Title: Ecosystem size predicts the probability of speciation in migratory freshwater fish

Short title: Ecosystem size predicts speciation

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ABSTRACT

Predicting speciation is a fundamental goal of research in evolutionary ecology. The probability of speciation is often positively correlated with ecosystem size. Although the mechanisms driving this correlation are generally difficult to identify, a shared geographic and ecological context provides a suitable condition to study the mechanisms that promote speciation in large ecosystems by reducing the number of factors to be considered. Here, we determined the correlation between speciation and ecosystem size, and discussed the underlying mechanisms of this relationship, using a probable parallel ecotype formation for freshwater fish. Our population genetic analysis revealed that speciation of the landlocked goby, *Rhinogobius* sp. YB, of the Ryukyu Archipelago, Japan, from its migratory ancestor, *R. brunneus*, occurred in parallel across five islands. Logistic regression analysis showed that speciation probability could be predicted using island size. The results suggest that ecosystem size predicts the occurrence of adaptation and reproductive isolation, likely through its association with three possible factors: divergent selection strength, population persistence, and occurrence probability of habitat separation.

Key words

ecological speciation, parallel evolution, island biogeography, approximate Bayesian
computation, speciation-area relationship, *Rhinogobius*

1 | INTRODUCTION

Understanding the patterns and mechanisms of speciation is the fundamental goal of evolutionary ecology (Coyne & Orr, 2004; Reznick & Ricklefs, 2009). As macroevolutionary patterns of speciation, such as differences in diversification rate among lineages or regions, are caused by the accumulation of individual speciation events, the patterns are expected to be strongly influenced by speciation mechanisms (i.e., evolution of reproductive isolation). However, the relationships between macropatterns and the underlying mechanisms are not well understood, because they are usually investigated separately (Rosenblum et al., 2012; Cutter & Gray, 2016; Rabosky, 2016; but see Rabosky & Matute, 2013). Explicit consideration of the speciation mechanism would be helpful for obtaining a causal explanation of how macroevolutionary patterns of speciation have been generated (Harvey et al., 2017; Kisel et al., 2012).

Ecosystem size, often represented by habitat area, has long been considered as one of the best predictors for variation in species richness (MacArthur & Wilson, 1967). Recent studies on species–area relationships also recognize "in situ speciation" as an important factor, in addition to immigration and extinction rates (Losos & Parent, 2009; Losos & Schluter, 2000; Wagner, Harmon, & Seehausen, 2014; Weigelt, Steinbauer, Cabral, & Kreft, 2016). The positive correlation between ecosystem size and speciation rate is supported by several empirical (Kisel & Barraclough, 2010; Parent & Crespi, 2006) and theoretical (Gavrilets & Vose, 2005; Rosindell & Phillimore, 2011) studies.

Several hypotheses have been proposed that explain how speciation rate, or speciation probability, is affected by ecosystem size through speciation processes. For example, the opportunity for geographical isolation, which impedes gene flow, is likely to increase in larger areas (Kisel & Barraclough, 2010; Losos & Schluter, 2000). As larger areas contain heterogeneous environments, this phenomenon might also promote diversification to new environments following speciation (Parent & Crespi, 2006). Moreover, larger areas allow larger population sizes and longer persistence of newly emerged species (Kisel, McInnes, Toomey, & Orme, 2011). However, these hypotheses have been rarely tested empirically, because studies have usually assessed speciation by considering various mechanisms simultaneously. Thus, it is difficult to evaluate the influence of different factors on the speciation process. This problem could be addressed by targeting a group with parallel diversification under the same mechanism (Lucek, Kristjánsson, Skúlason, & Seehausen, 2016; Vamosi, 2003). However, when using such an approach, it is important to first obtain evidence of repeated evolution under the same mechanism as the focal system.

Due to clear boundaries and replications, freshwater invasion by migratory fish in island habitats is a suitable case for testing the relationship between ecosystem size and occurrence of speciation. The East Asian goby, genus *Rhinogobius*, is one such fish group, in which the amphidromous (migratory) species *R. brunneus* might have repeatedly produced strictly freshwater populations (*Rhinogobius* sp. YB sensu Akihito, Sakamoto, Ikeda, & Aizawa, 2013) in the Ryukyu Archipelago of Japan (Kano, Nishida, & Nakajima, 2012; Nishida, 2001; Ohara, Takagi, Hashimoto, Miyazaki, & Hirashima, 2008). However, the number of times and geographical scales (i.e., islands, rivers, etc.) of the origin of the freshwater form of this goby have not yet been elucidated. Furthermore, the extent and factors of reproductive isolation between the amphidromous and freshwater forms have not been investigated.

We propose that the freshwater colonization of the goby in the Ryukyu Archipelago is a good model system for testing the correlation between ecosystem size and speciation probability for the following reasons. First, the ancestral amphidromous populations might have shared common evolutionary potential, because of possible gene flow through the sea during the larval period. Second, ecosystem age is similar among islands. According to geographical data, most islands in the Ryukyu Archipelago formed nearly simultaneously ~1.5 million years ago by the opening of straits between the islands (Osozawa et al., 2012). Third, ecological conditions are probably similar among the islands, because almost no freshwater fish species, except those of *Rhinogobius*, occur in the upper reaches of the rivers in the Ryukyu Archipelago (Kano et al., 2012; Yoshigou, 2014), resulting in few competitors and predators, which are important components of ecological opportunity (Wellborn & Langerhans, 2014; Yoder et al., 2010).

Using the simple system of *Rhinogobius* gobies, we primarily aimed to clarify whether the speciation probability of the freshwater form can be explained by ecosystem size. We first confirmed the existence of genetic isolation between the amphidromous and freshwater forms inhabiting the same islands or rivers. Next, we estimated where and how many times the freshwater forms originated, based on statistically explicit tests among demographic models that hypothesized parallel or single origin scenarios. We then examined whether speciation probability could be predicted by ecosystem size. The correlation between independent origins of the freshwater form inferred from demographic modelling and ecosystem size (e.g., island area) was tested statistically (see Figure 1, concept diagram representing our approach). On the basis of these results, we discuss the mechanisms producing the relationships between ecosystem size and the speciation process in this system.

2 | MATERIALS AND METHODS

2.1 | Study system

The freshwater resident form derived from the amphidromous species *Rhinogobius brunneus* is recognized as an independent species but has not yet been described because of taxonomic confusion. Previous studies (e.g., Akihito et al., 2013) tentatively used the name "*Rhinogobius* sp. YB" for this freshwater form. However, until its evolutionary status is clarified, we will use the code "FF" (freshwater form) for *Rhinogobius* sp. YB and "AF" (amphidromous form) for *R. brunneus* based on their life history modes.

The FF completes its life in freshwater; conversely, AF larvae hatch in rivers and immediately drift down to the sea and return to rivers after 2–3 months (Mizuno, 2001). The eggs and larvae of FF are larger than those of AF (Supporting Information methods and results S1). These traits are assumed to be an adaptation to the river environment, where small food items (i.e., plankton) are scarce and higher level of swimming ability in river currents is needed (Hirashima & Tachihara, 2000; Nishida, 2001; Shinomiya, Sasabe, Sakurai, & Kishino, 2005; Yamasaki, Nishida, Suzuki, Mukai, & Watanabe, 2015).

Although the distribution of the two species sometimes overlapped in a single river, their distributions were generally different. AF mainly lived in the middle to lower reaches of rivers. In fact, AF populations are found only in rivers shorter than 18 km in the central Honshu region of Japan (Tamada, 2005). The larvae of AF must rapidly reach the sea to avoid starvation because of the scarcity of small food in rivers (Iguchi & Mizuno, 1999; Moriyama, Yanagisawa, Mizuno, & Omori, 1998). Thus, they might not be able to reproduce effectively in areas far from the sea (Iguchi & Mizuno, 1999). By contrast, FF mainly live in the upper reaches of rivers, and are often found in the upper areas of waterfalls where no other fish species are distributed (Kano et al., 2012).

2.2 | Sampling

Samples were collected on seven islands where populations of FF have been recorded previously (locality code 2. Amami-Ohshima Is., 4. Tokunoshima Is., 5. Okinoerabujima Is., 6. Okinawajima Is., and 7. Kumejima Is. in Middle Ryukyu; 8. Ishigakijima Is. and 9. Iriomotejima Is. in South Ryukyu; Table S1; Figure 2; Ohara et al., 2008; Yoshigo, 2014). In addition, AF specimens were collected from three other islands (Figure 2). The specimens were identified by body colour patterns when fresh (Kano et al., 2012; Suzuki, Shibukawa, Yano, & Senou, 2004). Identification based on body colour was in agreement with the results of the genetic analysis, but some samples were difficult to identify or showed inconsistent genetic characteristics. When genetic data suggested that the focal specimens were not judged as hybrids based on the criteria described below and that incorrect identification based on morphology in the field was likely (see the next section and Supporting methods and results S1), these samples were removed from all subsequent analyses. If a sample was judged to be a hybrid, we tentatively named it based on morphology. As a result, 842 FF and 578 AF specimens from 52 points in 42 river systems were included in the analysis. Both forms were collected from nine river systems; they were sympatrically collected at seven points.

2.3 | Genetic data and population structure

Genetic data of *Rhinogobius* specimens were obtained by genotyping 20 nuclear microsatellite loci (Table S2; Ohara, Takahashi, & Takagi, 2004). Methods for molecular experiments and genotyping are described in the Supporting methods and results S1. Genotype data were deposited in Dryad (https://doi.org/10.5061/dryad.mpg4f4qvh). To assess the genetic features of the respective populations, we calculated the expected and observed heterozygosity (H_E and H_O, respectively) and allelic richness (*Rs*) for the respective populations. Pairwise F_{ST} and Jost's *D* were also calculated. We conducted analysis of molecular variance (AMOVA; Excoffier, Smouse, & Quattro, 1992) separately for AF and FF, to assess hierarchical genetic differentiation. To visualize relatedness among populations, we constructed a neighbour-joining tree among populations based on Nei's *Da* distance (Nei, Tajima, & Tateno, 1983) using poptree2 (Takezaki, Nei, & Tamura, 2010). The credibility of each clade was evaluated using 1,000 bootstrap resamplings.

To infer the existence and extent of gene flow and genetic isolation, we analysed the genetic structure of the population using structure version 2.3.4 (Lawson, van Dorp, & Falush, 2018; Pritchard, Stephen, & Donnelly, 2000). We prepared two data sets: one for both FF and AF populations from each island, and another for only AF populations from all islands. Evanno's Δ*K* (Earl & von Holdt, 2012; Evanno, Regnaut, & Goudet, 2005) was used as a reference for *K* value selection. Hybrid individuals were evaluated using *q* values; we arbitrarily judged specimens as hybrids (or individuals with hybrid origin) in cases where minor genetic components accounted for 10% or more of the aggregate (Vähä & Primmer, 2006). Detailed methods are provided in the Supporting methods and results S1.

2.4 | Testing the parallel formation of FF by ABC

Before testing the relationship between ecosystem size and speciation probability, we needed to infer the islands where speciation of FF occurred. To examine the single or parallel origins of FF statistically, we conducted a demographic model selection under the Approximate Bayesian Computation (ABC) framework (Beaumont, 2010). We briefly describe the procedures of model construction and model selection in this section (for details, see Supporting methods and results S1).

Our general model construction strategies for ABC analysis were as follows. First, we generated separate models using three geographical scales (i.e. within-islands, regional [Middle and South Ryukyu], and archipelago scales) and examined FF origins in each geographical scale to reduce the number of models and populations examined in a single analysis. Second, we examined both models with and without gene flow between AF and FF populations. This is because a simulation study suggests that gene flow could alter apparent phylogenetic relationships among populations when simple genetic distance was used (Bierne, Gagnaire, & David, 2013). Demographic model comparisons that consider gene flow can overcome this problem (Butlin et al., 2014).

In the within-islands analyses, we mainly examined two questions: whether FF had single or parallel origin, and whether gene flow between AF and FF existed on each island. We hypothesized several plausible divergence orders between populations based on the result of structure analysis, phylogeny and geographical locations for respective islands. Thereafter, we compared the models with single/parallel origins and with/without gene flow. Analyses were conducted for the five islands where FF is distributed in multiple rivers (i.e., Amami-Oshima Is., Tokunoshima Is., Okinawajima Is., Kumejima Is. and Iriomotejima Is.). We selected three (or two) river populations for each island to reduce the model complexities. Criteria for population selection are described in the Supporting methods and results S1. The constructed models (a total of 34 models) are described in Figure S1a–e. Summary statistics are given in Table S3.

For the among-islands within-region analyses, we constructed several plausible models separately for the regions of Tokunoshima Is. and Okinoerabujima Is., Middle Ryukyu, and South Ryukyu. Five to 10 models were constructed on the basis of the phylogenetic tree and geographical distance between islands. Finally, in the between-region analyses, we compared 10 models generated from the results of the previous analyses. All constructed models are described in the Supporting methods and results S1 and Figure S1f–I. Scripts that describe the models have been deposited in Dryad (https://doi.org/10.5061/dryad.mpg4f4qvh).

For model selection, we chose the model that had the highest posterior probability in the respective analyses. To evaluate the accuracy of model selection, we calculated a misclassification rate (i.e., the rate at which the focal model was selected despite the other model being true [type 2 error rate]).

2.5 | Correlation between ecosystem size and speciation probability

We first identified the islands on which the speciation of FF occurred based on the results of structure (genetic isolation) and ABC model selection (independent origin). The relationship between ecosystem size and speciation was analysed for the Middle and South Ryukyu islands. This is because these islands are assumed to be similar in age, were never connected to the continent after separation, and were not catastrophically affected by volcanic activity (Osozawa et al., 2012; Supporting methods and results S1). We acquired distribution information of the two forms from published literature (Yoshigou, 2014) and our own field survey, and we only chose the islands where either or both forms were distributed. This is because we assumed that speciation was not likely to have occurred on the island where either of these species is not currently distributed. We coded the occurrence of speciation in each island as follows: 1 for the island where speciation occurred, and 0 for the island where speciation did not occur. As a proxy of ecosystem size, we used island area (km^2; data from the Geospatial Information Authority of Japan), maximum catchment area (km^2), maximum river length (m) or the maximum number of waterfalls on each island (Supporting methods and results S1).

We performed one-parameter logistic regression analysis in the generalized linear model framework with binomial error structure for the response variable (speciation: 1, presence; 0, absence) using the glm package of r version 3.1.1 (R Core Team, 2014). Due to a strong positive correlation between the four variables (Pearson's correlation coefficient, 0.592–0.993, Supporting methods and results S1), we primarily used island area as the explanatory variable for the main result. Explanatory variables, except the number of waterfalls, were $\log_{10}$-transformed. To test the significance of explanatory variables, we conducted a likelihood ratio test using 10,000 rounds of parametric bootstrap sampling with a constant model as a null model that assumes no relationship between ecosystem variables and speciation probability. We calculated McFadden's pseudo R^2.

Furthermore, to examine the effect of the ecosystem size parameters other than island size (i.e., maximum catchment area, river length and number of waterfalls), we constructed another generalized linear model for speciation probability. We used the residuals from a regression between island size and each of the other ecosystem size parameters, together with the island size and their interaction, as explanatory variables. Stepwise model selections by Akaike information criterion (AIC) scores were conducted using the *step* function on r.

3 | RESULTS

3.1 | Basic summary statistics

Heterozygosity and allelic richness were generally higher in the AF populations than in the FF populations (Table S1, Figure S2a, b). The AF populations showed relatively little pairwise genetic differentiation within islands and among islands within regions (Tables S4–S6, Figure S2c, d). In comparison, the genetic differentiation of AF populations between regions was large (Tables S4–S6, Figure S2c, d). The FF populations often showed large genetic differentiation within islands and among islands within regions, as well as among regions (Tables S4–S6, Figure S2c, d).

3.2 | Genetic isolation and hybrids

In the AF data set, Evanno's Δ*K* showed the maximum value at $K = 2$; the populations in North plus Middle Ryukyu and South Ryukyu were clearly separated. In the data set for each island, including FF and AF populations, Δ*K* had a maximum value at $K = 2$ for all islands, except one (Amami-Oshima Is.). The two genetic clusters corresponded to the two forms, except on Okinawajima Is. (see below; Figure 3; Figure S3).

Suspected hybrid individuals were rare (2.0% of the total individuals). No suspected hybrid individuals were detected from five of the seven sympatric collection points. Several suspected hybrid individuals were detected in 11 FF and AF populations. Among these, all FF individuals that were identified based on morphology in the FFOK-4–1 and FFOK-4–2 populations (Okinawajima Is.; Figures 2 and 3; Figure S3) exhibited the genetic features of AF as the dominant component.

3.3 | Genetic relationships among populations

The neighbour-joining tree showed two divergent groups separated by the Kerama Gap in all of the FF and AF populations (bootstrap value, 97%; Figure 4). Each group included both forms, which we present as Group 1 (Honshu, North Ryukyu and Middle Ryukyu) and Group 2 (South Ryukyu), hereafter. In both groups, FF populations

on each island formed a monophyletic group (bootstrap value, 91%–100%), except those on two islands in Group 1 (Amami-Oshima Is., 67%; Okinawajima Is., 33%). In addition, FF populations on different islands (Tokunoshima Is. and Okinoerabujima Is.) formed a monophyletic group (89%). The AF populations within each group were closely related to each other, and the populations of each island in Group 1 tended to form a monophyletic group.

3.4 | Test for multiple origins of FF

In the within-island-scale analysis, the single origin model of FF was selected for all islands (Table 1 and Table S7; Figure 4 and Figure S4). Models including gene flow among all or partial populations of the two forms showed higher posterior probability than those not considering gene flow (Table 1 and Table S7; Figure 4 and Figure S4).

At the among-island scale, Group 1 in Middle Ryukyu and Group 2 in South Ryukyu were analysed separately. For Group 1, we first examined the single origin of FF in the adjoining islands, Tokunoshima Is. and Okinoerabujima Is., which was suggested by the phylogenetic analysis. ABC analysis supported their single origin (Table 1 and Table S7), and thus only FF on Tokunoshima Is. was used for subsequent analyses. The model selection for Group 1 strongly supported the four independent origins of FF (Table 1; Table S7). The model with gene flow between the two forms provided a higher Bayes factor (BF) than the model not considering gene flow (Table S7). In Group 2, the single origin of FF of Iriomotejima Is. and Ishigakijima Is. was supported (Table 1; Table S7). The model including gene flow between the AF and FF populations was better supported than that not considering gene flow (Table S7).

For the between-region scale, the neighbour-joining tree for populations suggested independent origins of FF in Groups 1 and 2. However, no conclusion could be drawn at this scale from ABC, because no single model was successfully selected, probably because of insufficient data (Table 1; Table S7).

3.5 | Correlation between speciation probability and ecosystem size

We confirmed the occurrence of AF or FF populations on 18 islands from the published literature and our field survey (Table S8). As we could not specify the islands where unique speciation occurred, we tested 20 alternative scenarios that hypothesized that speciation occurred in different combinations of the candidate islands (see Supporting methods and results S1, and Table S9 for details).

For all four data sets in the scenario of independent origins between the regions, speciation probability was significantly explained by island area (Table 2 and Table S9; Figure 5 and S5). The relationship was also significant for 12 of the 16 data sets in the nonindependent scenario (Table S9). Almost identical results were obtained for maximum catchment area and river length (Table 2 and Table S9; Figure S5). Furthermore, two of the four data sets for the independent origin scenario and five of the 16 data sets for the nonindependent scenario showed significant relationships between the number of waterfalls and speciation (Table 2 and Table S9). Model selection by AIC scores showed that the best model included no variables, except for island area, as the predictors for speciation probability in most data sets when the variables were controlled by island area (Table S9).

4 | DISCUSSION

Our results revealed that FF repeatedly evolved from AF in the Ryukyu Archipelago, and that the occurrence of FF was highly correlated with island size. These results suggest that the speciation of FF was promoted in larger ecosystems. In the following sections, we discuss the mechanisms of speciation and the causes of correlation between ecosystem size and speciation of FF.

4.1 | Reproductive isolation between the two forms and its evolution

Genetic isolation between the two forms was suggested, even at sympatric sites (Figure 3 and Figure S3); the results support that FF and AF are reproductively isolated. This genetic isolation between AF and FF cannot be explained by isolation by distance (IBD), because geographically isolated FF populations in different river systems showed closer relationships than FF and AF in the same river. This relationship was consistent in the respective islands. Some behavioural mechanisms might be responsible for this reproductive isolation, as reported for other species pairs of *Rhinogobius* (Mizuno, 1987), which share common reproductive features with intersexual behavioural interactions (Takahashi & Kohda, 2004). Differences in the breeding season might also contribute to their current reproductive isolation (AF, January to May; FF, March to June; Hirashima, 2016; Katoh, 1996; Tachihara, 2009). Although the presence of pre- and post-zygotic isolations has not been tested for our studied pair of species and their position along a speciation continuum (Nosil, 2012) is not clear, genetic isolation, as well as distinct life history divergence, support that FF populations should be treated as different biological species from AF populations.

Although AF and FF currently exhibit genetic isolation, our ABC analysis suggested that reproductive isolation between these two ecologically divergent forms evolved under the existence of gene flow. This result suggests that the evolution of reproductive isolation was not caused simply by allopatry and mutation-order mechanisms but by divergent ecological adaptation between the AF and FF populations (Seehausen & Wagner, 2014).

What is the factor that led to the evolution of their reproductive isolation? Previous studies have focused on the differences in food size for larvae between seas and rivers (Nishida, 2001). AF larvae generally feed on small food items available in seas. If larvae cannot reach the sea rapidly, large larvae might be favoured by directional selection in rivers (Closs, Hicks, & Jellyman, 2013; Kishi, 1979; Kondo, Maeda, Hirashima, & Tachihara, 2013; Mizuno, 1963). A mathematical model has shown that speciation could occur due to differences in favourable egg and larval size between the upper and lower reaches (Omori et al., 2012). Such empirical and theoretical evidence suggests that the primary factor in the evolution of reproductive isolation is divergent selection between the optimal combinations of the within-rivers distribution and larval size.

The role of barriers in a river should also be emphasized, because they might promote adaptation to freshwater habitats through reduced gene flow and the invasion of predators and competitors. During repeated sea-level fluctuations during the Pleistocene, steep marine terraces of limestone or coral reef developed in the coastal areas of the Ryukyu Archipelago (Machida, Ota, Kawana, Moriwaki, & Nagaoka, 2001). Such terraces would form many waterfalls near river mouths. Nishida (2001) and Kano et al. (2012) hypothesized an important role of waterfall formation in the landlocking process of FF. The relationship between such barriers and divergent selection should be further investigated to understand the early processes of landlocking.

Despite the existence of current reproductive isolation, suspected hybrid individuals were occasionally detected. Some hybridization might be explained by artificial disturbances in the distribution and migration schemes of AF. Six of the 11 populations containing suspected hybrids were collected from the waters above artificial dams; they included FFOK-4-1 and FFOK-4-2 populations of FF, which primarily exhibited genetic features of AF. Artificial dams would promote hybridization in the following process.

Artificial dams have promoted the establishment of a landlocked AF population (Tachihara, 2009), because there are small food items in reservoirs that the larvae of AF and hybrids would be able to use. This would induce a sympatric distribution of the two forms and facilitate the survival of hybrids in the upper reaches of the dam. These cases might be examples of human-mediated reverse speciation (Grabenstein & Taylor, 2017; Taylor et al., 2006).

4.2 | Multiple origins of FF

The AF and FF populations showed large divergence between the North/Middle Ryukyu (Group 1) and South Ryukyu (Group 2). The AF populations were closely related among islands within each region (Figures 3 and 4), suggesting that gene flow by larval drifting is effective at the regional scale, but is prevented between regions by the Kerama Gap.

A series of ABC analyses supported the parallel derivation of FF populations on respective islands. The estimated number of times speciation occurred was four or five. The uncertainty in the number is attributed to the unresolved relationship among the FF populations across the Middle and South Ryukyus, which could not be resolved by ABC analysis, probably owing to the limitation of microsatellite markers, such as allele size homoplasy. However, the following reasons support that the FF populations originated independently in each region; that is, FF originated five times. First, the independent origins of FF populations among islands within regions were supported (Table 1; Figure 4). Second, the simple tree analysis supported the dichotomous relationship of the populations between the North/Middle and South Ryukyus. Third, the two regions are separated by a deep strait, the Kerama Gap, which is considered to have not emerged above water since the Ryukyu Archipelago separated from the continent (Osozawa et al., 2012). This geographical barrier has also been noted for many other terrestrial animals, such as amphibians and reptiles (Matsui, Ito, et al., 2005; Matsui, Shimada, et al., 2005; Ota, 1998; Tominaga, Matsui, Eto, & Ota, 2015).

Our results suggest that the multiple origins of FF were an example of parallel speciation, which is the phenomenon whereby reproductive isolation repeatedly evolves under the same mechanism (Schluter & Nagel, 1995). Nosil (2012) proposed four criteria to distinguish parallel speciation: nonmonophyletic pattern of an ecotype; nonmonophyly of ecologically similar forms representing multiple origins, rather than the effect of gene flow or incomplete lineage sorting; positive correlation between reproductive isolation and ecological divergence; and the genetic basis of reproductive isolation. The ABC analysis, as well as the egg and larval size difference between FF and AF, indicated that our study system satisfies the former two criteria. In addition, the latter two criteria were probably satisfied because of the clear differences in life history and reproductive traits between the two forms (Yamasaki et al., 2015), although they need to be confirmed by conducting mate choice and common garden experiments in the future.

4.3 | Correlation of ecosystem size and speciation probability

Our logistic regression analysis showed that speciation probability was significantly explained by island size, river length and catchment area in most of the data sets under the various analysis conditions. This result suggests that some mechanisms promoting the speciation process tend to be more effective in larger ecosystems. As the number of waterfalls also explained speciation probability in some data sets, it also partly supported that waterfalls promote speciation in the goby.

Why is the speciation probability of FF positively correlated with ecosystem size? To answer this question, understanding the relationships between ecosystem size and the following three components related to the mechanism of speciation is necessary: (a) establishment of reproductive isolation, (b) persistence of diverged populations and (c) enhancement of the former two components by population separation (Allmon, 1992; Mayer, 1963).

First, the establishment of reproductive isolation would be promoted in larger ecosystems, because the strength of divergent selection is expected to be positively correlated with ecosystem size. Divergent selection between flowing and staying larvae would become stronger in longer rivers (i.e., larger ecosystems), as the spawning sites of AF are restricted within a certain distance from the sea owing to the mortality of drifting larvae (see above; Moriyama et al., 1998; Omori et al., 2012). Furthermore, divergent selection might have been stronger during glacial periods, when sea level was lower, and hence rivers became longer (Kondo et al., 2013). Therefore, the landscape in the period of low sea level might have affected patterns of speciation. However, unfortunately, we could not test the correlation between speciation probability and island size at the low sea level, represented by the Last Glacial Maximum (i.e., when sea level was −122 m), because the 18 islands investigated were estimated to have been merged into eight, and the statistical power was too low to detect the correlation (data not shown). Although the correlation between the strength of divergent selection and river length should be tested in the future, larger ecosystems might enhance reproductive isolation via divergent selection, when the extent of the focal environmental gradient is positively related to ecosystem size. This relationship might generally lead to the development of a correlation between speciation probability and ecosystem size in other systems as well.

Second, the amount of available space might increase with ecosystem size, which could result in the greater persistence of freshwater-adapted populations through an increase in population size. In longer rivers, the freshwater population could use larger areas in the upper reaches of the rivers, because the optimal distance between the spawning area and sea for AF does not increase with river length. A larger population size might reduce the risk of demographic extinction. In addition, extinction risk due to fusion with the amphidromous population might be alleviated in the larger freshwater populations. Furthermore, the reinforcement of reproductive isolation might be more effectively developed when the population sizes of the two secondarily contacted species are similar (Liou & Price, 1994). A larger population size is also beneficial for retaining adaptive alleles (Gavrilets & Vose, 2005) and reducing maladaptive gene flow (Hanski, Mononen, & Ovaskainen, 2011).

Third, the probability of habitat separation between rivers and seas might be positively correlated with ecosystem size, promoting the previously described two processes during speciation. Correlation between the number of waterfalls and river length suggests the more frequent emergence of barriers to migration in longer rivers. Furthermore, greater river length might hinder migration to the upper reaches. Such habitat separation in longer rivers might be important for population divergence, because the separation would reduce gene flow between FF and AF populations, and would impede the entrance of other predatory and competitive fishes in the upper reaches.

5 | CONCLUSIONS

We have confirmed that speciation probability is explained by ecosystem size in our goby system. This result suggests positive correlations between ecosystem size and several components of the speciation process, including the strength of divergent selection, population persistence and population separation frequency. These correlations could promote the establishment of reproductive isolation and the persistence of new populations, although further explicit tests for these relationships are necessary. These correlations could also be important for understanding species diversification mechanisms at the phylogenetic level. Simple systems, such as our parallel species pairs, could contribute to the development of theories that link the mechanisms of each speciation to macroevolutionary patterns of speciation.

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AUTHOR CONTRIBUTIONS

Y.Y.Y., M.N. and K.W. planned the project. Y.Y.Y., Y.K., N.O. and T.S. performed field surveys. Y.Y.Y. and H.T. conducted molecular experiments. Y.Y.Y. conducted population genetic and statistical analysis. Y.Y.Y. and K.W. wrote the first draft manuscript, and all authors contributed to the improvement of the manuscript.

DATA AVAILABILITY STATEMENT

The microsatellite genotype data and scripts of ABC analysis have been deposited in Dryad (https://doi.org/10.5061/dryad.mpg4f 4qvh). NGS data for developing microsatellite makers have been de- posited in DDBJ (accession no. DRA006388).

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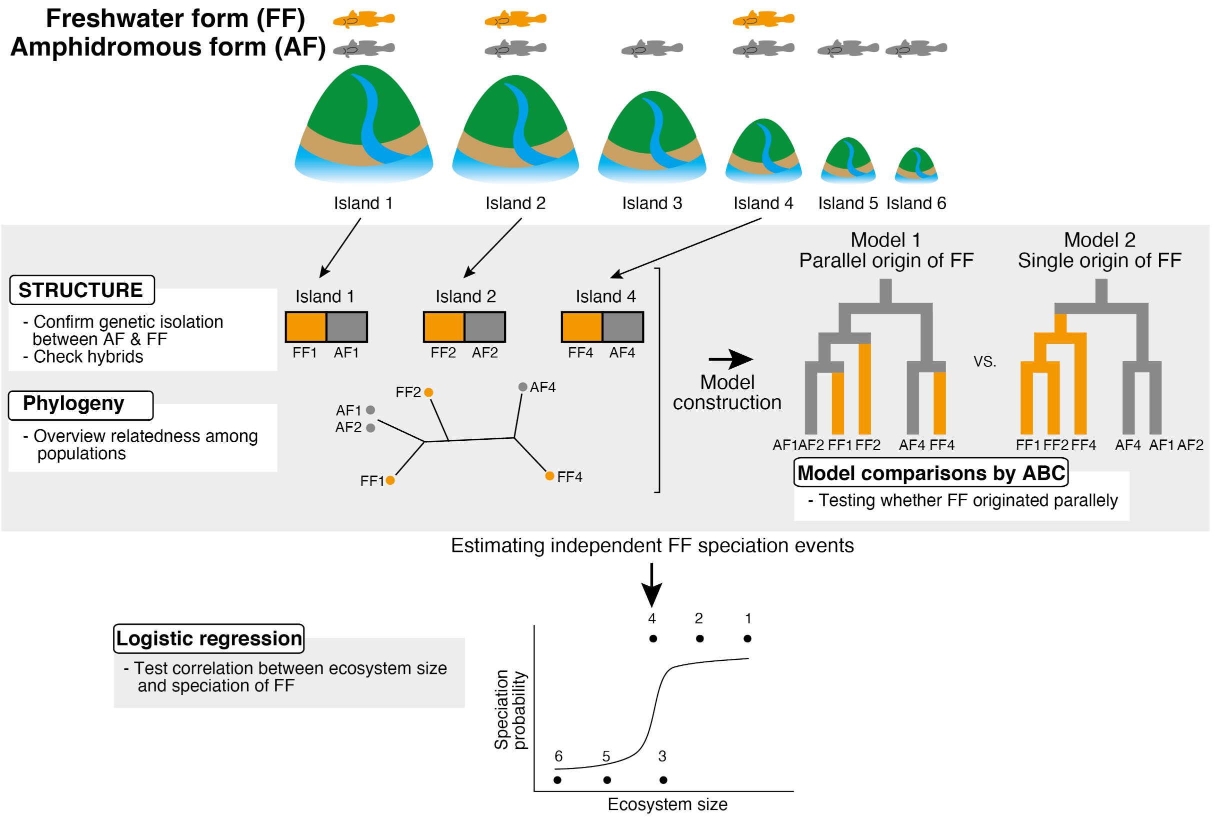
TABLE 1 Results of model selection by ABC analysis

Tested geographic scale	Origins of freshwater form in the best model	Gene flow	Posterior probability of the best model	Bayes factors of the best model against all models	Bayes factosr of the best model against another origin models	Type 2 error rate (all models)	Type 2 error rate (against another origin models)
Within-islands							
Amami-Oshima Is.	Single origin	Partial	0.5087	1.668-37.70	12.04-37.70	0.05-0.17	0.09-0.12
Tokunoshima Is.	Single origin	All	0.3128	1.355-2069	133.5 - 2069	0.02-0.11	0.05-0.07
Okinawajima Is.	Single origin	All	0.6357	1.754 - 4300	544.4 - 4300	0-0.04	0
Kumejima Is.	Single origin	Partial	0.3254	1.047 - 18735	4368- 18735	0.02-0.17	0.02-0.09
Iriomotejima Is.	Single origin	Partial	0.4544	1.321 - 309807	3247- 309807	0.01-0.15	0.01-0.15
Among-islands within-regions							
Middle Ryukyu	Originated in respective islands	All	0.4471	1.090-519.2	23.97-24.37	0-0.35	0
South Ryukyu	Single origin	All	0.8949	13.63 - 191.0	36.98 - 191.0	0-0.08	0-0.08
Tokunoshima Is. – Okinoerabujima Is.	Single origin	All	0.7461	4.680 - 122.6	9.419 -122.6	0.06-0.1	0.06-0.1
Among-regions							
Middle Ryukyu – South Ryukyu	Robust result could not obtain.	-	-	-	-	-	-

TABLE 2 Results of the logistic regression analysis

Explanatory variable	Data Set	*P* value	Difference of deviance	R^2
Island Area	Larger island	0.0016	12.265	0.577
	Smaller island	0.0061	8.650	0.407
Catchment Area	Larger island	0.0026	12.055	0.567
	Smaller island	0.0187	6.923	0.325
River Length	Larger island	0.0038	11.699	0.550
	Smaller island	0.0172	7.028	0.330
No.Waterfalls	Larger island	0.0013	13.712	0.645
	Smaller island	0.3277	1.407	0.066

Note: The results presented in this table are based on the assumption that the freshwater form (FF) has five independent origins. The data set column indicates the assumption of the islands where speciation occurred. Our ABC analysis indicated that FF in Tokunoshima Is. and Okinoerabujima Is., and Ishigakijima Is. and Iriomotejima Is. shared their origins. “Larger island” in the data set column assumed that the speciation of FF occurred in the larger island (i.e., Tokunoshima Is. and Iriomotejima Is.), whereas “smaller island” assumed that speciation occurred in the smaller island (i.e., Okinoerabujima Is. and Ishigakijima Is.). The *p* values for all combinations are presented in Table S9.



F I G U R E 1 Concept diagram of this study based on a hypothetical example. Our final goal was to determine whether ecosystem size explains the occurrence of speciation of the freshwater form (FF). To explain the study workflow, we postulate six islands with the amphidromous form (AF). FF was distributed in three islands among them. Four main analyses were conducted in this study. First, we confirmed genetic isolation between AF and FF by structure analysis for each island. Second, we estimated phylogenetic relationships among populations. Third, we tested independent speciation of FF by demographic comparison based on ABC analysis. The phylogenetic tree and geographical locations were used to construct demographic models. The occurrence of speciation in focal islands was identified by these three analyses. Finally, we tested the correlation between ecosystem size and occurrence of speciation by logistic regression analysis.

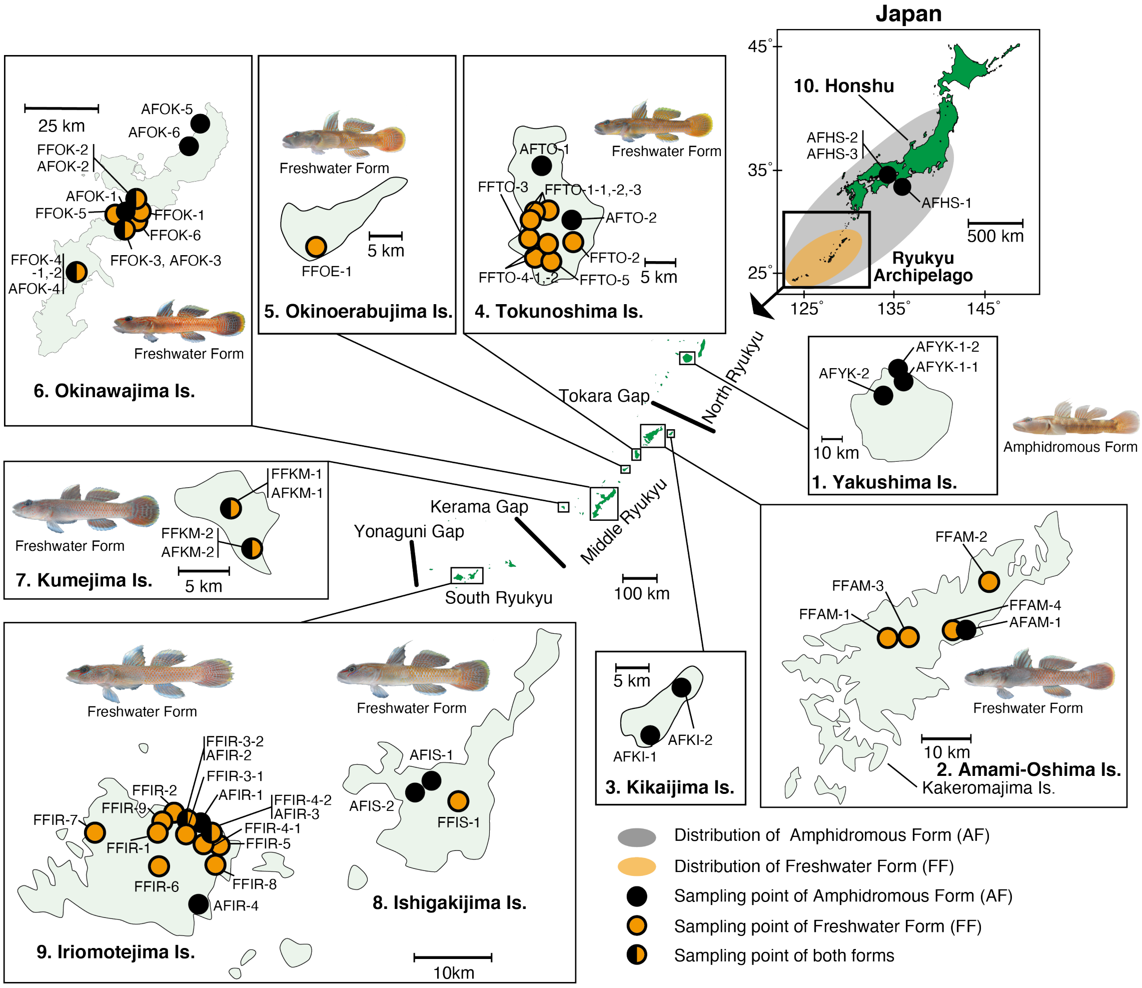
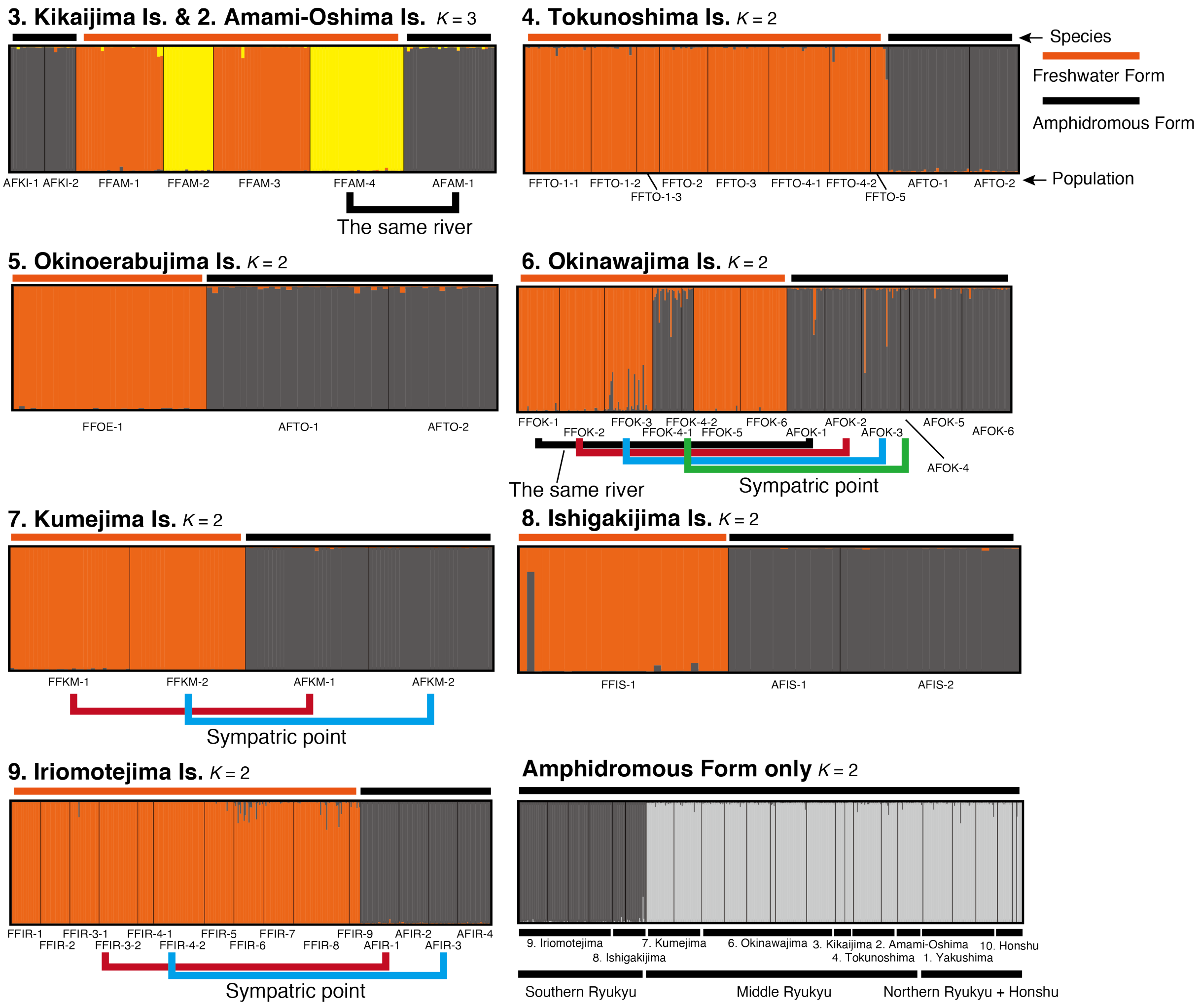
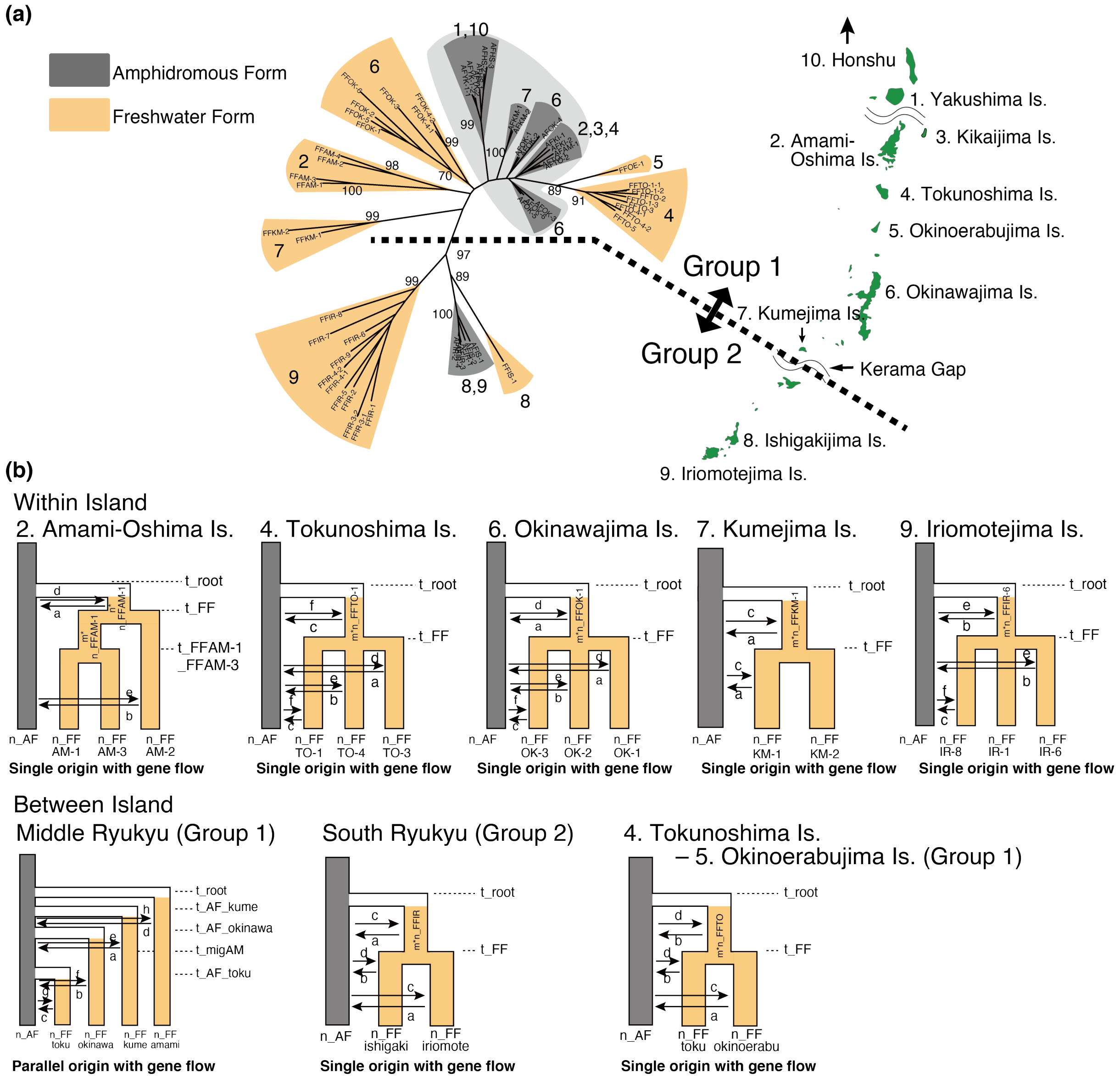


FIGURE 2

Samplingpointsinthisstudy.Themapintheupperrightboxindicatesdistributionrangesoftheamphidromousform(AF;grey) and the freshwater form (FF; orange) in Japan as a whole. The central map is the whole area of the Ryukyu Archipelago. Black and orange circles indicate the points from where AF and FF were collected, respectively. Sympatrically collected points are indicated by both colours.



F I G U R E 3 Results of genetic clustering analysis performed in structure (Amami-Oshima Is., *K* = 3; others, *K* = 2). Sampling points are indicated by black vertical bars in the respective bar plots. Horizontal bars at the top of the plot indicate morphological identification of respective specimens. Sympatric points are indicated by an additional annotation. The specimens morphologically identified as the freshwater form (FF) are presented in orange and yellow colours, whereas those identified as the amphidromous form (AF) are presented in grey.



F I G U R E 4 Population relationships and evolutionary scenarios of the amphidromous form (AF) and the freshwater form (FF). (a) Neighbour-joining tree based on Nei's *Da* distance of 20 microsatellites. Numbers on tree nodes indicate bootstrap values. Only bootstrap values >70% are indicated. Island numbers are indicated at tips. (b) The models selected by ABC analysis. AF and FF are represented by black and orange colours, respectively. Arrows between populations indicate gene flow. Only representative populations were used for ABC analysis to reduce the amount of calculation (see Materials and methods and Supporting methods and results S1).

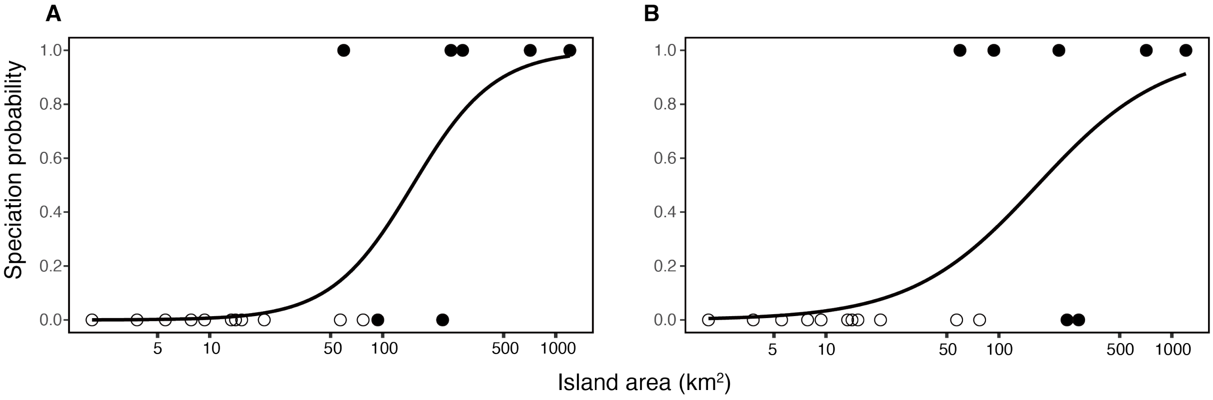


FIGURE 5 Results of logistic regression analysis between island size and speciation probability. Islands with the freshwater form (FF) are represented by filled circles, whereas those without FF are represented by open circles. Filled circles plotted on the *x*-axis (speciation probability = 0) are for the islands with FF that was assumed to be of nonindependent origin. Our ABC analysis indicated that FF in Tokunoshima Is. and Okinoerabujima Is., and Ishigakijima Is. and Iriomotejima Is. shared their origins. (a) Speciation of FF is assumed to have occurred in the larger islands (Tokunoshima Is. and Iriomotejima Is.). (b) Speciation is assumed to have occurred in the smaller islands (Okinoerabujima Is. and Ishigakijima Is.).

Supplemental methods and results S1: Complete version of Materials and Methods and Results

Materials and Methods

1. Study system

1.1 Study species

The genus *Rhinogobius* (Gobiidae) is the most speciose group of gobies occurring in freshwater. This group contains more than 85 species in East and Southeast Asia, and 18 species in Japan (Oijen et al., 2011; Yamasaki et al., 2015). The freshwater resident form derived from the amphidromous species *R. brunneus* is recognized as an independent species but has not been described to date because of taxonomic confusion. Previous studies (e.g., Akihito et al., 2013) tentatively used the name "*Rhinogobius* sp. YB" for this freshwater form. However, until its evolutionary status is clarified, we will use the code 'FF' (freshwater form) for *Rhinogobius* sp. YB and 'AF' (amphidromous form) for *R. brunneus* based on their life history modes.

The FF completes its life in freshwater; conversely, AF larvae hatch in rivers and immediately drift down to the sea and return to rivers after 2–3 months (Mizuno, 2001). The eggs and larvae of FF are larger than those of AF. The sizes of eggs and hatched larvae of respective forms and islands have already reported by some studies. As follows, the both egg and larval sizes are greater in FF than in AF. The mean and standard deviation of egg size of FF varies across islands; namely, long axis 3.07 and 3.36 mm, short axis 1.55 and 1.52 mm on Amami-Oshima Island (Kon et al., 2003); long axis 5.06 ± 0.39 mm, short axis 1.77 ± 0.10 mm on Amami-Oshima Is. (Shinomiya et al., 2005); long axis 3.4 and 4.4 mm, short axis 1.4 and 1.7 mm on Tokunoshima Island (measured from the Figure 2 of Oshiro, 1981), long axis 4.3 ± 0.2 mm, short axis 1.4 ± 0.1 mm on Okinawajima Island (Hirashima & Tachihara, 2000); long axis 5.4 mm, short axis 1.7 mm on Ishigakijima Island (measured from the Figure 2 of Oshiro, 1981). We also measured the egg size of FF spawned in a tank by one individual collected from Shirase River on Kumejima Island (long axis 3.52 ± 0.24 mm, short axis 1.31 ± 0.07 mm, n=26). The mean and standard deviation of egg size of AF was recorded on Okinawajima Island; namely, long axis 2.8 ± 0.1 mm, short axis 0.9 ± 0.04 mm (Kondo et al., 2013). The mean and standard deviation for notochord length of hatched larvae of FF varies across islands; namely, 5.0 mm on Amami-Oshima Is. (Kon et al., 2013);

5.96–6.60 mm on Amami-Oshima Is. (Shinomiya et al., 2004); 5.3 mm on Okinawajima Is. (Hirashima & Tachihara 2000). The mean and standard deviation in notochord length of hatched larvae of AF on Okinawajima Is. was 3.7 ± 0.2 mm (Kondo et al., 2013); 3.59 ± 0.087 mm on Shikoku Island in the Japanese archipelago (Moriyama et al., 1998). Fluvial species of this genus tend to produce larger eggs and larvae (Yamasaki et al., 2015). Such traits are considered to be an adaptation to river environments, where small food items (i.e., plankton) are scarce and higher level of swimming ability in river current is needed during the larval period (Nishida, 2001; Shinomiya et al., 2005; Hirashima & Tachihara, 2000; Yamasaki et al., 2015).

Although the distribution of the two species sometimes overlapped in a single river, the tendencies of their distributions were different. AF mainly lived in the middle to lower reaches of rivers. In fact, AF populations are actually only found in rivers shorter than 18 km in the central Honshu region of Japan (Tamada, 2005). The larvae of AF must rapidly reach the sea to avoid starvation because of the scarcity of small food in rivers (Moriyama, Yanagisawa, Mizuno, & Omori, 1998; Iguchi & Mizuno, 1999). Thus, they might not be able to reproduce effectively in areas far from the sea (Iguchi & Mizuno, 1999). On the other hand, FF mainly live in the upper reaches of rivers, and are often found in the upper areas of waterfalls where no other fishes are distributed (Kano et al., 2012).

1.2 Study area

The Ryukyu Archipelago is a series of islands located in the southwestern part of Japan (Figure 2). The islands separated simultaneously from the continent about 1.5 million years ago (Osozawa et al., 2012). Three deep straits (Tokara Gap, Kerama Gap, and Yonaguni Gap) divide this archipelago into three regions: North Ryukyu, Middle Ryukyu, and South Ryukyu. These gaps act as biogeographic barriers for terrestrial organisms (Ota 1998). On the islands of North Ryukyu, the biota was destroyed by pyroclastic flow 7300 years ago (Machida et al., 2001). AF is distributed in all three regions, as well as mainland Japan, whereas FF is only distributed in Middle and South Ryukyu (Yoshigou, 2014). In the Ryukyu Archipelago, primary freshwater fishes are almost absent, and most fishes are diadromous. Therefore, fish assemblages in freshwater areas are simple and similar among islands (Yoshigou, 2014).

2. Sampling

All animal experiments followed the rules, regulations, and guidelines relating to animal experimentation of Kyoto University. Sampling of FF and AF was conducted from June 2012 to March 2015 on seven islands where former populations have been recorded previously (Locality code 2. Amami-Oshima Is., 4. Tokunoshima Is., 5. Okinoerabujima Is., 6. Okinawajima Is., and 7. Kumejima Is. in Middle Ryukyu; 8. Ishigakijima Is. and 9. Iriomotejima Is. in South Ryukyu; Figure 2; Table S1; Ohara et al. 2008; Yoshigo, 2014). In addition, AF specimens were collected from Kikaijima Is. (Locality code 3) in Middle Ryukyu, Yakushima Is. (1) in North Ryukyu, and mainland Japan (10). The specimens were identified by body colour patterns under fresh conditions (Suzuki et al., 2004; Kano et al., 2012). Identification based on body colour was validated by the results of the genetic analysis; however, some samples were difficult to identify or showed inconsistent genetic characteristics (3.2% of specimens in total, including potential hybrids). When genetic data suggested the focal specimens were not judged as hybrids based on the criteria described below and that wrong identification based on morphology in the field was likely, these samples were removed from further analysis. In the case that a sample was judged to be a hybrid (see 4.2), we tentatively named it based on the morphology. It should be noted that we found that morphologically identified FFOK-4-1 and FFOK-4-2 populations of FF largely reflected the genetic features of AF (Figure 3 and Supporting Information Figure S3). We judged them as hybrid populations and did not remove any specimens from the analysis even if they were not judged as hybrid (see Discussion). Specimens were anesthetized with iced water or 2-phenoxy-ethanol, and then a fin was clipped and preserved in 99% ethanol. Most specimens were fixed in 10% formalin or 99% ethanol. As a result, 842 FF and 578 AF specimens from 52 points in 42 river systems were included in the population genetic analysis. The average numbers of localities and specimens per island were 5.2 and 142, respectively. Both forms were collected from nine river systems; they were sympatrically collected at seven points.

3. Molecular experiment

3.1 Microsatellite marker development

We developed new microsatellite markers following the methods of Takeshima et al.

(2017). Total genomic DNA was extracted from one AF specimen collected from DAIR-4 in Iriomotejima Island by using a Genomic DNA Purification Kit (Promega, Madison, Wisconsin, USA). We concentrated CA repeat regions by using the target capture method and sequenced them using the Roche 454 GS Junior system (Accession No. DRA006388). Primers and multiplex systems were designed using QDD ver. 2 (Meglecz et al., 2010) and Multiplex Manager v. 1.2 (Holleley & Geerts 2009), respectively. One out of four universal tail sequences was added to each forward primer for fluorescent labelling during PCR (Blacket et al., 2012).

3.2 DNA extraction, PCR, and genotyping

Total genomic DNA was extracted from the fin clip by using the Genomic DNA Purification Kit. Before PCR amplification, a droplet of 1.25 μL extracted DNA was placed on a 96 well plate and dried. Total 21 microsatellite markers (18 originally developed loci and three loci reported by Ohara et al. (2004)) were analyzed. We developed four multiplex sets and simultaneously amplified 4–10 loci (Table S2). For the markers that were developed, the final concentration of each forward and reverse primer was 1 and 2 μM, respectively. The 1 μM tailed fluorescent primer for each forward primer was also added to the multiplex reaction mixture. For the three loci reported by Ohara et al. (2004), 5′-fluorescent-labelled forward primers were used, and the final concentration of each forward and reverse primers was adjusted to 1 μM. PCR amplification was performed in a 4 μL volume containing 2.43 μL of ultrapure water, 0.066 μL of primer mix, and 1.5 μL of Type–IT Microsatellite PCR Kit (Qiagen, Hilden, Germany) with the dried DNA. The PCR settings for the originally developed markers included a first step of denaturation at 95°C for 5 min, followed by 35 cycles of the second step (denaturation: 94°C, 30 s; annealing: 63°C, 90 s; and extension: 72°C, 75 s), and the final extension at 72°C for 30 min. For the PCR for the loci of Ohara et al. (2004), the second step was changed as follows: 28 cycles of denaturation at 94°C for 30 s; annealing at 53°C for 90 s; and extension at 72°C for 60 s. We directly added 10 μL HiDi Formamide (Thermo Fisher Scientific, Waltham, MA, USA) and 0.2 μL of GeneScan 500Liz dye Size Standard or GeneScan 400HD Rox dye Size Standard (Thermo Fisher Scientific) for the respective PCR products. Next, we subjected the products to heat shock treatment (95°C, 5 min; 0°C, 5 min). The peak size data were acquired using ABI 3130xl sequencer (Applied Biosystems, Foster City, CA, USA) and were analyzed using GeneMapper v.4.0 (Applied Biosystems). The acquired allele size data were transformed for integral number by using tandem v.1.09 (Matschiner & Salzburger 2009).

We genotyped a total of 21 microsatellite loci for population genetic analyses (Table S2). Null alleles were checked using software Micro-checker ver.2.2.3 (van Oosterhout et al., 2004) under 100% interval condition for the 25 populations of *R. brunneus*, which were assumed to not be affected by the bottleneck effect. Null alleles were detected in several *R. brunneus* populations. We excluded locus br_b_04 from the analysis because null alleles were detected at this locus in both North Ryukyu and Middle Ryukyu populations. Null alleles in other loci occurred sporadically; hence, we used the other 20 loci for the following analysis to avoid reduction of information. Linkage disequilibrium among loci was tested using 10,000 times of permutation implemented in Arlequin ver.3.5 (Excoffier & Lischer 2010), and Bonferroni collection was applied to *P*-values to avoid type I errors. No significant linkage disequilibrium between loci was detected (adjusted $P \geq 0.05$). The final genotype data were deposited in dryad (doi: 10.5061/dryad.mpg4f4qvh).

4. Data analysis

4.1 Calculation of summary statistics and estimation of phylogenetic trees

We calculated the expected and observed heterozygosity (*He* and *Ho*, respectively), the effective number of alleles (*Ae*) for the respective populations, and population-pairwise F_{ST} and Jost's *D* by using GenoDive 2.0b27 (Meirmans & van Tienderen 2004). We also calculated allelic richness (*Rs*) of the respective populations by using FSTAT v2.9.3.2 (Goudet 1995). Phylogenetic relationships among populations were estimated based on *Nei's Da* distance by using the neighbor-joining method implemented in Poptree2 (Takezaki et al., 2010). The credibility of each clade was evaluated using 1,000 bootstrap resamplings. To assess hierarchical genetic differentiation, we conducted AMOVA (Excoffier, Smouse, & Quattro, 1992) implemented in GenoDive separately for AF and FF. The number of hierarchies to be tested was five. However, AMOVA could include only four hierarchies in one analysis. To deal with this problem, we conducted AMOVA separately in two geographic scales. In the among-islands within-regions scale, we set following four hierarchies: within-individuals, among-individuals, among-rivers, and among-islands. This analysis was separately conducted for Middle Ryukyu and South Ryukyu. In the among-regions scale, we set the following four hierarchies: within-individuals, among-individuals, among-islands, and among-regions. F_{ST}-analog distance was applied. Significance was tested using 999 permutations.

4.2 STRUCTURE analysis

To infer the existence and extent of gene flow and genetic isolation, we analyzed the genetic structure of the population using STRUCTURE v.2.3.4 (Pritchard, Stephen, & Donnelly, 2000; Lawson, van Dorp, & Falush, 2018). We prepared two datasets: one for both FF and AF populations from each island, and another for only AF populations from all islands. Because AF was not found on Okinoerabujima Is., the FF on the island were analyzed along with the AF from the nearest island, Tokunoshima Is. Admixture model with correlated allele frequencies was assumed. Markov Chain Monte Carlo was performed with 100,000 generations for burn-in and final 1,000,000 generations. Ten independent runs for each K from 1 to 10 were evaluated. After a run finished, we calculated Evanno's ΔK by using STRUCTURE Harvester (Evanno, Regnaut, & Goudet, 2005; Earl & von Holdt, 2012) was used for a reference for K value selection. Hybrid individuals were evaluated using q-values; we arbitrarily judged specimens as hybrids (or individuals with hybrid origin) in cases where minor genetic components accounted for 10% or more of the aggregate (Vähä & Primmer 2006).

4.3 Testing parallel speciation of FF by using ABC

To statistically examine the single or parallel origins of FF, and to estimate which FF populations shared their origins we conducted a demographic model selection under the approximate Bayesian computation (ABC framework , Beaumont, 2010; Bertorelle et al., 2010) implemented in ABCtoolbox v.1 (Wegmann et al.,. 2010) and R package '*abc*' v.2.1 (Csilléry et al., 2012). Coalescent simulation was conducted using fastsimcoal2 v.2.5.2.1.1 (Excoffier & Foll 2011; Excoffier et al., 2013). Summary statistics were calculated using arlsumstat v.3.5 for each simulation (Excoffier & Lischer 2010).

4.3.1 Prior distribution, summary statistics, and simulation

Prior distribution and summary statistics were determined after several preliminary analyses. When the range of the prior distribution of a parameter was across the digits, the value was $\log_{10}$ transformed. A uniform distribution for each parameter was assumed. We set a larger prior range for population size of AF (10^2–$10^{5.3}$) than for FF (10^2–$10^{4.7}$). The prior distribution of coalescent time (generation) was set to 10^3–$10^{6.2}$, considering that the Ryukyu Archipelago had separated from the continents 1.5 million years ago, and the generation time of the *Rhinogobius* species was one to two years (Yamasaki, personal observation). The prior distribution of the migration rate was set to 10^{-9}–10^{-3}. In the case that the models of two or more populations were merged, the ancestral population size was set to the range of 0.5 to 2 times of either of the derived populations. We applied a generalized stepwise mutation model for microsatellite evolution. Our data did not match the simulated data produced using the models under a previously reported average mutation rate of microsatellites in fish (common carp: 5.56×10^{-4}/locus/generation, 95% interval, 1.52×10^{-4}–1.63×10^{-3}, Yue et al., 2007) from principal component analysis (PCA) (see 4.3.3). Simulated data under several average mutation rates were tested, and then the value of 1.0×10^{-4} was selected, under which the generated data matched the acquired data. The prior distribution of the mutation rate for each locus was set to a Gamma distribution. The maximum difference of repeat number of alleles of each microsatellite in coalescent simulations was set to 45.

To capture information regarding population size and differentiation, we selected summary statistics listed in Table S3. Detailed formulae of respective summary statistics are described in the Arlequin 3.5 manual (Excoffier & Lischer 2010). A total of 46 to 132 summary statistics for each analysis were used according to the number of the analyzed populations. We performed 1.0×10^6 simulations for each demographic model.

4.3.2 General strategy for the construction of demographic models

Our general model construction strategies for ABC analysis were as follows. First, we generated separate models using three geographic scales, i.e. within-islands, regional (Middle and South Ryukyu), and archipelago scales, and examined FF origins in each geographic scale to reduce the number of models and populations examined in a single analysis. Second, we examined both models with and without gene flow between AF and FF populations. This is because a simulation study suggests that gene flow could alter apparent phylogenetic relationships among populations when simple genetic distance was used (Bierne, Gagnaire, & David, 2013). Demographic model comparisons that consider gene flow can overcome this problem (Butlin et al., 2014).

In the within-islands analyses, we mainly examined two questions: whether FF had single or parallel origin, and whether gene flow between AF and FF existed on each island. We hypothesized several plausible divergence orders between populations based on the result of STRUCTURE analysis, phylogeny, and geographic locations for respective islands. Thereafter, we compared the models with single/parallel origins and with/without gene flow. Analyses were conducted for the five islands where FF is distributed in multiple rivers (i.e., Amami-Oshima Is., Tokunoshima Is., Okinawajima Is., Kumejima Is., and Iriomotejima Is.). Ishigakijima Is. and Okinoerabujima Is. were not included in the analyses because the FF population was only found in one river system on each island. We selected three (or two) river populations for each island to reduce the model complexities and calculation loading. FF specimens from a single river system were merged to increase calculation accuracy. Populations were selected by the following criteria to extract information of population history as much as possible; geographically distant river systems, to avoid bias from shared population history among geographically nearby populations; and lower rates of missing data. The constructed models (a total of 34 models) are described in Supporting Information Figure S1A–E.

For the among-islands within-region analyses, we constructed several plausible models separately for the regions of Tokunoshima Is. and Okinoerabujima Is., Middle Ryukyu, and South Ryukyu. Five to ten models were constructed on the basis of the phylogenetic tree and geographic distance between islands. Gene flow settings followed the results of within-islands scale analysis. For each island, we selected only one FF population whose population size was the largest, as judged from *He* values. Finally, in the between-region analyses, we compared ten models generated from the results of the previous analyses. All constructed models are described in Figure S1F–I. Scripts that described models were deposited in Dryad (doi: 10.5061/dryad.mpg4f4qvh).

4.3.3 Prior check

We performed PCA by using *gfitpca* function implemented in *abc* package to check the validity of the prior distribution. We confirmed that the observed summary statistics included of the 90% envelope of each simulation result (data not shown).

4.3.4 Posterior probabilities of models

The posterior probability of each model based on the observed value was estimated using the *neuralnet* method, which is a non-linear regression method involving neural networks. We used *postpr* function implemented in the *abc* package. The regression step was performed using 30 neural networks and 10 hidden layer units. Five hidden layer units were set in the analysis of the archipelago scale, because an error occurred when 10 hidden layers were set. We used 1% of simulations with summary statistic values closest to the observed ones (tolerance rate = 1%). We conducted 10 calculations for each model selection by changing the tolerance rates from 0.1% to 1.0% with increments of 0.1% to evaluate the robustness of the results by using a tolerance rate of 1%.

4.3.5 Confidence in model selection

To evaluate the accuracy of the model selection, we calculated the misclassification rate by using function *cv4postpr* implemented in *abc* package. We randomly generated 100 pseudo–observed data sets (pods) of each model from the prior distribution and performed model selection for the respective pods with 10^5 simulations for each model. Model selection was performed using *neuralnet* method under 10 neural networks and 10 hidden layer units. Five hidden layer units were set in the analysis at the archipelago scale as in the calculation of posterior probabilities. Type 1 and type 2 errors were evaluated for each model: type 1 error rate is the probability that the other model was selected despite the focal model being true, and type 2 error rate is the probability that the focal model was selected despite the other model being true. For evaluating the accuracy of the model selection results, the type 2 error rate should be carefully considered (Cornuet et al., 2010; Lombert et al., 2014).

4.3.6 Estimating posterior distributions of parameters

We calculated the posterior distribution of each parameter under the selected model by using function *abc* implemented in the *abc* package. We retained 1% of simulations close to the observed summary statistics, and we performed regression analysis by using the *neuralnet* method under 30 neural networks and five hidden layer units. Parameters of population size and event time were log transformed before regression analysis.

4.3.7 Posterior predictive check

We checked whether the selected model could produce the observed value under the posterior distribution. We generated 1000 simulations under the posterior distribution of the selected model and calculated summary statistics. In addition to the originally used summary statistics, the following summary statistics were also calculated: the mean allelic range over loci for each population (R_pop) and its standard deviation (Rsd_pop), the mean allelic range over loci and populations (MEAN_R) and its standard deviation (MEAN_Rsd), and the mean total allelic range over loci and populations (TOT_R), and F_{IS} (FIS). Next, PCA using function *gfitpca* implemented in *abc* package was performed to check whether the observed summary statistics were included in the range of summary statistics generated from the posterior distribution.

5. Correlation between island size and speciation probability

We first identified the islands on which the speciation of FF occurred based on the results of STRUCTURE (genetic isolation) and ABC model selection (independent origin). The relationship between ecosystem size and speciation was analyzed for the Middle and South Ryukyu Islands between the Tokara Gap and Yonaguni Gap. This analysis was conducted because these islands are assumed to be similar in age, were never connected to any continent after separation, and were not catastrophically affected by volcanic activity (Osozawa et al., 2012). We acquired distribution information for the two forms from published literature (Yoshigou 2014) and our own field survey, and we only chose the islands where either or both forms were distributed. This is because we assumed that speciation was not likely to have occurred on the island where either of these species is not currently distributed. We coded the occurrence of speciation in each island as follows: 1 for the island where speciation occurred; 0 for the island where speciation did not occur. As a proxy of ecosystem size, we used island area (km^2; data obtained from Geospatial Information Authority of Japan), the maximum catchment area (km^2), the maximum river length (m), or the maximum number of waterfalls in each island. The data on rivers on the islands where FF is distributed were only obtained for rivers with FF. The latter three parameters were calculated using the 10 m mesh digital elevation model (Geographic Information Authority of Japan) by using ArcGIS10.3 (ESRI Japan, Tokyo). Because of strong positive correlations among the four variables (Pearson’s correlation coefficient: island size and catchment area, 0.959; island size and river length, 0.951; catchment area and river length, 0.993; island size and number of waterfalls, 0.592; catchment area and number of waterfalls, 0.865; river length and number of waterfalls, 0.865), we primarily used island area as the explanatory variable.

We performed one-parameter logistic regression analysis in the generalized linear model framework with binomial error structure for the response variable (speciation: 1, presence; 0, absence) using glm package of R v. 3.1.1 (R Core Team, 2014). Explanatory variables, except the number of waterfalls, were $\log_{10}$ transformed. To test the significance of explanatory variables, we conducted a likelihood ratio test using 10,000 rounds of parametric bootstrap sampling by using a constant model as the null model that assumes no relationship between ecosystem variables and speciation probability. We calculated McFadden's pseudo R^2 by using the following formula: $r^2 = 1 - (SSE/SST)$. In this formula, SSE and SST refer to the deviances of the focal and null models, respectively.

Furthermore, to examine the effect of the ecosystem size parameters other than island size (i.e., maximum catchment area, river length, and number of waterfalls), we constructed another generalized linear model for speciation probability. We used the residuals from a regression between island size and each of the other ecosystem-size parameters, together with the island size and their interaction, as explanatory variables. Stepwise model selections by AIC scores were conducted using *step* function on R.

Results

1. Basic summary statistics

Heterozygosity and allelic richness were generally higher in the AF populations than in the FF ones, possibly suggesting a larger current or historical population size in the former (AF: *He*, 0.296–0.554 and *Rs*, 1.94–3.65; FF: *He*, 0.070–0.390 and *Rs*, 1.21–3.08; Supporting Information Table S1, Figure S2A, B). The AF populations showed relatively little pairwise genetic differentiation within-islands (F_{ST} = -0.008–0.145; Jost's *D* = -0.009–0.102; Supporting Information Tables S4, 5, Figure S2C, D). In the case of the among-islands within-regions scale, pairwise genetic differentiation was moderate (F_{ST}, 0.022–0.168; Jost's *D*, 0.025–0.219). AMOVA showed significant differentiation in the among-rivers hierarchy in both Middle Ryukyu and South Ryukyu, and in the among-islands hierarchy in Middle Ryukyu (Supporting Information Table

S6). Most of the variation was explained by within-individuals hierarchy. Compared with this, the genetic differentiation of AF populations between regions was large (F_{ST}, 0.110–0.456; Jost's D, 0.124–0.613). AMOVA showed significant differentiation in both among-islands and among-regions hierarchies (Supporting Information Table S6). Variations were mainly explained by within-individuals, among-islands, and among-regions hierarchies. The FF populations often showed large genetic differentiation within-islands (F_{ST}, 0.003–0.804; Jost's D, 0.001–0.529; Supporting Information Tables S4, 5, Figure S2C, D) and among-islands within-regions (F_{ST}, 0.312–0.859; Jost's D, 0.146–0.778), as well as among-regions (F_{ST}, 0.507–0.914; Jost's D, 0.580–0.890). AMOVA for FF showed significant genetic differentiation in the hierarchies of among-individuals, among-rivers, among-islands, and among-regions, except among-islands in South Ryukyu (Supporting Information Table S6). In the among-islands within-regions scale analysis, genetic variation was mainly explained by within-individuals, among-rivers, and among-islands hierarchies.

2 Genetic isolation and hybrids

In the AF dataset, Evanno's ΔK showed the maximum value at $K = 2$; the populations in North plus Middle Ryukyu and South Ryukyu were clearly separated. In the dataset for each island, including FF and AF populations, ΔK had the maximum value at $K = 2$ for all islands, except one (Amami-Oshima Is.). The two genetic clusters corresponded to the two forms, except on Okinawajima Is. (see below; Figure 3 and Supporting Information Figure S3). ΔK on Amami-Oshima Is. showed the maximum value at $K = 3$, in which FF was further divided into two clusters. Suspected hybrid individuals (q-value, ≥10%) were rare (2.0% of total individuals). No suspected hybrid individuals were detected from five of the seven sympatric collection points. Several suspected hybrid individuals were detected in 11 FF and AF populations, including two FF populations on Tokunoshima Is. (FFTO-4-2, FFTO-5), three FF on Okinawajima Is. (FFOK-3, FFOK-4-1, and FFOK-4-2), one FF on Ishigakijima Is. (FFIS-1), three FF on Iriomotejima Is. (FFIR-3-1, FFIR-6, and FFIR-8), and two AF on Okinawajima Is. (AFOK-1, AFOK-3). Among these, all FF individuals that were identified based on morphology in the FFOK-4-1 and FFOK-4-2 populations (Okinawajima Is.; see Figures 2, 3 and Supporting Information Figure S3) exhibited the genetic features of AF as the dominant component. Except for these two populations, the proportion of suspected hybrid individuals ranged from 3.6% to 21.2% of individuals in a population. Potential hybrids found in the FF populations contained 10.1%–80.5% of the AF component, whereas those of the AF populations contained 25.6%–69.0% of the FF component.

3 Genetic relationships among populations

The neighbor-joining tree showed two divergent groups separated by the Kerama Gap in all of the FF and AF populations (bootstrap value, 97%; Figure 4). Each group included both forms, which we present as Group 1 (Honshu, North Ryukyu, and Middle Ryukyu) and Group 2 (South Ryukyu), hereafter.

In both groups, FF populations on each island formed a monophyletic group (bootstrap value, 89%–100%), except those on two islands in Group 1 (Amami-Oshima Is., 67%; Okinawajima Is., 33%). In addition, FF populations on different islands (Tokunoshimajima Is. and Okinoerabujima Is.) formed a monophyletic group (89%). The AF populations within each group were closely related to each other, and the populations of each island in Group 1 tended to form a monophyletic group.

4 Test for multiple origins of FF

In the within-island scale analysis, the single origin model of FF was selected for all islands (Table 1 and Supporting Information Table S7; Figure 4 and Supporting Information Figure S4). Models including gene flow among all or partial populations of the two forms showed higher posterior probability than those not considering gene flow (Table 1 and Supporting Information Table S7; Figure 4 and Supporting Information Figure S4). Type 2 error rates for the selected single origin model against alternative parallel origin models were generally low (Table 1 and Supporting Information Table S7; Figure 4 and S4).

At the among-island scale, Group 1 in Middle Ryukyu and Group 2 in South Ryukyu were analyzed separately. For Group 1, we first examined the single origin of FF in the adjoining islands, Tokunoshima Is. and Okinoerabujima Is., which was suggested by the phylogenetic analysis. ABC analysis supported their single origin (posterior probability (PP), 0.746; Bayes factor (BF), 9.42–122.57; Type 2 error rate, 0.06–0.1; BFs and Type 2 error rates are of the selected model against parallel origin models; Table 1 and Supporting Information Table S7; Figure S4); thus, only FF on

Tokunoshima Is. was used for subsequent analyses. The model selection for Group 1 strongly supported the four independent origins of FF (PP, 0.447; BF, 23.97–519.23; Type 2 error rate, 0; BFs and Type 2 error rates are of the selected model against the other non-four origin models; Tables 1 and S7; Figure S4). The model with gene flow between the two forms obtained higher BF than the model not considering gene flow (BF, 4.72; Type 2 error rate, 0.125). In Group 2, the single origin of FF of Iriomotejima Is. and Ishigakijima Is. was supported (PP, 0.895; BF, 36.98–191.0; Type 2 error rate, 0–0.08; BFs and Type 2 error rates are of the selected model against parallel origin models Tables 1 and S7; Figure S4). The model including gene flow between the AF and FF populations was better supported than that not considering gene flow (BF, 13.63; Type 2 error rate, 0.06).

For the between-region scale, the neighbor-joining tree for populations suggested independent origins of FF in Groups 1 and 2. However, we could not obtain a conclusion at this scale from ABC, because no single model was successfully selected, probably because of insufficient data (PP, 0.0024–0.14; Table S7; Figure S4).

5 Correlation between speciation probability and ecosystem size

We confirmed the occurrence of AF or FF populations on 18 islands from the published literature and our field survey (Supporting Information Table S8). As we could not conclude from the ABC analysis whether the FF population originated independently between Groups 1 and 2, we analyzed independent and non-independent scenarios between the Middle and South Ryukyus. In addition, because the single origin of FF was supported for Tokunoshima Is. and Okinoerabujima Is. populations, as well as for Ishigakijima Is. and Iriomotejima Is. populations, we could not conclude which island FF originated in. We developed four datasets for the independent scenario between Groups 1 and 2 with all possible combinations of islands in which speciation would have occurred independently: dataset 1, speciation in Tokunoshima Is. and Iriomotejima Is.; dataset 2, in Tokunoshima Is. and Ishigakijima Is.; dataset 3, Okinoerabujima Is. and Iriomotejima Is.; and dataset 4, Okinoerabujima Is. and Ishigakijima Is. We also developed 16 datasets for the non-independent scenario (Supporting Information Table S9).

For all four datasets in the scenario of independent origins between the regions, speciation probability was significantly explained by island area (P = 0.0016–0.0061, difference of deviance = 8.650–12.265, r^2 = 0.407–0.577; Table 2 and Supporting Information Table S9; Figure 5 and S5). The relationship was also significant for 12 of the 16 datasets in the non-independent scenario (Supporting Information Table S9). Almost identical results were obtained for the maximum catchment area and river length (Table 2 and Supporting Information Table S9). Furthermore, two of the four datasets for the independent origin scenario and five of the 16 datasets for the non-independent scenario, showed significant relationships between the number of waterfalls and speciation (Table 2 and Supporting Information Table S9). Model selection by AIC scores showed that the best model included no variables, except for island area, as the predictors for speciation probability in most datasets when the variables were controlled by the island area (Supporting Information Table S9).

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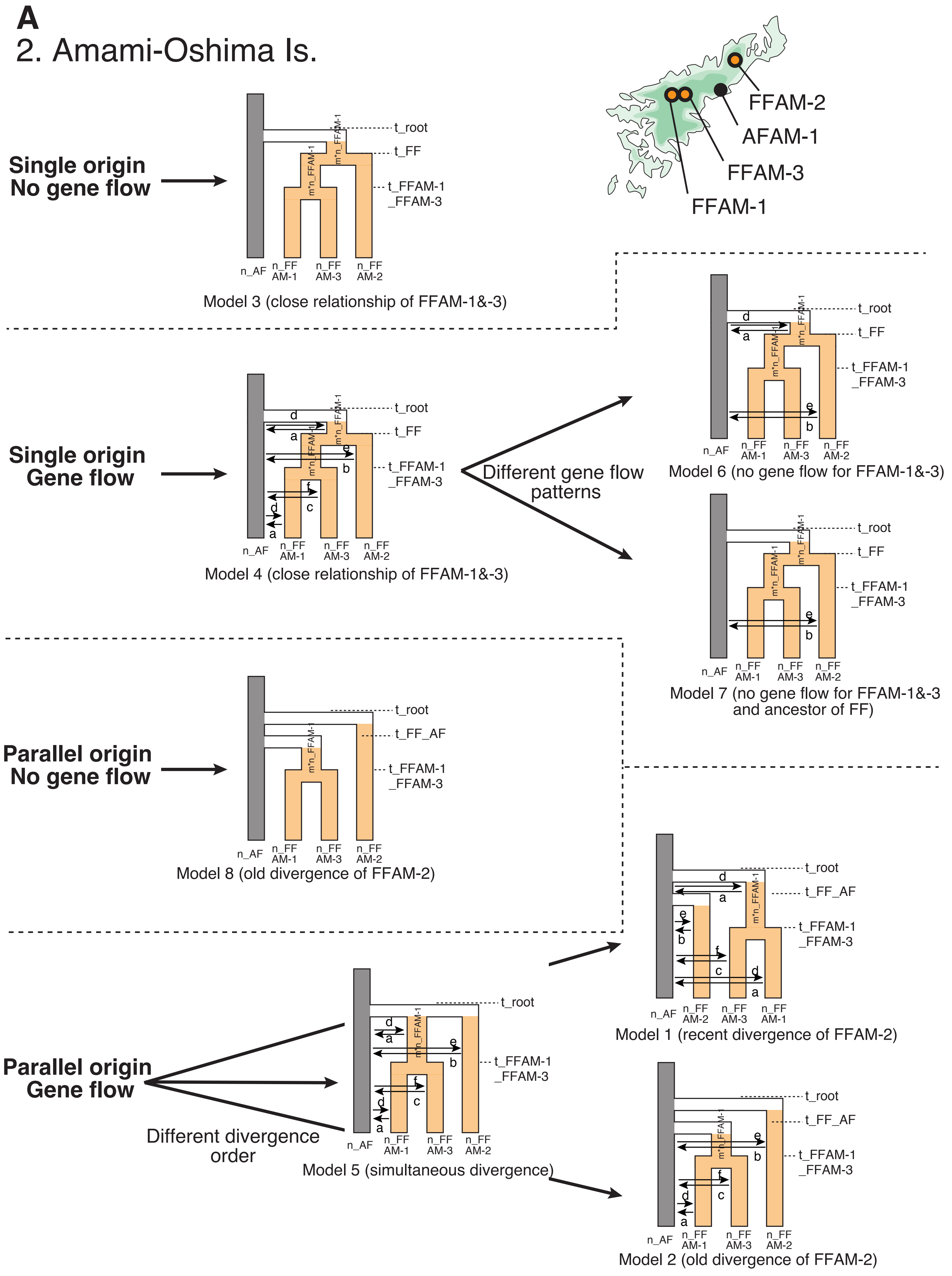
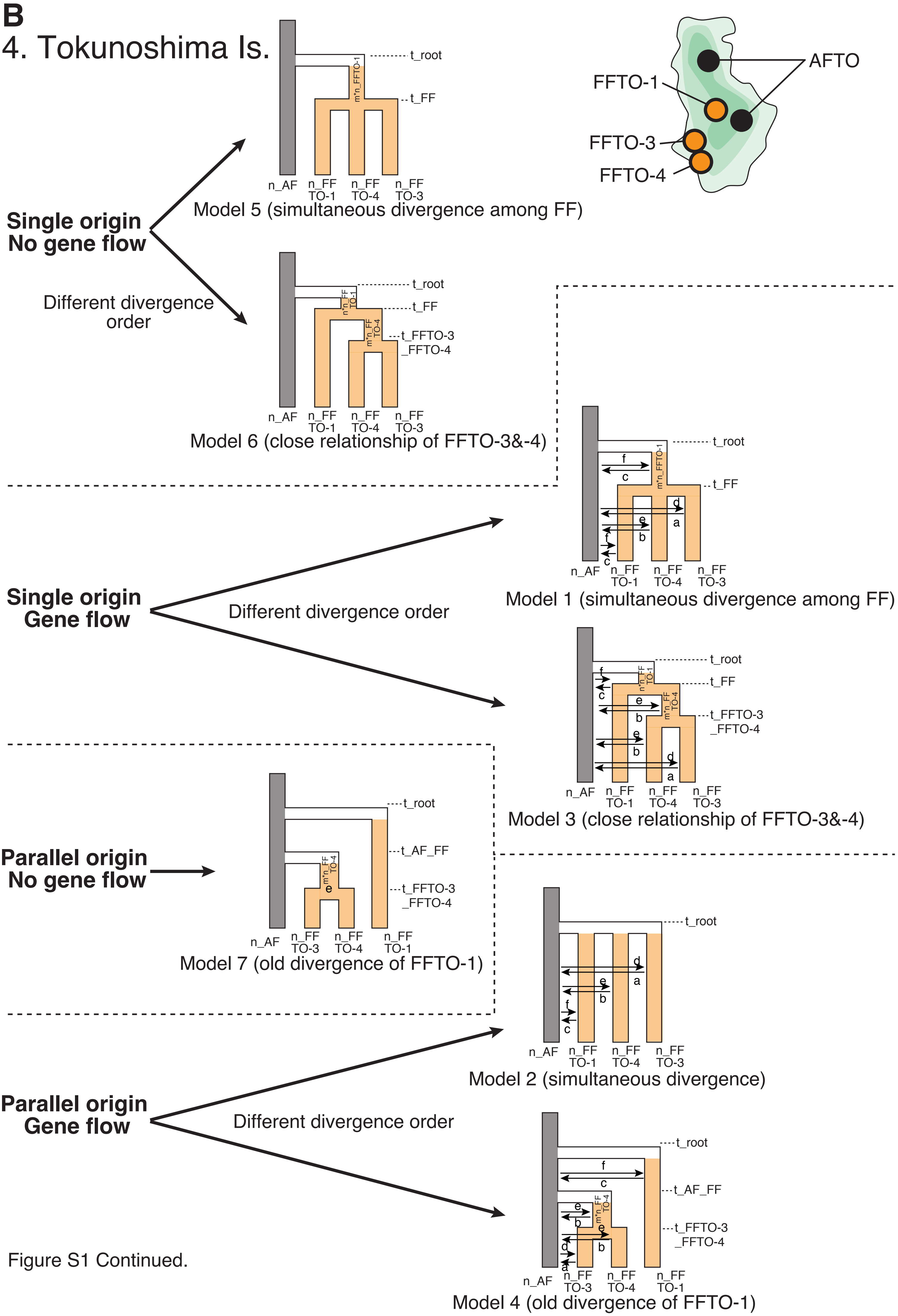


Figure S1 Tested demographic models and their relationships.



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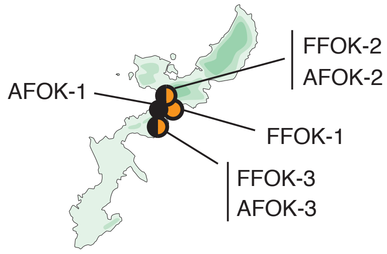
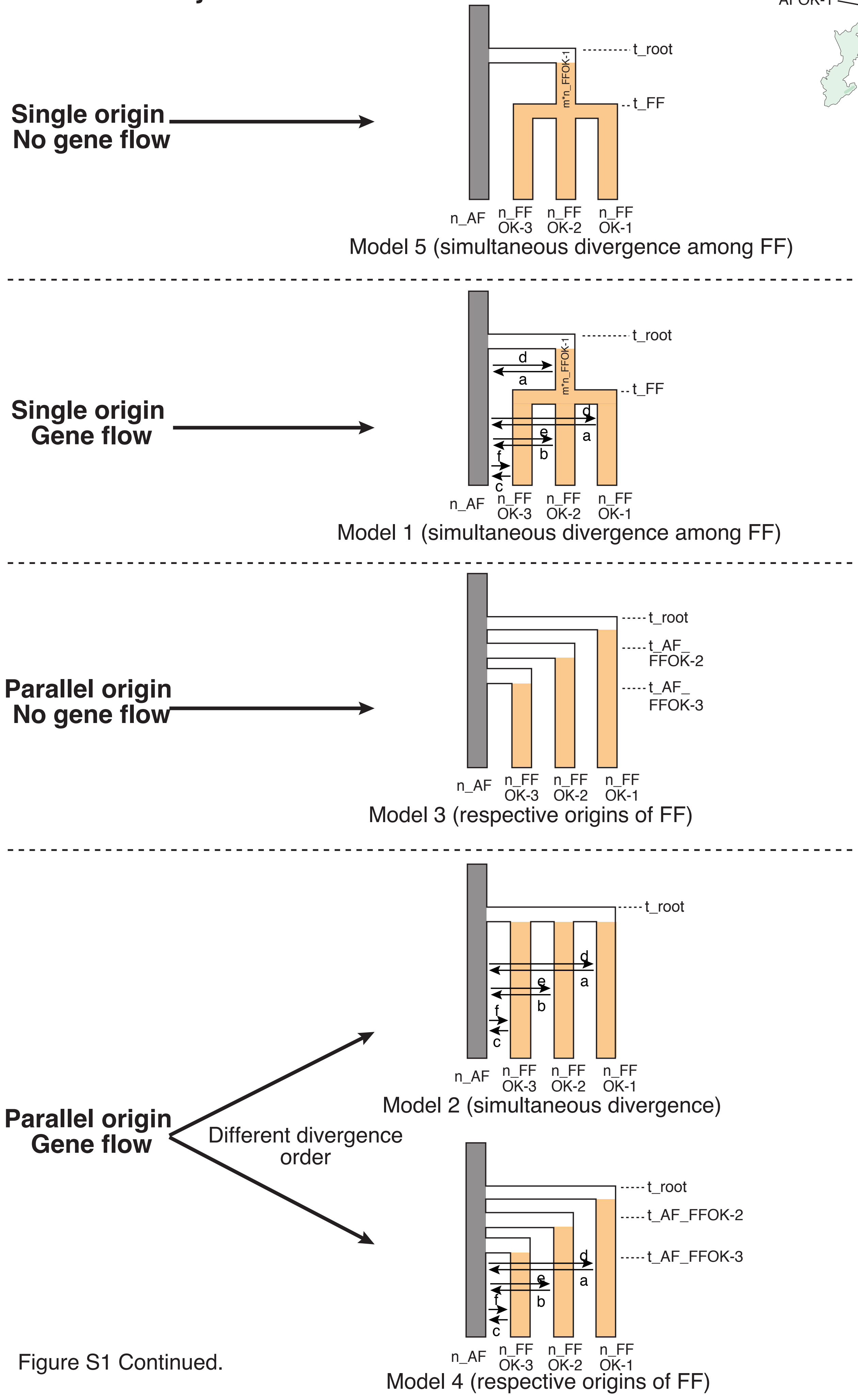
C

6. Okinawajima Is.





Model 5 (simultaneous divergence among FF)

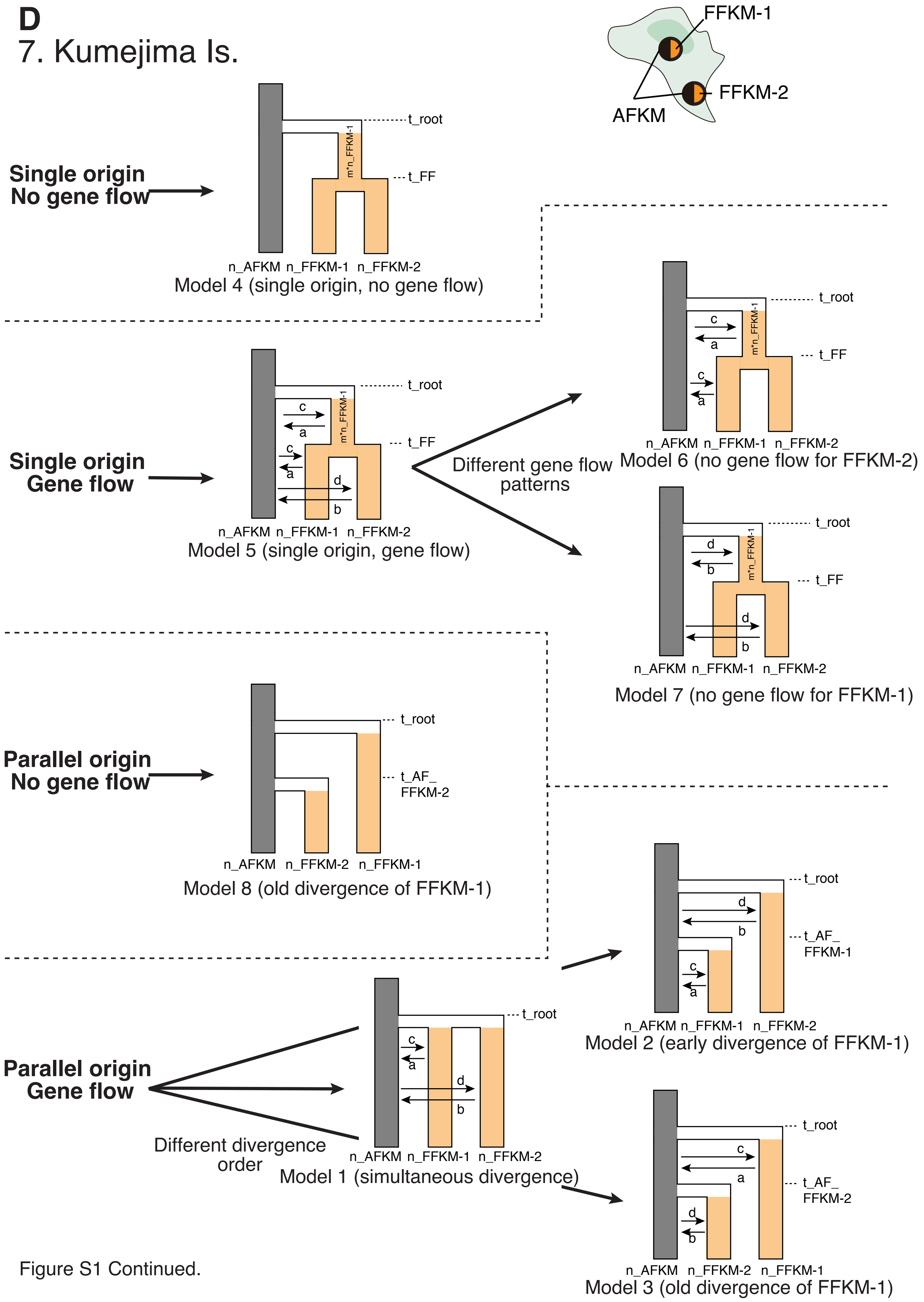
Model 1 (simultaneous divergence among FF)

Model 3 (respective origins of FF)

Model 2 (simultaneous divergence)

Model 4 (respective origins of FF)

Figure S1 Continued.



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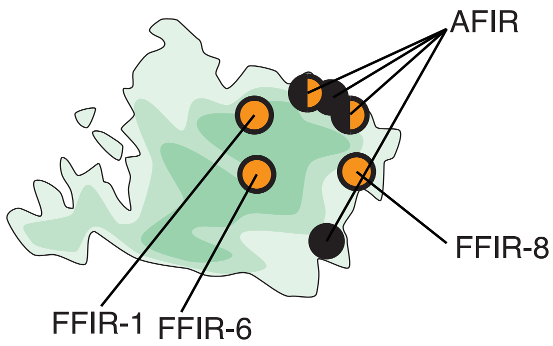
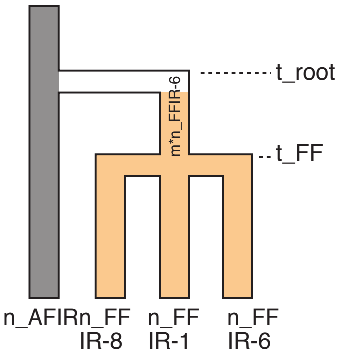
E

9. Iriomotejima Is.

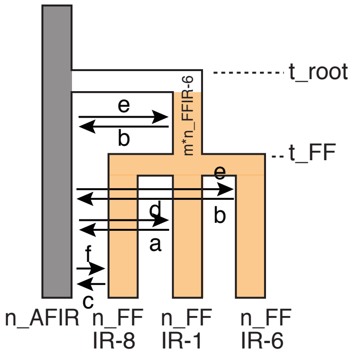


Single origin
No gene flow



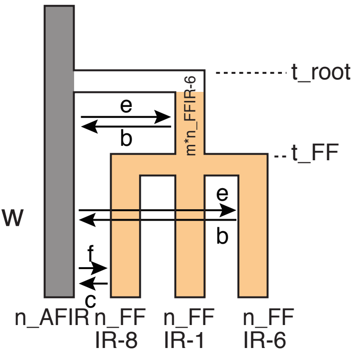
Model 1 (simultaneous divergence among FF)

Single origin
Gene flow



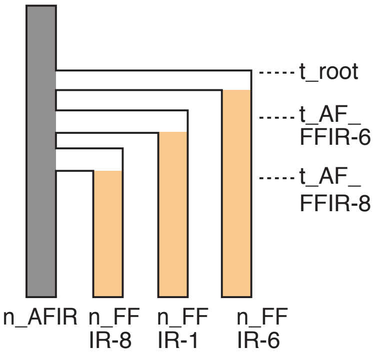
Model 3 (simultaneous divergence among FF)

Different gene flow patterns

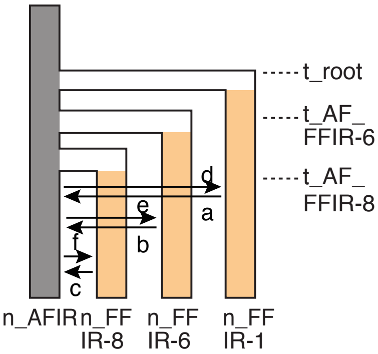


Model 6 (no gene flow for FFIR-1)

Parallel origin
No gene flow



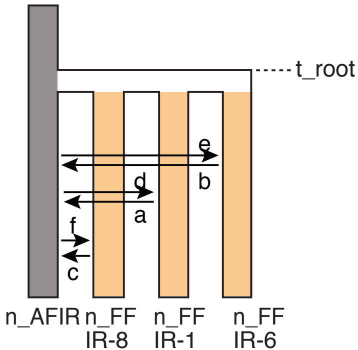
Model 2 (respective origins of FF)



Model 4 (respective origins of FF)

Parallel origin
Gene flow

Different divergence order

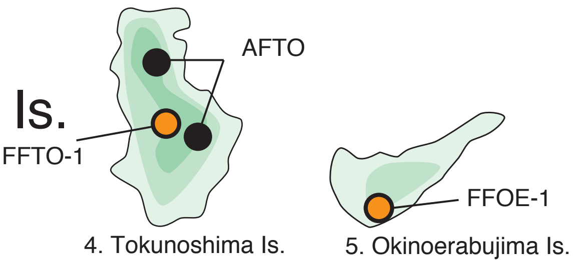


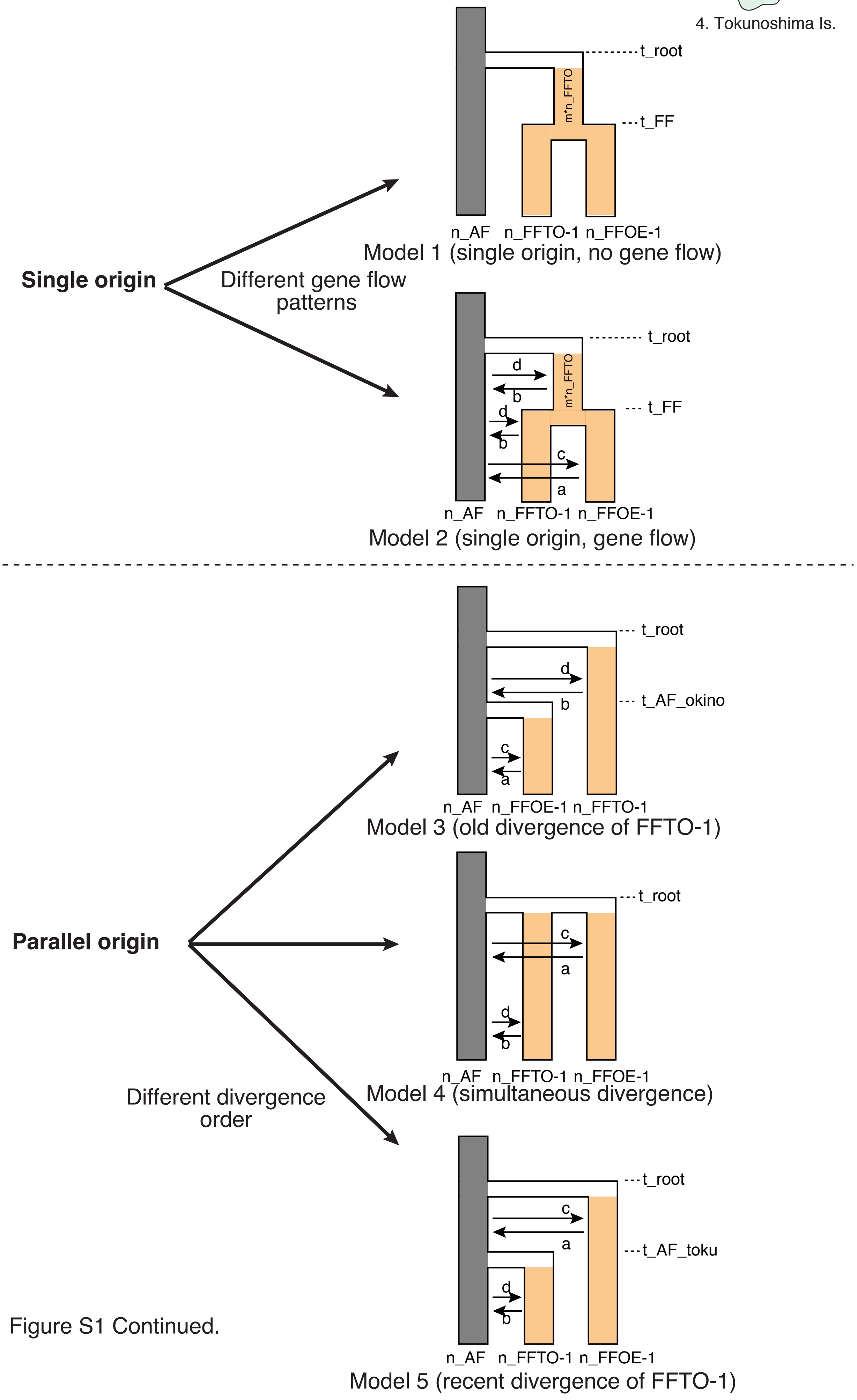
Model 5 (simultaneous divergence)

Figure S1 Continued.

F

4. Tokunoshima Is.– 5. Okinoerabujima Is.





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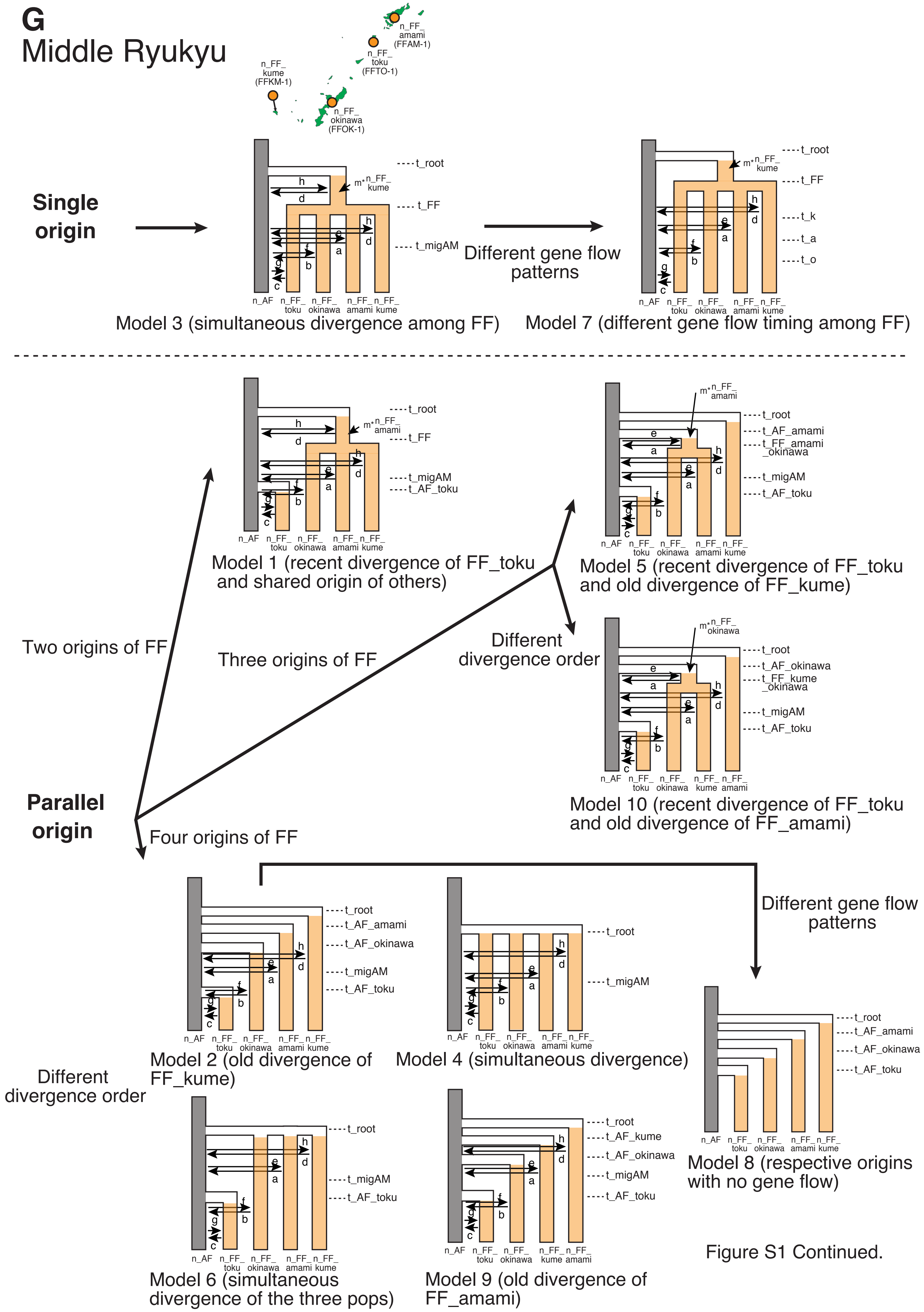

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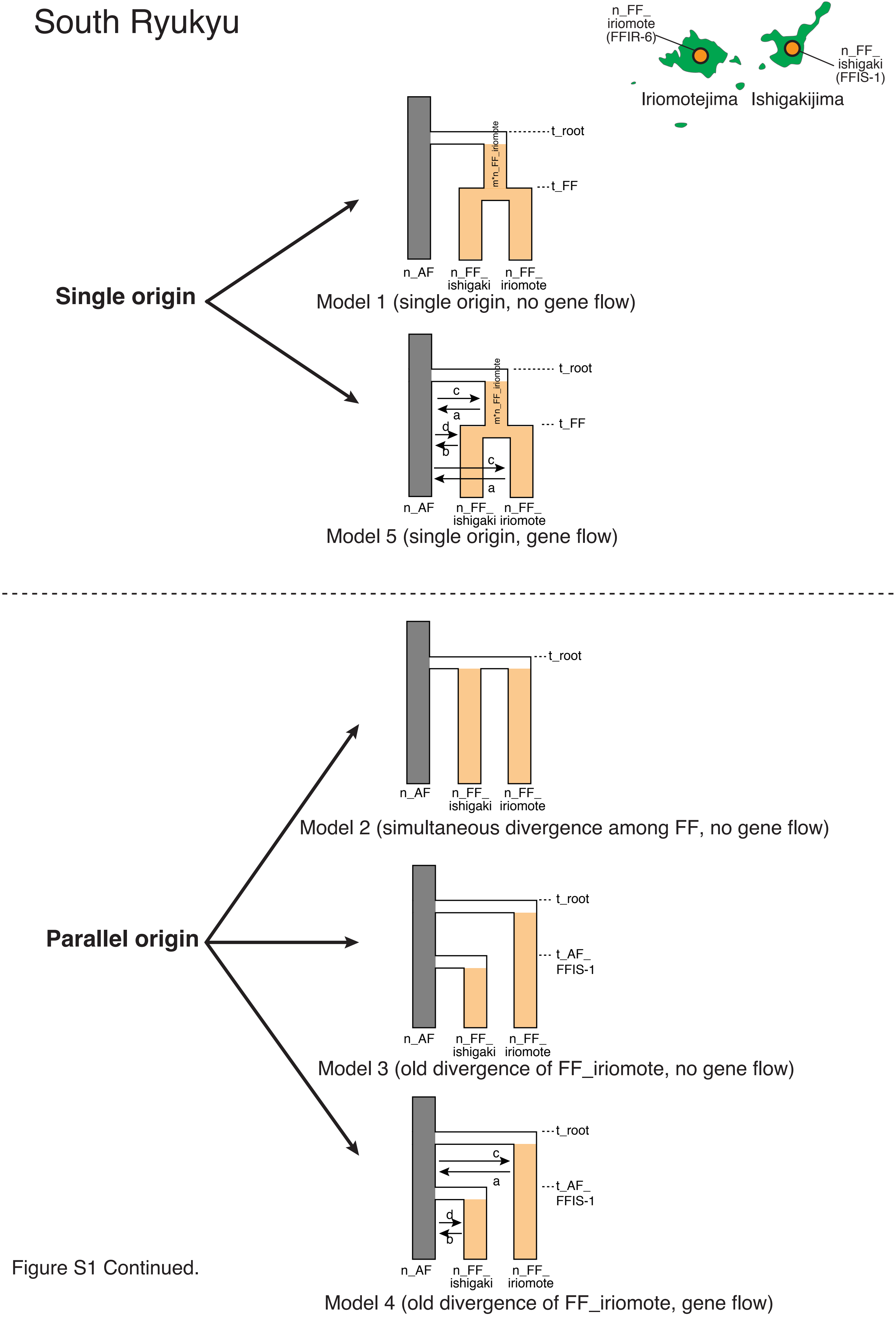
H

South Ryukyu



Model 1 (single origin, no gene flow)

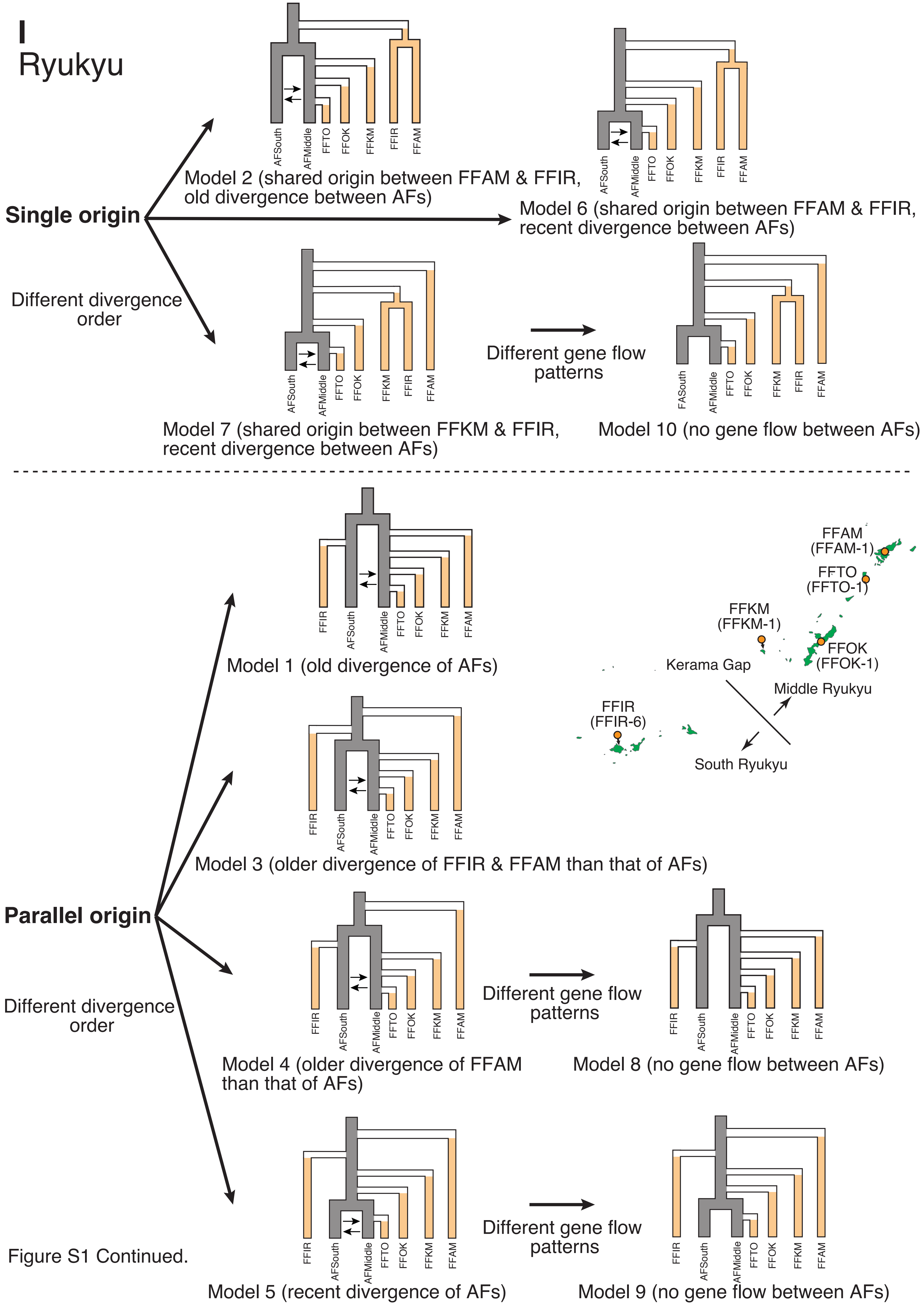
Model 5 (single origin, gene flow)

Model 2 (simultaneous divergence among FF, no gene flow)

Model 3 (old divergence of FF_iriomote, no gene flow)

Model 4 (old divergence of FF_iriomote, gene flow)

Figure S1 Continued.



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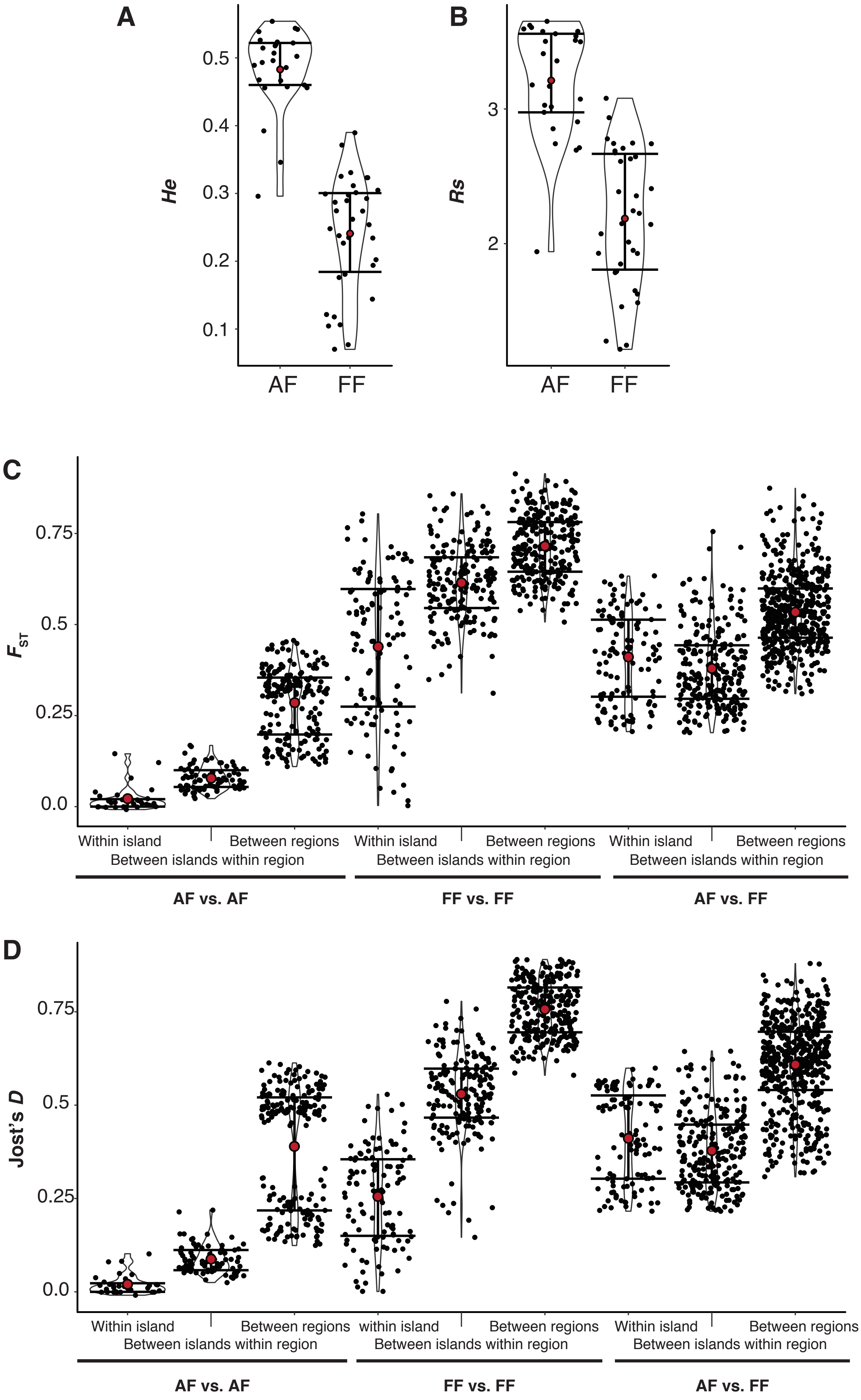


Figure S2 Distributions of summary statistics for genetic diversities within and between populations of the *Rhinogobius* species. Red dots and error bars indicate mean values and intermedian quantiles ranges, respectively. Genetic diversity values of populations were measured by expected heterozygosity (*He*, A) and allelic richness (*Rs*, B). Pairwise population differences were measured by F_{ST} (C) and Jost's *D* (D).

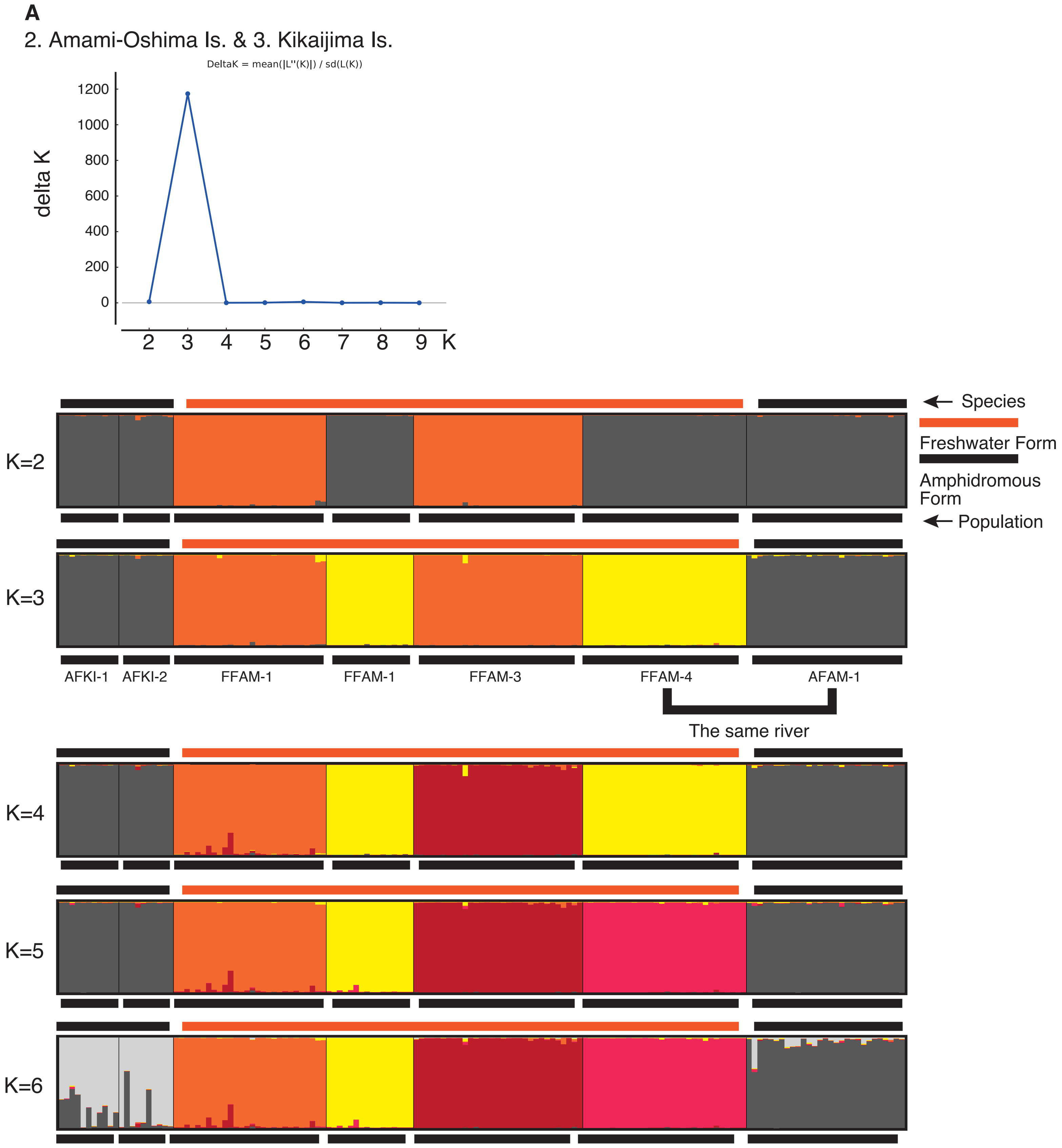
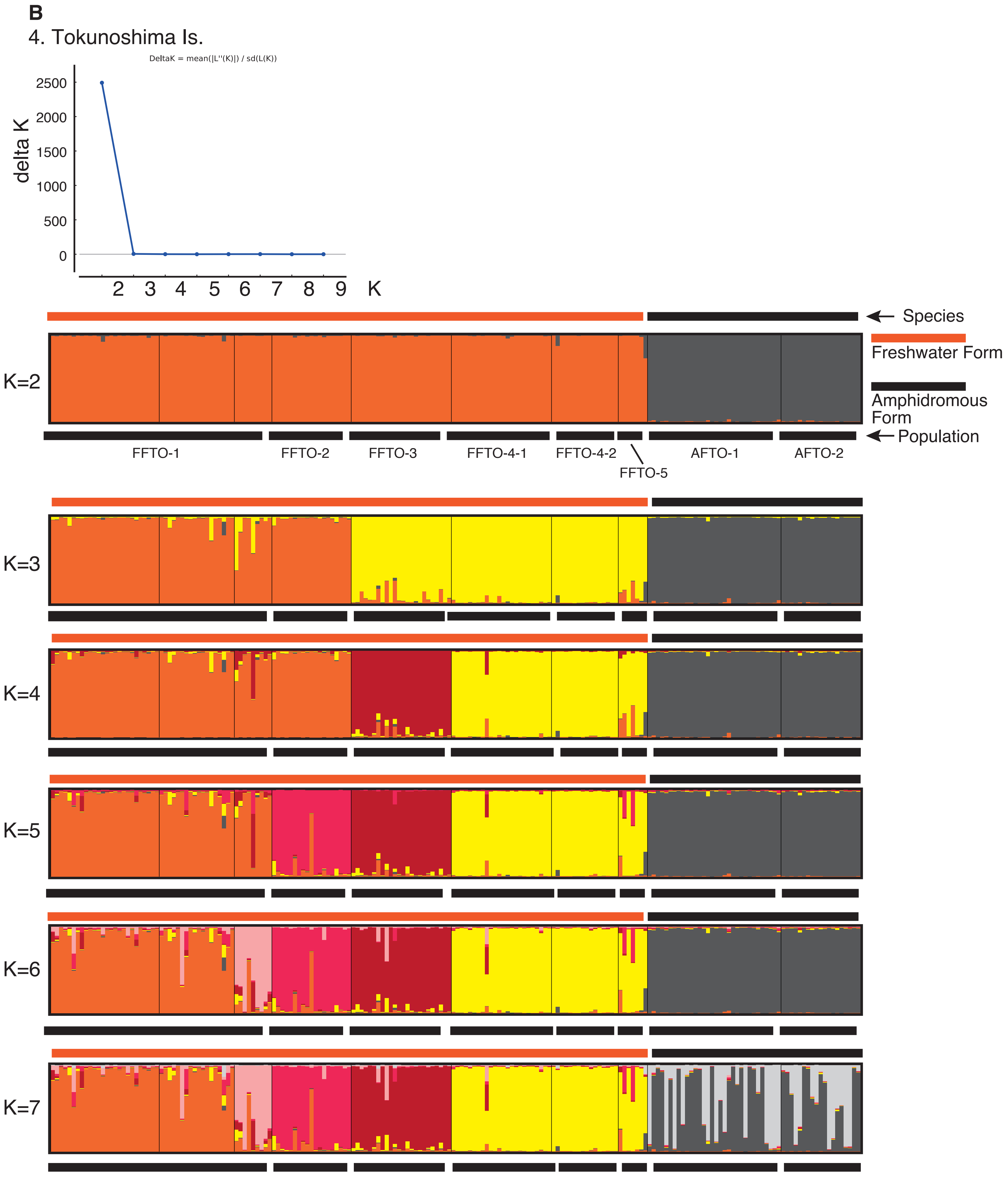


Figure S3 Results of STRUCTURE analysis for each island and AF. Sympatric points are indicated by additional annotation. Dominant genetic features in AF identified by morphology are shown in grey, whereas those in FF are shown in the other colours. Graphs of ΔK are also shown.



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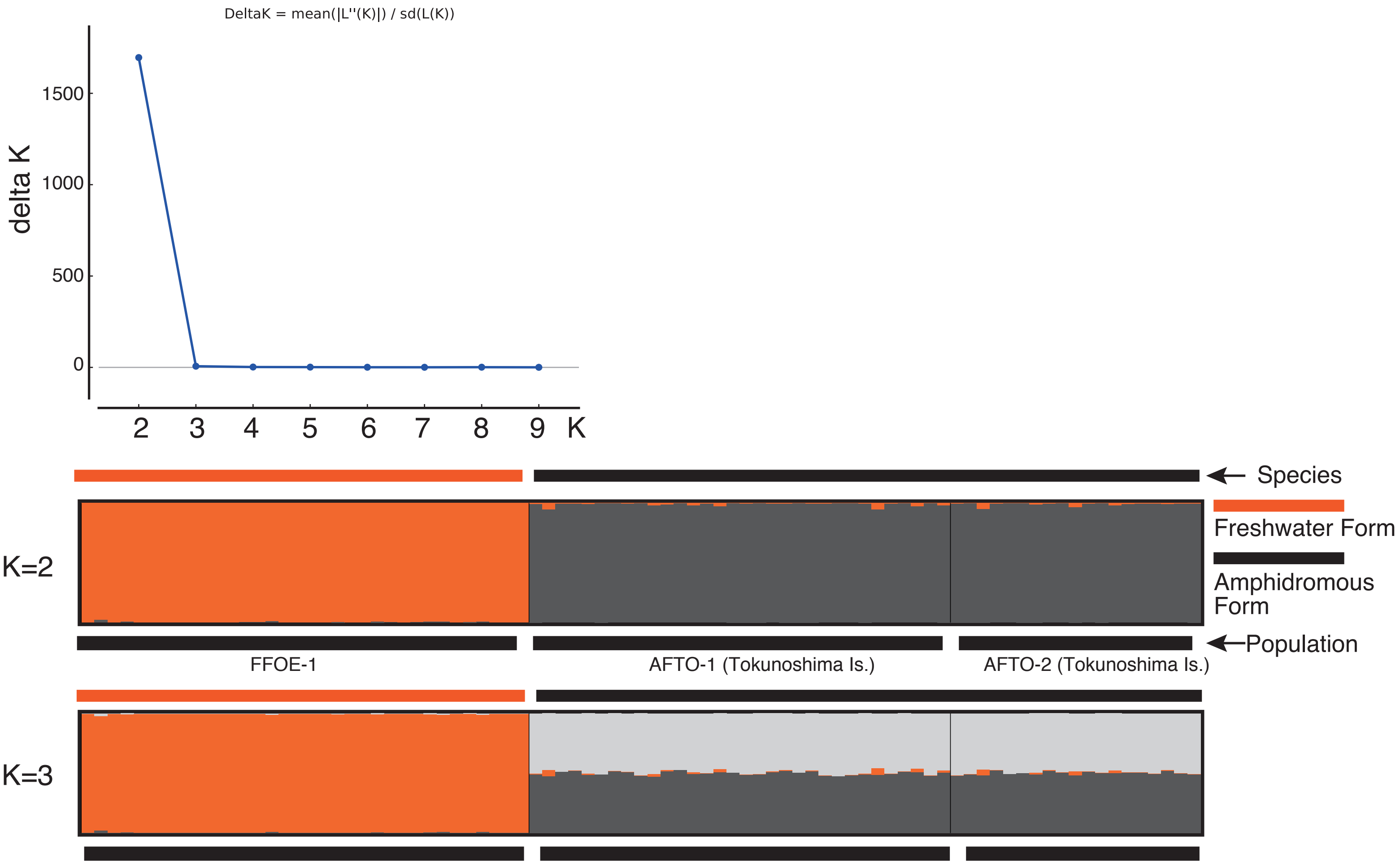
C

5. Okinoerabujima Is. (but specimens of *R. brunneus* collected in Tokunoshima Is. were used)



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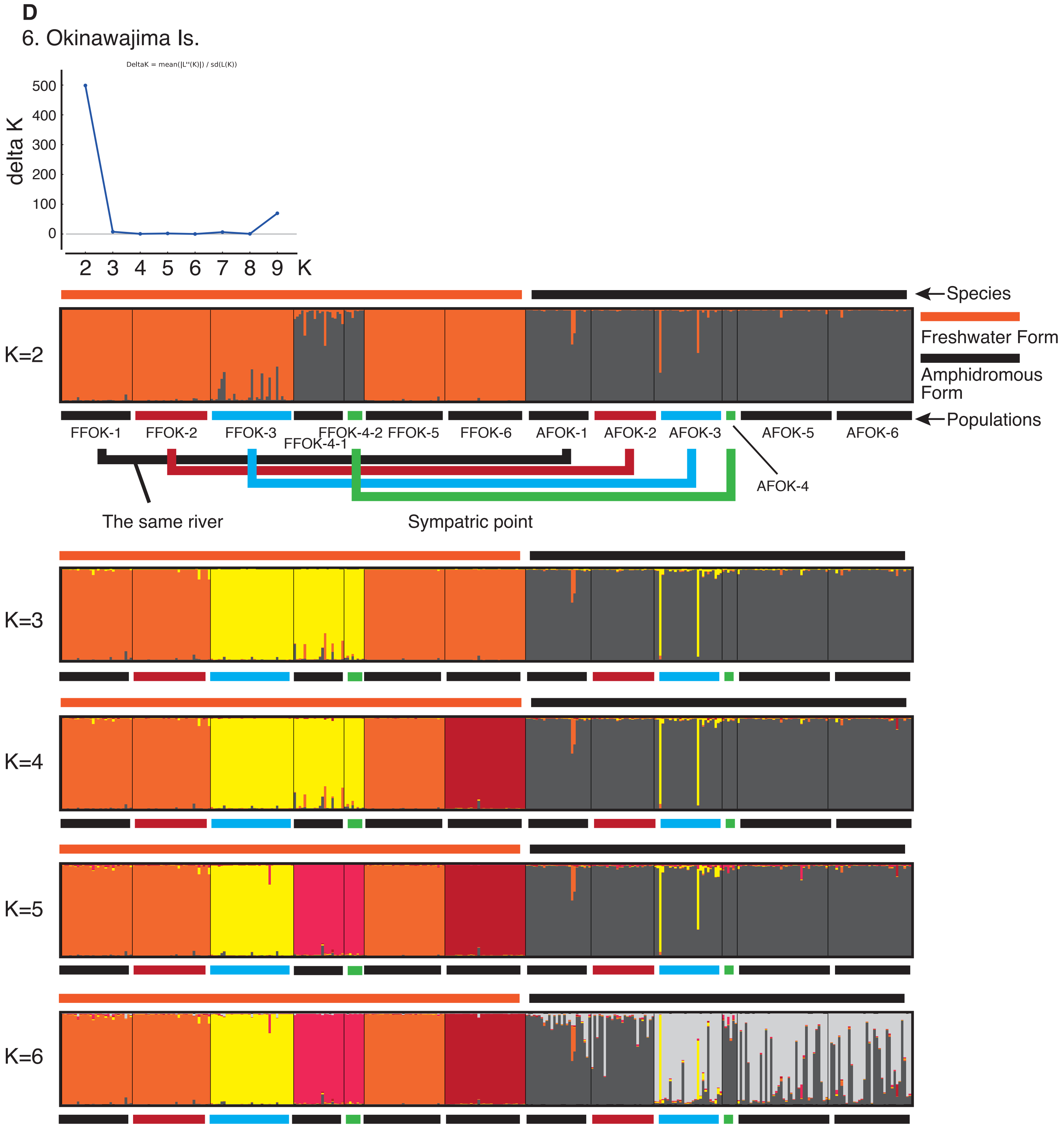

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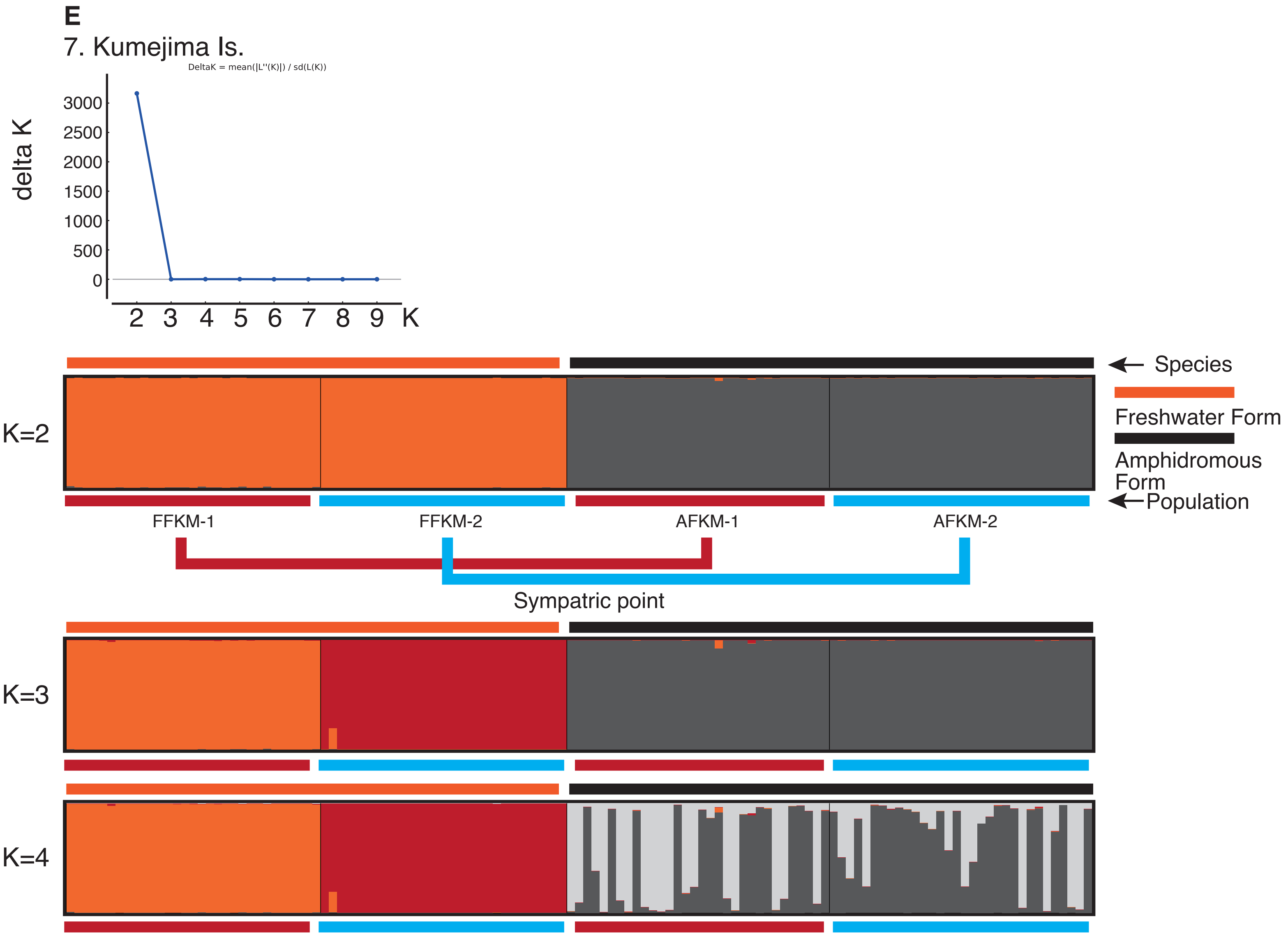

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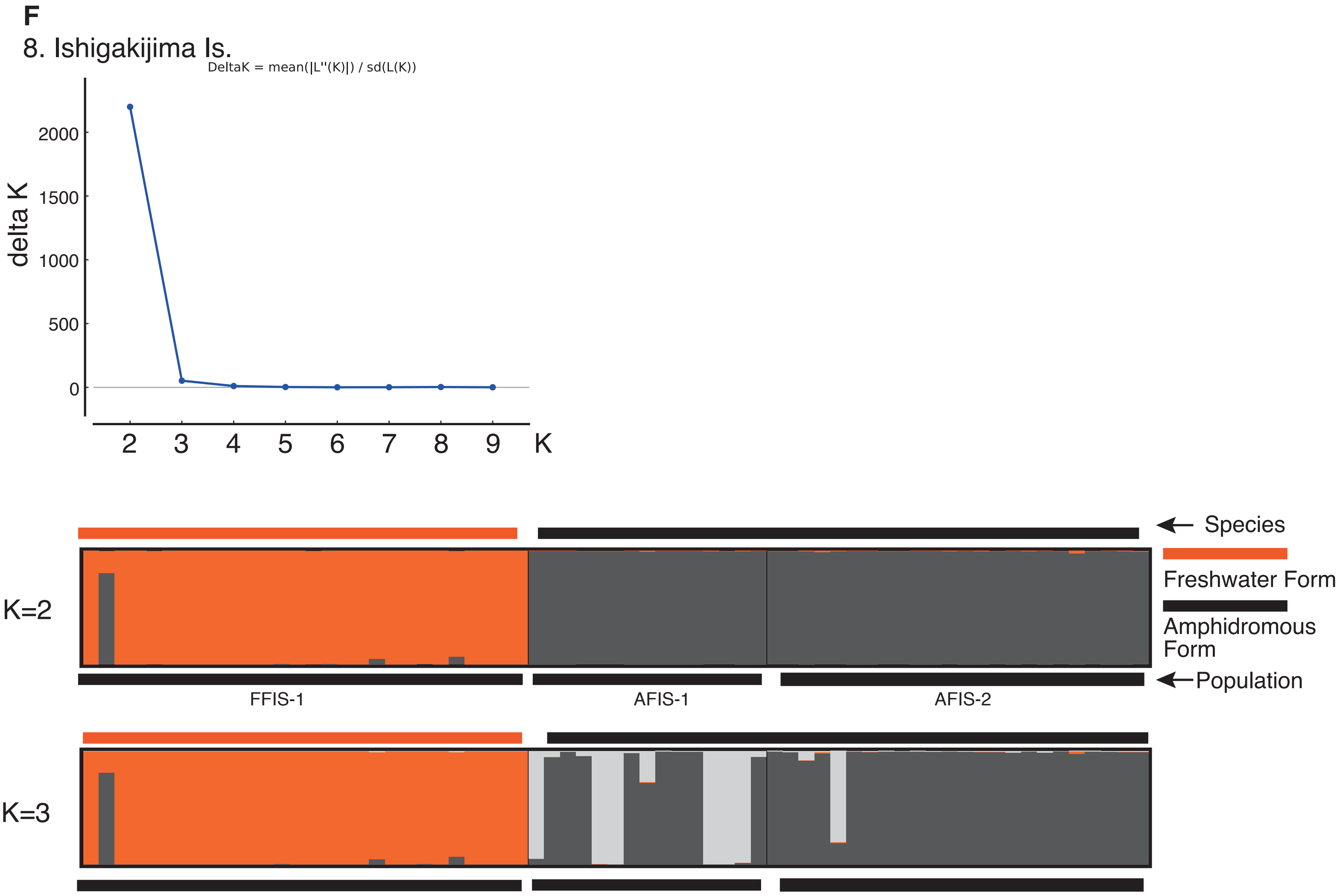

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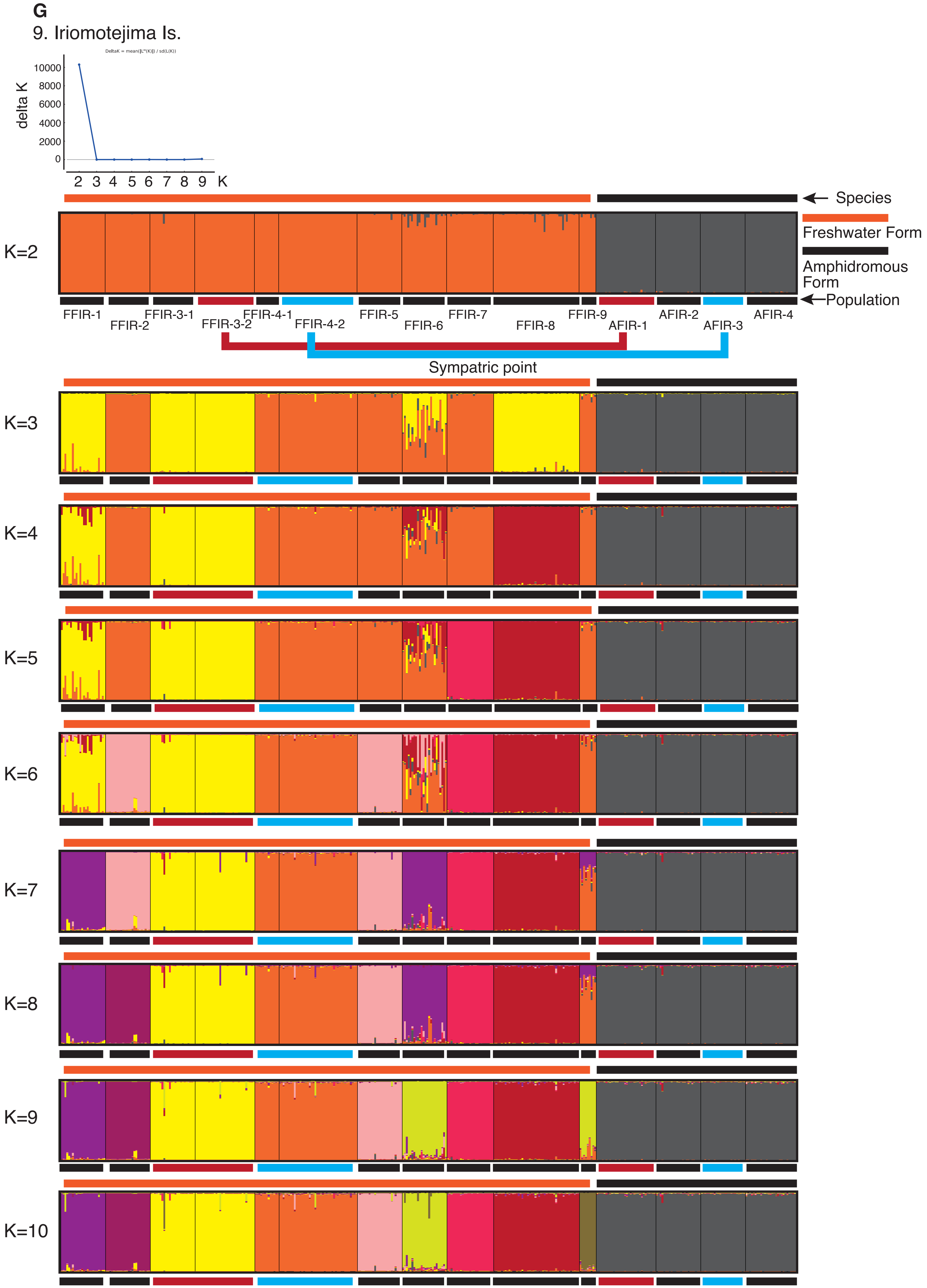

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H

Rhinogobius brunneus

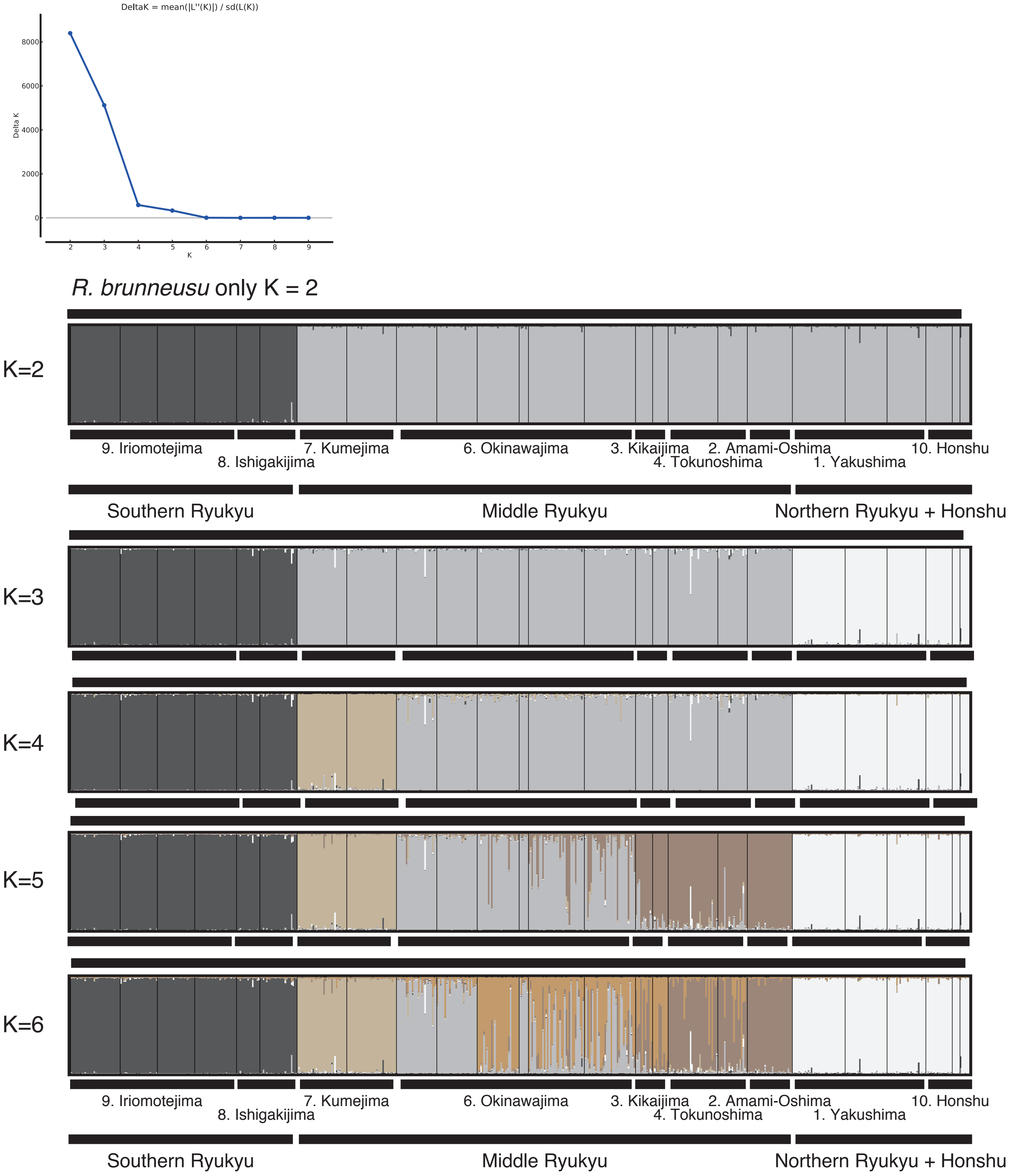
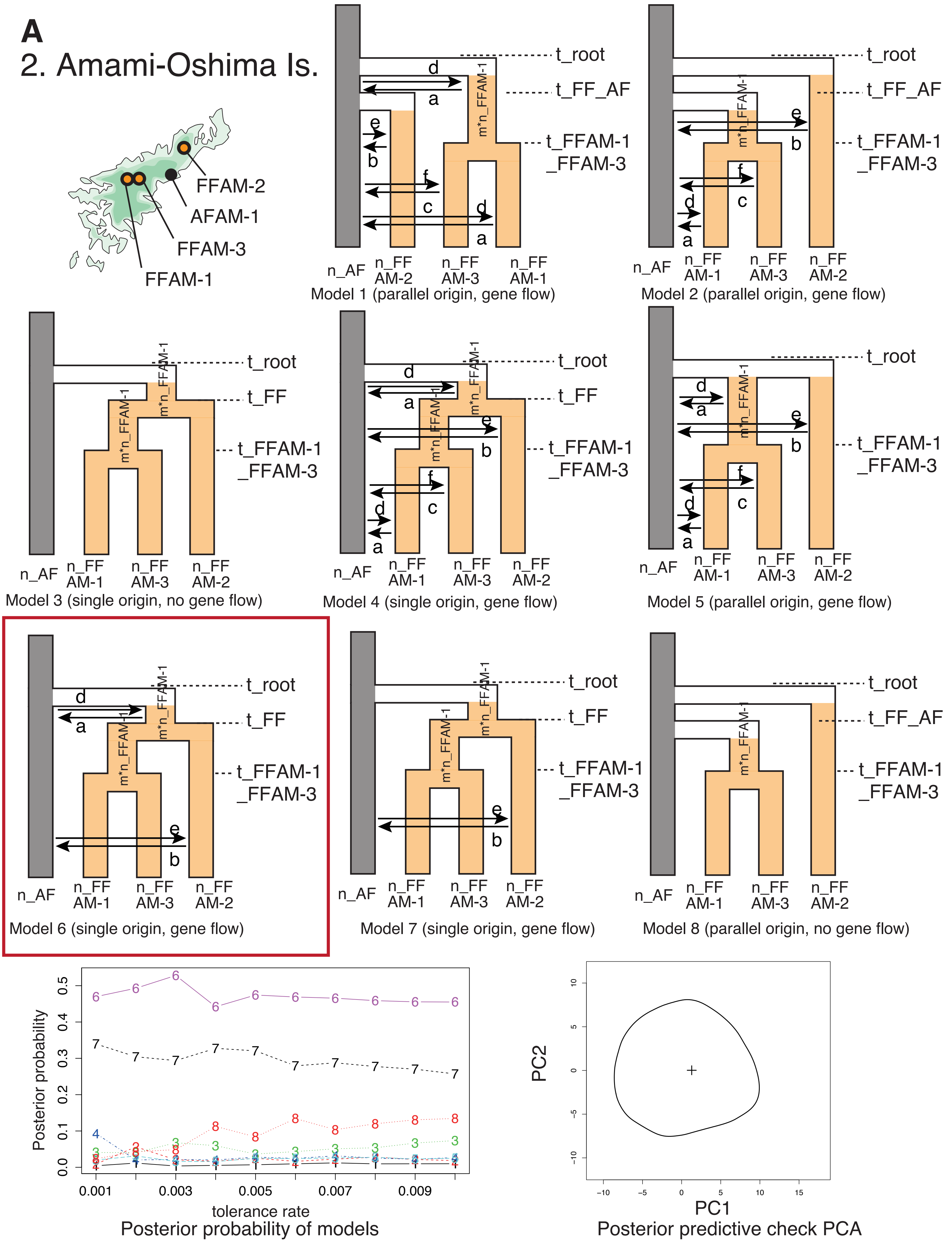


Fig. S3 Continued.



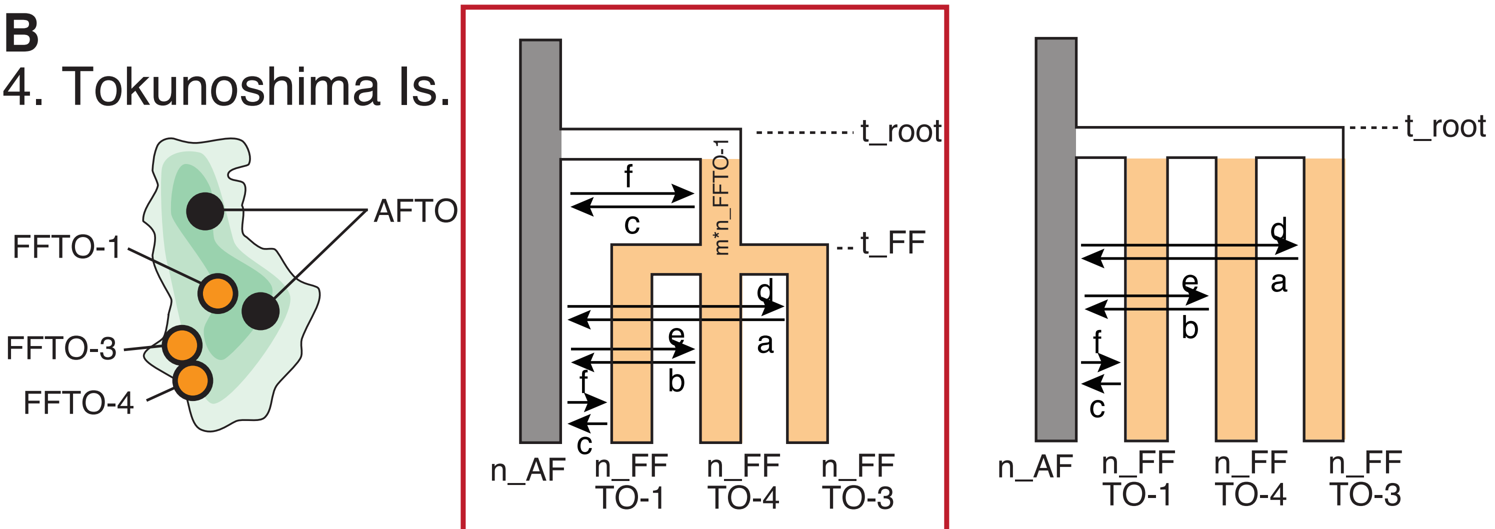
Posterior probability of models

Posterior predictive check PCA

Figure S4 Tested demographic models and results of ABC model selection. Result of posterior predictive check conducted using principal component analysis for the selected model is also shown. Amphidromous and fluvial forms are indicated by black and orange, respectively. Arrows between populations indicate gene flow. The model that was selected is enclosed in a red square.

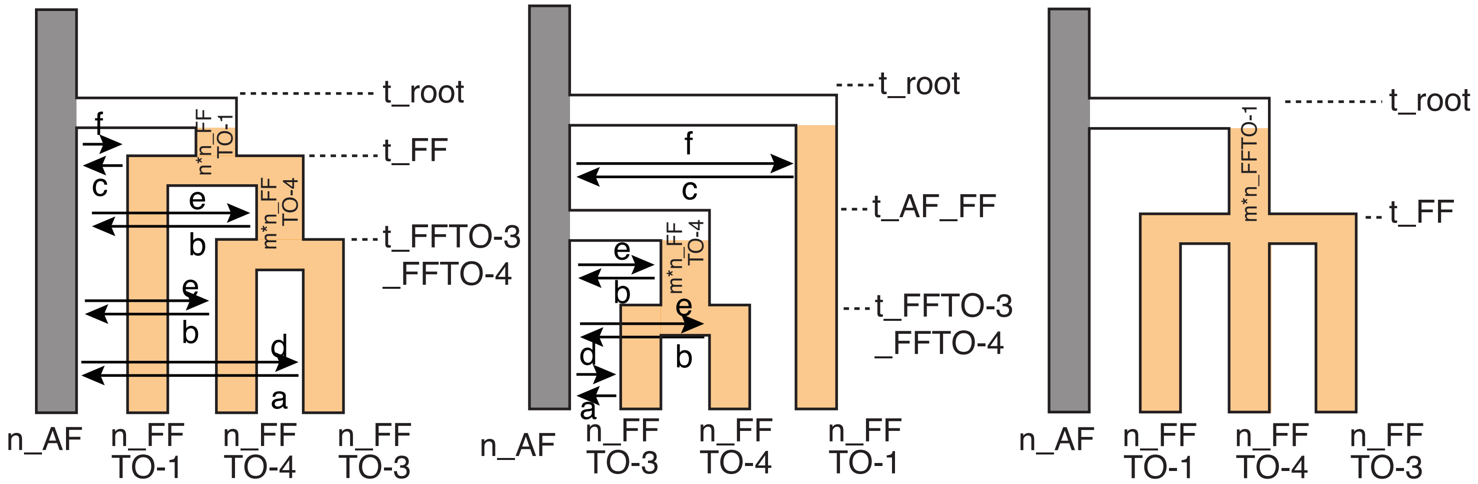
B

4. Tokunoshima Is.



Model 1 (single origin, gene flow)

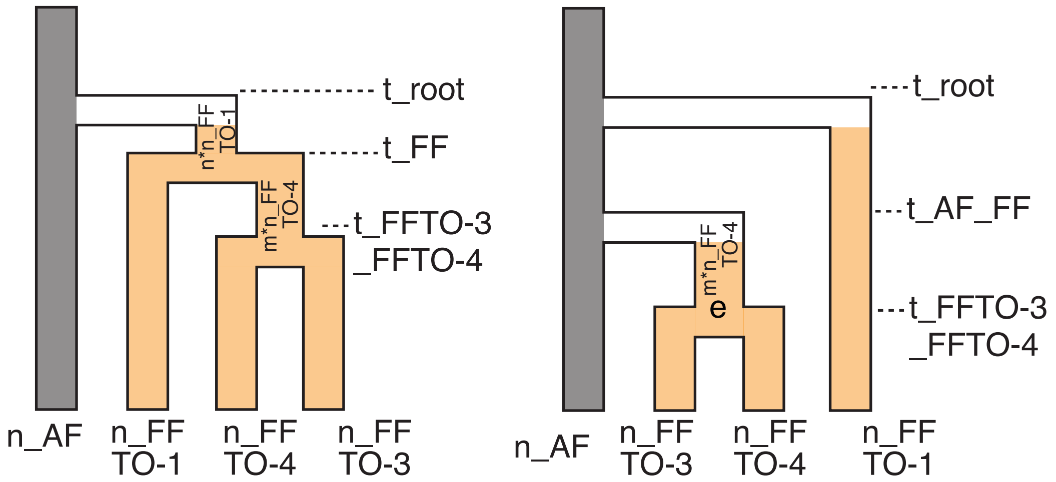
Model 2 (simultaneous divergence, gene flow)



Model 3 (single origin, gene flow)

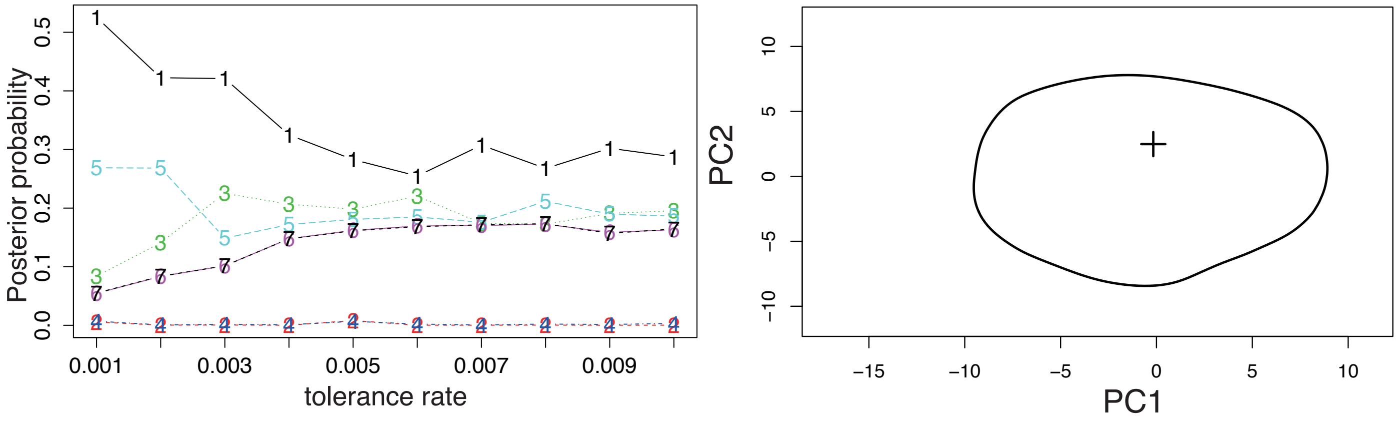
Model 4 (parallel origin, gene flow)

Model 5 (single origin, no gene flow)



Model 6 (single origin, no gene flow)

Model 7 (parallel origin, no gene flow)



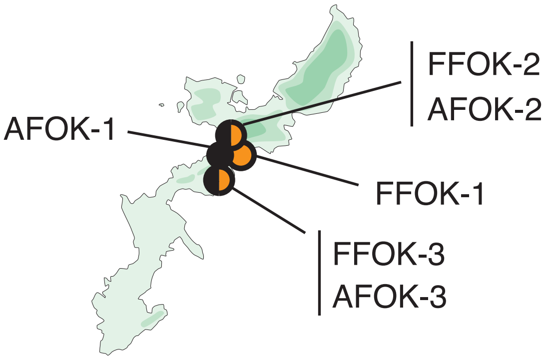
Posterior probability of models

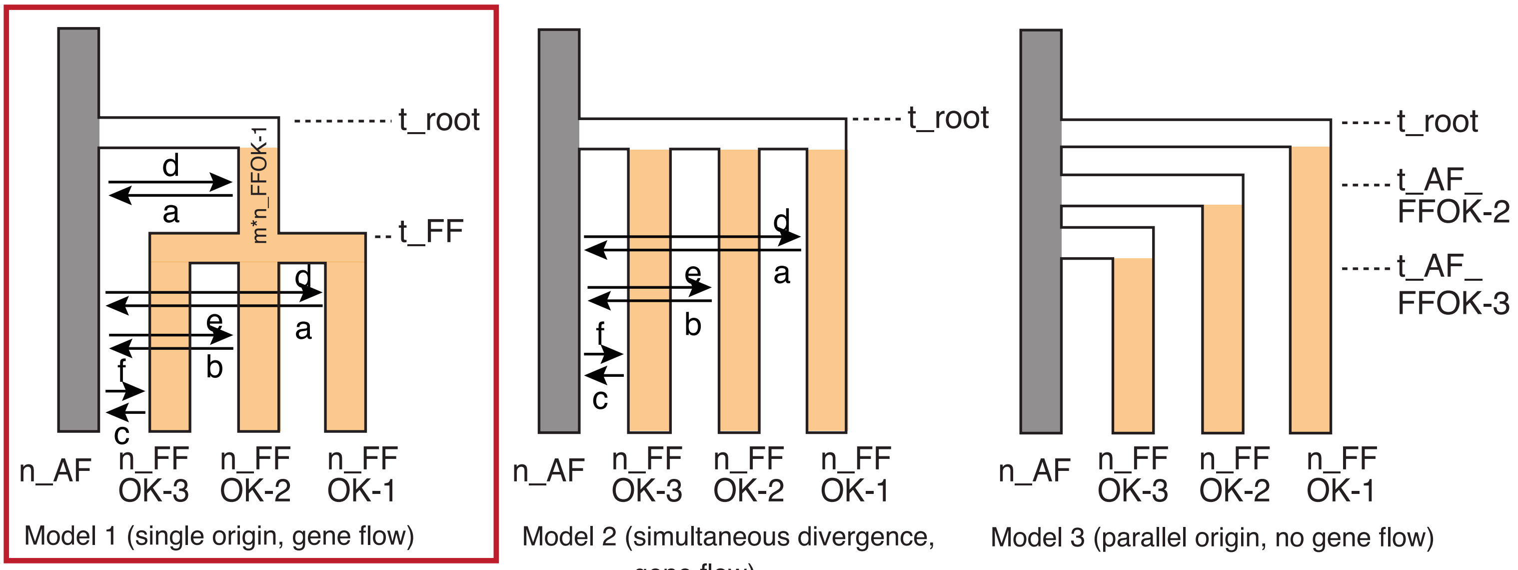
Posterior predictive check PCA

Figure S4 Continued

C

6. Okinawajima Is.

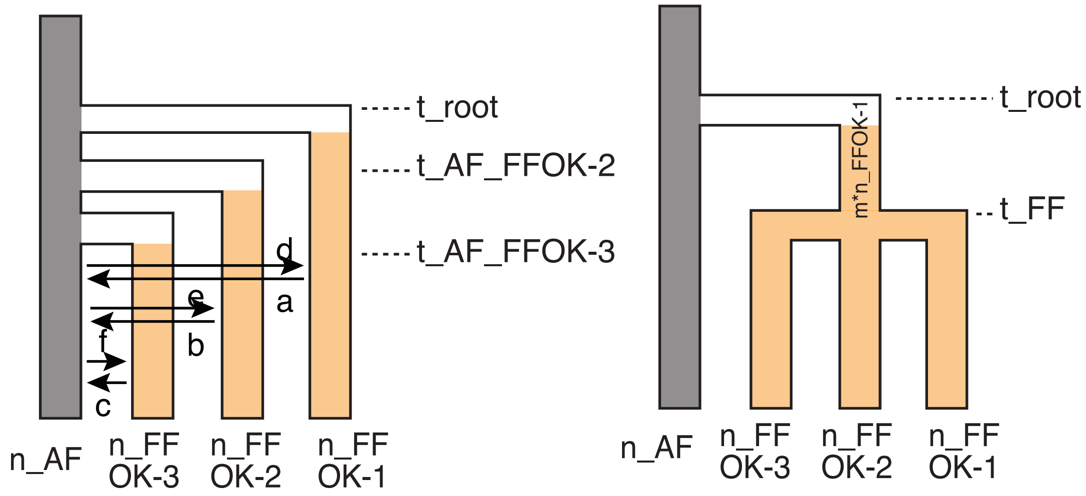




Model 1 (single origin, gene flow)

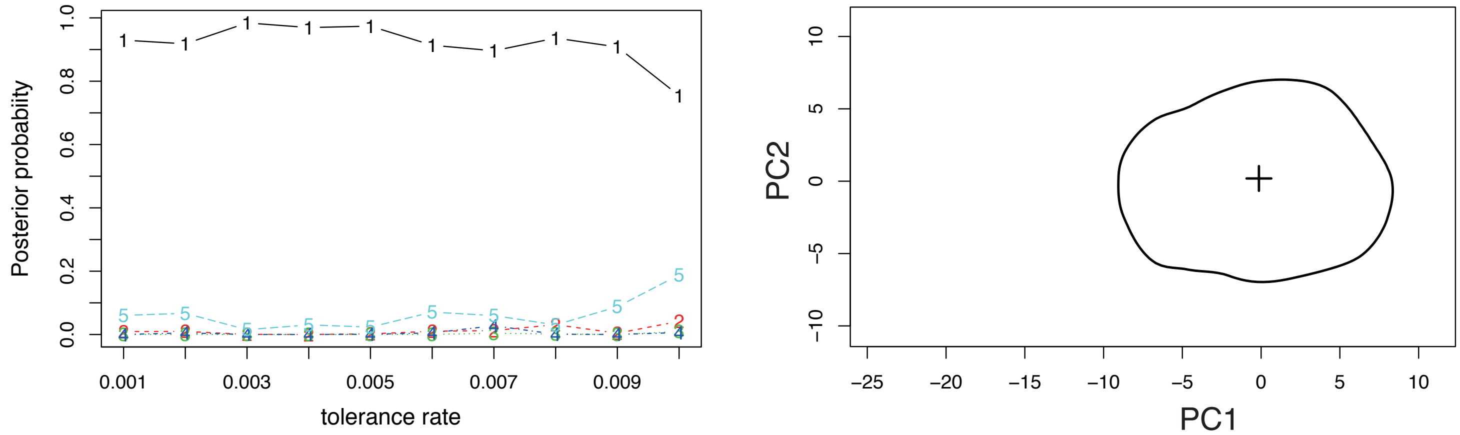
Model 2 (simultaneous divergence, gene flow)

Model 3 (parallel origin, no gene flow)



Model 4 (parallel divergence, gene flow)

Model 5 (single origin, no gene flow)



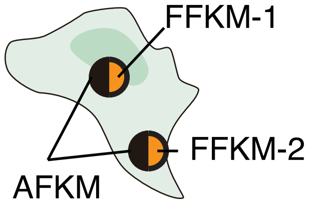
Posterior probability of models

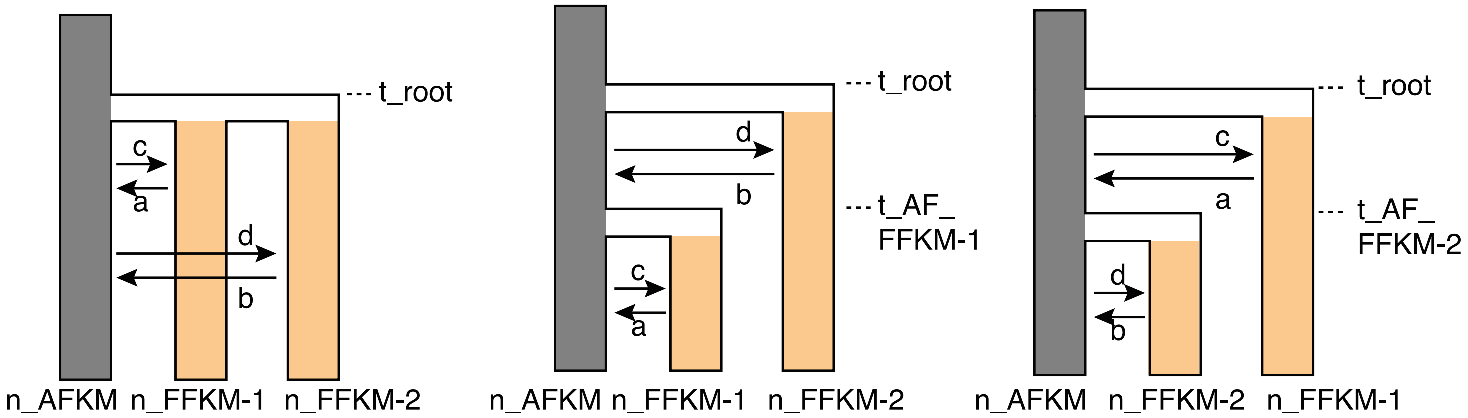
Posterior predictive check PCA

Figure S4 Continued

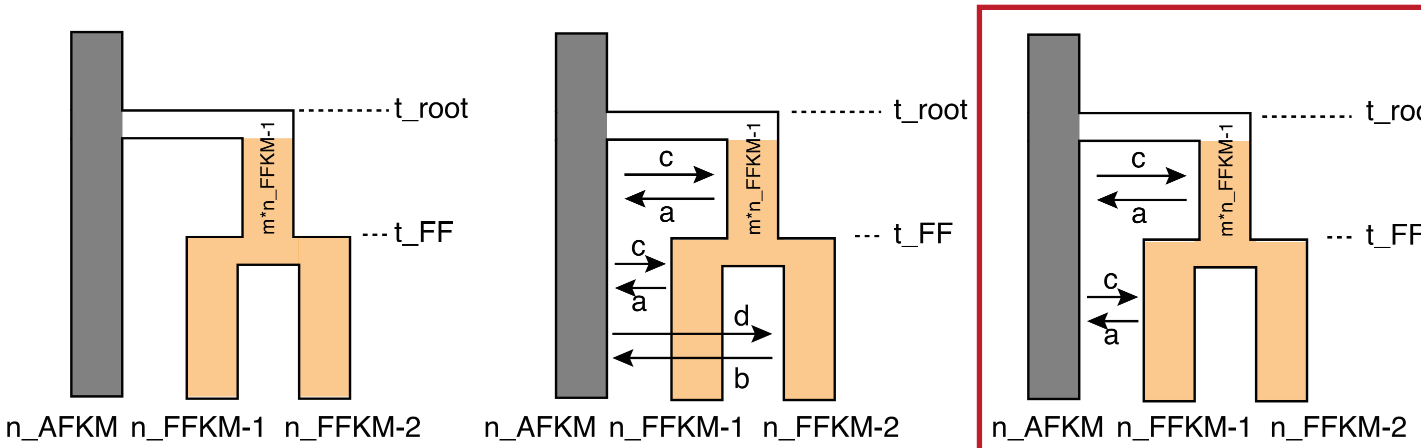
D

7. Kumejima Is.

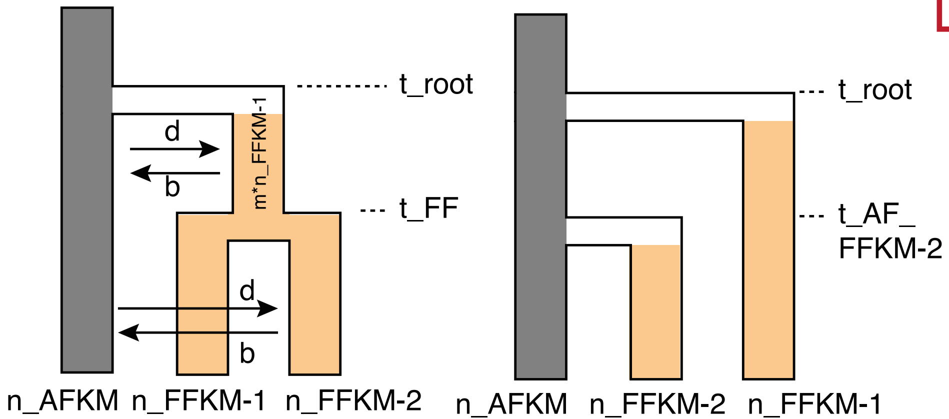




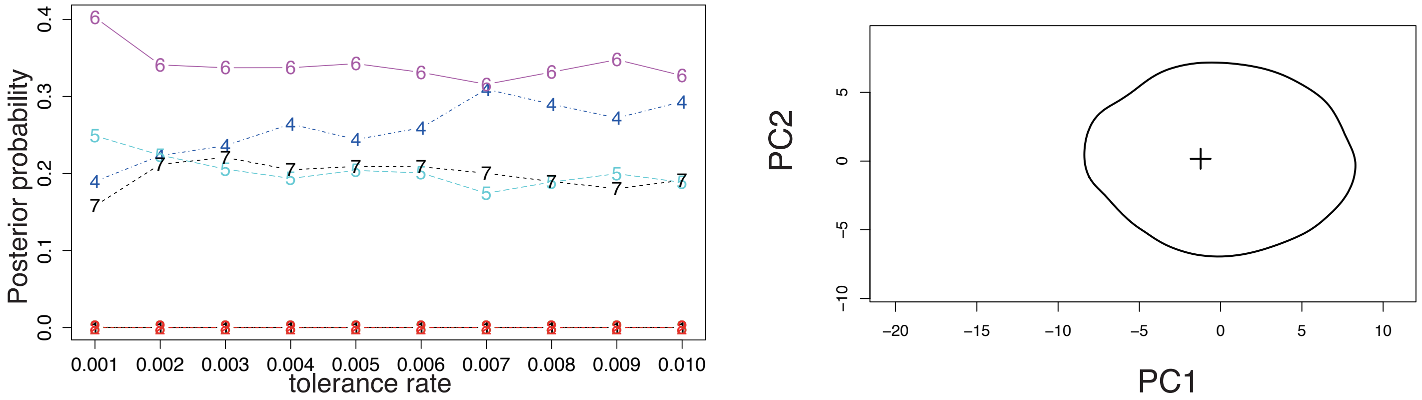
Model 1 (simultaneous origin, gene flow) Model 2 (parallel origin, gene flow) Model 3 (parallel origin, gene flow)



Model 4 (single origin, no gene flow) Model 5 (single origin, gene flow) Model 6 (single origin, gene flow)



Model 7 (single origin, gene flow) Model 8 (parallel origin, no gene flow)

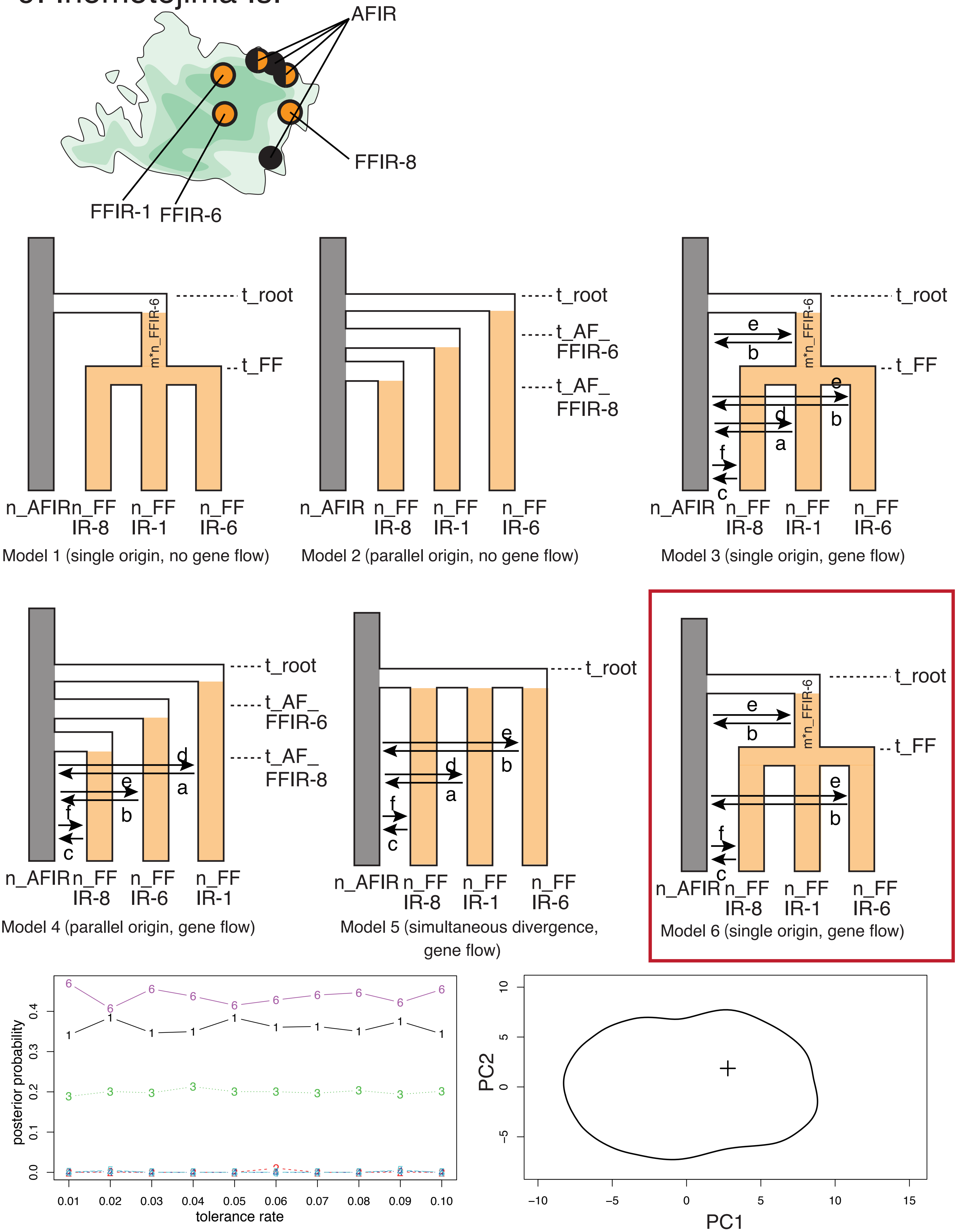


Posterior probability of models Posterior predictive check PCA

Figure S4 Continued

E

9. Iriomotejima Is.



Model 1 (single origin, no gene flow)

Model 2 (parallel origin, no gene flow)

Model 3 (single origin, gene flow)

Model 4 (parallel origin, gene flow)

Model 5 (simultaneous divergence, gene flow)

Model 6 (single origin, gene flow)

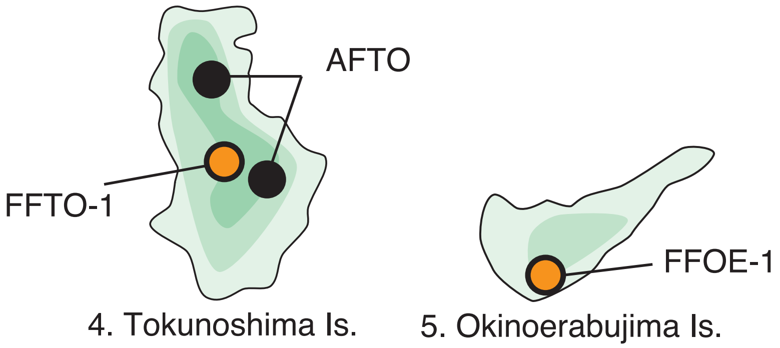
Posterior probability of models

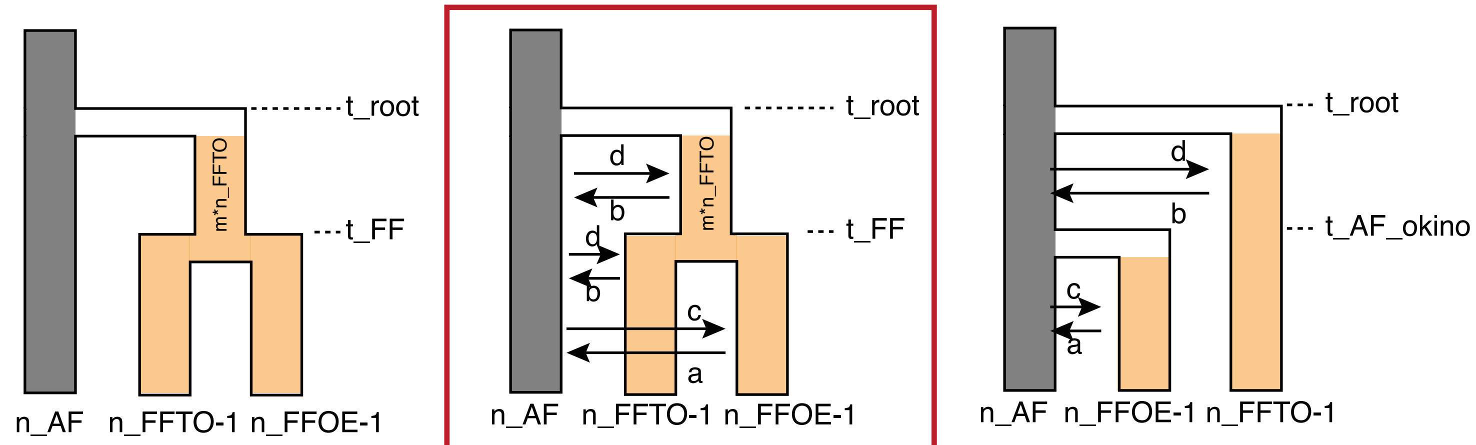
Posterior predictive check PCA

Figure S4 Continued

F

4. Tokunoshima Is.– 5. Okinoerabujima Is.

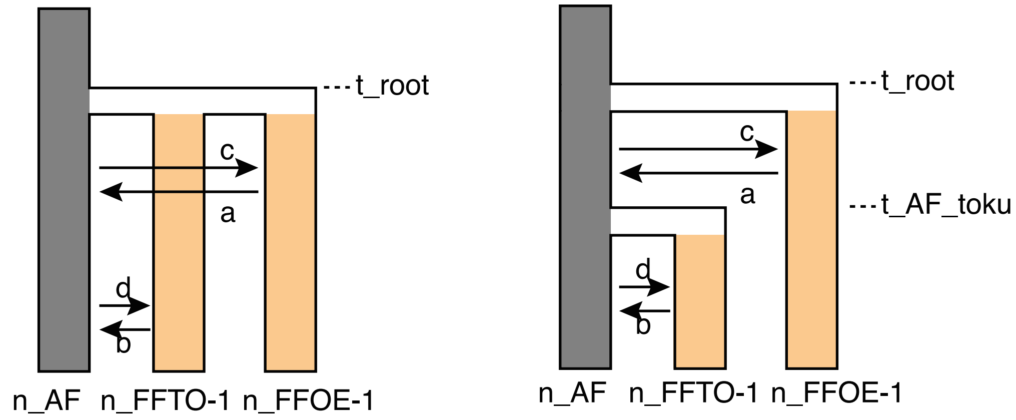




Model 1 (single origin, no gene flow)

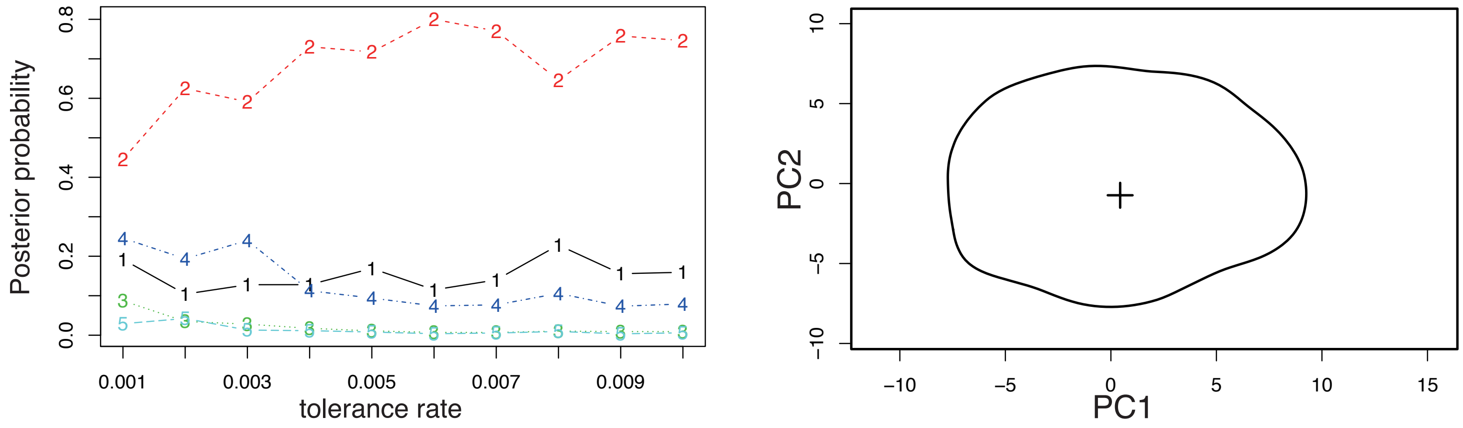
Model 2 (single origin, gene flow)

Model 3 (parallel origin, gene flow)



Model 4 (simultaneous divergence, gene flow)

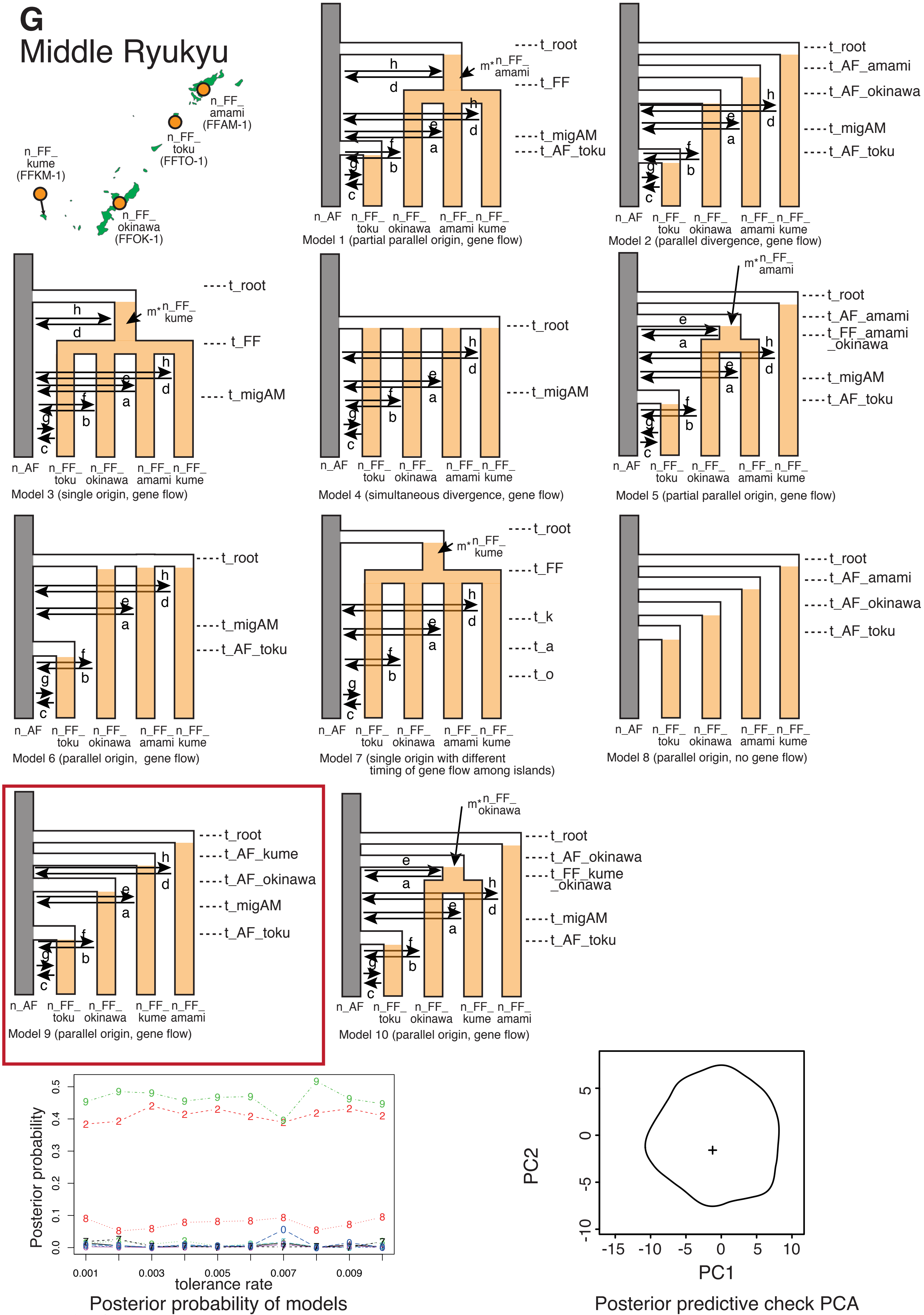
Model 5 (parallel origin, geneflow)



Posterior probability of models

Posterior predictive check PCA

Figure S4 Continued



Model 1 (partial parallel origin, gene flow)

Model 2 (parallel divergence, gene flow)

Model 3 (single origin, gene flow)

Model 4 (simultaneous divergence, gene flow)

Model 5 (partial parallel origin, gene flow)

Model 6 (parallel origin, gene flow)

Model 7 (single origin with different timing of gene flow among islands)

Model 8 (parallel origin, no gene flow)

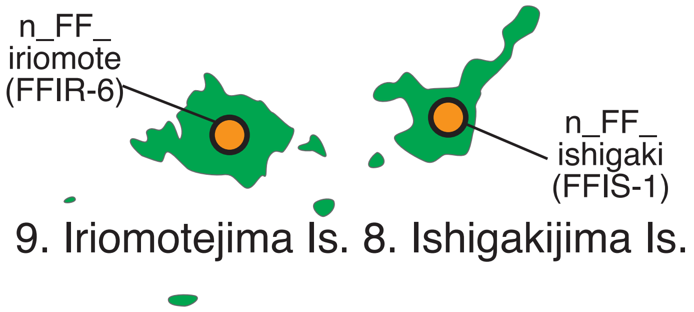
Model 9 (parallel origin, gene flow)

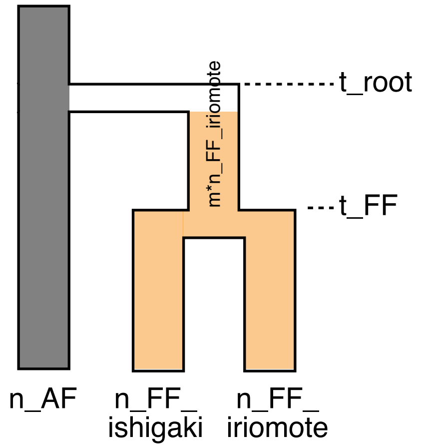
Model 10 (parallel origin, gene flow)

Figure S4 Continued

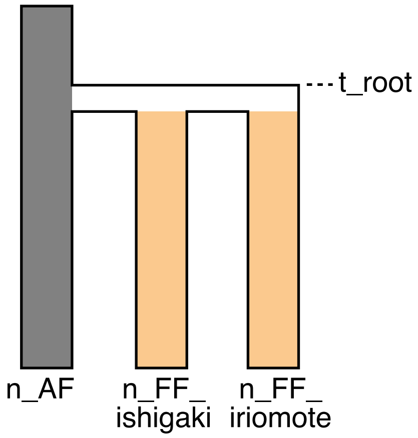
H

South Ryukyu

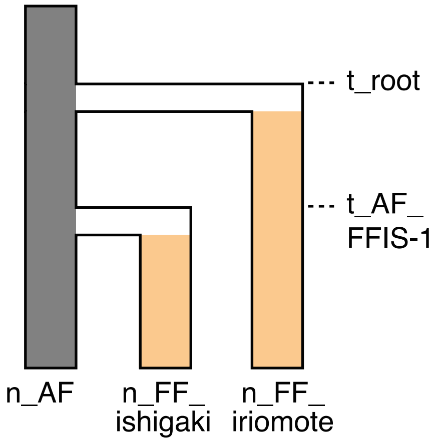




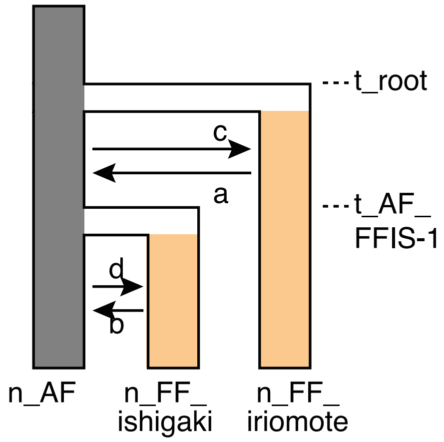
Model 1 (single origin, no gene flow)



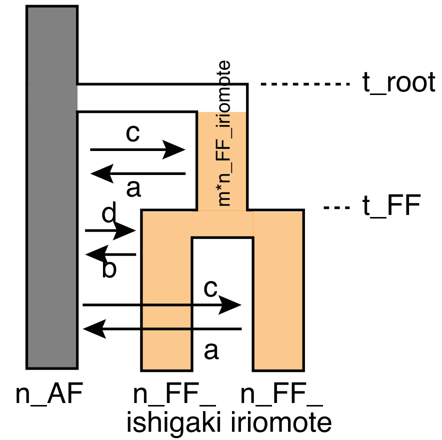
Model 2 (simultaneous divergence, no gene flow)



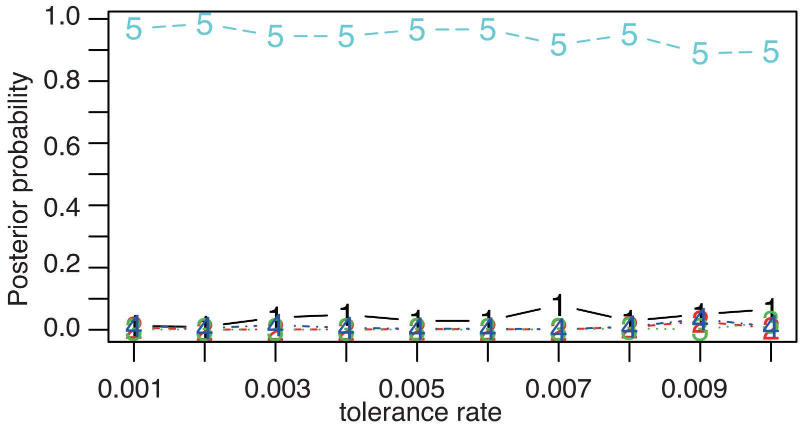
Model 3 (parallel origin, no gene flow)



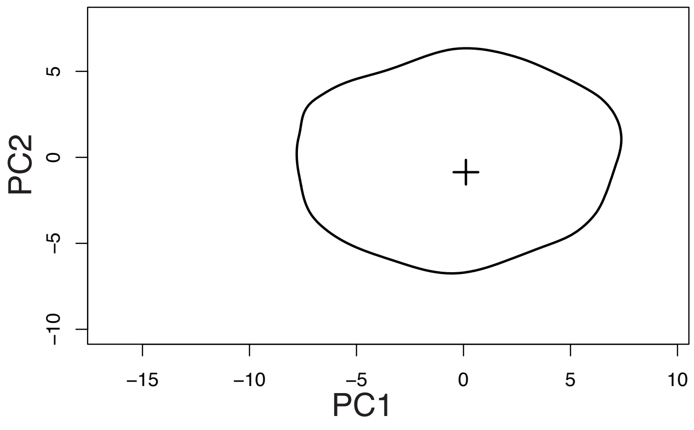
Model 4 (parallel origin, gene flow)



Model 5 (single origin, gene flow)



Posterior probability of models

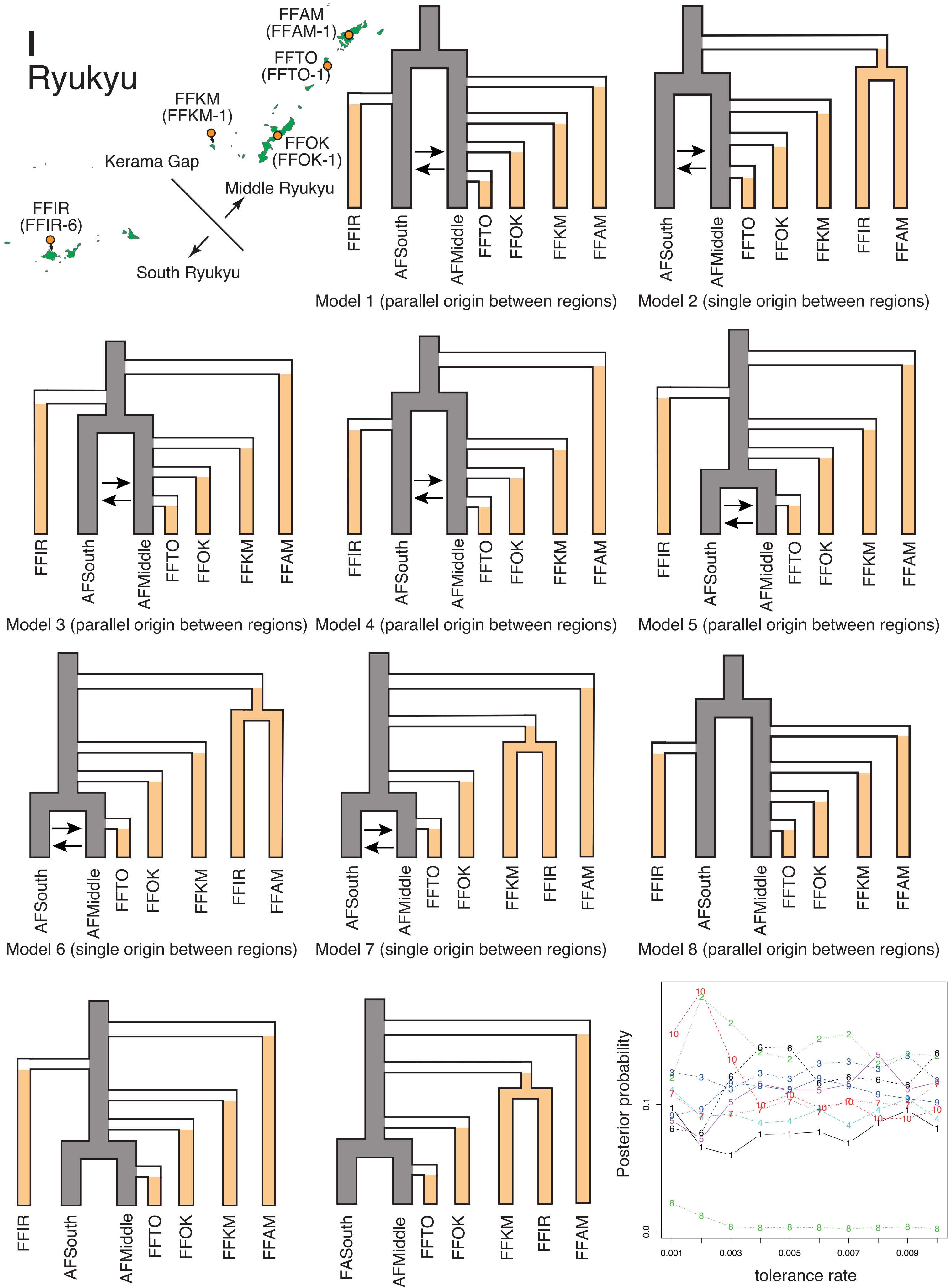


Posterior predictive check PCA

Figure S4 Continued

I

Ryukyu



Model 1 (parallel origin between regions)

Model 2 (single origin between regions)

Model 3 (parallel origin between regions)

Model 4 (parallel origin between regions)

Model 5 (parallel origin between regions)

Model 6 (single origin between regions)

Model 7 (single origin between regions)

Model 8 (parallel origin between regions)

Model 9 (parallel origin between regions)

Model 10 (single origin between regions)

Posterior probability of models

Parameters except gene flow between amphidromous form in Middle and South Ryukyu were omitted in this figure.

Figure S4 Continued

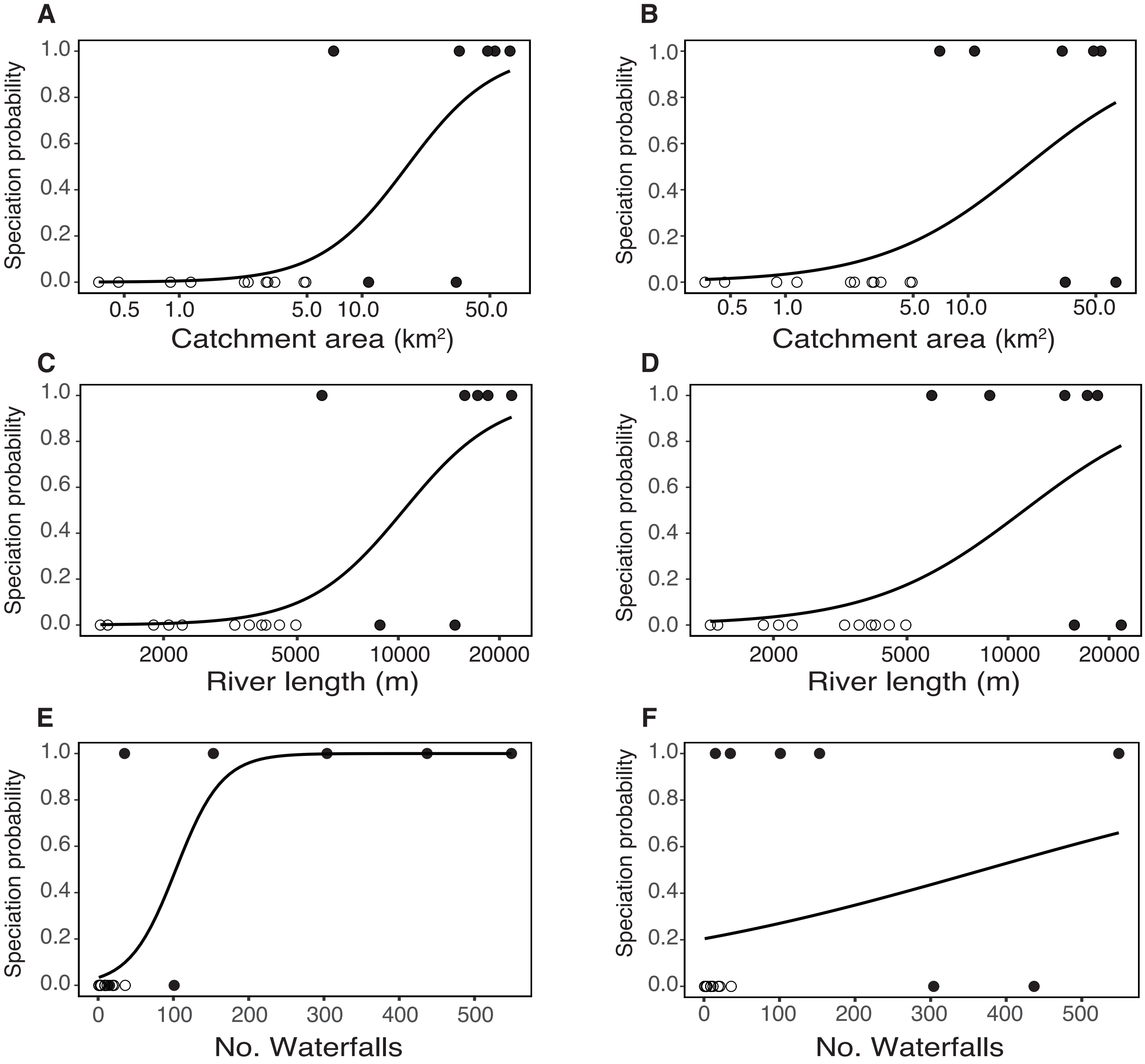


Figure S5 Results of logistic regression analysis between ecosystem size other than island size and speciation probability. Islands with the freshwater form (FF) are represented by filled circles, whereas those without FF are represented by open circles. Filled circles plotted on the x-axis (speciation probability = 0) are for the islands with FF that was assumed to be of non-independent origin. Our ABC analysis indicated that FF in Tokunoshima Is. and Okinoerabujima Is., and Ishigakijima Is. and Iriomotejima Is. shared their origins. Plots in the left colomun (A,C,E) assumed that the speciation of FF occurred in the larger island (Tokunoshima Is. and Iriomotejima Is.). Plots in the right colomun (B,D,F) assumed that speciation occurred in the smaller island (Okinoerabujima Is. and Ishigakijima Is.).

TableS1 Information about sampling point and summary statistics of each population.

Region	**Island**	**Form**	**River system**	**Point**	**Population Name**	**River length m**	**Catchment area ha**	**N**	**Ho**	**He**	**Rs**	**ABC**
Middle Ryukyu	Amami-Oshima	FF	Sumiyo	Sumiyo	FFAM-1	18478	4858	28	0.337	0.371	2.38575	Amami-Oshima/Middle Ryukyu/Ryukyu
			Akina	Akina	FFAM-2	9969	1135	16	0.228	0.235	2.6299	Amami-Oshima
			Kawauchi	Kawauchi	FFAM-3	12484	2817	31	0.239	0.234	1.65095	Amami-Oshima
			Asado	Asado-2	FFAM-4	13155	3238	30	0.128	0.181	2.77865	-
		AF	Asado	Asado-1	AFAM-1	13155	3238	29	0.507	0.507	3.5093	Amami-Oshima/Middle Ryukyu/Ryukyu
	Kikaijima	AF	Kikai-1	Kikai-1	AFKI-1	1859	69	11	0.495	0.514	3.3566	-
			Kikai-2	Kikai-2	AFKI-2	1825	56	10	0.438	0.489	3.5747	-
	Tokunoshima	FF	Akirigami	Akirigami-1	FFTO-1-1	15754	3400	26	0.312	0.325	2.70765	Tokunoshima/Tokunoshima-Okinoerabu/Middle Ryukyu/Ryukyu
				Akirigami-2	FFTO-1-2			18	0.304	0.323	2.74675	Tokunoshima/Tokunoshima-Okinoerabu/Middle Ryukyu/Ryukyu
				Akirigami-3	FFTO-1-3			9	0.3	0.323	2.61145	-
			Oose	Oose	FFTO-2	8262	886	19	0.25	0.254	2.74265	-
			Uwanaru	Uwanaru	FFTO-3	6791	403	24	0.253	0.262	2.68755	Tokunoshima
			Agon	Agon-1	FFTO-4-1	6958	492	24	0.3	0.311	2.0111	Tokunoshima
				Agon-2	FFTO-4-2			16	0.256	0.287	1.78625	Tokunoshima
			Shikaura	Shikaura	FFTO-5	9038	1184	7	0.279	0.298	1.7933	-
		AF	Manda	Manda	AFTO-1	8817	1361	32	0.51	0.522	3.5405	Tokunoshima/Tokunoshima-Okinoerabujima/Middle Ryukyu/Ryukyu
			Kametoku	Kametoku	AFTO-2	9034	969	19	0.526	0.539	3.49895	Tokunoshima/Tokunoshima-Okinoerabujima/Middle Ryukyu/Ryukyu
	Okinoerabujima	FF	Amata	Amata	FFOE-1	8813	10.8	34	0.2	0.227	1.94955	Tokunoshima-Okinoerabujima
	Okinawajima	FF	Sukuta	Sukuta-2	FFOK-1	5573	369	28	0.294	0.289	2.4092	Okinawajima/Middle Ryukyu/Ryukyu
			Yofuke	Yofuke	FFOK-2	4442	403	31	0.098	0.121	2.2433	Okinawajima
			Okukubi	Okukubi	FFOK-3	8967	1682	33	0.262	0.274	2.14875	Okinawajima
			Hija	Hija-1	FFOK-4-1	17218	5330	20	0.307	0.331	2.14305	-
				Hija-2	FFOK-4-2			8	0.296	0.293	2.07295	-
			Kyodafukuji	Kyodafukuj	FFOK-5	6445	479	32	0.169	0.176	2.35485	-
			Kushiookawa	Kushi	FFOK-6	5299	662	32	0.133	0.144	1.92765	-
		AF	Sukuta	Sukuta-1	AFOK-1			26	0.506	0.554	3.62115	Okinawajima/Middle Ryukyu/Ryukyu
			Yofuke	Yofuke	AFOK-2			25	0.533	0.542	3.55845	Okinawajima/Middle Ryukyu/Ryukyu
			Okukubi	Okukubi	AFOK-3			27	0.477	0.523	3.6047	-
			Hija	Hija-2	AFOK-4			6	0.475	0.493	3.16775	-
			Sate	Sade	AFOK-5	7213	670	36	0.517	0.526	3.5023	-
			Yona	Yona	AFOK-6	7700	1179	33	0.482	0.518	3.5941	-
	Kumejima	FF	Shirase	Shirase	FFKM-1	5925	699	31	0.241	0.274	1.9285	Kumejima/Middle Ryukyu/Ryukyu
			Suhara	Suhara	FFKM-2	3118	150	30	0.073	0.077	1.53105	Kumejima
		AF	Shirase	Shirase	AFKM-1			32	0.491	0.544	3.65115	Kumejima/Middle Ryukyu/ryukyu
			Suhara	Suhara	AFKM-2			32	0.494	0.52	3.5765	Kumejima
South Ryukyu	Ishigakijima	FF	Miyara	Sokohara	FFIS-1	14750	3275	28	0.234	0.301	2.64575	South Ryukyu
		AF	Arakawa	Arakawa	AFIS-1	2861	205	15	0.4	0.486	3.01515	South Ryukyu/Ryukyu
			Nagura	Nagura	AFIS-2	8423	1604	24	0.505	0.496	3.02725	South Ryukyu/Ryukyu
	Iriomotejima	FF	Pinai	Pinai	FFIR-1	4705	361	24	0.152	0.202	1.5609	Iriomotejima
			Kura	Kura	FFIR-2	2937	160	24	0.094	0.104	1.21535	-
			Geda	Geda-1	FFIR-3-1	2885	131	24	0.083	0.106	1.2767	-
				Geda-2	FFIR-3-2			32	0.078	0.07	1.24555	-
			Yuchin	YuchinR-1	FFIR-4-1	4266	498	13	0.233	0.248	2.6738	-
				YuchinR-2	FFIR-4-2			42	0.24	0.238	2.2249	-
				YuchinL	FFIR-5			24	0.103	0.118	1.62565	-
			Urauchi	Urauchi	FFIR-6	21736	6437	24	0.329	0.39	3.0796	Iriomotejima/South Ryukyu/Ryukyu
			Arabara	Arabara	FFIR-7	3697	179	25	0.181	0.194	1.8484	-
			Aira	Aira	FFIR-8	6130	557	46	0.289	0.305	2.9351	Iriomotejima
			Nishida	Nishida	FFIR-9	4759	476	9	0.3	0.299	2.74405	-
		AF	Geda	Geda-2	AFIR-1	4266	498	32	0.46	0.456	2.8527	Iriomotejima/South Ryukyu/Ryukyu
			Omija	Omija	AFIR-2	3395	227	24	0.508	0.502	3.1789	Iriomotejima/South Ryukyu/Ryukyu
			Yuchin	YuchinR-2	AFIR-3	4266	498	24	0.437	0.46	2.7118	-
			Nakama	Nakama	AFIR-4	15379	3355	27	0.437	0.466	2.9053	-
North Ryukyu	Yakushima	AF	Takinokawa	Nunobiki-1	AFYK-1-1	2000	70	34	0.426	0.457	2.97495	-
				Nunobiki-2	AFYK-1-2			27	0.417	0.456	3.07295	-
			Isso	Isso	AFYK-2	10521	1471	25	0.424	0.468	3.4101	-
Honshu	Honshu	AF	Esuno	Wakayama	AFHS-1			17	0.429	0.392	2.74215	-
			Betto	Kagawa-1	AFHS-2			5	0.31	0.296	2.6938	-
			Yoshida	Kagawa-2	AFHS-3			6	0.3	0.346	1.9406	-
Total			42 river syster	50 points	59 populations			**1420**				

Table S2 Primer pairs used in this study.

Locus name	Motif	Forward primer sequence (5' →3') for microsatellite analysis.	Reverse primer sequence (5' →3')	Tm value	Fluorescent	Size range (bp)	No. of alleles
Ohara et al (2004)							
Rhi-3	$(CA)_5(CA)_4(CA)_{10}$	GGATATTCTGTCTCTGTT	ATCTATTCCCTTTCTGTTTGTCT	53	6-FAM	131-163	9
Rhi-8	$(CA)_{18}$	ATACGCATAGTTTACCTTGA	CCTATGGTTTGAACTTGGGTGTG	53	HEX	155-195	8
Rhi-13	$(TG)_2(TG)_4(GT)_4$	GACTCGCCATCAAATACAAAAA	AGTCTCCTCCTCACCCGCACACC	53	NED	99-132	7
New loci (This study)							
br_a_02	（AC）$_{11}$	(GCCTTGCCAGCCCGC)ACTCCTAGCCTACAGCTCACTCG	GCGTCAATGCAGCACTATATTACC	63	VIC	82-126	22
br_a_05	（AC）$_{10}$	(GCCTCCCTCGCGCCA)CCACTCAAGGCATTCTCCAGTTT	ATGTTTCCTCTCACAACAATCGC	63	6-FAM	195-243	14
br_a_06	（AC）$_{9}$	(GCCTTGCCAGCCCGC)AACGTCATTATCAGATCCGCTCC	CTCCTAACTTGGCAATCACATGG	63	VIC	200-242	17
br_a_07	（AC）$_{12}$	(CAGGACCAGGCTACCGTG)AGTTCATCGATCCATTCACCAGA	CGTGGAGCTCTAAACAAGAGGTG	63	NED	174-226	14
br_a_08	（AC）$_{13}$	(CGGAGAGCCGAGAGGTG)GTTCGTCTTCATCCATCACCAGT	TAAGATTTGTGCAGATGCGAAGG	63	PET	194-252	17
br_a_09	（AC）$_{18}$	(GCCTCCCTCGCGCCA)CCAGCTGAACATGGTGTAGCTTT	TCTCAGCTGCCAGTGAACTGAAC	63	6-FAM	278-334	29
br_a_10	（AC）$_{11}$	(GCCTTGCCAGCCCGC)CGCTGTCAATCACGGTAAGAGTT	CCTATAAGCACGACCTCCATGTG	63	VIC	306-338	15
br_b_05	（AC）$_{12}$	(GCCTCCCTCGCGCCA) GGAGCGGAGTTGTTGTGTCTTAC	TGTCCCAAGATAGTGCACAAATG	63	6-FAM	182-280	45
br_b_06	（AC）$_{11}$	(GCCTTGCCAGCCCGC) ATCCTTAGGCCAACACAAAGCTC	TTAACCATATGCAAACCTCTCCC	63	VIC	190-243	22
br_c_01	（AC）$_{13}$	(GCCTCCCTCGCGCCA) TGCAGTGGTTGTGTTGAAAGGTA	CCTTGCACAGATGTGTCTTAGCAT	63	6-FAM	100-156	20
br_c_02	（AC）$_{10}$	(GCCTTGCCAGCCCGC) GACAGCAGCACACTCCTAAGCTC	CAGATCCAGATCCTCTGTTGACAT	63	VIC	111-135	8
br_c_05	（AC）$_{10}$	(GCCTCCCTCGCGCCA) TGGCTCTAGAACTCTTGATGATGG	GCACAGTATAGACGCTCTGCACAT	63	6-FAM	212-286	35
br_c_06	（AC）$_{10}$	(GCCTTGCCAGCCCGC) CTGAGCAGGACAGGAAGGAAATC	TGAATTGTTTGGACCATGAGACAG	63	VIC	195-283	39
br_c_07	（AC）$_{14}$	(CAGGACCAGGCTACCGTG) CCGTTTGACCGACTTCTTAAGGT	TTATCCTCACGCCTCCTTTCTTC	63	NED	209-251	17
br_c_08	（AC）$_{10}$	(CGGAGAGCCGAGAGGTG) TCTTGCATGACCACAATGTCAAC	AAGCTTGGTTTGTTTCCCTCTTG	63	PET	222-258	15
br_c_09	（AC）$_{10}$	(GCCTCCCTCGCGCCA) TCCCACCAAACTAAGCCACAATA	GCTCCTCTGATGGTACTTGCTCA	63	6-FAM	334-386	22
br_c_10	（AC）$_{11}$	(GCCTTGCCAGCCCGC) GACAGGAGCTCTGATCATCTCCA	CCACCATCCACCTCTATAACTCTTTC	63	VIC	340-380	17

The sequence in parentheses in forward primers indicate in tail sequence for universal fluorescent primers (Blacket et al., 2012).

Table S3 List of summary statistics used in ABC analysis.

Summary statistics	Abbreviation	Analysis the summary statistics used
Mean number of alleles over loci for each population	K_pop	All analysis
Standard deviation of Mean number of alleles over loci for each population	Ksd_pop	All analysis
Mean number of alleles over loci and population	MEAN_K	All analysis
Standard deviation of mean number of alleles over loci and population	SD_K	All analysis
Mean total number of alleles over loci	TOT_K	All analysis
Mean heterozygosity over loci for each population	H_pop	All analysis
Standard deviation of mean heterozygosity over loci for each population	Hsd_pop	All analysis
Mean heterozygosity over loci and population	MEAN_H	All analysis
Standard deviation of Mean heterozygosity over loci and population	SD_H	All analysis
Mean total heterozygosity	ALL_H	All analysis
Mean Graza–Williamson statistic over loci for each population	GW_pop	All analysis
Standard deviation of mean Graza–Williamson statistic over loci for each population	GWSD_pop	All analysis
Mean Graza–Williamson statistic over loci and population	MEAN_GW	All analysis
Standard deviation of mean Graza–Williamson statistic over loci and population	SD_GW	All analysis
Mean Graza–Williamson statistic over all populations	TOT_GW	All analysis
Mean modified Graza–Williamson statistic over loci for each population	NGW_pop	All analysis
Standard deviation of mean modified Graza–Williamson statistic over loci for each population	NGWSD_pop	All analysis
Mean modified Graza–Williamson statistic over loci and population	MEAN_NGW	All analysis
Standard deviation of mean modified Graza–Williamson statistic over loci and population	SD_NGW	All analysis
Global Fst	FST	All analysis
Global Fit	FIT	All analysis
Pairwise Fst	FST_pop1_pop2	All analysis
Mean number of pairwise differences over populations	PI_pop1_pop2	All analysis
Mean delta mu-square	DMUSQ_pop1_pop2	All analysis
Mean allele range over loci for each population	R_pop	Posterior predictive check only
Standard deviation of mean allele range over loci for each population	Rsd_pop	Posterior predictive check only
Mean allelic range over loci and populations	MEAN_R	Posterior predictive check only
Standard deviation of mean allelic range over loci and populations	MEAN_Rsd	Posterior predictive check only
Mean total allelic range over loci and populations	TOT_R	Posterior predictive check only
Global Fis	FIS	Posterior predictive check only

Table S4 Pairwise FST values.

						Amami-Oshima					Kikaijima		Tokunoshima										Okinoerabujima	Okinawajima													Kumejima				Ishigakijima			Iriomotejima															Yakushima			Honshu		
						FF				AF	AF		FF								AF		FF	FF							AF						FF		AF		FF	AF		FF											AF				AF			AF		
Region	**Island**	**species**	**River system**	**point**	**Population Name**	FFAM-1	FFAM-2	FFAM-3	FFAM-4	AFAM-1	AFKI-1	AFKI-2	FFTO-1-1	FFTO-1-2	FFTO-1-3	FFTO-2	FFTO-3	FFTO-4-1	FFTO-4-2	FFTO-5	AFTO-1	AFTO-2	FFOE-1	FFOK-1	FFOK-2	FFOK-3	FFOK-4-1	FFOK-4-2	FFOK-5	FFOK-6	AFOK-1	AFOK-2	AFOK-3	AFOK-4	AFOK-5	AFOK-6	FFKM-1	FFKM-2	AFKM-1	AFKM-2	FFIS-1	AFIS-1	AFIS-2	FFIR-1	FFIR-2	FFIR-3-1	FFIR-3-2	FFIR-4-1	FFIR-4-2	FFIR-5	FFIR-6	FFIR-7	FFIR-8	FFIR-9	AFIR-1	AFIR-2	AFIR-3	AFIR-4	AFYK-1-1	AFYK-1-2	AFYK-2	AFHS-1	AFHS-2	AFHS-3
Middle Ryukyu	Amami-Oshima	FF	Sumiyo	Sumiyo	FFAM-1	--	0.513	0.164	0.582	0.396	0.392	0.39	0.517	0.515	0.52	0.564	0.587	0.531	0.542	0.516	0.337	0.351	0.564	0.516	0.624	0.543	0.473	0.47	0.616	0.622	0.338	0.348	0.381	0.406	0.356	0.361	0.588	0.73	0.333	0.365	0.57	0.468	0.449	0.676	0.705	0.728	0.767	0.617	0.649	0.699	0.54	0.651	0.593	0.58	0.461	0.436	0.464	0.46	0.43	0.427	0.425	0.452	0.493	0.499
			Akina	Akina	FFAM-2	0.513	--	0.617	0.411	0.354	0.428	0.41	0.57	0.576	0.594	0.623	0.621	0.521	0.562	0.564	0.351	0.362	0.641	0.6	0.717	0.597	0.547	0.569	0.705	0.743	0.353	0.363	0.392	0.47	0.36	0.354	0.642	0.82	0.351	0.388	0.67	0.565	0.534	0.764	0.816	0.818	0.854	0.708	0.713	0.806	0.624	0.74	0.665	0.676	0.548	0.531	0.559	0.555	0.445	0.442	0.428	0.499	0.55	0.551
			Kawauchi	Kawauchi	FFAM-3	0.164	0.617	--	0.653	0.473	0.5	0.5	0.603	0.612	0.635	0.658	0.671	0.622	0.646	0.642	0.409	0.443	0.647	0.611	0.714	0.634	0.568	0.597	0.7	0.704	0.436	0.443	0.467	0.545	0.432	0.444	0.677	0.807	0.422	0.446	0.651	0.571	0.539	0.752	0.789	0.803	0.832	0.717	0.72	0.785	0.629	0.73	0.656	0.686	0.535	0.522	0.546	0.54	0.511	0.516	0.518	0.566	0.637	0.635
			Asado	Asado	FFAM-4	0.582	0.411	0.653	--	0.438	0.529	0.519	0.605	0.621	0.645	0.645	0.644	0.569	0.608	0.635	0.418	0.441	0.697	0.652	0.759	0.626	0.615	0.641	0.731	0.76	0.426	0.437	0.462	0.563	0.429	0.424	0.678	0.825	0.416	0.451	0.704	0.628	0.583	0.794	0.835	0.837	0.864	0.757	0.745	0.824	0.675	0.774	0.694	0.736	0.588	0.574	0.603	0.595	0.496	0.508	0.497	0.563	0.625	0.613
		AF	Asado	Asado	AFAM-1	0.396	0.354	0.473	0.438	--	0.105	0.096	0.339	0.318	0.294	0.362	0.356	0.308	0.341	0.276	0.089	0.085	0.38	0.365	0.48	0.387	0.293	0.276	0.467	0.527	0.12	0.123	0.128	0.127	0.104	0.105	0.461	0.613	0.165	0.168	0.506	0.366	0.367	0.597	0.636	0.652	0.693	0.52	0.577	0.626	0.463	0.578	0.531	0.479	0.391	0.361	0.391	0.391	0.206	0.198	0.186	0.25	0.269	0.28
	Kikaijima	AF	Kikai-1	Kikai-1	AFKI-1	0.392	0.428	0.5	0.529	0.105	--	0.046	0.325	0.304	0.278	0.37	0.369	0.29	0.319	0.24	0.045	0.042	0.351	0.369	0.553	0.4	0.284	0.268	0.516	0.587	0.047	0.046	0.045	0.059	0.022	0.038	0.495	0.708	0.1	0.116	0.506	0.347	0.343	0.629	0.693	0.709	0.764	0.534	0.597	0.675	0.444	0.609	0.535	0.472	0.371	0.333	0.365	0.36	0.156	0.154	0.143	0.238	0.268	0.27
			Kikai-2	Kikai-2	AFKI-2	0.39	0.41	0.5	0.519	0.096	0.046	--	0.335	0.319	0.295	0.392	0.37	0.273	0.332	0.248	0.057	0.048	0.379	0.386	0.561	0.404	0.285	0.269	0.544	0.626	0.057	0.061	0.068	0.072	0.049	0.05	0.489	0.712	0.104	0.121	0.532	0.368	0.361	0.65	0.72	0.732	0.785	0.563	0.622	0.701	0.467	0.633	0.554	0.503	0.39	0.349	0.385	0.384	0.182	0.171	0.152	0.245	0.256	0.269
	Tokunoshima	FF	Akirigami	Akirigami-1	FFTO-1-1	0.517	0.57	0.603	0.605	0.339	0.325	0.335	--	0.003	0.105	0.139	0.278	0.246	0.257	0.225	0.277	0.278	0.362	0.508	0.641	0.546	0.459	0.478	0.607	0.658	0.268	0.281	0.291	0.325	0.265	0.279	0.607	0.75	0.313	0.333	0.601	0.488	0.475	0.692	0.736	0.751	0.788	0.615	0.645	0.731	0.557	0.639	0.604	0.587	0.479	0.46	0.482	0.48	0.393	0.396	0.385	0.447	0.491	0.498
				Akirigami-2	FFTO-1-2	0.515	0.576	0.612	0.621	0.318	0.304	0.319	0.003	--	0.099	0.149	0.265	0.228	0.236	0.198	0.26	0.259	0.349	0.5	0.65	0.545	0.45	0.474	0.607	0.678	0.256	0.269	0.274	0.314	0.25	0.264	0.603	0.77	0.304	0.318	0.602	0.483	0.467	0.707	0.76	0.775	0.814	0.626	0.656	0.752	0.557	0.657	0.611	0.596	0.479	0.455	0.481	0.477	0.382	0.382	0.372	0.438	0.49	0.494
				Akirigami-3	FFTO-1-3	0.52	0.594	0.635	0.645	0.294	0.278	0.295	0.105	0.099	--	0.225	0.23	0.207	0.242	0.197	0.234	0.232	0.412	0.511	0.683	0.537	0.454	0.483	0.626	0.701	0.239	0.253	0.247	0.286	0.231	0.235	0.596	0.806	0.286	0.296	0.604	0.448	0.44	0.718	0.79	0.803	0.847	0.633	0.661	0.78	0.54	0.684	0.6	0.591	0.458	0.425	0.458	0.45	0.347	0.346	0.335	0.422	0.478	0.462
			Oose	Oose	FFTO-2	0.564	0.623	0.658	0.645	0.362	0.37	0.392	0.139	0.149	0.225	--	0.352	0.297	0.32	0.308	0.304	0.31	0.439	0.57	0.721	0.6	0.506	0.548	0.682	0.714	0.316	0.325	0.339	0.389	0.304	0.319	0.637	0.802	0.351	0.378	0.638	0.541	0.517	0.742	0.796	0.807	0.841	0.667	0.681	0.781	0.597	0.709	0.625	0.645	0.526	0.508	0.534	0.524	0.422	0.428	0.416	0.489	0.545	0.543
			Uwanaru	Uwanaru	FFTO-3	0.587	0.621	0.671	0.644	0.356	0.369	0.37	0.278	0.265	0.23	0.352	--	0.223	0.284	0.255	0.295	0.295	0.475	0.578	0.7	0.568	0.505	0.544	0.66	0.719	0.291	0.316	0.296	0.345	0.278	0.279	0.612	0.77	0.333	0.332	0.622	0.492	0.473	0.72	0.766	0.781	0.816	0.642	0.662	0.771	0.586	0.681	0.614	0.621	0.486	0.46	0.489	0.485	0.384	0.386	0.375	0.454	0.503	0.485
			Agon	Agon-1	FFTO-4-1	0.531	0.521	0.622	0.569	0.308	0.29	0.273	0.246	0.228	0.207	0.297	0.223	--	0.05	0.059	0.245	0.24	0.386	0.518	0.653	0.535	0.468	0.474	0.62	0.691	0.241	0.257	0.254	0.302	0.234	0.235	0.575	0.733	0.276	0.298	0.601	0.488	0.468	0.703	0.748	0.761	0.798	0.63	0.654	0.745	0.57	0.666	0.619	0.598	0.485	0.462	0.484	0.484	0.343	0.336	0.326	0.407	0.436	0.427
				Agon-2	FFTO-4-2	0.542	0.562	0.646	0.608	0.341	0.319	0.332	0.257	0.236	0.242	0.32	0.284	0.05	--	0.104	0.288	0.281	0.412	0.539	0.699	0.554	0.507	0.523	0.651	0.729	0.275	0.293	0.29	0.364	0.269	0.277	0.601	0.779	0.308	0.328	0.613	0.504	0.481	0.726	0.779	0.793	0.832	0.655	0.674	0.776	0.578	0.695	0.632	0.621	0.503	0.479	0.503	0.498	0.373	0.368	0.359	0.447	0.492	0.476
			Shikaura	Shikaura	FFTO-5	0.516	0.564	0.642	0.635	0.276	0.24	0.248	0.225	0.198	0.197	0.308	0.255	0.059	0.104	--	0.213	0.206	0.312	0.509	0.697	0.545	0.447	0.478	0.643	0.728	0.209	0.224	0.212	0.257	0.203	0.205	0.592	0.817	0.258	0.278	0.613	0.448	0.433	0.732	0.811	0.821	0.865	0.653	0.673	0.799	0.556	0.698	0.618	0.607	0.459	0.426	0.455	0.454	0.33	0.317	0.31	0.407	0.471	0.449
		AF	Manda	Manda	AFTO-1	0.337	0.351	0.409	0.418	0.089	0.045	0.057	0.277	0.26	0.234	0.304	0.295	0.245	0.288	0.213	--	-0.008	0.32	0.308	0.429	0.338	0.232	0.207	0.42	0.467	0.056	0.057	0.063	0.055	0.038	0.035	0.422	0.568	0.087	0.103	0.465	0.315	0.314	0.552	0.595	0.608	0.651	0.472	0.531	0.587	0.409	0.522	0.482	0.426	0.333	0.303	0.33	0.331	0.146	0.134	0.125	0.18	0.215	0.227
			Kametoku	Kametoku	AFTO-2	0.351	0.362	0.443	0.441	0.085	0.042	0.048	0.278	0.259	0.232	0.31	0.295	0.24	0.281	0.206	-0.008	--	0.351	0.325	0.48	0.347	0.237	0.212	0.453	0.517	0.046	0.053	0.057	0.054	0.031	0.028	0.429	0.611	0.08	0.094	0.477	0.313	0.312	0.575	0.627	0.64	0.691	0.486	0.553	0.62	0.411	0.553	0.494	0.436	0.334	0.301	0.329	0.329	0.134	0.122	0.11	0.168	0.198	0.205
	Okinoerabujima	FF	Amata	Amata	FFOE-1	0.564	0.641	0.647	0.697	0.38	0.351	0.379	0.362	0.349	0.412	0.439	0.475	0.386	0.412	0.312	0.32	0.351	--	0.57	0.685	0.582	0.521	0.559	0.664	0.719	0.307	0.32	0.307	0.41	0.299	0.311	0.645	0.785	0.386	0.405	0.659	0.553	0.527	0.742	0.78	0.8	0.829	0.688	0.69	0.77	0.621	0.712	0.653	0.667	0.536	0.518	0.547	0.54	0.476	0.475	0.473	0.549	0.609	0.611
	Okinawajima	FF	Sukuta	Sukuta	FFOK-1	0.516	0.6	0.611	0.652	0.365	0.369	0.386	0.508	0.5	0.511	0.57	0.578	0.518	0.539	0.509	0.308	0.325	0.57	--	0.367	0.463	0.431	0.475	0.233	0.554	0.298	0.311	0.31	0.377	0.303	0.307	0.596	0.749	0.318	0.32	0.626	0.542	0.51	0.709	0.759	0.773	0.807	0.677	0.694	0.749	0.594	0.708	0.651	0.636	0.529	0.504	0.534	0.526	0.395	0.395	0.404	0.453	0.507	0.529
			Yofuke	Yofuke	FFOK-2	0.624	0.717	0.714	0.759	0.48	0.553	0.561	0.641	0.65	0.683	0.721	0.7	0.653	0.699	0.697	0.429	0.48	0.685	0.367	--	0.602	0.589	0.671	0.445	0.673	0.451	0.456	0.445	0.596	0.43	0.437	0.7	0.859	0.457	0.463	0.756	0.676	0.633	0.821	0.869	0.873	0.894	0.815	0.787	0.861	0.717	0.82	0.74	0.79	0.634	0.624	0.653	0.64	0.544	0.553	0.557	0.642	0.75	0.744
			Okukubi	Okukubi	FFOK-3	0.543	0.597	0.634	0.626	0.387	0.4	0.404	0.546	0.545	0.537	0.6	0.568	0.535	0.554	0.545	0.338	0.347	0.582	0.463	0.602	--	0.408	0.426	0.567	0.634	0.318	0.328	0.267	0.405	0.319	0.316	0.59	0.727	0.357	0.351	0.642	0.52	0.503	0.693	0.715	0.757	0.79	0.664	0.676	0.729	0.572	0.7	0.644	0.645	0.524	0.506	0.537	0.528	0.434	0.439	0.437	0.498	0.553	0.552
			Hija	Hija-1	FFOK-4-1	0.473	0.547	0.568	0.615	0.293	0.284	0.285	0.459	0.45	0.454	0.506	0.505	0.468	0.507	0.447	0.232	0.237	0.521	0.431	0.589	0.408	--	0.144	0.558	0.615	0.251	0.25	0.24	0.272	0.233	0.246	0.541	0.681	0.259	0.271	0.558	0.418	0.411	0.674	0.726	0.738	0.78	0.605	0.636	0.709	0.507	0.645	0.576	0.583	0.432	0.402	0.428	0.427	0.366	0.363	0.351	0.421	0.466	0.472
				Hija-2	FFOK-4-2	0.47	0.569	0.597	0.641	0.276	0.268	0.269	0.478	0.474	0.483	0.548	0.544	0.474	0.523	0.478	0.207	0.212	0.559	0.475	0.671	0.426	0.144	--	0.625	0.694	0.235	0.231	0.225	0.259	0.219	0.225	0.562	0.762	0.231	0.251	0.594	0.432	0.428	0.729	0.796	0.813	0.858	0.667	0.684	0.782	0.538	0.705	0.622	0.622	0.45	0.419	0.45	0.446	0.333	0.323	0.317	0.389	0.478	0.461
			Kyodafukuji	Kyodafukuji	FFOK-5	0.616	0.705	0.7	0.731	0.467	0.516	0.544	0.607	0.607	0.626	0.682	0.66	0.62	0.651	0.643	0.42	0.453	0.664	0.233	0.445	0.567	0.558	0.625	--	0.641	0.421	0.434	0.427	0.545	0.414	0.418	0.663	0.813	0.452	0.437	0.711	0.639	0.601	0.786	0.834	0.838	0.863	0.773	0.76	0.826	0.684	0.788	0.713	0.753	0.604	0.59	0.619	0.608	0.482	0.485	0.496	0.563	0.653	0.659
			Kushi	Kushi	FFOK-6	0.622	0.743	0.704	0.76	0.527	0.587	0.626	0.658	0.678	0.701	0.714	0.719	0.691	0.729	0.728	0.467	0.517	0.719	0.554	0.673	0.634	0.615	0.694	0.641	--	0.496	0.507	0.513	0.633	0.489	0.5	0.715	0.854	0.493	0.51	0.719	0.634	0.607	0.78	0.838	0.844	0.869	0.775	0.752	0.833	0.675	0.779	0.702	0.746	0.602	0.594	0.618	0.604	0.551	0.567	0.577	0.652	0.746	0.732
		AF	Sukuta	Sukuta	AFOK-1	0.338	0.353	0.436	0.426	0.12	0.047	0.057	0.268	0.256	0.239	0.316	0.291	0.241	0.275	0.209	0.056	0.046	0.307	0.298	0.451	0.318	0.251	0.235	0.421	0.496	--	-0.001	0.029	0.011	0.017	0.012	0.428	0.589	0.061	0.073	0.443	0.307	0.304	0.537	0.57	0.602	0.65	0.454	0.523	0.566	0.387	0.516	0.467	0.406	0.328	0.288	0.317	0.319	0.141	0.138	0.123	0.179	0.184	0.207
			Yofuke	Yofuke	AFOK-2	0.348	0.363	0.443	0.437	0.123	0.046	0.061	0.281	0.269	0.253	0.325	0.316	0.257	0.293	0.224	0.057	0.053	0.32	0.311	0.456	0.328	0.25	0.231	0.434	0.507	-0.001	--	0.032	0.008	0.017	0.014	0.428	0.595	0.059	0.071	0.456	0.322	0.319	0.548	0.586	0.614	0.661	0.473	0.538	0.578	0.396	0.535	0.478	0.419	0.341	0.302	0.331	0.333	0.149	0.146	0.131	0.195	0.203	0.22
			Okukubi	Okukubi	AFOK-3	0.381	0.392	0.467	0.462	0.128	0.045	0.068	0.291	0.274	0.247	0.339	0.296	0.254	0.29	0.212	0.063	0.057	0.307	0.31	0.445	0.267	0.24	0.225	0.427	0.513	0.029	0.032	--	0.04	0.015	0.016	0.444	0.597	0.093	0.095	0.476	0.324	0.324	0.551	0.586	0.619	0.665	0.474	0.537	0.581	0.408	0.529	0.498	0.421	0.351	0.315	0.346	0.345	0.174	0.168	0.156	0.227	0.245	0.255
			Hija	Hija	AFOK-4	0.406	0.47	0.545	0.563	0.127	0.059	0.072	0.325	0.314	0.286	0.389	0.345	0.302	0.364	0.257	0.055	0.054	0.41	0.377	0.596	0.405	0.272	0.259	0.545	0.633	0.011	0.008	0.04	--	0.018	0.009	0.511	0.755	0.073	0.083	0.524	0.32	0.327	0.634	0.729	0.747	0.805	0.553	0.61	0.712	0.426	0.627	0.512	0.485	0.355	0.31	0.347	0.345	0.159	0.156	0.139	0.225	0.252	0.258
			Sade	Sade	AFOK-5	0.356	0.36	0.432	0.429	0.104	0.022	0.049	0.265	0.25	0.231	0.304	0.278	0.234	0.269	0.203	0.038	0.031	0.299	0.303	0.43	0.319	0.233	0.219	0.414	0.489	0.017	0.017	0.015	0.018	--	-0.001	0.427	0.568	0.067	0.073	0.451	0.317	0.318	0.534	0.566	0.594	0.635	0.461	0.519	0.56	0.394	0.509	0.471	0.41	0.339	0.305	0.333	0.332	0.136	0.131	0.119	0.189	0.199	0.212
			Yona	Yona	AFOK-6	0.361	0.354	0.444	0.424	0.105	0.038	0.05	0.279	0.264	0.235	0.319	0.279	0.235	0.277	0.205	0.035	0.028	0.311	0.307	0.437	0.316	0.246	0.225	0.418	0.5	0.012	0.014	0.016	0.009	-0.001	--	0.426	0.578	0.072	0.075	0.465	0.325	0.323	0.544	0.579	0.607	0.649	0.472	0.532	0.57	0.406	0.523	0.48	0.426	0.343	0.308	0.337	0.338	0.136	0.13	0.116	0.183	0.19	0.206
	Kumejima	FF	Shirase	Shirase	FFKM-1	0.588	0.642	0.677	0.678	0.461	0.495	0.489	0.607	0.603	0.596	0.637	0.612	0.575	0.601	0.592	0.422	0.429	0.645	0.596	0.7	0.59	0.541	0.562	0.663	0.715	0.428	0.428	0.444	0.511	0.427	0.426	--	0.535	0.438	0.448	0.643	0.546	0.517	0.729	0.773	0.781	0.811	0.698	0.708	0.748	0.583	0.709	0.644	0.659	0.536	0.509	0.539	0.535	0.479	0.473	0.47	0.533	0.568	0.545
			Suhara	Suhara	FFKM-2	0.73	0.82	0.807	0.825	0.613	0.708	0.712	0.75	0.77	0.806	0.802	0.77	0.733	0.779	0.817	0.568	0.611	0.785	0.749	0.859	0.727	0.681	0.762	0.813	0.854	0.589	0.595	0.597	0.755	0.568	0.578	0.535	--	0.565	0.578	0.761	0.683	0.641	0.842	0.893	0.895	0.914	0.838	0.793	0.882	0.714	0.833	0.746	0.832	0.643	0.635	0.66	0.65	0.608	0.617	0.615	0.702	0.821	0.786
		AF	Shirase	Shirase	AFKM-1	0.333	0.351	0.422	0.416	0.165	0.1	0.104	0.313	0.304	0.286	0.351	0.333	0.276	0.308	0.258	0.087	0.08	0.386	0.318	0.457	0.357	0.259	0.231	0.452	0.493	0.061	0.059	0.093	0.073	0.067	0.072	0.438	0.565	--	0.022	0.432	0.31	0.306	0.528	0.56	0.589	0.633	0.453	0.515	0.555	0.375	0.5	0.454	0.389	0.325	0.287	0.314	0.317	0.155	0.153	0.137	0.185	0.18	0.201
			Suhara	Suhara	AFKM-2	0.365	0.388	0.446	0.451	0.168	0.116	0.121	0.333	0.318	0.296	0.378	0.332	0.298	0.328	0.278	0.103	0.094	0.405	0.32	0.463	0.351	0.271	0.251	0.437	0.51	0.073	0.071	0.095	0.083	0.073	0.075	0.448	0.578	0.022	--	0.449	0.327	0.323	0.542	0.573	0.599	0.642	0.465	0.525	0.578	0.396	0.519	0.47	0.408	0.344	0.305	0.335	0.337	0.158	0.157	0.144	0.198	0.201	0.217
South Ryukyu	Ishigakijima	FF		Sokohara	FFIS-1	0.57	0.67	0.651	0.704	0.506	0.506	0.532	0.601	0.602	0.604	0.638	0.622	0.601	0.613	0.613	0.465	0.477	0.659	0.626	0.756	0.642	0.558	0.594	0.711	0.719	0.443	0.456	0.476	0.524	0.451	0.465	0.643	0.761	0.432	0.449	--	0.391	0.364	0.637	0.697	0.716	0.755	0.617	0.64	0.686	0.497	0.632	0.549	0.571	0.393	0.369	0.384	0.367	0.502	0.509	0.508	0.559	0.592	0.575
		AF	Arakawa	Arakawa	AFIS-1	0.468	0.565	0.571	0.628	0.366	0.347	0.368	0.488	0.483	0.448	0.541	0.492	0.488	0.504	0.448	0.315	0.313	0.553	0.542	0.676	0.52	0.418	0.432	0.639	0.634	0.307	0.322	0.324	0.32	0.317	0.325	0.546	0.683	0.31	0.327	0.391	--	0.079	0.483	0.497	0.538	0.606	0.42	0.473	0.549	0.305	0.477	0.384	0.361	0.086	0.078	0.086	0.082	0.383	0.38	0.374	0.43	0.452	0.434
			Nagura	Nagura	AFIS-2	0.449	0.534	0.539	0.583	0.367	0.343	0.361	0.475	0.467	0.44	0.517	0.473	0.468	0.481	0.433	0.314	0.312	0.527	0.51	0.633	0.503	0.411	0.428	0.601	0.607	0.304	0.319	0.324	0.327	0.318	0.323	0.517	0.641	0.306	0.323	0.364	0.079	--	0.526	0.552	0.571	0.624	0.467	0.522	0.565	0.361	0.498	0.423	0.419	0.051	0.043	0.059	0.05	0.37	0.366	0.364	0.402	0.425	0.409
	Iriomotejima	FF	Pinai	Pinai	FFIR-1	0.676	0.764	0.752	0.794	0.597	0.629	0.65	0.692	0.707	0.718	0.742	0.72	0.703	0.726	0.732	0.552	0.575	0.742	0.709	0.821	0.693	0.674	0.729	0.786	0.78	0.537	0.548	0.551	0.634	0.534	0.544	0.729	0.842	0.528	0.542	0.637	0.483	0.526	--	0.617	0.546	0.594	0.532	0.528	0.651	0.299	0.6	0.454	0.541	0.522	0.505	0.527	0.517	0.584	0.598	0.599	0.655	0.721	0.696
			Kura	Kura	FFIR-2	0.705	0.816	0.789	0.835	0.636	0.693	0.72	0.736	0.76	0.79	0.796	0.766	0.748	0.779	0.811	0.595	0.627	0.78	0.759	0.869	0.715	0.726	0.796	0.834	0.838	0.57	0.586	0.586	0.729	0.566	0.579	0.773	0.893	0.56	0.573	0.697	0.497	0.552	0.617	--	0.733	0.784	0.592	0.505	0.679	0.471	0.695	0.534	0.624	0.543	0.532	0.556	0.539	0.628	0.648	0.65	0.718	0.817	0.791
			Geda	Geda-1	FFIR-3-1	0.728	0.818	0.803	0.837	0.652	0.709	0.732	0.751	0.775	0.803	0.807	0.781	0.761	0.793	0.821	0.608	0.64	0.8	0.773	0.873	0.757	0.738	0.813	0.838	0.844	0.602	0.614	0.619	0.747	0.594	0.607	0.781	0.895	0.589	0.599	0.716	0.538	0.571	0.546	0.733	--	0.016	0.619	0.557	0.766	0.454	0.683	0.546	0.643	0.564	0.559	0.581	0.567	0.642	0.662	0.663	0.736	0.829	0.804
				Geda-2	FFIR-3-2	0.767	0.854	0.832	0.864	0.693	0.764	0.785	0.788	0.814	0.847	0.841	0.816	0.798	0.832	0.865	0.651	0.691	0.829	0.807	0.894	0.79	0.78	0.858	0.863	0.869	0.65	0.661	0.665	0.805	0.635	0.649	0.811	0.914	0.633	0.642	0.755	0.606	0.624	0.594	0.784	0.016	--	0.682	0.595	0.804	0.503	0.734	0.584	0.714	0.61	0.611	0.633	0.617	0.681	0.704	0.707	0.78	0.874	0.853
			Yuchin	YuchinR-1	FFIR-4-1	0.617	0.708	0.717	0.757	0.52	0.534	0.563	0.615	0.626	0.633	0.667	0.642	0.63	0.655	0.653	0.472	0.486	0.688	0.677	0.815	0.664	0.605	0.667	0.773	0.775	0.454	0.473	0.474	0.553	0.461	0.472	0.698	0.838	0.453	0.465	0.617	0.42	0.467	0.532	0.592	0.619	0.682	--	0.039	0.588	0.282	0.468	0.446	0.294	0.479	0.457	0.486	0.474	0.525	0.536	0.53	0.603	0.672	0.646
				YuchinR-2	FFIR-4-2	0.649	0.713	0.72	0.745	0.577	0.597	0.622	0.645	0.656	0.661	0.681	0.662	0.654	0.674	0.673	0.531	0.553	0.69	0.694	0.787	0.676	0.636	0.684	0.76	0.752	0.523	0.538	0.537	0.61	0.519	0.532	0.708	0.793	0.515	0.525	0.64	0.473	0.522	0.528	0.505	0.557	0.595	0.039	--	0.531	0.332	0.472	0.473	0.33	0.524	0.514	0.537	0.523	0.576	0.589	0.587	0.644	0.692	0.675
				YuchinL	FFIR-5	0.699	0.806	0.785	0.824	0.626	0.675	0.701	0.731	0.752	0.78	0.781	0.771	0.745	0.776	0.799	0.587	0.62	0.77	0.749	0.861	0.729	0.709	0.782	0.826	0.833	0.566	0.578	0.581	0.712	0.56	0.57	0.748	0.882	0.555	0.578	0.686	0.549	0.565	0.651	0.679	0.766	0.804	0.588	0.531	--	0.373	0.684	0.504	0.628	0.565	0.55	0.582	0.557	0.626	0.644	0.645	0.715	0.812	0.79
			Urauchi	Urauchi	FFIR-6	0.54	0.624	0.629	0.675	0.463	0.444	0.467	0.557	0.557	0.54	0.597	0.586	0.57	0.578	0.556	0.409	0.411	0.621	0.594	0.717	0.572	0.507	0.538	0.684	0.675	0.387	0.396	0.408	0.426	0.394	0.406	0.583	0.714	0.375	0.396	0.497	0.305	0.361	0.299	0.471	0.454	0.503	0.282	0.332	0.373	--	0.382	0.292	0.271	0.377	0.344	0.369	0.358	0.45	0.455	0.452	0.498	0.53	0.509
			Arabara	Arabara	FFIR-7	0.651	0.74	0.73	0.774	0.578	0.609	0.633	0.639	0.657	0.684	0.709	0.681	0.666	0.695	0.698	0.522	0.553	0.712	0.708	0.82	0.7	0.645	0.705	0.788	0.779	0.516	0.535	0.529	0.627	0.509	0.523	0.709	0.833	0.5	0.519	0.632	0.477	0.498	0.6	0.695	0.683	0.734	0.468	0.472	0.684	0.382	--	0.52	0.421	0.498	0.485	0.506	0.501	0.577	0.589	0.592	0.653	0.72	0.703
			Aira	Aira	FFIR-8	0.593	0.665	0.656	0.694	0.531	0.535	0.554	0.604	0.611	0.6	0.625	0.614	0.619	0.632	0.618	0.482	0.494	0.653	0.651	0.74	0.644	0.576	0.622	0.713	0.702	0.467	0.478	0.498	0.512	0.471	0.48	0.644	0.746	0.454	0.47	0.549	0.384	0.423	0.454	0.534	0.546	0.584	0.446	0.473	0.504	0.292	0.52	--	0.473	0.425	0.394	0.421	0.408	0.513	0.52	0.518	0.565	0.595	0.578
			Nishida	Nishida	FFIR-9	0.58	0.676	0.686	0.736	0.479	0.472	0.503	0.587	0.596	0.591	0.645	0.621	0.598	0.621	0.607	0.426	0.436	0.667	0.636	0.79	0.645	0.583	0.622	0.753	0.746	0.406	0.419	0.421	0.485	0.41	0.426	0.659	0.832	0.389	0.408	0.571	0.361	0.419	0.541	0.624	0.643	0.714	0.294	0.33	0.628	0.271	0.421	0.473	--	0.43	0.401	0.434	0.421	0.484	0.492	0.487	0.561	0.624	0.592
		AF	Geda	Geda-2	AFIR-1	0.461	0.548	0.535	0.588	0.391	0.371	0.39	0.479	0.479	0.458	0.526	0.486	0.485	0.503	0.459	0.333	0.334	0.536	0.529	0.634	0.524	0.432	0.45	0.604	0.602	0.328	0.341	0.351	0.355	0.339	0.343	0.536	0.643	0.325	0.344	0.393	0.086	0.051	0.522	0.543	0.564	0.61	0.479	0.524	0.565	0.377	0.498	0.425	0.43	--	0.007	0.006	-0.001	0.391	0.39	0.388	0.432	0.456	0.443
			Omija	Omija	AFIR-2	0.436	0.531	0.522	0.574	0.361	0.333	0.349	0.46	0.455	0.425	0.508	0.46	0.462	0.479	0.426	0.303	0.301	0.518	0.504	0.624	0.506	0.402	0.419	0.59	0.594	0.288	0.302	0.315	0.31	0.305	0.308	0.509	0.635	0.287	0.305	0.369	0.078	0.043	0.505	0.532	0.559	0.611	0.457	0.514	0.55	0.344	0.485	0.394	0.401	0.007	--	0	0	0.354	0.353	0.35	0.394	0.415	0.401
			Yuchin	YuchinR2	AFIR-3	0.464	0.559	0.546	0.603	0.391	0.365	0.385	0.482	0.481	0.458	0.534	0.489	0.484	0.503	0.455	0.33	0.329	0.547	0.534	0.653	0.537	0.428	0.45	0.619	0.618	0.317	0.331	0.346	0.347	0.333	0.337	0.539	0.66	0.314	0.335	0.384	0.086	0.059	0.527	0.556	0.581	0.633	0.486	0.537	0.582	0.369	0.506	0.421	0.434	0.006	0	--	-0.002	0.381	0.381	0.378	0.424	0.449	0.433
			Nakama	Nakama	AFIR-4	0.46	0.555	0.54	0.595	0.391	0.36	0.384	0.48	0.477	0.45	0.524	0.485	0.484	0.498	0.454	0.331	0.329	0.54	0.526	0.64	0.528	0.427	0.446	0.608	0.604	0.319	0.333	0.345	0.345	0.332	0.338	0.535	0.65	0.317	0.337	0.367	0.082	0.05	0.517	0.539	0.567	0.617	0.474	0.523	0.557	0.358	0.501	0.408	0.421	-0.001	0	-0.002	--	0.38	0.38	0.377	0.424	0.448	0.433
North Ryukyu	Yakushima	AF	Takinokawa	Nunobiki-1	AFYK-1-1	0.43	0.445	0.511	0.496	0.206	0.156	0.182	0.393	0.382	0.347	0.422	0.384	0.343	0.373	0.33	0.146	0.134	0.476	0.395	0.544	0.434	0.366	0.333	0.482	0.551	0.141	0.149	0.174	0.159	0.136	0.136	0.479	0.608	0.155	0.158	0.502	0.383	0.37	0.584	0.628	0.642	0.681	0.525	0.576	0.626	0.45	0.577	0.513	0.484	0.391	0.354	0.381	0.38	--	-0.002	0.004	0.084	0.147	0.129
				Nunobiki-2	AFYK-1-2	0.427	0.442	0.516	0.508	0.198	0.154	0.171	0.396	0.382	0.346	0.428	0.386	0.336	0.368	0.317	0.134	0.122	0.475	0.395	0.553	0.439	0.363	0.323	0.485	0.567	0.138	0.146	0.168	0.156	0.131	0.13	0.473	0.617	0.153	0.157	0.509	0.38	0.366	0.598	0.648	0.662	0.704	0.536	0.589	0.644	0.455	0.589	0.52	0.492	0.39	0.353	0.381	0.38	-0.002	--	-0.001	0.078	0.133	0.113
			Isso	Isso	AFYK-2	0.425	0.428	0.518	0.497	0.186	0.143	0.152	0.385	0.372	0.335	0.416	0.375	0.326	0.359	0.31	0.125	0.11	0.473	0.404	0.557	0.437	0.351	0.317	0.496	0.577	0.123	0.131	0.156	0.139	0.119	0.116	0.47	0.615	0.137	0.144	0.508	0.374	0.364	0.599	0.65	0.663	0.707	0.53	0.587	0.645	0.452	0.592	0.518	0.487	0.388	0.35	0.378	0.377	0.004	-0.001	--	0.068	0.12	0.111
Honshu	Honshu	AF	Esuno	Wakayama	AFHS-1	0.452	0.499	0.566	0.563	0.25	0.238	0.245	0.447	0.438	0.422	0.489	0.454	0.407	0.447	0.407	0.18	0.168	0.549	0.453	0.642	0.498	0.421	0.389	0.563	0.652	0.179	0.195	0.227	0.225	0.189	0.183	0.533	0.702	0.185	0.198	0.559	0.43	0.402	0.655	0.718	0.736	0.78	0.603	0.644	0.715	0.498	0.653	0.565	0.561	0.432	0.394	0.424	0.424	0.084	0.078	0.068	--	0.121	0.145
			Betto	Kagawa-1	AFHS-2	0.493	0.55	0.637	0.625	0.269	0.268	0.256	0.491	0.49	0.478	0.545	0.503	0.436	0.492	0.471	0.215	0.198	0.609	0.507	0.75	0.553	0.466	0.478	0.653	0.746	0.184	0.203	0.245	0.252	0.199	0.19	0.568	0.821	0.18	0.201	0.592	0.452	0.425	0.721	0.817	0.829	0.874	0.672	0.692	0.812	0.53	0.72	0.595	0.624	0.456	0.415	0.449	0.448	0.147	0.133	0.12	0.121	--	0.019
			Yoshida	Kagawa-2	AFHS-3	0.499	0.551	0.635	0.613	0.28	0.27	0.269	0.498	0.494	0.462	0.543	0.485	0.427	0.476	0.449	0.227	0.205	0.611	0.529	0.744	0.552	0.472	0.461	0.659	0.732	0.207	0.22	0.255	0.258	0.212	0.206	0.545	0.786	0.201	0.217	0.575	0.434	0.409	0.696	0.791	0.804	0.853	0.646	0.675	0.79	0.509	0.703	0.578	0.592	0.443	0.401	0.433	0.433	0.129	0.113	0.111	0.145	0.019	--

ble S5 Pairwise Jost'D values.

						Amami-Oshima					Kikaijima		Tokunoshima										Okinoerabujima	Okinawajima													Kumejima				Ishigakijima			Iriomotejima															Yakushima			Honshu		
						FF				AF	AF		FF								AF		FF	FF							AF						FF		AF		FF	AF		FF											AF				AF			AF		
Region	Island	species	River system	point	Population Name	FFAM-1	FFAM-2	FFAM-3	FFAM-4	AFAM-1	AFKI-1	AFKI-2	FFTO-1-1	FFTO-1-2	FFTO-1-3	FFTO-2	FFTO-3	FFTO-4-1	FFTO-4-2	FFTO-5	AFTO-1	AFTO-2	FFOE-1	FFOK-1	FFOK-2	FFOK-3	FFOK-4-1	FFOK-4-2	FFOK-5	FFOK-6	AFOK-1	AFOK-2	AFOK-3	AFOK-4	AFOK-5	AFOK-6	FFKM-1	FFKM-2	AFKM-1	AFKM-2	FFIS-1	AFIS-1	AFIS-2	FFIR-1	FFIR-2	FFIR-3-1	FFIR-3-2	FFIR-4-1	FFIR-4-2	FFIR-5	FFIR-6	FFIR-7	FFIR-8	FFIR-9	AFIR-1	AFIR-2	AFIR-3	AFIR-4	AFYK-1-1	AFYK-1-2	AFYK-2	AFHS-1	AFHS-2	AFHS-3
Middle Ryukyu	Amami-Oshima	FF	Sumiyo	Sumiyo	FFAM-1	0.000	0.486	0.084	0.529	0.514	0.472	0.448	0.573	0.574	0.599	0.611	0.668	0.590	0.600	0.575	0.416	0.435	0.539	0.520	0.522	0.558	0.490	0.474	0.582	0.551	0.437	0.444	0.495	0.468	0.461	0.458	0.675	0.757	0.428	0.468	0.669	0.631	0.617	0.855	0.771	0.868	0.877	0.774	0.766	0.778	0.718	0.746	0.725	0.736	0.608	0.592	0.610	0.611	0.538	0.525	0.529	0.506	0.533	0.571
			Akina	Akina	FFAM-2	0.486	0.000	0.491	0.178	0.360	0.411	0.359	0.536	0.530	0.538	0.537	0.547	0.421	0.453	0.445	0.374	0.371	0.534	0.547	0.491	0.519	0.486	0.453	0.585	0.621	0.392	0.395	0.432	0.414	0.400	0.376	0.630	0.706	0.394	0.437	0.768	0.720	0.709	0.890	0.830	0.851	0.859	0.769	0.770	0.832	0.791	0.760	0.781	0.732	0.712	0.713	0.721	0.733	0.475	0.455	0.434	0.459	0.413	0.452
			Kawauchi	Kawauchi	FFAM-3	0.084	0.491	0.000	0.502	0.522	0.482	0.455	0.580	0.582	0.608	0.614	0.667	0.605	0.620	0.595	0.424	0.451	0.548	0.550	0.539	0.590	0.498	0.492	0.598	0.553	0.484	0.482	0.517	0.503	0.479	0.486	0.713	0.778	0.467	0.489	0.675	0.649	0.638	0.854	0.799	0.872	0.879	0.794	0.793	0.815	0.741	0.744	0.724	0.738	0.610	0.605	0.611	0.616	0.559	0.548	0.557	0.548	0.575	0.608
			Asado	Asado	FFAM-4	0.529	0.178	0.502	0.000	0.414	0.462	0.417	0.512	0.514	0.524	0.480	0.497	0.422	0.441	0.466	0.403	0.401	0.581	0.575	0.566	0.505	0.522	0.479	0.596	0.595	0.423	0.428	0.461	0.447	0.437	0.413	0.630	0.688	0.419	0.457	0.745	0.725	0.693	0.890	0.835	0.853	0.859	0.778	0.778	0.809	0.788	0.767	0.774	0.745	0.689	0.679	0.693	0.704	0.485	0.484	0.461	0.474	0.434	0.446
		AF	Asado	Asado	AFAM-1	0.514	0.360	0.522	0.414	0.000	0.121	0.105	0.370	0.349	0.335	0.375	0.356	0.316	0.369	0.304	0.104	0.101	0.344	0.382	0.414	0.396	0.311	0.299	0.442	0.522	0.154	0.155	0.155	0.146	0.124	0.123	0.544	0.644	0.219	0.214	0.696	0.571	0.582	0.848	0.817	0.878	0.879	0.748	0.755	0.809	0.709	0.764	0.730	0.712	0.593	0.575	0.603	0.609	0.241	0.230	0.218	0.283	0.305	0.330
	Kikaijima	AF	Kikai-1	Kikai-1	AFKI-1	0.472	0.411	0.482	0.462	0.121	0.000	0.049	0.312	0.294	0.284	0.326	0.320	0.256	0.293	0.231	0.051	0.050	0.248	0.337	0.394	0.361	0.269	0.261	0.416	0.491	0.058	0.055	0.051	0.064	0.025	0.042	0.538	0.645	0.128	0.140	0.618	0.529	0.527	0.778	0.739	0.804	0.808	0.680	0.686	0.722	0.623	0.688	0.664	0.627	0.536	0.513	0.532	0.529	0.168	0.167	0.157	0.249	0.283	0.299
			Kikai-2	Kikai-2	AFKI-2	0.448	0.359	0.455	0.417	0.105	0.049	0.000	0.311	0.299	0.291	0.338	0.304	0.224	0.293	0.227	0.063	0.054	0.267	0.345	0.376	0.349	0.256	0.245	0.436	0.541	0.068	0.071	0.076	0.076	0.054	0.054	0.499	0.599	0.128	0.143	0.654	0.554	0.549	0.802	0.776	0.833	0.836	0.716	0.726	0.752	0.652	0.716	0.689	0.669	0.559	0.530	0.556	0.564	0.195	0.181	0.162	0.246	0.250	0.279
	Tokunoshima	FF	Akirigami	Akirigami-1	FFTO-1-1	0.573	0.536	0.580	0.512	0.370	0.312	0.311	0.000	0.001	0.056	0.067	0.161	0.152	0.155	0.135	0.289	0.281	0.212	0.455	0.491	0.508	0.414	0.423	0.499	0.566	0.286	0.297	0.302	0.284	0.278	0.289	0.657	0.718	0.361	0.374	0.685	0.612	0.624	0.811	0.776	0.847	0.850	0.673	0.684	0.791	0.695	0.623	0.695	0.660	0.599	0.595	0.595	0.605	0.425	0.421	0.408	0.443	0.452	0.488
				Akirigami-2	FFTO-1-2	0.574	0.530	0.582	0.514	0.349	0.294	0.299	0.001	0.000	0.053	0.071	0.147	0.137	0.136	0.114	0.276	0.266	0.192	0.433	0.464	0.497	0.398	0.411	0.468	0.569	0.284	0.293	0.291	0.276	0.267	0.280	0.633	0.700	0.361	0.364	0.682	0.621	0.625	0.831	0.794	0.867	0.870	0.685	0.697	0.804	0.705	0.641	0.708	0.675	0.616	0.606	0.610	0.617	0.418	0.409	0.398	0.433	0.446	0.481
				Akirigami-3	FFTO-1-3	0.599	0.538	0.608	0.524	0.335	0.284	0.291	0.056	0.053	0.000	0.111	0.117	0.120	0.138	0.111	0.258	0.252	0.237	0.444	0.454	0.469	0.407	0.417	0.459	0.552	0.283	0.293	0.274	0.261	0.258	0.258	0.598	0.678	0.357	0.353	0.681	0.582	0.600	0.808	0.768	0.842	0.845	0.670	0.681	0.784	0.681	0.660	0.672	0.652	0.594	0.575	0.589	0.588	0.377	0.371	0.362	0.419	0.418	0.428
			Oose	Oose	FFTO-2	0.611	0.537	0.614	0.480	0.375	0.326	0.338	0.067	0.071	0.111	0.000	0.189	0.169	0.173	0.162	0.304	0.295	0.245	0.500	0.545	0.543	0.425	0.440	0.559	0.578	0.332	0.335	0.345	0.306	0.312	0.324	0.637	0.699	0.396	0.421	0.690	0.664	0.666	0.837	0.807	0.869	0.871	0.674	0.688	0.780	0.720	0.689	0.673	0.673	0.657	0.654	0.656	0.654	0.437	0.434	0.417	0.450	0.432	0.462
			Uwanaru	Uwanaru	FFTO-3	0.668	0.547	0.667	0.497	0.356	0.320	0.304	0.161	0.147	0.117	0.189	0.000	0.115	0.148	0.128	0.284	0.267	0.289	0.520	0.527	0.484	0.425	0.444	0.527	0.625	0.288	0.313	0.277	0.251	0.268	0.261	0.581	0.637	0.356	0.336	0.649	0.534	0.548	0.776	0.729	0.803	0.805	0.619	0.641	0.791	0.684	0.629	0.645	0.618	0.550	0.528	0.539	0.550	0.368	0.358	0.345	0.390	0.375	0.373
			Agon	Agon-1	FFTO-4-1	0.590	0.421	0.605	0.422	0.316	0.256	0.224	0.152	0.137	0.120	0.169	0.115	0.000	0.023	0.028	0.240	0.225	0.225	0.458	0.490	0.471	0.414	0.397	0.503	0.624	0.245	0.259	0.246	0.244	0.233	0.226	0.555	0.614	0.296	0.313	0.662	0.596	0.593	0.818	0.776	0.840	0.844	0.686	0.690	0.801	0.716	0.670	0.720	0.659	0.603	0.590	0.589	0.604	0.337	0.319	0.308	0.365	0.345	0.350
				Agon-2	FFTO-4-2	0.600	0.453	0.620	0.441	0.369	0.293	0.293	0.155	0.136	0.138	0.173	0.148	0.023	0.000	0.048	0.303	0.282	0.232	0.473	0.515	0.479	0.463	0.446	0.516	0.656	0.299	0.314	0.300	0.315	0.283	0.286	0.584	0.641	0.352	0.365	0.664	0.634	0.629	0.828	0.774	0.849	0.853	0.700	0.702	0.805	0.724	0.692	0.734	0.676	0.644	0.634	0.632	0.640	0.383	0.366	0.358	0.417	0.398	0.400
			Shikaura	Shikaura	FFTO-5	0.575	0.445	0.595	0.466	0.304	0.231	0.227	0.135	0.114	0.111	0.162	0.128	0.028	0.048	0.000	0.228	0.218	0.146	0.425	0.440	0.465	0.381	0.382	0.461	0.582	0.240	0.251	0.224	0.221	0.219	0.216	0.566	0.632	0.311	0.321	0.681	0.578	0.578	0.812	0.777	0.845	0.848	0.686	0.689	0.788	0.709	0.660	0.703	0.655	0.587	0.573	0.576	0.588	0.346	0.321	0.319	0.383	0.377	0.385
		AF	Manda	Manda	AFTO-1	0.416	0.374	0.424	0.403	0.104	0.051	0.063	0.289	0.276	0.258	0.304	0.284	0.240	0.303	0.228	0.000	-0.009	0.278	0.309	0.361	0.336	0.238	0.216	0.388	0.438	0.068	0.069	0.073	0.062	0.043	0.039	0.486	0.577	0.109	0.126	0.620	0.473	0.476	0.747	0.735	0.779	0.783	0.649	0.657	0.734	0.593	0.646	0.625	0.603	0.478	0.459	0.480	0.486	0.163	0.150	0.141	0.194	0.240	0.262
			Kametoku	Kametoku	AFTO-2	0.435	0.371	0.451	0.401	0.101	0.050	0.054	0.281	0.266	0.252	0.295	0.267	0.225	0.282	0.218	-0.009	0.000	0.294	0.318	0.382	0.329	0.238	0.220	0.398	0.470	0.058	0.065	0.068	0.063	0.036	0.032	0.473	0.576	0.104	0.117	0.622	0.482	0.483	0.752	0.731	0.777	0.781	0.661	0.664	0.737	0.594	0.667	0.628	0.621	0.484	0.464	0.483	0.489	0.149	0.135	0.124	0.178	0.218	0.234
	Okinoerabujima	FF	Amata	Amata	FFOE-1	0.539	0.534	0.548	0.581	0.344	0.248	0.267	0.212	0.192	0.237	0.245	0.289	0.225	0.232	0.146	0.278	0.294	0.000	0.453	0.463	0.463	0.401	0.409	0.500	0.589	0.266	0.274	0.252	0.280	0.261	0.265	0.603	0.670	0.388	0.401	0.684	0.581	0.587	0.792	0.748	0.853	0.858	0.675	0.676	0.740	0.696	0.669	0.698	0.657	0.591	0.575	0.592	0.597	0.472	0.451	0.448	0.496	0.497	0.531
	Okinawajima	FF	Sukuta	Sukuta	FFOK-1	0.520	0.547	0.550	0.575	0.382	0.337	0.345	0.455	0.433	0.444	0.500	0.520	0.458	0.473	0.425	0.309	0.318	0.453	0.000	0.146	0.336	0.336	0.369	0.090	0.335	0.305	0.314	0.304	0.312	0.310	0.306	0.577	0.653	0.340	0.325	0.697	0.683	0.655	0.801	0.795	0.867	0.872	0.790	0.792	0.788	0.739	0.779	0.793	0.719	0.676	0.652	0.670	0.671	0.395	0.386	0.404	0.410	0.421	0.487
			Yofuke	Yofuke	FFOK-2	0.522	0.491	0.539	0.566	0.414	0.394	0.376	0.491	0.464	0.454	0.545	0.527	0.490	0.515	0.440	0.361	0.382	0.463	0.146	0.000	0.377	0.375	0.395	0.140	0.316	0.393	0.386	0.361	0.367	0.379	0.370	0.576	0.674	0.423	0.410	0.809	0.707	0.706	0.853	0.849	0.887	0.889	0.851	0.850	0.845	0.807	0.830	0.839	0.761	0.708	0.691	0.710	0.709	0.498	0.481	0.488	0.521	0.541	0.582
			Okukubi	Okukubi	FFOK-3	0.558	0.519	0.590	0.505	0.396	0.361	0.349	0.508	0.497	0.469	0.543	0.484	0.471	0.479	0.465	0.336	0.329	0.463	0.336	0.377	0.000	0.291	0.287	0.381	0.459	0.314	0.320	0.232	0.329	0.316	0.303	0.543	0.582	0.383	0.354	0.720	0.589	0.603	0.721	0.625	0.781	0.787	0.712	0.709	0.697	0.642	0.728	0.743	0.709	0.630	0.619	0.642	0.640	0.442	0.439	0.439	0.467	0.479	0.503
			Hija	Hija-1	FFOK-4-1	0.490	0.486	0.498	0.522	0.311	0.269	0.256	0.414	0.398	0.407	0.425	0.425	0.414	0.463	0.381	0.238	0.238	0.401	0.336	0.375	0.291	0.000	0.079	0.396	0.452	0.276	0.265	0.244	0.228	0.244	0.256	0.502	0.477	0.288	0.290	0.580	0.482	0.503	0.736	0.700	0.748	0.754	0.646	0.654	0.676	0.586	0.629	0.625	0.658	0.513	0.491	0.497	0.508	0.392	0.380	0.368	0.410	0.417	0.450
				Hija-2	FFOK-4-2	0.474	0.453	0.492	0.479	0.299	0.261	0.245	0.423	0.411	0.417	0.440	0.444	0.397	0.446	0.382	0.216	0.220	0.409	0.369	0.395	0.287	0.079	0.000	0.429	0.497	0.272	0.255	0.238	0.216	0.237	0.239	0.497	0.468	0.264	0.276	0.625	0.528	0.557	0.797	0.719	0.815	0.821	0.727	0.725	0.720	0.651	0.684	0.714	0.690	0.560	0.546	0.556	0.562	0.347	0.326	0.324	0.350	0.382	0.394
			Kyodafukuji	Kyodafukuji	FFOK-5	0.582	0.585	0.598	0.596	0.442	0.416	0.436	0.499	0.468	0.459	0.559	0.527	0.503	0.516	0.461	0.388	0.398	0.500	0.090	0.140	0.381	0.396	0.429	0.000	0.340	0.393	0.400	0.380	0.389	0.394	0.383	0.569	0.636	0.462	0.413	0.753	0.716	0.706	0.845	0.847	0.881	0.884	0.844	0.842	0.843	0.803	0.839	0.825	0.803	0.703	0.686	0.705	0.704	0.436	0.419	0.435	0.449	0.466	0.518
			Kushi	Kushi	FFOK-6	0.551	0.621	0.553	0.595	0.522	0.491	0.541	0.566	0.569	0.552	0.578	0.625	0.624	0.656	0.582	0.438	0.470	0.589	0.335	0.316	0.459	0.452	0.497	0.340	0.000	0.494	0.496	0.497	0.485	0.499	0.497	0.660	0.732	0.509	0.516	0.712	0.630	0.666	0.725	0.750	0.791	0.795	0.743	0.740	0.763	0.702	0.703	0.728	0.666	0.648	0.642	0.643	0.640	0.534	0.536	0.554	0.587	0.612	0.622
		AF	Sukuta	Sukuta	AFOK-1	0.437	0.392	0.484	0.423	0.154	0.058	0.068	0.286	0.284	0.283	0.332	0.288	0.245	0.299	0.240	0.068	0.058	0.266	0.305	0.393	0.314	0.276	0.272	0.393	0.494	0.000	-0.001	0.035	0.015	0.020	0.014	0.514	0.623	0.079	0.092	0.588	0.488	0.484	0.719	0.668	0.767	0.773	0.635	0.647	0.680	0.568	0.643	0.605	0.591	0.493	0.454	0.480	0.488	0.165	0.163	0.147	0.205	0.215	0.252
			Yofuke	Yofuke	AFOK-2	0.444	0.395	0.482	0.428	0.155	0.055	0.071	0.297	0.293	0.293	0.335	0.313	0.259	0.314	0.251	0.069	0.065	0.274	0.314	0.386	0.320	0.265	0.255	0.400	0.496	-0.001	0.000	0.038	0.010	0.019	0.015	0.497	0.612	0.075	0.087	0.599	0.507	0.505	0.725	0.684	0.772	0.776	0.660	0.668	0.684	0.573	0.670	0.616	0.602	0.510	0.473	0.497	0.506	0.172	0.170	0.153	0.220	0.231	0.262
			Okukubi	Okukubi	AFOK-3	0.495	0.432	0.517	0.461	0.155	0.051	0.076	0.302	0.291	0.274	0.345	0.277	0.246	0.300	0.224	0.073	0.068	0.252	0.304	0.361	0.232	0.244	0.238	0.380	0.497	0.035	0.038	0.000	0.046	0.017	0.017	0.515	0.605	0.118	0.115	0.630	0.491	0.499	0.712	0.669	0.772	0.776	0.641	0.647	0.677	0.583	0.636	0.651	0.585	0.515	0.484	0.513	0.514	0.199	0.193	0.181	0.257	0.282	0.304
			Hija	Hija	AFOK-4	0.468	0.414	0.503	0.447	0.146	0.064	0.076	0.284	0.276	0.261	0.306	0.251	0.244	0.315	0.221	0.062	0.063	0.280	0.312	0.367	0.329	0.228	0.216	0.389	0.485	0.015	0.010	0.046	0.000	0.020	0.011	0.513	0.596	0.091	0.096	0.603	0.453	0.476	0.674	0.665	0.741	0.743	0.629	0.646	0.662	0.543	0.625	0.559	0.581	0.479	0.446	0.471	0.477	0.165	0.163	0.147	0.212	0.227	0.252
			Sade	Sade	AFOK-5	0.461	0.400	0.479	0.437	0.124	0.025	0.054	0.278	0.267	0.258	0.312	0.268	0.233	0.283	0.219	0.043	0.036	0.261	0.310	0.379	0.316	0.244	0.237	0.394	0.499	0.020	0.019	0.017	0.020	0.000	-0.001	0.510	0.608	0.083	0.086	0.599	0.483	0.491	0.717	0.684	0.769	0.772	0.638	0.646	0.686	0.567	0.634	0.613	0.576	0.496	0.468	0.493	0.494	0.152	0.147	0.135	0.211	0.222	0.245
			Yona	Yona	AFOK-6	0.458	0.376	0.486	0.413	0.123	0.042	0.054	0.289	0.280	0.258	0.324	0.261	0.226	0.286	0.216	0.039	0.032	0.265	0.306	0.370	0.303	0.256	0.239	0.383	0.497	0.014	0.015	0.017	0.011	-0.001	0.000	0.491	0.600	0.087	0.087	0.613	0.490	0.492	0.718	0.684	0.773	0.776	0.646	0.655	0.681	0.580	0.644	0.616	0.600	0.497	0.464	0.492	0.497	0.149	0.142	0.128	0.197	0.206	0.230
	Kumejima	FF	Shirase	Shirase	FFKM-1	0.675	0.630	0.713	0.630	0.544	0.538	0.499	0.657	0.633	0.598	0.637	0.581	0.555	0.584	0.566	0.486	0.473	0.603	0.577	0.576	0.543	0.502	0.497	0.569	0.660	0.514	0.497	0.515	0.513	0.510	0.491	0.000	0.248	0.542	0.538	0.724	0.661	0.645	0.857	0.839	0.882	0.885	0.832	0.823	0.764	0.677	0.760	0.748	0.759	0.668	0.633	0.654	0.665	0.537	0.507	0.506	0.542	0.512	0.491
			Suhara	Suhara	FFKM-2	0.757	0.706	0.778	0.688	0.644	0.645	0.599	0.718	0.700	0.678	0.699	0.637	0.614	0.641	0.632	0.577	0.576	0.670	0.653	0.674	0.582	0.477	0.468	0.636	0.732	0.623	0.612	0.605	0.596	0.608	0.600	0.248	0.000	0.599	0.596	0.720	0.627	0.655	0.817	0.810	0.837	0.838	0.780	0.775	0.776	0.695	0.743	0.780	0.765	0.668	0.650	0.652	0.667	0.590	0.564	0.552	0.584	0.590	0.541
		AF	Shirase	Shirase	AFKM-1	0.428	0.394	0.467	0.419	0.219	0.128	0.128	0.361	0.361	0.357	0.396	0.356	0.296	0.352	0.311	0.109	0.104	0.388	0.340	0.423	0.383	0.288	0.264	0.462	0.509	0.079	0.075	0.118	0.091	0.083	0.087	0.542	0.599	0.000	0.026	0.566	0.486	0.482	0.710	0.669	0.756	0.761	0.637	0.643	0.678	0.538	0.621	0.582	0.550	0.481	0.445	0.466	0.477	0.182	0.181	0.164	0.211	0.208	0.240
			Suhara	Suhara	AFKM-2	0.468	0.437	0.489	0.457	0.214	0.140	0.143	0.374	0.364	0.353	0.421	0.336	0.313	0.365	0.321	0.126	0.117	0.401	0.325	0.410	0.354	0.290	0.276	0.413	0.516	0.092	0.087	0.115	0.096	0.086	0.087	0.538	0.596	0.026	0.000	0.578	0.497	0.496	0.712	0.667	0.747	0.750	0.629	0.638	0.704	0.560	0.634	0.594	0.559	0.500	0.461	0.488	0.496	0.179	0.179	0.165	0.217	0.221	0.247
South Ryukyu	Ishigakijima	FF		Sokohara	FFIS-1	0.669	0.768	0.675	0.745	0.696	0.618	0.654	0.685	0.682	0.681	0.690	0.649	0.662	0.664	0.681	0.620	0.622	0.684	0.697	0.809	0.720	0.580	0.625	0.753	0.712	0.588	0.599	0.630	0.603	0.599	0.613	0.724	0.720	0.566	0.578	0.000	0.384	0.371	0.597	0.606	0.667	0.669	0.631	0.636	0.600	0.515	0.572	0.528	0.572	0.399	0.385	0.376	0.359	0.626	0.628	0.632	0.650	0.626	0.616
		AF	Arakawa	Arakawa	AFIS-1	0.631	0.720	0.649	0.725	0.571	0.529	0.554	0.612	0.621	0.582	0.664	0.534	0.596	0.634	0.578	0.473	0.482	0.581	0.683	0.707	0.589	0.482	0.528	0.716	0.630	0.488	0.507	0.491	0.453	0.483	0.490	0.661	0.627	0.486	0.497	0.384	0.000	0.082	0.439	0.345	0.410	0.421	0.429	0.418	0.448	0.332	0.414	0.355	0.391	0.081	0.082	0.083	0.080	0.544	0.540	0.543	0.586	0.613	0.594
			Nagura	Nagura	AFIS-2	0.617	0.709	0.638	0.693	0.582	0.527	0.549	0.624	0.625	0.600	0.666	0.548	0.593	0.629	0.578	0.476	0.483	0.587	0.655	0.706	0.603	0.503	0.557	0.706	0.666	0.484	0.505	0.499	0.476	0.491	0.492	0.645	0.655	0.482	0.496	0.371	0.082	0.000	0.595	0.525	0.572	0.579	0.573	0.568	0.575	0.449	0.516	0.451	0.534	0.049	0.044	0.058	0.049	0.529	0.523	0.533	0.549	0.579	0.563
	Iriomotejima	FF	Pinai	Pinai	FFIR-1	0.855	0.890	0.854	0.890	0.848	0.778	0.802	0.811	0.831	0.808	0.837	0.776	0.818	0.828	0.812	0.747	0.752	0.792	0.801	0.853	0.721	0.736	0.797	0.845	0.725	0.719	0.725	0.712	0.674	0.717	0.718	0.857	0.817	0.710	0.712	0.597	0.439	0.595	0.000	0.291	0.219	0.214	0.320	0.323	0.357	0.179	0.371	0.301	0.357	0.566	0.554	0.550	0.550	0.737	0.748	0.752	0.758	0.749	0.719
			Kura	Kura	FFIR-2	0.771	0.830	0.799	0.835	0.817	0.739	0.776	0.776	0.794	0.768	0.807	0.729	0.776	0.774	0.777	0.735	0.731	0.748	0.795	0.849	0.625	0.700	0.719	0.847	0.750	0.668	0.684	0.669	0.665	0.684	0.684	0.839	0.810	0.669	0.667	0.606	0.345	0.525	0.291	0.000	0.321	0.335	0.269	0.234	0.265	0.291	0.402	0.341	0.321	0.504	0.494	0.490	0.485	0.730	0.744	0.743	0.755	0.745	0.720
			Geda	Geda-1	FFIR-3-1	0.868	0.851	0.872	0.853	0.878	0.804	0.833	0.847	0.867	0.842	0.869	0.803	0.840	0.849	0.845	0.779	0.777	0.853	0.867	0.887	0.781	0.748	0.815	0.881	0.791	0.767	0.772	0.772	0.741	0.769	0.773	0.882	0.837	0.756	0.747	0.667	0.410	0.572	0.219	0.321	0.000	0.001	0.305	0.289	0.412	0.273	0.382	0.359	0.352	0.552	0.553	0.544	0.545	0.780	0.795	0.792	0.831	0.822	0.793
				Geda-2	FFIR-3-2	0.877	0.859	0.879	0.859	0.879	0.808	0.836	0.850	0.870	0.845	0.871	0.805	0.844	0.853	0.848	0.783	0.781	0.858	0.872	0.889	0.787	0.754	0.821	0.884	0.795	0.773	0.776	0.776	0.743	0.772	0.776	0.885	0.838	0.761	0.750	0.669	0.421	0.579	0.214	0.335	0.001	0.000	0.306	0.288	0.412	0.270	0.395	0.361	0.360	0.559	0.561	0.551	0.552	0.781	0.796	0.793	0.833	0.825	0.796
			Yuchin	YuchinR-1	FFIR-4-1	0.774	0.769	0.794	0.778	0.748	0.680	0.716	0.673	0.685	0.670	0.674	0.619	0.686	0.700	0.686	0.649	0.661	0.675	0.790	0.851	0.712	0.646	0.727	0.844	0.743	0.635	0.660	0.641	0.629	0.638	0.646	0.832	0.780	0.637	0.629	0.631	0.429	0.573	0.320	0.269	0.305	0.306	0.000	0.013	0.285	0.198	0.239	0.326	0.154	0.565	0.560	0.567	0.559	0.686	0.698	0.688	0.738	0.734	0.717
				YuchinR-2	FFIR-4-2	0.766	0.770	0.793	0.778	0.755	0.686	0.726	0.684	0.697	0.681	0.688	0.641	0.690	0.702	0.689	0.657	0.664	0.676	0.792	0.850	0.709	0.654	0.725	0.842	0.740	0.647	0.668	0.647	0.646	0.646	0.655	0.823	0.775	0.643	0.638	0.636	0.418	0.568	0.323	0.234	0.289	0.288	0.013	0.000	0.268	0.210	0.253	0.336	0.166	0.559	0.557	0.563	0.552	0.696	0.707	0.700	0.742	0.743	0.727
				YuchinL	FFIR-5	0.778	0.832	0.815	0.809	0.809	0.722	0.752	0.791	0.804	0.784	0.780	0.791	0.801	0.805	0.788	0.734	0.737	0.740	0.788	0.845	0.697	0.676	0.720	0.843	0.763	0.680	0.684	0.677	0.662	0.686	0.681	0.764	0.776	0.678	0.704	0.600	0.448	0.575	0.357	0.265	0.412	0.412	0.285	0.268	0.000	0.203	0.404	0.312	0.353	0.570	0.553	0.566	0.541	0.748	0.755	0.753	0.781	0.796	0.782
			Urauchi	Urauchi	FFIR-6	0.718	0.791	0.741	0.788	0.709	0.623	0.652	0.695	0.705	0.681	0.720	0.684	0.716	0.724	0.709	0.593	0.594	0.696	0.739	0.807	0.642	0.586	0.651	0.803	0.702	0.568	0.573	0.583	0.543	0.567	0.580	0.677	0.695	0.538	0.560	0.515	0.332	0.449	0.179	0.291	0.273	0.270	0.198	0.210	0.203	0.000	0.253	0.210	0.210	0.447	0.424	0.432	0.420	0.608	0.613	0.619	0.637	0.654	0.629
			Arabara	Arabara	FFIR-7	0.746	0.760	0.744	0.767	0.764	0.688	0.716	0.623	0.641	0.660	0.689	0.629	0.670	0.692	0.660	0.646	0.667	0.669	0.779	0.830	0.728	0.629	0.684	0.839	0.703	0.643	0.670	0.636	0.625	0.634	0.644	0.760	0.743	0.621	0.634	0.572	0.414	0.516	0.371	0.402	0.382	0.395	0.239	0.253	0.404	0.253	0.000	0.384	0.212	0.503	0.499	0.492	0.504	0.700	0.703	0.708	0.730	0.713	0.711
			Aira	Aira	FFIR-8	0.725	0.781	0.724	0.774	0.730	0.664	0.689	0.695	0.708	0.672	0.673	0.645	0.720	0.734	0.703	0.625	0.628	0.698	0.793	0.839	0.743	0.625	0.714	0.825	0.728	0.605	0.616	0.651	0.559	0.613	0.616	0.748	0.780	0.582	0.594	0.528	0.355	0.451	0.301	0.341	0.359	0.361	0.326	0.336	0.312	0.210	0.384	0.000	0.391	0.438	0.406	0.421	0.408	0.627	0.629	0.631	0.655	0.643	0.624
			Nishida	Nishida	FFIR-9	0.736	0.732	0.738	0.745	0.712	0.627	0.669	0.660	0.675	0.652	0.673	0.618	0.659	0.676	0.655	0.603	0.621	0.657	0.719	0.761	0.709	0.658	0.690	0.803	0.666	0.591	0.602	0.585	0.581	0.576	0.600	0.759	0.765	0.550	0.559	0.572	0.391	0.534	0.357	0.321	0.352	0.360	0.154	0.166	0.353	0.210	0.212	0.391	0.000	0.514	0.504	0.518	0.506	0.646	0.655	0.655	0.703	0.703	0.676
		AF	Geda	Geda-2	AFIR-1	0.608	0.712	0.610	0.689	0.593	0.536	0.559	0.599	0.616	0.594	0.657	0.550	0.603	0.644	0.587	0.478	0.484	0.591	0.676	0.708	0.630	0.513	0.560	0.703	0.648	0.493	0.510	0.515	0.479	0.496	0.497	0.668	0.668	0.481	0.500	0.399	0.081	0.049	0.566	0.504	0.552	0.559	0.565	0.559	0.570	0.447	0.503	0.438	0.514	0.000	0.007	0.005	####	0.539	0.536	0.542	0.575	0.595	0.586
			Omija	Omija	AFIR-2	0.592	0.713	0.605	0.679	0.575	0.513	0.530	0.595	0.606	0.575	0.654	0.528	0.590	0.634	0.573	0.459	0.464	0.575	0.652	0.691	0.619	0.491	0.546	0.686	0.642	0.454	0.473	0.484	0.446	0.468	0.464	0.633	0.650	0.445	0.461	0.385	0.082	0.044	0.554	0.494	0.553	0.561	0.560	0.557	0.553	0.424	0.499	0.406	0.504	0.007	0.000	0.000	0.000	0.501	0.501	0.507	0.539	0.566	0.554
			Yuchin	YuchinR2	AFIR-3	0.610	0.721	0.611	0.693	0.603	0.532	0.556	0.595	0.610	0.589	0.656	0.539	0.589	0.632	0.576	0.480	0.483	0.592	0.670	0.710	0.642	0.497	0.556	0.705	0.643	0.480	0.497	0.513	0.471	0.493	0.492	0.654	0.652	0.466	0.488	0.376	0.083	0.058	0.550	0.490	0.544	0.551	0.567	0.563	0.566	0.432	0.492	0.421	0.518	0.005	0.000	0.000	####	0.520	0.519	0.526	0.555	0.578	0.563
			Nakama	Nakama	AFIR-4	0.611	0.733	0.616	0.704	0.609	0.529	0.564	0.605	0.617	0.588	0.654	0.550	0.604	0.640	0.588	0.486	0.489	0.597	0.671	0.709	0.640	0.508	0.562	0.704	0.640	0.488	0.506	0.514	0.477	0.494	0.497	0.665	0.667	0.477	0.496	0.359	0.080	0.049	0.550	0.485	0.545	0.552	0.559	0.552	0.541	0.420	0.504	0.408	0.506	####	0.000	####	0.000	0.525	0.526	0.530	0.566	0.590	0.576
North Ryukyu	Yakushima	AF	Takinokawa	Nunobiki-1	AFYK-1-1	0.538	0.475	0.559	0.485	0.241	0.168	0.195	0.425	0.418	0.377	0.437	0.368	0.337	0.383	0.346	0.163	0.149	0.472	0.395	0.498	0.442	0.392	0.347	0.436	0.534	0.165	0.172	0.199	0.165	0.152	0.149	0.537	0.590	0.182	0.179	0.626	0.544	0.529	0.737	0.730	0.780	0.781	0.686	0.696	0.748	0.608	0.700	0.627	0.646	0.539	0.501	0.520	0.525	0.000	-0.002	0.003	0.070	0.129	0.112
				Nunobiki-2	AFYK-1-2	0.525	0.455	0.548	0.484	0.230	0.167	0.181	0.421	0.409	0.371	0.434	0.358	0.319	0.366	0.321	0.150	0.135	0.451	0.386	0.481	0.439	0.380	0.326	0.419	0.536	0.163	0.170	0.193	0.163	0.147	0.142	0.507	0.564	0.181	0.179	0.628	0.540	0.523	0.748	0.744	0.795	0.796	0.698	0.707	0.755	0.613	0.703	0.629	0.655	0.536	0.501	0.519	0.526	-0.002	0.000	-0.001	0.065	0.114	0.096
			Isso	Isso	AFYK-2	0.529	0.434	0.557	0.461	0.218	0.157	0.162	0.408	0.398	0.362	0.417	0.345	0.308	0.358	0.319	0.141	0.124	0.448	0.404	0.488	0.439	0.368	0.324	0.435	0.554	0.147	0.153	0.181	0.147	0.135	0.128	0.506	0.552	0.164	0.165	0.632	0.543	0.533	0.752	0.743	0.792	0.793	0.688	0.700	0.753	0.619	0.708	0.631	0.655	0.542	0.507	0.526	0.530	0.003	-0.001	0.000	0.057	0.105	0.097
Honshu	Honshu	AF	Esuno	Wakayama	AFHS-1	0.506	0.459	0.548	0.474	0.283	0.249	0.246	0.443	0.433	0.419	0.450	0.390	0.365	0.417	0.383	0.194	0.178	0.496	0.410	0.521	0.467	0.410	0.350	0.449	0.587	0.205	0.220	0.257	0.212	0.211	0.197	0.542	0.584	0.211	0.217	0.650	0.586	0.549	0.758	0.755	0.831	0.833	0.738	0.742	0.781	0.637	0.730	0.655	0.703	0.575	0.539	0.555	0.566	0.070	0.065	0.057	0.000	0.080	0.102
			Betto	Kagawa-1	AFHS-2	0.533	0.413	0.575	0.434	0.305	0.283	0.250	0.452	0.446	0.418	0.432	0.375	0.345	0.398	0.377	0.240	0.218	0.497	0.421	0.541	0.479	0.417	0.382	0.466	0.612	0.215	0.231	0.282	0.227	0.222	0.206	0.512	0.590	0.208	0.221	0.626	0.613	0.579	0.749	0.745	0.822	0.825	0.734	0.743	0.796	0.654	0.713	0.643	0.703	0.595	0.566	0.578	0.590	0.129	0.114	0.105	0.080	0.000	0.010
			Yoshida	Kagawa-2	AFHS-3	0.571	0.452	0.608	0.446	0.330	0.299	0.279	0.488	0.481	0.428	0.462	0.373	0.350	0.400	0.385	0.262	0.234	0.531	0.487	0.582	0.503	0.450	0.394	0.518	0.622	0.252	0.262	0.304	0.252	0.245	0.230	0.491	0.541	0.240	0.247	0.616	0.594	0.563	0.719	0.720	0.793	0.796	0.717	0.727	0.782	0.629	0.711	0.624	0.676	0.586	0.554	0.563	0.576	0.112	0.096	0.097	0.102	0.010	0.000

Table S6. Results of AMOVA analysis.

Geographic scales	Form	Source of variation	%var	Statistics	*F* values	*P* values
Among-islands within-regions	AF	Within-individuals	87.8	*F*IT	0.122	-
		Among-individuals	4.4	*F*IS	0.048	0.001
		Among-rivers in Middle Ryukyu	1.7	*F*SC	0.018	0.001
		Among-islands in Middle Ryukyu	6.2	*F*CT	0.062	0.001
		Within-individuals	91.8	*F*IT	0.082	-
		Among-individuals	2.8	*F*IS	0.03	0.016
		Among-rivers in South Ryukyu	1.7	*F*SC	0.018	0.001
		Among-islands in South Ryukyu	3.7	*F*CT	0.037	0.057
	FF	Within-individuals	34.9	*F*IT	0.651	-
		Among-individuals	3.2	*F*IS	0.083	0.001
		Among-rivers in Middle Ryukyu	30.9	*F*SC	0.448	0.001
		Among-islands in Middle Ryukyu	31	*F*CT	0.31	0.001
		Within-individuals	29.4	*F*IT	0.706	-
		Among-individuals	3.3	*F*IS	0.101	0.001
		Among-rivers in South Ryukyu	36.5	*F*SC	0.527	0.001
		Among-islands in South Ryukyu	30.8	*F*CT	0.308	0.1
Among-regions	AF	Within-individuals	68.1	*F*IT	0.319	-
		Among-individuals	4.1	*F*IS	0.057	0.001
		Among-islands	5.3	*F*SC	0.068	0.001
		Among-regions	22.5	*F*CT	0.225	0.002
	FF	Within-individuals	26.7	*F*IT	0.733	-
		Among-individuals	22.5	*F*IS	0.457	0.001
		Among-islands	34	*F*SC	0.409	0.001
		Among-regions	16.8	*F*CT	0.168	0.038

Table S7

Detail results of ABC analysis. For each ABC analysis, the following data are listed: prior distribution, posterior distribution, observed summary statistics, confusion matrix, mean model posterior probabilities and Bayes Factors.

Amami-Oshima

Prior distribution (Model6)

parameter name	log10_a	log10_b	log10_d	log10_e	log10_n_AFAM-1	log10_n_FFAM-2	log10_n_FFAM-3	log10_n_FFAM-1	log10_t_FF	log10_t_root	t_FFAM-1_FI	m	n	p	a	b	d	e	n_AFAM-1	n_FFAM-2	n_FFAM-3	n_FFAM-1	t_FF	t_root	t_FFAM-1_FFAM-3
distribution	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Min.	-3	-3	-3	-3	2	2	2	2	3	3	3	0.5	0.5	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Max.	-9	-9	-9	-9	5.3	4.7	4.7	4.7	6.2	6.2	6.2	2	2	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Complex parameter	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	10^(log10_a)	10^(log10_b)	10^(log10_d)	10^(log10_e)	log10_n_AFA	log10_n_FFA	log10_n_FFA	log10_n_FFA	0^(log10_t_FF	^(log10_t_roo	^(log10_t_FFAM-1_FFAM-3)

Posterior distribution (Model6)

parameter name	log10_a	log10_b	log10_d	log10_e	log10_n_AFAM-1	log10_n_FFAM-2	log10_n_FFAM-3	log10_n_FFAM-1	log10_t_FF	log10_t_root	t_FFAM-1_FI	m	n	p	a	b	d	e	n_AFAM-1	n_FFAM-2	n_FFAM-3	n_FFAM-1	t_FF	t_root	t_FFAM-1_FFAM-3
Min.	-9.688245188	-9.261749857	-9.447602948	-10.43091199	2.148707771	2.051890226	2.020025768	2.210023534	2.932256647	2.8493256	2.9351179	0.4689047	0.4833346	-0.0080614	2.01E-10	6.00E-10	3.56E-10	4.43E-11	143.36576	117.17763	102.44895	167.82318	864.92098	803.93566	860.3889627
Weighted 2.5% Perc.	-8.880829517	-8.840722165	-8.688545393	-8.454426684	3.253432034	2.565699428	2.698025807	3.028594802	3.227351115	3.6598599	3.0116441	0.5243041	0.5307589	0.1834049	1.28E-09	1.46E-09	2.05E-09	4.14E-09	1781.4591	359.11492	499.0369	1071.8358	1689.4299	4617.6306	1028.082447
Weighted Median	-5.749200821	-6.034464377	-5.103343321	-5.131292527	4.162760391	3.141155135	3.397724724	3.71612343	3.715414707	4.7243364	3.2674309	1.1091171	1.1665536	0.513816	1.82E-06	9.28E-07	8.01E-06	7.97E-06	14366.955	1353.314	2484.0608	5160.7724	5198.8158	53111.368	1850.996534
Weighted Mean	-5.851660078	-6.049782859	-5.457287905	-5.445428834	4.146442013	3.119337361	3.38485093	3.695395918	3.724955177	4.8218666	3.31287	1.1549767	1.194043	0.5004376	8.45E-05	5.89E-05	0.0001353	5.28E-05	20915.059	1493.5832	3127.6158	6335.3111	6647.4153	235572.24	2431.910009
Weighted Mode	-3.961825664	-8.208226706	-3.646448158	-4.625548898	4.149616233	3.172005233	3.414502848	3.766201104	3.714934422	4.2238142	3.094914	0.6180184	0.6370036	0.5723542	4.05E-06	-6.10E-07	1.76E-06	1.32E-05	7606.3026	1187.7615	1863.8561	3366.7669	3652.2375	20583.992	1255.456084
Weighted 97.5% Perc.	-3.139786642	-3.260632003	-3.024833339	-3.415798945	4.915242934	3.553061048	4.017398908	4.278223536	4.292053651	6.1541921	3.864486	1.9513652	1.952053	0.7499216	0.0007518	0.0005524	0.0009655	0.0003933	82097.119	3521.8727	10210.235	18859.953	19595.932	1424183.2	7289.668274
Max.	-2.287622263	-2.859568273	-2.390938534	-1.834875376	5.348809863	4.306579685	4.613133261	4.67851205	5.288952643	6.6873637	4.6276368	2.0394319	2.021237	0.9216372	0.0051932	0.001373	0.0042044	0.0133041	214464.83	19818.999	39244.593	45826.93	204761.56	4869082.7	41920.22715

Observed Summary Statistics Value

Summary statistics	K_FFAM-1	K_FFAM-2	K_FFAM-3	K_AF	Ksd_FFAM-1	Ksd_FFAM-2	Ksd_FFAM-3	Ksd_AF	mean_K	sd_K	tot_K
Observed Value	4.6	2.3	2.5	7.5	5.11345	1.83819	1.93309	5.64288	4.225	2.41851	10.75

Summary statistics	H_FFAM-1	H_FFAM-2	H_FFAM-3	H_AF	Hsd_FFAM-1	Hsd_FFAM-2	Hsd_FFAM-3	Hsd_AF	mean_H	sd_H	tot_H
Observed Value	0.370812	0.234677	0.233783	0.50702	0.319123	0.289914	0.28524	0.33781	0.336573	0.130605	0.53725

Summary statistics	GW_FFAM-1	GW_FFAM-2	GW_FFAM-3	GW_AF	GWsd_FFAM-1	GWsd_FFAM-2	GWsd_FFAM-3	GWsd_AF	mean_GW	sd_GW	tot_GW
Observed Value	0.809459	0.389957	0.685698	0.727478	0.192735	0.140586	0.256188	0.225266	0.653148	0.182836	0.716245

Summary statistics	NGW_FFAM-1	NGW_FFAM-2	NGW_FFAM-3	NGW_AF	NGWsd_FFAM-1	NGWsd_FFAM-2	NGWsd_FFAM-3	NGWsd_AF	mean_NGW	sd_NGW
Observed Value	0.316684	0.186962	0.195131	0.513304	0.202424	0.117843	0.108306	0.201813	0.30302	0.152223

Summary statistics	R_FFAM-1	R_FFAM-2	R_FFAM-3	R_AF	Rsd_FFAM-1	Rsd_FFAM-2	Rsd_FFAM-3	Rsd_AF	mean_R	sd_R	tot_R
Observed Value	6.6	8.8	5.81818	11.5263	7.37564	4.2374	6.64557	10.9766	8.18612	2.55973	14.5

Summary statistics	FIS	FST	FIT
Observed Value	0.0248456	0.425806	0.440072

Summary statistics	FST_FFAM-2_FFAM-1	FST_FFAM-3_FFAM-1	FST_FFAM-3_FFAM-2	FST_AF_FFAM-1	FST_AF_FFAM-2	FST_AF_FFAM-3
Observed Value	0.518432	0.165651	0.615835	0.397943	0.354383	0.473672

Summary statistics	PI_FFAM-2_FFAM-1	PI_FFAM-3_FFAM-1	PI_FFAM-3_FFAM-2	PI_AF_FFAM-1	PI_AF_FFAM-2	PI_AF_FFAM-3
Observed Value	12.5831	7.01757	12.1764	14.2669	11.9246	13.933

Summary statistics	MUSQ_FFAM-2_FFAM-	MUSQ_FFAM-3_FFAM-	MUSQ_FFAM-3_FFAM-	MUSQ_AF_FFAM-	MUSQ_AF_FFAM-	MUSQ_AF_FFAM-3
Observed Value	15.2019	5.91293	6.84931	28.9158	5.34731	16.0727

Confusion matrix based on 100 samples for each model (neuralnet, tolerance rate=0.01).

model focal \ selected	1	2	3	4	5	6 (best model)	7	8
1 (Parallel origin, gene flow)	0.32	0.2	0	0.15	0.14	0.04	0.02	0.13
2 (Parallel origin, gene flow)	0.18	0.48	0.01	0.09	0.17	0.05	0	0.02
3 (Single origin, no gene flow)	0	0.01	0.81	0	0	0.03	0.04	0.11
4 (Single origin, gene flow)	0.17	0.16	0.07	0.26	0.18	0.05	0.07	0.04
5 (Parallel origin, gene flow)	0.18	0.27	0.03	0.14	0.18	0.12	0.02	0.06
6 (Single origin, restricted gene flow)	0.03	0.02	0.15	0.02	0.01	0.36	0.16	0.25
7 (Single origin, restricted gene flow)	0.03	0	0.27	0.01	0.01	0.2	0.29	0.19
8 (Parallel origin, no gene flow)	0.01	0	0.13	0	0	0.04	0.03	0.79

Mean model posterior probabilities (neuralnet, tolerance rate=0.01)

model focal \ selected	1	2	3	4	5	6 (best model)	7	8
1 (Parallel origin, gene flow)	0.2295	0.1968	0.0092	0.1814	0.2052	0.0518	0.0389	0.0872
2 (Parallel origin, gene flow)	0.1891	0.3154	0.0158	0.1673	0.2271	0.0396	0.0249	0.0208
3 (Single origin, no gene flow)	0.0135	0.0147	0.4751	0.0446	0.0174	0.1342	0.2075	0.093
4 (Single origin, gene flow)	0.1786	0.1775	0.0463	0.2324	0.1934	0.0735	0.0681	0.0302
5 (Parallel origin, gene flow)	0.2015	0.2103	0.0181	0.1833	0.2146	0.0762	0.0524	0.0436
6 (Single origin, restricted gene flow)	0.0649	0.0503	0.1311	0.0849	0.0621	0.2387	0.2084	0.1596
7 (Single origin, restricted gene flow)	0.0571	0.0319	0.1672	0.0723	0.048	0.2252	0.2698	0.1284
8 (Parallel origin, no gene flow)	0.0632	0.0282	0.1034	0.0299	0.0379	0.1332	0.1141	0.49

Bayes Factor (neuralnet, tolerance rate=0.01)

numerator \ denominator	1	2	3	4	5	6	7	8
1 (Parallel origin, gene flow)	1	0.5373	0.1342	0.3741	0.3947	0.0217	0.0384	0.0735
2 (Parallel origin, gene flow)	1.8611	1	0.2498	0.6962	0.7345	0.0404	0.0716	0.1368
3 (Single origin, no gene flow)	1.8611	1	0.2498	0.6962	0.7345	0.0404	0.0716	0.1368
4 (Single origin, gene flow)	7.4518	4.004	1	2.7875	2.9411	0.1619	0.2865	0.5476
5 (Parallel origin, gene flow)	2.5337	1.3614	0.34	0.9478	1	0.055	0.0974	0.1862
6 (Single origin, restricted gene flow)	46.0352	24.7355	6.1777	17.22	18.1691	1	1.77	3.3831
7 (Single origin, restricted gene flow)	26.0084	13.9748	3.4902	9.7288	10.265	0.565	1	1.9113
8 (Parallel origin, no gene flow)	13.6074	7.3115	1.826	5.09	5.3705	0.2956	0.5232	1

Table S7 (Continued)

Tokunoshima

Prior distribution (Model1)

parameter name	**log10_n_AFTO**	**log10_n_FFTO-4**	**log10_n_FFTO-1**	**log10_n_FFTO-3**	**log10_t_FF**	**log10_t_root**	**log_a**	**log_b**	**log_c**	**log_d**	**log_e**	**log_f**	**m**	**p**	**a**	**b**	**c**	**d**	**e**	**f**	**n_AFTO**	**n_FFTO-4**	**n_FFTO-1**	**n_FFTO-3**	**t_FF**	**t_root**
distribution	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Min.	2	2	2	2	3	3	-9	-9	-9	-9	-9	-9	0.5	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Max.	5.3	4.7	4.7	4.7	6.2	6.2	-3	-3	-3	-3	-3	-3	2	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Complex parameter	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	10^(log10_a)	10^(log10_b)	10^(log10_c)	10^(log10_d)	10^(log10_e)	10^(log10_f)	10^(log10_n_AFTO)	10^(log10_n_FFTO-4)	10^(log10_n_FFTO-1)	10^(log10_n_FFTO-3)	10^(log10_t_FF)	10^(log10_t_root)

Posterior distribution (Model1)

parameter name	**log10_n_AFTO**	**log10_n_FFTO-4**	**log10_n_FFTO-1**	**log10_n_FFTO-3**	**log10_t_FF**	**log10_t_root**	**log_a**	**log_b**	**log_c**	**log_d**	**log_e**	**log_f**	**m**	**p**	**a**	**b**	**c**	**d**	**e**	**f**	**n_AFTO**	**n_FFTO-4**	**n_FFTO-1**	**n_FFTO-3**	**t_FF**	**t_root**
Min.	2.806621339	2.116182292	2.201555834	2.419102158	2.806713725	2.74163814	-9.450201829	-9.633612015	-9.478277609	-9.253909274	-9.402711499	-9.740325909	0.46811023	-0.011780559	3.26E-10	2.31E-10	4.44E-10	5.20E-10	4.18E-10	2.15E-10	675.2262373	118.8410321	157.1864122	263.8589956	584.8185335	642.5137943
Weighted 2.5% Perc.	3.429824279	2.91132051	2.854444308	3.088151593	2.991217137	3.280792587	-8.9174322	-8.898617743	-8.798390571	-8.859721234	-8.904164258	-8.539945709	0.525238496	0.218514744	1.20E-09	1.20E-09	1.89E-09	1.36E-09	1.31E-09	2.44E-09	2724.214565	768.2931065	714.1165077	1190.300136	962.9139787	2105.654271
Weighted Median	4.050193787	3.597146054	3.62245139	3.710513837	3.295586529	4.445679726	-5.971689247	-5.887720429	-5.333141151	-5.648746588	-5.564529899	-4.6927291	1.031109976	0.526750674	1.07E-06	1.22E-06	4.51E-06	2.27E-06	2.82E-06	2.07E-05	11152.73624	3921.533151	4194.083041	5111.49013	1971.531907	28551.57269
Weighted Mean:	4.047075388	3.584334357	3.605717457	3.701726334	3.374926875	4.558475855	-6.020794352	-5.954769468	-5.594912264	-5.763583526	-5.769524192	-5.244238516	1.102350622	0.516966062	5.96E-05	5.71E-05	9.72E-05	8.71E-05	8.13E-05	0.00011969	14171.88937	5067.643737	5538.497957	6285.432826	6179.850249	163508.3018
Weighted Mode	4.105660297	3.63795658	3.634609247	3.715003498	3.16995544	3.904127149	-3.773003426	-3.834890428	-3.545999358	-3.603589397	-3.696967315	-4.137987155	0.609576716	0.538568403	4.84E-07	7.25E-07	1.38E-06	1.00E-06	3.86E-06	-3.50E-06	7317.39962	2571.839605	2141.203149	3924.687184	2452.91197	13984.66192
Weighted 97.5% Perc.	4.644603312	4.193653539	4.259667258	4.263031263	4.285119848	6.093931894	-3.275147713	-3.259453503	-3.129532522	-3.240459918	-3.251738966	-3.149270183	1.932612241	0.7631989	0.000535864	0.000513347	0.000651373	0.000589436	0.000585083	0.00082005	42881.5475	16185.8368	18094.87646	18383.70345	21171.04172	1143861.067
Max.	5.399078444	4.645826156	4.717599474	4.688592279	6.06931587	6.559059066	-2.973490895	-2.79830814	-2.720958118	-2.86926084	-2.517730551	-2.234854856	2.041769927	0.931583562	0.00096041	0.001544948	0.00183694	0.001409813	0.003709343	0.006998659	238742.0939	48017.34928	51865.24316	48727.88337	1304689.467	3218707.559

Observed Summary Statistics Value

Summary statistics	**K_FFTO-3**	**K_FFTO-4**	**K_FFTO-1**	**K_AFTO**	**Ksd_FFTO-3**	**Ksd_FFTO-4**	**Ksd_FFTO-1**	**Ksd_AFTO**	**mean_K**	**sd_K**	**tot_K**
Observed Value	3.15	2.8	4.4	8.45	2.88873	2.70672	4.41767	7.08947	4.7	2.59262	9.85

Summary statistics	**H_FFTO-3**	**H_FFTO-4**	**H_FFTO-1**	**H_AFTO**	**Hsd_FFTO-3**	**Hsd_FFTO-4**	**Hsd_FFTO-1**	**Hsd_AFTO**	**mean_H**	**sd_H**	**tot_H**
Observed Value	0.262258	0.309161	0.324758	0.526077	0.264561	0.290201	0.305237	0.338558	0.355564	0.116737	0.474944

Summary statistics	**GW_FFTO-3**	**GW_FFTO-4**	**GW_FFTO-1**	**GW_AFTO**	**GWsd_FFTO-3**	**GWsd_FFTO-4**	**GWsd_FFTO-1**	**GWsd_AFTO**	**mean_GW**	**sd_GW**	**tot_GW**
Observed Value	0.667612	0.685444	0.607993	0.756569	0.261519	0.29896	0.26461	0.163251	0.679404	0.0611817	0.739408

Summary statistics	**NGW_FFTO-3**	**NGW_FFTO-4**	**NGW_FFTO-1**	**NGW_AFTO**	**NGWsd_FFTO-3**	**NGWsd_FFTO-4**	**NGWsd_FFTO-1**	**NGWsd_AFTO**	**mean_NGW**	**sd_NGW**
Observed Value	0.307032	0.27283	0.378335	0.643602	0.225687	0.206968	0.201916	0.225501	0.40045	0.167954

Summary statistics	**R_FFTO-3**	**R_FFTO-4**	**R_FFTO-1**	**R_AFTO**	**Rsd_FFTO-3**	**Rsd_FFTO-4**	**Rsd_FFTO-1**	**Rsd_AFTO**	**mean_R**	**sd_R**	**tot_R**
Observed Value	7.2	6.69231	8.27778	12.4444	10.0726	8.36047	8.25908	11.4029	8.65363	2.61224	12.7

Summary statistics	**FIS**	**FST**	**FIT**
Observed Value	0.0431306	0.262106	0.293931

Summary statistics	**FSt_FFTO-4_FFTO-3**	**FSt_FFTO-1_FFTO-3**	**FSt_FFTO-1_FFTO-4**	**FST_AFTO_FFTO-3**	**FST_AFTO_FFTO-4**	**FST_AFTO_FFTO-1**
Observed Value	0.233804	0.265177	0.233429	0.274302	0.257181	0.271697

Summary statistics	**PI_FFTO-4_FFTO-3**	**PI_FFTO-1_FFTO-3**	**PI_FFTO-1_FFTO-4**	**PI_AFTO_FFTO-3**	**PI_AFTO_FFTO-4**	**PI_AFTO_FFTO-1**
Observed Value	7.43464	7.96141	8.2402	11.185	11.3353	11.7025

Summary statistics	**DMUSQ_FFTO-4_FFTO-3**	**DMUSQ_FFTO-1_FFTO-3**	**DMUSQ_FFTO-1_FFTO-4**	**DMUSQ_AFTO_FFTO-3**	**DMUSQ_AFTO_FFTO-4**	**DMUSQ_AFTO_FFTO-1**
Observed Value	0.909784	5.33136	4.68833	14.3849	12.1673	6.54198

Confusion matrix based on 100 samples for each model (neuralnet, tolerance rate=0.01).

model focal \ selected	**1(best model)**	**2**	**3**	**4**	**5**	**6**	**7**
1 (Single origin, gene flow)	0.4	0.37	0.06	0.06	0.09	0.01	0.01
2 (Parallel origin, gene flow)	0.16	0.66	0.02	0.08	0.07	0	0.01
3 (Single origin, gene flow)	0.16	0.28	0.23	0.26	0.01	0.04	0.02
4 (Parallel origin, gene flow)	0.07	0.12	0.17	0.48	0	0	0.16
5 (Single origin, no gene flow)	0.06	0.04	0	0	0.76	0.012	0.02
6 (Single origin, no gene flow)	0	0.01	0.01	0.01	0.35	0.51	0.011
7 (Parallel origin, gene flow)	0.01	0	0	0.07	0.04	0.09	0.79

Yellow mark indicates type2 error rate.

Mean model posterior probabilities (neuralnet, tolerance rate=0.01)

model focal \ selected	**1(best model)**	**2**	**3**	**4**	**5**	**6**	**7**
1 (Single origin, gene flow)	0.3639	0.2337	0.1547	0.1066	0.0935	0.0305	0.0172
2 (Parallel origin, gene flow)	0.2264	0.4204	0.128	0.1232	0.0593	0.0171	0.0256
3 (Single origin, gene flow)	0.1908	0.1739	0.2697	0.2375	0.032	0.0503	0.0457
4 (Parallel origin, gene flow)	0.0885	0.1214	0.2536	0.3652	0.0061	0.0121	0.1532
5 (Single origin, no gene flow)	0.1213	0.0387	0.0384	0.0078	0.5539	0.2074	0.0326
6 (Single origin, no gene flow)	0.0303	0.0158	0.0576	0.0236	0.279	0.4784	0.1152
7 (Parallel origin, gene flow)	0.0176	0.0195	0.0545	0.1165	0.0379	0.1097	0.6442

Bayes Factor (neuralnet, tolerance rate=0.01)

numerator \ denominator	**1**	**2**	**3**	**4**	**5**	**6**	**7**
1 (Single origin, gene flow)	1.00	1083.09	1.47	88.30	1.54	1.76	1.7489
2 (Parallel origin, gene flow)	0.00	1.00	0.00	0.08	0.00	0.00	0.0016
3 (Single origin, gene flow)	0.68	737.14	1.00	60.10	1.05	1.20	1.1903
4 (Parallel origin, gene flow)	0.01	12.27	0.02	1.00	0.02	0.02	0.0198
5 (Single origin, no gene flow)	0.65	702.12	0.95	57.24	1.00	1.14	1.1337
6 (Single origin, no gene flow)	0.57	614.95	0.83	50.13	0.88	1.00	0.993
7 (Parallel origin, gene flow)	0.5718	619.302	0.8401	50.489	0.882	1.0071	1

Table S7 (Continued)

Okinawajima

Prior distribution (Model1)

parameter name	log10_n_AFOK	log10_n_FFOK-3	log10_n_FFOK-2	log10_n_FFOK-1	log10_t_FF	log10_t_root	log10_a	log10_b	log10_c	log10_d	log10_e	log10_f	m	p	a	b	c	d	e	f	n_AFOK	n_FFOK-3	n_FFOK-2	n_FFOK-1	t_FF	t_root
distribution	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Min.	2	2	2	2	3	3	-3	-3	-3	-3	-3	-3	0.5	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Max.	5.3	4.7	4.7	4.7	6.2	6.2	-9	-9	-9	-9	-9	-9	2	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Complex parameter	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	10^(log10_a)	10^(log10_b)	10^(log10_c)	10^(log10_d)	10^(log10_e)	10^(log10_f)	10^(log10_n_AFOK)	10^(log10_n_FFOK-3)	10^(log10_n_FFOK-2)	10^(log10_n_FFOK-1)	10^(log10_t_FF)	10^(log10_t_root)

Posterior distribution (Model1)

parameter name	log10_n_AFOK	log10_n_FFOK-3	log10_n_FFOK-2	log10_n_FFOK-1	log10_t_FF	log10_t_root	log10_a	log10_b	log10_c	log10_d	log10_e	log10_f	m	p	a	b	c	d	e	f	n_AFOK	n_FFOK-3	n_FFOK-2	n_FFOK-1	t_FF	t_root
Min.	2.470037117	2.106607131	2.003392575	2.095989707	2.683380616	2.652998433	-9.060979986	-9.781111918	-9.603851946	-13.40190103	-10.27498397	-9.987746822	0.426683355	0.002010761	8.69E-10	1.32E-10	2.69E-10	4.05E-14	5.18E-11	1.03E-10	286.155762	135.3008481	99.93796288	127.7847617	482.28055	381.9607394
Weighted 2.5% Perc.	3.186550594	2.661357783	2.300956732	2.529202748	2.915524281	3.221252646	-8.828417622	-8.909141876	-8.892325358	-8.325405866	-8.966637061	-8.898442663	0.515057032	0.298567721	1.49E-09	1.22E-09	1.29E-09	4.73E-09	1.06E-09	1.26E-09	1559.319773	466.5309642	197.5145846	331.6786578	826.6239371	1599.611816
Weighted Median	3.934064082	3.360566165	3.025112952	3.27140576	3.291617878	4.493656379	-5.486372376	-5.771689018	-5.85816251	-5.101049492	-5.485215013	-5.353632771	1.126172133	0.56638306	3.23E-06	1.66E-06	1.41E-06	7.90E-06	3.20E-06	4.42E-06	8652.286334	2354.47759	1059.215297	1865.958051	1967.465405	30152.06798
Weighted Mean	3.936032289	3.341316983	3.015862985	3.249219428	3.35124467	4.564056664	-5.655413265	-5.89812345	-5.925949505	-5.414555547	-5.812634772	-5.648030195	1.159918912	0.558853108	0.000107896	5.63E-05	6.51E-05	5.06E-05	4.56E-05	7.59E-05	12876.71173	2900.696014	1467.73636	2338.990216	4592.557803	159496.0951
Weighted Mode	3.9210869	3.39067497	3.031550832	3.278921219	3.190582822	4.046258811	-3.565084669	-3.90443231	-3.834071824	-4.371626383	-4.237852751	-3.917545848	0.640429423	0.6127895	2.23E-06	1.41E-06	2.20E-06	8.22E-07	1.31E-06	2.08E-06	4683.487533	1454.737661	509.7203752	1104.935793	1739.571732	10249.11298
Weighted 97.5% Perc.	4.701418456	3.938166571	3.699935549	3.848942833	4.166162823	6.038663315	-3.087717092	-3.329447231	-3.279852204	-3.454177995	-3.440025963	-3.269300016	1.921441713	0.776864847	0.000801836	0.000449686	0.000538957	0.000349559	0.000349811	0.000539677	50651.86405	8892.370115	5014.450747	7081.232675	14763.24385	1060457.27
Max.	5.208638033	4.444154965	4.419639911	4.405605859	5.975096954	6.363076	-2.80826801	-2.867905968	-2.806998277	-2.660569437	-2.76384924	-2.592757571	2.045246187	0.964151752	0.001371122	0.001256278	0.001634339	0.002152299	0.001697525	0.002525621	163617.7769	28358.71962	26854.03131	26488.15756	962325.273	2226872.47

Observed Summary Statistics Value

Summary statistics	K_FFOK-1	K_FFOK-2	K_FFOK-3	K_AFOK	Ksd_FFOK-1	Ksd_FFOK-2	Ksd_FFOK-3	Ksd_AFOK	mean_K	sd_K	tot_K
Observed Value	2.8	2.2	2.95	7.9	1.47256	1.36111	2.08945	5.85707	3.9625	2.64492	9.7

Summary statistics	H_FFOK-1	H_BbOK-2	H_FFOK-3	H_AFOK	Hsd_FFOK-1	Hsd_FFOK-2	Hsd_FFOK-3	Hsd_AFOK	mean_H	sd_H	tot_H
Observed Value	0.288875	0.120941	0.273701	0.549793	0.239761	0.197719	0.307525	0.295097	0.308328	0.177948	0.498571

Summary statistics	GW_FFOK-1	GW_FFOK-2	GW_FFOK-3	GW_AFOK	GWsd_FFOK-1	GWsd_FFOK-2	GWsd_FFOK-3	GWsd_AFOK	mean_GW	sd_GW	tot_GW
Observed Value	0.672185	0.612805	0.503191	0.686937	0.288557	0.379484	0.25459	0.243243	0.61878	0.0834543	0.660295

Summary statistics	NGW_FFOK-1	NGW_FFOK-2	NGW_FFOK-3	NGW_AFOK	NGWsd_FFOK-1	NGWsd_FFOK-2	NGWsd_FFOK-3	NGWsd_AFOK	mean_NGW	sd_NGW
Observed Value	0.244927	0.20997	0.254996	0.56015	0.198128	0.21371	0.235732	0.256007	0.317511	0.162907

Summary statistics	R_FFOK-1	R_FFOK-2	R_FFOK-3	R_AFOK	Rsd_FFOK-1	Rsd_FFOK-2	Rsd_FFOK-3	Rsd_AFOK	mean_R	sd_R	tot_R
Observed Value	5.35294	6.92308	10	12.5263	5.25525	7.1933	8.66025	10.085	8.70058	3.19849	14.9

Summary statistics	FIS	FST	FIT
Observed Value	0.0600406	0.379787	0.417025

Summary statistics	FSt_FFOK-2_FFOK-1	FSt_FFOK-3_FFOK-1	FSt_FFOK-3_FFOK-2	FST_AFOK_FFOK-1	FST_AFOK_FFOK-2	FST_AFOK_FFOK-3
Observed Value	0.369919	0.466347	0.605607	0.27425	0.390591	0.293323

Summary statistics	PI_FFOK-2_FFOK-1	PI_FFOK-3_FFOK-1	PI_FFOK-3_FFOK-2	PI_AFOK_FFOK-1	PI_AFOK_FFOK-2	PI_AFOK_FFOK-3
Observed Value	6.37385	10.3268	9.92937	11.7598	11.6712	11.7937

Summary statistics	DMUSQ_FFOK-2_FFOK-1	DMUSQ_FFOK-3_FFOK-1	DMUSQ_FFOK-3_FFOK-2	DMUSQ_AFOK_FFOK-1	DMUSQ_AFOK_FFOK-2	DMUSQ_AFOK_FFOK-3
Observed Value	2.1967	9.99437	9.74943	9.99219	10.1139	20.6324

Confusion matrix based on 100 samples for each model (neuralnet, tolerance rate=0.01).

model focal \ selected	1 (best model)	2	3	4	5
1 (Single origin, gene flow)	0.85	0	0.01	0	0.14
2 (Parallel origin, gene flow)	0	0.73	0.08	0.19	0
3 (Parallel origin, no gene flow)	0	0.03	0.86	0.11	0
4 (Parallel origin, gene flow)	0	0.28	0.17	0.55	0
5 (Single origin, no gene flow)	0.04	0	0	0	0.96

Yellow mark indicates type2 error rate.

Mean model posterior probabilities (neuralnet, tolerance rate=0.01)

model focal \ selected	1 (best model)	2	3	4	5
1 (Single origin, gene flow)	0.7957	0.0073	0.0083	0.0094	0.1793
2 (Parallel origin, gene flow)	0.0071	0.5949	0.1312	0.2637	0.0031
3 (Parallel origin, no gene flow)	0.0033	0.0726	0.7346	0.1873	0.0022
4 (Parallel origin, gene flow)	0.0126	0.3331	0.1715	0.481	0.0017
5 (Single origin, no gene flow)	0.1331	0.0032	0.0025	0.0021	0.8591

Bayes Factor (neuralnet, tolerance rate=0.01)

numerator \ denominator	1	2	3	4	5
1 (Single origin, gene flow)	1.00	544.36	4300.22	1065.07	1.75
2 (Parallel origin, gene flow)	0.00	1.00	7.90	1.96	0.00
3 (Parallel origin, no gene flow)	0.00	0.13	1.00	0.25	0.00
4 (Parallel origin, gene flow)	0.00	0.51	4.04	1.00	0.00
5 (Single origin, no gene flow)	0.57	310.34	2451.54	607.19	1.00

Table S7 (Continued)

Kumejima

Prior distribution (Model 6)

parameter name	log10_n_AFKM	log10_n_FFKM-2	log10_n_FFKM-1	log10_t_FF	log10_t_root	log10_a	log10_b	log10_c	log10_d	m	p	a	b	c	d	n_AFKM	n_FFKM-2	n_FFKM-1	t_FF	t_root
distribution	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	NA	NA	NA	NA	NA	NA	NA	NA	NA
Min.	2	2	2	3	3	-9	-9	-9	-9	0.5	0	NA	NA	NA	NA	NA	NA	NA	NA	NA
Max.	5.3	4.7	4.7	6.2	6.2	-3	-3	-3	-3	2	1	NA	NA	NA	NA	NA	NA	NA	NA	NA
Complex parameter	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	10^(log10_a)	10^(log10_b)	10^(log10_c)	10^(log10_b)	10^(log10_n_AFKM)	10^(log10_n_FFKM-2)	10^(log10_n_FFKM-1)	10^(log10_n_t_FF)	10^(log10_t_root)

Posterior distribution (Model 6)

parameter name	log10_n_AFKM	log10_n_FFKM-2	log10_n_FFKM-1	log10_t_FF	log10_t_root	log_a	log_c	m	p	a	c	n_AFKM	n_FFKM-2	n_FFKM-1	t_FF	t_root
Min.	2.416127171	2.004640794	2.195688172	2.571801336	2.506533198	-11.03135065	-11.94135622	0.350029579	0.119638824	9.19E-12	1.66E-12	256.9803544	101.0271525	155.7156975	356.0300794	320.6380399
Weighted 2.5% Perc.	3.349392787	2.214602831	2.667328393	2.807337785	3.115649547	-8.863888873	-9.459927484	0.51226449	0.34271048	1.35E-09	3.76E-10	2210.427301	163.425521	466.8124526	616.3542291	1306.729313
Weighted Median	3.9063289	2.812843055	3.191056472	3.222978094	4.226772144	-5.412483207	-6.082777496	1.207500815	0.573843802	3.82E-06	8.86E-07	8050.746861	646.9069959	1561.363319	1619.003405	16957.61468
Weighted Mean	3.906568278	2.795631761	3.170139926	3.245222085	4.347789913	-5.74975406	-6.488813004	1.208351047	0.568498288	3.59E-05	4.18E-06	9966.727385	765.334502	1680.490703	2064.426182	92120.93428
Weighted Mode	3.843857634	2.843821278	3.209075825	3.167078368	3.918224242	-4.657233417	-5.454441533	0.711134174	0.571936334	3.88E-06	7.67E-08	5824.187544	505.2645714	1472.223727	1031.97428	5801.871497
Weighted 97.5% Perc.	4.442243706	3.314469105	3.565015759	3.798425659	5.809010545	-3.601695366	-4.589844626	1.927135582	0.764119195	0.000251621	2.74E-05	27658.72477	2064.018942	3687.98735	6016.462052	649944.7837
Max.	5.217529632	4.101331001	3.972027084	4.490901997	6.377450717	-2.248523711	-3.633882552	2.06084598	0.886429859	0.005984198	0.000239331	160577.8217	12546.79442	9468.430179	29648.41896	2419445.977

Observed Summary Statistics Value

Summary statistics	K_FFKM-1	K_FFKM-2	K_AFKM	Ksd_FFKM-1	Ksd_FFKM-2	Ksd_AFKM	mean_K	sd_K	tot_K
Observed Value	2.65	1.5	6.85	1.53125	0.688247	5.35355	3.66667	2.81617	8.25

Summary statistics	H_FFKM-1	H_FFKM-2	H_AFKM	Hsd_FFKM-1	Hsd_FFKM-2	Hsd_AFKM	mean_H	sd_H	tot_H
Observed Value	0.273834	0.0765779	0.537819	0.219506	0.148743	0.29866	0.296077	0.231424	0.569533

Summary statistics	GW_FFKM-1	GW_FFKM-2	GW_AFKM	GWsd_FFKM-1	GWsd_FFKM-2	GWsd_AFKM	mean_GW	sd_GW	tot_GW
Observed Value	0.564947	0.522009	0.671573	0.26537	0.328004	0.225123	0.586176	0.0770089	0.664282

Summary statistics	NGW_FFKM-1	NGW_FFKM-2	NGW_AFKM	NGWsd_FFKM-1	NGWsd_FFKM-2	NGWsd_AFKM	mean_NGW	sd_NGW
Observed Value	0.29725	0.175673	0.543082	0.247376	0.135949	0.280676	0.338668	0.187174

Summary statistics	R_FFKM-1	R_FFKM-2	R_AFKM	Rsd_FFKM-1	Rsd_FFKM-2	Rsd_AFKM	mean_R	sd_R	tot_R
Observed Value	5.77778	5.25	13.6471	5.07074	3.99106	12.879	8.22495	4.7031	13.95

Summary statistics	FIS	FST	FIT
Observed Value	0.0915018	0.478775	0.526468

Summary statistics	FSt_FFKM-2_FFKM-1	FST_AFKM_FFKM-1	FST_AFKM_FFKM-2
Observed Value	0.541478	0.415315	0.514248

Summary statistics	PI_FFKM-2_FFKM-1	PI_AFKM_FFKM-1	PI_AFKM_FFKM-2
Observed Value	7.49005	14.3749	14.2251

Summary statistics	DMUSQ_FFKM-2_FFKM-1	DMUSQ_AFKM_FFKM-1	DMUSQ_AFKM_FFKM-2
Observed Value	17.6762	21.6765	31.2206

Confusion matrix based on 100 samples for each model (neuralnet, tolerance rate=0.01).

model focal \ selected	1	2	3	4	5	6 (best model)	7	8
1 (Parallel origin, gene flow)	26	30	13	3	4	4	5	15
2 (Parallel origin, gene flow)	10	50	21	1	1	5	4	8
3 (Parallel origin, gene flow)	8	15	30	0	3	9	9	26
4 (Single origin, no gene flow)	2	2	0	75	0	9	9	3
5 (Parallel origin, gene flow)	1	24	12	13	19	12	13	6
6 (Single origin, restricted gene flow)	7	19	0	23	6	31	8	6
7 (Single origin, restricted gene flow)	3	4	7	28	3	1	34	20
8 (Parallel origin, no gene flow)	1	1	7	4	0	0	3	84

Yellow mark indicates type2 error rate.

Mean model posterior probabilities (neuralnet, tolerance rate=0.01)

model focal \ selected	1	2	3	4	5	6 (best model)	7	8
1 (Parallel origin, gene flow)	0.24	0.2216	0.1552	0.028	0.1058	0.0798	0.0679	0.1016
2 (Parallel origin, gene flow)	0.1801	0.2934	0.1855	0.0183	0.1169	0.0958	0.0539	0.0561
3 (Parallel origin, gene flow)	0.1604	0.153	0.2137	0.0121	0.1105	0.0707	0.0939	0.1857
4 (Single origin, no gene flow)	0.0308	0.0232	0.0153	0.4492	0.1015	0.1906	0.1533	0.0361
5 (Parallel origin, gene flow)	0.1108	0.1474	0.1272	0.0917	0.2154	0.1435	0.1129	0.0511
6 (Single origin, restricted gene flow)	0.0995	0.1232	0.0632	0.1674	0.1608	0.2594	0.0909	0.0357
7 (Single origin, restricted gene flow)	0.0754	0.0609	0.0921	0.1677	0.109	0.0935	0.2644	0.1369
8 (Parallel origin, no gene flow)	0.1039	0.0553	0.1594	0.0444	0.0429	0.0247	0.093	0.4765

Bayes Factor (neuralnet, tolerance rate=0.01)

numerator \ denominator	1	2	3	4	5	6 (best model)	7	8
1 (Parallel origin, gene flow)	1	8.3092	6.1755	0.0002	0.0003	0.0002	0.0003	3.2552
2 (Parallel origin, gene flow)	0.1203	1	0.7432	0	0	0	0	0.3918
3 (Parallel origin, gene flow)	0.1619	1.3455	1	0	0.0001	0	0.0001	0.5271
4 (Single origin, no gene flow)	4463.2158	37085.7043	27562.3749	1	1.5558	0.8965	1.5339	14528.6928
5 (Parallel origin, gene flow)	2868.7132	23836.6803	17715.6004	0.6427	1	0.5763	0.9859	9338.2561
6 (Single origin, restricted gene flow)	4978.2329	41365.0782	30742.8378	1.1154	1.7354	1	1.7109	16205.18
7 (Single origin, restricted gene flow)	2909.7535	24177.6918	17969.0427	0.6519	1.0143	0.5845	1	9471.8508
8 (Parallel origin, no gene flow)	0.3072	2.5526	1.8971	0.0001	0.0001	0.0001	0.0001	1

Table S7 (Continued)

Iriomotejima

Prior distribution (Model 6)

parameter name	log10_n_AFIR	log10_n_FFIR-8	log10_n_FFIR-1	log10_n_FFIR-6	log10_t_FF	log10_t_root	log10_b	log10_c	log10_e	log10_f	m	p	b	c	e	f	n_AFIR	n_FFIR-8	n_FFIR-1	n_FFIR-6	t_FF	t_root
distribution	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Min.	2	2	2	2	3	3	-9	-9	-9	-9	0.5	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Max.	5.3	4.7	4.7	4.7	6.2	6.2	-3	-3	-3	-3	2	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Complex parameter	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	10^(log10_b)	10^(log10_c)	10^(log10_e)	10^(log10_f)	10^(log10_n_AFIR)	10^(log10_n_FFIR-8)	10^(log10_n_FFIR-1)	10^(log10_n_FFIR-6)	10^(log10_t_FF)	10^(log10_t_root)

posterior distribution (Model 6)

parameter name	log10_n_AFIR	log10_n_FFIR-8	log10_n_FFIR-1	log10_n_FFIR-6	log10_t_FF	log10_t_root	log10_b	log10_c	log10_e	log10_f	m	p	b	c	e	f	n_AFIR	n_FFIR-8	n_FFIR-1	n_FFIR-6	t_FF	t_root
Min.	1.915487029	2.21968195	2.15476663	2.441619089	2.747147682	2.473732259	-11.21508222	-9.626500114	-9.801559582	-9.465448368	0.29780842	0.002710558	5.72E-12	2.07E-10	1.47E-10	3.15E-10	84.25277643	159.0992715	131.1922672	276.0443047	565.6402479	314.429606
Weighted 2.5% Perc.	2.782904526	2.953914706	2.720987649	3.087323057	2.924291202	3.111579607	-9.584977969	-8.615824726	-9.115491716	-8.704787727	0.446573465	0.288991886	2.57E-10	2.54E-09	7.62E-10	1.91E-09	620.2293597	881.255958	518.6265397	1181.967206	857.4029643	1274.29255
Weighted Median	3.715629567	3.659029266	3.232449278	3.772326725	3.297647403	4.258229583	-6.102813347	-5.730094717	-5.695216583	-5.559136046	1.028367829	0.546874289	7.55E-07	1.98E-06	1.96E-06	2.70E-06	5346.47333	4408.27543	1688.731104	5837.187609	2023.113308	17819.842
Weighted Mean	3.686588187	3.654443527	3.221828394	3.76793801	3.335202315	4.372551088	-6.454943357	-5.819280903	-5.966328467	-5.699428759	1.075953693	0.539573701	7.99E-06	6.28E-05	3.53E-05	8.11E-05	7832.198196	5961.144974	1883.967953	7715.033089	2769.863067	96475.62062
Weighted Mode	3.775550466	3.661780701	3.242285543	3.757131713	3.256977797	3.894817905	-5.040524556	-3.890349528	-4.25135968	-3.722119858	0.671001832	0.57290055	4.38E-07	8.69E-07	2.21E-06	-5.80E-08	2846.357543	2402.654168	1470.19855	3671.504606	1310.110453	8970.047402
Weighted 97.5% Perc.	4.45841304	4.322372895	3.632882996	4.404183987	3.94036625	5.850348299	-4.231739617	-3.323883092	-3.585472019	-3.197150551	1.858439401	0.752515902	5.61E-05	0.000496538	0.00025481	0.000609329	29675.48484	20143.94118	4299.770343	24963.88018	8869.999928	701214.2751
Max.	5.160344328	4.628358594	4.012198264	5.137285861	4.829166001	6.493866008	-3.291207014	-2.849310272	-2.591596757	-2.511623696	2.094541059	0.860199351	0.000477437	0.001502305	0.00244674	0.003012237	147579.5789	40978.71266	10703.12864	132535.9065	72536.52188	2969775.821

Observed Summary Statistics Value

Summary statistics	K_FFIR-1	K_FFIR-6	K_FFIR-8	K_AFIR	Ksd_FFIR-1	Ksd_FFIR-6	Ksd_FFIR-8	Ksd_AFIR	mean_K	sd_K	tot_K
Observed Value	2.35	3.75	3.75	5.85	1.81442	2.4034	4.35135	4.51051	3.925	1.44309	8.85

Summary statistics	H_FFIR-1	H_FFIR-6	FFIR-8	H_AFIR	Hsd_FFIR-1	Hsd_FFIR-6	Hsd_FFIR-8	Hsd_AFIR	mean_H	sd_H	tot_H
Observed Value	0.201064	0.388779	0.30482	0.477427	0.223632	0.288172	0.302482	0.262433	0.343023	0.117997	0.542345

Summary statistics	GW_FFIR-1	GW_FFIR-6	GW_FFIR-8	GW_AFIR	GWsd_FFIR-1	GWsd_FFIR-6	GWsd_FFIR-8	GWsd_AFIR	mean_GW	sd_GW	tot_GW
Observed Value	0.713468	0.720055	0.542658	0.689927	0.273476	0.26706	0.263749	0.224724	0.666527	0.0835859	0.658672

Summary statistics	NGW_FFIR-1	NGW_FFIR-6	NGW_FFIR-8	NGW_AFIR	NGWsd_FFIR-1	NGWsd_FFIR-6	NGWsd_FFIR-8	NGWsd_AFIR	mean_NGW	sd_NGW
Observed Value	0.216348	0.328606	0.265182	0.506789	0.132975	0.183321	0.148052	0.280571	0.329231	0.126981

Summary statistics	R_FFIR-1	R_FFIR-6	R_FFIR-8	R_AFIR	Rsd_FFIR-1	Rsd_FFIR-6	Rsd_FFIR-8	Rsd_AFIR	mean_R	sd_R	tot_R
Observed Value	5.92857	6.22222	16.7692	8.63158	10.4695	5.54718	27.7853	6.29118	9.3879	5.06769	17.45

Summary statistics	FIS	FST	FIT
Observed Value	0.0589495	0.399616	0.435008

Summary statistics	FST_FFIR-6_FFIR-1	FST_FFIR-8_FFIR-1	FST_FFIR-8_FFIR-6	FST_AFIR_FFIR-1	FST_AFIRIR_FFIR-6	FST_AFIR_FFIR-8
Observed Value	0.304243	0.455915	0.294781	0.48297	0.35409	0.39128

Summary statistics	PI_FFIR-6_FFIR-1	PI_FFIR-8_FFIR-1	PI_FFIR-8_FFIR-6	PI_AFIR_FFIR-1	PI_AFIRIR_FFIR-6	PI_AFIR_FFIR-8
Observed Value	8.36632	9.52423	9.57088	14.1875	13.5054	12.9078

Summary statistics	DMUSQ_FFIR-6_FFIR-1	DMUSQ_FFIR-8_FFIR-1	DMUSQ_FFIR-8_FFIR-6	DMUSQ_AFIR_FFIR-1	DMUSQ_AFIRIR_FFIR-6	DMUSQ_AFIR_FFIR-8
Observed Value	7.36113	11.5983	3.47136	25.9701	14.0454	20.1645

Confusion matrix based on 100 samples for each model (neuralnet, tolerance rate=0.01).

model focal \ selected	1	2	3	4	5	6(best model)
1 (Single origin, no gene flow)	0.9	0.03	0.01	0	0	0.06
2 (Parallel origin, no gene flow)	0.02	0.88	0	0.07	0.02	0.01
3 (Single origin, gene flow)	0.16	0.03	0.29	0.1	0.22	0.2
4 (Parallel origin, gene flow)	0	0.25	0.03	0.48	0.19	0.05
5 (Parallel origin, gene flow)	0.04	0.09	0.09	0.16	0.47	0.15
6 (SIngle origin, gene flow)	0.14	0.11	0.1	0.07	0.1	0.48

Yellow mark indicates type2 error rate.

Mean model posterior probabilities (neuralnet, tolerance rate=0.01)

model focal \ selected	1	2	3	4	5	6 (best model)
1 (Single origin, no gene flow)	0.6662	0.0294	0.0985	0.0044	0.0271	0.1743
2 (Parallel origin, no gene flow)	0.028	0.6313	0.0299	0.1906	0.0667	0.0536
3 (Single origin, gene flow)	0.123	0.0432	0.3061	0.1296	0.2042	0.1939
4 (Parallel origin, gene flow)	0.0059	0.2157	0.1167	0.3654	0.2155	0.0808
5 (Parallel origin, gene flow)	0.0368	0.0825	0.205	0.197	0.3357	0.1429
6 (SIngle origin, gene flow)	0.1299	0.0732	0.2285	0.0924	0.1365	0.3395

Bayes Factor (neuralnet, tolerance rate=0.01)

numerator \ denominator	1	2	3	4	5	6
1 (Single origin, no gene flow)	1	94024.0848	1.7085	234566.4108	2458.9742	0.7571
2 (Parallel origin, no gene flow)	0	1	0	2.4947	0.0262	0
3 (Single origin, gene flow)	0.5853	55033.272	1	137294.1532	1439.2631	0.4432
4 (Parallel origin, gene flow)	0	0.4008	0	1	0.0105	0
5 (Parallel origin, gene flow)	0.0004	38.2371	0.0007	95.392	1	0.0003
6 (SIngle origin, gene flow)	1.3208	124183.7803	2.2565	309807.2552	3247.7286	1

Table S7 (Continued)

Tokunoshima_Okinoerabujima

Prior distribution (Model2)

parameter name	log10_a	log10_b	log10_c	log10_d	log10_n_AF	log10_n_okino	log10_n_toku	log10_t_FF	log10_t_root	m	p	a	b	c	d	n_AF	n_okino	n_toku	t_FF	t_root
distribution	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	NA	NA	NA	NA	NA	NA	NA	NA	NA
Min.	-9	-9	-9	-9	2	2	2	3	3	0.5		NA	NA	NA	NA	NA	NA	NA	NA	NA
Max.	-3	-3	-3	-3	5.3	4.7	4.7	6.2	6.2	2		NA	NA	NA	NA	NA	NA	NA	NA	NA
Complex parameter	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	10^(log10_a)	10^(log10_b)	10^(log10_c)	10^(log10_d)	10^(log10_n_AF)	10^(log10_n_okino)	10^(log10_n_toku)	10^(log10_t_FF)	10^(log10_t_root)

Posterior distribution (Model2)

parameter name	log10_a	log10_b	log10_c	log10_d	log10_n_AF	log10_n_okino	log10_n_toku	log10_t_FF	log10_t_root	m	p	a	b	c	d	n_AF	n_okino	n_toku	t_FF	t_root
Min.	-10.14958659	-11.11341166	-11.45255462	-11.16476095	2.776673139	2.061336903	2.360266768	2.074409034	2.401879147	0.404548429	0.003573449	7.15E-11	6.89E-12	3.48E-12	6.82E-12	591.8862858	114.8724309	227.2451764	118.0719184	250.5689687
Weighted 2.5% Perc.	-9.202913073	-9.023659958	-8.941294563	-8.899285843	3.443063722	2.558173848	3.069487412	2.585305711	3.074086215	0.514615452	0.242243218	6.31E-10	9.55E-10	1.13E-09	1.21E-09	2738.742395	360.0914213	1161.64389	382.5846214	1196.245616
Weighted Median	-5.961562108	-5.348512608	-5.909820868	-5.452163411	4.050707087	3.27214837	3.710535377	3.241885296	4.424051541	1.146281297	0.532173827	1.10E-06	4.49E-06	1.22E-06	3.45E-06	11172.29011	1869.353565	5143.961394	1746.746089	26421.55556
Weighted Mean	-6.116380114	-5.784742914	-6.09210827	-5.690588205	4.053608151	3.246556204	3.698837717	3.347693538	4.452163395	1.176857129	0.524192096	3.82E-05	4.56E-05	1.75E-05	3.99E-05	14562.28311	2244.978483	6264.689698	7467.92739	113792.1471
Weighted Mode	-4.3469019	-4.50111073	-5.950859573	-5.511585451	4.003350363	3.328487865	3.714023312	3.1567225	3.890017278	0.666153834	0.579110955	-2.36E-06	-2.27E-06	-8.21E-07	2.27E-06	7453.902105	1283.334464	3690.010605	661.3093564	8150.788215
Weighted 97.5% Perc.	-3.500079707	-3.449034485	-3.847886318	-3.449370538	4.67254187	3.822723853	4.251151813	4.79650326	5.847947266	1.924979731	0.757162432	0.000315004	0.000348579	0.000140908	0.000347709	46575.89176	6619.335656	17901.79924	62485.42911	701379.1444
Max.	-2.542248289	-2.359737163	-2.920104543	-2.606485662	5.102251631	4.405683442	4.668525192	5.832934866	6.368778078	2.070120686	0.920796071	0.002853665	0.004411571	0.001196782	0.002424363	124846.5407	24946.85325	47142.42174	675162.9522	2326504.085

Observed Summary Statistics Value

Summary statistics	K_okino	K_toku	K_AF	Ksd_okino	Ksd_toku	Ksd_AF	mean_K	sd_K	tot_K
Observed Value	2.35	4.4	8.45	1.53125	4.41767	7.08947	5.06667	3.10416	9.4

Summary statistics	H_okino	H_toku	H_AF	Hsd_okino	Hsd_toku	Hsd_AF	mean_H	sd_H	tot_H
Observed Value	0.226868	0.324758	0.526077	0.268593	0.305237	0.338558	0.359234	0.152555	0.4863

Summary statistics	GW_okino	GW_toku	GW_AF	GWsd_okino	GWsd_toku	GWsd_AF	mean_GW	sd_GW	tot_GW
Observed Value	0.586317	0.607993	0.756569	0.241392	0.26461	0.163251	0.650293	0.0926739	0.722554

Summary statistics	NGW_okino	NGW_toku	NGW_AF	NGWsd_okino	NGWsd_toku	NGWsd_AF	mean_NGW	sd_NGW
Observed Value	0.246524	0.382195	0.649745	0.197962	0.202091	0.224729	0.426155	0.205173

Summary statistics	R_okino	R_toku	R_AF	Rsd_okino	Rsd_toku	Rsd_AF	mean_R	sd_R	tot_R
Observed Value	6.38462	8.27778	12.4444	7.98476	8.25908	11.4029	9.03561	3.10018	12.45

Summary statistics	FIS	FST	FIT
Observed Value	0.0437566	0.299879	0.330513

Summary statistics	FST_toku_okino	FST_AF_okino	FST_AF_toku
Observed Value	0.343439	0.303634	0.271697

Summary statistics	PI_toku_okino	PI_AF_okino	PI_AF_toku
Observed Value	8.33941	10.9974	11.7025

Summary statistics	DMUSQ_toku_okino	DMUSQ_AF_okino	DMUSQ_AF_toku
Observed Value	1.69281	3.63525	6.54198

Confusion matrix based on 100 samples for each model (neuralnet, tolerance rate=0.01).

model focal \ selected	1	2 (best model)	3	4	5
1 (Single origin, no gene flow)	0.85	0.08	0.01	0.05	0.01
2 (Single origin, gene flow)	0.23	0.29	0.16	0.17	0.15
3 (Parallel origin, gene flow)	0.02	0.07	0.37	0.24	0.3
4 (Parallel origin, gene flow)	0.08	0.1	0.22	0.37	0.23
5 (Parallel origin, gene flow)	0.04	0.06	0.17	0.15	0.58

Yellow mark indicates type2 error rate.

Mean model posterior probabilities (neuralnet, tolerance rate=0.01)

model focal \ selected	1	2 (best model)	3	4	5
1 (Single origin, no gene flow)	0.7214	0.1837	0.0197	0.0531	0.022
2 (Single origin, gene flow)	0.2064	0.3135	0.1605	0.184	0.1356
3 (Parallel origin, gene flow)	0.0195	0.1454	0.3236	0.2543	0.2572
4 (Parallel origin, gene flow)	0.08	0.1616	0.2381	0.2938	0.2265
5 (Parallel origin, gene flow)	0.0314	0.1381	0.2532	0.2236	0.3537

Bayes Factor (neuralnet, tolerance rate=0.01)

numerator \ denominator	1	2	3	4	5
1 (Single origin, no gene flow)	1.00	0.21	17.36	2.01	26.19
2 (Single origin, gene flow)	4.68	1.00	81.23	9.42	122.57
3 (Parallel origin, gene flow)	0.06	0.01	1.00	0.12	1.51
4 (Parallel origin, gene flow)	0.50	0.11	8.62	1.00	13.01
5 (Parallel origin, gene flow)	0.04	0.01	0.66	0.08	1.00

Table S7 (Continued)

Middle Ryukyu

Prior distribution (Model 9)

parameter name	log10_n_AF	log10_n_FF_amami	log10_n_FF_kume	log10_n_FF_okinawa	log10_n_FF_toku	log10_t_AF_kume	log10_t_AF_okinawa	log10_t_AF_toku	log10_t_migAM	log10_t_root
distribution	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform
Min.	2	2	2	2	2	3	3	3	3	3
Max.	5.3	4.7	4.7	4.7	4.7	6.2	6.2	6.2	6.2	6.2
Complex parameter	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

parameter name	log10_a	log10_b	log10_c	log10_d	log10_e	log10_f	log10_g	log10_h	p
distribution	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform
Min.	-3	-3	-3	-3	-3	-3	-3	-3	0
Max.	-9	-9	-9	-9	-9	-9	-9	-9	1
Complex parameter	NA	NA	NA	NA	NA	NA	NA	NA	NA

parameter name	a	b	c	d	e	f	g	h
distribution	NA	NA	NA	NA	NA	NA	NA	NA
Min.	NA	NA	NA	NA	NA	NA	NA	NA
Max.	NA	NA	NA	NA	NA	NA	NA	NA
Complex parameter	10^(log10_a)	10^(log10_b)	10^(log10_c)	10^(log10_d)	10^(log10_e)	10^(log10_f)	10^(log10_g)	10^(log10_h)

parameter name	n_AF	n_FF_amami	n_FF_kume	n_FF_okinawa	n_FF_toku	t_AF_kume	t_AF_okinawa	t_AF_toku	t_migAM	t_root
distribution	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Min.	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Max.	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Complex parameter	10^(log10_n_AF)	10^(log10_n_FF_amami)	10^(log10_n_FF_kume)	10^(log10_n_FF_okinawa)	10^(log10_n_FF_toku)	10^(log10_t_AF_kume)	10^(log10_t_AF_okinawa)	10^(log10_t_AF_toku)	10^(log10_t_migAM)	10^(log10_t_root)

Posterior distribution (Model 9)

parameter name	log10_n_AF	log10_n_FF_amami	log10_n_FF_kume	log10_n_FF_okinawa	log10_n_FF_toku	log10_t_AF_kume	log10_t_AF_okinawa	log10_t_AF_toku	log10_t_migAM	log10_t_root
Min.	2.515932389	1.928028296	2.014834638	1.984707728	2.00707657	3.145233619	3.004846334	2.877973342	2.913833761	3.436966624
Weighted 2.5% Perc.	3.645682495	2.705697791	2.221728838	2.145762034	2.602727452	3.770487707	3.441788565	3.037054959	3.190853327	4.210516157
Weighted Median	4.535063745	3.695012386	3.225344224	3.220492419	3.679509021	4.632633114	4.068283985	3.293149866	3.654190819	5.560978208
Weighted Mean	4.525815799	3.651123659	3.220042025	3.199351956	3.659327368	4.70426877	4.133202545	3.343679312	3.675360952	5.456470587
Weighted Mode	4.533936785	3.820844794	3.411052097	3.439022543	3.66595809	4.38750784	3.981764829	3.198773185	3.534742501	5.983430186
Weighted 97.5% Perc.	5.281118445	4.351156003	4.240545986	4.235369382	4.52792648	5.914152025	5.238440916	3.905770258	4.294795956	6.308150913
Max.	5.616444114	4.610816782	4.839682943	4.674744573	4.691854056	6.65184099	6.134771395	4.66805346	5.728802089	6.657055374

parameter name	log_a	log_b	log_c	log_d	log_e	log_f	log_g	log_h	p
Min.	-9.110623281	-9.153692197	-9.345605485	-9.97106862	-10.48226683	-9.270976144	-9.228641811	-9.267241605	-0.018745348
Weighted 2.5% Perc.	-8.727498544	-8.860402677	-8.929837428	-9.082391497	-9.164531523	-8.648965354	-8.927847126	-8.164336911	0.205117447
Weighted Median	-5.111002905	-5.608374585	-6.010291728	-4.862163437	-5.856261481	-5.271934656	-6.006617423	-4.067953627	0.51106773
Weighted Mean	-5.47760657	-5.758118518	-6.016227365	-5.457161362	-6.218087953	-5.527629157	-6.021962732	-4.654099873	0.503655554
Weighted Mode	-3.906302305	-3.665579041	-3.824516189	-4.045299065	-4.97247662	-3.815210138	-3.568875184	-3.34487359	0.514877917
Weighted 97.5% Perc.	-3.081820521	-3.155843012	-3.244955021	-3.395941409	-4.101654671	-3.116602055	-3.239931664	-2.497924441	0.760574815
Max.	-2.822831525	-2.983179258	-2.948039801	-2.760885808	-3.04031623	-2.187044083	-2.987419393	-1.639176956	0.895097821

parameter name	a	b	c	d	e	f	g	h
Min.	7.06E-10	7.45E-10	5.41E-10	1.12E-10	3.28E-11	4.67E-10	5.35E-10	4.38E-10
Weighted 2.5% Perc.	1.74E-09	1.38E-09	1.22E-09	8.72E-10	7.07E-10	2.18E-09	1.14E-09	6.69E-09
Weighted Median	7.26E-06	2.45E-06	1.03E-06	1.43E-05	1.40E-06	5.08E-06	9.48E-07	8.08E-05
Weighted Mean	0.000103456	8.84E-05	6.84E-05	7.33E-05	1.16E-05	9.78E-05	6.49E-05	0.000498404
Weighted Mode	3.15E-06	1.24E-06	-1.47E-07	1.54E-06	3.38E-07	-3.19E-06	2.08E-07	1.01E-05
Weighted 97.5% Perc.	0.000776532	0.000687988	0.000605431	0.000425498	7.97E-05	0.000742942	0.000552076	0.003083635
Max.	0.001413372	0.001005896	0.001130982	0.001804595	0.000981153	0.006280042	0.000951987	0.025961717

parameter name	n_AF	n_FF_amami	n_FF_kume	n_FF_okinawa	n_FF_toku	t_AF_kume	t_AF_okinawa	t_AF_toku	t_migAM	t_root
Min.	319.2687035	85.38682423	101.9785528	99.30479396	101.0141641	1370.922201	1024.017513	761.4456485	805.501497	2727.357864
Weighted 2.5% Perc.	4298.196681	515.8147627	166.4240244	143.512365	401.5625167	5922.811402	2812.404443	1095.905562	1553.033556	16233.85957
Weighted Median	33141.01212	4938.798864	1679.68186	1695.584983	4828.902364	42765.08105	11868.04426	1972.224064	4518.103771	363980.5972
Weighted Mean	50608.49071	6679.324402	3453.774205	3477.764307	8327.352923	128692.2115	28160.30139	2634.549528	6161.179225	579235.9126
Weighted Mode	14684.0877	2007.829395	630.1194652	561.8360028	1809.478321	21704.32791	6110.714289	1460.381887	2474.597486	82836.94965
Weighted 97.5% Perc.	187436.5835	22215.47585	17431.89075	17571.87469	34497.18328	835303.8483	175253.7513	8069.871065	19894.59361	2033283.063
Max.	405626.2736	38623.44926	68692.65173	47933.667	50225.70298	4553299.515	1358549.616	46881.51871	539502.8465	4585734.959

Observed Summary Statistics Value

Summary statistics	K_1	K_2	K_3	K_4	K_5	Ksd_1	Ksd_2	Ksd_3	Ksd_4	Ksd_5	mean_K	sd_K	tot_K
Observed Value	2.65	2.8	4.4	4.6	12.05	1.53125	1.47256	4.41767	5.11345	9.94974	5.3	3.87734	14.35

Summary statistics	H_1	H_2	H_3	H_4	H_5	Hsd_1	Hsd_2	Hsd_3	Hsd_4	Hsd_5	mean_H	sd_H	tot_H
Observed Value	0.273834	0.288875	0.324758	0.370812	0.571991	0.219506	0.239761	0.305237	0.319123	0.299479	0.366054	0.121036	0.621406

Summary statistics	GW_1	GW_2	GW_3	GW_4	GW_5	GWsd_1	GWsd_2	GWsd_3	GWsd_4	GWsd_5	mean_GW	sd_GW	tot_GW
Observed Value	0.564947	0.672185	0.607993	0.809459	0.717653	0.26537	0.288557	0.26461	0.192735	0.222763	0.674447	0.0955332	0.688728

Summary statistics	NGW_1	NGW_2	NGW_3	NGW_4	NGW_5	NGWsd_1	NGWsd_2	NGWsd_3	NGWsd_4	NGWsd_5	mean_NGW	sd_NGW
Observed Value	0.156938	0.156497	0.214441	0.221478	0.548467	0.0938338	0.0752668	0.113899	0.171366	0.222273	0.259564	0.164398

Summary statistics	R_1	R_2	R_3	R_4	R_5	Rsd_1	Rsd_2	Rsd_3	Rsd_4	Rsd_5	mean_R	sd_R	tot_R
Observed Value	5.77778	5.35294	8.27778	6.6	15.75	5.07074	5.25525	8.25908	7.37564	12.0257	8.3517	4.28446	19

Summary statistics	FIS	FST	FIT
Observed Value	0.0933461	0.372194	0.430797

Summary statistics	FST_2_1	FST_3_1	FST_3_2	FST_4_1	FST_4_2	FST_4_3	FST_5_1	FST_5_2	FST_5_3	FST_5_4
Observed Value	0.597144	0.599805	0.498581	0.593372	0.519027	0.524987	0.359291	0.251116	0.244667	0.294268

Summary statistics	PI_2_1	PI_3_1	PI_3_2	PI_4_1	PI_4_2	PI_4_3	PI_5_1	PI_5_2	PI_5_3	PI_5_4
Observed Value	13.7416	14.9434	12.1804	15.267	13.2503	14.1455	14.1308	12.0294	12.1935	13.6638

Summary statistics	DMUSQ_2_1	DMUSQ_3_1	DMUSQ_3_2	DMUSQ_4_1	DMUSQ_4_2	DMUSQ_4_3	DMUSQ_5_1	DMUSQ_5_2	DMUSQ_5_3	DMUSQ_5_4
Observed Value	12.4761	32.3385	17.8408	16.6124	26.9178	19.2818	24.8019	9.91446	5.28855	22.4146

Confusion matrix based on 100 samples for each model (neuralnet, tolerance rate=0.01).

model focal \ selected	1	2	3	4	5	6	7	8	9 (Best Model)	10
1 (Parallel origin, gene flow)	0.29	0	0.04	0.04	0.14	0.22	0.9	0	0	0.18
2 (Parallel origin, gene flow)	0	0.45	0	0	0	0	0	0.2	0.35	0
3 (Single origin, gene flow)	0.5	0	0.38	0.22	0.07	0.1	0.14	0	0	0.4
4 (Parallel origin, gene flow)	0.5	0	0.21	0.3	0.06	0.09	0.2	0	0	0.09
5 (Parallel origin, gene flow)	0.12	0	0.09	0.05	0.43	0.15	0.04	0	0	0.12
6 (Parallel origin, gene flow)	0.16	0	0.06	0.02	0.07	0.43	0.06	0	0	0.2
7 (Single origin, gene flow)	0.08	0	0.06	0.04	0.01	0.6	0.73	0	0	0.2
8 (Parallel origin, no gene flow)	0	0.06	0	0	0	0	0	0.89	0.05	0
9 (Parallel origin, gene flow)	0	0.41	0	0	0	0	0	0.15	0.44	0
10 (Parallel origin, gene flow)	0.1	0	0.08	0.06	0.03	0.15	0.04	0	0	0.54

Yellow mark indicates type2 error rate.

Mean model posterior probabilities (neuralnet, tolerance rate=0.01)

model focal \ selected	1	2	3	4	5	6	7	8	9 (Best Model)	10
1 (Parallel origin, gene flow)	0.2271	0.0122	0.0943	0.0964	0.1433	0.1795	0.0697	0.006	0.0123	0.1591
2 (Parallel origin, gene flow)	0.0094	0.3988	0.0048	0.0052	0.0083	0.0109	0.0039	0.1845	0.365	0.0091
3 (Single origin, gene flow)	0.0922	0.0059	0.2955	0.2071	0.0982	0.0773	0.1288	0.0032	0.0058	0.086
4 (Parallel origin, gene flow)	0.0832	0.0056	0.2084	0.2651	0.0911	0.0859	0.149	0.0039	0.0061	0.1017
5 (Parallel origin, gene flow)	0.1398	0.0142	0.1004	0.1058	0.3358	0.1262	0.0443	0.008	0.014	0.1115
6 (Parallel origin, gene flow)	0.1821	0.0112	0.0755	0.1039	0.1264	0.2583	0.0564	0.0073	0.015	0.164
7 (Single origin, gene flow)	0.0842	0.0049	0.1284	0.1183	0.0427	0.0603	0.5023	0.0073	0.005	0.0465
8 (Parallel origin, no gene flow)	0.005	0.1774	0.0024	0.0034	0.0062	0.0068	0.0061	0.6639	0.125	0.0037
9 (Parallel origin, gene flow)	0.0092	0.3863	0.0044	0.0053	0.008	0.011	0.0049	0.1274	0.434	0.0095
10 (Parallel origin, gene flow)	0.1442	0.0095	0.1034	0.0961	0.0863	0.1416	0.045	0.0045	0.0117	0.3578

Bayes Factor (neuralnet, tolerance rate=0.01)

numerator \ denominator	1	2	3	4	5	6	7	8	9	10
1 (Parallel origin, gene flow)	1.00	0.01	0.13	2.62	0.44	2.74	0.13	0.02	0.01	1.66
2 (Parallel origin, gene flow)	173.88	1.00	22.00	455.14	76.91	476.39	22.36	4.33	0.92	288.06
3 (Single origin, gene flow)	7.91	0.05	1.00	20.69	3.50	21.66	1.02	0.20	0.04	13.10
4 (Parallel origin, gene flow)	0.38	0.00	0.05	1.00	0.17	1.05	0.05	0.01	0.00	0.63
5 (Parallel origin, gene flow)	2.26	0.01	0.29	5.92	1.00	6.19	0.29	0.06	0.01	3.75
6 (Parallel origin, gene flow)	0.36	0.00	0.05	0.96	0.16	1.00	0.05	0.01	0.00	0.60
7 (Single origin, gene flow)	7.78	0.04	0.98	20.36	3.44	21.31	1.00	0.19	0.04	12.88
8 (Parallel origin, no gene flow)	40.19	0.23	5.08	105.19	17.78	110.10	5.17	1.00	0.21	66.58
9 (Parallel origin, gene flow)	189.52	1.09	23.97	496.06	83.83	519.23	24.37	4.72	1.00	313.97
10 (Parallel origin, gene flow)	0.60	0.00	0.08	1.58	0.27	1.65	0.08	0.02	0.00	1.00

Table S7 (Continued)

South Ryukyu

Prior distribution (Model 5)

parameter name	log10_a	log10_b	log10_c	log10_d	log10_n_AF	log10_n_ishigaki	log10_n_iriomote	log10_t_FF	log10_t_root	m	p	a	b	c	d	n_AF	n_ishigaki	n_iriomote	t_FF	t_root
distribution	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	uniform	NA	NA	NA	NA	NA	NA	NA	NA	NA
Min.	-9	-9	-9	-9	2	2	2	3	3	0.5	0	NA	NA	NA	NA	NA	NA	NA	NA	NA
Max.	-3	-3	-3	-3	5.3	4.7	4.7	6.2	6.2	2	1	NA	NA	NA	NA	NA	NA	NA	NA	NA
Complex parameter	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	10^(log10_a)	10^(log10_b)	10^(log10_c)	10^(log10_b)	10^(log10_n_AF)	10^(log10_ishigaki)	10^(log10_iriomote)	10^(log10_t_FF)	10^(log10_t_root)

Posterior distribution (Model5)

parameter name	log10_a	log10_b	log10_c	log10_d	log10_n_AF	log10_n_ishigaki	log10_n_iriomote	log10_t_FF	log10_t_root	m	p	a	b	c	d	n_AF	n_ishigaki	n_iriomote	t_FF	t_root
Min.	-10.41018112	-10.10277534	-10.00713071	-10.50807508	2.611704817	1.993488455	2.135259187	2.789609709	2.818403745	0.43645659	0.0003027	3.36E-11	8.17E-11	9.95E-11	3.66E-11	431.1793174	99.24520694	138.3037164	630.2111403	618.7346758
Weighted 2.5% Perc.	-9.134330709	-8.683549288	-8.826107389	-8.053864892	3.247355058	2.612327062	2.908432549	3.250282209	3.605341131	0.541477846	0.29644687	7.21E-10	2.02E-09	1.49E-09	9.30E-09	1763.714134	413.9688356	819.0888356	1750.357478	4025.782063
Weighted Median	-5.349287518	-5.262004739	-5.017281743	-4.771362921	3.893367898	3.269444635	3.626680308	3.818292744	4.88005598	1.238407052	0.528120686	4.53E-06	5.50E-06	9.72E-06	1.69E-05	7846.83798	1857.881138	4234.648749	6589.026835	76234.0719
Weighted Mean	-5.846756557	-5.584088808	-5.528189056	-5.072548038	3.890743197	3.251866104	3.602818945	3.895147357	4.911209857	1.244904324	0.521514117	3.65E-05	7.64E-05	6.14E-05	0.000168655	10349.16041	2219.046264	5216.152089	20220.76185	316656.6385
Weighted Mode	-4.386709355	-4.239063231	-4.118923658	-4.025084745	3.887053211	3.292880034	3.694422564	3.780748221	4.37540734	0.745433858	0.532950304	2.87E-06	-7.07E-07	3.26E-06	7.90E-06	5052.568074	1390.244892	2791.688958	5319.192251	17784.51235
Weighted 97.5% Perc.	-3.622195581	-3.200261519	-3.387626355	-2.87117254	4.518010446	3.778079715	4.191778683	5.140157887	6.321292904	1.959613182	0.713528915	0.000248307	0.000639776	0.000406212	0.001303584	33213.58103	5983.949561	15377.31758	140239.5293	2094257.497
Max.	-2.730132231	-2.0709959	-2.359728293	-1.925656583	5.236961662	4.499816253	4.669800824	6.247419837	6.858308816	2.054196232	0.824551573	0.001899799	0.00860596	0.004333239	0.011842609	175350.0396	31366.23533	44667.67009	1823148.674	7157235.775

Observed Summary Statistics Value

Summary statistics	K_iriomote	K_ishigaki	K_AF	Ksd_iriomote	Ksd_ishigaki	Ksd_AF	mean_K	sd_K	tot_K
Observed Value	3.75	3.1	7.3	2.4034	1.33377	4.78044	4.71667	2.26072	8.8

Summary statistics	H_iriomote	H_ishigaki	H_AF	Hsd_iriomote	Hsd_ishigaki	Hsd_AF	mean_H	sd_H	tot_H
Observed Value	0.388779	0.299456	0.50118	0.288172	0.241195	0.260336	0.396472	0.101081	0.569886

Summary statistics	GW_iriomote	GW_ishigaki	GW_AF	GWsd_iriomote	GWsd_ishigaki	GWsd_AF	mean_GW	sd_GW	tot_GW
Observed Value	0.720055	0.660067	0.653008	0.26706	0.260751	0.245748	0.67771	0.0368415	0.648847

Summary statistics	NGW_iriomote	NGW_ishigaki	NGW_AF	NGWsd_iriomote	NGWsd_ishigaki	NGWsd_AF	mean_NGW	sd_NGW
Observed Value	0.324162	0.267627	0.539343	0.216599	0.168378	0.223509	0.377044	0.143369

Summary statistics	R_iriomote	R_ishigaki	R_AF	Rsd_iriomote	Rsd_ishigaki	Rsd_AF	mean_R	sd_R	tot_R
Observed Value	6.22222	5.05882	12.0526	5.54718	2.92555	7.13733	7.77789	3.74746	13.35

Summary statistics	FIS	FST	FIT
Observed Value	0.0909702	0.349889	0.409029

Summary statistics	FST_ishigaki_iriomote	FST_AF_iriomote	FST_AF_ishigaki
Observed Value	0.501156	0.324191	0.331076

Summary statistics	PI_ishigaki_iriomote	PI_AF_iriomote	PI_AF_ishigaki
Observed Value	13.4829	13.3516	12.4218

Summary statistics	DMUSQ_ishigaki_iriomote	DMUSQ_AF_iriomote	DMUSQ_AF_ishigaki
Observed Value	13.1287	12.8723	7.13103

Confusion matrix based on 100 samples for each model (neuralnet, tolerance rate=0.01).

model focal \ selected	1	2	3	4	5 (best model)
1 (Single origin, no gene flow)	0.79	0.14	0.01	0	0.06
2 (Parallel origin, no gene flow)	0.03	0.84	0.04	0.01	0.08
3 (Parallel origin, no gene flow)	0.02	0.33	0.62	0	0.03
4 (Parallel origin, gene flow)	0	0	0	100	0
5 (Single origin, Gene flow,best model)	0.3	0.11	0.04	0	0.55

Yellow mark indicates type2 error rate.

Mean model posterior probabilities (neuralnet, tolerance rate=0.01)

model focal \ selected	1	2	3	4	5 (best model)
1 (Single origin, no gene flow)	0.461226746	0.088258646	0.043990076	0.000303527	0.162031194
2 (Parallel origin, no gene flow)	0.088916008	0.552662745	0.234758924	0.000154347	0.068301858
3 (Parallel origin, no gene flow)	0.060454802	0.274156831	0.499342396	0.015673549	0.081498049
4 (Parallel origin, gene flow)	0.000361667	0.00125748	0.023494941	0.477026376	0.008149881
5 (Single origin, Gene flow,best model)	0.178577648	0.098446936	0.090713468	0.010823468	0.384182543

Bayes Factor (neuralnet, tolerance rate=0.01)

numerator \ denominator	1	2	3	4	5
1 (Single origin, no gene flow)	1	14.01	2.7125	6.1901	0.0733
2 (Parallel origin, no gene flow)	0.0714	1	0.1936	0.4418	0.0052
3 (Parallel origin, no gene flow)	0.3687	5.1649	1	2.282	0.027
4 (Parallel origin, gene flow)	0.1615	2.2633	0.4382	1	0.0118
5 (Single origin, Gene flow,best model)	13.6333	191.002	36.9807	84.3915	1

Table S7 (Continued)

Ryukyu

Observed Summary Statistics Value

summary statistics	**K_iriomote**	**K_kume**	**K_okinawa**	**K_toku**	**K_amami**	**K_AF_north**	**K_AF_south**	**Ksd_iriomote**	**Ksd_kume**	**Ksd_okinawa**	**Ksd_toku**	**Ksd_amami**	**Ksd_AF_north**	**Ksd_AF_south**	**mean_K**	**sd_K**	**tot_K**
Observed Value	3.9	2.7	3.1	4.45	4.8	7.4	12.3	2.35975	1.59275	1.44732	4.43046	5.21738	4.75062	9.93717	5.52143	3.35657	16.75

summary statistics	**H_iriomote**	**H_kume**	**H_okinawa**	**H_toku**	**H_amami**	**H_AF_north**	**H_AF_south**	**Hsd_iriomote**	**Hsd_kume**	**Hsd_okinawa**	**Hsd_toku**	**Hsd_amami**	**Hsd_AF_north**	**Hsd_AF_south**	**mean_H**	**sd_H**	**tot_H**
Observed Value	0.400709	0.276203	0.305	0.326737	0.382825	0.506299	0.574718	0.286351	0.223413	0.231406	0.306826	0.312612	0.259003	0.297136	0.39607	0.10934	0.683888

summary statistics	**GW_iriomote**	**GW_kume**	**GW_okinawa**	**GW_toku**	**GW_amami**	**GW_AF_north**	**GW_AF_south**	**GWsd_iriomote**	**GWsd_kume**	**GWsd_okinawa**	**GWsd_toku**	**GWsd_amami**	**GWsd_AF_north**	**GWsd_AF_south**	**mean_GW**	**sd_GW**	**tot_GW**
Observed Value	0.596521	0.548082	0.478161	0.579161	0.601921	0.576826	0.570073	0.361611	0.289505	0.395811	0.296955	0.366161	0.300105	0.351067	0.564392	0.0419276	0.356417

summary statistics	**NGW_iriomote**	**NGW_kume**	**NGW_okinawa**	**NGW_toku**	**NGW_amami**	**NGW_AF_north**	**NGW_AF_south**	**NGWsd_iriomote**	**NGWsd_kume**	**NGWsd_okinawa**	**NGWsd_toku**	**NGWsd_amami**	**NGWsd_AF_north**	**NGWsd_AF_south**	**mean_NGW**	**sd_NGW**
Observed Value	0.107054	0.0470869	0.0684315	0.101614	0.0743156	0.159436	0.274882	0.149158	0.038491	0.0728588	0.135335	0.0764772	0.167159	0.311092	0.118974	0.0775722

summary statistics	**R_iriomote**	**R_kume**	**R_okinawa**	**R_toku**	**R_amami**	**R_AF_north**	**R_AF_south**	**Rsd_iriomote**	**Rsd_kume**	**Rsd_okinawa**	**Rsd_toku**	**Rsd_amami**	**Rsd_AF_north**	**Rsd_AF_south**	**mean_R**	**sd_R**	**tot_R**
Observed Value	20.6667	14.4444	31.3333	16.8889	35.625	24	43	33.3766	38.3869	39.7995	37.3881	58.2888	39.4856	54.0643	26.5655	10.4629	90.65

summary statistics	**FIS**	**FST**	**FIT**
Observed Value	0.102062	0.384027	0.446895

summary statistics	**FST_kume_iriomote**	**FST_okinawa_iriomote**	**FST_okinawa_kume**	**FST_toku_iriomote**	**FST_toku_kume**	**FST_toku_okinawa**	**FST_amami_iriomote**	**FST_amami_kume**	**FST_amami_okinawa**	**FST_amami_toku**	**FST_AF_north_iriomote**	**FST_AF_north_kume**	**FST_AF_north_okinawa**	**FST_AF_north_toku**	**FST_AF_north_amami**	**FST_AF_south_iriomote**	**FST_AF_south_kume**	**FST_AF_south_okinawa**	**FST_AF_south_toku**	**FST_AF_south_amami**	**FST_AF_south_AF_north**
Observed Value	0.575327	0.579388	0.586098	0.557793	0.595885	0.49019	0.526715	0.581072	0.500887	0.515678	0.319456	0.465398	0.459614	0.438372	0.408936	0.352726	0.356829	0.248316	0.242821	0.291398	0.283472

summary statistics	**PI_kume_iriomote**	**PI_okinawa_iriomote**	**PI_okinawa_kume**	**PI_toku_iriomote**	**PI_toku_kume**	**PI_toku_okinawa**	**PI_amami_iriomote**	**PI_amami_kume**	**PI_amami_okinawa**	**PI_amami_toku**	**PI_AF_north_iriomote**	**PI_AF_north_kume**	**PI_AF_north_okinawa**	**PI_AF_north_toku**	**PI_AF_north_amami**	**PI_AF_south_iriomote**	**PI_AF_south_kume**	**PI_AF_south_okinawa**	**PI_AF_south_toku**	**PI_AF_south_amami**	**PI_AF_south_AF_north**
Observed Value	15.7151	16.6719	14.0204	16.1648	15.0533	12.4401	16.5391	15.6529	13.7809	14.5124	13.6424	15.6878	15.979	15.3615	15.5275	15.7377	14.2531	12.3003	12.2968	14.0354	15.1204

summary statistics	**DMUSQ_kume_iriomote**	**DMUSQ_okinawa_iriomote**	**DMUSQ_okinawa_kume**	**DMUSQ_toku_iriomote**	**DMUSQ_toku_kume**	**DMUSQ_toku_okinawa**	**DMUSQ_amami_iriomote**	**DMUSQ_amami_kume**	**DMUSQ_amami_okinawa**	**DMUSQ_amami_toku**	**DMUSQ_AF_north_iriomote**	**DMUSQ_AF_north_kume**	**DMUSQ_AF_north_okinawa**	**DMUSQ_AF_north_toku**	**DMUSQ_AF_north_amami**	**DMUSQ_AF_south_iriomote**	**DMUSQ_AF_south_kume**	**DMUSQ_AF_south_okinawa**	**DMUSQ_AF_south_toku**	**DMUSQ_AF_south_amami**	**DMUSQ_AF_south_AF_north**
Observed Value	18.2243	18.3329	12.6695	21.4015	24.8697	19.8034	23.8487	17.6696	13.054	23.5592	19.1938	15.0099	6.85663	16.6374	14.1494	15.0493	16.5047	11.5923	8.92655	13.5864	13.3101

Confusion matrix based on 100 samples for each model (neuralnet, tolerance rate=0.01).

model focal \ selected	1	2	3	4	5	6	7	8	9	10
1	0.13	0.08	0.06	0.11	0.03	0.09	0.09	0.32	0.04	0.05
2	0.03	0.29	0.09	0.21	0.05	0.05	0.03	0.16	0.03	0.06
3	0.1	0.18	0.1	0.19	0.05	0.07	0.08	0.1	0.07	0.06
4	0.11	0.09	0.08	0.19	0.01	0.11	0.05	0.22	0.05	0.09
5	0.05	0.05	0.05	0.02	0.07	0.28	0.14	0.02	0.1	0.22
6	0.02	0.06	0.03	0.04	0.09	0.29	0.1	0.03	0.21	0.13
7	0.02	0.01	0.05	0.06	0.04	0.17	0.24	0	0.16	0.25
8	0.05	0	0.01	0.01	0	0	0	0.88	0.01	0.04
9	0.03	0.03	0.04	0.04	0.05	0.07	0.08	0.06	0.27	0.33
10	0	0.06	0.02	0.05	0.05	0.06	0.18	0.05	0.21	0.32

Mean model posterior probabilities (neuralnet, tolerance rate=0.01)

model focal \ selected	1	2	3	4	5	6	7	8	9	10
1	0.1448	0.1123	0.1085	0.1295	0.0753	0.0732	0.0691	0.1847	0.054	0.0485
2	0.1304	0.1672	0.1465	0.1412	0.0717	0.082	0.0608	0.0837	0.0627	0.0537
3	0.13	0.1374	0.1463	0.1537	0.077	0.0699	0.0709	0.0738	0.0722	0.0687
4	0.1339	0.1096	0.1162	0.1346	0.0783	0.0786	0.0828	0.1198	0.075	0.0713
5	0.0696	0.0877	0.0861	0.0735	0.1337	0.1431	0.1377	0.0137	0.1248	0.13
6	0.0706	0.0981	0.0869	0.0741	0.1275	0.1649	0.1227	0.0196	0.1239	0.1116
7	0.0587	0.0634	0.0765	0.071	0.1207	0.1127	0.1941	0.0089	0.1171	0.1767
8	0.1742	0.059	0.0605	0.1101	0.0126	0.0126	0.0134	0.5112	0.0223	0.0242
9	0.0552	0.0707	0.0783	0.0659	0.1134	0.1088	0.1238	0.0351	0.1678	0.1809
10	0.0525	0.0691	0.0731	0.0647	0.1042	0.0922	0.166	0.0268	0.1457	0.2057

Bayes Factor (neuralnet, tolerance rate=0.01)

numerator \ denominator	1	2	3	4	5	6	7	8	9	10
1	1	0.5872	0.6843	0.9137	0.6929	0.5795	0.6997	33.3996	0.8009	0.8466
2	1.7029	1	1.1652	1.556	1.18	0.9869	1.1914	56.8751	1.3638	1.4416
3	1.4614	0.8582	1	1.3354	1.0127	0.847	1.0225	48.8113	1.1705	1.2372
4	1.0944	0.6427	0.7489	1	0.7584	0.6343	0.7657	36.553	0.8765	0.9265
5	1.4431	0.8475	0.9875	1.3186	1	0.8363	1.0097	48.1998	1.1558	1.2217
6	1.7255	1.0133	1.1807	1.5767	1.1957	1	1.2073	57.6313	1.382	1.4608
7	1.4293	0.8393	0.978	1.306	0.9904	0.8283	1	47.7376	1.1447	1.21
8	0.0299	0.0176	0.0205	0.0274	0.0207	0.0174	0.0209	1	0.024	0.0253
9	1.2486	0.7332	0.8544	1.1409	0.8652	0.7236	0.8736	41.7024	1	1.057
10	1.1812	0.6937	0.8083	1.0793	0.8185	0.6846	0.8264	39.4521	0.946	1

Table S8 Geographic data of respective islands.

Island Name	Freshwater form distribution	Latitude	Longitude	Area (km ^{2})	Area log10	Catchment area (km ^{2})	Catchment area log10	Length (m)	Length log	No. Steep Slopes
Okinawajima Is.	1	26°35′	128°2′	1206.93	3.082	53.30	1.727	17218	4.236	152
Amami-Oshima Is.	1	28°16′	129°20′	712.5	2.853	48.58	1.686	18478	4.267	548
Iriomotejima Is.	1	24°20′	123°50′	289.6	2.462	64.37	1.809	21736	4.337	435
Tokunoshima Is.	1	27°45′	128°57′	247.9	2.394	34.00	1.531	15754	4.197	304
Ishigakijima Is.	1	24°24′	124°11′	222.2	2.347	32.75	1.515	14750	4.169	101
Okinoerabujima Is.	1	27°22′	128°35′	93.7	1.972	10.84	1.035	8813	3.945	15
Kakeromajima Is.	0	28°7′	129°14′	77.3	1.888	2.99	0.475	3601	3.556	26
Kumejima Is.	1	26°22′	126°46′	59.5	1.775	6.99	0.844	5925	3.773	35
Kikaijima Is.	0	28°18′	129°57′	57.0	1.755	4.81	0.683	4957	3.695	5
Iheyajima Is.	0	27°3′	127°58′	20.7	1.315	4.93	0.693	4428	3.646	2
Tokashikijima Is.	0	26°11′	127°21′	15.3	1.185	3.33	0.522	4029	3.605	19
Izenajima Is.	0	26°56′	127°56′	14.1	1.150	3.05	0.484	3918	3.593	3
Ukejima Is.	0	28°1′	129°15′	13.3	1.125	2.38	0.377	2275	3.357	21
Yorojima Is.	0	28°2′	129°9′	9.4	0.971	2.27	0.356	3257	3.513	12
Yagajijima Is.	0	26°40′	128°0′	7.8	0.893	1.16	0.063	2072	3.316	0
Miyagijima Is.	0	26°22′	128°0′	5.5	0.744	0.90	-0.048	1867	3.271	2
Akajima Is.	0	26°12′	127°17′	3.8	0.580	0.46	-0.333	1364	3.135	4
Hamahigajima Is.	0	26°19′	127°57′30″	2.1	0.320	0.36	-0.441	1297	3.113	0

Table S9 The results of statistical test and AIC model selection of logistic regression analysis for respective combinations of islands where speciation observed. 1 indicated speciation occurred, 0 indicated speciation did not occur.

Combinations of islands		Originate in respective regions				Share the origin in respective regions															
	Island name	Dataset 1	Dataset 2	Dataset 3	Dataset 4	Dataset 5	Dataset 6	Dataset 7	Dataset 8	Dataset 9	Dataset 10	Dataset 11	Dataset 12	Dataset 13	Dataset 14	Dataset 15	Dataset 16	Dataset 17	Dataset 18	Dataset 19	Dataset 20
	Okinawajima Is.	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0
	Amami-Oshima Is.	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	1	1	1	1
	Tokunoshima Is.	1	1	0	0	1	1	0	0	0	0	1	0	1	1	0	0	1	1	0	0
	Kumejima Is.	1	1	1	1	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1
	Okinoerabujima Is.	0	0	1	1	0	0	1	1	0	0	0	1	0	0	1	1	0	0	1	1
	Iriomotejima Is.	1	0	1	0	1	0	1	0	1	0	0	0	1	0	1	0	1	0	1	0
	Ishigakijima Is.	0	1	0	1	0	1	0	1	0	1	0	0	0	1	0	1	0	1	0	1
	Kakeromajima Is.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Kikaijima Is.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Tokashikijima Is.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Iheyajima Is.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Izenajima Is.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Ukejima Is.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Yorojima Is.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Yagajijima Is.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Miyagijima Is.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Akajima Is.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Hamahigajima Is.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Maximum likelihood ratio t	Explanatory variables	Dataset 1	Dataset 2	Dataset 3	Dataset 4	Dataset 5	Dataset 6	Dataset 7	Dataset 8	Dataset 9	Dataset 10	Dataset 11	Dataset 12	Dataset 13	Dataset 14	Dataset 15	Dataset 16	Dataset 17	Dataset 18	Dataset 19	Dataset 20
P values	Area	0.0016	0.0026	0.0054	0.0061	0.0001	0.002	0.005	0.0064	0.0068	0.0093	0.0073	0.0253	0.024	0.0317	0.0534	0.0606	0.0342	0.046	0.0733	0.0868
	Catchment Area	0.0026	0.0069	0.008	0.0187	0.0003	0.0041	0.0046	0.0113	0.0105	0.025	0.0242	0.0637	0.0191	0.0322	0.0479	0.082	0.0214	0.0346	0.0518	0.0899
	River Length	0.0038	0.0046	0.0077	0.0172	0.0006	0.0031	0.0057	0.0115	0.0101	0.0294	0.0239	0.0596	0.0212	0.0307	0.0502	0.0789	0.0191	0.0295	0.0464	0.0729
	No. Waterfall	0.0013	0.0697	0.0449	0.3277	2.00E-04	0.0347	0.0203	0.2627	0.0177	0.2163	0.0628	0.3241	0.1269	0.587	0.5181	0.8131	0.0055	0.0879	0.0614	0.4257

Model Selection	Explanatory variables	Dataset 1	Dataset 2	Dataset 3	Dataset 4	Dataset 5	Dataset 6	Dataset 7	Dataset 8	Dataset 9	Dataset 10	Dataset 11	Dataset 12	Dataset 13	Dataset 14	Dataset 15	Dataset 16	Dataset 17	Dataset 18	Dataset 19	Dataset 20
AIC scores	Island Area only	**19.478**	**13.005**	**13.922**	**15.965**	8.953	**4**	9.145	**12.471**	**13.366**	**13.939**	**14.678**	**14.382**	**16.682**	**16.532**	**17.063**	**18.315**	**18.729**	**17.553**	**18.016**	**19.113**
	Residuals of Catchment Area only	22.943	25.059	24.389	24.723	11.391	22.913	22.251	22.589	21.623	22.548	21.551	21.362	20.472	23.069	22.803	22.977	22.407	22.835	23.067	23.042
	Island Area + Residuals of Catchment Area	21.405	14.835	15.868	17.96	**6**	6	**6**	14.454	15.092	15.926	16.417	16.015	17.809	17.646	18.991	20.131	20.701	17.371	19.46	20.316
	Island Area * Residuals of Catchment Area	22.78	16.82	16.004	19.9	8	8	8	16.357	15.368	17.847	17.585	16.982	18.61	19.578	20.991	22.084	22.69	17.905	20.579	21.091
	Island Area only	**19.478**	**13.005**	**13.922**	**15.965**	8.953	**4**	9.145	**12.471**	**13.366**	**13.939**	**14.678**	**14.382**	**16.682**	**16.532**	**17.063**	**18.315**	**18.729**	17.553	**18.016**	**19.113**
	Residual of River Length only	23.067	25.018	24.386	24.88	11.646	22.888	22.274	22.76	22.026	22.34	21.326	21.368	21.006	23.058	22.734	23.012	22.567	22.726	23.062	22.873
	Island Area + Residual of River Length	21.107	14.918	15.832	17.932	**6**	6	**6**	14.351	15.276	15.935	16.272	15.99	18.098	17.902	19.025	20.064	20.727	**17.084**	19.201	19.669
	Island Area * Residual of River Length	22.611	16.908	15.996	19.764	8	8	8	15.937	14.921	17.852	17.32	17.138	18.757	19.893	21.019	22.051	22.615	17.652	20.199	20.856
	Island Area only	19.478	**13.005**	**13.922**	**15.965**	8.953	**4**	9.145	**12.471**	13.366	**13.939**	**14.678**	**14.382**	**16.682**	**16.532**	17.063	**18.315**	18.729	17.553	**18.016**	19.113
	Residuals of No. Waterfall only	20.894	24.196	20.881	22.692	9.13	22.551	19.758	21.339	16.818	21.989	18.335	20.969	18.718	20.977	15.981	18.731	**9.806**	23.03	22.305	22.913
	Island Area + Residuals of No. of Waterfall	21.288	13.13	14.906	17.963	10.952	6	**6**	14.442	**6**	15.538	15.159	16.38	17.679	18.52	**15.828**	19.161	11.775	14.038	19.719	20.019
	Island Area * Residuals of No. of Waterfall	**15.168**	15.081	16.756	19.49	**8**	8	8	16.087	8	17.538	16.986	18.377	18.832	20.438	16.985	21.052	13.672	**8**	18.523	**14.982**