

### Electronic Supplementary Material

Olah G\*, Heinsohn RG, Brightsmith DJ, and Peakall R (2017). The application of non-invasive genetic tagging reveals new insights into the clay lick use by macaws in the Peruvian Amazon. *Conservation Genetics*

doi:10.1007/s10592-017-0954-6

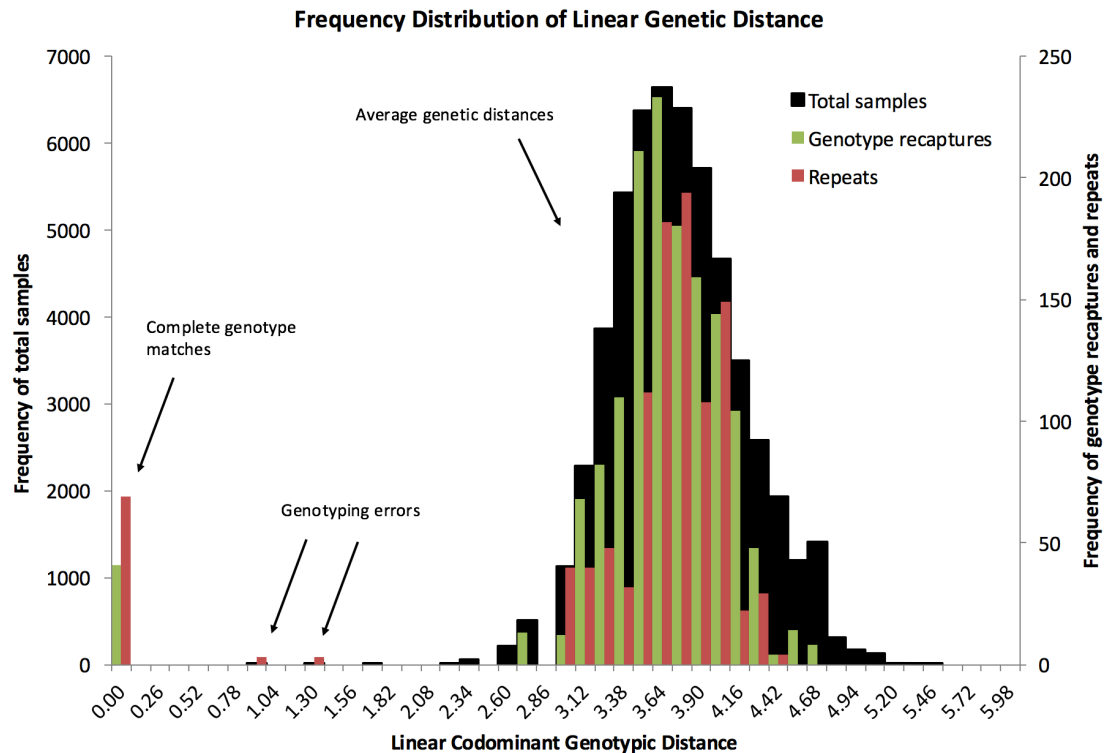
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**Table S1.** Pairwise population genetic differentiations of red-and-green macaws (*Ara chloropterus*) between clay licks.  $F_{ST}$  values below diagonal;  $P$  values based on 10,000 permutations are shown above diagonal. Clay licks are in geographical order from south to north.

	$P$						
	<b>Tavara</b> (N = 22)	<b>Colorado</b> (N = 10)	<b>Chuncho</b> (N = 114)	<b>Explorers</b> (N = 18)	<b>Posada</b> (N = 12)	<b>Heath</b> (N = 23)	<b>Piedras</b> (N = 22)
<b>Tavara</b>	-	0.108	0.031*	0.033*	0.447	0.005*	0.025*
<b>Colorado</b>	0.011	-	0.36	0.21	0.117	0.067	0.452
<b>Chuncho</b>	0.007*	0.001	-	0.183	0.379	0.004*	0.063
$F_{ST}$ <b>Explorers</b>	0.012*	0.007	0.003	-	0.067	0.004*	0.035*
<b>Posada</b>	0	0.014	0.001	0.013	-	0.278	0.457
<b>Heath</b>	0.017*	0.013	0.011*	0.019*	0.004	-	0.461
<b>Piedras</b>	0.012*	0	0.005	0.012*	0	0	-

\*Significant ( $P < 0.05$ ) population genetic differentiations

**Figure S1.** Frequency distribution of pairwise genetic distances [following Smouse and Peakall (1999)] among red-and-green macaws (*Ara chloropterus*) of different individuals (black, N=221), genotype recaptures (green, N=49), and PCR repeats (red, N=42).



Peakall et al. (1995) described a pairwise genetic distance measure for a meaningful comparison of allozyme and random amplified polymorphic DNA (RAPD) data. A slight modification of this scheme was presented in Smouse and Peakall (1999) to calculate the genetic distance between a pair of individuals for multiallelic codominant loci. According to this scheme, in a system of three codominant alleles (e.g. A, B, and C) the linear distances between different homozygotes (e.g. AA and BB) are scaled to be '2' units apart, while the heterozygotes are a linear distance of '1' from each homozygote with shared allele (e.g. AB and AA). The linear distance between heterozygotes sharing a single allele (e.g. AB and AC) is '1', and that between any heterozygote and a homozygote not sharing any alleles (e.g. AB and CC) is ' $\sqrt{3}$ '. The distance between any genotype and itself is '0'. Extending the calculations to more than three

alleles, the only difference is that the linear distance between two non-overlapping heterozygotes (e.g. AB and CD) is ' $\sqrt{2}$ '. For multiple loci, the total genetic distance between two individuals is the sum of distances at each locus.

Peakall R, Smouse PE, and Huff DR (1995) Evolutionary implications of allozyme and RAPD variation in diploid populations of dioecious buffalograss

*Buchloë dactyloides*. *Molecular Ecology* 4:135-148

doi:10.1111/j.1365-294X.1995.tb00203.x

Smouse PE and Peakall R (1999) Spatial autocorrelation analysis of individual multiallele and multilocus genetic structure. *Heredity* 82:561-573

doi:10.1038/sj.hdy.6885180