

Supplementary Material

Olah G, Smith AL, Asner GP, Brightsmith DJ, Heinsohn RG, Peakall R (2016) Exploring dispersal barriers using landscape genetic resistance modelling in scarlet macaws of the Peruvian Amazon. *Landscape Ecology* doi:10.1007/s10980-016-0457-8

Table S1. Average genetic variation of nine polymorphic microsatellite loci for scarlet macaw (*Ara macao*).

Locus	<i>N</i>	Size range (bp)	<i>N_a</i>	<i>N_e</i>	<i>H_O</i>	<i>H_E</i>	<i>F</i>
SCMA 22	163	114-160	18	12.527	0.926	0.920	-0.007
SCMA 32	158	175-211	16	10.432	0.829	0.904	0.083
SCMA 34	164	151-189	17	7.898	0.841	0.873	0.037
SCMA 33	166	174-212	18	10.297	0.867* (1)	0.903	0.039
SCMA 26	160	210-240	14	8.994	0.831* (2)	0.889	0.065
SCMA 09	164	112-136	12	5.197	0.787	0.808	0.026
SCMA 14	163	220-252	14	8.538	0.773	0.883	0.124
SCMA 30	156	206-246	17	9.402	0.885	0.894	0.010
SCMA 31	138	137-169	15	8.264	0.877	0.879	0.002
Mean			15.7	9.061	0.846	0.884	0.042

Presented are locus code, number of samples (*N*), fragment size ranges, number of alleles (*N_a*), effective number of alleles (*N_e*), observed heterozygosity (*H_O*), expected heterozygosity (*H_E*) and fixation index (*F*).

*Significant ($P < 0.05$) departure from HWE. The number of populations is given in parentheses.

Table S2. Genetic variation from three populations of scarlet macaw (*Ara macao*) for nine polymorphic microsatellite loci.

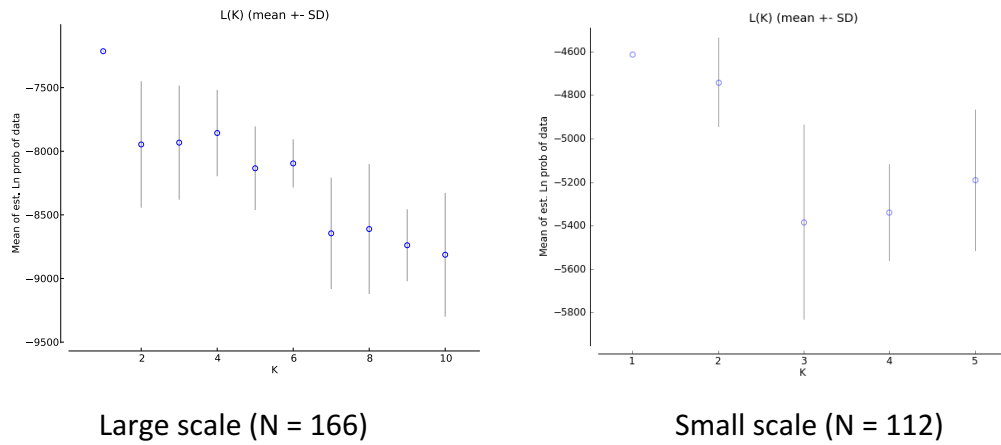
Population	<i>N</i>	<i>Na</i>	<i>Ne</i>	<i>H_O</i>	<i>H_E</i>	<i>F</i>
Lower Tambopata	54	13.78	8.69	0.833* (1)	0.875	0.048
Upper Tambopata	82	14.11	8.77	0.866* (2)	0.881	0.018
Candamo	30	11.11	7.58	0.817	0.862	0.052
Mean		13	8.35	0.838	0.873	0.040

Number of individuals sampled (*N*), number of alleles (*Na*), effective number of alleles (*Ne*), observed heterozygosity (*H_O*), expected heterozygosity (*H_E*) and inbreeding coefficient (*F*) are given. Populations are arranged from south to north.

*Significant ($P < 0.05$) departure from HWE. Number of loci given in parentheses.

Figure S1. Results from (A) STRUCTURE Harvester (Earl and vonHoldt 2012) and (B) GENELAND indicated that a single genetic cluster was most likely the case.

(A)



(B)

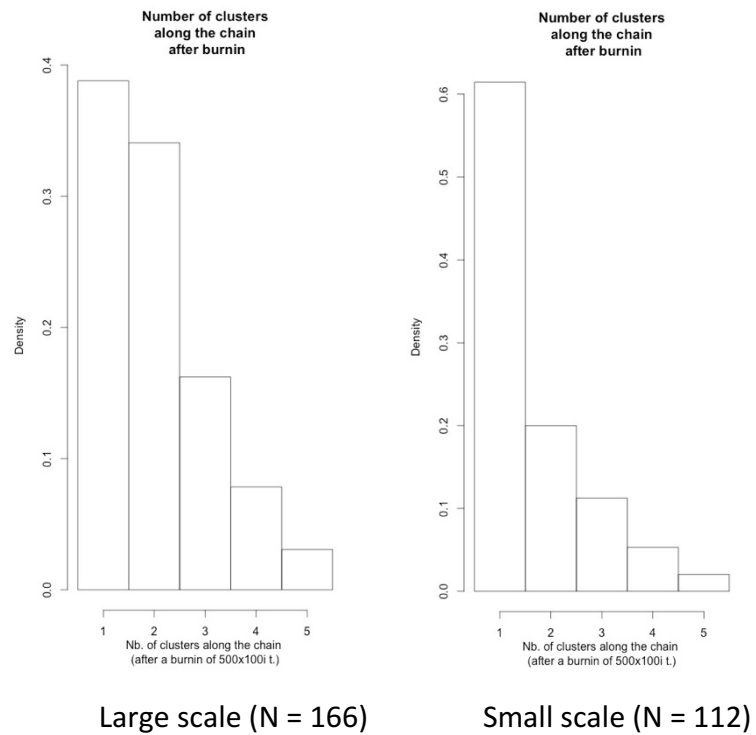


Figure S2. Sex specific spatial genetic autocorrelation analysis for scarlet macaw (*Ara macao*). The graph shows comparison of correlations for females versus males across study sites: pairwise genetic distance (rc) for increasing distance class sizes (blue), 95% CI about the null hypothesis of a random distribution of scarlet macaw (red), 95% confidence error bars about rc as determined by bootstrapping (black).

