

## Appendix

We assume discrete generations and a polygynous mating system where all females have equal mating success. Individuals are haploid, which leads to 8 female genotypes ( $A_1M_1N_1$ ,  $A_1M_1N_2$ , ...,  $A_2M_2N_2$ ) and 12 male phenogenotypes ( $A_1M_1N_11$ ,  $A_1M_1N_12$ ,  $A_1M_1N_22$ ,  $A_1M_2N_12$ , ...,  $A_2M_2N_23$ ) in the basic model, where the last digit, 1-3, denotes which song interval category the male's songs fall in. The male phenogenotypes occur with frequencies  $xm_1$ ,  $xm_2$ , ...,  $xm_{12}$  in the population and female genotypes occur with frequencies  $xf_1, \dots, xf_8$ . Each of these phenotypes and genotypes is tracked within two separate populations (these indexes are left out below for simplicity).

The life cycle starts every year at the time of dispersal, where a percentage of young adults,  $m$ , from each population disperses to the other habitat. We assume that dispersal is independent of genetic background and we compare different dispersal rates ( $m = 0.01, 0.05, 0.1$ ). Here  $m$  specifically represents the proportion of each population that consists of migrants, measured after migration occurs, leading to the standard population genetic equations for migration between two islands.

After dispersal, females search for mates. There is a probability that a choosy female may remain unmated; the frequency of choosy females (females with the A2 allele) who mate is calculated as:

$$xf_i^c = \frac{(1 - c(\alpha_p(1 - f_p) + \alpha_m(1 - f_m)))xf_i}{\bar{w}_c}$$

Where  $c$  is the strength of costs,  $\alpha_p$  is the strength of female preference for pure song,  $\alpha_m$  is the strength of preference for mixed song, and  $f_p$  and  $f_m$  are the frequency of males singing pure and mixed song, respectively. Selection against preference is bounded such that the frequency of choosy females following selection is never  $< 0$ .  $\bar{w}_c$  is the mean fitness resulting from costs, calculated as the sum of the numerators of the  $xf_i^c$ .

Females and males mate and produce offspring. The mating table (table A1) summarizes all the possible matings that can occur in the population under the basic model and the version where hybrids have preferences, with each cell in the table corresponding to a coefficient of mating (see Table 1 legend). Specifically the frequency of each mated pair is equal to the product of the corresponding male and female frequencies after migration and preference costs multiplied by the indicated coefficient of mating, with each row of the mating table normalized so that female genotype has equal mating success. The frequency of each mated pair can be represented in the matrix  $M$  where

$$M_{i,j} = \frac{F_{i,j}xf_i^c xm_j^m}{\sum_k F_{i,k}xm_k^m}. \quad (A1)$$

Here  $F$  is the matrix of coefficients presented in Table A1 and the superscript  $m$  indicates the frequency after migration. The version of the model where hybrids with weak predispositions can learn parental song is presented further below.

Offspring are produced from each mated pair  $M_{i,j}$  using the standard assumptions of segregation in haploids assuming free recombination between each pair of loci. Only the genotype of males, not the song that they sing, is transmitted to zygotes in the next generation. This leads to 8 genotypes in zygotes with identical frequencies in both males and females, indexed as  $x_1^z$  through  $x_8^z$  equaling the frequencies of  $A_1M_1N_1$ ,  $A_1M_1N_2$ , ...,  $A_2M_2N_2$ .

The exact frequency of each phenogentotype acquired by males in the next generation will depend on the frequency of weak predispositions in the population as well as which songs are present in the parental generation. In the basic model, hybrids ( $M_1N_2$  and  $M_2N_1$  males) produce songs from the mixed range (category 2) only, so their phenogentotype frequencies are equal to the frequencies in the zygote stage, where  $xm_3 = x_2^z$ ,  $xm_4 = x_3^z$ ,  $xm_9 = x_6^z$  and  $xm_{10} = x_7^z$ . With a probability  $1-B$ , the frequency of strong predispositions, non-hybrid males will sing songs from either category 1 or 3 depending on whether he has the genetic combination  $M_1N_1$  or  $M_2N_2$ . The rest of the non-hybrid males will learn obliquely under weak predispositions with probability  $B$ . Juvenile males with weak predispositions hear songs from all three categories and learn either songs from I) the categories that he can produce songs from (for  $M_1N_1$  allele juveniles this means categories 1 or 2 and for  $M_2N_2$  allele juveniles songs from category 2 or 3), or II) the mixed category when the juvenile by mistake tries to learn songs from the wrong allele specific song category (for  $M_1N_1$  allele juveniles, category 3, and for  $M_2N_2$  allele juveniles, category 1). These outcomes occur in proportion to how common songs from each category are in the entire population. The resulting male phenogentotypes will thus be:

$$\begin{aligned}
 xm_1^s &= (1-B)x_1^z + Bs_1x_1^z \\
 xm_2^s &= B(s_2 + s_3)x_1^z \\
 xm_5^s &= B(s_1 + s_2)x_4^z \\
 xm_6^s &= (1-B)x_4^z + Bs_3x_4^z \\
 xm_7^s &= (1-B)x_5^z + Bs_1x_5^z \\
 xm_8^s &= B(s_2 + s_3)x_5^z \\
 xm_{11}^s &= B(s_1 + s_2)x_8^z \\
 xm_{12}^s &= (1-B)x_8^z + Bs_3x_8^z
 \end{aligned} \tag{A2}$$

where the superscript z indicates the frequency in zygotes, the superscript s indicates after song learning and  $s_1$  through  $s_3$  indicate the frequency of songs 1-3 sung by adults of the previous generation, as follows:

$$\begin{aligned}
 s_1 &= xm_1^m + xm_7^m \\
 s_2 &= xm_2^m + xm_3^m + xm_4^m + xm_5^m + xm_8^m + xm_9^m + xm_{10}^m + xm_{11}^m \\
 s_3 &= xm_6^m + xm_{12}^m
 \end{aligned}$$

The last step in the life cycle is natural selection. Hybrids suffer from lower viability, with strength  $s_E$ .

$$\begin{aligned} xm_p &= \frac{xm_p}{\bar{w}}, \\ xm_h &= \frac{xm_h(1-s_E)}{\bar{w}} \end{aligned} \tag{A3}$$

where  $\bar{w}$  equals the frequency of purebreds plus  $1-s_E$  times the frequency of hybrids. The index  $p$  indicates pure males (i.e. males with the combination  $M_1N_1$  or  $M_2N_2$ ) and the index  $h$  indicates hybrid males.

When hybrids with weak predispositions can learn parental song the male genotypes expand from 12 to 20, indexed in the order specified in the column headers of Table A2. Table A2 becomes the table of coefficients F used to create the mating table M specified in equation (A1). Offspring production follows the procedure described above. Juvenile males learn song according to the following set of equations:

$$\begin{aligned} xm_1^s &= (1-B)x_1^{\bar{z}} + Bs_1x_1^{\bar{z}} \\ xm_2^s &= B(s_2 + s_3)x_1^{\bar{z}} \\ xm_3^s &= Bs_1x_2^{\bar{z}} \\ xm_4^s &= (1-B)x_2^{\bar{z}} + Bs_2x_2^{\bar{z}} \\ xm_5^s &= Bs_3x_2^{\bar{z}} \\ xm_6^s &= Bs_1x_3^{\bar{z}} \\ xm_7^s &= (1-B)x_3^{\bar{z}} + Bs_2x_3^{\bar{z}} \\ xm_8^s &= Bs_3x_3^{\bar{z}} \\ xm_9^s &= B(s_1 + s_2)x_4^{\bar{z}} \\ xm_{10}^s &= (1-B)x_4^{\bar{z}} + Bs_3x_4^{\bar{z}} \\ xm_{11}^s &= (1-B)x_5^{\bar{z}} + Bs_1x_5^{\bar{z}} \\ xm_{12}^s &= B(s_2 + s_3)x_5^{\bar{z}} \\ xm_{13}^s &= Bs_1x_6^{\bar{z}} \\ xm_{14}^s &= (1-B)x_6^{\bar{z}} + Bs_2x_6^{\bar{z}} \\ xm_{15}^s &= Bs_3x_6^{\bar{z}} \\ xm_{16}^s &= Bs_1x_7^{\bar{z}} \\ xm_{17}^s &= (1-B)x_7^{\bar{z}} + Bs_2x_7^{\bar{z}} \\ xm_{18}^s &= Bs_3x_7^{\bar{z}} \\ xm_{19}^s &= B(s_1 + s_2)x_8^{\bar{z}} \\ xm_{20}^s &= (1-B)x_8^{\bar{z}} + Bs_3x_8^{\bar{z}} \end{aligned} \tag{A5}$$

where now

$$s_1 = xm_1^m + xm_3^m + xm_6^m + xm_{11}^m + xm_{13}^m + xm_{16}^m$$

$$s_2 = xm_2^m + xm_4^m + xm_7^m + xm_9^m + xm_{12}^m + xm_{14}^m + xm_{17}^m + xm_{19}^m .$$

$$s_3 = xm_5^m + xm_8^m + xm_{10}^m + xm_{15}^m + xm_{18}^m + xm_{20}^m$$

Viability selection then acts as specified in equation (A3).

		Males												
		A <sub>1</sub>						A <sub>2</sub>						
		M <sub>1</sub> N <sub>1</sub> 1	M <sub>1</sub> N <sub>1</sub> 2	M <sub>1</sub> N <sub>2</sub> 2	M <sub>2</sub> N <sub>1</sub> 2	M <sub>2</sub> N <sub>2</sub> 2	M <sub>2</sub> N <sub>2</sub> 3	M <sub>1</sub> N <sub>1</sub> 1	M <sub>1</sub> N <sub>1</sub> 2	M <sub>1</sub> N <sub>2</sub> 2	M <sub>2</sub> N <sub>1</sub> 2	M <sub>2</sub> N <sub>2</sub> 2	M <sub>2</sub> N <sub>2</sub> 3	
Females	A <sub>1</sub>	M <sub>1</sub> N <sub>1</sub>	1	1	1	1	1	1	1	1	1	1	1	
		M <sub>1</sub> N <sub>2</sub>	1	1	1	1	1	1	1	1	1	1	1	
		M <sub>2</sub> N <sub>1</sub>	1	1	1	1	1	1	1	1	1	1	1	
		M <sub>2</sub> N <sub>2</sub>	1	1	1	1	1	1	1	1	1	1	1	
	A <sub>2</sub>	M <sub>1</sub> N <sub>1</sub>	1+ $\alpha_p$	1+ $\alpha_m$	1+ $\alpha_m$	1+ $\alpha_m$	1+ $\alpha_m$	1	1+ $\alpha_p$	1+ $\alpha_m$	1+ $\alpha_m$	1+ $\alpha_m$	1+ $\alpha_m$	1
		M <sub>1</sub> N <sub>2</sub>	1	1+ $\alpha_h$	1+ $\alpha_h$	1+ $\alpha_h$	1+ $\alpha_h$	1	1	1+ $\alpha_h$	1+ $\alpha_h$	1+ $\alpha_h$	1+ $\alpha_h$	1
		M <sub>2</sub> N <sub>1</sub>	1	1+ $\alpha_h$	1+ $\alpha_h$	1+ $\alpha_h$	1+ $\alpha_h$	1	1	1+ $\alpha_h$	1+ $\alpha_h$	1+ $\alpha_h$	1+ $\alpha_h$	1
		M <sub>2</sub> N <sub>2</sub>	1	1+ $\alpha_m$	1+ $\alpha_m$	1+ $\alpha_m$	1+ $\alpha_m$	1+ $\alpha_p$	1	1+ $\alpha_m$	1+ $\alpha_m$	1+ $\alpha_m$	1+ $\alpha_m$	1+ $\alpha_p$

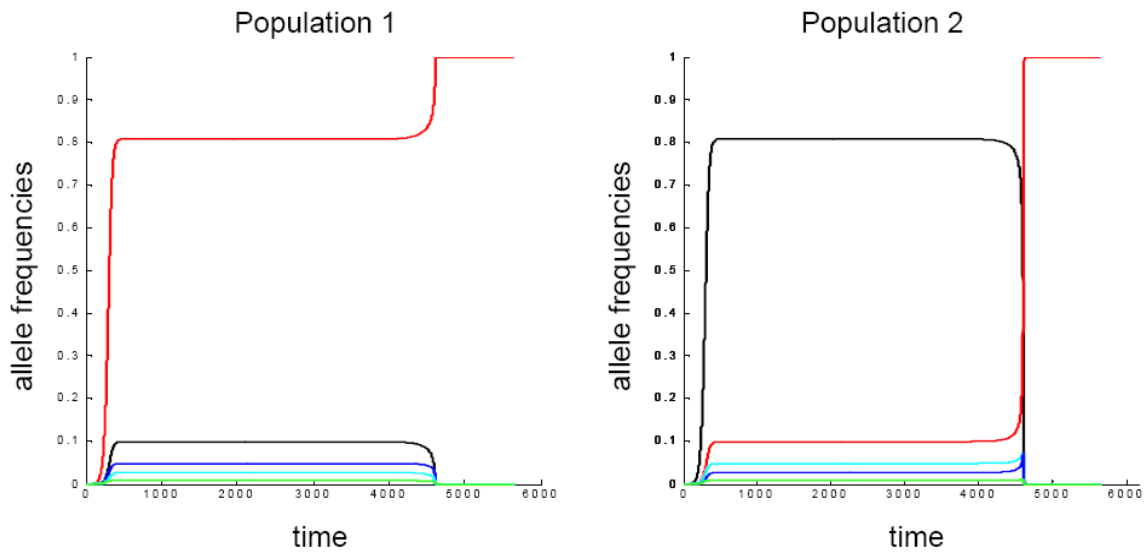
**Table A1.** The mating table, showing all the possible matings that can occur in the population under the basic model and in the version where hybrid females have preferences. These matings occur within each of the two populations under consideration. The genotypes of the females are shown down the right hand side of the table and the phenogenotypes of the males are shown across the top. The value in each cell represents the coefficient of mating, specifically how much more likely a given female is to mate with that particular type of male as opposed to a male that she does not prefer, given that she encounters one of each. In the basic model,  $a_h = 0$ . In the version of the model where hybrids have a preference,  $a_h = a_p$ .

Fig. A1 (next page). A) Changes in phenogenotypes after the introduction of  $A_2$  in both habitats for a case with an unstable equilibrium for the maintenance of local dialects ( $B = 0.1$ ,  $\alpha_p = 8$ ,  $s_E = 0.85$ ,  $m = 0.05$ ). In general we find this unstable equilibrium after  $A_2$  is introduced (unstable equilibria for the maintenance of both dialects before the introduction of  $A_2$  is discussed in the text) when migration is high ( $m = 0.05$ ), and is the frequency of weak predispositions is low. Only phenogenotypes with  $A_2$  are shown (as a given phenogenotype with  $A_2$  increases the corresponding phenogenotype with  $A_1$  decreases, since the two frequencies always sum to 1). The lines are color coded in the same manner in both habitats, where  $A_2M_1N_11$  is the red line and  $A_2M_2N_23$  is the black line. Other visible phenogenotype frequencies are as follows: Purple =  $A_2M_2N_12$ , Turquoise =  $A_2M_2N_22$ , Green =  $A_2M_1N_22$ .

B) The dominant eigenvalue for the Jacobian matrix for the example in A. When this value is greater than 1 it indicates unstable dynamics, while a value less than 1 indicates stability. Time is starting when  $A_2$  is introduced. Combining the two graphs from A1A with this one, it is possible to see that the population is not at a stable equilibrium prior to the great change in phenogenotype frequencies.

Figure A1

A)



B)

