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Papio Baboon Species Indicative *Alu* Elements

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[†]Membership in the Baboon Genome Analysis Consortium is listed as supplementary file S1, Supplementary Material online.

Abstract

The genus of *Papio* (baboon) has six recognized species separated into Northern and Southern clades, each comprised of three species distributed across the African continent. Geographic origin and phenotypic variants such as coat color and body size have commonly been used to identify different species. The existence of multiple hybrid zones, both ancient and current, have complicated efforts to characterize the phylogeny of *Papio* baboons. More recently, mitochondrial DNA (mtDNA) and Y-chromosome genetic markers have been utilized for species identification with particular focus on the hybrid zones. *Alu* elements accumulate in a random manner and are a novel source of identical by descent variation with known ancestral states for inferring population genetic and phylogenetic relationships. As part of the Baboon Genome Analysis Consortium, we assembled an *Alu* insertion polymorphism database of nearly 500 *Papio*-lineage specific insertions representing all six species and performed population structure and phylogenetic analyses. In this study, we have selected a subset of 48 species indicative *Alu* insertions and demonstrate their utility as genetic systems for the identification of baboon species within *Papio*. Individual elements from the panel are easy to genotype and can be used in a hierarchical fashion based on the original level of uncertainty. This *Alu*-48 panel should serve as a valuable tool during the maintenance of pedigree records in captive populations and assist in the forensic identification of fossils and potential hybrids in the wild.

Key words: retrotransposon, population genomics, evolutionary biology.

Introduction

Baboons (genus *Papio*) cover a large geographic region on the African continent (Boissinot et al. 2014; Jolly 1993; Newman et al. 2004). There are currently six recognized species of *Papio* baboons: *P. anubis* (olive), *P. hamadryas* (hamadryas), *P. papio* (guinea), *P. cynocephalus* (yellow), *P. kindae* (kinda), and *P. ursinus* (chacma) (Jolly et al. 2011; Zinner et al. 2013). The six species are separated primarily into a Northern clade (olive, guinea, and hamadryas) and a Southern clade (yellow, kinda, and chacma), but the existence of natural hybrid zones, both ancient and current, located near species boundaries have been widely studied (Bergman et al. 2008; Nagel 1973; Phillips-Conroy and Jolly 1986; Szmulewicz et al. 1999). The population biology observed in the living populations shows strong evidence for active current hybrid zones

between 1) *P. anubis* and *P. hamadryas*, 2) *P. anubis* and *P. cynocephalus*, 3) *P. kindae* and *P. ursinus*, 4) *P. kindae* and *P. cynocephalus*, and 5) *P. anubis* and *P. papio*. The manuscript from the Baboon Genome Analysis Consortium (Rogers et al. under revision) reported strong evidence for multiple episodes of ancient and recent admixture involving several of the recognized species, suggesting that genetic exchange and gene flow is ongoing in extant populations.

Investigators commonly use morphological characteristics, phenotypic variation and geographic locale/social groups to identify baboon species (Jolly 1993; Phillips-Conroy et al. 1991). In hybrid zones, baboon species origins are inferred using variation in coat color, body size and more recently by using genetic markers such as mitochondrial DNA (mtDNA) (Keller et al. 2010; Kopp et al. 2014; Newman et al. 2004;

Zinner et al. 2013), Y-chromosome markers (Jolly et al. 2011) and microsatellites (Bergman et al. 2008; Charpentier et al. 2012; Tung et al. 2008). Most genetic variation among hybrid baboons is introduced by unidirectional introgression of males mating with native females of the other parental species, thus changing the Y-chromosome genomic component while leaving the native mitochondrial genome intact (Jolly et al. 2011; Keller et al. 2010). Alternatively, using neutral autosomal genetic markers such as retrotransposons, LINEs (long interspersed elements) and *Alu*, may help decipher these complex evolutionary relationships (Boissinot et al. 2014; Szmulewicz et al. 1999).

Retrotransposons have been shown to be highly valuable genetics systems to infer the evolutionary relationships between different species (Konkel et al. 2010; Murata et al. 1993; Ray et al. 2005b; Shedlock and Okada 2000). These markers, especially *Alu* elements and to a lesser extent L1, are now commonly used to investigate phylogenetic and population genetic relationships within the primate orders (Batzer and Deininger 1991; Konkel et al. 2010; Ray and Batzer 2005; Roos et al. 2004; Shedlock and Okada 2000; Stoneking et al. 1997; Xing et al. 2007). *Alu* elements are used more commonly, as they are easy to genotype with a single PCR reaction due to their relatively small size (~300 bp). Retrotransposons such as *Alu* elements are identical-by-descent, have a known directionality or ancestral state and are inexpensive to genotype (Ray et al. 2006). The amplification of *Alu* elements has been ongoing in primate genomes for about 65 million years (Batzer and Deininger 2002; Roy-Engel et al. 2008). They mobilize via a “copy and paste” mechanism through an RNA intermediate, a process termed “target-primed reverse transcription” (TPRT) (Luan et al. 1993). *Alu* elements are nonautonomous and utilize the enzymatic machinery of autonomous LINE elements (L1) to mobilize (Batzer and Deininger 2002; Comeaux et al. 2009; Dewannieux et al. 2003). Due to the staggered DNA cuts of the genome by the L1-derived endonuclease during TPRT, *Alu* insertions are flanked by short sequences of duplicated host DNA called Target Site Duplications (TSDs) that can be used to identify the insertion event.

Because understanding the taxonomy of baboons is complicated and *Alu* elements are robust genetic systems for resolving primate phylogenies, we employed *Papio* lineage specific *Alu* elements in the quest to resolve the phylogenetic relationship among *Papio* baboons as part of the Baboon Genome Analysis Consortium. For this larger study, we identified over 500 *Alu* insertion polymorphisms specific to the *Papio* lineage with representative elements ascertained from all six *Papio* species (Rogers et al. under revision). A final data set of 494 insertion events were used in that study to analyze the phylogeny and population structure across 79 different baboons. Although a complete statistically robust reconstruction of *Papio* phylogeny remained elusive, even when using retrotransposons, the population Structure program was able

to identify the existence of six distinct population clusters, one for each recognized species, and detect species admixture among some baboons, making this *Alu* panel a powerful tool in species identification. However, having such a large data set is cumbersome and not quite feasible for use in most field studies or captive breeding colonies. The goal of this study was to assemble a subset ($\leq 10\%$) of species informative *Alu* insertions, and demonstrate their utility as genetic markers for the identification of *Papio* baboons.

Materials and Methods

DNA Samples

A complete list of all the DNA samples used in this study is shown in supplementary file S2, Supplementary Material online and is also available in the supplementary material, of the manuscript submitted as part of the Baboon Genome Analysis Consortium (Rogers et al. under revision). Briefly, the DNA panel included 79 individual baboon samples, 15 olive baboons (*P. anubis*) including DNA from the reference olive baboon individual (27861), 2 Guinea baboons (*P. papio*), 2 hamadryas baboons (*P. hamadryas*), 3 chacma baboons (*P. ursinus*), 15 wild caught kinda baboons (*P. kindae*) from Zambia, and 42 yellow baboons (*P. cynocephalus*) consisting of 12 captive yellow baboons from the Southwest National Primate Research Center in San Antonio, TX (SFBR-Y), which are likely descendants of baboons captured in Amboseli National Park, Kenya, and 30 wild caught yellow baboons from the Mikumi National Park in Tanzania. All the baboon DNA samples were subjected to whole genome amplification (WGA) using the illustra GenomiPhi V2 DNA amplification kit (GE Healthcare Life Sciences, Marlborough, MA, USA). This was required to obtain sufficient DNA template for PCR analysis of over 500 polymorphic *Alu* insertions as part of the Baboon Genome Analysis Consortium. To insure that WGA DNA was suitable for this parent study, we compared original stock DNA to WGA DNA for baboon sample 27861 (used in the reference genome assembly labelled Panu_2.0 in NCBI and papAnu2 in Ensembl) in eight PCR assays in which 27861 appeared heterozygous for the *Alu* insertion while being absent from Panu_2.0. In all eight cases, the genotype using the stock DNA matched the genotype using the WGA DNA. Furthermore, in a previous study comparing stock DNA and WGA DNA (Ray et al. 2005a) genotypes were 97% (473 out of 489) consistent between the original DNA and the WGA DNA. Each of the 16 (of 489) disagreements (3%) represented a single allele aberration (i.e., between heterozygous and homozygous). The ability to determine the inferred ancestry of each individual was unaffected and was 100% consistent between the original stock and WGA DNA. Therefore, WGA DNA was used throughout this study with confidence.

Alu Insertion Polymorphisms

All loci used in this study were designed as part of the Baboon Genome Analysis Consortium (Rogers et al. under revision) and ascertained from the baboon reference genome (Panu_2.0) of *P. anubis*, or computationally derived from sequence data from the diversity panel samples (described in detail elsewhere [Rogers et al. under revision, supplementary methods, Jordan et al. In preparation]). Briefly, whole genome sequencing data generated from diversity panel baboons (16098, 34472, 34474, 97124, 28755, 28547, and 30388) were downloaded from the Baylor College of Medicine Human Genome Sequencing Center File Transfer Database. In-house Python scripts were used to predict the insertion coordinates of taxon-specific *Alu* insertion candidates by aligning second generation sequencing reads both to a consensus *Alu* sequence (*AluY*) (Jurka et al. 2005) and to the reference baboon assembly (Panu_2.0) with the Burrows Wheeler Aligner (BWA mem) (Li and Durbin 2009). A confidence score was calculated for each candidate *Alu* locus to filter out candidates lacking sufficient computational support. The confidence score was calculated using an in-house algorithm based on several criteria, such as the number of supporting reads, number of reads that mapped both to the reference genome and the consensus *Alu* sequence, location within the consensus *Alu* to which reads mapped, local read depth and average read depth throughout the genome. To determine a reliable cutoff score, we performed PCR validation experiments on a small panel of baboon diversity samples. This was done to confirm the presence of the candidate loci in the diversity sample from which they were computationally detected, and the absence of those loci in the baboon reference genome. A complete list of the 48 *Alu* elements selected for this study, including the locus-specific oligonucleotide primers for PCR and genomic coordinates, is shown in supplementary file S2, Supplementary Material online.

Polymerase Chain Reaction

Oligonucleotide primers for PCR for all loci used in this study were designed as part of the Baboon Genome Analysis Consortium (Rogers et al. under revision). Briefly, the genomic coordinates of potential *Alu* insertions, plus 500 bp flanking both ends of the predicted insertion point, were extracted from the reference genome Panu_2.0. Orthologous human and rhesus macaque sequences were also aligned. Primer 3 software was used in all cases, either manually (Rozen and Skaletsky 2000) or using a modified version (Untergasser et al. 2012). PCR amplifications were performed in 25 μ l reactions containing 25 ng of template DNA; 200 nM of each oligonucleotide primer; 1.5 mM MgCl₂; 10 \times PCR buffer (1 \times :50 mM KCl; 10 mM TrisHCl, pH 8.4); 0.2 mM dNTPs; and 1–2 U *Taq*

DNA polymerase. PCR reactions were performed under the following conditions: initial denaturation at 94 °C for 60 s, followed by 32 cycles of denaturation at 94 °C for 30 s, 30 s at optimum annealing temperature (usually 57 °C), and extension at 72 °C for 30 s. PCRs were terminated with a final extension at 72 °C for 2 min. 20 μ l of each PCR product were fractionated in a horizontal gel chamber on a 2% agarose gel containing 0.2 μ g/ml ethidium bromide for 60 min at 185V. UV-fluorescence was used to visualize the DNA fragments and images were saved using a BioRad ChemiDoc XRS imaging system (Hercules, CA).

Selection of the *Alu*-48 Panel

Structure analysis as reported for the Baboon Genome Analysis Consortium (Rogers et al. under revision) revealed that the 12 yellow baboons from the Southwest National Primate Research Center in San Antonio, TX (SFBR-Y) all exhibited evidence of mixed ancestry with olive baboons. Therefore, these 12 were removed from consideration for the initial construction of the species indicative markers. The *Alu*-48 panel of loci were selected from the larger data set of 494 *Alu* insertion polymorphisms using a combination of allele frequency data and empirical observation of agarose gels. Following gel electrophoresis, genotypic data were recorded for each allele as follows: an individual who was homozygous present for a given *Alu* locus was assigned the code 1, 1; homozygous absent, 0, 0; and heterozygous, 1, 0. This binomial data sheet was used to calculate the allele frequency for each *Alu* insertion across each population group for the final data set of 494 *Alu* insertion polymorphisms reported in the manuscript submitted as part of the Baboon Genome Analysis Consortium (Rogers et al. under revision). This binomial data sheet is also available on the Batzer Lab website (<https://biosci-batzerlab.biology.lsu.edu/>, last accessed June 6, 2017) under publications for the Baboon Genome Consortium manuscript as supplementary file S1, genotypes worksheet. In addition to using the calculated allele frequencies, gel chromatographs were also visually inspected, with selection for loci appearing to exhibit strong presence in a given species while also mostly absent from the other five species. From this filtered list of loci, seven to ten candidates representative of each of the six species were selected and the panel narrowed to 48 *Alu* loci.

Structure Analysis

Once the small panel of 48 species indicative markers was determined, population structure analyses were performed using Structure 2.3.4 software (Falush et al. 2003) to confirm that the *Alu*-48 panel properly identified six population clusters. Using genotype data from unlinked markers, this software performs a model-based clustering method to infer the population structure. For our initial analysis, the information regarding the origin of the samples was omitted. The analyses

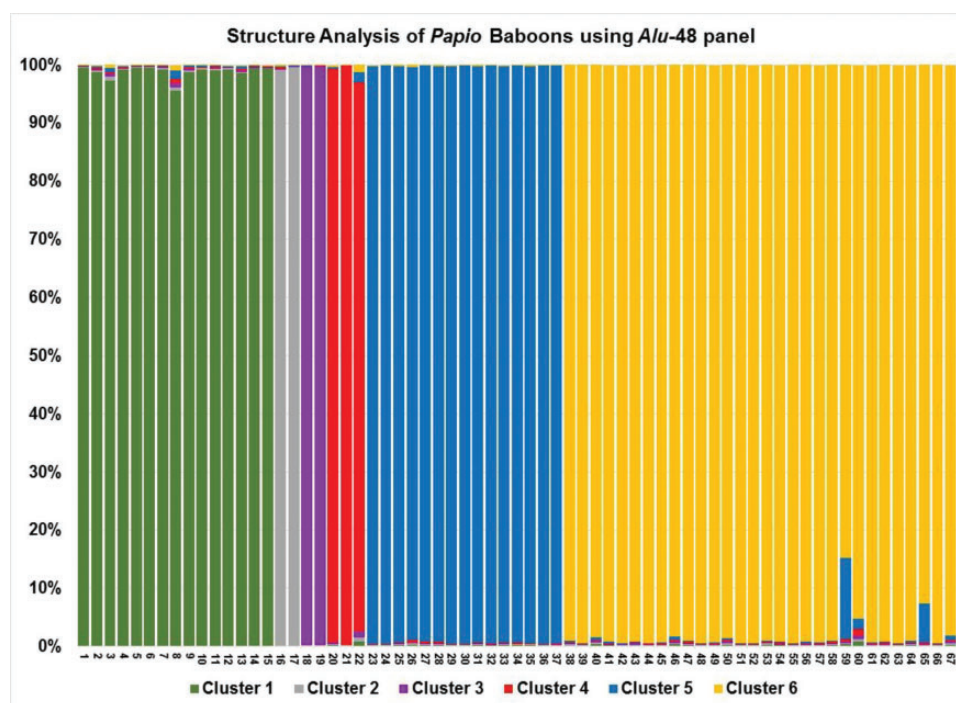


FIG. 1.—Structure analysis of 67 *Papio* baboon individuals using the *Alu*-48 panel. The y axis shows the probability of assignment of each individual to six population clusters. The x axis shows baboons numbered 1–67 listed in the same order as [supplementary file S3, Supplementary Material](#) online. Individuals 1–15 are olive baboons (*P. anubis*), 16–17 are hamadryas baboons (*P. hamadryas*), 18–19 are Guinea baboons (*P. papio*), 23–37 are kinda baboons (*P. kindae*), and 38–67 are yellow baboons (*P. cynocephalus*) from the Mikumi National Park, Tanzania. $K=6$ population clusters matches the recognized number of *Papio* species and captures the majority of structure in the data.

were performed under the admixture model which assumes that individuals may have mixed ancestry. To determine the value of K (where K equals the number of population clusters) with the highest likelihood, initially K was set from 1 to 8. The initial burn-in period was set at 10,000 iterations and followed by a run-length of 10,000 steps and repeated twice. These settings were based on the readme.pdf file downloaded with the software “Document for Structure Software version 2.3” listing suitable starting parameters for small data sets. The alpha statistic stabilized by about 2,000 of the 10,000 post-burn-in iterations in each of the duplicate runs indicating these settings were adequate. The most likely value of K was calculated to be six based on the “estimated ln prob of data” scores generated by Structure.

The authors of Structure indicate that this method is generally accurate with small data sets, such as this one, but acknowledge it is still an estimate of K . Therefore, the discriminant analysis of principal components (DAPC) method was also used on the *Alu*-48 panel (Jombart et al. 2010). DAPC is a nonmodel based method to estimate the number of population clusters in a data set using the *adegenet* package (Jombart 2008) for the R software (R Development Core Team 2016). The DAPC method also determined $K=6$.

Next, with K set to 6, another Structure analysis was performed under the admixed model using the known population information. The 12 SFBR yellow baboons (SFBR-Y) were

assigned as “unknowns” or population “0” to determine if the *Alu*-48 panel could detect their admixed ancestry. Based on Structure’s estimate of the most likely population(s) of origin, samples were then assigned to each of the two potential source populations, Olive (population 1) and then Yellow (population 6), and admixture estimates were calculated for three parental generations. The Structure results were compared with the expected ancestry based on pedigree records for these animals obtained from the SFBR.

Results

Here, we report a subset of 48 *Papio* lineage-specific *Alu* insertion polymorphisms from the Baboon Genome Analysis Consortium (Rogers et al. under revision) with species indicative distributions. A complete list of these 48 elements, including the locus specific oligonucleotide primers for PCR and genomic coordinates, is shown in [supplementary file S2, Supplementary Material](#) online. The Structure output using the *Alu*-48 panel across 67 *Papio* baboon individuals is plotted as [figure 1](#), showing each individual assigns to their respective species cluster with near 100% probability. $K=6$ clusters captures the majority of structure in the data and matches the number of recognized *Papio* species. The allele frequency data for each locus in the *Alu*-48 panel, sorted by *Papio* species, is shown in [table 1](#). The allele frequency data for the 12

Table 1Allele Frequency Distribution Data for Each *Alu*-48 Locus, Sorted by *Papio* Species

	Loci	Olive	Hamadryas	Guinea	Chacma	Kinda	Yellow	SFBR-Y
1	Bab_LPL	0.333	0.750	0.000	0.000	0.000	0.000	0.292
2	TB_3063	1.000	1.000	1.000	0.000	0.000	0.000	0.292
3	TB_3084	0.800	0.500	0.000	0.000	0.000	0.000	0.417
4	69388	0.833	0.000	0.000	0.000	0.000	0.000	0.250
5	46912	0.833	0.000	0.000	0.000	0.000	0.000	0.083
6	27402	0.667	0.000	0.000	0.000	0.000	0.000	0.292
7	27523	0.633	0.000	0.000	0.000	0.000	0.000	0.333
8	11507	0.300	0.000	0.000	0.000	0.000	0.000	0.000
9	TB_3040	0.533	0.000	0.000	0.000	0.000	0.000	0.083
10	TB_3023	0.400	0.000	0.000	0.000	0.000	0.000	0.083
11	TB_76	0.433	0.000	0.000	0.000	0.000	0.000	0.125
12	Ham-09	0.000	1.000	0.000	0.000	0.000	0.000	0.000
13	Ham-16	0.000	1.000	0.000	0.000	0.000	0.000	0.000
14	Ham-27	0.000	1.000	0.000	0.000	0.000	0.000	0.000
15	Ham-28	0.000	1.000	0.000	0.000	0.000	0.000	0.000
16	Ham-41	0.000	1.000	0.000	0.000	0.000	0.000	0.000
17	Ham-43	0.000	1.000	0.000	0.000	0.000	0.000	0.000
18	Ham-44	0.000	1.000	0.000	0.000	0.000	0.000	0.000
19	G47-0	0.000	0.000	1.000	0.000	0.000	0.000	0.000
20	G47-13	0.000	0.000	1.000	0.000	0.000	0.000	0.000
21	G47-17	0.000	0.000	1.000	0.000	0.000	0.000	0.000
22	G47-28	0.000	0.000	1.000	0.000	0.000	0.000	0.000
23	G88-9	0.000	0.000	1.000	0.000	0.000	0.000	0.000
24	G88-19	0.000	0.000	1.000	0.000	0.000	0.000	0.000
25	G88-20	0.000	0.000	1.000	0.000	0.000	0.000	0.000
26	C-16	0.000	0.000	0.000	1.000	0.000	0.000	0.000
27	C-38	0.000	0.000	0.000	1.000	0.000	0.000	0.000
28	C-44	0.000	0.000	0.000	1.000	0.000	0.000	0.000
29	C-05	0.000	0.000	0.000	0.667	0.000	0.000	0.000
30	C-36	0.000	0.000	0.000	0.833	0.000	0.000	0.000
31	C-42	0.000	0.000	0.000	0.833	0.000	0.000	0.000
32	C-49	0.000	0.000	0.000	0.667	0.000	0.000	0.000
33	K-20	0.000	0.000	0.000	0.000	0.733	0.000	0.000
34	K-29	0.000	0.000	0.000	0.000	0.767	0.000	0.000
35	K-30	0.000	0.000	0.000	0.000	0.500	0.000	0.000
36	K-74-85	0.000	0.000	0.000	0.000	0.833	0.017	0.000
37	K-17	0.000	0.000	0.000	0.000	0.600	0.000	0.000
38	K2-10	0.000	0.000	0.000	0.000	0.867	0.017	0.000
39	K-33	0.000	0.000	0.000	0.000	1.000	0.000	0.083
40	T2-103	0.000	0.000	0.000	0.000	0.000	0.600	0.083
41	Y-90	0.000	0.000	0.000	0.000	0.000	0.879	0.125
42	Y-65	0.000	0.000	0.000	0.000	0.000	0.414	0.167
43	Y-71	0.000	0.000	0.000	0.000	0.000	0.810	0.375
44	Y-141	0.000	0.000	0.000	0.000	0.000	0.733	0.292
45	Y-108	0.000	0.000	0.000	0.000	0.000	0.776	0.292
46	Y-119	0.000	0.000	0.000	0.000	0.000	0.914	0.250
47	T2-25	0.000	0.000	0.000	0.000	0.000	0.367	0.042
48	T2-29	0.000	0.000	0.000	0.000	0.000	0.567	0.083

NOTE.—Colored fields indicate the species from which the locus was ascertained. Bold font indicates an allele frequency >0.000.

yellow baboon (*P. cynocephalus*) samples originally obtained from the Southwest National Primate Center in San Antonio, TX (SFBR-Y) are listed separately in table 1 due to their

predetermined admixture with olive baboons (*P. anubis*) (see Methods). Colored fields in table 1 indicate the species from which the locus was ascertained. Bold font indicates an

Table 2

Inferred Population Structure: Probability of Assignment to Each Population Cluster

	Given Pop	Proportional Membership to Population Clusters						Number of Individuals
		1	2	3	4	5	6	
Unknown (SFBR-Y)	0	0.436	0.030	0.022	0.033	0.061	0.419	12
<i>P. anubis</i>	1	1.000	0.000	0.000	0.000	0.000	0.000	15
<i>P. hamadryas</i>	2	0.000	1.000	0.000	0.000	0.000	0.000	2
<i>P. papio</i>	3	0.000	0.000	1.000	0.000	0.000	0.000	2
<i>P. ursinus</i>	4	0.000	0.000	0.000	0.999	0.000	0.000	3
<i>P. kindae</i>	5	0.000	0.000	0.000	0.000	1.000	0.000	15
<i>P. cynocephalus</i>	6	0.000	0.000	0.000	0.000	0.002	0.998	30

NOTE.—Colored fields highlight species assignment to population clusters. Cluster 1 (olive), cluster 2 (gray), cluster 3 (lavender), cluster 4 (red), cluster 5 (blue), and cluster 6 (yellow).

allele frequency > 0.000. The *Alu*-48 panel consists of 11 *Alu* insertions present in olive baboons, ten ascertained from the olive baboon (*P. anubis*) reference genome, (Panu_2.0), and one previously published *Alu* locus with a history of genotype data collected from a known *anubis/hamadryas* hybrid zone (Szmulewicz et al. 1999). The polymorphic *Alu* insertion used in that study, located in the baboon *lipoprotein lipase* (LPL) gene, was genotyped in a total of 179 baboon individuals, 58 *anubis*, 66 *hamadryas*, and 55 hybrids, providing valuable allele frequency data for these populations. The same *Alu* locus was also included in a later study (Boissinot et al. 2014) and was genotyped in 45 baboon individuals, reinforcing the historical precedent for including it in our analysis. We also selected seven *Alu* insertions ascertained from *P. hamadryas* diversity sample 97124 that were homozygous present in both *P. hamadryas* samples we had available and homozygous absent in 77 other baboon genomes. Similarly, we selected seven *Alu* insertions ascertained from *P. papio* diversity samples (28547 or 30388) with 100% allele frequency in both Guinea baboons and absence in all 77 others. The seven *Alu* insertions each ascertained from *P. ursinus* and *P. kindae* baboons, and the remaining nine on the panel ascertained from *P. cynocephalus*, are not completely fixed present in these selected species, but do exhibit high allele frequencies and are nearly exclusive for the targeted species (table 1). Genotype data for the *Alu*-48 panel across all 79 *Papio* baboon individuals (including a *T. gelada* individual as the out-group) are shown in supplementary file S3, Supplementary Material online.

To demonstrate the utility of our *Alu*-48 panel as genetic markers for the species specific identification of *Papio* baboons we performed a population structure analysis using Structure 2.3.4 software (Falush et al. 2003) and included 67 of our 79 total samples (the 12 SFBR-Y were omitted here). The most likely value of *K* was determined to be six (see Materials and Methods), matching the number of recognized species and consistent with our previous findings (Rogers et al. under revision). Next, Structure was run again, setting *K* = 6, and including the 12 SFBR-Y samples as population “0”, or

unknowns. The results of this Structure analysis were obtained in <5 min using a 3.6 GHz processor and are shown in table 2. The 12 SFBR-Y samples as a group exhibit nearly equal membership to olive and yellow clusters with no single individual being assigned to either population with >73% probability as reflected in the data set calculations (table 3). Although not an exact match, these findings are generally consistent with the proportional admixture reported for the larger data set (Rogers et al. under revision). For example, the probability of assignment to the olive and yellow clusters, respectively, for SFBR-Y sample 6968 was 72%/28% and for sample 1X2117 was 22%/78% in that study, compared with 61%/27% and 12%/66% shown here (table 3). Pedigree records obtained from the SFBR indicated that all 12 SFBR-Y samples had at least one olive baboon ancestor within a recent generation while in captivity. In addition, these animals are likely descendants of baboons captured in the Amboseli National Park, Kenya, where a yellow/olive hybrid zone has been well documented (Alberts and Altmann 2001; Charpentier et al. 2012; Samuels and Altmann 1986). These data provided evidence to support our *Alu*-based findings of admixture within these individuals. This demonstrates that our *Alu*-48 panel can be used to identify each of the six species of *Papio* baboons, as well as detect the likelihood of admixture.

However, our *Alu*-48 panel was unable to accurately infer the proportional ancestry, or degree of olive/yellow mixture derived from previous generations. As with field studies, most species identification within captive breeding programs has been largely based on phenotypic and behavioral observations of the animals. Therefore, the potential for multigenerational hybridization events can easily produce a phenotypically “yellow” baboon with mixed ancestry. To test our *Alu*-48 panel in this regard, we performed a subsequent Structure analysis, first assigning each of the SFBR-Y individuals to the Olive cluster and then each to the Yellow cluster to allow the software, with the given data set, to assign admixture going back three generations. The results of this ancestry test using the *Alu*-48 panel were uninformative. With the exception of sample 1x2117 the Structure analysis for ancestry indicated

Table 3

Structure Analysis of 12 SFBR-Y Individuals as Unknowns

Proportional Membership to Population Clusters						
Pop 0 ID	1 Olive	2 Hamadryas	3 Guinea	4 Chacma	5 Kinda	6 Yellow
6968	0.607	0.032	0.021	0.030	0.038	0.273
1x1763	0.352	0.063	0.032	0.039	0.047	0.467
1x2092	0.725	0.016	0.014	0.020	0.025	0.200
9166	0.350	0.024	0.025	0.027	0.033	0.542
1x1786	0.447	0.024	0.021	0.047	0.060	0.401
1x3027	0.545	0.018	0.017	0.036	0.046	0.338
9481	0.286	0.030	0.036	0.041	0.045	0.562
8919	0.289	0.073	0.031	0.063	0.072	0.472
9656	0.547	0.017	0.018	0.024	0.023	0.371
1x2117	0.115	0.016	0.017	0.027	0.167	0.658
1x2798	0.529	0.028	0.019	0.024	0.156	0.243
8820	0.440	0.015	0.012	0.015	0.018	0.502

NOTE.—Probability of assignment to each population cluster.

assignment to the Olive cluster was more likely with essentially no ability to detect which previous parental generation(s) contributed the Yellow and Olive components of the admixture (data not shown). This is not surprising given the limited number of informative loci and representative samples from each species. Estimating admixture proportions can be especially challenging if there are very few representatives of the parental populations within the data set and as such admixture estimates in these situations should be treated with caution (Falush et al. 2003; Pritchard et al. 2000). In this case, no baboons from previous generations from the Amboseli region were represented in our database.

Discussion

The availability of whole genome sequence data for all six *Papio* baboon species allowed *Alu* elements to be ascertained from individuals other than the olive baboon reference genome (Panu_2.0) and thus increased the analytical power of the data set across species. However, there are clear limitations to using a panel with a reduced number of genetic markers. A data set is only as useful as the members it contains. As shown in table 2, there were representative samples from *P. anubis*, *P. kindae* and *P. cynocephalus* with $N = 15$, 15, and 30, respectively. But, there were only two samples each from *P. hamadryas* and *P. papio* and only three from *P. ursinus*, one of which (18736) was likely “wild caught” originally and could have some possible admixture from neighboring population(s) of yellow or kinda baboons. Therefore, calculations of mixed ancestry are only as accurate as the depth of the parental generations represented in the data set. Our *Alu*-48 panel was reasonably successful at detecting the olive/yellow admixture of the SFBR-Y samples, but not at inferring the proportion of mixed ancestry because those parental generations were not

available in the data set. Similarly, the two hamadryas samples in our data set are both males, originally from the Awash National Park in Ethiopia, a recognized hybrid zone between olive and hamadryas with social groups exhibiting mixed ancestry to varying degrees (Phillips-Conroy et al. 1991). These samples were not specifically labeled as hybrid individuals, but rather as “Awash hamadryas” baboons. The population Structure analysis for the Baboon Genome Analysis Consortium using the full data set of 494 *Alu* insertion polymorphisms detected about 25–30% admixture with olive (Rogers et al. under revision). When these two samples are subjected to a secondary Structure analysis using the population information provided, first assigning both to the hamadryas cluster and then both to the olive cluster, the admixture analysis assigns them both to the hamadryas cluster with 100% probability. This is due to the absence of individuals from nonadmixed parental generation populations in the data set. In fact, there is some evidence that some or all of the females initially classified as “pure anubis” females observed in the Awash region may have themselves been hybrids (Phillips-Conroy et al. 1991). Thus, this reinforces the need for caution with regard to sweeping conclusions regarding mixed ancestry within a limited data set.

It was not the purpose of this study to provide a comprehensive “one size fits all” *Alu*-based solution to solving the complex identification of *Papio* baboons. That is clearly unrealistic given the complex demographic and population genetic history of the species complex. Rather, the purpose of this study was to introduce a panel of *Alu* insertions with species indicative allele frequencies that used collectively provide an inference of *Papio* species identification. Individual sets of species indicative markers could be used empirically based on the initial level of ancestral uncertainty, such as in hybrid zones. The *Alu*-48 panel presented here was intentionally filtered from a larger database to select for high frequency alleles targeting six *Papio* species. The purpose of estimating the value of K clusters using both the Structure program (Falush et al. 2003) and DAPC (Jombart et al. 2010) was to insure that the true value of K could be set at six in Structure to infer species identity using the *Alu*-48 panel.

The Structure analysis on this data set is accomplished quickly (<5 min using a 3.6 GHz processor). *Alu* elements are relatively easy and inexpensive to genotype and represent a distinct advantage over large scale SNP genotyping or whole genome sequencing. They are also identical by descent, neutral autosomal markers with known directionality rather than gender derived (Y-chromosome or mtDNA). This *Alu*-48 panel is not intended to replace any of the existing methods for species identification, but rather it is to be used in conjunction with other widely established techniques. Baboon samples from known localities could be characterized using the most appropriate markers from the *Alu*-48 panel, adding to the genetic data collected for these individuals. Male introgression into hybrid zones transfers nuclear and Y-chromosome genetic

data while the mitochondrial DNA of the native female parent of the other species remains unchanged. Adding more nuclear genetic markers, especially identical by descent *Alu* elements, collected throughout baboon populations, should provide another tool to help investigators. We are hopeful that the *Alu*-48 panel reported here will also assist with the maintenance of pedigrees at research centers with captive populations such as the Southwest National Primate Research Center in San Antonio, TX and the German Primate Center in Goettingen, Germany. The gradual accumulation of multigenerational genotype data from known parental matings using this genetic marker system should lead to more robust proportional ancestry estimates in the future. Such an improved data set may also be useful to augment morphological (Ackermann et al. 2014) and other methods in the forensic identification of potential hybrids from fossil records and wild populations.

Supplementary Material

Supplementary data are available at *Genome Biology and Evolution* online.

Authors' Contributions

J.A.W. and M.A.B. designed the research and wrote the paper; J.A.W., V.E.J., C.J.S., T.O.B., C.L.M., C.P.S., E.C.B., A.R., and B.N.C. conducted the experiments; M.K.K. and T.O.B. performed the *Alu* repeat analysis of the Panu_2.0 genome assembly; V.E.J., C.J.S., and T.O.B. performed the computational analysis of the whole genome sequencing data generated from diversity panel baboons downloaded from the Baylor College of Medicine Human Genome Sequencing Center File Transfer Database. All authors read and approved the final manuscript.

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A.R. conducted experiments for this project in the Department of Biological Sciences, LSU-Baton Rouge as a participant in the Louisiana Biomedical Research Network (LBRN) while completing a degree in the Department of Biological and Physical Sciences at Northwestern State University of Louisiana, Natchitoches, LA. B.N.C. conducted experiments for this project in the Department of Biological Sciences, LSU-Baton Rouge as a member of the NIH Biomedical Research Experience for Veterinary Scholars.

Competing Interests

The authors declare that they have no competing interests.

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