Comparative analysis of microsatellite variability in five macaw species (Psittaciformes, Psittacidae): Application for conservation

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Abstract

Cross-amplification was tested and variability in microsatellite primers (designed for Neotropical parrots) compared, in five macaw species, viz., three endangered blue macaws (Cyanopsitta spixii [extinct in the wild], Anodorhynchus leari [endangered] and Anodorhynchus hyacinthinus [vulnerable]), and two unthreatened red macaws (Ara chloropterus and Ara macao). Among the primers tested, 84.6% successfully amplified products in C. spixii, 83.3% in A. leari, 76.4% in A. hyacinthinus, 78.6% in A. chloropterus and 71.4% in A. macao. The mean expected heterozygosity estimated for each species, and based on loci analyzed in all the five, ranged from 0.33 (A. hyacinthinus) to 0.85 (A. macao). As expected, the results revealed lower levels of genetic variability in threatened macaw species than in unthreatened. The low combined probability of genetic identity and the moderate to high potential for paternity exclusion, indicate the utility of the microsatellite loci set selected for each macaw species in kinship and population studies, thus constituting an aid in planning in-situ and ex-situ conservation.

Key words: conservation, cross-amplification, macaw, microsatellite, Psittaciformes.
tionships were unknown), 30 wild hyacinth macaws from the Pantanal (state of Mato Grosso do Sul), 31 wild red-and-green macaws from the Pantanal, and 28 wild scarlet macaws from the southeast of the state of Pará, all in Brazil. Samples of the latter three species were obtained from nestlings. Only one chick per nest was studied. All the samples were preserved in absolute ethanol and stored frozen at the Laboratório de Genética e Evolução Molecular de Aves (LGEMA), Instituto de Biociências, Universidade de São Paulo. Total DNA was extracted from blood samples, according to standard protocol, with proteinase K digestion and phenol: chloroform (Bruford et al., 1992).

Primer pairs were tested for 19 di- and tetranucleotide microsatellite loci. Seven of these were designed for Ara ararauna (UnaCT21, UnaCT32, UnaCT43, UnaCT74 and UnaGT55; Caparroz et al., 2003; UnaCT41int; Gebhardt and Waits, 2008; UnaCT35 F 5’TCTATCCCTTTTGTG AGC3’ and UnaCT35 R 5’TAGCTAGATTTTCTTCTC TG3’; R. Caparroz, unpublished), eight for Amazona guildingui (AgGT07, AgGT08, AgGT12, AgGT17, AgGT21, AgGT81, AgGT19 and AgGT32; Russello et al., 2001, 2005), two for Anodorhynchus hyacinthinus (Scott K. Davis, unpublished; MAC 436 F 5’GCACCAAAACA CAACATCTATTC3’ and MAC 436 R 5’TGGGACAC CAATGTAATTTG3’, and HYA 1172 F 5’GATCCTTTG CTTAAAGACAGATGTC3’ and HYA 1172 R 5’GAGTGAAATACACATTCAGCTTCTG3’), and two for Psittacus erithacus (Pee/c109 11 and Pee/c109 16; Taylor and Parkin, 2007). In each primer pair, the forward one had an additional 5’ M13 sequence tail (5’-TGTAAAACGACG GCCAGT-3’) (Schuelke, 2000), so as to enable applying the universal dye-labelling method (Boutin-Ganache et al., 2001).

We initially tested the potential cross-amplification of each locus (Table 1) with two to four samples from each species. PCR was carried out in a total volume of 12 μL with 20-50 ng of template DNA, 10 mM of Tris-HCl, 50 mM of KCl, 1.5 mM of MgCl2, 200 μM of each dNTP, 0.2 μM of a M13 fluorescent primer (FAM, HEX or NED, Applied Biosystems, CA), 0.1 μM of an M13 tailed forward primer, 0.3 μM of a reverse primer and 0.5 unit of Taq polymerase (Pharmacia). PCR conditions were: initial denaturation at 95 °C for 10 min; followed by 35 cycles of 95 °C for 1 min, 52-58 °C (see Table 1) for 40 s and, 72 °C for 40 s; and a final extension of 72 °C for 7 min. Amplification products were visualized in 1.5% agarose gel and fragments sized by comparison with the 1 kb Plus DNA ladder (Invitrogen). Any amplification that produced fragments with similar sizes to those observed in source species was considered successful. Allele sizes were determined on an ABI 377 DNA sequencer (Applied Biosystems) for blue macaws, and a MegaBACE 1000 (GE Healthcare) for red macaws, using a weight standard (TAMRA 500C or GeneScan -500 ROX STANDARD, Applied Biosystem) in

| Loci       | Size T °C | T °C | Size T °C | T °C | Size T °C | T °C |
|------------|----------|------|----------|------|----------|------|
| UnaCT21    | 237-245  | 58   | 285-290  | 56   | 265-275  | 58   |
| UnaCT32    | 290-295  | 58   | 285-290  | 56   | 265-275  | 58   |
| UnaCT35    | 127-129  | 56   | 290-295  | 58   | 265-275  | 58   |
| UnaCT43    | 212-217  | 56   | 285-290  | 56   | 265-275  | 58   |
| UnaCT55    | 188-190  | 58   | 265-275  | 58   | 265-275  | 58   |
| UnaCT41int | 134-136  | 58   | 265-275  | 58   | 265-275  | 58   |
| AgGT07     | 141-145  | 58   | 212-217  | 56   | 285-290  | 56   |
| AgGT17     | 125-129  | 56   | 285-290  | 56   | 265-275  | 58   |
| MAC416     | 181-185  | 58   | 285-290  | 56   | 265-275  | 58   |
| MAC12      | 238-245  | 58   | 285-290  | 56   | 265-275  | 58   |
| MAC11      | 238-245  | 58   | 285-290  | 56   | 265-275  | 58   |
| MAC10      | 238-245  | 58   | 285-290  | 56   | 265-275  | 58   |
| MAC9       | 238-245  | 58   | 285-290  | 56   | 265-275  | 58   |
| MAC8       | 238-245  | 58   | 285-290  | 56   | 265-275  | 58   |

- NT – not tested, - no amplification, * - touch down PCR method (decreasing 0.5 °C per cycle).
each sample lane. Profile analysis was undertaken with GeneScan and Genotyper 2.1 (Applied Biosystems), or MegaBACE Genetic Profiler Software Suite v2.2 (GE Healthcare). A fragment from one homozygous individual from each species was also sequenced, using the Big Dye Terminator Cycle Sequencing Kit (Applied Biosystems), to check for the presence of microsatellite loci.

The number of alleles per locus, observed and expected heterozygosities (Nei, 1978), paternity exclusion (Q, Weir, 1996) and genetic identity probabilities (Paetkau et al., 1995) were estimated using Identity 1.0 (Wagner and Sefc, 1999). Deviation from Hardy-Weinberg expectation and linkage equilibrium were analyzed with Genepop 4.0 (Raymond and Rousset, 1995), and by applying the Bonferroni correction to account for multiple comparisons. Genotyping errors, due to null alleles, stutter bands or allele dropouts, were analyzed using Micro-checker 2.2.3 (van Oosterhout et al., 2004).

Among the heterologous primer pairs tested, eleven of thirteen (84.6%) amplified products in the Spix’s macaw, 10 of 12 (83.3%) in the Lear’s, 13 of 17 (76.4%) in the hyacinth,11 of 14 (78.6%) in the red-and-green, and 10 of 14 (71.4%) in the scarlet macaw (Table 1). Sequencing results showed that the repeat units are the same as those in source species. Among these successfully amplified loci, six were polymorphic in the Spix’s (54.5%) and Lear’s macaws (60%), eleven in the hyacinth (84.3%), and ten in the red-and-green (90.9%) and scarlet (100%). The number of alleles per polymorphic locus ranged from two to five in the Spix’s macaw, two to six in the Lear’s macaw, two to seven in the hyacinth, two to 12 in the red-and-green, and five to 15 in the scarlet (Table 1).

All the pairs of polymorphic loci were in linkage equilibrium in all the species studied. Sporadic cases of departure from Hardy-Weinberg equilibrium (HWE, p < 0.01) were found in the blue macaw species: locus UnaCT43 in the Spix’s; UnaCT35 and MAC436 in the Lear’s; and MAC436, UnaCT41, and Pee/c109 in the hyacinth macaw (Table 2). Analysis with Micro-Checker software revealed null alleles at all these loci. Expected heterozygosity across all the loci in Hardy Weinberg equilibrium were 0.55 in the Spix’s macaw, 0.62 in the Lear’s, 0.40 in the hyacinth, 0.55 in the red-and-green, and 0.74 in the scarlet (Table 2).

Threatened species, usually present in small populations, are more vulnerable to loss of genetic diversity through processes such as genetic drift and inbreeding. Thus, it was expected that levels of genetic variability in the threatened species studied would be lower than in the unthreatened. This proved to be so, results showing lower levels of genetic variability in the threatened blue macaws than in the unthreatened red. On considering only the four loci UnaCT21, UnaCT43, UnaCT74 and AgGT21, which successfully amplified in all the species, expected mean heterozygosis in the three blue macaws proved to be lower than in the two red (Table 2). Furthermore, monomorphic
loci were more frequently observed in the former. This is in accordance with results from DNA fingerprinting, showing a certain correlation between genetic similarity among pairs of individuals and the level of threat. In the extinct Spix’s macaw, the similarity is 64% (Caparroz et al., 2001b), in the vulnerable hyacinth, 34% (Miyaki C. Y., unpublished results), and in the unthreatened red-and-green, 27% (Caparroz et al., 2001a). Moreover, 21 single locus minisatellite markers also showed higher variability in red-and-green macaws than in the hyacinth (Faria and Miyaki, 2006).

The Spix’s macaw, already rare since its discovery, is now extinct in the wild (Ridgely, 1981, Sick, 1981). Although most of the Spix samples analyzed were from wild individuals, given the rarity of the species, they are all possibly related, a possible reflection of its historically small wild population.

In 2003, the population of Lear’s macaws was estimated to be around 450 individuals (Menezes et al., 2006). This species occurs in a small area in the state of Bahia (Brazil). As most likely all the individuals analyzed here came from this very same, small wild population, the low genetic variability levels observed here could be thus related. However, as the relationships among these individuals are unknown, it is possible that genetic variability levels are biased, due to possible kinship among some.

The population of the hyacinth is the largest among the blue macaws. It is estimated to be around 6,500 individuals, with 5,000 in the Pantanal alone (Birdlife International, 2010). However, its mean expected heterozygosity has proved to be relatively low, compared to that estimated in the unthreatened red-and-green, 27% (Caparroz et al., 2001a). Moreover, 21 single locus minisatellite markers also showed higher variability in red-and-green macaws than in the hyacinth (Faria and Miyaki, 2006).

This study placed in evidence that, in the macaw species analyzed, the cross-amplification of previously developed microsatellite loci can increase the availability of markers to address both ecological and population questions. The low combined-probabilities of genetic identity, and the moderate to high probabilities of paternity exclusion (Table 2), indicate the utility of these microsatellite sets in studying parentage and population differentiation, a valuable aid in planning in-situ and ex-situ conservation action.

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