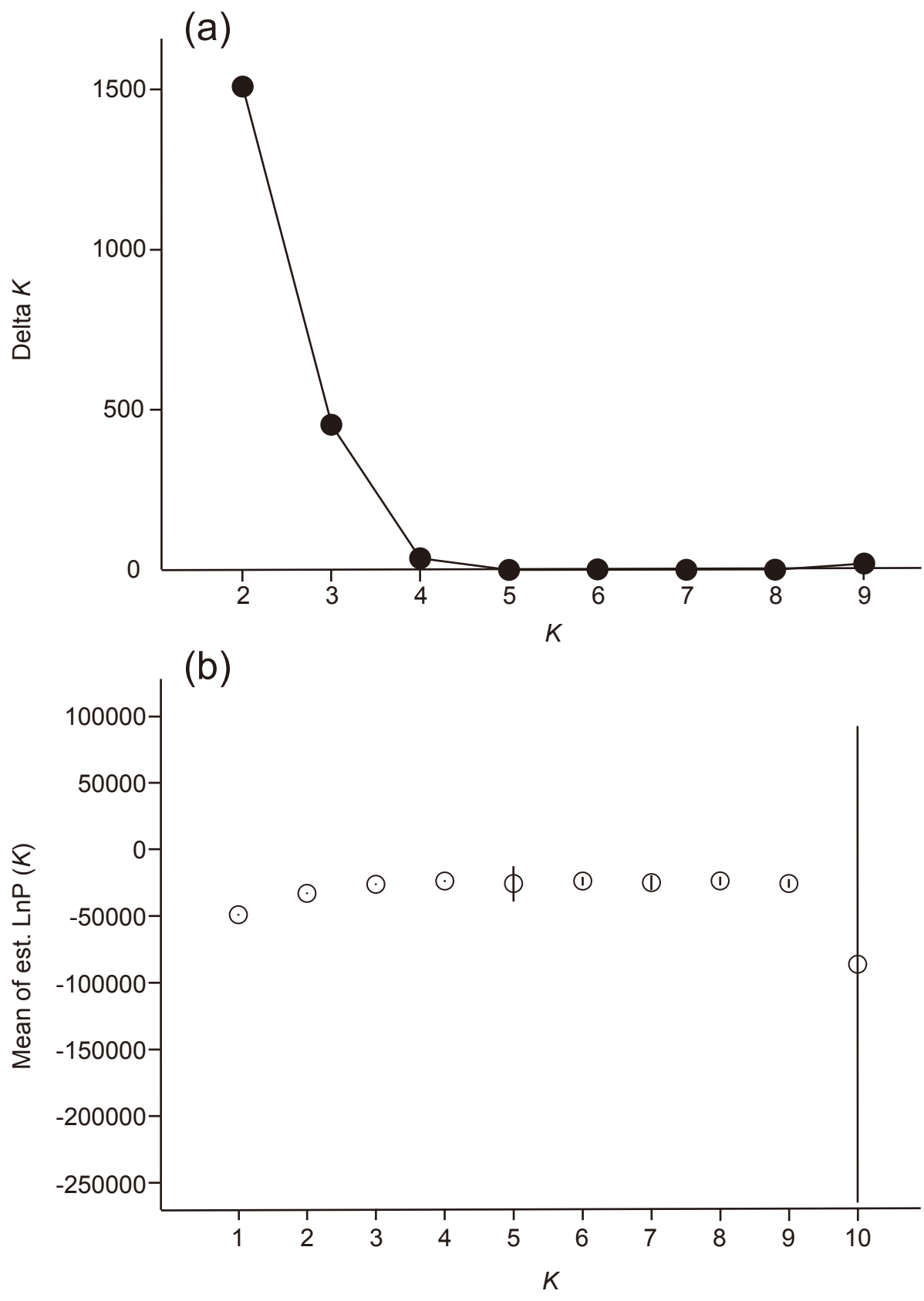


Fig. S1. Delta *K* values (a) and LnP (*K*) (b) in each of *K* cluster in STRUCTURE analysis.

Table S2. Prior distributions of the parameters used in DIYABC.

parameter	Probability distribution	Minimum	Maximum
Effective population size			
N1	uniform	10	50,000
N2	uniform	10	50,000
N3	uniform	10	50,000
Na	uniform	10	150,000
Time scale in generations			
t1	uniform	10	50,000
t2	uniform	10	100,000
t3	uniform	10	100,000
Admixture			
ra	uniform	0.1	0.9

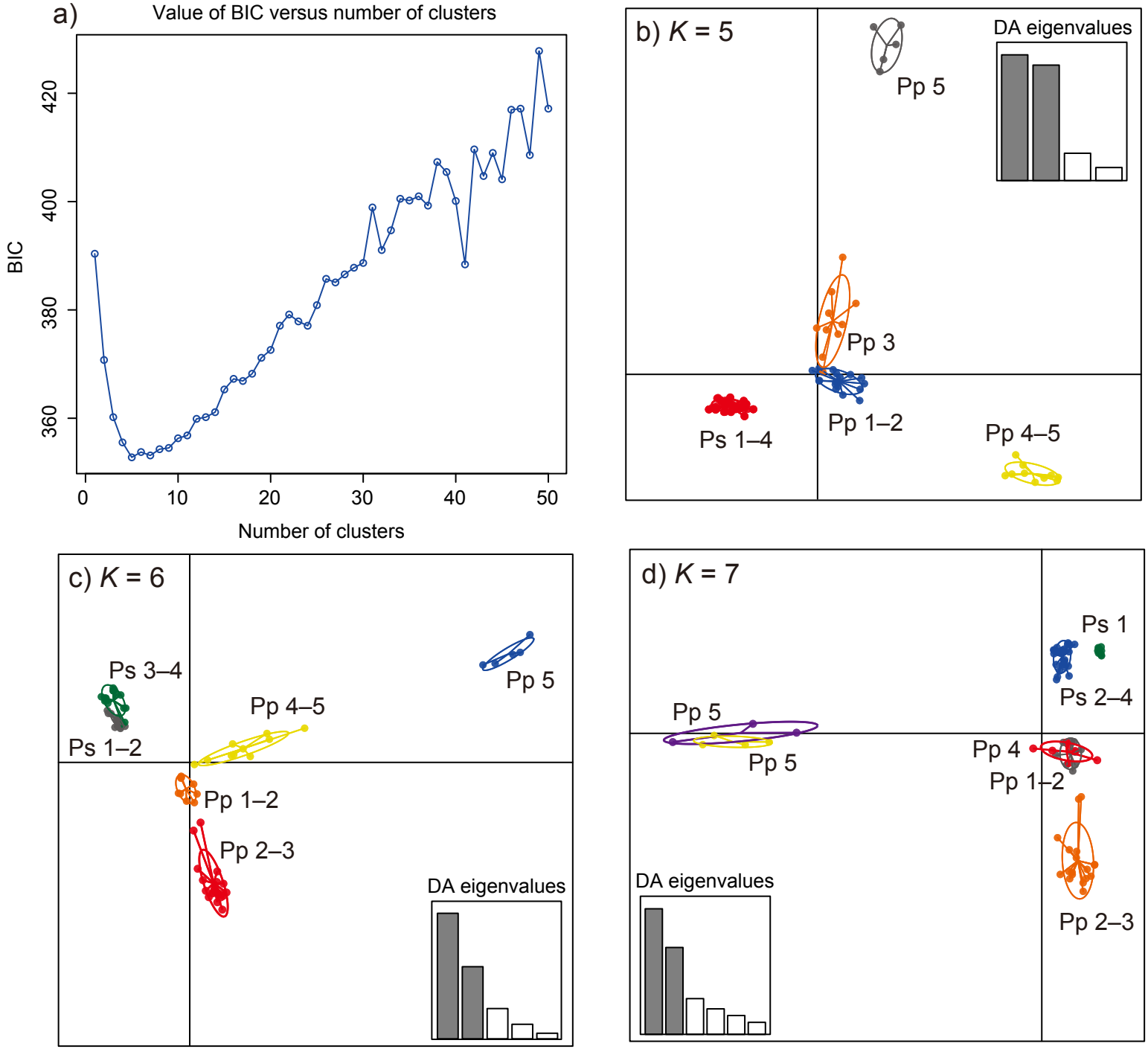


Fig. S2. BIC values in each of *K* cluster (a). Discriminant analysis of principal components scatter plot at *K* = 5 (b), *K* = 6 (c), and *K* = 7 (d) based on the *Eisenia bicyclis* collected in the present study.

Table S3. Original demographic parameters estimated by DIYABC in Scenario 6.

Parameter		Mean	Median	Mode	Quantile 2.5%	Quantile 5.0%	Quantile 95.0%	Quantile 97.5%
Effective population size	N1	9,690	9,770	9,730	4,570	5,620	13,500	14,100
	N2	34,800	35,300	36,300	22,800	25,300	42,700	45,100
	N3	37,700	39,000	45,900	18,400	22,000	49,000	49,500
	Na	144,000	145,000	146,000	129,000	134,000	149,000	150,000
Time scale in generations	t1	12,200	9,400	373	375	708	33,500	38,300
	t2	28,400	28,800	34,900	5,580	8,180	47,800	51,100
	t3	43,400	44,000	45,900	24,600	28,100	56,800	60,000

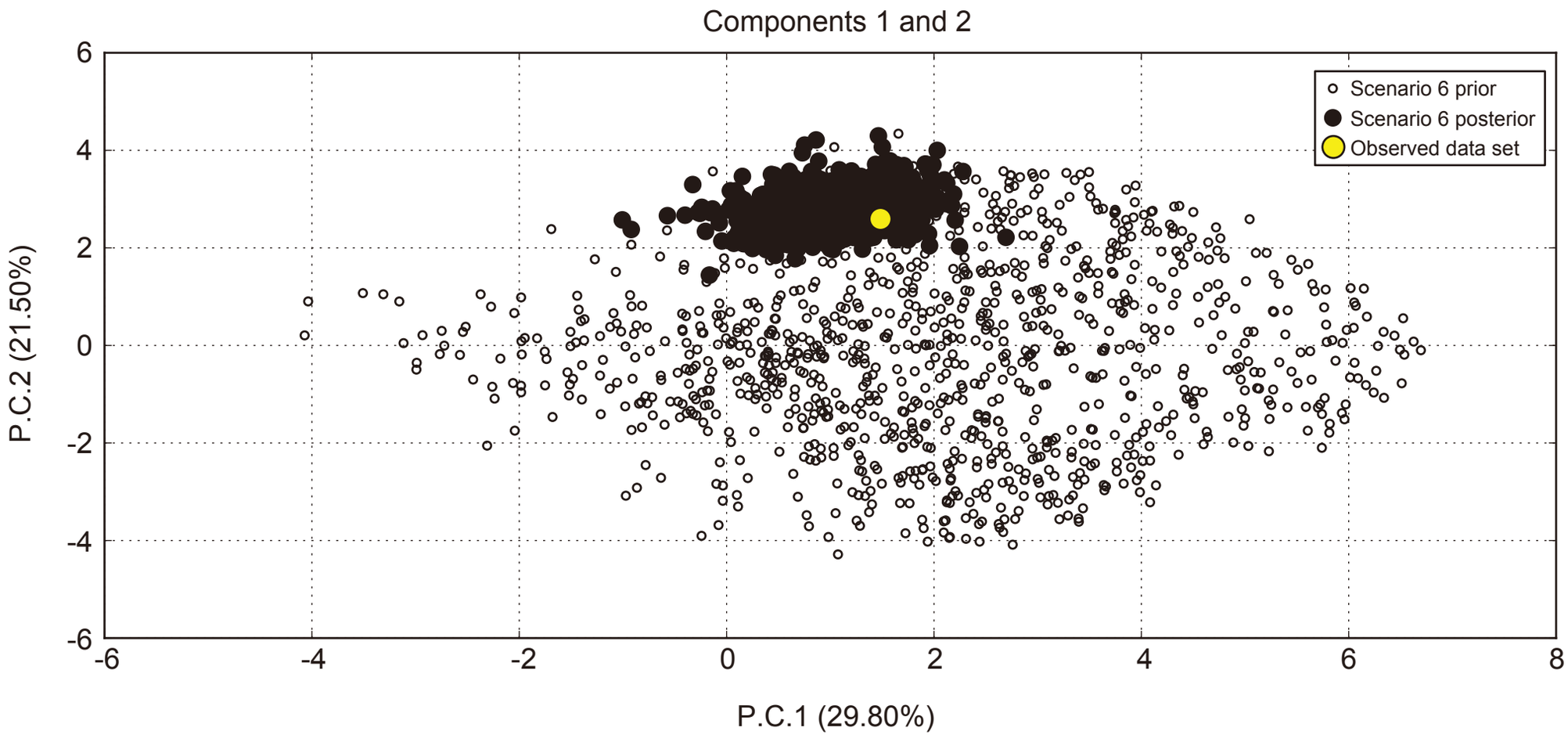


Fig. S3. PCA on summary statistics of the best-supported scenario 6 based on 1,000 simulations in DIYABC analysis.