Appendix 1

Figure A1. Results of a null model with identical parameters to those used in the experimental model (Figure 1), but with the females’ discrimination ability set to zero: females ignore male individuality signals while choosing mates, and all the measured genotypes in this model thus evolve only under neutral processes. Global number of genotypes (red symbols) and mean genotypes per patch (blue symbols) across a range of levels of population fragmentation (x-axis). Large symbols: genotypes visible to females that would be evolving under sexual selection if it were active (Figure 1); small symbols: genotypes invisible to females and evolving only under neutral processes. Data are means from 40 replicate model runs with standard deviations, collected after 50,000 model time steps. The number of patches in the global population varies between 1 and 50 (x-axis), with six rates of dispersal between patches (separate panels) including no dispersal. The top axis rug (red ticks) marks levels of fragmentation at which global signal diversity is significantly different from signal diversity in the single-patch system. The x-axis rug (blue ticks) marks levels of fragmentation at which local signal diversity is significantly different from local signal diversity at the immediately preceding level. Rugs were calculated using linear models with number of genotypes as the response variable and fragmentation (restricted to the two levels of interest) as a factor.
Figure A2. Mean pairwise $F_{ST} \pm SE$ for signalling (large symbols) and non-signalling (small symbols) loci at dispersal rates of 0.001 (black), 0.01 (red) and 0.1 (blue) in the 20-patch system (equilibrium density of 500 individuals per patch). In the model, patches were distributed in a circular arrangement so that there was a maximum distance of 10 units between patches. Data are means of 40 replicate runs of the model, collected after 50 000 model time steps. Because each replicate run generated multiple distance points and $F_{ST}$ estimates, we analysed the effect of dispersal rate and distance on mean pairwise $F_{ST}$ using a linear mixed-effects model (LMM) with replicate modelled as a random effect. As expected under an isolation-by-distance model, $F_{ST}$ increased with distance between pairs of patches, and pairwise $F_{ST}$ increased with decreasing probability of inter-patch dispersal. The rate of $F_{ST}$ increase with inter-patch distance was influenced by the dispersal rate, with the greatest increase in isolation-by-distance at the lowest levels of dispersal, resulting in a significant interaction LMM: (dispersal rate * inter-patch distance: $F_{1,2757} = 258$, $p << 0.001$). Pairwise mean $F_{ST}$ was significantly different between signalling and non-signalling patches at all distances for the dispersal rate of 0.001. When dispersal was 0.01 there was no difference in mean pairwise $F_{ST}$ for distances 1 or 2 (both $F < 1.59$, both $p > 0.207$), and for the highest dispersal of 0.1 this comparison was significant only for distances 8, 9 and 10 (for distances < 8: all $F_{1,1559} < 2.45$, $p > 0.118$, for distance $\geq 8$: $F_{1,1559} > 4.74$, $p < 0.030$).
Figure A3. The number of genotypes in a single population of the 10-patch system over an arbitrary 50,000 time-step period in the middle of the model run. The heatmap colours represent the 1000 possible genotype combinations. Signalling genotypes (left panels) show more genetic diversity and stability than non-signalling genotypes (right panels) across the range of dispersal rates tested (horizontal rows).
Figure A4. Proportion of matings where there is an ‘impersonation’ (i.e. the female mates with a male other than the best male, but which carries the same signal as the best male) for a subset of dispersal rates and patch sizes. Data collected from periods of 10 timesteps towards the end of simulation runs. Errors are SEs; open bars represent a 10 patch system, red bars 20 patches, blue bars 50 patches.