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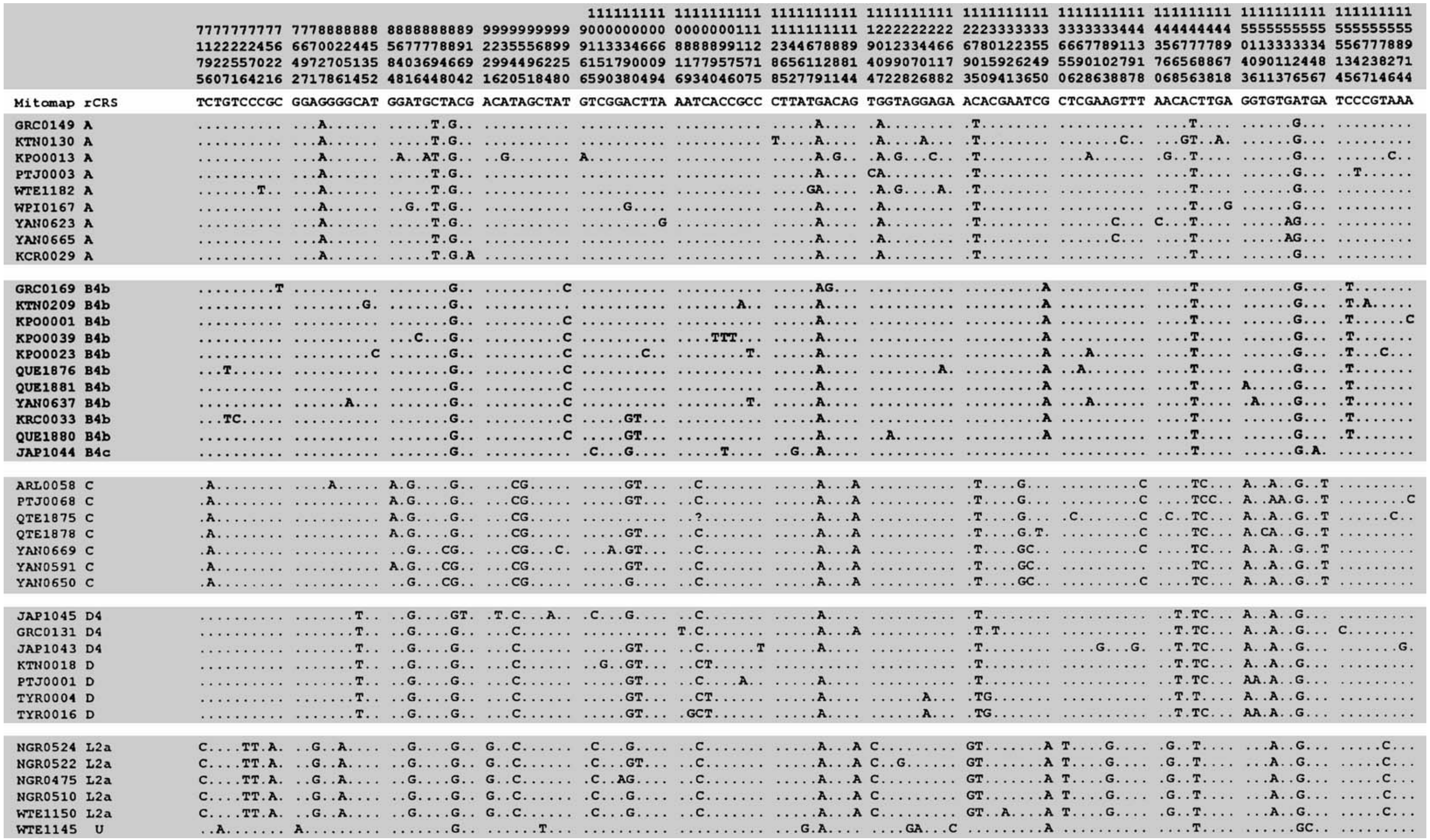
Correction: Mitochondrial DNA Variation in Amerindians

To the Editor:

We thank Yao et al. (2003 [in this issue]) for calling our attention to inconsistencies in our data reporting mitochondrial DNA variations in Amerindians (Silva et al. 2002). We reviewed the original chromatograms and resequenced all the samples (forward and reverse). On the basis of the reanalysis of the initial data and sequencing that has been repeated, we conclude that most criticisms of Yao et al. are correct. We identified two sources of problems: (*a*) alignment with a variant CRS (Macaulay et al. 1999) and (*b*) mutations missed at regions of low-quality chromatograms in one (forward or reverse) of the first sequencing. Elimination of these two problems, by a second (and, in a few cases, a third) sequencing, careful manual checking of the chromatograms, and use of the correct rCRS reference sequence (MITOMAP) eliminated the discrepancies. A summary of all 40 corrected sequences is presented in figure 1, and the general pattern is similar to that recently reported by Herrnstadt et al. (2002). The presence of a private mutation in more than one individual or the absence of a basal mutation probably represent examples of homoplasy or of reverse mutations. Extensive homoplasy within the coding region of mtDNA has been documented (Eyre-Walker et al. 1999; Herrnstadt et al. 2002) and will probably be found more often as the number of mtDNA samples sequenced increases. For instance, the group C basal mutation 9545G was found in one individual from the haplogroup A, whereas private mutation 14460G was found in two individuals who belong to haplogroups A and D, and 15670C is present in one individual who belongs to haplogroup A and two who belong to haplogroup C (Herrnstadt et al. 2002). The finding of two similar private mutations (12406A) in two individuals of the same tribe (TYR0004 and TYR0016) is probably the consequence of a single mutational event, as is the occurrence of the reverse mutation 8584 in two individuals of another tribe (YAN0669 and YAN0650).

Recalculation of the age estimates for the four founder haplogroups on the basis of the reviewed data continues



						111111111	1111111111	1111111111	1111111111	1111111111	1111111111	111111111	1111111111	111111111
		7777777777	7778888888	8888888889	9999999999	9000000000	0000000111	1111111111	1222222222	2223333333	3333333444	444444444	5555555555	555555555
		1122222456	6670022445	5677778891	2235556899	9113334666	8888899112	2344678889	9012334466	6780122355	6667789113	356777789	0113333334	556777889
		7922557022	4972705135	8403694669	2994496225	6151790009	1177957571	8656112881	4099070117	9015926249	5590102791	766568867	4090112448	134238271
		5607164216	2717861452	4816448042	1620518480	6590380494	6934046075	8527791144	4722826882	3509413650	0628638878	068563818	3611376567	456714644
Mitomap	rCRS	TCTGTCCCGC	GGAGGGGCAT	GGATGCTACG	ACATAGCTAT	GTCGGACTTA	AATCACCGCC	CTTATGACAG	TGGTAGGAGA	ACACGAATCG	CTCGAAGTTT	AACACTTGA	GGTGTGATGA	TCCCGTAAA
GRC0149	A	....	...A......	.....T.G..	....	....	....	.....A....	.A........	.T........	....	....T....	......G...	....
KTN0130	A	....	...A......	.....T.G..	....	....	....	T....A....	.A....A...	.T........	.......C..	...GT..A.	......G...	....
KPO0013	A	....	...A......	.A..AT.G..	..G.......	A.........	....	.....A.G..	.A.G...C..	.T........	...A......	.G..T....	......G...	......C..
PTJ0003	A	....	...A......	.....T.G..	....	....	....	.....A....	CA........	.T........	....	....T....	......G...	..T......
WTE1182	A	.......T..	...A......	.....T.G..	....	....	....	....GA....	.A.G....A.	.T........	....	....T....	......G...	....
WPI0167	A	....	...A......	..G..T.G..	....	.....G....	....	.....A....	.A........	.T........	....	....T...G	......G...	....
YAN0623	A	....	...A......	.....T.G..	....	.........G	....	.....A....	.A........	.T........	......C...	C...T....	.....AG...	....
YAN0665	A	....	...A......	.....T.G..	....	....	....	.....A....	.A........	.T........	......C...	....T....	.....AG...	....
KCR0029	A	....	...A......	.....T.G.A	....	....	....	.....A....	.A........	.T........	....	....T....	......G...	....
GRC0169	B4b	.........T	....	.......G..	C	....	....	.....AG...	....	.........A	....	....T....	......G...	.T.......
KTN0209	B4b	....	........G.	.......G..	....	....	.......A..	.....A....	....	.........A	....	....T....	......G...	.T.A.....
KPO0001	B4b	....	....	.......G..	C	....	....	.....A....	....	.........A	....	....T....	......G...	.T......C
KPO0039	B4b	....	....	...C...G..	C	....	....TTT...	.....A....	....	.........A	....	....T....	......G...	.T.......
KPO0023	B4b	....	C	.......G..	C	.......C..	........T.	.....A....	....	.........A	...A......	....T....	......G...	.T...C...
QUE1876	B4b	...T......	....	.......G..	C	....	....	.....A....	........A.	.........A	..A.......	....T....	......G...	.T.......
QUE1881	B4b	....	....	.......G..	C	....	....	.....A....	....	.........A	....	....T....	A.....G...	.T.......
YAN0637	B4b	....	......A...	.......G..	C	....	........T.	.....A....	....	.........A	...A......	....T....	.A....G...	.T.......
KRC0033	B4b	...TC.....	....	.......G..	C	.....GT...	....	.....A....	....	.........A	....	....T....	......G...	.T.......
QUE1880	B4b	....	....	.......G..	C	.....GT...	....	.....A....	..A.......	.........A	....	....T....	......G...	.T.......
JAP1044	B4c	....	....	.......G..	....	.C...G....	....T.....	..G..A....	....	....	....	....T....	......G.A.	....
ARL0058	C	.A........	....A.....	A.G....G..	...CG.....	.....GT...	..C.......	.....A...A	....	.T...G....	C	....TC...	A..A..G..T	....
PTJ0068	C	.A........	....	A.G....G..	...CG.....	.....GT...	..C.......	.....A...A	....	.T...G....	C	....TCC..	A..AA.G..T	C
QTE1875	C	.A........	....	A.G....G..	...CG.....	....	..?.......	.....A...A	....	.T...G....	.C.......C	.C..TC...	A..A..G..T	......C..
QTE1878	C	.A........	....	A.G....G..	...CG.....	.....GT...	..C.......	.....A...A	....	.T...G.T..	C	....TC...	A.CA..G..T	....
YAN0669	C	.A........	....	..G...CG..	...CG...C.	...A.GT...	..C.......	.....A...A	....	.T...GC...	C	....TC...	A..A..G..T	....
YAN0591	C	.A........	....	A.G...CG..	...CG.....	.....GT...	..C.......	.....A...A	....	.T...GC...	....	....TC...	A..A..G..T	....
YAN0650	C	.A........	....	..G...CG..	...CG.....	.....G....	..C.......	.....A...A	....	.T...GC...	C	....TC...	A..A..G..T	....
JAP1045	D4	....	.......T..	..G....GT.	.T.C...A..	.C...G....	..C.......	.....A....	....	.T........	....	..T.TC...	A..A..G...	....
GRC0131	D4	....	.......T..	..G....G..	...C......	....	T.C.......	.....A...A	....	.T.T......	....	..T.TC...	A..A..G...	C........
JAP1043	D4	....	.......T..	..G....G..	...C......	.....GT...	..C......T	.....A....	....	.T........	....G...G.	..T.TC...	A..A..G...	.......G.
KTN0018	D	....	.......T..	..G....G..	...C......	..G..GT...	..CT......	....	....	.T........	....	..T.TC...	A..A..G...	....
PTJ0001	D	....	.......T..	..G....G..	...C......	.....GT...	..C....A..	.....A....	....	.T........	....	..T.TC...	AA.A..G...	....
TYR0004	D	....	.......T..	..G....G..	...C......	.....GT...	..CT......	.....A....	......A...	.TG.......	....	..T.T....	A..A..G...	....
TYR0016	D	....	.......T..	..G....G..	...C......	.....GT...	.GCT......	.....A....	......A...	.TG.......	....	..T.TC...	AA.A..G...	....
NGR0524	L2a	C....TT.A.	..G..A....	..G....G..	G..C......	.C...G....	..C.......	.....A...A	C.........	GT.......A	T....G....	.G..T....	...A..G...	.....C...
NGR0522	L2a	C....TT.A.	..G..A....	..G....G..	G..C......	.C...GT...	..C.......	.....A...A	C..G......	GT.......A	T....G....	.G..T....	...A..G...	.....C...
NGR0475	L2a	C....TT.A.	..G..A....	..G....G..	G..C......	.C..AG....	..C.......	.....A...A	C.........	GT.......A	T....G....	.G..T....	...A..G...	.....C...
NGR0510	L2a	C....TT.A.	..G..A....	..G....G..	G..C......	.C...G....	..C.......	.....A...A	C.........	GT.......A	T....G....	.G..T....	...A..G...	.....C...
WTE1150	L2a	C....TT.A.	..G..A....	..G....G..	G..C......	.C...G....	..C.......	.....A...A	C.........	GT..A....A	T....G....	.G..T....	...A..G...	.....C...
WTE1145	U	..A.......	A.........	.......G..	......T...	....	....	...G.A....	....GA...C	.........A	....	....T....	......GC..	....

Figure 1 Data matrix showing the corrected informative nucleotide positions for the 8.8-kb mtDNA segment for 40 individuals sequenced by us

Table 1

Nucleotide Diversity and Age Estimates for mtDNA Belonging to the Four Founder Haplogroups of New World Natives

Haplogroup	No. of Sequences	Genetic Diversity[a] (SE)	Mean Age in Years[b] (95% CI)
A	10	0.73 (0.15)	15,398 (12,052–18,744)
B	11	0.75 (0.14)	15,819 (12,659–18,970)
C	9	0.64 (0.13)	13,520 (10,616–17,425)
D	5	0.86 (0.18)	18,144 (14,137–22,151)
Weighted mean		0.75 (0.15)	15,720 (12,366–19,074)

[a] $\pi(\times 10^{-3})$.

[b] Calculated as in Silva et al. (2002).

to show similarities between the four haplogroups and does not differ significantly from the previously published values (table 1). This supports our primary conclusion in favor of a single migration wave, with a mean age for the four haplogroups of 12,366–19,074 years before present.

The revised versions of the sequences have been submitted to GenBank.

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Electronic-Database Information

The URL for data presented herein is as follows:

MITOMAP, http://www.mitomap.org (for a human mitochondrial genome database)

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Reply to Silva et al.

To the Editor:

Silva et al. (2003 [in this issue]) have certainly improved their data by eliminating many of the errors in the current version of the data matrix, and they have admitted most of their innocent mistakes. Their efforts and atti-