

A Compendium of Human Mitochondrial DNA Control Region: Development of an International Standard Forensic Database

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A compendium of human mitochondrial DNA (mtDNA) control region types has been constructed. This updated compilation indexes over 10,000 population-specific mtDNA nucleotide sequences in a standardized format. The sequences represent mtDNA types from the Scientific Working Group on DNA Analysis Methods (SWGAM) mtDNA database and from the public literature. The SWGAM data are considered to be of higher quality than the public data, particularly for counting the number of times a particular haplotype has been observed.

Key words: base sequence; databases, factual; DNA; DNA, mitochondrial; forensic medicine; gene frequency; genetics, population; molecular sequence data; United States

The analysis of the first and second hypervariable segments (HV1 and HV2) of the control region of human mitochondrial genome (mtDNA) has proven to be a useful tool for forensic identification (1), medical genetics (2), population (3) and evolutionary studies (4), and anthropological reconstruction (5). A concordance (ie, a compilation/compendium) of nucleotide substitutions in HV1 and HV2 was first constructed in 1996 (6) and made available via the Internet (<http://shelob.bioanth.cam.ac.uk/mtDNA>). Since then, additional mtDNA population data have been developed, thus warranting another update.

In recent years, mtDNA typing has become increasingly important in forensics (7,8). As the number of individuals typed increases, it is becoming more difficult to access sequence data quickly and easily. It is particularly desirable to determine if a sequence is relatively rare or common for identity purposes (9). Currently, the Federal Bureau of Investigation (FBI) and others use the Scientific Working Group on DNA Analysis Methods (SWGAM) database (N=4,142) for estimating the relative rarity of a mtDNA profile. The compilation of other public mtDNA population data can be useful in some identity cases, as well as in other fields of genetic study.

The resulting reference list of types is in a standardized format, arranged by continent/country of origin and ethnicity, and includes all the population-specific mtDNA. The assembled data are referenced to the publication or source in which they originally appeared. The Compendium is an ongoing SWGAM project.

Material and Methods

A survey of sequences from the published literature and the sequence databases GenBank and EMBL was conducted (Table 1). The mtDNA nucleotide sequence data contributed to the authors for inclusion in the original concordance and contributions to SWGAM are also included. All sequence information is included in the compilation.

The SWGAM data contain sequences for nucleotide positions (np) for both HV1 (np 16024-16365) and HV2 (np 73-340) for each individual. Sequence data are described as those np sites that are different from the Cambridge Reference Sequence (CRS) (82).

All sequences are compiled by continent and country of origin and numbered according to a standard 14 character ("XXX.XXX.XXXXX") format (Table 2). In this format, the first three characters identify the continent/country of origin. All country codes are the official country code designations published by the United Nations (86) and are text characters. For example, DEU defines Germany, and ESP defines Spain. Three zeros ("000") are used in this field to identify sequences that cannot be attributed to a particular country.

The next three characters identify the population (Table 3). These characters can be either text or numeric. Text identifies major population groups generally used by law enforcement agencies, such as "AFR" for African; "ASN" for Asian; "CAU" for Caucasian; and "HIS" for Hispanic. Exceptions to this arise from contributions from the field of archaeology/anthropology, such as "ANC" for ancient people; "NED" for Neanderthal; and "TIM" for Tyrolean Ice Man. Otherwise, a three-digit numerical designation is given to identify a particular subgroup. For example, "154" identifies Native Americans of the Navajo tribe.

The third set of digits identifies the individual sequence within a particular group. These numbers are consecutive within a particular group and are assigned arbitrarily in the order in which they are entered into the Compendium. Thus, the sequence identifier "USA.154.000201" is the 201st Navajo mtDNA sequence from the United States. Similarly, "000.AFR.000003" is the 3rd sequence of African origin for which a country was not defined. In instances where types arise

from individuals residing in territories that are governed by other countries, the first three characters identify the country in political control and the next three identify the people living in the territory. For example, the Polynesian people of New Britain in Melanesia are identified by "area code" 315. However, the island belongs politically to the United Kingdom. Therefore, the first sequence in a series from this group is identified "GBR.315.000001".

Results and Discussion

A total of 10,828 mtDNA sequences were obtained: 4,142 from SWGDAM and 6,686 from the published literature/EMBL and GenBank (Table 1). Other tabular information includes provenance, number of populations, number of mtDNA types per population, sequence range, and contributing author.

Miller et al (6) previously reported that when compiling data from a number of sources inconsistencies may arise. During data collection, a few substitutions in some published and SWGDAM sequences were clearly reviewed to be anomalous. When problems were suspected, authors were contacted and asked to confirm their nucleotide sequence. Usually, minor sequence errors were corrected with the author's assistance. However, there are instances with the public literature data where an author has not yet responded to our requests or has asked that an incorrectly reported substitution not be corrected until the laboratory could publish an erratum. Those requests have been honored. However, the following disclaimer has been added to the published data: "This compendium of human mtDNA control region types is compiled from nucleotide sequence data available in the public domain. Every attempt has been made by the editors to ensure the accuracy of the data provided herein. However, some inaccuracies and inconsistencies may exist in the literature. It is possible that some errors still remain. The authors do not accept responsibility or legal liability for the accuracy of reported nucleotide sequences. If errors in the compendium are observed, we would appreciate you bringing them to our attention for subsequent correction". We recommend the use of published sequence data for investigative or research purposes only and not for the assignment of weight regarding forensic matches.

Nucleotide numbering schemes (for example, those given in refs. 23,27,87) that have deviated from that originally published by Anderson and coworkers (82) have been changed in order to standardize sites of substitution. Where authors have not conformed to a standardized numbering system, some confusion resulting in ambiguity may arise. For example, Barbujani et al (68) used a different numbering system to denote *nps* than the forensic science community currently uses. Table 4 provides an example of the conversion of their data to be consistent with those data in this Compendium.

Nucleotide additions that are not normally assigned positional numbers in the CRS have been assigned suffixes (X.1, X.2, etc.). For consistency, we have chosen to number additions to the right of homopolymeric stretches. In the study of HV2 by Batista and coworkers (33), for example, additional

cytosines (C's) were labeled 303.1, 303.2, and 313.1. In our nomenclature, these same sites are numbered 309.1, 309.2, and 315.1. It is not altogether uncommon to find that insertions and deletions in the polycytosine stretch of HV1 (*np* 16184-16193) are left unrecorded. Therefore, caution must be exercised while attempting to derive meaningful population-based frequency information from this area.

In homopolymeric stretches, the assignment of *np* numbers for additions or deletions is done to minimize the number of substitutions recorded, unless *np* numbers were specifically designated by the original author.

The same number of individuals reported in an original publication may not comport with that described in the Compendium. This is due to the fact that while all mtDNA types, or lineages, may have been reported in a publication, the total number of individuals sharing each mtDNA type was not specified. In such instances, each mtDNA type is reported as a single individual. This underestimates the total number of individuals represented. Therefore, estimating the rarity of a mtDNA profile from non-SWGDAM data should be undertaken with caution. However, a search of the published data may be informative about the general occurrence of a mtDNA profile and its ethno-geopolitical distribution.

The same mtDNA types may be published multiple times, especially those that aim at inter-population comparison. Such sequence data, however, are not always unambiguously attributed to its source. Attempts have been made not to place duplicate sequences in the Compendium.

Inconsistencies exist between the number of sequences that appear in the published literature on a given population and the number of sequences that have been submitted to GenBank for that population. This may indicate the submission of haplotypes/lineages rather than individual data. It is, nonetheless, confusing. Attempts have been made to reconcile numbers of sequences in the literature with numbers of sequences in GenBank/EMBL. In addition, GenBank/EMBL accession numbers may not accurately reflect the numbers of individuals originally reported.

Sequences have been removed from (or not included in) the Compendium due either to an inconsistent assignment of mitotypes to populations or to inconsistent definitions of the populations/groups themselves. For example, Shields et al (87) note that lineage 59 occurs in the Inupiaq (p. 553, column 2 of their paper) as well as in a single Yakima individual. However, Table 3 (p. 556) of their paper shows lineage 59 belonging to one Yakima and to one West Greenland Eskimo.

Ambiguous and undetermined *nps* in published sequences are provided within the sequence data to denote the possibility of additional substitutions. Ambiguities may also denote nucleotide sequence heteroplasmy (e.g., in 74: *np* 16169 of Tsar Nicholas is reported to be either a C or a T). In all cases, the nomenclature of the International Union of Pure and Applied Chemistry (IUPAC) is used. To facilitate fu-

Table 1. Populations represented in the mtDNA Population Database. The forensic dataset consists of groups designated as SWGDAM (asterisk) in the column labeled Ref. (reference number). The Public dataset is composed of groups for which a literature reference is provided

Region/ country	Population	Identification code	No.	Nucleotide positions used	Ref.	Region/ country	Population	Identification code	No.	Nucleotide positions used	Ref.
Africa						Zambia	ND	ZMB.AFR	1	16048-16569; 15 1-41	
Algeria	Ghardaia	DZA.AFR	78	16090-16370	10	Zimbabwe	ND	ZWE.AFR	1	16048-16569; 15 1-41	
Benin	ND ^a	BEN.AFR	13	16190-16370	11	America, North					
Botswana	Herero	BWA.337	20	16204-16381; 63-374	12	Belize	Carib	BLZ.345	28	16067-16344	24
Central African Republic	Mbuti Pygmy	CAF.320	5	71-270	13	Canada	Bella Coola	CAN.030	22	16024-16383	25
Central African Republic	ND	CAF.320	19	16024-16381; 63-374	14	Canada	Bella Coola	CAN.030	4	16030-16370	26
Central African Republic	ND	CAF.AFR	10	16028-16569; 15 1-41	15	Canada	Haida	CAN.080	18	16024-16383	25
Democratic Republic of Congo	ND	COD.AFR	1	16028-16569; 15 1-41	15	Canada	ND	CAN.CAU	1	16086-16519	15
Eastern Senegal	Niokolo Madenka	SEN.327	119	16024-16368; 64-375	16	Canada	Nuu-Chah-Nulth	CAN.328	63	16024-16383	27
Egypt	Ancient people	EGY.ANC	1	16210-16254	17	Costa Rica	Quitirisi	CRI.319	27	16003-16392	28
Egypt	ND	EGY.AFR	24	16024-16365; 73-340	*b	Guatemala	Santa Cruz de Quiche	GTM.296	23	16022-16363	29
Guinea, Equatorial	Bubi	GNQ.325	50	16024-16383	18	Mexico	Yucatan Peninsula	MEX.138	4	16030-16370	26
Guinea, Sub-Saharan	ND	GIN.334	11	15997-16339	19	ND	Native American	000.333	72	16129-16569	30
Ivory Coast	ND	IVC.AFR	1	16086-16519	15	ND	Nuu-Chah	USA.328	2	16024-16400	31
Kenya	ND	KEN.AFR	1	16086-16519	15	ND	Ojibwa/Chippewa	USA.305	3	16030-16370	26
Malawi	ND	MWI.AFR	7	16082-16353; 64-324	20	ND	Pima	USA.173	3	16030-16370	26
Morocco	Rif Mountains	MAR.332	18	15997-16399	19	ND	Tlingit	USA.252	2	16030-16370	26
Namibia	Kung!	NAM.336	25	16024-16381; 63-374	12	Panama	Boruca	PAN.302	2	16030-16370	26
Niger	Ancient peoples	NER.ANC	2	16037-16420	21	Panama	Embera	PAN.329	39	16040-16400	32
Niger	Bantu-speaking	NER.318	24	16082-16353; 64-324	20	Panama	Guayami	PAN.301	1	16030-16370	26
Nigeria	ND	NGA.AFR	1	16086-16519	15	Panama	Guaymi/ Ngobe	PAN.301	46	16040-16400	32
Nigeria	ND	NGA.AFR	7	16024-16389	22	Panama	Kuna	PAN.298	64	16030-16400; 39-380	33
Nigeria	Yoruban	NGA.007	14	16024-16381; 63-374	12	Panama	Wouman	PAN.330	32	16040-16400	32
ND	Mbanderu	BWA.342	7	16024-16381; 63-374	14	United States	African American	USA.AFR	795	16024-16365; 73-340	*b
ND	Naron	BWA.341	1	16024-16381; 63-374	14	United States	Apache	USA.008	1	16030-16370	26
ND	ND	000.AFR	3	16086-16519	15	United States	Apache	USA.008	180	16024-16365; 73-340	*b
Sierra Leone	ND	SKE.AFR	110	16024-16365; 73-340	*b	USA	Asian American	USA.ASN	1	16024-16381	14
South Africa	Biaka	ZAF.314	18	16024-16381; 63-374	23	USA	European American	USA.CAU	1406	16024-16365; 73-340	*b
South Africa	Biaka	ZAF.314	5	71-270	13	USA	Hawaiian	USA.087	2	16192-16420	34
South Africa	Nguni	ZAF.310	14	71-270	13	USA	Hawaiian	USA.087	15	16193-16370	11
South Africa	ND	ZAFCAU	1	16048-16569; 15 1-41	15	USA	Hispanic American	USA.HIS	694	16024-16365; 73-340	*b
South Africa	San	ZAF.311	14	71-270	13	USA	Navajo	USA.154	2	16030-16370	26
South Africa	Sotho-Tswana	ZAF.312	22	71-270	13	USA	Navajo	USA.154	150	16024-16365; 73-340	*b
South Africa	Tsonga	ZAF.313	14	71-270	13	USA	ND	USA.AFR	3	16129-16365; 73-340	35
Tanzania	Hazda	TZA.343	17	16024-16381; 63-374	12	USA	Oneota	USA.331	52	16056-16409	36
Uganda	ND	UGA.AFR	1	16048-16569; 15 1-41	15	USA	Windover	USA.295	14	16151-16317	37
						America, South					
						Argentina	Mapuche	ARG.297	39	16050-16400; 70-370	38
						Argentina	Mutaco	ARG.303	3	16030-16370	26
						Brazil	African origin	BRA.AFR	42	16024-16365	39
						Brazil	Amazon region, ND	BRA.300	92	16047-16405	40
						Brazil	Ancient people	BRA.ANC	18	16047-16380	41

Table 1. Continued...

Region/ country	Population	Identification code	No.	Nucleotide positions used	Ref.	Region/ country	Population	Identification code	No.	Nucleotide positions used	Ref.
Brazil	Krahoa	BRA.304	3	16030-16370	26	Korea, South	ND	KOR.ASN	64	16086-16519	46
Brazil	Surucucu, Catrimani	BRA.299	50	16003-16393; 30-396	42	Krygyzstan	Kirghiz	KGZ.ASN	96	16024-16383	51
Brazil	Ticuna	BRA.344	3	16030-16370	26	Laos	H'mong	LAO.ASN	1	16190-16370	11
Brazil	Yanomama	BRA.299	3	16030-16370	26	Malaysia	ND	MYS.ASN	1	16217-16261	11
Columbia	Ancient People	COL.ANC	6	16049-16401	43	Malaysia	ND	MYS.ASN	6	71-270	13
Tristan da Cunha	Indigenous	GBR.340	5	15996-16401; 29-408	44	Malaysia	Sabah	MYS.ASN	36	16064-16375	45
Venezuela	ND	VEN.338	1	16030-16370	26	Mongolia	ND	MNG.ASN	83	16020-16400	53
Asia						ND	ND	000.ASN	13	71-270	13
Cambodia	ND	KHM.ASN	12	71-270	13	ND	ND	000.ASN	14	16024-16381; 63-374	12
China	Hong Kong	CHN.ASN	20	16024-16400	31	ND	ND	000.ASN	23	16024-16389; 56-374	22
China	ND	CHN.ASN	2	16024-16381; 63-374	14	Philippines	ND	PHL.ASN	1	16024-16381	14
China	ND	CHN.ASN	4	16086-16519	15	Philippines	ND	PHL.ASN	1	16086-16519	15
China	ND	CHN.ASN	1	16190-16370	11	Philippines	ND	PHL.ASN	35	16189-16375	45
China	ND	CHN.ASN	16	71-270	13	Thailand	ND	THA.ASN	69	16024-16569; 1-576	*b
China	Taiwan	CHN.ASN	34	16064/16189- 16375	45	Viet Nam	ND	VNM.ASN	9	71-270	13
China	Taiwan	CHN.ASN	6	16030-16370	26	Australia					
China	Taiwan	CHN.ASN	1	16024-16381	14	New Zealand	Aotearoa	NZL.ASN	24	16189-16375	45
China	Taiwan	CHN.ASN	65	16048-16569; 1-41	46	New Zealand	Chatham Islands	NZL.317	1	16192-16420	34
China	Taiwan	CHN.ASN	28	16024-16390	47	New Zealand	Maori	NZL.323	292	16189-16365	54
China	Siberia	CHN.306	1	16030-16370	26	ND	ND	AUS.294	9	16190-16370	11
India	Karnataka, Kerala: Havik	IND.CAU	48	15997-16401; 29-408	48	ND	ND	AUS.CAU	1	16086-16519	15
India	Kumtata- luka: Murki	IND.CAU	50	15997-16401; 29-408	48	ND	Waripiri and Pallintji / Ngyiambaa	AUS.326	115	15997-16377	55
India	ND	IND.CAU	1	16086-16519	15	Europe					
Indonesia	Moluccas and Nusa Tenggara Islands	IDN.ASN	27	16024-16395	49	Austria	Ancient people	AUT.ANC	1	16056-16402	56
Indonesia	ND	IDN.ASN	1	16086-16519	15	Austria	Caucasian	AUT.CAU	101	16024-16400; 30-394	57, *b
Indonesia	ND	IDN.ASN	1	16024-16381	23	Bulgaria	Caucasian	BGR.CAU	30	15997-16400; 30-406	58
Indonesia	ND	IDN.ASN	7	16190-16370	11	Denmark	Caucasian	DNK.CAU	19	16024-16324; 63-332	59
Japan	Chiose	JPN.ASN	1	16190-16379	15	Denmark	Caucasian	DNK.CAU	28	16069-16365	60
Japan	Kano	JPN.ASN	3	16190-16379	15	Estonia	Caucasian	EST.CAU	1	16024-16381; 63-374	23
Japan	ND	JPN.ASN	163	16024-16365; 73-340	*b	Estonia	Caucasian	EST.CAU	28	16024-16383	61
Japan	ND	JPN.ASN	1	16024-16381; 63-374	23	Faroe Islands	Caucasian	DNK.CAU	22	16024-16324; 63-332	59
Japan	ND	JPN.ASN	100	16024-16399; 56-373	50	Finland	Caucasian	FIN.CAU	50	16024-16383	61
Japan	ND	JPN.ASN	62	16048-16569; 1-41	15	Finland	Caucasian	FIN.CAU	32	16024-16383	62
Japan	ND	JPN.ASN	1	16190-16370	11	Finland	Central and Southern	FIN.CAU	29	16090-16365	60
Japan	ND	JPN.ASN	19	71-270	13	Finland	Saami	FIN.CAU	298	16024-16383	61
Japan	Ryukyu/ Okinawa	JPN.ASN	50	16190-16379	15	France	Ancient People	FRA.ANC	3	16037-16420	21
Japan	Suttu	JPN.ASN	2	16190-16379	15	France	Caucasian	FRA.CAU	109	16024-16365; 73-340	*b
Japan	Taka	JPN.ASN	3	16190-16379	15	France	Caucasian	FRA.CAU	2	16086-16519	15
Japan	Toda	JPN.ASN	1	16190-16379	15	France	Caucasian	FRA.CAU	20	71-270	13
Japan	Urawa	JPN.ASN	1	16190-16379	15	France	Chambery	FRA.CAU	18	16024-16324; 63-322	59
Kazakhstan	Kazakh	KAZ.ASN	55	16024-16383	51	Germany	Caucasian	DEU.CAU	200	15996-16569; 1-618	63
Kazakhstan	Uighurs	KAZ.ASN	54	16024-16383	51	Germany	Caucasian	DEU.CAU	50	16024-16365; 73-340	64
Korea	ND	KOR.ASN	182	16024-16365; 73-340	*b	Germany	Caucasian	DEU.CAU	109	16024-16365; 73-340	65
Korea	ND	KOR.ASN	4	16030-16370	52						
Korea	ND	KOR.ASN	3	16086-16519	15						
Korea	ND	KOR.ASN	2	71-270	13						

Table 1. Continued...

Region/ country	Population	Identification code	No.	Nucleotide positions used	Ref.	Region/ country	Population	Identification code	No.	Nucleotide positions used	Ref.
Germany	Caucasian	DEU.CAU	107	16090-16365	60	Turkey	Western Region	TUR.CAU	22	16090-16365	60
Germany	Neanderthal	DEU.NED	1	16023-16400	66	UK	Cambridge Reference Sequence	GBR.CRS	1	All	82
Greece	ND	GRC.CAU	1	16024-16409	67	UK	Caucasian	GBR.CAU	5	16086-16519	15
Iceland	Caucasian	ISL.CAU	39	16024-16383	61	UK	Caucasian	GBR.CAU	100	16024-16400; 83, 30-394	83,
Iceland	Caucasian	ISL.CAU	14	16069-16365	60	UK	Cornwall	GBR.CAU	20	16024-16324; 59 63-322	60
Iceland	Caucasian	ISL.CAU	21	16024-16324; 59 63-322	59	UK	Cornwall	GBR.CAU	50	16069-16365	60
Italy	Caucasian	ITA.CAU	21	106-357	68	UK	Glasgow	GBR.CAU	3	16020-16478; 84 84-327	84
Italy	Sardinia	ITA.CAU	46	16024-16409	67	UK	Hebrides	GBR.CAU	19	16024-16324; 59 63-322	59
Italy	South Tyrol and Trentino	ITA.CAU	62	16024-16383	69	UK	Northern Ireland	GBR.CAU	37	16024-16324; 59 63-322	59
Italy	Tuscany	ITA.CAU	47	16051-16362; 70 57-319	70	UK	Northumber land	GBR.CAU	19	16024-16324; 59 63-322	59
Netherlands	Caucasian	NLD.CAU	1	16048-16569; 15 1-41	15	UK	Orkney Islands	GBR.CAU	89	16024-16324; 59 63-322	59
Norway	Caucasian	NOR.CAU	30	16024-16324; 71 63-322	71	UK	Wales	GBR.CAU	92	16090-16365	60
Norway	Saami	NOR.CAU	197	15997-16401	71	Oceania					
ND	Caucasian	000.CAU	107		13 ^c	Cook Islands	ND	COK.317	79	16189-16375	45
ND	Saami	000.CAU	100	15997-16401	61	Marques	Polynesian	FRA.317	19	16189-16375	45
Portugal	Caucasian	PRT.CAU	40	16090-16370	10	Marshall Islands	ND	MHL.317	5	16189-16375	45
Portugal	Caucasian	PRT.CAU	30	16090-16365	60	Melanesia	New Britain	GBR.315	2	16192-16420	34
Russia	Evenk and Tungus	RUS.307	11	16030-16370	26	Micronesia	Kapingamar angi	FSM.316	16	16189-16375	45
Russia	Itel'men	RUS.321	46	16000-16525	73	Micronesia	Kosrae (Caroline Islands)	FSM.316	1	16192-16420	34
Russia	Karelian	RUS.CAU	83	16024-16383	61	ND	Polynesian	FRA.317	3	16189-16375	45
Russia	Koryk	RUS.324	147	16000-16525	73	ND	Yap	FSM.316	1	16192-16420	34
Russia	Nivkh	RUS.308	2	16030-16370	26	Papua New Guinea	Highland	PNG.339	3	16190-16370	11
Russia	Romanov	RUS.CAU	11	16020-16400; 74 48-408	74	Papua New Guinea	ND	PNG.339	19	16024-16381; 23 63-374	23
Russia	Udegey	RUS.309	3	16030-16370	26	Papua New Guinea	ND	PNG.339	23	16024-16595	49
Russia	Volga	RUS.CAU	34	16024-16383	61	Papua New Guinea	ND	PNG.339	1	16086-16519	15
Saudi Arabia, Israel, and Yemin	Bedouins, Arabs, and Jews	000.MLE	39	16024-16409	67	Papua New Guinea	ND	PNG.339	9	16164/16189- 16375	45
Spain	Andalusia	ESP.CAU	15	16090-16370	10	Samoa, American	ND	WSM.317	24	16024-16395; 49 41-401	49
Spain	Basques	ESP.CAU	45	16024-16383	75	Samoa, American	ND	WSM.317	17	16190-16370	11
Spain	Basques	ESP.CAU	42	16090-16370	10	Samoa, American	Savai'i and Upola	WSM.317	24	16064-16375	45
Spain	Basques	ESP.CAU	55	16069-16365	60	Sao Tome Society Islands	Bioko Island	STP.AFR	95	16024-16383	18
Spain	Canary Islands- Tenerife	ESP.322	54	15997-16399	19	Society Islands	Polynesian	FRA.317	1	16192-16420	34
Spain	Catalonia	ESP.CAU	15	16090-16370	10	Tahiti	Polynesian	FRA.317	4	16189-16375	45
Spain	Caucasian	ESP.CAU	30	16090-16365	60	Tonga	Polynesian	TGO.317	6	16064-16375	45
Spain	Caucasian	ESP.CAU	78	16024-16569; 76, 1-576	76, * ^b	Tonga	Polynesian	TGO.317	1	16024-16381; 23 63-374	23
Spain	Caucasian	ESP.CAU	11	16090-16370	10	Tonga	Polynesian	TGO.317	2	16190-16370	11
Spain	Caucasian	ESP.CAU	18	15997-16399	19	Vanuatau	Nguna	VUT.315	41	16041-16400	34
Spain	Galacia	ESP.CAU	92	16024-16383	77	Vanuatau	ND	VUT.315	1	16041-16400	85
Spain	Northern Region	ESP.CAU	30	16090-16370	10	Vanuatau	ND	VUT.315	51	16064-16375	45
Spain	Zaragoza	ESP.CAU	103	16024-16391; 78, 60-380	78, * ^b						
Switzerland	Caucasian	CHE.CAU	154	16020-16400; 79 40-400	79						
Switzerland	Caucasian	CHE.CAU	74	16024-16383	80						
Switzerland	Caucasian	CHE.CAU	1	16086-16519	15						
Turkey	ND	TUR.CAU	29	16097-16400; 58 30-400	58						
Turkey	ND	TUR.CAU	45	16024-16401	81						

*ND – Not defined.

^bSWGDM – Scientific Working Group for DNA Analysis Methods.^cReferences 13,14,15,22,48,72.

Table 2. Country codes used in the sequence identifier to designate the country of origin (86)

Country	Code	Adjective	Country	Code	Adjective
Afghanistan (the Islamic State of)	AFG	Afghan	Djibouti (the Republic of)	DJI	Djibouti (of); a Djiboutian
Albania (the Republic of)	ALB	Albanian	Dominica (the Commonwealth of)	DMA	Dominica (of)
Algeria (the People's Democratic Republic of)	DZA	Algerian	Dominican Republic (the)	DOM	Dominican
Andorra (the Principality of)	AND	Andorran	Ecuador (the Republic of)	ECU	Ecuadorian
Angola (the Republic of)	AGO	Angolan	Egypt (the Arab Republic of)	EGY	Egyptian
Antigua and Barbuda	ATG	Antigua and Barbuda (of)	El Salvador (the Republic of)	SLV	Salvadoran
Argentina (the Argentine Republic)	ARG	Argentine	Equatorial Guinea (the Republic of)	GNQ	Equatorial Guinea (of)
Armenia (the Republic of)	ARM	Armenian	Eritrea	ERI	Eritrean
Australia	AUS	Australian	Estonia (the Republic of)	EST	Estonian
Austria (the Republic of)	AUT	Austrian	Ethiopia (Federal Democratic Republic of)	ETH	Ethiopian
Azerbaijan (the Azerbaijani Republic)	AZE	Azerbaijani	Fiji (the Republic of)	FJI	Fiji (of)
Bahamas (the Commonwealth of the)	BHS	Bahamian	Finland (the Republic of)	FIN	Finnish; a Finn
Bahrain (the State of)	BHR	Bahraini	France (the Republic of)	FRA	French; a Frenchman
Bangladesh (the People's Republic of)	BGD	Bangladesh (of) / a Bangladeshi	Gabon (the Republic of)	GAB	Gabonese
Barbados	BRB	Barbadian	Gambia (the Republic of the)	GMB	Gambian
Belarus (the Republic of)	BLR	Belarusian	Georgia	GEO	Georgian
Belgium (the Kingdom of)	BEL	Belgian	Germany (the Federal Republic of)	DEU	German
Belize	BLZ	Belizean	Ghana (the Republic of)	GHA	Ghanaian
Benin (the Republic of)	BEN	Beninese	Greece (the Hellenic Republic of)	GRC	Greek
Bhutan (the Kingdom of)	BTN	Bhutanese	Grenada	GRD	Grenadian
Bolivia (the Republic of)	BOL	Bolivian	Guatemala (the Republic of)	GTM	Guatemalan
Bosnia and Herzegovina	BIH	Bosnia and Herzegovina (of)	Guinea (the Republic of)	GIN	Guinean
Botswana (the Republic of)	BWA	Botswana (of)	Guinea-Bissau (the Republic of)	GNB	Guinea-Bissau (of)
Brazil (the Federative Republic of)	BRA	Brazilian	Guyana (the Republic of)	GUY	Guyanese
Brunei Darussalam	BRN	Brunei Darussalam (of)	Haiti (the Republic of)	HTI	Haitian
Bulgaria (the Republic of)	BGR	Bulgarian	Holy See (the); also known as the Vatican City State	VAT	Holy See (of the)
Burkina Faso	BFA	Burkina Faso (of)	Honduras (the Republic of)	HND	Honduran
Burundi (the Republic of)	BDI	Burundian/ (of) Burundi	Hungary (the Republic of)	HUN	Hungarian
Cambodia (the Kingdom of)	KHM	Cambodian	Iceland (the Republic of)	ISL	Icelandic; an Icelander
Cameroon (the Republic of)	CMR	Cameroonian	India (the Republic of)	IND	Indian
Canada	CAN	Canadian	Indonesia (the Republic of)	IDN	Indonesian
Cape Verde (the Republic of)	CPV	Cape Verdean	Iran (the Islamic Republic of)	IRN	Iranian
Central African Republic (the)	CAF	Central African, of the Central African Republic	Iraq (the Republic of)	IRQ	Iraqi
Chad (the Republic of)	TCD	Chadian	Ireland: also known as Eire	IRL	Irish; an Irishman
Chile (the Republic of)	CHL	Chilean	Israel (the State of)	ISR	Israeli
China (the People's Republic of) including Taiwan province	CHN	Chinese (Taiwanese)	Italy (the Republic of)	ITA	Italian
Colombia (the Republic of)	COL	Colombian	Ivory Coast (the Republic of the)	IVC	
Comoros (the Islamic Federal Republic of)	COM	Comorian	Jamaica	JAM	Jamaican
Congo (the Democratic Republic of)	COD	Congolese; of the Democratic Republic of the Congo	Japan	JPN	Japanese
Congo (the Republic of the)	COG	Congolese	Jordan (the Hashemite Kingdom of)	JOR	Jordanian
Cook Islands (the)	COK	Cook Islands (of the)	Kazakhstan (the Republic of)	KAZ	Kazakh
Costa Rica (the Republic of)	CRI	Costa Rican	Kenya (the Republic of)	KEN	Kenyan
Cote d'Ivoire (the Republic of)	CIV	Ivorian	Kiribati	KIR	Kiribati (of)
Croatia (the Republic of)	HRV	Croatian	Korea (the Democratic People's Republic of)	PRK	Korea (of the Democratic People's Republic of)
Cuba (the Republic of)	CUB	Cuban	Kuwait (the State of)	KWT	Kuwaiti
Cyprus (the Republic of)	CYP	Cypriot	Kyrgyzstan: also known as the Kyrgyz Republic	KGZ	Kyrgyz
Czech Republic (the)	CZE	Czech	Lao People's Democratic Republic (the)	LAO	Lao; a Lao
Denmark (the Kingdom of)	DNK	Danish; a Dane	Latvia (the Republic of)	LVA	Latvian
			Lebanon: also known as the Lebanese Republic	LBN	Lebanese
			Lesotho (the Kingdom of)	LSO	Lesotho (of)
			Liberia (the Republic of)	LBR	Liberian

Table 2. Continued...

Country	Code	Adjective	Country	Code	Adjective
Libyan Arab Jamahiriya (the Socialist People's)	LBY	Libyan	Saint Lucia	LCA	Saint Lucian
Liechtenstein (the Principality of)	LIE	Liechtenstein (of)	Saint Vincent and the Grenadines	VCT	Saint Vincent and the Grenadines (of)
Lithuania (the Republic of)	LTU	Lithuanian	Samoa (the Independent State of)	WSM	Samoa
Luxembourg (the Grand Duchy of)	LUX	Luxembourg (of)	San Marino (the Republic of)	SMR	San Marino (of)
Macedonia (the former Yugoslav Republic of)	MKD	Macedonia (of the former Yugoslav Republic of)	Sao Tome and Principe (the Democratic Republic of)	STP	Sao Tome and Principe (of)
Madagascar (the Republic of)	MDG	Malagasy	Saudi Arabia (the Kingdom of)	SAU	Saudi Arabian
Malawi (the Republic of)	MWI	Malawian	Senegal (the Republic of)	SEN	Senegalese
Malaysia	MYS	Malaysian	Seychelles (the Republic of)	SYC	Seychelles (of); a Seychellois
Maldives (the Republic of)	MDV	Maldivian	Sierra Leone (the Republic of)	SKE	Sierra Leonean
Mali (the Republic of)	MLI	Malian	Singapore (the Republic of)	SGP	Singaporean
Malta (the Republic of)	MLT	Maltese	Slovakia: also known as the Slovak Republic	SVK	Slovak
Marshall Islands (the Republic of the)	MHL	Marshall Islands (of the), Marshallese	Slovenia (the Republic of)	SVN	Slovene
Mauritania (the Islamic Republic of)	MRT	Mauritanian	Solomon Islands	SLB	Solomon Islands (of)
Mauritius (the Republic of)	MUS	Mauritian	Somalia: also known as the Somali Democratic Republic	SOM	Somali
Mazambique (the Republic of)	MOZ	Mozambican	South Africa (the Republic of)	ZAF	South African
Mexico: also known as the United Mexican States	MEX	Mexican	Spain (the Kingdom of)	ESP	Spanish; a Spaniard
Micronesia (the Federated States of)	FSM	Micronesia (of the Federated States of)	Sri Lanka (the Democratic Socialist Republic of)	LKA	Sri Lankan, (of) Sri Lanka
Monaco (the Principality of)	MCO	Monegasque	Sudan (the Republic of the)	SDN	Sudanese
Mongolia	MNG	Mongolian	Suriname (the Republic of)	SUR	Surinamese
Morocco (the Kingdom of)	MAR	Moroccan	Swaziland (the Kingdom of)	SWZ	Swazi
Myanmar (the Union of)	MMR	Myanmar	Sweden (the Kingdom of)	SWE	Swedish; a Swede
Namibia (the Republic of)	NAM	Namibian	Switzerland: also known as the Swiss Confederation	CHE	Swiss
Nauri (the Republic of)	NRU	Nauruan	Syrian Arab Republic (the)	SYR	Syrian
Nepal (the Kingdom of)	NPL	Nepalese	Tajikistan (the Republic of)	TJK	Tajik
Netherlands (the Kingdom of the)	NLD	Netherlands; a Netherlander	Thailand (the Kingdom of)	THA	Thai
New Zealand	NZL	New Zealand (of); a New Zealander	Togo: also known as the Togolese Republic	TGO	Togolese
Nicaragua (the Republic of)	NIC	Nicaraguan	Tonga (the Kingdom of)	TON	Tongan
Niger (the Republic of the)	NER	Niger (of the)	Trinidad and Tobago (the Republic of)	TTO	Trinidad and Tobago (of)
Nigeria (the Federal Republic of)	NGA	Nigerian	Tunisia (the Republic of)	TUN	Tunisian
Norway (the Kingdom of)	NOR	Norwegian	Turkey (the Republic of)	TUR	Turkish; a Turk
Oman (the Sultanate of)	OMN	Omani	Turkmenistan	TKM	Turkmen
Pakistan (the Islamic Republic of)	PAK	Pakistan (of); a Pakistani	Tuvalu	TUV	Tuvaluan
Palau (the Republic of)	PLW	Palau (of)	Uganda (the Republic of)	UGA	Ugandan
Panama (the Republic of)	PAN	Panamanian	Ukraine	UKR	Ukrainian
Papua New Guinea	PNG	Papua New Guinea (of); a Papua New Guinean	United Arab Emirates (the)	ARE	United Arab Emirates (of the)
Paraguay (the Republic of)	PRY	Paraguayan	United Kingdom of Great Britain and Northern Ireland (the)	GBR	British, of the United Kingdom (of Great Britain and Northern Ireland)
Peru (the Republic of)	PER	Peruvian	United Republic of Tanzania (the)	TZA	Tanzanian
Philippines (the Republic of the)	PHL	Philippine; a Filipino	United States of America (the)	USA	American, of the United States of America
Poland (the Republic of)	POL	Polish; a Pole	Uruguay (the Eastern Republic of)	URY	Uruguayan
Portugal: also known as the Portuguese Republic	PRT	Portuguese	Uzbekistan (the Republic of)	UZB	Uzbek
Qatar (the State of)	QAT	Qatar (of)	Vanuatu (the Republic of)	VUT	Vanuatu (of)
Korea (the Republic of)	KOR	Korea (of the Republic of)	Venezuela (the Republic of)	VEN	Venezuelan
Moldova (the Republic of)	MDA	Moldovan	Viet Nam (the Socialist Republic of)	VNM	Vietnamese
Romania	ROM	Romanian	Yemen (the Republic of)	YEM	Yemeni; a Yemenite
Russian Federation (the)	RUS	Russian Federation, Russian (of the)	Yugoslavia	YUG	Yugoslav
Rwanda: also known as the Twandese Republic	RWA	Rwandan	Zambia (the Republic of)	ZMB	Zambian
Saint Kitts and Nevis	KNA	Saint Kitts and Nevis (of)	Zimbabwe (the Republic of)	ZWE	Zimbabwean

Table 3. Codes (alphabetic and numeric) used in the sequence identifier to designate group or ethnic affiliation

Tribe	Code	Region	Country	Tribe	Code	Region	Country
Aborigine	0.294	ND ^a	Australia	Chumash	0.048	California	USA
Aborigine	0.326	Waripiri and Paalintji/Ngyambaa	Australia	Clatsop	0.049	Pacific Northwest	USA
Achumawi	0.001	California	USA	Coahuiltec	0.050	Southwest	USA
African origin	AFR	ND		Coast Salish	0.051	Pacific Northwest	USA
AfroCaribbean	AFC	ND		Cochimi	0.052	California	USA
Ahtena	0.002	Subarctic	USA	Cocopa	0.053	Southwest	USA
Algonkin	0.003	Subarctic	USA	Coeur d'Alene	0.054	Plateau	USA
Alsea	0.004	Pacific Northwest	USA	Columbia	0.055	Plateau	USA
Alutiq	0.005	Arctic	USA	Colville	0.056	Plateau	USA
Amazon region: undefined	0.300	Amazon Region	Brazil	Comanche	0.057	Great Plains	USA
Amazon region: Yanomami	0.299	Roraima	Brazil	Comox	0.058	Pacific Northwest	USA
Anasazi	0.006	Southwest	USA	Concho	0.059	Southwest	USA
Ancient	ANC	Ancient people	ND	Coos	0.060	Pacific Northwest	USA
Apache, Aravaipa	0.009	Southwest	USA	Coquille	0.061	Pacific Northwest	USA
Apache, Chiricahua	0.010	Southwest	USA	Costanoan	0.062	California	USA
Apache, Jicarilla	0.011	Southwest	USA	Cowichan	0.063	Pacific Northwest	USA
Apache, Kiowa	0.012	Great Plains	USA	Cowlitz	0.064	Pacific Northwest	USA
Apache, Lipan	0.013	Southwest	USA	Cree	0.065	Subarctic	USA
Apache, Mescalero	0.014	Southwest	USA	Crow	0.066	Great Plains	USA
Apache, Mimbreno	0.015	Southwest	USA	Cupeno	0.067	California	USA
Apache, ND	0.008	North America	USA	Dakota	0.068	Great Plains	USA
Apache, San Carlos	0.016	Southwest	USA	Dogrib	0.069	Subarctic	USA
Apache, Tonto	0.017	Southwest	USA	Duwamish	0.070	Pacific Northwest	USA
Apache, White Mountain	0.018	Southwest	USA	Embera	0.329	Eastern Region	Panama
Apache, Yavapai	0.019	Southwest	USA	Esselen	0.071	California	USA
Arapaho	0.020	Great Plains	USA	Evenk/Tungus	0.307	Siberia	Russia
Arikara	0.021	Great Plains	USA	Eyak	0.072	Subarctic	USA
Asian origin	ASN	ND		Fang	0.334	Sub-Saharan	Guinea
Assiniboin	0.022	Great Plains	USA	Flathead	0.073	Plateau	USA
Athabaskan	0.023	Subarctic	USA	Gabrielino	0.074	California	USA
Atsugewi	0.024	California	USA	Gitksan	0.075	Pacific Northwest	USA
Aztec	0.025	Middle America	USA	Goshute	0.076	Great Basin	USA
Bannock	0.026	Great Basin	USA	Gros Ventre	0.077	Great Plains	USA
Bantu-Speaking	0.318	South Eastern Africa	ND	Guachichil	0.078	Southwest	USA
Bear River Indians	0.027	California	USA	Guaicura	0.079	California	USA
Beaver	0.028	Subarctic	USA	Guam	0.335	Mariana Islands (South)/Guamanian	USA
Bella Bella	0.029	Pacific Northwest	USA	Guayami/Ngobe	0.301	Western Region	Panama
Bella Coola	0.030	Pacific Northwest	USA	Haida	0.080	Pacific Northwest	USA/Canada
Beothuk	0.031	Subarctic	USA	Haisla	0.081	Pacific Northwest	USA
Berber	0.332	Northern Morocco: Rif Mountains	Morocco	Halchidhoma	0.082	Southwest	USA
Biaka	0.314	ND	South Africa	Halyikwamai	0.083	Southwest	USA
Blackfoot	0.032	Great Plains	USA	Han	0.084	Subarctic	USA
Blood	0.033	Great Plains	USA	Hare	0.085	Subarctic	USA
Boruca	0.302	Western Region	Panama	Havasupai	0.086	Southwest	USA
Bubi	0.325	Bioko Island	Equatorial Guinea	Hawaiian	0.087	Pacific Islands	USA
Cahto	0.034	California	USA	Hazda	0.343	Africa	The United Republic of Tanzania
Cahuilla	0.035	California	USA	Herero!	0.337	South Western Africa	Botswana
Cambridge Reference Sequence	CRS			Hidatsa	0.088	Great Plains	USA
Canary Islander	0.322	West Coast North Africa	Spain	Hispanic origin	HIS	ND	
Caribs	CAR	ND	Caribbean Area	Hoh	0.089	Pacific Northwest	USA
Carrier	0.036	Subarctic	USA	Hohokam	0.090	Southwest	USA
Caucasian	CAU	ND		Hope	0.091	Southwest	USA
Cayuse	0.037	Plateau	USA	Hope-Tewa	0.092	Southwest	USA
Chastacosta	0.038	Pacific Northwest	USA	Huchnom	0.093	California	USA
Chehalis	0.039	Pacific Northwest	USA	Huetar	0.319	Quitirrisi	Costa Rica
Chelan	0.040	Plateau	USA	Huichol	0.094	Southwest	USA
Chemehuevi	0.041	Great Basin	USA	Hupa	0.095	California	USA
Cheyenne	0.042	Great Plains	USA	Inca	0.096	Middle America	USA
Chilcotin	0.043	Subarctic	USA	Ingalik	0.097	Subarctic	USA
Chilula	0.044	California	USA	Innu	0.098	Subarctic	USA
Chimariko	0.045	California	USA	Inuit	0.099	Arctic	USA
Chinook	0.046	Pacific Northwest	USA	Inupiat	0.100	Arctic	USA
Chipewyan	0.047	Subarctic	USA	Iowa	0.101	Great Plains	USA
				Itel'men	0.321	Kamchatka	Russia
				Jumano	0.102	Southwest	USA
				Kalapuya	0.103	Pacific Northwest	USA
				Kalispel	0.104	Plateau	USA

Table 3. Continued...

Tribe	Code	Region	Country	Tribe	Code	Region	Country
Kansa	0.105	Great Plains	USA	Nez Perce	0.155	Plateau	USA
Karankawa	0.106	Southwest	USA	Nguni	0.310	ND	South Africa
Karok	0.107	California	USA	Niokolo Mandenka	0.327	Eastern Senegal	Senegal
Kaska	0.108	Subarctic	USA	Niska	0.156	Pacific Northwest	USA
Kawaiisu	0.109	Great Basin	USA	Nisqually	0.157	Pacific Northwest	USA
Kichai	0.110	Great Plains	USA	Nomlaki	0.158	California	USA
Kiliwa	0.111	California	USA	Nongatl	0.159	California	USA
Kiowa	0.112	Great Plains	USA	Nooksack	0.160	Pacific Northwest	USA
Kitanemuk	0.113	California	USA	Nootka	0.161	Pacific Northwest	USA
Klallam	0.114	Pacific Northwest	USA	Nuu-chah-nulth	0.328	Pacific Northwest	USA/Canada
Klamath	0.115	Plateau	USA	Ojibwa/Chippewa	0.305	North Central States (MN, ND)	USA
Klickitat	0.116	Plateau	USA	Okanagan	0.162	Plateau	USA
Kohuana	0.117	Southwest	USA	Olmec	0.163	Middle America	USA
Kootenai	0.118	Plateau	USA	Omaha	0.164	Great Plains	USA
Koryak	0.324	Kamchatka Peninsula	Russia	Oneota	0.331	Illinois: Norris Farms cemetery	USA
Koyukon	0.119	Subarctic	USA	Osage	0.165	Great Plains	USA
Kraho	0.304	ND	Brazil	Oto	0.166	Great Plains	USA
Kuitsh	0.120	Pacific Northwest	USA	Paipai	0.167	California	USA
Kumeyaay	0.121	California	USA	Paiute	0.168	Great Basin	USA
Kuna	0.298	South Eastern Coastline	Panama	Palouse	0.169	Plateau	USA
Kung	0.336	South Western Africa	Namibia	Papua	0.339	ND	Papua New Guinea
Kutchin	0.122	Subarctic	USA	Patwin	0.170	California	USA
Kwakiutl	0.123	Pacific Northwest	USA	Pawnee	0.171	Great Plains	USA
Kwalhioqua	0.124	Pacific Northwest	USA	Piegan	0.172	Great Plains	USA
Lake	0.125	Plateau	USA	Pima	0.173	Southwest	USA
Lakota	0.126	Great Plains	USA	Piro	0.174	Southwest	USA
Lassik	0.127	California	USA	Pojoaque	0.175	Southwest	USA
Latgawa	0.128	Pacific Northwest	USA	Polynesia	0.317	South Pacific Islanders	ND
Lillooet	0.129	Plateau	USA	Pomo	0.176	California	USA
Luiseno	0.130	California	USA	Ponca	0.177	Great Plains	USA
Lummi	0.131	Pacific Northwest	USA	Pueblo, Acoma	0.179	Southwest	USA
Maidu	0.132	California	USA	Pueblo, Cochiti	0.180	Southwest	USA
Makah	0.133	Pacific Northwest	USA	Pueblo, Isleta	0.181	Southwest	USA
Makiritare	0.338	ND	Venezuela	Pueblo, Jemez	0.182	Southwest	USA
Mandan	0.134	Great Plains	USA	Pueblo, Keres	0.183	Southwest	USA
Manso	0.135	Southwest	USA	Pueblo, Laguna	0.184	Southwest	USA
Maori	0.323	Polynesia	New Zealand	Pueblo, Nambe	0.185	Southwest	USA
Mapuche	0.297	Patagonian Region	Argentina	Pueblo, Not Defined	0.178	Southwest	USA
Maricopa	0.136	Southwest	USA	Pueblo, Pecos	0.186	Southwest	USA
Mataco	0.303	ND	Argentina	Pueblo, Picuris	0.187	Southwest	USA
Mattole	0.137	California	USA	Pueblo, San Felipe	0.188	Southwest	USA
Maya	0.138	Middle America	USA	Pueblo, San	0.189	Southwest	USA
Mayo	0.139	Southwest	USA	ldefonso			
Mbanderu	0.342	ND	Botswana	Pueblo, San Juan	0.190	Southwest	USA
Melanesia	0.315	South Pacific Islanders	ND	Pueblo, Sandia	0.191	Southwest	USA
Metis	0.140	Subarctic	USA	Pueblo, Santa Ana	0.192	Southwest	USA
Micronesia	0.316	South Pacific Islanders	ND	Pueblo, Santa Clara	0.193	Southwest	USA
Middle Eastern Europeans	MLE	Middle East	Europe	Pueblo, Santo Domingo	0.194	Southwest	USA
Mimbreno	0.141	Southwest	USA	Pueblo, Taos	0.195	Southwest	USA
Missouri	0.142	Great Plains	USA	Pueblo, Tesugue	0.196	Southwest	USA
Miwok	0.143	California	USA	Pueblo, Tewa	0.197	Southwest	USA
Mixtec	0.144	Middle America	USA	Pueblo, Tompiro	0.198	Southwest	USA
Modoc	0.145	Plateau	USA	Pueblo, Towa	0.199	Southwest	USA
Mogollon	0.146	Southwest	USA	Pueblo, Ysleta del Sur	0.200	Southwest	USA
Mohave	0.147	Southwest	USA	Pueblo, Zia	0.201	Southwest	USA
Mono	0.148	California	USA	Puyallup	0.202	Pacific Northwest	USA
Mountain	0.149	Subarctic	USA	Pygmy	0.320	Central Africa	Central African Republic and DR Congo
Muckleshoot	0.150	Pacific Northwest	USA	Quapaw	0.203	Great Plains	USA
Nakipa	0.151	California	USA	Quiche	0.296	Santa Cruz de Quiche	Guatemala
Nakota	0.152	Great Plains	USA	Quileute	0.204	Pacific Northwest	USA
Nanaimo	0.153	Pacific Northwest	USA	Quinault	0.205	Pacific Northwest	USA
Naron	0.341	ND	Botswana	Salinan	0.206	California	USA
Native American	0.333	ND	North/South America				
Navajo	0.154	Southwest	USA				

Table 3. Continued...

Tribe	Code	Region	Country	Tribe	Code	Region	Country
Salish	0.207	Pacific Northwest	USA	Tolowa	0.254	California	USA
Samish	0.208	Pacific Northwest	USA	Toltec	0.255	Middle America	USA
San	0.311	ND	South Africa	Tristan da Cunha	0.340	Southern Atlantic Ocean	Great Britain
Sanpoil	0.209	Plateau	USA	Tssetsaut	0.256	Subarctic	USA
Sarsi	0.210	Great Plains	USA	Tsimshian	0.257	Pacific Northwest	USA
Sauk-Suiattle	0.211	Pacific Northwest	USA	Tsonga	0.313	ND	South Africa
Sechelt	0.212	Pacific Northwest	USA	Tubatulabal	0.258	California	USA
Sekani	0.213	Subarctic	USA	Tutchone	0.259	Subarctic	USA
Seri	0.214	Southwest	USA	Tututni	0.260	Pacific Northwest	USA
Serrano	0.215	California	USA	Twana	0.261	Pacific Northwest	USA
Shasta	0.216	California	USA	Umatilla	0.262	Plateau	USA
Shoalwater	0.217	Pacific Northwest	USA	Umpqua, Cow Creek Band	0.264	Pacific Northwest	USA
Shoshone	0.218	Great Basin	USA	Umpqua, ND	0.263	Pacific Northwest	USA
Shuswap	0.219	Plateau	USA	Umpqua, Upper	0.265	Pacific Northwest	USA
Siletz	0.220	Pacific Northwest	USA	Unangan	0.266	Arctic	USA
Sinkyone	0.221	California	USA	Unknown	UNK	ND	ND
Siuslaw	0.222	Pacific Northwest	USA	USA, Guam	GUA		USA
Skagit	0.223	Pacific Northwest	USA	Ute	0.267	Great Basin	USA
Skokomish	0.224	Pacific Northwest	USA	Waco	0.268	Great Plains	USA
Slavey	0.225	Subarctic	USA	Wailaki	0.269	California	USA
Snohomish	0.226	Pacific Northwest	USA	Walapai	0.270	Southwest	USA
Snoqualmie	0.227	Pacific Northwest	USA	Walapai	0.270	Southwest	USA
Sobaipuri	0.228	Southwest	USA	Walla Walla	0.271	Plateau	USA
Songhees	0.229	Pacific Northwest	USA	Wappo	0.272	California	USA
Sotho-Tswana	0.312	ND	South Africa	Wasco	0.273	Pacific Northwest	USA
Spokan	0.230	Plateau	USA	Washoe	0.274	Great Basin	USA
Squamish	0.231	Pacific Northwest	USA	Wenatchee	0.275	Plateau	USA
Squaxin Island	0.232	Pacific Northwest	USA	Whilkut	0.276	California	USA
Steilacoom	0.233	Pacific Northwest	USA	Wichita	0.277	Great Plains	USA
Stillaguamish	0.234	Pacific Northwest	USA	Windover	0.295	Windover ancient arch. site	USA
Suma	0.235	Southwest	USA	Wintun	0.278	California	USA
Suquamish	0.236	Pacific Northwest	USA	Wishram	0.279	Plateau	USA
Swinomish	0.237	Pacific Northwest	USA	Wiyot	0.280	California	USA
Tagish	0.238	Subarctic	USA	Wounan	0.330	Eastern Region	Panama
Tahltan	0.239	Subarctic	USA	Yahi	0.281	California	USA
Takelma	0.240	Pacific Northwest	USA	Yakima	0.282	Plateau	USA
Tanaina	0.241	Subarctic	USA	Yana	0.283	California	USA
Tano	0.242	Southwest	USA	Yaqui	0.284	Southwest	USA
Tarahumara	0.243	Southwest	USA/Mexico	Yaquina	0.285	Pacific Northwest	USA
Tataviam	0.244	California	USA	Yellowknife	0.286	Subarctic	USA
Tawakoni	0.245	Great Plains	USA	Yokuts	0.287	California	USA
Tenana	0.246	Subarctic	USA	Yoruban	0.007	ND	Nigeria
Tenino	0.247	Plateau	USA	Yuki	0.288	California	USA
Tepehuan	0.248	Southwest	USA	Yuma	0.289	Southwest	USA
Thompson	0.249	Plateau	USA	Yup'ik	0.290	Arctic	USA
Tibetan	0.306	Tibet	China	Yurok	0.291	California	USA
Tillamook	0.250	Pacific Northwest	USA	Zapotec	0.292	Middle America	USA
Tiwa	0.251	Southwest	USA	Zuni	0.293	Southwest	USA
Tlingit	0.252	Pacific Northwest	USA				
Tohono O'odham	0.253	Southwest	USA				

^aND – not determined/defined.

Table 4. The nucleotide positions listed by Barbuji et al (68) are listed together with the standardized *nps* to which they most likely correspond

Sequence/number	Nucleotide/position											Reported mitotype	
Sequence 13 ^a	G	G	C	C	-	C	C			T	T	C	47C 94C 145C 158G 205C 208C 209C 213T 246T
Barbuji Number	150	158	190	205	206	208	208C	209 ^c	209 ^d	213	219	223	
Our number ^b (based on CRS)	255	263	295	309.1	309.2	310	315.1	315.1	315.2	315	321	325	
Sequence 13	G	G	C	C	-			C	C	T	T	C	152C 199C 250C 263G 309.1C 315T 315.1C 315.2C 348T

^aThe haploype of sample 13 is listed in Figure 2 of Barabujani et al (68).

^bOur assignment of *np* is that of Anderson et al (82).

^cIf Barbuji et al (68) 208 *np* is T or blank, then it is replaced with 315.1C.

^dIf Barbuji et al (68) *np* 208 is C, then it is replaced with 315.2C.

ture contributions a standardized format should be developed that is consistent with the structure in the Compendium. Finally, the original concordance search format has been replaced by the FBI-developed searching program "MitoSearch," and searching algorithms are included in Combined DNA Index System to support the Missing Persons and Forensic Indices. The database will be made available via *Forensic Science Communications* (<http://www.fbi.gov>). The data contained in this Compendium cannot represent all data currently available; mtDNA population data are being developed and disseminated continuously. In fact, by the time this Compendium is published, the web-based data will be augmented compared with the data included in this Compendium. Furthermore, in an attempt to remain current and correct, we invite submissions of new sequence data for inclusion in future editions and welcome comments from users. We also especially welcome corrections in the public literature data that may be due to transcriptional errors on the authors' part, incorrect conversion of nomenclature on our part, or errors on our part due to manual transcription of the data into the Compendium. Updates to the Compendium will be made when sufficient data become available. Finally, it is our intention to archive whole mtDNA genome information when it becomes available.

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References

- Holland MM, Fisher DL, Mitchell LG, Rodriquez WC, Canik JJ, Meril CR, et al. Mitochondrial DNA sequence analysis of human skeletal remains: identification of remains from the Vietnam war. *J Forensic Sci* 1993;38:542-53.
- Wallace DC. Mitochondrial DNA in aging and disease. *Scientific American* 1997 August; p. 40-7.
- Budowle B, Wilson MR, DiZinno JA, Stauffer C, Fasano MA, Holland MM, et al. Mitochondrial DNA regions HVI and HVII population data. *Forensic Sci Int* 1999;103:23-35.
- Stoneking M. Mitochondrial DNA and human evolution. *J Bioenerg Biomembr* 1994;26:251-9.
- Cann R. Human dispersal and diversity. *Trends in Evolutionary Ecology* 1993;8:27-30.
- Miller KWP, Dawson JL, Hagelberg E. A concordance of nucleotide substitutions in the first and second hypervariable segments of the human mtDNA control region. *Int J Legal Med* 1996;109:107-13.
- Wilson MR, Stoneking M, Holland MM, DiZinno JA. Guidelines for the use of mitochondrial DNA sequencing in forensic science. *Crime Laboratory Digest* 1993;20:68-77.
- Wilson MR, DiZinno JA, Polansky D, Roplogle J, Budowle B. Validation of mitochondrial DNA sequencing for forensic casework analysis. *Int J Legal Med* 1995;108:68-74.
- National Research Council. NRC Report II: The evaluation of forensic evidence. Washington (DC): National Academy Press; 1996.
- Corte-Real HB, Macaulay VA, Richards MB, Hariti G, Issad MS, Cabon-Thomsen A, et al. Genetic diversity in the Iberian Peninsula determined from mitochondrial sequence analysis. *Ann Hum Genet* 1996;60:331-50.
- Lum JK, Rickards O, Ching C, Cann RL. Polynesian mitochondrial DNAs reveal three deep maternal lineage clusters. *Hum Biol* 1994;66:567-90.
- Vigilant L, Stoneking M, Harpending H, Hawkes K, Wilson AC. African populations and the evolution of human mitochondrial DNA. *Science* 1991;253:1503-7.
- Jorde LB, Bamshad MJ, Watkins WS, Zenger R, Fraley AE, Krakowiak PA, et al. Origins and affinities of modern humans: a comparison of mitochondrial and nuclear genetic data. *Am J Hum Genet* 1995;57:523-38.
- Vigilant L, Pennington R, Harpending H, Kocher TD, Wilson AC. Mitochondrial DNA sequences in single hairs from a southern African population. *Proc Natl Acad Sci U S A* 1989;86:9350-4.
- Horai S, Hayasaka K. Intraspecific nucleotide sequence differences in the major noncoding region of human mitochondrial DNA. *Am J Hum Genet* 1990;46:828-42.
- Graven L, Passarino G, Semino O, Boursot P, Santachiara-Benerecetti S, Langanzy A, et al. Evolutionary correlation between control region sequence and restriction polymorphisms in the mitochondrial genome of a large Senegalese Mandenka sample. *Mol Biol Evol* 1995;12:334-45.
- Pääbo S. Ancient DNA: extraction, characterization, molecular cloning, and enzymatic amplification. *Proc Natl Acad Sci U S A* 1989;86:1939-43.
- Mateu E, Comas D, Calafell F, Perez-Lezaun A, Abade A, Bertranpetit J. A tale of two islands: population history and mtDNA sequence variation of Bioko and Sao Tome, Gulf of Guinea. *Am J Hum Genet* 1997;61:507-18.
- Pinto F, Gonzalez AM, Hernandez M, Larruga JM, Cabrera VM. Genetic relationship between the Canary Islanders and their African and Spanish ancestors inferred from mtDNA sequences. *Ann Hum Genet* 1996;60:321-30.
- Soodyall H, Vigilant L, Hill AV, Stoneking M, Jenkins T. mtDNA control-region sequence variation suggests multiple independent origins of an Asian-specific 9-bp deletion in sub-Saharan Africans. *Am J Hum Genet* 1996;58:595-608.
- Hanni C, Begue A, Laudet V, Stehelin D, Brosseau T, Amouyel P, et al. Molecular typing of neolithic human bones. *Journal of Archaeological Science* 1995;22:649-58.
- Stoneking M, Hedgecock D, Higuchi RG, Vigilant L, Erlich HA, Arnheim N, et al. Population variation of human mtDNA control region sequences detected by enzymatic amplification and sequence-specific oligonucleotide probes. *Am J Hum Genet* 1991;48:370-82.
- Vigilant L. Control region sequences from African populations and the evolution of human mitochondrial DNA [dissertation]. Berkeley (CA): University of California; 1990.
- Monsalve MV, Hagelberg E. Mitochondrial DNA polymorphisms in Carib people from Belize. *Proc R Soc Lond B Biol Sci* 1997;264:1217-24.

- 25 Ward RH, Redd A, Valencia D, Fraizer B, Pääbo S. Genetic and linguistic differentiation in the Americas. *Proc Natl Acad Sci U S A* 1993;90:10663-7.
- 26 Torroni A, Sukernik RI, Schurr TG, Starikovskaya YB, Cabell MF, Crawford MH, et al. mtDNA variation of Aboriginal Siberians reveals distinct genetic affinities with Native Americans. *Am J Hum Genet* 1993;53:591-608.
- 27 Ward RH, Frazier BL, Dew-Jager K, Pääbo S. Extensive mitochondrial diversity within a single Amerindian tribe. *Proc Natl Acad Sci U S A* 1991;88:8720-4.
- 28 Santos M, Ward RH, Barrantes R. mtDNA variation in the Chibcha Amerindian Huetar from Costa Rica. *Hum Biol* 1994;66:963-77.
- 29 Boles TC, Snow CC, Stover E. Forensic DNA testing on skeletal remains from mass graves: a pilot project in Guatemala. *J Forensic Sci* 1995;40:349-55.
- 30 Horai S, Kondo R, Nakagawa-Hattori Y, Hayashi S, Sonoda S, Tajima K. Peopling of the Americas, founded by four major lineages of mitochondrial DNA. *Mol Biol Evol* 1993;10:23-47.
- 31 Betty DJ, Chin-Atkins AN, Croft L, Sraml M, Eastal S. Multiple independent origins of the COII/tRNA^{Lys} intergenic 9-bp mtDNA deletion in aboriginal Australians. *Am J Hum Genet* 1996;58:428-33.
- 32 Kolman CJ, Bermingham E, Cooke R, Ward RH, Arias TD, Guionneau SF. Reduced mtDNA diversity in the Ngobe Amerinds of Panama. *Genetics* 1995;140:275-83.
- 33 Batista O, Kolman CJ, Bermingham E. Mitochondrial DNA diversity in the Kuna Amerinds of Panama. *Hum Mol Genet* 1995;4:921-9.
- 34 Hagelberg E, Clegg JB. Genetic polymorphisms in prehistoric Pacific Islanders determined by analysis of ancient bone DNA. *Proc R Soc Lond B Biol Sci* 1993;252:163-70.
- 35 Aquadro CF, Greenberg BD. Human mtDNA variation and evolution: analysis of nucleotide sequences from seven individuals. *Genetics* 1983;103:287-312.
- 36 Stone AC, Stoneking M. mtDNA analysis of a prehistoric Oneota population: implications for the peopling of the New World. *Am J Hum Genet* 1998;62:1153-70.
- 37 Hauswirth WW, Dickel CD, Rowold DJ, Hauswirth MA. Inter- and intrapopulation studies of ancient humans. *Experientia* 1994;50:585-91.
- 38 Ginther C, Corach D, Penacino GA, Rey JA, Carnese FR, Hutz MH, et al. Genetic variation among the Mapuche Indians from the Patagonian region of Argentina: mitochondrial DNA sequence variation and allele frequencies of several nuclear genes. In: Pena SDJ, Chakraborty R, Epplen JT, Jeffreys AJ, editors. *DNA fingerprinting: state of the science*. Basel: Birkhauser Verlag; 1993. p. 211-9.
- 39 Catira-Bortolini M, Zago MA, Salzano FM, Silva-Junior WA, Luiz Bonatto S, Da Salva MCBO, et al. Evolutionary and anthropological implications of mitochondrial DNA variation in African Brazilian populations. *Hum Biol* 1997;69:141-59.
- 40 Santos SE, Ribetio-dos-Santos AK, Meyer D, Zago MA. Multiple founder haplotypes of mitochondrial DNA in Amerindians revealed by RFLP and sequencing. *Ann Hum Genet* 1996;60:305-19.
- 41 Ribetio-dos-Santos AK, Santos SE, Machado AL, Guapindaia V, Zago MA. Heterogeneity of mtDNA haplotypes in pre-Columbian natives of the Amazon Region. *Am J Phys Anthropol* 1996;101:29-37.
- 42 Easton RD, Merriwether DA, Crews DE, Ferrell RE. mtDNA variation in the Yanomami: evidence for additional New World founding lineages. *Am J Hum Genet* 1996;59:213-25.
- 43 Monsalve MV, Cardenas F, Guhl F, Delaney AD, Devine DV. Phylogenetic analysis of mtDNA lineages in South American mummies. *Ann Hum Genet* 1996;60:293-303.
- 44 Roberts DF, Soodyall H. Population ancestry on Tristan da Cunha: the evidence of the individual. In: Mascie-Taylor CGN, Boyce AJ, editors. *Molecular biology and human diversity*. Cambridge: Cambridge University Press; 1996. p. 196-204.
- 45 Sykes B, Leibold A, Low-Beer J, Tetzner S, Richards M. The origins of the Polynesians: an interpretation from mitochondrial lineage analysis. *Am J Hum Genet* 1995;57:1463-75.
- 46 Horai S, Murayama K, Hayasaka K, Matsubayashi S, Hattori Y, Fucharoen G, et al. mtDNA polymorphism in East Asian populations, with special reference to the peopling of Japan. *Am J Hum Genet* 1996;59: 579-90.
- 47 Melton T, Clifford S, Martinson J, Batzer M, Stoneking M. Genetic evidence for the proto-Austronesian homeland in Asia: mtDNA and nuclear DNA variation in Taiwanese aboriginal tribes. *Am J Hum Genet* 1998;63:204-12.
- 48 Mountain JL, Herbert JM, Bhattacharyya S, Underhill PA, Ottolenghi C, Gadgil M, et al. Demographic history of India and mtDNA-sequence diversity. *Am J Hum Genet* 1995;56:979-92.
- 49 Redd AJ, Takezaki N, Sherry ST, McGarvey ST, Sofro ASM, Stoneking M. Evolutionary history of the COII/tRNA^{Lys} intergenic 9 base pair deletion in human mitochondrial DNAs from the Pacific. *Mol Biol Evol* 1995;12:604-15.
- 50 Seo Y, Stradmann-Bellinghausen B, Rittner C, Takahama K, Schneider PM. Sequence polymorphism of mitochondrial DNA control region in Japanese. *Forensic Sci Int* 1998;97:155-64.
- 51 Comas D, Calafell F, Mateu E, Perez-Lezaun A, Bosch E, Martinez-Arias R, et al. Trading genes along the Silk Road: mtDNA sequences and the origin of Central Asian populations. *Am J Hum Genet* 1998;63:1824-38.
- 52 Torroni A, Schurr TG, Cabell MF, Brown MD, Neel JV, Larsen M, et al. Asian affinities and continental radiation of the four founding native American mtDNAs. *Am J Hum Genet* 1993;53:563-90.
- 53 Kolman CJ, Sambuughin N, Bermingham E. Mitochondrial DNA analysis of Mongolian populations and implications for the origin of New World founders. *Genetics* 1996;142:1321-34.
- 54 Murray-McIntosh R, Scrimshaw BJ, Hatfield PJ, Penny D. Testing migration patterns and estimating founding population size in Polynesia by using human mtDNA sequences. *Proc Natl Acad Sci U S A* 1998;95:9047-52.
- 55 van Holst Pellekaan S, Frommer S, Sned JA, Boettcher B. Mitochondrial control-region sequence variation in Aboriginal Australians. *Am J Hum Genet* 1998;62: 435-49.
- 56 Handt O, Richards M, Trommsdorff M, Kilger L, Simanannen J, Georgiev O, et al. Molecular genetic analyses of the Tyrolean Ice Man. *Science* 1994;264:1775-8.
- 57 Parson W, Parsons TJ, Scheithauer R, Holland MM. Population data for 101 Austrian Caucasian mitochondrial DNA D-loop sequences: application of mtDNA sequence analysis to a forensic case. *Int J Legal Med* 1998;111:124-32.
- 58 Calafell F, Underhill P, Tolun A, Angelcheva D, Kalaydjieva Z. From Asia to Europe: mitochondrial

- DNA sequence variability in Bulgarians and Turks. *Ann Hum Genet* 1996;60:35-49.
- 59 Miller KWP. Molecular genetic analysis of human populations in Orkney and the North Atlantic Region [dissertation]. Cambridge (UK): University of Cambridge; 1996.
- 60 Richards M, Corte-Real H, Forster P, Macaulay V, Wilkinson-Herbots H, Demaine A, et al. Paleolithic and Neolithic lineages in the European mitochondrial gene pool. *Am J Hum Genet* 1996;59:185-203.
- 61 Sajantila A, Lahermo P, Anttinen T, Lukka M, Sistonen P, Savontaus M-L, et al. Genes and languages in Europe: an analysis of mitochondrial lineages. *Genome Research* 1995;5:42-52.
- 62 Lahermo P, Sajantila A, Sistonen P, Lukka M, Aula P, Peltonen L, Savontaus ML. The genetic relationship between the Finns and the Finnish Saami (Lapps): analysis of nuclear DNA and mtDNA. *Am J Hum Genet* 1996;58:1309-22.
- 63 Lutz S, Weisser H-J, Heizmann J, Pollak S. Location and frequency of polymorphic positions in the mtDNA control region of individuals from Germany. *Int J Legal Med* 1998;111:67-77.
- 64 Baasner A, Schafer C, Junge A, Madea B. Polymorphic sites in human mtDNA control region sequences: population data and maternal inheritance. *Forensic Sci Int* 1998;98:169-78.
- 65 Pfeiffer H, Brinkmann B, Huhne J, Rolf B, Morris AA, Steighner R, et al. Expanding the forensic German mitochondrial DNA control region database: genetic diversity as a function of sample size and microgeography. *Int J Legal Med* 1999;112:291-8.
- 66 Krings M, Stone A, Schmitz RW, Krainitzki H, Stoneking M, Pääbo S. Neandertal DNA sequences and the origin of modern humans. *Cell* 1997;90: 19-30.
- 67 Di Rienzo A, Wilson AC. Branching pattern in the evolutionary tree for human mitochondrial DNA. *Proc Natl Acad Sci U S A* 1991;88:1597-601.
- 68 Barbujani G, Stenico M, Excoffier L, Nigro L. Mitochondrial DNA sequence variation across linguistic and geographic boundaries in Italy. *Hum Biol* 1996; 68:201-15.
- 69 Stenico ML, Nigro L, Bertorelle G, Calafell F, Capitano M, Corrain C, et al. High mitochondrial DNA sequence diversity in linguistic isolates of the Alps. *Am J Hum Genet* 1996;59:1363-75.
- 70 Francalacci P, Bertranpetit J, Calafell F, Underhill PA. Sequence diversity of the control region of mtDNA in Tuscany and its implication for the peopling of Europe. *Am J Phys Anthropol* 1996;100:443-60.
- 71 Dupuy BM, Olaisen B. mtDNA sequences in the Norwegian Saami and main populations. In: Carracedo A, Brinkmann B, Bär W, editors. *Advances in forensic haemogenetics*: 6. Berlin: Springer-Verlag; 1996. p. 23-5.
- 72 Hopwood A, Mannucci A, Sullivan K. DNA typing from human faeces. *Int J Legal Med* 1996;108:237-43.
- 73 Schurr TG, Sukernik RI, Starikovskaya YB, Wallace DC. Mitochondrial DNA variation in Koryaks and Ite' men: population replacement in the Okhotsk Sea-Bering Sea region during the Neolithic. *Am J Phys Anthropol* 1999; 108:1-39.
- 74 Gill P, Ivanov PL, Kimpton C, Piercy R, Benson N, Tully G, et al. Identification of the remains of the Romanov family by DNA analysis. *Nat Genet* 1994;6:130-5.
- 75 Bertranpetit J, Sala J, Calafell F, Underhill PA, Moral P, Comas D. Human mitochondrial DNA variation and the origin of the Basques. *Ann Hum Genet* 1995;59: 63-81.
- 76 Alonso A, Martin P, Albarran C, Garcia O, Sancho M. Rapid detection of sequence polymorphisms in the human mitochondrial DNA control region by polymerase chain reaction and single strand conformation analysis in mutation detection enhancement gels. *Electrophoresis* 1996;17:1299-301.
- 77 Salas A, Comas D, Lareu MV, Bertranpetit J, Carracedo A. mtDNA analysis of the Galician population: a genetic edge of European variation. *Eur J Hum Genet* 1998;6:365-75.
- 78 Martinez-Jarreta B, Prades A, Calafell F, Budowle B. Mitochondrial DNA HVI and HVII variation in a North-East Spanish population. *J Forensic Sci* 2000; 45:1162-3.
- 79 Dimo-Simonin N, Grange F, Taroni F, Brandt-Casadevall C, Mangin P. Forensic evaluation of mtDNA in a population from Southwest Switzerland. *Int J Legal Med* 2000;113:89-97.
- 80 Pult I, Sajantila A, Simonainen J, Georgiev O, Schaffner W, Pääbo S. Mitochondrial DNA sequences from Switzerland reveal striking homogeneity of European populations. *Biological Chemistry Hoppe-Seyler* 1994;375: 837-40.
- 81 Comas D, Calafell F, Mateu E, Perez-Lezaun A, Bertranpetit J. Geographic variation in human mitochondrial DNA control region sequence: the population history of Turkey and its relationship to the European populations. *Mol Biol Evol* 1996;13:1067-77.
- 82 Anderson S, Bankier AT, Barrell BG, de Bruijn MHL, Coulson AR, Drouin J, et al. Sequence and organization of the human mitochondrial genomes. *Nature* 1981; 290:457-65.
- 83 Piercy R, Sullivan KM, Benson N, Gill P. The application of mitochondrial DNA typing to the study of white Caucasian genetic identification. *Int J Legal Med* 1993;106:85-90.
- 84 Thomas MG, Cook CE, Miller KW, Waring MJ, Hagelberg E. Molecular instability in the COII-tRNA^{Lys} intergenic region of the human mitochondrial genome: multiple origins of the 9-bp deletion and heteroplasmy for expanded repeats. *Philos Trans R Soc Lond B Biol Sci* 1998;353:955-65.
- 85 Hagelberg E, Goldman N, Lio P, Whelan S, Schiefenhovel W, Glegg JB, et al. Evidence for mitochondrial DNA recombination in a human population of island Melanesia. *Proc R Soc Lond B Biol Sci* 1999; 266:485-92.
- 86 United Nations. Terminology Bulletin No.347/Rev.1: Country Names. New York (NY): United Nations Office of Conference and Support Services; 1997. p. 1-50.
- 87 Shields GF, Schmiechen AM, Frazier BL, Redd A, Voevoda MI, Reed JK, et al. mtDNA sequences suggest a recent evolutionary divergence for Beringian and northern North American populations. *Am J Hum Genet* 1993;53:549-62.

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