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Population differentiation at a regional scale in spadefoot toads: contributions of distance and divergent selective environments

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Abstract

The causes of population differentiation can provide insight into the origins of early barriers to gene flow. Two key drivers of population differentiation are geographic distance and local adaptation to divergent selective environments. When reproductive isolation arises because some populations of a species are under selection to avoid hybridization while others are not, population differentiation and even speciation can result. Spadefoot toad populations *Spea multiplicata* that are sympatric with a congener have undergone reinforcement. This reinforcement has resulted not only in increased reproductive isolation from the congener, but also in the evolution of reproductive isolation from nearby and distant conspecific allopatric populations. We used multiple approaches to evaluate the contributions of geographic distance and divergent selective environments to population structure across this regional scale in *S. multiplicata*, based on genotypes from six nuclear microsatellite markers. We compared groups of populations varying in both geographic location and in the presence of a congener. Hierarchical F-statistics and results from cluster analyses and discriminant analyses of principal components all indicate that geographic distance is the stronger contributor to genetic differentiation among *S. multiplicata* populations at a regional scale. However, we found evidence that adaptation to divergent selective environments also contributes to population structure. Our findings highlight how variation in the balance of evolutionary forces acting across a species' range can lead to variation in the relative contributions of geographic distance and local adaptation to population differentiation across different spatial scales.

Key words: cascade reinforcement, character displacement, reproductive isolation, spatial scale, *Spea multiplicata*, speciation.

Elucidating the causes of genetic differentiation between populations of a single species can provide important insight into the speciation process, because the origins of early barriers to gene flow may often be concealed by evolutionary divergence after speciation (Via 2009). Even though incompletely isolated populations may not all proceed to complete reproductive isolation and species status (Nosil et al. 2009b), the mechanisms underlying population differentiation

are key for explaining biological diversity. Further, understanding the relative contributions of geographic distance and divergent selection, two potential factors underlying genetic differentiation, can shed light on longstanding questions about the importance of genetic drift versus selection in speciation (Coyne and Orr 2004).

Local adaptation is an important driver of population differentiation and speciation (Shafer and Wolf 2013; Sexton et al. 2014). When

populations adapt to different environments, gene flow between them may be reduced for multiple reasons (Schluter 2001; Rundle and Nosil 2005). When migrants mate with residents, any offspring that are phenotypically intermediate or otherwise mismatched to the environment are likely to be selected against, resulting in extrinsic postzygotic reproductive isolation (Hatfield and Schluter 1999; Pfennig and Rice 2007; Fuller 2008; Arnegard et al. 2014). Local adaptation may also reduce the likelihood of such matings. If migrants from alternate environments are maladapted to local conditions, they are less likely to survive to successfully reproduce (“immigrant inviability,” *sensu* Nosil et al. 2005). Likewise, when local adaptation results in the divergence of sexual signals or mating preferences, premating isolation can arise (Jiggins et al. 2004; Snowberg and Benkman 2007; Pfennig and Rice 2014).

Such mating trait divergence can not only arise when populations adapt to divergent ecological environments, but also when populations vary in the presence of an interacting species (Hoskin and Higgie 2010; Pfennig and Rice 2014). For instance, when some populations of a species co-occur with a closely related species while other populations do not (i.e., sympatric and allopatric populations, respectively), selection will act differently in these two environments. As a result of selection to avoid interspecific mating interactions or hybridization, sympatric populations might undergo reproductive character displacement (RCD) or reinforcement (Pfennig and Pfennig 2012); allopatric populations, on the other hand, do not. When the resulting divergence in mating traits between allopatric and sympatric populations results in reproductive isolation, speciation can occur. This process has been called both “RCD speciation” (Hoskin and Higgie 2010) and “cascade reinforcement” (Ortiz-Barrientos et al. 2009), and recent empirical and theoretical results suggest it may be an important initiator of speciation (Hoskin et al. 2005; Jaenike et al. 2006; McPeck and Gavrilets 2006, Pfennig and Ryan 2006, Svensson et al. 2006, Lemmon 2009, Porretta and Urbanelli 2012; Bewick and Dyer 2014; Pfennig and Rice 2014).

The reduction in gene flow because of adaptation to divergent selective environments has been called both “isolation by ecology” (IBE; Edelaar et al. 2012) and “isolation by adaptation” (IBA; Nosil et al. 2008). Yet, although IBE is an important and widespread pattern of gene flow (Shafer and Wolf 2013; Sexton et al. 2014), levels of gene flow are often affected by geographic distance as well (“isolation by distance” or IBD; Wright 1943). If dispersal is limited, then the likelihood of mating should be inversely related to the geographic distance separating individuals. In such a scenario, genetic drift alone can lead to population genetic differentiation. Understanding the relative contributions of divergent selective environments and geographic distance to population differentiation is further complicated by the fact that the two factors are often confounded; populations separated by large distances are more likely to experience different selective environments than are populations separated by small distances. Further, the relative roles of contributors to population structure may fluctuate across the landscape, due to variation in demographic parameters, the strength of divergent selection, or other factors.

Here, we examine the relative contributions of geographic distance and divergent selective environments to population differentiation at a regional scale in a system that exhibits both limited dispersal and reinforcement—the spadefoot toad *Spea multiplicata*. Premating isolation is present in this species between populations that have and have not undergone reinforcement, at both local and regional scales (Pfennig 2000; Pfennig and Rice 2014). At the local scale, population

differentiation is associated with this difference in selective environment (Rice and Pfennig 2010; Pfennig and Rice 2014); however, whether divergent selective environments contribute strongly to population structure at the regional scale remains unknown. To address this topic, we used multiple approaches to estimate population structure between groups of populations that varied in both selective environment and geographic location.

Materials and Methods

Study system

The overall goal of this study was to evaluate the contributions of geographic distance and divergent selective environments to population differentiation at a regional scale in the spadefoot toad *Spea multiplicata*. This species ranges from the southwestern United States into Mexico (Stebbins 2003). In the southwestern United States, *S. multiplicata*'s range overlaps broadly with the range of a congener, *S. bombifrons* (Stebbins 2003). During much of the year, individuals hibernate underground, emerging only during the summer months to breed and to feed (Bragg 1944, 1945). These species are explosive breeders in ephemeral ponds, formed during the summer rainy season (Bragg 1945). Where the ranges of the two species overlap, ponds vary locally in species composition: Some ponds contain only one species, while others contain both (Pfennig and Murphy 2000, 2002).

In ponds where the two species co-occur, they occasionally hybridize (Simovich and Sassaman 1986; Pfennig and Simovich 2002; Pfennig et al. 2012). This hybridization is costly for *S. bombifrons* in certain environments and always costly for *S. multiplicata* (Pfennig and Simovich 2002). As an indirect effect of selection against hybridization in sympatry, female *S. multiplicata* in sympatry versus allopatry with *S. bombifrons* experience divergent selective pressure on mate preferences. Allopatric *S. multiplicata* females can obtain fitness benefits by choosing males with faster calls (Pfennig 2000). In contrast, because the fast calls of *S. multiplicata* are similar to the calls of *S. bombifrons* males, sympatric *S. multiplicata* females lessen their risk of hybridizing by preferring males with slower call rates (Pfennig 2000). Consistent with the occurrence of reinforcement in sympatric populations, hybridization frequency has declined over time (Pfennig 2003). As a result of this divergent selection on female preferences between sympatric and allopatric *S. multiplicata*, premating reproductive isolation has evolved at both local (Pfennig and Rice 2014) and regional scales (Pfennig 2000): Females from both distant and nearby allopatric ponds prefer the calls of males from their own environments over the calls of males from sympatric ponds, and vice versa. Reinforcement has therefore led indirectly to the evolution of reproductive isolation in this species.

As a result of the reproductive isolation that has evolved between *S. multiplicata* populations in sympatry and allopatry with *S. bombifrons*, populations from the different selective environments should show signs of differentiation, relative to populations from the same selective environment. This prediction has been supported at a local scale by population genetic analyses of southeastern Arizona sympatric and allopatric populations (i.e., “East” populations, Figure 1, Table 1; Rice and Pfennig 2010, Pfennig and Rice 2014). At this scale, divergent selection contributes more to population differentiation than geographical distance (Pfennig and Rice 2014). Yet, although premating reproductive isolation has also been demonstrated between sympatric and more distant western allopatric populations (Pfennig 2000),



Figure 1. Map of *Spea multiplicata* population locations. Inset at upper left indicates map region. Black circles, west allopatric populations; white circle, central/west allopatric population; triangles, east populations. Triangle color indicates selective environment, with blue triangles as allopatric, and orange triangles as sympatric. Populations labeled following Table 1.

Table 1. Sampling and location information

Population code	N	UTM Northing (m)	UTM Easting (m)	Geographical category	Selective environment category
FT	12	3,513,168.81	680,005.47	East	Sympatry
SD	16	3,521,287.58	684,419.76	East	Sympatry
BP	18	3,529,290.03	679,851.46	East	Allopatry
HC	10	3,513,359.11	680,335.65	East	Sympatry
JC	10	3,534,202.38	676,772.4	East	Allopatry
PO	13	3,515,338.54	682,464.08	East	Sympatry
RT	19	3,535,263.87	677,991.59	East	Allopatry
SH	11	3,516,255.27	681,712.24	East	Sympatry
TR	10	3,534,235.32	677,745.99	East	Allopatry
YW	19	3,502,192.61	680,817.35	East	Allopatry
SRV	16	3,475,853.35	538,989.31	West	Allopatry
EL ^a	25	3,501,820.85	541,362.27	West	Allopatry
HE ^a	25	3,477,602.55	585,843.69	Central/West ^b	Allopatry

^aNew genotypic data presented in this study. Genotypes from the other eleven populations were previously generated for Pfennig and Rice (2014) and re-analyzed for this study.

^bThis population is classified as Central in the three geographic grouping scheme, and West in the two geographic grouping scheme.

the extent of population differentiation between populations at this larger scale, and the relative contributions of divergent selection versus geographic distance, remain unknown.

Sampling and genotyping

We analyzed genetic differentiation among 13 populations of *S. multiplicata* (Figure 1, Table 1) at 6 previously published microsatellite loci: Sb8 (Pfennig & Rice 2014), Spea C7, Spea D111, Spea D103 (Van Den Bussche et al. 2009), Sm14, and Sm25 (Rice et al. 2008). Each population was categorized based on its relative geographical location (Table 1, Figure 1; West, Central, or East) and its selective

environment (Table 1, Figure 1; Sympatry = *S. bombifrons* present, Allopatry = *S. bombifrons* absent). Genotypes from 11 of the 13 populations were generated for another study (Pfennig and Rice 2014; Table 1) and were reanalyzed for this study. We extracted DNA from *S. multiplicata* tissues that were collected from two additional populations located at least 65 km west of the *S. bombifrons* range edge (Figure 1; Table 1; tissues collected by K. and D. Pfennig). The DNA was extracted using a Qiagen (Valencia, California, USA) DNeasy Blood & Tissue Kit, following the manufacturer's instructions. We used a three-primer system to amplify the microsatellite markers, following Pfennig & Rice (2014). Sample sizes ranged from 10 to 25 per population (Table 1), similar to or greater than sample

sizes used in previous studies of population structure in this system (Rice and Pfennig 2008, 2010; Pfennig and Rice 2014; Rice et al. 2009). Although small sample sizes per population can decrease ability to accurately estimate allele frequencies, they are still useful for measuring genetic distance (Kalinowski 2005; Pruett and Winker 2008). Our choice to sample more populations over increasing sample sizes per population maximized our power to detect structure between groups of populations (Fitzpatrick 2009). Additionally, all of the genotypes from populations in sympatry with *S. bombifrons* were previously verified to be from pure-species *S. multiplicata* (Pfennig and Rice 2014). Thus, population differentiation cannot be explained by introgression with *S. bombifrons*.

Analyses

We used probability tests in Genepop 4.2 (Raymond and Rousset 1995; Rousset 2008) as implemented by Genepop on the Web (<http://genepop.curtin.edu.au>), to test for Hardy Weinberg Equilibrium and for genotypic linkage disequilibrium between all locus pairs across all populations. We also ran global tests for Hardy Weinberg for each locus across all populations using Fisher's method. The default Markov chain parameters were used for both linkage disequilibrium and Hardy Weinberg Equilibrium tests (i.e., 1,000 step dememorization, 100 batches, and 1,000 iterations per batch). Because only one locus was in Hardy Weinberg Equilibrium (see Results), we used Micro-Checker (van Oosterhout et al. 2004) to test whether the deviations from Hardy Weinberg were consistent with the presence of null alleles, using 1,000 randomizations and Bonferroni correction for multiple testing. Null alleles can affect estimates of population structure (Chapuis and Estoup 2006; Carlsson 2008; Guillot et al. 2008), so the Oosterhout correction algorithm was implemented in Micro-Checker (van Oosterhout et al. 2004) to estimate null allele frequencies and to generate corrected allele frequencies and genotypes for use in subsequent analyses where possible (see below).

We used several approaches to test for contributions of geographic distance and divergent selective environments on conspecific population differentiation in *S. multiplicata*. First, we assigned the populations to groups based on either geography or selective environment (Figure 1; Table 1). If geographic distance contributes more to the observed population differentiation than divergent selective environments, then the geographic population grouping should explain a greater proportion of the variation in genotype frequencies than the selective environment grouping. If the different selective environments make a greater contribution to population differentiation, however, then the opposite should be true.

To do this, we first used Analyses of Molecular Variance (AMOVA) in Arlequin 3.5 (Excoffier and Lischer 2010) to estimate population structure for our entire dataset. The 13 populations were grouped in three ways (Figure 1; Table 1), and hierarchical F -statistics were calculated to test which grouping explained the greatest percentage of variation in microsatellite genotypes (Crispo et al. 2006). We calculated F_{ST} and other F -statistics throughout instead of R_{ST} because simulations have shown that F_{ST} outperforms R_{ST} in conditions of moderate to small sample sizes and numbers of loci (Gaggiotti et al. 1999). The populations were placed either in three geographic groups (i.e., West, Central, East), in two geographic groups (i.e., West, East), or in two selective environment groups (i.e., Sympatric, Allopatric). In each of these cases, we calculated global F_{ST} and F_{CT} as weighted averages across loci. F_{ST} values indicate the proportion of the total variation in allele frequency that is explained by variation among the 13 populations, while F_{CT} values

indicate the proportion of the total variation in allele frequency that is explained by the geographic or selective groupings. We also calculated the same F -statistics for each locus individually. Because null alleles were likely present in our data (see "Results" section), we calculated F_{ST} and F_{CT} for each locus a second time using corrected allele frequencies. Global F -statistics were not calculated for the null allele-corrected data because corrected data could only be input in a format that does not allow multi-locus analyses in Arlequin. Significance of the F -statistics was estimated using 10,000 permutations of the data.

We next used the adegenet package (Jombart 2008; Jombart and Ahmed 2011) in R version 3.2.1 (R Core Team 2015) to assess the genetic population structure present among our different population groupings using Discriminant Analyses of Principal Components (DAPC) (Jombart et al. 2010). DAPC does not rely on assumptions of Hardy Weinberg Equilibrium (Jombart et al. 2010). It first transforms multi-locus genetic data into a set of fewer, uncorrelated variables using a principal components analysis; a discriminant analysis is then applied to a set of retained principal components, such that the variation between defined groups is maximized. In addition to allowing graphical assessment of population structure, DAPC also calculates the proportion of successful reassignment of individuals to their previously defined groups, based on the discriminant functions. A high proportion of successful reassignment indicates that the groups are genetically distinct, while a lower proportion suggests little structure between the groups. To test for contributions of geographic distance and selective environment on population structure in *S. multiplicata*, we performed DAPC analyses using the three previously described population groupings. If geographic distance contributes more than divergent selective environments to population structure in *S. multiplicata*, then we expected higher proportions of successful reassignment to geographic groups than to selective environment groups. Alternatively, if divergent selective environments contribute more, then higher proportions of successful reassignment to selective environment groups were expected. Because retaining too many principal components can lead to inflated reassignment success, we followed the recommendations of the DAPC tutorial and performed an a-score optimization to determine the optimal number of principal components to retain for each DAPC analysis. We then ran DAPC three times for each population grouping, retaining different numbers of principal components: 1) the optimal number based on a-score optimization; 2) the minimum optimal number across all groupings (i.e., 7; see "Results" section); and 3) the maximum optimal number across all groupings (i.e., 41; see "Results" section). Based on our results, we performed an additional DAPC analysis on a combined geographic and selective environment grouping (Figure 1; Table 1; i.e., West/Central allopatry, East allopatry, and Sympatry), and retained only the optimal number of principal components based on a-score optimization.

We also assessed evidence of population structure without prior groupings, and asked whether genetic clustering corresponded more clearly with geography or selective environment. To do this, we estimated the number of genetic clusters present in our microsatellite dataset using a spatially explicit Bayesian model implemented by the program Geneland (Guillot et al. 2005, 2008; Guillot 2008), version 4.0.5. If divergent selective environments contribute more to population differentiation in *S. multiplicata* than distance, then we expected to find two clusters corresponding to the selective environments. Likewise, if geographic distance is a stronger contributor, then we expected two or three clusters corresponding with the geographic groupings. Geneland defines genetic clusters by

assuming Hardy Weinberg Equilibrium within populations (Guillot et al. 2005); however, it also incorporates an optional algorithm to improve the accuracy of inferences when null alleles are present (Guillot et al. 2008). To estimate the number of genetic clusters present in our data, we ran ten independent runs of Geneland under each of two different sets of modeling parameters. Both parameter sets included the spatial model (incorporating 100 m coordinate uncertainty), the null allele filtering algorithm, a maximum of 13 populations, 1,000,000 Markov chain Monte Carlo (MCMC) iterations with every 1,000th iteration saved, and 200 saved iterations discarded as burn-in. The spatial coordinates were expressed in the Universal Transverse Mercator (UTM) coordinate system (Table 1). The first parameter set used the uncorrelated allele frequency model, and the second set used the correlated allele frequency model. Even though the correlated allele frequency model is likely to be a more accurate reflection of the biology of *S. multiplicata*, and may have more power to detect subtle population differentiation (Guillot 2008), it may also be less robust to deviations from model assumptions. For this reason, we followed the suggestions of the Geneland manual, and ran both correlated and uncorrelated allele frequency models. We checked that the 10 independent runs under each parameter set inferred similar numbers of clusters, in order to ensure that we ran Geneland for enough iterations. We then ran longer, single runs of Geneland under each parameter set, with 2,000,000 MCMC iterations, every 1,000th iteration saved, and 400 saved iterations discarded as burn-in, to obtain final estimates of cluster number. We visualized probability of population assignment to genetic clusters using the program *distruct* 1.1 (Rosenberg 2004).

It is important to note that although the preceding analyses allow us to test predictions about the relative contributions of geographic grouping versus selective environment on population differentiation, they do not allow us to directly compare the relative contributions of these effects in a single analysis. This is unfortunate, because ecological differences will often be confounded with geographic distance (Sexton et al. 2014), which is the case in our system (Figure 1). In recent years, a number of approaches have been developed to address this problem (e.g., Bradburd et al. 2013; Wang 2013b). Here, we employed three approaches in an effort to address this issue.

First, we performed a two-factor AMOVA to simultaneously estimate the effects of geography and selective environment on genetic variation. We used the PopGenReport package (Adamack and Gruber 2014) in R version 3.2.2 (R Core Team 2015) to calculate pairwise genetic distances among all individuals, based on Kosman and Leonard's (2005) genetic distance measure. We then used the *adonis* function in the *vegan* package (Oksanen et al. 2015) to run a two-factor AMOVA. As factors, we used geographic group (two levels: West, East) and selective environment (two levels: Sympatric, Allopatric). Significance was estimated with *F*-tests based on sequential sums of squares, using 1,000 permutations of the raw data.

The two-factor AMOVA tests the explanatory power of categorical variables; therefore, it does not include an explicit test for a linear relationship between geographic and genetic distance. Thus, we also performed a multiple matrix regression with randomization (MMRR) in R version 3.2.2 (R Core Team 2015) using the script supplied by Wang (2013a, 2013b) to simultaneously estimate the contributions of geographic distance and divergent selective environments to population differentiation. Our response matrix for this analysis was population pairwise F_{ST} , calculated in Arlequin 3.5 (Excoffier and Lischer 2010) without correcting for the presence of null alleles. We included all combinations of three predictor matrices: 1) a binary selective environment contrast matrix, with 0 representing a comparison between two

populations from the same selective environment, and 1 representing a comparison between two populations from different selective environments; 2) a Euclidean (i.e., straight line) geographic distance matrix, with pairwise distances calculated from the population UTM coordinates (Table 1); and 3) an environmental cost distance matrix (following Wang and Summers 2010). An environmental cost path analysis, also known as least-cost path analysis, determines the length of the most likely dispersal path by weighting potential dispersal paths between populations by predicted climate and elevation requirements for the species.

To calculate the environmental cost distance matrix, we first performed species distribution modeling to predict the environmentally suitable range for *S. multiplicata*. We extracted contemporary climate and elevation data (averages for years 1950–2000) from the WorldClim database (worldclim.org, Hijmans et al. 2005) at 30 arc-second resolution, and cropped the climate and elevation layers to include areas between latitudes 23°N–40°N and longitudes 96°W–113°W. We used all 19 bioclimatic variables, representing trends in temperature and precipitation, seasonality, and extreme or limiting environmental factors, plus elevation for our species distribution modeling. We obtained 268 georeferenced species occurrence locations from across the entire range of *S. multiplicata* based on the samples from this study (Table 1) plus records from 22 museums (data provided by A. Chuncó; Chuncó et al. 2012). After filtering out any samples occurring in the same grid cell, 236 records were left for building our distribution model. We used MAXENT version 3.3.3k (Phillips et al. 2006) to predict habitat suitability at each grid cell of the study area, with values ranging from 0 (unsuitable habitat) to 1 (fully suitable habitat). We then inverted the suitability values to create friction landscapes (i.e., cost values), and calculated pairwise environmental cost distances (i.e., least-cost paths) among our 13 populations using *SDMtoolbox* (Etherington 2011; Brown 2014) in ArcMap (ver. 10.2.2; ESRI, Redlands, CA, USA).

All matrices were standardized by subtracting the matrix mean from each value and dividing by the matrix standard deviation, as recommended in the MMRR tutorial (Wang 2013a). *P*-values were calculated using 10,000 permutations of the data. The predictor matrix with the largest significant regression coefficient contributes the most to population differentiation at this regional scale (Wang 2013b; Nanninga et al. 2014).

Thirdly, we performed one final DAPC analysis on the subset of individuals within the East geographic group, grouped by selective environment (Figure 1; Table 1). We retained only the optimal number of principal components based on a-score optimization. With this analysis, we examined the assignment of individuals from the YW population, which experiences an allopatric selective environment (Table 1), but is geographically nearer to the sympatric populations (Figure 1). If selective environment contributes to population structure, then individuals from the YW population should be correctly assigned to the allopatric selective environment grouping; however, if geographic distance is the sole contributor to population structure, then individuals from the YW population should instead be assigned to the sympatric selective environment grouping.

Results

Linkage disequilibrium and Hardy Weinberg equilibrium

Of 195 possible population–locus pair combinations, only six showed significant departures from linkage equilibrium at $P < 0.05$. When combined across populations, all locus pairs were in linkage

equilibrium ($P > 0.19$). Our six loci therefore provided independent data on population structure, and we retained genotypes from all six loci for subsequent analyses. Of the 78 possible population–locus combinations, five could not be tested for departure from Hardy Weinberg Equilibrium, either because the locus exhibited no polymorphism in a particular population (three of five cases, all Sb8), or

Table 2. Summary of tests for Hardy Weinberg Equilibrium and null alleles

	Sb8	SpeaC7	SpeaD111	Sm25	Sm14	SpeaD103
FT	N/A	X			X	N/A
SD	X		X		X	N/A
BP	X	X		X	X	
HC	X	X	X			
JC	X	X	X	X		
PO	X	X	X	X	X	
RT	N/A	X				
SH	X	X	X		X	
TR	X	X	X			
YW	X	X	X	X	X	
SRV	N/A	X			X	
EL	X			X		
HE			X	X		

Gray shading: significant evidence of null allele; X: significant deviation from Hardy Weinberg Equilibrium; N/A: no information because allele is fixed or failed to amplify.

because the locus failed to amplify in all individuals of a particular population (two of five cases, all SpeaD103). A majority of the remaining 73 population–locus combinations showed evidence of departure from Hardy Weinberg equilibrium at $P < 0.05$ (Table 2). In most cases, the pattern of departure from Hardy Weinberg equilibrium was consistent with the presence of a null allele (Table 2). Allele frequencies and genotypes corrected for the presence of null alleles using the Oosterhout algorithm in Micro-Checker (van Oosterhout et al. 2004) were therefore used when possible in our analyses of population structure.

Population structure

Results from the AMOVAs comparing different groupings of the full dataset are presented in Table 3. F_{ST} values were significantly greater than zero for individual loci and for the global weighted average across loci. Although individual locus F_{ST} values tended to decrease after correction for the presence of null alleles, they remained significantly greater than zero. Additionally, F_{ST} values were universally higher than corresponding F_{CT} values. Global weighted average F_{CT} values were significantly greater than zero for two of the population grouping schemes (Table 3), with a higher global F_{CT} for two geographic groups versus two selective environment groups. This suggests that grouping the populations into two geographic groups explains a higher proportion of the total genotypic variation than does grouping by selective environment. At the individual locus level, only one to three loci exhibited significant F_{CT} values,

Table 3. AMOVA results comparing different groupings of the full dataset

	Sb8	SpeaC7	SpeaD111	Sm25	Sm14	SpeaD103 ^a	Global ^b
A. Three geographic groups (West, Central, East)							
F_{ST} , uncorrected (<i>P</i> -value)	0.13333 (0.000)	0.08004 (0.000)	0.08016 (0.000)	0.10425 (0.000)	0.05578 (0.000)	0.05090 (0.002)	0.08520 (0.000)
F_{ST} , corrected (<i>P</i> -value)	0.15638 (0.000)	0.04704 (0.004)	0.04671 (0.000)	0.07942 (0.000)	0.01982 (0.013)	0.03702 (0.017)	
F_{CT} , uncorrected (<i>P</i> -value)	−0.05181 (0.741)	0.01057 (0.233)	0.00271 (0.340)	0.05371 (0.027)	0.01729 (0.115)	0.02763 (0.056)	0.01364 (0.133)
F_{CT} , corrected (<i>P</i> -value)	0.01320 (0.371)	0.03602 (0.038)	0.01385 (0.183)	0.06412 (0.005)	0.00056 (0.442)	0.01102 (0.236)	
B. Two geographic groups (West, East)							
F_{ST} , uncorrected (<i>P</i> -value)	0.15561 (0.000)	0.08981 (0.000)	0.09075 (0.000)	0.11507 (0.000)	0.05258 (0.000)	0.05877 (0.003)	0.09391 (0.000)
F_{ST} , corrected (<i>P</i> -value)	0.17967 (0.000)	0.05445 (0.003)	0.05525 (0.000)	0.08758 (0.000)	0.02103 (0.015)	0.04619 (0.018)	
F_{CT} , uncorrected (<i>P</i> -value)	0.00572 (0.248)	0.02772 (0.052)	0.02458 (0.076)	0.07073 (0.011)	0.00960 (0.201)	0.04074 (0.012)	0.03023 (0.003)
F_{CT} , corrected (<i>P</i> -value)	0.06468 (0.097)	0.04713 (0.011)	0.02961 (0.054)	0.07366 (0.004)	0.00284 (0.283)	0.02883 (0.043)	
C. Two selective environment groups (Sympatry, Allopatry)							
F_{ST} , uncorrected (<i>P</i> -value)	0.14488 (0.000)	0.08158 (0.000)	0.09652 (0.000)	0.09318 (0.000)	0.05983 (0.000)	0.03564 (0.002)	0.08898 (0.000)
F_{ST} , corrected (<i>P</i> -value)	0.14756 (0.000)	0.03341 (0.003)	0.05564 (0.000)	0.06817 (0.000)	0.02471 (0.013)	0.03690 (0.017)	
F_{CT} , uncorrected (<i>P</i> -value)	−0.01786 (0.612)	0.01520 (0.085)	0.03528 (0.015)	0.02409 (0.092)	0.02378 (0.029)	−0.00566 (0.620)	0.02043 (0.003)
F_{CT} , corrected (<i>P</i> -value)	−0.00801 (0.407)	0.00684 (0.217)	0.02881 (0.021)	0.03036 (0.058)	0.00953 (0.118)	0.00747 (0.279)	

^aLocus for which two populations (FT and SD) failed to amplify, so F-statistics calculated with only 11 populations.

^bWeighted average over five loci (not including SpeaD103), for 13 populations.

Boldfaced values indicate statistical significance at $P < 0.05$.

Table 4. Summary of DAPCs

Population grouping scheme	Number of discriminant functions	Optimal number PCs	Proportion of overall correct assignment			
			Optimal number PCs retained	7 PCs retained ^a	41 PCs retained ^a	Mean for 7 and 41 PCs retained
A. Three geographic groups	2	41	0.887	0.721	0.887	0.804
B. Two geographic groups	1	7	0.804	0.804	0.917	0.861
C. Two selective environment groups	1	8	0.775	0.784	0.887	0.836

^aData used to calculate mean proportion of overall correct assignment.

depending on the grouping scheme and whether the data had been corrected for null alleles. Unlike for F_{ST} , many individual locus F_{CT} values actually increased upon correction for the presence of null alleles, particularly for the two geographic grouping schemes (Table 3, Panels A and B). Thus, although the global weighted average F_{CT} values were of similar magnitude for the two geographic groups (Table 3, Panel B) and the two selective environment groups (Table 3, Panel C), the presence of null alleles likely affected estimates of F_{CT} for individual loci in opposite directions for these two groups.

The optimal number of principal components to retain in our DAPC analyses varied among the population grouping schemes, with a minimum of seven principal components retained, and a maximum of 41 (for two and three geographic groups, respectively; Table 4). DAPC scatter plots indicated that the eastern populations were relatively distinct from the western and central

populations along the first discriminant function axis, while the western and central populations exhibited more subtle structure along the second discriminant function axis (Figure 2A). When grouping the populations into either two geographic or two selective environment groups, some separation was evident along the first discriminant function axis, but in both cases, substantial overlap remained (Figs. 2B and 2C). Likewise, the proportion of overall correct assignment to original groups was higher for the three geographic groups than for the two geographic or two selective environment groups (Table 4). However, as expected, the relative values of the proportion of overall correct assignment were dependent on the number of principal components retained in each DAPC (Table 4). To allow direct comparisons of correct assignment proportions among the population grouping schemes, we calculated a mean proportion of overall correct assignment

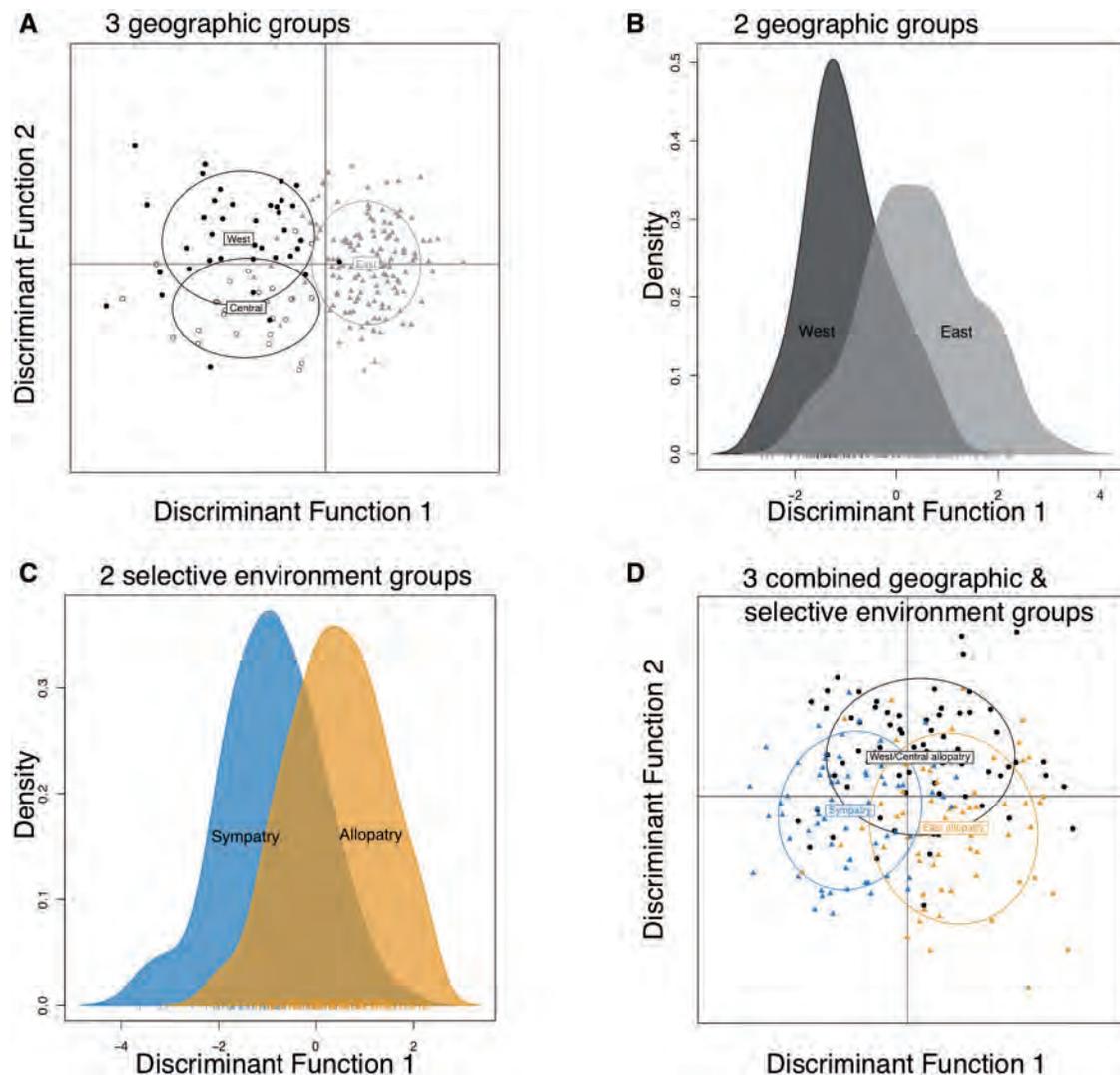


Figure 2. Scatterplots of DAPC for each of four different population grouping schemes. Each panel depicts DAPC results when the optimal number of principal components was retained, as determined by a-score optimization (see text, Table 5). A) Three geographic groups, with black circles indicating the west group, white circles indicating the central group, and gray triangles indicating the east group. Inertia ellipses are labeled with the group name. B) Two geographic groups, with the dark gray distribution indicating the west group and the light gray distribution indicating the east group. C) Two selective environment groups, with the blue distribution indicating the sympatric group and the orange distribution indicating the allopatric group. D) Three combined geographic and environmental groups, with black circles representing West/Central allopatry, orange triangles representing East allopatry, and blue triangles representing sympatry. Inertia ellipses are labeled with the group name.

based on assignments using the minimum and maximum optimal numbers of principal components (7 and 41 PCs, respectively; Table 4). This mean value was highest for the two geographic groups (Table 4). Breaking down the proportion of correct assignment by group when retaining the optimal number of principal components shows that the East geographic group is genetically distinct (Figure 3A and 3B) because of its accurate assignment. The proportion of correct reassignment to the West geographic group was higher when the Central population (HE) was not lumped in with the two populations farther west (SRV and EL; Figure 3A and 3B), suggesting that the HE population is slightly differentiated from EL and SRV. The higher proportion of correct reassignment for the Allopatry versus the Sympatry selective environment groups (Figure 3C) is likely because the Allopatry group contains both West/Central and East populations, which are genetically distinct from each other (Figure 2A). The scatter plot for the combined geographic and selective environment grouping shows some separation between the Sympatry and Allopatry selective environments along the first discriminant function axis (Figure 2D). This structure combined with the subtle separation between the West/Central allopatry populations and the remaining populations along the second discriminant function axis (Figure 2D) suggests that both geography and selective environment contribute to population differentiation.

The two sets of 10 independent Geneland runs, using either the uncorrelated or the correlated allele frequency models, were consistent in the number of clusters inferred, with the uncorrelated allele frequency model inferring two clusters in all ten runs, and the correlated allele frequency model inferring either five or six clusters (Table 5). The consistency of inferred cluster number suggested that Geneland runs of at least 1,000,000 MCMC iterations were of appropriate length. In a single run of 2,000,000 MCMC iterations, the uncorrelated allele frequency model again inferred two genetic clusters (Figure 4). These clusters corresponded to the West and East population groups (Figs. 1 and 4). The correlated allele frequency model inferred the presence of six genetic clusters after a run of 2,000,000 MCMC iterations (Figure 5). However, the five clusters showed no clear correspondence to any geographic or selective environment grouping (Figure 5).

Consistent with the DAPC results (Figure 2D), the two-factor AMOVA also indicated that both geographic grouping and selective environment explain the observed genetic variation (Table 6), but the higher partial R^2 value for geographic group suggested that this factor explains a greater proportion of the genetic variation than does selective environment. When the order of the factors is switched, both remain significant, and the partial R^2 remains higher for geographic group (data not shown). The overall MMRR model, however, was not significant ($R^2=0.007$, $F=0.179$, $P=0.961$),

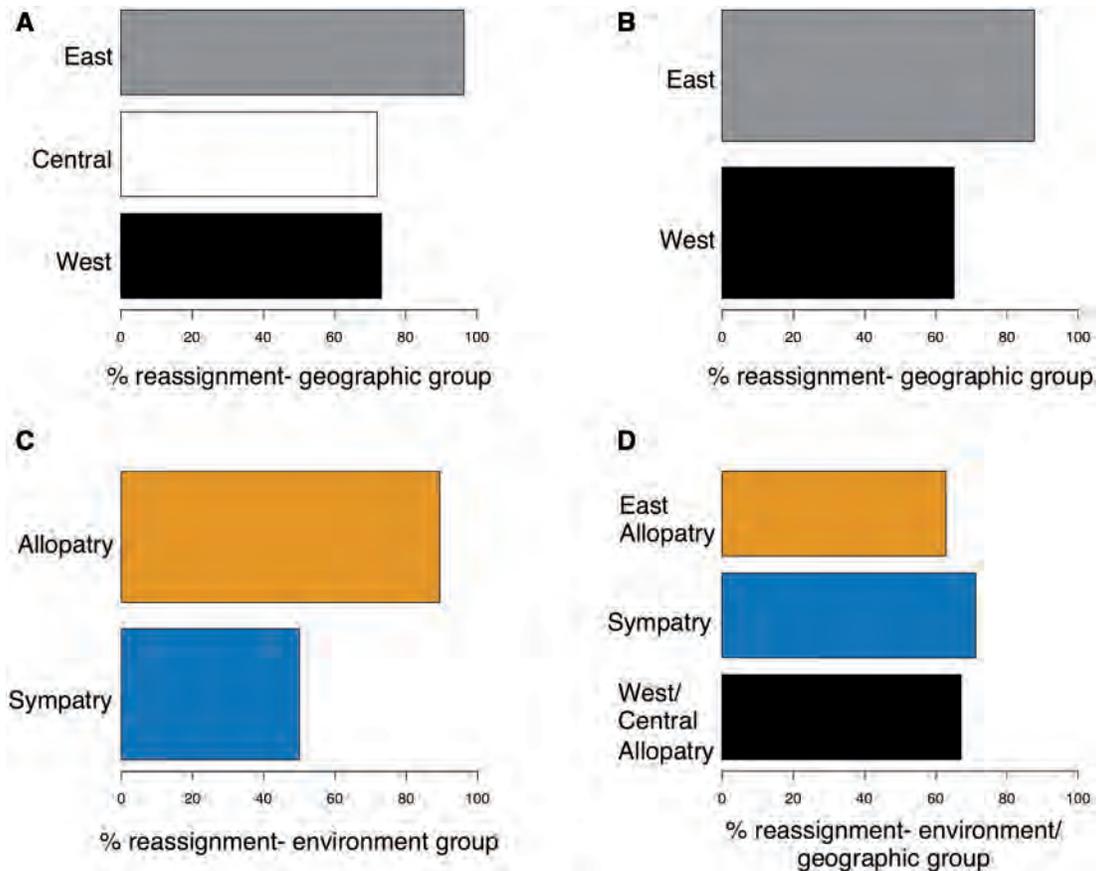


Figure 3. Percent correct reassignment to original population group by DAPC, for each of four different population grouping schemes. Each panel depicts DAPC results when the optimal number of principal components was retained, as determined by a-score optimization (see text, Table 4). In each panel, the group names are on the left. Colors correspond to Figure 2. A) Three geographic groups; B) two geographic groups; C) two selective environment groups; and (D) three combined geographic and selective environment groups.

Table 5. Summary of independent Geneland runs under two modeling parameter sets

Run	Inferred number of clusters (Mode height of posterior distribution, %)	Mean of posterior probability distribution
Uncorrelated allele frequencies		
1	2 (43.25)	-3529.57243
2	2 (45.50)	-3541.22173
3	2 (46.50)	-3543.586784
4	2 (45.00)	-3524.145509
5	2 (49.25)	-3575.041492
6	2 (45.88)	-3510.737678
7	2 (48.50)	-3546.914796
8	2 (41.00)	-3491.46949
9	2 (49.88)	-3552.511677
10	2 (44.50)	-3531.811381
Correlated allele frequencies		
1	5 (70.88)	-1493.8793
2	6 (36.50)	-1024.9787
3	6 (35.88)	-1648.6143
4	5 (68.88)	-1531.3952
5	6 (29.88)	-745.1921
6	5 (62.13)	-1419.4386
7	5 (55.63)	-1746.0225
8	6 (42.88)	-677.9943
9	5 (61.75)	-1958.0136
10	6 (58.13)	-137.5810

suggesting that none of the three explanatory matrices—selective environment contrast, Euclidean geographic distance, or environmental cost distance—explained a significant amount of the variation in population pairwise F_{ST} at this scale. With the DAPC reassignment of YW population individuals to selective environments, we found that 16 of 19 YW individuals were assigned to the allopatric selective environment (84.2%). This result was consistent with selective environment contributing to population structure at a more local scale.

Discussion

We evaluated the extent of population differentiation present at a regional scale among populations of *S. multiplicata* that are allopatric and sympatric with the congener, *S. bombifrons*. We then examined the relative contributions of divergent selective environments and geographic distance for explaining the observed population differentiation. To do this, we used multiple approaches to estimate population structure based on microsatellite genotypes from 13 populations, varying in selective environment and geographic location. Our hierarchical AMOVA (Table 3), DAPC (Table 4), two-factor AMOVA (Table 6) and Geneland (Figure 4) results indicate that geographic distance contributes more strongly to moderate population differentiation across a regional scale. However, evidence from both the hierarchical (Table 3) and two-factor AMOVAs (Table 6), and the DAPC analyses (Figure 2D) also support a role for divergent selective environments, particularly at a more local scale.

Our estimates of F_{ST} indicate the presence of moderate population differentiation, with estimates significantly higher than zero globally ($F_{ST} \sim 0.09$) and for each individual locus (Table 3). There was variation between F_{ST} estimates that were and were not corrected for the presence of null alleles, as expected based on

simulation results (Chapuis and Estoup 2006) and our own previous work in this system (Rice and Pfennig 2010; Pfennig and Rice 2014). However, even after correcting for null alleles, F_{ST} remained significantly greater than zero at every locus. Our finding of population differentiation at this regional scale was consistent with our expectations, based on *S. multiplicata*'s limited opportunities for dispersal and on previous research in this system at a smaller spatial scale (Rice and Pfennig 2008, 2010; Rice et al. 2009, Pfennig and Rice 2014). However, the level of differentiation present among our populations was lower than expected for two reasons. First, a previous study of local population structure among the East *S. multiplicata* populations (Figure 1, Table 1) resulted in F_{ST} values that were only slightly lower than estimates from this study (Pfennig and Rice 2014), even though the populations in this study span nearly six times the distance. Second, at similar or even smaller spatial scales, amphibian species often exhibit higher levels of population structure than what we found (Burns et al. 2004; Arens et al. 2006).

Several nonmutually exclusive factors can explain why the level of population differentiation in *S. multiplicata* was lower than expected. First, the microsatellite markers we chose for this study were a subset of those used in Pfennig and Rice (2014), which renders the F_{ST} estimates not directly comparable between the two studies. Additionally, the high variability of microsatellite markers can result in underestimates of population differentiation (Hedrick 1999). Second, it is possible that *S. multiplicata* have a greater capacity for dispersal than many amphibian species. Although a moderate level of dispersal is likely among several of our East ponds because of the small distances separating them (< 5 km), we think this is unlikely as a general explanation for our findings; this species lives in a desert environment, and spends much of the year hibernating in underground burrows (Bragg 1944, 1945). Finally, demographic factors, such as recent range expansions or large population sizes, can affect levels of population differentiation (Hewitt 2000; Johansson et al. 2006; Wellenreuther et al. 2011). Genetic differentiation of the East *S. multiplicata* populations (Figure 1) based on mitochondrial *cytochrome b* sequences suggests that these populations have not undergone recent population growth or range expansion (Rice and Pfennig 2008). However, additional research is needed on the phylogeography and demography of *S. multiplicata* populations across the species range to evaluate demographic history as an explanation for our findings.

Our results suggest that at a regional scale, geographic distance contributes more to the observed population differentiation in *S. multiplicata* than does selective environment. The two geographic groups explained a greater proportion of the total variation in genotype frequencies than did the three geographic or the two selective environment groups (Table 3). When the number of retained principal components for DAPC was standardized across the three grouping schemes, the two geographic groups had the highest mean proportion of overall correct assignment (Table 4). The higher partial R^2 value for geographic grouping in the two-factor AMOVA also suggest this factor explained more of the genetic variation (Table 6). Finally, the uncorrelated allele frequency model in Geneland inferred two genetic clusters (Figure 4A) with strong correspondence to the two geographic groups (Figure 4B). This result contrasts with contributions to population structure at a local scale; Pfennig and Rice (2014) found that selective environment explained more of the population differentiation among the East populations (Figure 1) than did geography. Our finding that 84.2% of the individuals from the YW population were assigned to the allopatric selective environment by a DAPC, even though located nearer to other sympatric populations, is consistent with Pfennig and Rice (2014).

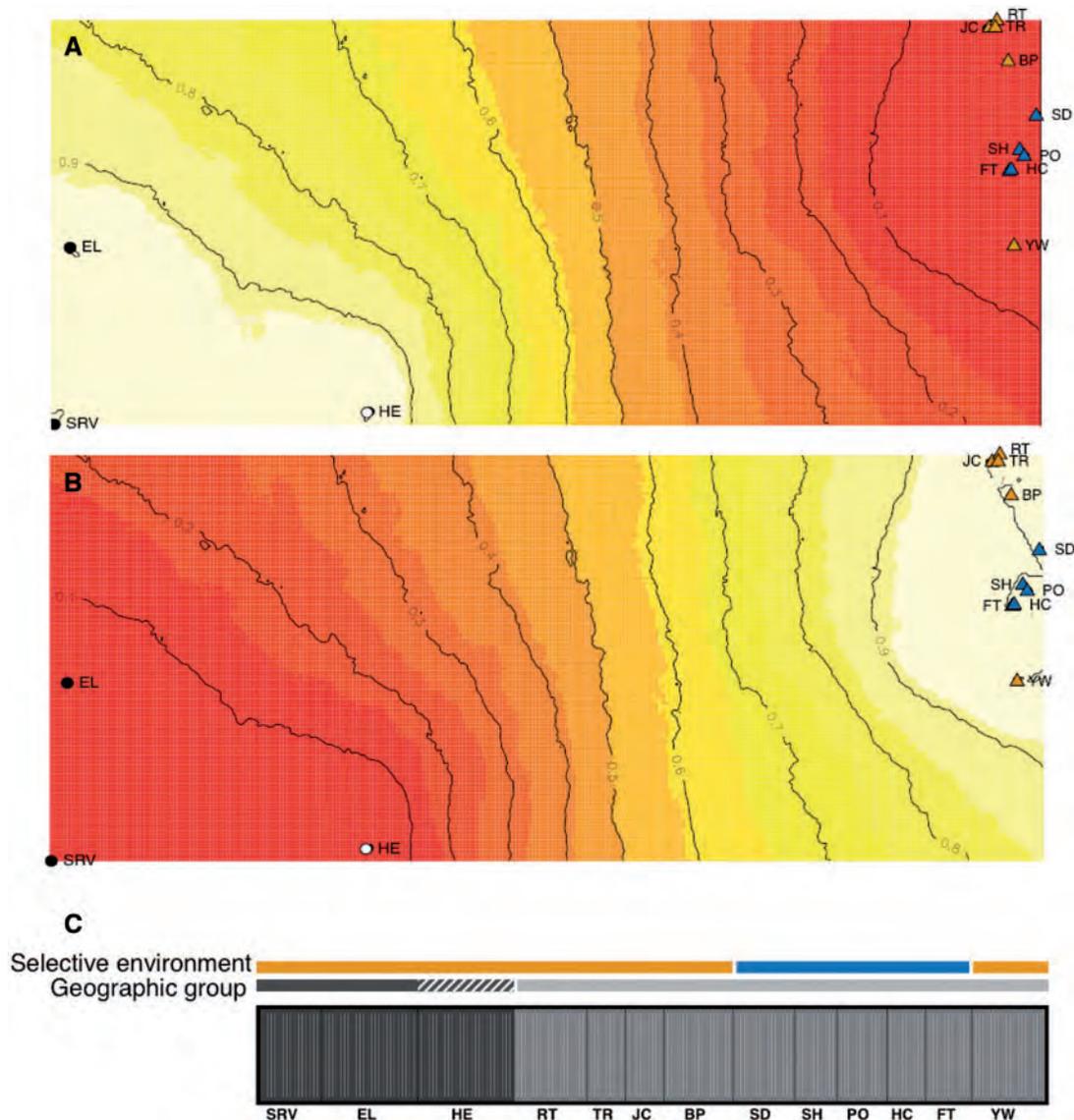


Figure 4. Geneland results for the uncorrelated allele frequency model. Run length was equal to 2,000,000 MCMC iterations, with two as the inferred number of clusters with the highest posterior probability. Heat maps illustrate the posterior probability of membership in A) cluster 1 or B) cluster 2. Lighter colors indicate higher posterior probability of membership in a given cluster. (C) dendrogram visualizing the population assignment by Geneland, to each of the inferred clusters. Colors correspond to inferred clusters (dark gray, cluster 1; light gray, cluster 2), with the height of each color indicating the probability of assignment to each inferred cluster. Individuals are grouped by sampling location (Table 1, Figure 1). Bars above the figure identify the selective environment group (allopatry, orange; sympatry, blue) and the geographic group (West, dark gray; Central, white; East, light gray) assignments for each population.

Variation might often exist across a species' range in the strength of particular evolutionary mechanisms, providing an explanation for why the key contributors to population differentiation have the potential to vary with spatial scale. For instance, populations of the European flounder at the edges of the species range exhibit genetic structuring and population sizes suggestive of founder events, while population structure in other parts of the range is more strongly associated with environmental or life history variation (Hemmer-Hansen et al. 2007). As noted earlier, one possible explanation for the lower than expected population differentiation in *S. multiplicata* at this regional scale is that the populations from the geographic groups differ in their recent demographic histories. Demography is expected to affect the strength of both genetic drift and natural

selection. The greater contribution of selective environment over distance for explaining structure in the East populations might also be a result of the higher potential for gene flow between populations in the sympatric and allopatric selective environments. Populations in the two environments occur within 30 km of each other (Figure 1), so even a low level of dispersal may swamp out the predicted isolation by distance pattern of gene flow. Although gene flow is expected to erode differentiation due to local adaptation, divergent selection may be strong enough in the East populations to maintain associations between population structure and selective environment. Divergent selection on female mate preferences has led to the evolution of pre-mating reproductive isolation between sympatric and allopatric populations (Pfennig and Rice 2014). Divergent ecological

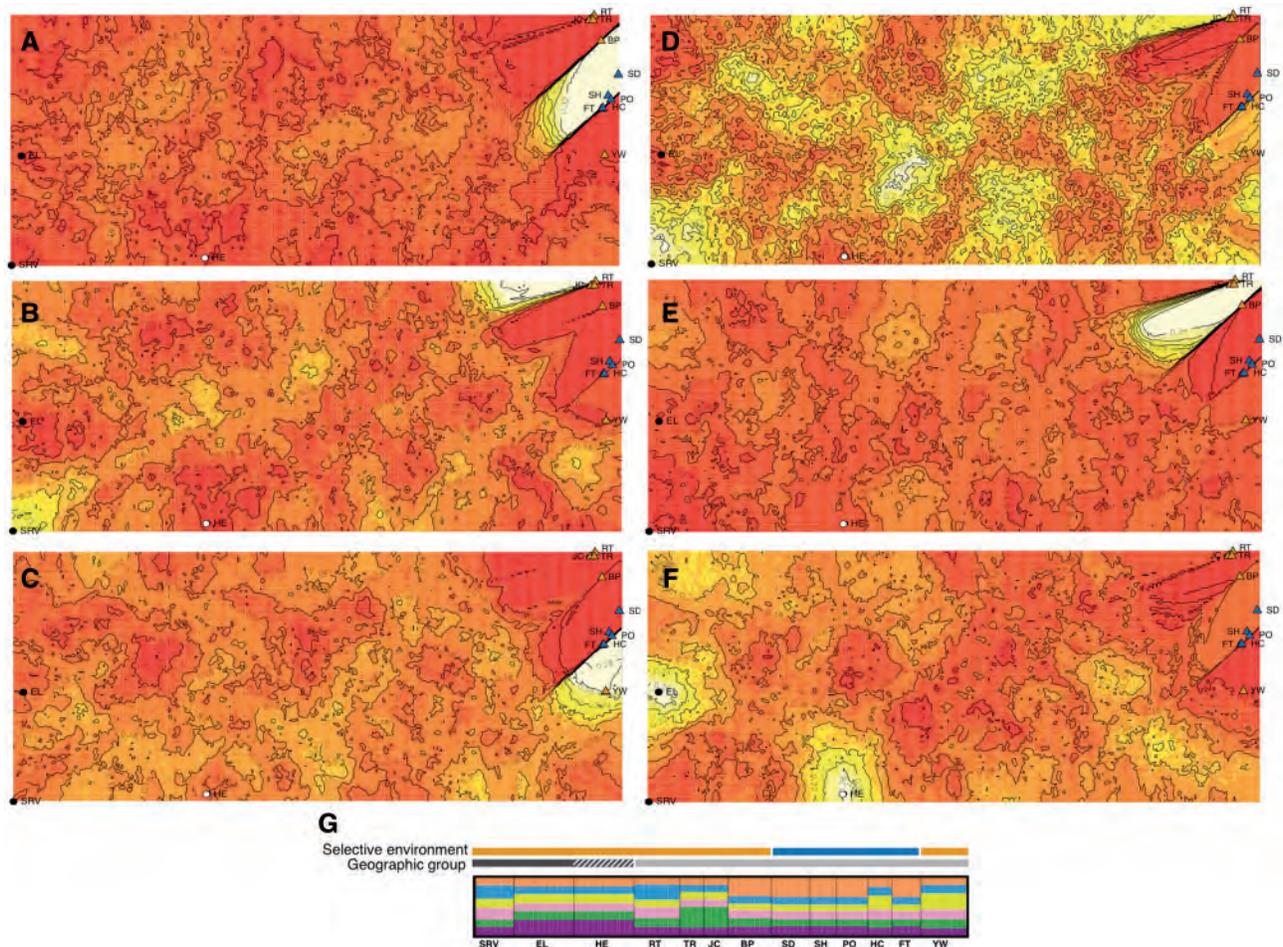


Figure 5. Geneland results for the correlated allele frequency model. Run length was equal to 2,000,000 MCMC iterations, with six as the inferred number of clusters with the highest posterior probability. Heat maps illustrate the posterior probability of membership in A) cluster 1, B) cluster 2, C) cluster 3, D) cluster 4, E) cluster 5 and F) cluster 6. Lighter colors indicate higher posterior probability of membership in a given cluster. G) distrupt plot visualizing the population assignment by Geneland, to each of the inferred clusters. Colors correspond to inferred clusters (orange, cluster 1; blue, cluster 2; yellow, cluster 3; pink, cluster 4; green, cluster 5; purple, cluster 6), with the height of each color indicating the probability of assignment to each inferred cluster. Individuals are grouped by sampling location (Table 1, Figure 1). Bars above the figure identify the selective environment group (allopatry, orange; sympatry, blue) and the geographic group (West, dark gray; Central, white; East, light gray) assignments for each population.

Table 6. Two-factor AMOVA testing the relative effects of geographic group vs. selective environment on genetic distance

Factor	df	SS	MS	F	Partial R^2	P
Geographic group	1	11.6	11.6	13.1	0.06	<0.001
Selective environment	1	4.5	4.5	5.1	0.02	<0.001
Residuals	201	178.3	0.9		0.92	
Total	203	194.5			1.0	

selection is also present between the East allopatric and sympatric populations of *S. multiplicata*. Ecological character displacement has occurred between *S. multiplicata* and *S. bombifrons* in tadpole morph production, resource use, and morphology (Pfennig and Murphy 2000; Pfennig et al. 2007; Rice et al. 2009) in sympatric populations, but not in allopatric populations. This divergence in ecological selective pressures between sympatric and allopatric populations has led to extrinsic postzygotic reproductive isolation (Pfennig and Rice 2007). Hence, the balance between selection, genetic drift, and gene flow likely varies across different spatial scales in *S. multiplicata*, affecting patterns of population differentiation.

Although our results suggest that distance contributes more to population differentiation at a regional scale than does selective environment, we found evidence that a portion of the population structure is associated with the divergent environments of allopatry and sympatry. The two selective environment groups exhibited a significant global weighted average F_{CT} value (Table 3). In addition, the DAPC illustrated some separation between allopatric and sympatric population groups (Figs. 2C, 2D). When geographical grouping and selective environment were considered simultaneously in the two-factor AMOVA, both were identified as significant contributors to genetic variation. Finally, individuals from the YW population were more frequently assigned to the correct selective environment group by DAPC than to the nearest geographic group. Using a different analysis, Rice and Pfennig (2010) also found that YW was more genetically similar to other allopatric populations than to nearby sympatric populations.

That these presumably neutral microsatellite markers exhibit any structure associated with divergent selection is somewhat surprising. Although divergence due to selection can be detected with neutral markers (Rice and Pfennig 2010; Rosenblum and Harmon

2011, Edelaar et al. 2012), theoretical and empirical results suggest that it often may not be (Crispo et al. 2006; Thibert-Plante and Hendry 2009, 2010; Hoskin and Higgie 2010). Levels of genetic differentiation are expected to vary across the genome for populations that have adapted to divergent selective environments, with the highest levels of differentiation often present at and near loci involved in local adaptation and reproductive isolation (Nosil et al. 2009a; Cruickshank and Hahn 2014). Consistent with expectations of variable differentiation across the genome, only one to two of the six loci exhibited significant F_{CTs} for sympatric versus allopatric population groups (Tables 3). Genome-wide studies will be necessary to evaluate the extent of genetic divergence between sympatric and allopatric *S. multiplicata* populations, and to identify specific loci associated with reproductive isolation and local adaptation.

In sum, our results indicate that at a regional scale, geographic distance contributes more to patterns of genetic differentiation among *S. multiplicata* populations than does selective environment. This result contrasts with genetic structure in this species at a more local scale, which is associated with divergent selective environments, and highlights the potential of reinforcement to initiate genetic differentiation. In general, variation across a species' range in the balance of evolutionary forces at work can result in differences in the key contributors to genetic differentiation among locations and spatial scales.

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