

# Social selection parapatry in Afrotropical sunbirds

Jay P. McEntee,<sup>1,2,3</sup> Joshua V. Peñalba,<sup>1,4</sup> Chacha Werema,<sup>5</sup> Elia Mulungu,<sup>6</sup> Maneno Mbilinyi,<sup>7</sup> David Moyer,<sup>8</sup> Louis Hansen,<sup>9</sup> Jon Fjeldså,<sup>9</sup> and Rauri C. K. Bowie<sup>1</sup>

<sup>1</sup>Museum of Vertebrate Zoology and Department of Integrative Biology, University of California, Berkeley, California 94720

<sup>2</sup>Current Address: Department of Biology, University of Florida, P. O. Box 118525, 220 Bartram Hall, Gainesville, Florida 32611

<sup>3</sup>E-mail: jaymcentee@gmail.com

<sup>4</sup>Current Address: Australian National University, Canberra

<sup>5</sup>Department of Zoology and Wildlife Conservation, University of Dar-es-salaam, Dar-es-salaam, Tanzania

<sup>6</sup>P. O. Box 934, Iringa, Tanzania

<sup>7</sup>Tanzania Bird Atlas, Iringa, Tanzania

<sup>8</sup>Field Museum of Natural History, Chicago, Illinois 60605

<sup>9</sup>Center for Macroecology, Evolution and Climate, University of Copenhagen, Denmark

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The extent of range overlap of incipient and recent species depends on the type and magnitude of phenotypic divergence that separates them, and the consequences of phenotypic divergence on their interactions. Signal divergence by social selection likely initiates many speciation events, but may yield niche-conserved lineages predisposed to limit each others' ranges via ecological competition. Here, we examine this neglected aspect of social selection speciation theory in relation to the discovery of a noncircular species border between sunbirds. We find that *Nectarinia moreaui* and *Nectarinia fuelleborni* meet in a ~6 km wide contact zone, as estimated by molecular cline analysis. These species exploit similar bioclimatic niches, but sing highly divergent learned songs, consistent with divergence by social selection. Cline analyses suggest that within-species stabilizing social selection on song-learning predispositions maintains species differences in song despite both hybridization and cultural transmission. We conclude that ecological competition between *moreaui* and *fuelleborni* contributes to the stabilization of the species border, but that ecological competition acts in conjunction with reproductive interference. The evolutionary maintenance of learned song differences in a hybrid zone recommend this study system for future studies on the mechanisms of learned song divergence and its role in speciation.

**KEY WORDS:** Bird song, cline, hybrid zone, HZAR, sexual selection, species borders.

Social selection, or selection on signals due to interactive intraspecific competition for resources (West-Eberhard 2014), can drive evolutionary divergence between populations in the presence or absence of ecological differences (West-Eberhard 1983). Our definition of social selection is inclusive of sexual selection on signals. In the absence of ecological differences, the capacity of social selection to drive signal divergence stems from the potential for run-

away selection via choice mechanisms (Fisher 1930), an absence of finite limits to social competition advantages from trait modification (Darwin 1871; West-Eberhard 1983; West-Eberhard 2014), and the efficacy of novel signals (West-Eberhard 1983). Social selection-driven signal divergence can directly lead to speciation when it causes sufficient prezygotic reproductive isolation (West-Eberhard 1983) or socially mediated postzygotic reproductive



isolation (Kawata and Yoshimura 2000; Seehausen and Schluter 2004; Stelkens et al. 2008; van der Sluijs et al. 2008).

Because social selection speciation could result in species with little to no ecological divergence, the products of speciation by social selection may be predisposed to intense ecological competition when in contact. Accordingly, West-Eberhard (1983) hypothesized that speciation with a strong social selection component should frequently predispose resultant lineages to mutual exclusion from ecological competition. By this “social selection parapathy” hypothesis, signal divergence can occur with minimal or no ecological divergence, yielding lineages that engage in strong resource and interference competition when they interact, stabilizing parapathy via ecological competition (see also, Case and Taper 2000; Case et al. 2005). Further, lineages subject to social selection divergence may be prone to preferential aggregation with conspecifics (Stamps 1988; Hahn and Silverman 2006), which should reinforce stable parapathy, or decrease cline width (Payne and Krakauer 1997). While the roles of both social selection and niche conservatism in speciation have recently been central foci of research (Peterson et al. 1999; Wiens and Graham 2005; Pyron et al. 2015), the particulars of West-Eberhard’s social selection parapathy hypothesis have received little attention.

Parapatric boundaries should be most frequently encountered in the tropics, where biological factors should set range limits more frequently than in temperate regions (Darwin 1859; MacArthur 1972). Such boundaries may form where ecological gradients are shallow or absent, as their existence need not depend on advantages accrued via local adaptation on either side of the boundary (Barton and Hewitt 1985; Case and Taper 2000; Case et al. 2005). As is true generally of parapatric boundaries, noncotal parapatric boundaries (those with shallow or no environmental gradient) may occur more frequently in the tropics, where strong niche conservatism should be more common because of higher climatic constancy through time (Fjelds  et al. 2012). While several narrow, tropical parapatric boundaries without obvious environmental gradients have been described (see e.g., Hall and Moreau 1970; Krabbe and Schulenberg 1997; Sanchez-Gonzalez et al. 2015), detailed studies of the maintenance of these noncotal parapatric distributions are uncommon (but see Brumfield et al. 2001).

Here, we examine the divergence and shared range boundary between the sunbird sibling species *Nectarinia moreaui* and *Nectarinia fuelleborni* in southern Tanzania in the context of the social selection parapathy hypothesis. These taxa exhibit similar habitat requirements, being found exclusively in sky island montane forests in eastern Africa. Their parapatric boundary occurs within a mountain block of the Eastern Arc Mountains known as the Udzungwa Mountains. Though only subtle differences in plumage exist between the two species (Bowie et al. 2004), males of the two species sing strikingly different territorial songs

(McEntee 2014). Their abutting distributions present the opportunity to examine the processes that stabilize the species border of sibling species with highly divergent signals and similar habitat requirements.

We propose that testing “social selection parapathy” would minimally require examining the following subhypotheses: (1) social selection is the primary mechanism for signal divergence; (2) each species’ range is not limited by aspects of the environment outside of the presence of the sibling species, either by an abiotic gradient or a geographic barrier to dispersal (Case et al. 2005); (3) ecological competition is intense where there is local co-occurrence; and (4) reproductive interference, inclusive of selection against hybrids, is insufficient to explain the totality of fitness loss for either species at their shared range boundary. The last two of these criteria together distinguish social selection parapathy from the tension zone model of hybrid zones, wherein viability selection against hybrids alone is responsible for reinforcing parapathy (Barton and Hewitt 1985).

We address the first of these subhypotheses by examining several alternative hypotheses to explain the striking song divergence between *N. moreaui* and *N. fuelleborni*. The songs are used in male–male competition (McEntee 2014), and likely also attract or manipulate potential mates (Catchpole and Slater 2008), however we do not yet have evidence on how songs influence mate choice. As the songs are extremely complex, and as sunbirds are oscine songbirds, the songs are almost certainly developed through learning (Catchpole and Slater 2008). We therefore consider the possibility that these signals evolve by cultural mechanisms in addition to those mechanisms that would apply to unlearned signals. We consider the following hypotheses to explain song divergence (Podos and Warren 2007; Wilkins et al. 2013): (1) acoustic adaptation, (2) a byproduct mechanism where song divergence is a consequence of morphological change, (3) genetic and/or cultural drift, and (4) social selection independent of ecological differences. Evidence consistent with the last of these possibilities would constitute the best support for social selection as a driver of divergence.

With respect to the second subhypothesis, we (1) use bioclimatic niche modeling to test whether bioclimatic niches decline in suitability past the parapatric boundary, which would indicate that an abiotic gradient plays a role in limiting the species range, and (2) we use molecular data to test for local syntopy of the two morphologically cryptic species, where syntopy would discount a geographic barrier to dispersal as the sole cause of parapathy. We discuss the third subhypothesis based on a null model-based test of bioclimatic niche similarity between species (this study) and evidence from a previous study indicating that interspecific interference competition is strong between territorial males of the two species (McEntee 2014). With respect to the fourth criterion, we test for hybridization by examining support for admixture using

DNA sequence data from 132 individuals. A lack of evidence for hybridization despite strong sampling in the range boundary vicinity would suggest that reproductive interference has a limited role in the stabilization of parapatry, whereas rampant hybridization would suggest that reproductive interference instead of ecological competition is primarily responsible for the stabilization of parapatry.

Beyond providing a possible case of social selection parapatry, the meeting of recent or incipient species with highly divergent learned song provides the opportunity to investigate learned song divergence's role in speciation. Learned song has received a great deal of attention as a signal that may be important to bird speciation (Baptista and Trail 1992; Grant and Grant 1996; Slabbekoorn and Smith 2002; Lachlan and Servedio 2004; Verzijden et al. 2012; Wilkins et al. 2013), both because song-learning birds are especially diverse and because learned songs appear especially labile. Essential for song to have a central role in speciation, though, is its robustness to convergence during secondary contact of divergent species (Cody 1969; Haavie et al. 2004; Seddon and Tobias 2010; Secondi et al. 2011; Verzijden et al. 2012). If learned song differences help prevent the merging of incipient species, accrued differences must be maintained when interspecific interactions make cultural transmission across species and/or gene flow of song-determining alleles possible. Here, we examine the robustness of song divergence to contact using cline analyses of molecular and phenotypic data. If cultural transmission across species is frequent where *moreaui* and *fuelleborni* interact, song phenotype clines should be gradual compared to molecular clines, and the song cline may be displaced from molecular clines. If cultural transmission is limited or absent across species, then the two clines should be coincident and concordant. The latter possibility would suggest that learned song behaves much like other quantitative traits under stabilizing selection within species, and further that the genetic basis of learned song predispositions are distinct for each species.

#### STUDY TAXA AND GEOGRAPHIC SETTING

*Nectarinia* (née *Cinnyris*) *moreaui* and *N. fuelleborni* (alternately classified as the subspecies *N. (Cinnyris) mediocris fuelleborni*) are sunbirds of Eastern Afrotropical forest and forest edges. Bowie et al. (2004) found that *moreaui* and *fuelleborni* are characterized by 4–6% mtDNA sequence divergence, that mtDNA gene trees are reciprocally monophyletic, and provided evidence that both mtDNA lineages are found within forest habitats of the Udzungwa Mountains, Tanzania (see also, Stuart et al. 1987; Fjeldså et al. 2010; McEntee 2013; Werema et al. 2014). The Udzungwa, much like the other Eastern Arc Mountain blocks (e.g., Ukaguru, Usambara, Uluguru), had largely been considered a single biogeographic sky island unit for forest-dependent birds (Fjeldså and Rabol 1995; Fjeldså and Bowie 2008; Fjeldså et al.

2010), such that the existence of two divergent taxa within the northeastern Udzungwa was unexpected.

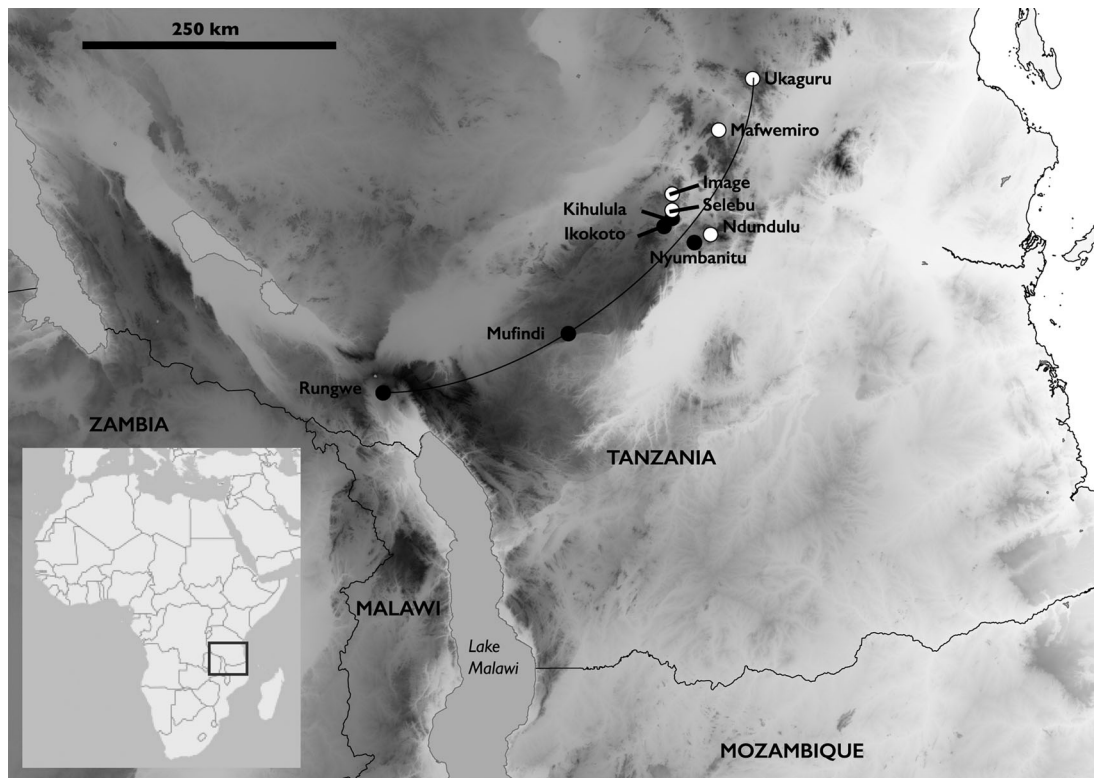
The forest areas inhabited by both species are constant environments that persisted in a similar state through the climatic fluctuations during the Pleistocene (Mumbi et al. 2008). The build-up of avian paleo- and neo-endemic diversity in the northeast Udzungwa provides further evidence that these areas have maintained stable environments through time (Fjeldså and Bowie 2008; Fjeldså et al. 2012). In contrast to contact zones where interspecific interactions have been attributed to recent anthropogenic changes to local environments, the *moreaui*–*fuelleborni* contact zone occurs largely in tracts of mature forest with high environmental stability.

## Methods

### MOLECULAR METHODS—SAMPLING, LABORATORY PROCEDURES, AND MOLECULAR ANALYSES

Tissue and blood samples were acquired from multiple field expeditions and museum collections. We sampled 132 individuals encompassing 14 different populations (Table S5). DNA extraction was performed using Qiagen DNEasy blood and tissue kits. Sanger sequencing was performed for the mtDNA gene ND2, the Z-linked intron loci CHDZ, MUSK, and BRM, and the autosomal introns 11,836 and 18,142 (Goodwin 1997; Griffiths and Korn 1997; Sorenson et al. 1999; Backstrom et al. 2008; Kimball et al. 2009) (further details in Supporting Information). Sequences were checked for quality and aligned using the MAFFT alignment algorithm (Kato et al. 2005) within Geneious Pro 5.1.6 (2010). Nuclear introns were phased probabilistically into haplotypes using the program PHASE (Stephens et al. 2001). Population structure and individual population membership were investigated using the Bayesian population assignment algorithm of the program *structure* (Hubisz et al. 2009). The number of populations  $K$  was set to two based on initial results where  $K$  was allowed to take values from 1 to 8 (Table S1). Results of Bayesian population assignment are depicted from (a) a *structure* run where only nuclear intron haplotypes were included (Fig. 2), compared against mtDNA haplotypes scored as either *fuelleborni* or *moreaui* in origin; and (b) a *structure* run where nuclear intron and mtDNA haplotypes were both included (Fig. S1). We used a cutoff value of .90 posterior probability of assignment to designate “pure” individuals of either species from *structure* output. Individuals were dichotomously scored for mtDNA species origin by inspecting the alignment.

To provide an indication of the level of within-species population structure, multilocus  $K_{st}$  indices (Hudson et al. 1992) were calculated in DNAsp (Librado and Rozas 2009). Because we sought to understand whether populations structure exists *within* species in these analyses, individuals with mixed ancestry, as



**Figure 1.** Map of the study area, with named localities mentioned in the text. The circular arc transect shown was used to reduce the spatial dimensionality of the data for cline analyses. Coloration indicates elevation: green shades = lower elevation and brown shades = higher elevation (for grayscale figure: lighter colors = lower elevation, darker colors = higher elevation). Green dots (white in grayscale) are sampling localities dominated by *N. moreaui*. Blue dots (black in grayscale) are sampling localities dominated by *N. fuelleborni*.

evidenced by low probability of assignment (<90%) to both *moreaui* and *fuelleborni* in structure analyses, were excluded from the calculation of multilocus  $K_{st}$ . Inclusion of mixed-ancestry individuals could prevent accurate inference of within-species population structure by inflating within species diversity. To prevent overestimation of structure because of limited sampling, only populations with sampling of five or more individuals were included in this analysis. As we were interested in the magnitude of population structure in the vicinity of the contact zone, only those populations within the cline-fitting area were included when estimating multilocus  $K_{st}$  indices (Fig. 1), which resulted in the exclusion of the Misuku Hills population of *N. fuelleborni*. Inclusion of this population may have resulted in higher estimates of population structure within *fuelleborni*, as this population is distant from our nearest sampled population (~60 km), and well isolated from it by unsuitable habitat.

### SONG RECORDING AND ANALYSIS

Sound recordings were made in the field in 2008–2010 using Sennheiser ME-67 shotgun microphones and Marantz solid-state recorders (models PMD660, PMD670, and PMD671; 16 bit precision, 44.1 or 48 kHz sampling rate). Two additional *N. fuelle-*

*borni* recordings were obtained from the Macaulay Library, Cornell University Lab of Ornithology. Values for song variables were obtained for each of 14 measurements from sonograms visualized in Luscinia (Lachlan 2007, see Supporting Information for further recording details, measurement definitions, and procedures). Mean individual values were then calculated from the set of songs measured for each individual, with the individual as our unit of analysis. Each vector of mean individual values was scaled by its standard deviation in R (R Core Team 2012) before MANOVA and principal components analysis in JMP 9 (SAS Institute Inc 2010). The first principal component was used to represent song variation in cline analyses. We present MANOVA results only for allopatric populations, to avoid inclusion of individuals of mixed-ancestry.

Analyzed song number per individual varied from 1 to 30 songs (mean = 3.3, SD = 3.2), which were exclusively sampled from songs sung in bout form (i.e., multiple songs were sung consecutively with a fairly regular intersong interval). Some individuals were banded prior to sound recording, and were identified by band combination. For unbanded individuals, a minimum distance of 60 m between recording localities was used to establish separation between individual samples. This minimum distance

threshold was selected based on extensive observation of territorial behavior (McEntee 2013, 2014), including of banded males, and from observations of the typical densities of territorial males (J.P.M. pers. obs.).

### BILL MEASUREMENTS

Culmen length, defined as the distance between the distal tip and the notch where the culmen meets the skull, was measured for male museum specimens using digital calipers. A single observer (J.P.M.) measured 141 male culmens. We retained the 122 measurements derived from populations along the cline transect (Fig. 1) for cline analyses.

### CLINE ANALYSES

To analyze individual- and population-level geographic variation in genotypes and phenotypes, we first reduced the spatial dimensionality of the data by assigning each population a position along a circular arc transect. We fixed the northernmost and southernmost sampling populations as the endpoints of the circular arc, and then adjusted the arc's radius in ArcMap 10 (ESRI 2011) such that it evenly split the set of populations at the center of the contact zone (Fig. 1). Population positions in one dimension were then assigned by finding the nearest point along the 504.5 km arc for each sampled population.

The goals of cline analyses were twofold: to estimate the center and width of molecular and phenotypic clines as parameters of cline models, and to test for coincidence and concordance among molecular and phenotypic clines. Using the R package HZAR (Derryberry et al. 2014), we fit and compared clines for three traits: a molecular hybrid index (q-scores from STRUCTURE analyses of nuclear molecular variation, see e.g., Yannic et al. 2008; Devitt et al. 2011; Gowen et al. 2014; Johnson et al. 2015 for the use of a molecular hybrid index in cline analysis), song PC1 scores, and culmen length (see Supporting Information for additional cline fitting details). To ease visualization of the results, we normalized each of the three trait distributions prior to fitting so that their ranges were [0, 1] using the following equation:

$$z_i = \frac{x_i - \min(x)}{\max(x) - \min(x)},$$

where  $x$  is a trait vector,  $x_i$  is the  $i$ th observation of a vector, and  $z_i$  is the normalized value of the  $i$ th observation.

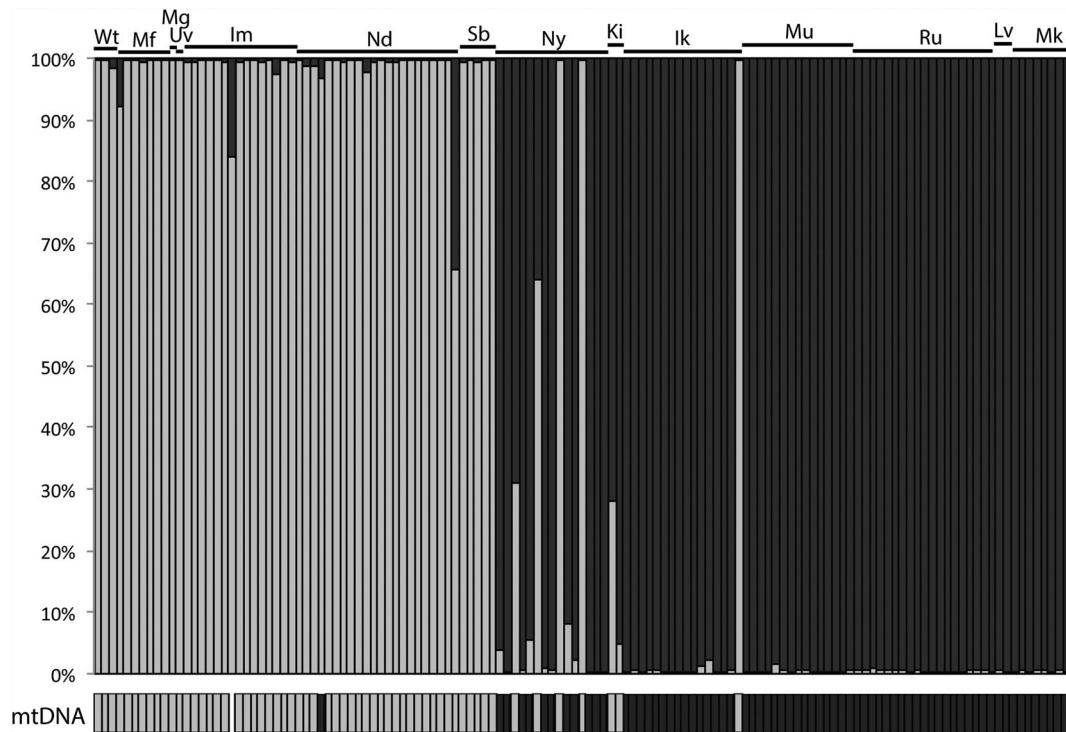
In HZAR, clines were fit with five different possible architectures: a sigmoid cline with or without exponential tails (Szymura and Barton 1986, 1991; Barton and Gale 1993; Brumfield et al. 2001; Derryberry et al. 2014). We then compared models representing each of the five architectures using model selection by AICc to determine a single preferred model architecture for each trait, and then extracted the maximum likelihood model parameters. For each architecture-trait combination, we made ini-

tial model fits (chain length =  $1 \times 10^6$  generations, burn-in =  $5 \times 10^5$  generations) to optimize the covariance matrix used in three separate subsequent MCMC chains (Derryberry et al. 2014). These three secondary MCMC chains were then concatenated ( $9 \times 10^6$  generations) for postprocessing and analysis. We checked for adequate mixing and convergence in cline parameter estimation by visualizing sampling trajectories with the R package coda (Plummer et al. 2006).

### NICHE MODELING AND NICHE SIMILARITY TEST

Strong ecological competition between species in secondary contact requires that the niches of the two species are strongly conserved. To assess the hypothesis that our focal species' niches are strongly conserved, we test whether their bioclimatic niches are more similar than expected under a null hypothesis. In the test we employ, the "background similarity" test of Warren et al. (2008), rejecting the null hypothesis can indicate that the niches of compared taxa are more similar or more divergent than expected by chance, where we explicitly account for the environmental variation present in the area where the species distributions occur. To generate a null distribution of similarity scores, we compare the geographically projected bioclimatic niche model of species X, where the niche model is generated from known occurrences of species X, with a set of niche models generated from pseudo-randomly selected points from a buffer area (background) around the occurrence points of species Y. Sets of background samples for each species were selected from buffer areas that were created by generating circles with 100-km radii around each of the true occurrence points. We use two niche similarity metrics: the ecological niche overlap metric Schoener's  $D$  (Schoener 1968), and a distance metric  $I$  (Warren et al. 2008, 2010; see Supporting Information).

We built niche models from 19 and 25 occurrence points for *N. moreaui* and *N. fuelleborni*, respectively. Background sample niche models were constructed from 19 background samples in the buffer area of *N. fuelleborni*, and 25 from the buffer area of *N. moreaui*. This process was repeated 100 times to generate null distributions. We used the maximum entropy modeling software Maxent to build niche models (Phillips et al. 2006). For each occurrence point, we extracted seven BIOCLIM variables (BIO1: annual mean temperature, BIO2: mean diurnal temperature range, BIO5: maximum temperature of warmest month, BIO6: minimum temperature of coldest month, BIO12: annual precipitation, BIO13: precipitation of wettest month, BIO14: precipitation of driest month) at a resolution of 2.5 arc-minutes (Hijmans et al. 2005). These seven BIOCLIM variables were chosen because they capture a large proportion of the climatic variation across space, and their levels of correlation are low over large areas of the globe (Jiménez-Valverde et al. 2009). We projected resulting niche models onto a geographic space including the range of both species.



**Figure 2.** Probability of assignment to *N. moreaui* (light gray) and *N. fuelleborni* (dark gray) as determined from a *structure* analysis using nuclear intron haplotypes (top). The corresponding mtDNA lineage (*moreaui* or *fuelleborni*) for each individual is also shown (bottom). Note two instances of mito-nuclear discordance. Population abbreviations are as follows: Wt, Wota; Mf, Mafwemiro; Mg, Mang'alisa; Uv, Uvidunda; Im, Image; Nd, Ndundulu; Sb, Selebu; Ny, Nyumbanitu; Ki, Kihulula; Ik, Ikokoto; Mu, Mufindi; Ru, Rungwe; Lv, Livingstone Mountains; Mk, Misuku Hills.

## Results

### MOLECULAR SEQUENCE DATA

Of the six molecular loci, *N. moreaui* exhibited a small but statistically significant  $K_{st}$  for MUSK (.073), with small and statistically insignificant  $K_{st}$  for the other loci (Table S2). *Nectarinia fuelleborni* exhibited small but statistically significant  $K_{st}$  for ND2 (.066) and MUSK (.110), with statistically insignificant  $K_{st}$  for the other loci (Table S2). Population structure for ND2 and MUSK in *fuelleborni* was driven by differences between the Rungwe and Udzungwa mountain blocks, which are separated by the Makambako Gap, a known biogeographic break (Burgess et al. 2007). The minimal structure was somewhat unexpected, given that many bird species with similar distributions exhibit strong structure among the same mountain blocks (Bowie and Fjeldså 2005; Fjeldså et al. 2010). The minimal structure in both species suggest that dispersal has maintained connectivity among geographically isolated populations, and further suggest that the parapatric boundary is unlikely to be explained by highly limited dispersal among forest patches.

In the combined mitochondrial and nuclear sequence dataset, population assignment in *structure* revealed that seven of 132 sampled individuals have mixed ancestry. Five individuals had mixed nuclear genomes, and two individuals exhibited cyto-nuclear dis-

cordance. The seven individuals of mixed ancestry came from four populations: Kihulula, Nyumbanitu, Image, and Ndundulu (Fig. 2). Sympatry of pure parental species was revealed from molecular analyses at two localities: Nyumbanitu and Ikokoto (Figs. 1 and 2).

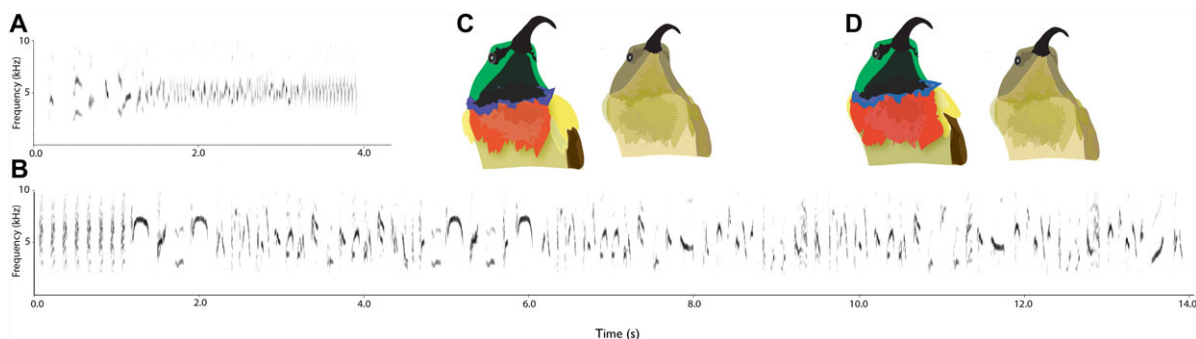
### SPECIES-LEVEL PHENOTYPIC DIVERGENCE

#### Songs

Representative sonograms can be found in Figure 3 (A and B). MANOVA following scaling and centering of all 14 variables was significant for differences between allopatric populations of the two species ( $n_1 = 38$  *fuelleborni*,  $n_2 = 41$  *moreaui*,  $F = 268.87$ ,  $df = 1$ ,  $P < 1 \times 10^{-15}$ ). The first principal component corresponded strongly with species differences. Loadings for PC1 for all nine variables with statistically significant differences in individual ANOVAs (Tables S3 and S4) had absolute value  $> .45$ , indicating correlation among these variables along the axis of species differences.

#### Culmen lengths

Mean  $\pm$  SD male culmen lengths were  $23.29 \pm 1.02$  for *N. fuelleborni* and  $24.89 \pm 1.01$  for *N. moreaui* ( $n_1 = 51$  *fuelleborni*,  $n_2 = 92$  *moreaui*, linear-mixed model with population nested



**Figure 3.** Representative sonograms and depictions of *Nectarinia moreaui* (A and C, male on left and female on right) and *N. fuelleborni* (B and D, same), respectively (reprinted from McEntee 2014 with permission from Oxford University Press). The large difference in song duration is representative of species differences. See online version for color depictions of birds.

within species and Satterthwaite approximations to  $df$ ,  $t = 5.728$ , residual  $d.f. = 135$ ,  $P = 1.22 \times 10^{-5}$ , Hedges'  $g$  for comparison of species means = 1.58). Individuals with mixed ancestry were excluded from this comparison. There is substantial overlap in culmen length between species (Fig. S2).

### Ecological niche

Species distribution models from Maxent had high prediction value for the training set for both species (*fuelleborni* AUC: .966; *moreaui* AUC: .988). In relativized contribution and permutation tests performed using Maxent, temperature variables had a higher impact than precipitation variables.

For both species, response curves for Maxent models developed independently for individual predictor variables generally indicate increasing suitability with decreasing mean annual temperature, maximum temperature of warmest month, and minimum temperature of coldest month. Suitability for both species is highest at intermediate diurnal temperature ranges relative to the background. For *moreaui*, suitability was highest at intermediate values of annual precipitation and precipitation of the wettest month, and for low values of precipitation of the driest month. For *fuelleborni*, suitability increased with annual precipitation and precipitation of the wettest month.

Predictions projected into the range of the sister species resulted in remarkably high concordance between the projected niche and the sister species' localities (Fig. 4A), including of localities maximally distant (~900 km, see Fig. 4) from the contact zone. Results of the background similarity test, performed in ENMTools (Warren et al. 2010), are shown in Figure 4B. Compared to the null distributions of niche similarity scores generated from comparing background point models of species X with the actual distribution model for species Y, niche models for *fuelleborni* and *moreaui* had higher similarity scores for both ecological indices calculated: Schoener's D and I. We reject the null hypothesis in all four comparisons, indicating bioclimatic niche conservatism.

### CLINES

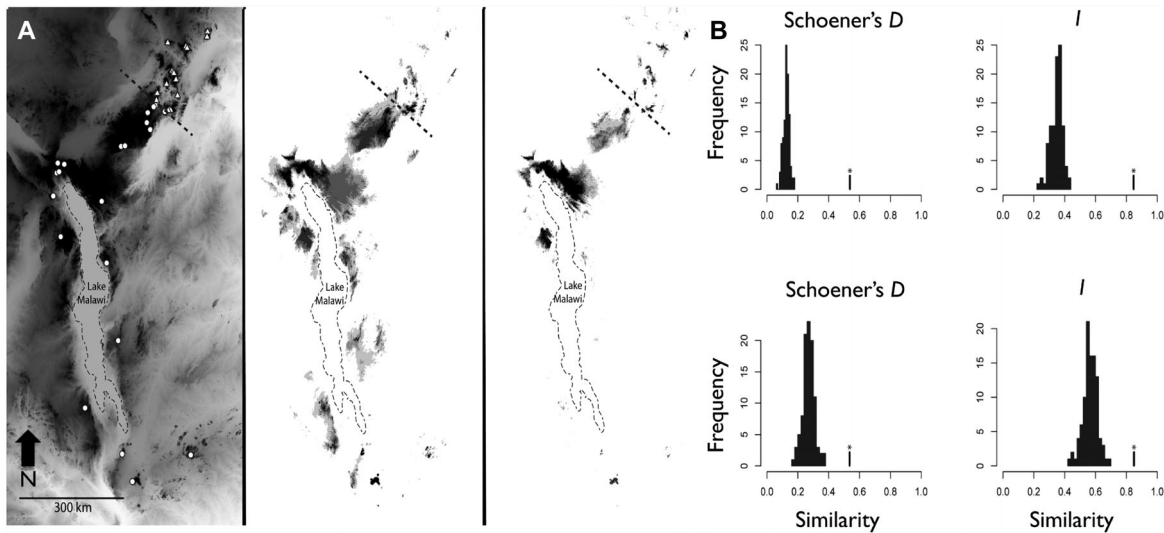
Relative support for cline architectures by trait are shown in Table 1. Cline center and width estimates for the molecular index and song clines were coincident and concordant, with center ~163 km and width ~6 km. The center of the molecular and song clines corresponded closely to the positions of Nyumbanitu and Kihulula forests along the transect.

The culmen length cline was not coincident with the molecular and song clines (95% credible intervals did not overlap). The culmen length cline's center was shifted ~8 km north of the molecular index and song cline centers. The culmen length cline was also broader in width than the molecular index cline (95% credible intervals did not overlap), while there was a small amount of overlap between the 95% credible intervals for culmen length and song cline widths.

## Discussion

### EVIDENCE FOR SOCIAL SELECTION PARAPATRY

West-Eberhard's (West-Eberhard 1983) "social selection parapatry" hypothesis is an appealingly plausible explanation for how stable range boundaries could arise between species with similar ecological niches. Models support the notion that (incipient) species with similar, even identical, ecological niches may establish stable mutual species borders or "mosaic sympatry," and may thus persist for long-time periods within a finite domain (M'Gonigle et al. 2012). As indicated in the Introduction, we suggest that support for the social selection parapatry hypothesis would minimally require support for these four subhypotheses: (1) social selection is the primary mechanism for signal divergence; (2) each species' range is not limited by aspects of the environment outside of the presence of the sibling species, either by an abiotic gradient or a geographic barrier to dispersal (Case et al. 2005); (3) ecological competition is intense where there is local co-occurrence; and (4) reproductive interference, inclusive of selection against hybrids, is insufficient to explain the totality



**Figure 4.** (A) From left to right: occurrence points for *Nectarinia moreaui* (triangles) and *N. fuelleborni* (circles) with elevation shown across their distributions (darker colors at higher elevations); Maxent niche model output for *fuelleborni*, with darker color indicating higher suitability; equivalent model for *moreaui*. (B) Results of background similarity tests performed in ENMTools. Starred bars for the niche similarity indices Schoener's *D* and *I* are similarity scores from niche models predicting the distribution of the other species (top: *fuelleborni* model predicting *moreaui* suitability, bottom: *moreaui* model predicting *fuelleborni* suitability). Distributions shown are null distributions generated from niche models developed for sets of "background" points within 100 km buffers around occurrence points. The greater similarity seen in niche models generated from the actual sister taxa distributions as compared to the null distributions indicates strong niche conservatism. See Methods for additional details.

**Table 1.** Cline models.

Trait	Center	Width	$\Delta$ AIC	Tails	Parameters
Song PC1			3.88	None	7
<b>Song PC1</b>	<b>163.0 (161.3–165.0)</b>	<b>5.9 (0.8–9.5)</b>	<b>0</b>	<b>Left</b>	<b>9</b>
<b>Song PC1</b>			<b>0.31</b>	<b>Right</b>	<b>9</b>
<b>Song PC1</b>			<b>0.14</b>	<b>Mirror</b>	<b>9</b>
Song PC1			5.07	Both	11
Molecular index			15.95	None	7
Molecular index			17.30	Left	9
<b>Molecular index</b>	<b>163.7 (159.1–164.8)</b>	<b>3.7 (0.3–5.5)</b>	<b>0</b>	<b>Right</b>	<b>9</b>
Molecular index			11.57	Mirror	9
Molecular index			5.21	Both	11
<b>Culmen length</b>	<b>155.1 (140.4–158.8)</b>	<b>21.4 (8.6–54.0)</b>	<b>0</b>	<b>None</b>	<b>7</b>
Culmen length			4.54	Left	9
Culmen length			5.24	Right	9
Culmen length			9.78	Mirror	9
Culmen length			9.80	Both	11

Center and width estimates with 95% confidence intervals for the preferred modeled cline architectures for each of the three examined traits. For each trait, models with  $\Delta$ AIC < 2 are shown in bold.

of fitness loss for either species at their shared range boundary. We review the evidence for each of these hypotheses from the *moreaui*–*fuelleborni* parapatric boundary.

With respect to the first subhypothesis above, we show that a signal, male territorial song, is highly divergent between *moreaui* and *fuelleborni* (see Table S3 and Fig. S2), whereas an eco-

morphological trait (culmen length, see Results and Fig. S3), and bioclimatic niche (Fig. 4) are more subtly divergent. Here, we assess the evidence that each of the following mechanisms has contributed to the described song divergence: acoustic adaptation, byproduct mechanism from natural selection on other traits (e.g., morphology that constrains sound production, Podos 1996),



genetic and/or cultural drift (Podos and Warren 2007; Wilkins et al. 2013), and social selection independent of environmental differences experienced by populations. We argue that, of these possibilities, social selection independent of ecological or morphological differences is the most plausible primary mechanism for song divergence. However, the action of social selection together with genetic drift may be important, as suggested by models incorporating both processes (Lande 1981; Uyeda et al. 2009).

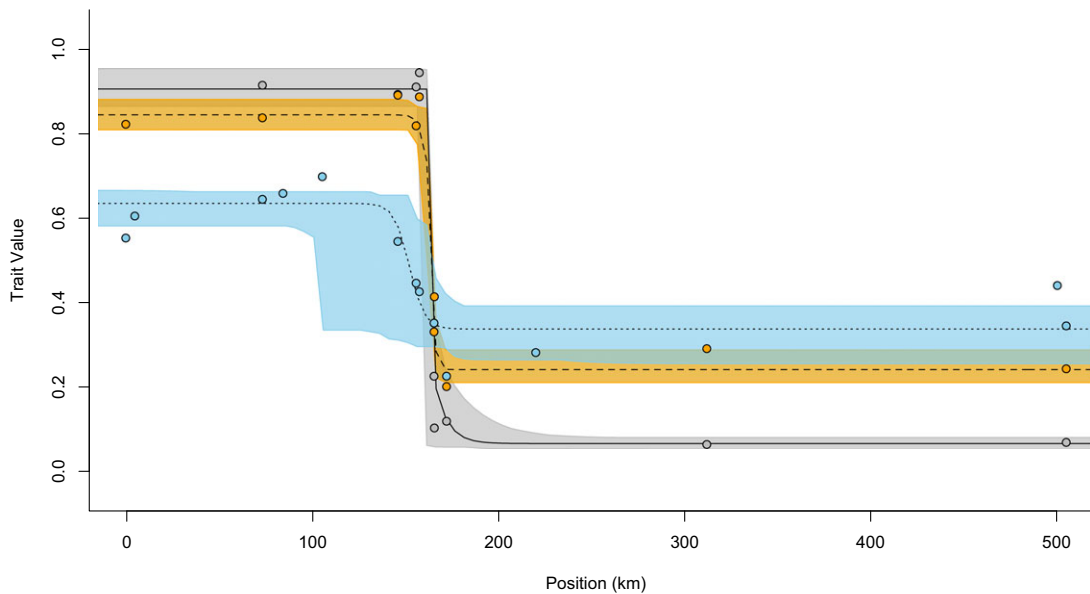
Under the “acoustic adaptation hypothesis,” aspects of the environment serve to alter the efficacy of acoustic signals by impeding or promoting the transmission of certain sounds (Morton 1975; Wiley and Richards 1982, Endler 1993). Selection can then drive the evolution of acoustic signals by sorting sounds that vary in transmission. The acoustic adaptation hypothesis predicts divergence when the acoustic environments experienced by different populations are consistently different. With respect to sound transmission properties of the habitats or micro-habitats used by *N. moreaui* and *N. fuelleborni*, it is unlikely that such differences exist for two reasons: the species have similar niches, and each species sings across a large variety of microhabitats that must have different transmission properties. In this study, we provide evidence regarding the former, in the form of the background similarity tests indicating that the focal species use extremely similar bioclimatic niche space. With respect to the latter, natural history observations indicate the two species sing from a broad variety of forest and forest edge microhabitats, suggesting broad variation within each species and extensive overlap between species in the acoustic properties that each experiences (McEntee 2013). Overall, the constraints on the transmission of song are likely to be quite similar, and highly variable within species, for *moreaui* and *fuelleborni*. Mediation of divergence by shifted acoustic constraints is then unlikely to contribute substantively to their strong song divergence.

The “byproduct hypothesis” requires phenotypic change in a trait with pleiotropic effects on song. Multiple studies have shown that bill morphology divergence is associated with song divergence (Podos 2001; Seddon 2005). The mean of *N. moreaui*’s culmen lengths is greater than that of *N. fuelleborni*, suggesting that pleiotropic effects on trills are possible. However, one prediction of the byproduct hypothesis for song is that “ecologically” selected traits and song must covary among populations. Cline analyses show that *N. moreaui* populations at Ndundulu and Selebu sing species-typical songs despite possessing smaller (more *fuelleborni*-like) bills relative to other *N. moreaui* populations, indicative of a subtle decoupling of bill length and song phenotype variation. This decoupling runs counter to the prediction of the byproduct hypothesis that song and bill phenotypes should tightly covary among populations (Wilkins et al. 2013, Table 2). Additionally, the dramatic divergence in song duration (Table S3) and fine-scale spectro-temporal aspects of song structure (e.g.,

coefficient of variation in interval duration, Table S3) cannot easily be explained by pleiotropic effects of bill divergence. Our study thus discounts a strong role for bill morphology in song divergence.

Random genetic drift can explain song divergence if different alleles underlying song variation fix in different species from ancestral standing genetic variation. A prediction from this genetic drift model is isolation-by-distance in song phenotype aspects that are vertically inherited. While we do not specifically test this hypothesis here, we note that the song phenotype dimension presented (PC1) is strongly conserved across space within species (Fig. 5) while being strongly divergent among species. This pattern suggests that different processes are at play within versus between species (Campbell et al. 2010), which is confirmed in a separate study specifically examining population-level song variation (McEntee et al. unpubl. ms.). Strong conservatism in song phenotypes among spatially isolated populations, including some that have accrued substantial divergence at molecular markers (Table S2, McEntee et al. unpubl. ms.), suggests that stabilizing selection prevents random genetic drift alone from driving song phenotype divergence among population isolates within species. Cultural drift, meanwhile, could explain the use of different song elements among populations within species, but is unlikely to account for the gross structural divergences of *moreaui* and *fuelleborni* song (Table S3), which are likely underlain by distinct, innate predispositions (Marler and Sherman 1985).

The failure of the acoustic adaptation, byproduct, and drift mechanisms to explain song divergence, together with evidence that niches are strongly conserved, leaves social selection independent of environmental differences as the most plausible primary mechanism of divergence, consistent with the social selection parapatry hypothesis. What is perhaps most interesting about song divergence in this case is strong within-species conservatism despite dramatic divergence between *N. moreaui* and *N. fuelleborni* (Fig. 5), and despite geographic isolation within species providing the potential for further divergence (Bowie et al. 2004; Table S2). Intraspecific conservatism despite geographic isolation is suggestive of stabilizing selection (Charlesworth et al. 1982; Estes and Arnold 2007). However, if stabilizing selection on song prevents among-population divergence within species, what processes can explain strong divergence between species? We suggest range expansion-associated divergence as a possibility (Mila et al. 2007). We hypothesize that *N. fuelleborni* arose as a daughter species of *N. moreaui* during an ancient southward range expansion, with a concomitant relaxation of stabilizing selection on song phenotype that permitted rapid divergence (Kaneshiro 1976), followed by secondary contact. This hypothesis could account for both the striking divergence in song between *N. fuelleborni* and *N. moreaui*, and the comparatively limited geographic variation within each species.



**Figure 5.** Cline analysis (HZAR) results for the molecular hybrid index (in color figure online = gray), song PC1 (in color figure online = orange), and culmen length (in color figure online = blue). Lines indicate the maximum likelihood cline for each trait (molecular hybrid index = solid; song PC1 = long dashes; culmen length = short dashes), from the model with the minimum AIC value for that trait. Shaded areas represent 95% credible intervals. Points are mean values for populations included in the cline analyses (see online version for color). When the clines are restricted to a common scale, the culmen length cline occupies the narrowest range of trait values because the maximum and minimum individual culmen length values lie far from the population means.

With respect to the second subhypothesis of social selection parapatry, neither a geographic barrier nor an abiotic gradient can explain the range border of either species in the northeast Udzungwa. Evidence for local syntopy and hybridization precludes the possibility that a geographic barrier divides the two species ranges. An abiotic gradient, meanwhile, is extremely unlikely to be more important than the presence of heterospecifics in limiting each species' range. The results of the niche models and background similarity tests presented here (Fig. 4) indicate that the environment is suitable for each species well beyond the range edge, extending to the opposite edge of the range of the sibling species. We acknowledge that we have not tested an additional possibility, that biotic factors outside of the sibling species interactions (e.g., plant food availability) play a major role in limiting the range of either species. However, the striking ecological similarity of the two species suggests that their populations are unlikely to be independently regulated. With respect to food plant species, both species are generalists in their exploitation of nectar (Dowsett-Lemaire 1989; J. P. M. pers. obs.), and both frequently feed on the same widespread plants (*Tecoma capensis*, *Halleria lucida*, *Dombeya* sp., *Leonotis* spp., J. P. M., pers. obs.) in the vicinity of the parapatric boundary. Consequently, we conclude that the range of each species is limited primarily by the presence of the sibling species, and not by other aspects of the environment.

For the third subhypothesis, that the two species are in strong ecological competition where they locally cooccur, our evidence comes from a previous experimental territorial intrusion study (McEntee 2014) and from natural history observation. In the territorial intrusion study, populations of both species near the species border exhibited strong aggressive responses to heterospecific mounts following approaches initiated by heterospecific or conspecific song playback (see Fig. 5 in McEntee 2014). This result suggests that interspecific interference competition for territories should be strong where there is local occurrence. At the only site where pure individuals of both species hold adjacent territories, we have observed extended aggressive chases among males of the two species. Such territorial disputes are further suggestive of resource competition, where suitable breeding territory is a shared resource. Collectively, the experimental and observational evidence is consistent with the social selection parapatry hypothesis, which requires strong ecological competition between species.

With respect to the fourth subhypothesis above, the combination of incomplete reproductive isolation and selection against hybrids can generate Allee effects for the locally rare species via reproductive interference (Hochkirch et al. 2007; Gröning and Hochkirch 2008) near mutual species borders (Case et al. 2005). It is theoretically possible then for reproductive interference to limit species ranges even where ecological competition is not strong. However, because reproductive interference may

combine with ecological competition to set Allee effects in nature, teasing out their relative effects is likely to be difficult. The strongest support for West-Eberhard's social selection parapatry hypothesis, which specifies ecological competition and less so reproductive interference as the driver of mutual exclusion, would come from parapatric distributions where no reproductive interference occurred. In this study, individuals of mixed ancestry comprise seven of the 75 individuals (9.3%) sampled from sites where genes from both species were sampled (Fig. 2). While this proportion is likely to be an overestimate of contact zone hybrid formation because of intensive sampling effort where syntopy of parental forms was discovered, it is nonetheless clear that prezygotic reproductive isolation is incomplete. This result raises two issues: the role of signal divergence in speciation and whether parapatry could be stabilized entirely by reproductive interference in this case. While social selection against hybrids due to poor signaling traits may occur, the existence of hybridization raises the possibility that genetic incompatibilities may contribute to the fitness disadvantages of individuals with mixed ancestry, perhaps indicating a less important role for signal divergence in the speciation process. However, genetic incompatibilities appear to accumulate slowly in many birds (Price and Bouvier 2002), such that even if genetic incompatibilities occur at present, early signal divergence may have caused lowered rates of hybridization during contact earlier in the speciation process. Population-level studies examining fitness outcomes in the hybrid zone would be helpful to tease out some of these issues. With respect to the stabilization of parapatry, we must conclude that reproductive interference via selection against hybrids is likely a contributor to the range limits of *fuelleborni* and *moreaui* at their shared range boundary. However, because evidence indicates strong ecological similarity between species, reproductive interference, and ecological competition can be seen as combining to limit the range of each species. Teasing out the relative strength of effects of reproductive interference and ecological competition on range limits would be a productive avenue of future research (Thum 2007; Kishi et al. 2009). Of the four examined subhypotheses for social selection parapatry, the insufficiency of reproductive interference to explain range limits remains the most challenging to support with evidence. It is, moreover, surprising that birds with such different songs do not exhibit more complete prezygotic reproductive isolation. Even dramatic divergence in signals is insufficient then to completely prevent hybridization attempts, such that reproductive interference could play a role in stabilizing avian parapatric boundaries even where (attempted) hybridization has not yet been documented.

#### **ROBUSTNESS OF LEARNED SONG DIVERGENCE TO SECONDARY CONTACT AND HYBRIDIZATION**

The role of learned song in bird speciation remains an open question that falls into the larger debate regarding plasticity's impor-

tance in divergence (West-Eberhard 2005; Pfennig et al. 2010; Verzijden et al. 2012). The combination of learned song's lability and its role in mate choice suggests it could promote speciation by reducing or impeding gene flow. However, the song learning process can result in heterospecific copying (Helb et al. 1985; Laiolo 2012). Divergent learned song may then be a weak barrier to hybridization (Secondi et al. 2003; Haavie et al. 2004; Qvarnström et al. 2006; Secondi et al. 2011; Vokurkova et al. 2013). There is more potential for learned song differences to prevent gene flow if song predispositions and adult song phenotypes have codiverged with preferences or response functions. Experiments have shown that certain aspects of song phenotypes tend to be constrained by innate song predispositions, namely duration, frequency range, organization (gross structure), and element (syllable) morphology (Thorpe 1958; Nottebohm 1968; Marler and Peters 1977; Marler and Sherman 1985; Soha and Marler 2000; Catchpole and Slater 2008). Thus (incipient) species bearing divergence in these aspects are less likely to converge on contact. *N. moreaui* and *N. fuelleborni* song differences include divergence in all of the listed aspects likely to be constrained by innate predispositions, rendering these species' contact zone an important case study for how song predisposition divergence impacts the robustness of learned song divergence to secondary contact with hybridization.

The coincidence and concordance of molecular and song clines (Tables 1 and S4, Fig. 5) suggest that song behaves much as a quantitative trait under within-species stabilizing selection across the *N. moreaui*-*N. fuelleborni* contact zone, and indeed suggests that heterospecific copying has not broadened the song cline, as would be predicted from interspecific cultural transmission in parapatry. It is important to note, though, that not all intermediate values for learned song come from mixed-ancestry individuals. At least one of the intermediate values for song in the contact zone was exhibited by an individual that scored as pure *moreaui* at a molecular level in our *structure* analyses. Therefore, those individuals with intermediate song phenotypes may represent hybrids as well as pure individuals. Thus, in the geographic context analyzed here, song behaves much like a typical quantitative trait, but heterospecific copying is apparent within one contact zone population. If heterospecific copying is disadvantageous (Qvarnström et al. 2006), selection against locally rare heterospecifics exhibiting mismatched genotypes and phenotypes might complement selection against hybrids in reinforcing the stability of the cline.

## *Conclusions*

We have provided evidence that *N. moreaui* and *N. fuelleborni* may be viewed as a case of social selection parapatry. Our evidence includes demonstrating (1) that the two species have

diverged strongly in a signal (learned song) while showing strong conservatism in bioclimatic niche, and (2) that interspecific interactions, not an ecological gradient or geographic barrier, play a primary role in limiting the range of each species. We add this evidence to experimental evidence from a previous article (McEntee 2014) indicating that interference competition between species is intense where these species make contact. While interspecific competition is apparent and clearly plays some role in limiting the range of each species, we cannot yet rule out the possibility that reproductive interference in the form of selection against hybrids is involved in restricting the range of each species. The relative contribution of ecological competition and reproductive interference in limiting the ranges of parapatric species may be difficult to distinguish, but doing so should be a focus of future research. We advocate, however, that investigators of hybrid zones study competitive interactions, individual movement, and relative population densities across hybrid zones in addition to studying hybridization, to understand which factors stabilize parapatry.

The abrupt spatial turnover in highly divergent song phenotypes, concordant with genotypes, recommends the *moreaui-fuelleborni* hybrid zone for future study on song divergence and speciation. Strong divergence in multiple aspects of song phenotype in these two species, together with the possibility of examining the phenotypes of hybrids, may allow for identification of the molecular changes underpinning divergent song predispositions in recent species.

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#### DATA ARCHIVING

Molecular sequence data have been archived in GenBank under accession numbers KX131279-KX132075. Song and bill measurements have been made accessible via the Dryad Digital Repository <http://dx.doi.org/10.5061/dryad.1fc41>.

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## Supporting Information

Additional Supporting Information may be found in the online version of this article at the publisher's website:

**Table S1.** Estimation of the number of populations ( $K$ ) in *structure* (Hubisz et al. 2009) from analyses of haplotypes for 132 individuals at five nuclear introns (11836, 18142, BRM, CHDZ, MUSK).

**Table S2.** Summary statistics from DNA sequences at 5 nuclear loci and the mtDNA gene ND2.

**Table S3.** Song variable mean and standard deviation by species, with 'effect size' estimates for the difference in means calculated as the absolute value of Hedges'  $g$  (Hedges 1981), and statistical test p-values from ANOVAs for each individual variable.

**Table S4.** Loadings on Principal Components from PCA on song variables,  $n = 101$  individuals (variables are identical to those in Table S2), and cumulative variance explained.

**Table S5.** Cline center and width estimates for preferred model architectures for each trait.

**Table S6.** Samples used for molecular analyses with localities and museum voucher numbers indicated.

**Figure S1.** Probability of assignment to *Nectarinia moreaui* (green) and *N. fuelleborni* (purple) from a *structure* analysis where ND2 haplotypes are scored as *moreaui* or *fuelleborni* in origin and included as a diploid marker with one known and one unknown state.

**Figure S2.** Histogram of the coefficient of variation of peak frequency, scored for each individual as the mean across songs.

**Figure S3.** Histogram of culmen length by species.