Phylogeny of Mitochondrial DNA Macrohaplogroup N in India, Based on Complete Sequencing: Implications for the Peopling of South Asia

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To resolve the phylogeny of the autochthonous mitochondrial DNA (mtDNA) haplogroups of India and determine the relationship between the Indian and western Eurasian mtDNA pools more precisely, a diverse subset of 75 macrohaplogroup N lineages was chosen for complete sequencing from a collection of >800 control-region sequences sampled across India. We identified five new autochthonous haplogroups (R7, R8, R30, R31, and N5) and fully characterized the autochthonous haplogroups (R5, R6, N1d, U2a, U2b, and U2c) that were previously described only by first hypervariable segment (HVS-I) sequencing and coding-region restriction-fragment–length polymorphism analysis. Our findings demonstrate that the Indian mtDNA pool, even when restricted to macrohaplogroup N, harbors at least as many deepest-branching lineages as the western Eurasian mtDNA pool. Moreover, the distribution of the earliest branches within haplogroups M, N, and R across Eurasia and Oceania provides additional evidence for a three-founder-mtDNA scenario and a single migration route out of Africa.

Introduction

The “population genomics” era has emerged in the research of human mtDNA (Hedges 2000; Richards and Macaulay 2001) by utilization of complete or nearly complete mtDNA sequences to infer the prehistoric dispersal of modern humans and the phylogeny of the major mtDNA lineages in Europe, Africa, America, Oceania (Australia and Papua New Guinea), and East Asia (Ingman et al. 2000; Finnilä et al. 2001; Maca-Meyer et al. 2001, 2003; Torroni et al. 2001; Derbeneva et al. 2002*b*; Herrnstadt et al. 2002, 2003; Ingman and Gyllensten 2003; Kong et al. 2003; Mishmar et al. 2003; Reidla et al. 2003). However, complete phylogenetic information was hitherto not available for South Asia and for India in particular, an important area that served as a major corridor of modern human dispersal out of Africa (Cann 2001) and that hosts a diverse conglomerate of people with different morphological, genetic, cultural, and linguistic characteristics. Quite a number of mtDNA studies that focus on the first hypervariable segment (HVS-I) of the control region have been applied to various Indian populations and have provided some insights into the genetic structure of the populations in this area (Kaur et al. 2002; Basu et al. 2003; Kivisild et al. 2003*a*; Roy et al. 2003 and references therein). In addition to India-specific M subhaplogroups (i.e., M2, M3, M4, M5, and M6), some autochthonous haplogroups, including U2a, U2b, U2c, and many unclassified lineages within the nested macrohaplogroups R and N, have been observed in Indian populations (Passarino et al. 1996; Kivisild et al. 1999*a*, 1999*b*, 2003*a*, 2003*b*; Bamshad et al. 2001; Basu et al. 2003; Quintana-Murci et al. 2004). However, since these studies were based mainly on HVS-I plus a few coding-region RFLPs, none of those haplogroups had yet been fully characterized. Moreover, some western Eurasian haplogroups also occur in India at low frequencies (Passarino et al. 1996; Kivisild et al. 2003*b*; Quintana-Murci et al. 2004)—or even at high frequencies, in particular regions (Forster et al. 2002). Although rather detailed phylogenies of western Eurasian mtDNA lineages have been obtained by Finnilä et al. (2001), Maca-Meyer et al. (2001), and Herrnstadt et al. (2002) (which were, however, in minor conflict with one another), no Indian counterpart was hitherto available for comparison. Although most of the mtDNA line-

Received August 4, 2004; accepted for publication September 8, 2004; electronically published October 1, 2004.

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0002-9297/2004/7506-0004$15.00

ages of western Eurasian ancestry must have a rather recent entry date (<10 thousand years ago [kya] [Kivisild et al. 1999*a*]), it is not clear whether one would also have to consider some early offshoots of the western Eurasian mtDNA phylogeny that are specific to India and neighboring regions. To resolve these problems and prepare the grounds for future extensive phylogeographic screening, it is necessary to contrast the mtDNA phylogeny of Indians with that of western Eurasians, on the basis of complete sequencing executed on a diverse collection of mtDNAs.

Complete sequence information from India is also urgently needed in the forensic field. In the past, forensic studies have predominantly described the general pattern of mtDNA control sequence variation in western Eurasian and East Asian individuals (Allard et al. 2002, 2004). Recently, however, coding-region SNPs in European populations have increasingly been utilized in forensics, especially for discriminating frequent control-region haplotypes that are poorly characterized by HVS-I and -II alone (Brandstätter et al. 2003; Coble et al. 2004; Quintáns et al. 2004). Similar studies of the mtDNA variation in other (sub)continents are still pending.

Complete mtDNA information for South Asia is also highly relevant to medical studies of mitochondrial diseases. To perform systematic studies of the major mitochondrial diseases (Leber hereditary optic neuropathy [LHON]; mitochondrial encephalomyopathy, lactic acidosis, and strokelike episodes [MELAS]; etc.) in patients with South Asian matrilineal ancestries, at least a basal outline of the total mtDNA phylogeny in this subcontinent is indispensable—see, for example, articles by Rocha et al. (1999) and Kong et al. (2004) for studies involving African, European, and East Asian haplogroup backgrounds.

Since control-region sequences of the Asian-specific macrohaplogroup M can hardly be confused with western Eurasian sequences (except for subhaplogroup M1 [Quintana-Murci et al. 1999]), we focused on macrohaplogroup N in India, which appeared to be totally missing or at least severely underrepresented in all previous worldwide studies of complete mtDNA variation (Ingman et al. 2000; Maca-Meyer et al. 2001; Cavalli-Sforza and Feldman 2003; Mishmar et al. 2003).

Material and Methods

Sampling

In the present study, 75 mtDNA lineages were selected from >800 samples across India, with the goal that at least one representative was chosen from each western Eurasian haplogroup and each group of previously unclassified haplotypes (authors' unpublished data). Samples were from the following populations: Reddy (R) and Thogataveera (T) from Andhrapradesh, South India; Bhargava (A), Chaturvedi (B), and other Brahmin (C) from Uttarpradesh, North India; and Rajbhansi from West Bengal (SW) and the Khasi population from Meghalaya (S), both located in Northeast India.

DNA Amplification and Sequencing

DNA was amplified using 15 pairs of primers (Kong et al. 2003) (table 1). After being purified on spin columns (Watson BioTechnologies), the 15 overlapping fragments were sequenced by means of PCR primers and 47 internal primers (Kong et al. 2003) (table 2) and BigDye Terminator chemistry (Applied Biosystems). Sequencing was performed on a 3700 DNA Analyzer (Applied Biosystems), and the resulting sequences were handled with the DNASTAR software (DNASTAR). Mutations were scored relative to the revised Cambridge Reference Sequence (rCRS [Andrews et al. 1999]). The 75 complete sequences have been submitted to GenBank (accession numbers AY713976–AY714050).

Quality Control

To avoid the kinds of errors and artifacts that have affected some earlier analyses of mtDNA coding-region variation, we utilized a strict quality-control procedure, similar to that of Kong et al. (2003). First, each base was sequenced from at least two independent amplifications. Second, all private mutations (i.e., mutations on a terminal branch of a single sequence) and all indels (insertions and deletions), as well as some seemingly unusual recurrent substitutions (such as transition 16266

Table 1

Primer Pairs for Amplification and Sequencing

Light mtDNA Strand		Heavy mtDNA Strand	
Primer	Location (5′→3′) in rCRS	Primer	Location (5′→3′) in CRS
L394	375–394	H1782	1801–1782
L1466	1445–1466	H3054	3074–3054
L2796	2777–2796	H3674	3693–3674
L3644	3625–3644	H5099	5118–5099
L4887	4866–4887	H5832	5851–5832
L5781	5762–5781	H6899	6918–6899
L6869	6850–6869	H7990	8009–7990
L7882	7861–7882	H9212	9231–9212
L9198	9181–9198	H10660	10679–10660
L10519	10498–10519	H11689	11708–11689
L11338	11319–11338	H12603	12623–12603
L12334	12315–12334	H13666	13685–13666
L13612	13593–13612	H14591	14610–14591
L14575	14556–14575	H16048	16067–16048
L15996	15975–15996	H408	429–408

NOTE.—The annealing temperature for all primer pairs was 53°C.

Table 2

The Inner Primers for the Complete Sequencing

Primer[a]	Location (5′→3′) in rCRS
L713	696–712
H902	922–902
L1156	1138–1156
H1172	1190–1172
L2025	2004–2025
H2053	2073–2053
L2415	2395–2415
H2426	2444–2426
L3179	3160–3179
H3274	3293–3274
L4210	4189–4210
H4227	4247–4227
L4499	4480–4499
H4792	4813–4792
L5278	5259–5278
H5442	5461–5442
L6337	6318–6337
H6367	6387–6367
L7356	7337–7356
H7406	7427–7406
L8215	8196–8215
H8345	8366–8345
L8581	8563–8581
H8861	8882–8861
L9794	9774–9794
H9848	9867–9848
L10170	10147–10170
H10356	10376–10356
L11004	10985–11004
H11081	11100–11081
L11718	11692–11718
H11944	11963–11944
L12028	12008–12028
H12341	12361–12341
L12572	12553–12572
H12878	12897–12878
L13049	13031–13049
H13124	13143–13124
L14054	14035–14054
H14186	14206–14186
L14989	14970–14989
H15086	15105–15086
L15391	15372–15391
H15400	15419–15400
L16209	16190–16209
H16498	16517–16498
L29	8–29

[a] "L" and "H" refer to light and heavy strands of mtDNA, respectively.

in A65 and B53 and transition 15326 in A165 and S4), were confirmed by independent PCR and sequencing.

Database Comparison

To differentiate between the Indian and western Eurasian mtDNA lineages, it is necessary to combine all published sequences sampled from western Eurasia (Ingman et al. 2000; Finnilä et al. 2001; Maca-Meyer et al. 2001; Rose et al. 2001; Taylor et al. 2001; Derbeneva et al. 2002*a*; Herrnstadt et al. 2002, 2003; Ingman and Gyllensten 2003; Mishmar et al. 2003; Reidla et al. 2003; Coble et al. 2004) and compare them with the Indian sequences. To clearly display and distinguish these lineages from our Indian samples and avoid confusion with haplogroup designation, we refer to particular samples from the articles cited above by use of the initials (first name and surname) of the first author as a prefix—that is, MI, SF, NM, GR, RT, OD, CH, IG, DM, MR, and MC, followed by "#" and the original sample code, albeit in lowercase instead of capital letters.

Haplogroup Nomenclature

We adopt the nomenclature system of Richards et al. (1998). For new basal subhaplogroups of N and R, we would reserve the codes N5–N8, R5–R8, and R30–R39 for South Asian mtDNAs. Although we regard it as admissible to widen the definition of some previously named haplogroups in light of new complete sequence information, the correction of haplogroup names (such as "J2a" for the incorrect "J1a") is done with the understanding that the obsolete names should not be recycled and are thus blocked henceforth to avoid misunderstanding.

Results

Autochthonous Indian Haplogroups

In our study, a number of novel haplogroups have emerged and then been named according to the rules of the notational system (see the "Material and Methods" section). The new haplogroup N5 is characterized by (at most) six transitions in the coding region (at sites 1719, 5063, 7076, 9545, 11626, and 13434) and two in the control region (at sites 16111 and 16311), as supported by lineage R148 and the authors' unpublished data. The two lineages T1 and C35, which share seven coding-region mutations (at sites 1442, 6248, 9051, 9110, 10289, 13105, and 13830) and four control-region mutations (at sites 16260, 16261, 16319, and 16362), constitute a new subhaplogroup of haplogroup R, designated as "R7." Another new haplogroup, R8, is recognizable by five specific mutations (at sites 2755, 3384, 7759, 9449, and 13215). We tentatively group five R-derived branches into haplogroup R30 on the basis of the shared 8584 transition and combine three branches with a common 15884 transition into haplogroup R31. Since recurrent mutations have been observed at each of these sites, this classification needs to be corroborated by future screening for related lineages.

With the present mtDNA phylogeny, we can redefine or revise the definitions of several haplogroups that were previously characterized only by control-region sequence and/or coding-region RFLPs. Haplogroup N1d is broadened by requiring only two control-region mutations (16301 and 16356) plus one coding-region mutation, 953 (recognizable by RFLP site −951*Mbo*I [Quintana-Murci et al. 2004]). Haplogroup U2b is further characterized by mutations 146, 2706, 5186T, 12106, and 13149 in addition to 15049 (i.e., −15047*Hae*III [Quintana-Murci et al. 2004]). Haplogroup U2c is redefined by requiring five mutations: 152, 5790A, 14935, 15061, and 16234, of which mutations 5790A and 15061 were previously recognized by RFLP typing (i.e., as +5789*Tag*I and −15060*Mbo*I [Quintana-Murci et al. 2004]). The transition at 8023 (recognized by +8020*Mbo*I/+8022*Taq*I [Quintana-Murci et al. 2004]), shared by our sample R94 and samples from Quintana-Murci et al. (2004), may characterize a major subbranch of U2c. In addition to having mutations at 8594 (corresponding to −8592*Mbo*I) and 16304 (Quintana-Murci et al. 2004), haplogroup R5 is further characterized by another three mutations, at 10754, 14544, and 16524. It is not clear at this point whether the 16266 transition defines R5 as a whole or just the main subbranch of R5, since 16266 seems to be prone to back mutation in this haplogroup. A similar caveat holds for hypervariable site 16129 in haplogroup R6. Finally, it has now become evident that U2a is defined only by the rare transversion 16206C (Kivisild et al. 1999*b*), and no additional motif is found in the coding region.

Haplogroups Shared by Indians and Western Eurasians: Reappraisal of the Western Eurasian mtDNA Phylogeny

Many of the Indian mtDNA lineages belonging to typical western Eurasian haplogroups (such as I, H, V, J1, T2, K, U2e, U7, and U5a) can be integrated into the western Eurasian phylogeny unambiguously (fig. 1). Some haplogroups, however, have to be redefined in order to accommodate deep-rooted lineages, which were newly identified in our Indian samples. For instance, haplogroup I1 is broadened by requiring only two mutations, 6734 and 16311, and embraces one subbranch, designated as "I1a" (the former haplogroup I1 [Herrnstadt et al. 2002]), which is further characterized by the 3447 and 8616T mutations. The definition of haplogroup W1 is also broadened by requiring only the 7864 transition. Then, three subhaplogroups can be identified: W1a and W1b (corresponding to the former haplogroups W1 and W2, respectively [Finnilä et al. 2001]) and W1c (defined by mutation 14148). A new haplogroup, N2, was erected to capture the sister lineage of haplogroup W found in the Mansi (Derbeneva et al. 2002*a*). It turns out that haplogroup U3 has only four characteristic mutations (150, 14139, 15454, and 16343), and its main subbranch, formerly identified as "U3" by Richards et al. (2000) and Herrnstadt et al. (2002), is designated as "U3a" here. Our study also fully characterized some haplogroups that were previously described by use of control-region data and RFLP analysis, such as N1, (pre-HV)1, HV2, J1b, J1b1, U1, R1, and R2 (Richards et al. 1998, 2000; Macaulay et al. 1999; Quintana-Murci et al. 2004), and identified a number of subhaplogroups: N1b1, V1, V1a, V2, V2a, J1c, J1c1, J2a, J2b, T1a, T1b, U2d, U5a1, K1a, K1a1, K1a2, K1b, K1c, and K2a (fig. 1). In particular, the former haplogroup J1a (Richards et al. 1998), however, is proven to be one subbranch of J2 on the basis of coding-region sequences (Finnilä et al. 2001; Rose et al. 2001; Herrnstadt et al. 2002, 2003) and is therefore renamed "J2a" here (thus retaining the suffix "a"). Since virtually all haplogroup T1b sequences bearing the mutational motif 16126-16189-16243-16294 (Richards et al. 2000) are also mutated at 16163, we assume that 16163 is a basal mutation of T1; therefore, the T1b sequences from Finnilä et al. (2001) seem to have experienced a back mutation at this site. The provisional definition of haplogroup U2d was inferred from the coding-region mutations reported in patient 3 from the study by Crimi et al. (2002) and from the control-region mutations in some other samples (Richards et al. 2000; Bulayeva et al. 2003; Comas et al. 2004; Quintana-Murci et al. 2004). This haplogroup seems to have a predominantly Near Eastern distribution and might share the 16189 mutation with U2e by ancestry.

Discussion

Reconciliation of the Conflicts among Published Western Eurasian Data Sets

With the help of the basal western Eurasian phylogeny constructed here (fig. 1), some obvious conflicts among different data sets could be reconciled. Take the data of Finnilä et al. (2001) as an example. There, transition 12414 had likely been transferred from the haplogroup W sequences to the haplogroup X sequences by mistake. The 10550 transition (characteristic of haplogroup K) had been omitted from all K1 sequences and the 3447 transition from all but one I1 sequence (i.e., SF#104). In other data sets, the typical shortcomings include random oversights of mutations (e.g., at sites 8701, 12308, and 12372 in the haplogroup U1a lineage IG#k4b) or recombination by sample mix-up in singular cases. Particularly problematic are the early data of Maca-Meyer et al. (2001), which were generated through manual sequencing. Many of their western Eurasian lineages lack one to three mutations; the haplogroup I lineage might even have received the 15452A transversion from some haplogroup JT lineage through sample mix-up. We have therefore made only limited use of these data in esti-

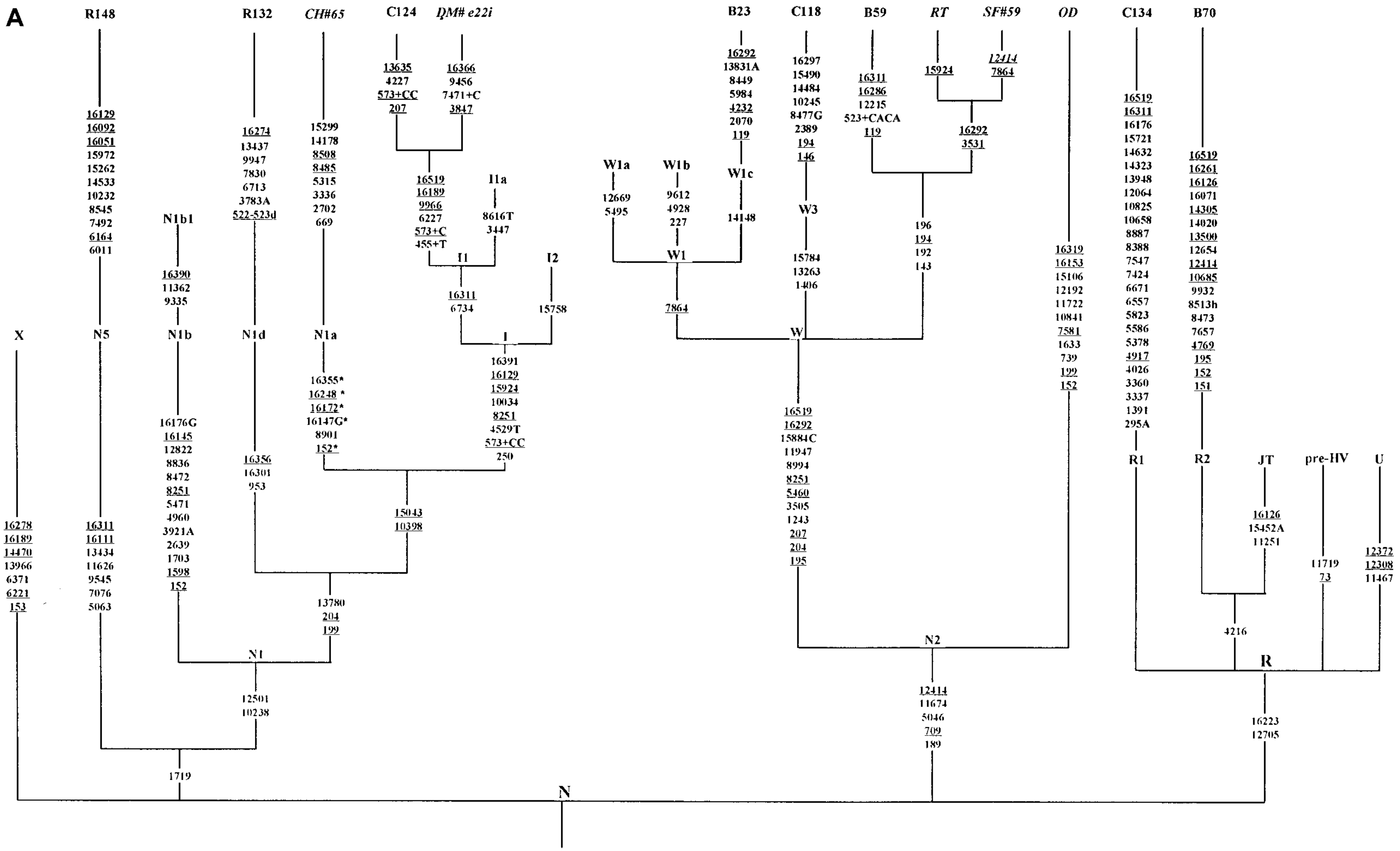
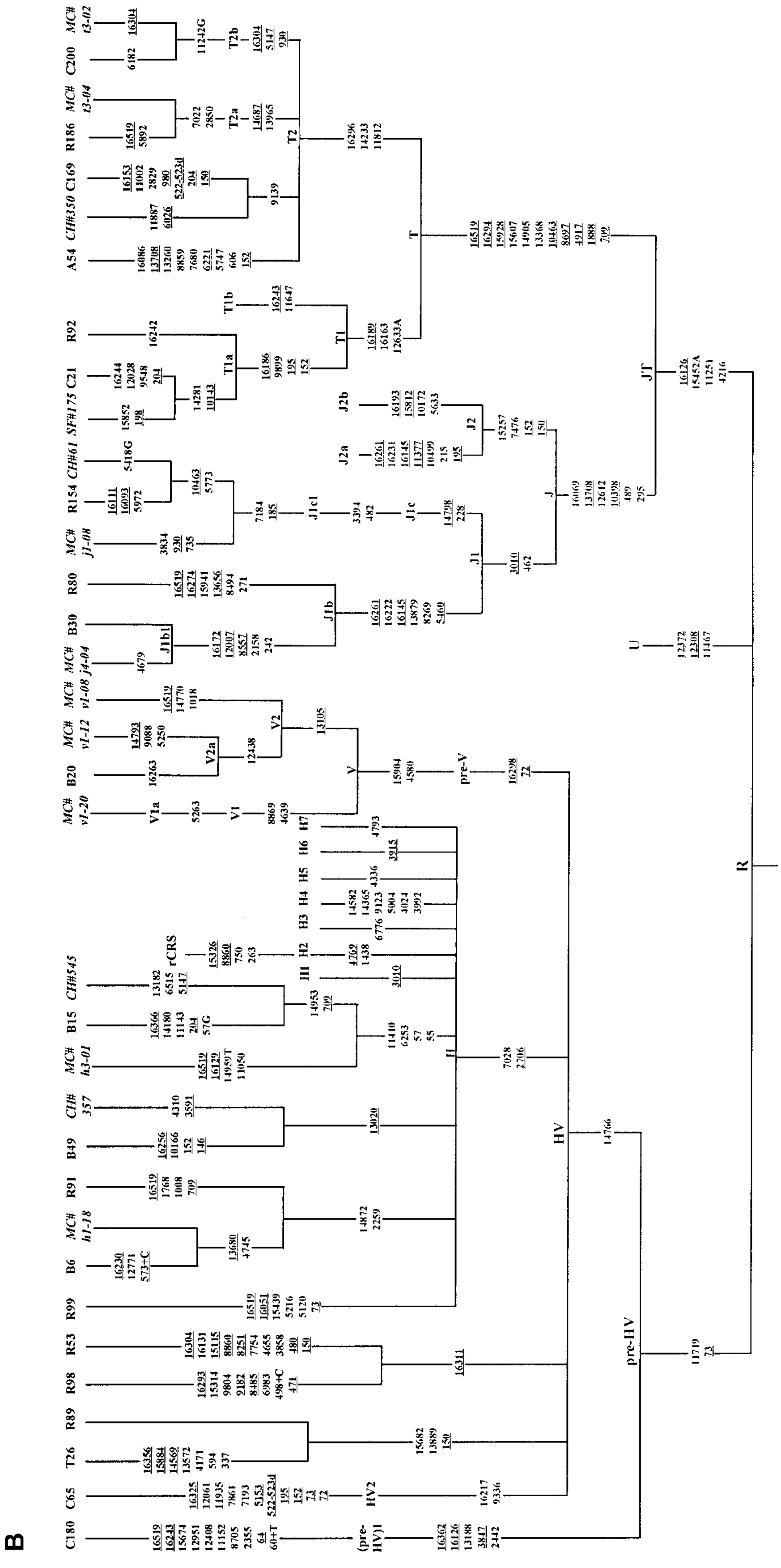


Figure 1 Phylogenetic tree of 75 Indian complete mtDNA sequences. Parts A, B, C, and D of the figure are the phylogenies of the N, pre-HV and JT, U, and Indian autochthonous R haplogroups, respectively. Mutations are scored relative to the rCRS (Andrews et al. 1999). Indian populations: A = Bhargava, B = Chaturvedi, C = Brahmin, R = Reddy, S = Khasi, SW = Rajbhansi, T = Thogataveera. Twenty-five additional complete sequences were taken from the literature (Finnilä et al. 2001; Maca-Meyer et al. 2001; Taylor et al. 2001; Derbeneva et al. 2002*a*; Herrnstadt et al. 2002, 2003; Ingman and Gyllensten 2003; Mishmar et al. 2003; Coble et al. 2004), and we referred to particular samples from these articles by SF, NM, RT, OD, CH, IG, DM, and MC, respectively, followed by "#" and the original sample code. Suffixes A, C, G, and T indicate transversions; "d" denotes a deletion, and a plus sign (+) denotes an insertion; recurrent mutations are underlined; "h" indicates heteroplasmy; and italics highlight likely oversights. Mutations in the single reported haplogroup N1a lineage labeled by an asterisk (*) are our reconstruction. The linkage between coding- and control-region mutations in the new haplogroup U2d is tentative. Since the variation at 16519 is extremely hypervariable, only the most parsimonious solution is offered here. For haplogroups H and U5, see articles by Loogväli et al. (2004) and Tambets et al. (2004), respectively.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C180
C65
T26
R89
R98
R53
R99
B6
MC# h1-18
R91
B49
CI# 357
MC# h3-01
B15
CH#545
rCRS
MC# v1-20
B20
MC# v1-12
MC# v1-08
MC# j4-04
B30
R80
MC# j1-08
R154
CH#61
SF#175
C21
R92
A54
CH#350
C169
R186
MC# t3-04
C200
MC# t3-02
16519 16243 15674 12951 12408 11152 8705 2355 64 60+T
(pre-HV)1
16362 16126 13188 3847 2442
16325 12061 11935 7861 7193 5153 522-523d 195 152 73 72
HV2
16217 9336
16356 15884 14569 13572 4171 594 337
15682 13889 150
16293 15314 9804 2182 8485 6983 498+C 471
16304 16131 15115 8860 8251 7754 4655 3858 480 150
16311
16519 16051 15439 5216 5120 73
16230 12771 573+C
13680 4745
16519 1768 1008 709
14872 2259
16256 10166 152 146
4310 3591
13020
16519 16129 14959T 11050
16366 14180 11143 204 57G
13182 6515 5147
14953 709
11410 6253 57 55
H
15326 8860 750 263
H1 H2 H3 H4 H5 H6 H7
3010
4769 1438
6776
14582 14365 9123 5004 4024 3992
4336
3915
4793
7028 2706
HV
14766
pre-HV
11719 73
V1a
5263
V1
8869 4639
16263
14793 9088 5250
V2a
12438
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V2
13105
V
15904 4580
pre-V
16298 72
4679
J1b1
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J1b
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J1c1
3394 482
J1c
14798 228
J1
3010 462
J2a
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J2b
16193 15812 10172 5633
J2
15257 7476 152 150
J
16069 13708 12612 10398 489 295
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T1a
16186 9899 195 152
T1b
16243 11647
T1
16189 16163 12633A
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11887 6026
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9139
16519 5892
7022 2850
T2a
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6182
16304
11242G
T2b
16304 5147 930
T2
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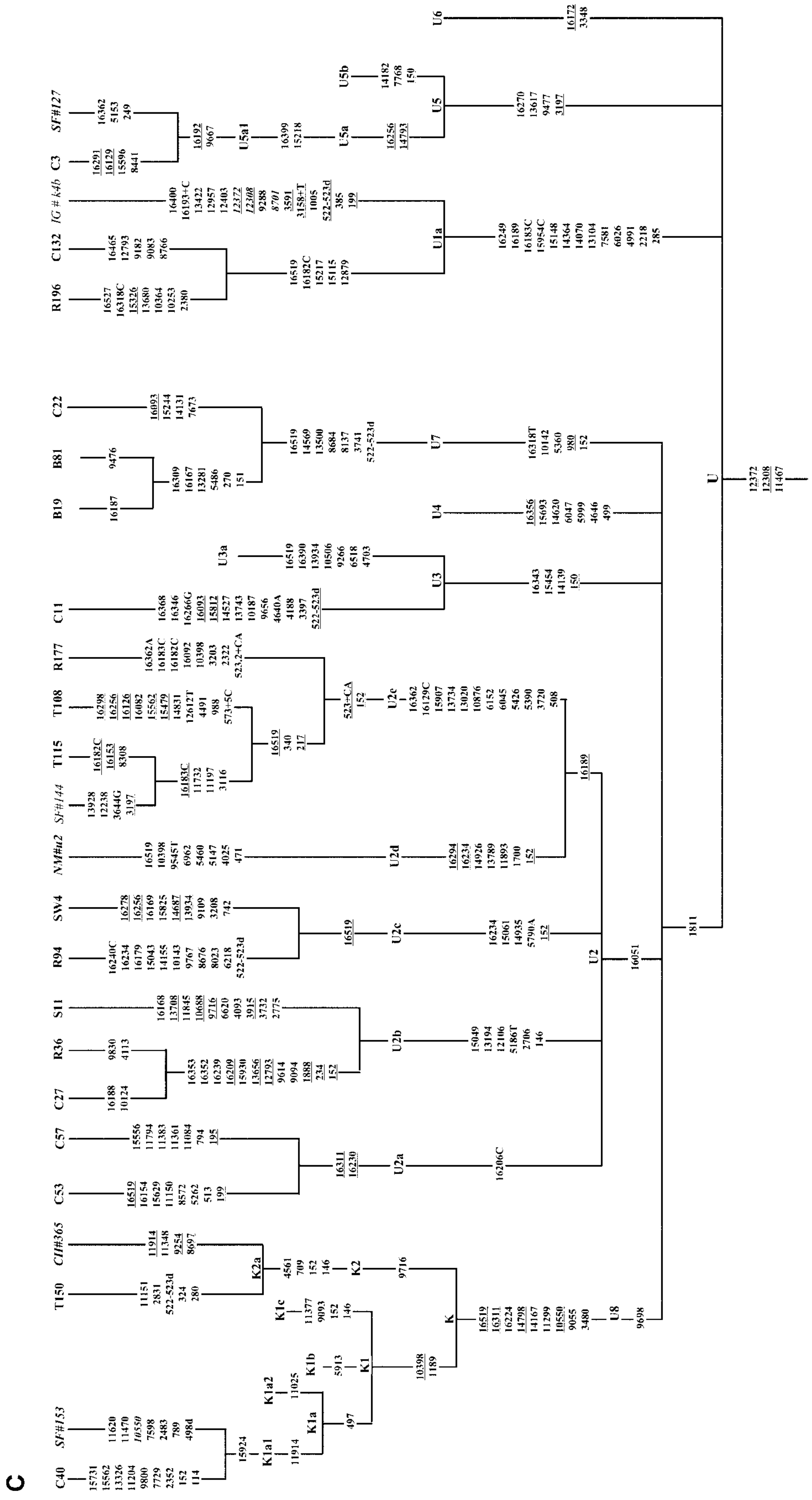
R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K
U8
U2a
U2b
U2c
U2d
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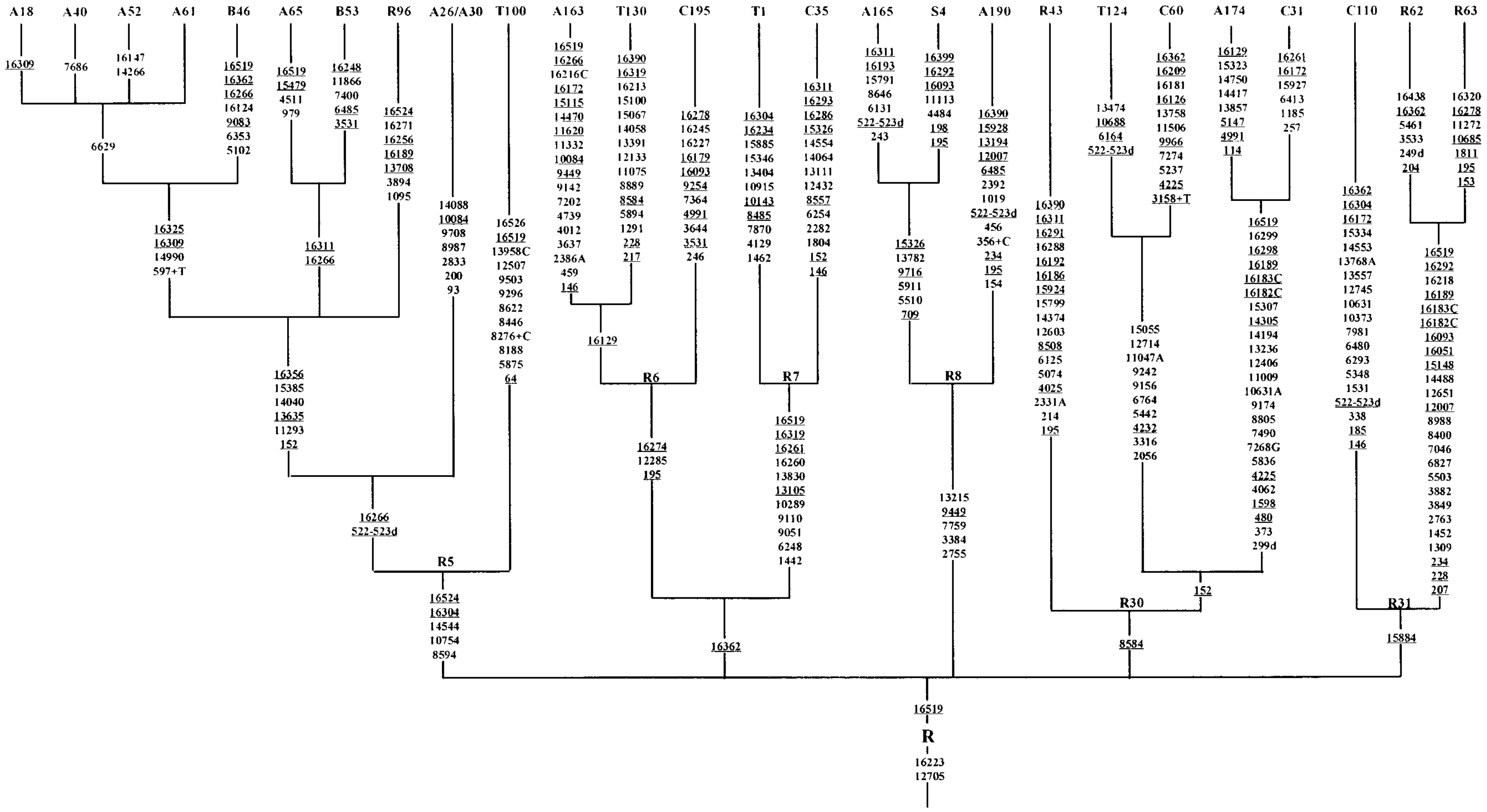
U5b
U5
U6
U

D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A40
A52
A61
B46
A65
B53
R96
A26/A30
T100
A163
T130
C195
T1
C35
A165
S4
A190
R43
T124
C60
A174
C31
C110
R62
R63
16309
7686
16147 14266
16519 16362 16266 16124 9083 6353 5102
16519 15479 4511 979
16248 11866 7400 6485 3531
16524 16271 16256 16189 13708 3894 1095
14088 10084 9708 8987 2833 200 93
16526 16519 13958C 12507 9503 9296 8622 8446 8276+C 8188 5875 64
16519 16266 16216C 16172 15115 14470 11620 11332 10084 9449 9142 7202 4739 4012 3637 2386A 459 146
16390 16319 16213 15100 15067 14058 13391 12133 11075 8889 8584 5894 1291 228 217
16278 16245 16227 16179 16093 9254 7364 4991 3644 3531 246
16304 16234 15885 15346 13404 10915 10143 8485 7870 4129 1462
16311 16293 16286 15326 14554 14064 13111 12432 8557 6254 2282 1804 152 146
16311 16193 15791 8646 6131 522-523d 243
16399 16292 16093 11113 4484 198 195
16390 15928 13194 12007 6485 2392 1019 522-523d 456 356+C 234 195 154
16390 16311 16291 16288 16192 16186 15924 15799 14374 12603 8508 6125 5074 4025 2331A 214 195
13474 10688 6164 522-523d
16362 16209 16181 16126 13758 11506 9966 7274 5237 4225 3158+T
16129 15323 14750 14417 13857 5147 4991 114
16261 16172 15927 6413 1185 257
16362 16304 16172 15334 14553 13768A 13557 12745 10631 10373 7981 6480 6293 5348 1531 522-523d 338 185 146
16438 16362 5461 3533 249d 204
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6629
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16311 16266
16356 15385 14040 13635 11293 152
16266 522-523d
R5
16524 16304 14544 10754 8594
16129
R6
16274 12285 195
R7
16519 16319 16261 16260 13830 13105 10289 9110 9051 6248 1442
16362
15326 13782 9716 5911 5510 709
R8
13215 9449 7759 3384 2755
15055 12714 11047A 9242 9156 6764 5442 4232 3316 2056
16519 16299 16298 16189 16183C 16182C 15307 14305 14194 13236 12406 11009 10631A 9174 8805 7490 7268G 5836 4225 4062 1598 480 373 299d
152
R30
8584
16519 16292 16218 16189 16183C 16182C 16093 16051 15148 14488 12651 12007 8988 8400 7046 6827 5503 3882 3849 2763 1452 1309 234 228 207
R31
15884
16519
R
16223 12705

mating and representing the basal western Eurasian mtDNA variation. As for the coding-region data published (or corrected) more recently (Herrnstadt et al. 2002, 2003; Mishmar et al. 2003; Coble et al. 2004), the congruence in the basal parts of the phylogeny is assured.

The Phylogeny of mtDNA Haplogroup N in India

The total phylogeny of all mtDNA lineages found in India is partially interwoven with the western Eurasian mtDNA phylogeny but includes numerous basal branches that are absolutely absent in Europe. These findings, first demonstrated by Kivisild et al. (1999*a,* 1999*b*) on the basis of HVS-I data, stand the test of complete sequence information. In India, a minority of lineages are of western Eurasian ancestry; the ancestral population probably entered Pakistan and India either from the west (Iran) or the north (via Central Asia) (see Quintana-Murci et al. 2004). In the opposite direction, gene flow was apparently more limited and not very far-reaching: for example, in the data provided by Quintana-Murci et al. (2004), we can find 4 (i.e., 1 haplogroup R5, 1 N5, and 2 M lineages) of 42 mtDNA lineages from (southern) central Iran but only a single lineage (from macrohaplogroup M) of 95 in northern and western Iran that belongs to (potentially) autochthonous South Asian haplogroups. Only one R5 lineage is found in the Iraqi sample of Al-Zahery et al. (2003). Farther to the (north)west, in the Caucasus area and Turkey, such lineages are virtually absent. In the Central Asian data set of Comas et al. (2004), only 6 of 232 lineages belong to South Asian haplogroups (2 from U2a, 1 from U2c, 2 from R5, and possibly 1 from M4). This clear-cut phylogeographic pattern underscores the autochthonous status of the frequent Indian haplogroups U2a, U2b, U2c, and R5–R7. For the less frequent haplogroups (R8, R30, R31, N1d, and N5), comparative HVS-I information would suggest their indigenous status, too, but focused searches of neighboring mtDNA pools by screening characteristic coding-region sites are necessary to confirm this.

Recognition of Indigenous Indian Haplogroup N Lineages

In the study of the mtDNA of patients with mitochondrial diseases whose matrilines are of unknown continental origin, the total worldwide complete mtDNA pool is necessary for comparison. When MITOMAP is consulted for mutation status, mtDNA lineages from South Asia would inevitably go unidentified, and many of their characteristic mutations would be shunted into the category of “novel” mutations. Then, some of these seemingly novel mutations, which might even be regarded as candidates for pathological mutations, are, in fact, specific to new haplogroups. For instance, Pulkes et al. (2003) analyzed 13 mitochondrial genomes from patients with classic mitochondrial phenotypes but reported only those “novel” mutations that were not listed in MITOMAP at the time. Even with respect to this restricted information, five of those mtDNA lineages can then be classified unambiguously here: the mtDNA types of patients 3, 5, and 15 belong to western Eurasian haplogroups (T2a, I1a, and (pre-HV)1, respectively), whereas those of patients 7 and 10 are of South Asian ancestry. Indeed, the mtDNA of patient 7 harbors the three transitions at 8594, 10754, and 14544, which are characteristic of haplogroup R5; moreover, the 8987 and 9708 mutations indicate some closer relationship with haplotype A26/A30 from our Indian sample. Patient 10 carries four specific mutations (3384, 7759, 9449, and 13215) that define haplogroup R8.

When only HVS-I data together with RFLP results (for the coding region) are available, one can nevertheless often predict haplogroup status by near-matching with the haplogroup motifs. Take the haplogroup N data from Kivisild et al. (2003*a*), for example. We can assign their haplotype 39 to N5 and haplotypes 45 and 46 to R7 without ambiguity. Further, haplotypes 40, 41, and 48 may belong to haplogroup R6, whereas haplotype 42 may belong to R5. Therefore, we are optimistic that our basal phylogeny of haplogroup N in South Asia covers most of the Indian autochthonous lineages. However, we have to concede that there may still be some minor haplogroups that remain to be determined for the coding region.

In the absence of any coding-region information, one can still predict (sub)haplogroup status for the vast majority of Indian HVS-I and HVS-II sequences from haplogroup N via (near-)matching with well-classified haplotypes. For instance, the data of Forster et al. (2002) are conspicuous for their extremely high proportion of haplogroup U1a lineages. This haplogroup status can be confirmed in view of the presence of the full U1a motif (i.e., 16189-16249-73-263-285). We arrive at the same count of 16 sequences belonging to haplogroup U2 as do Forster et al. (2002): namely, five to U2a, seven to U2b, and four to U2c. Then, five lineages are members of R5 (#133, #152, #221, #63b, and #25), two of R6 (#77 and #78), one of R8 (#141), and nine of R31 (#84, #101, #107, #117, #135, #140, #168, #200, and #201). Only ~10 potential haplogroup R lineages cannot be classified unambiguously (some of which may belong to R8). Haplogroups N5 and N1d do not seem to appear in these data.

Different Layers of mtDNA Haplogroups in India

Since there is thus no evidence that the offshoots R5, R6, R7, R8, R30, and R31 arose west of the Indian subcontinent, one can approximately calculate the time

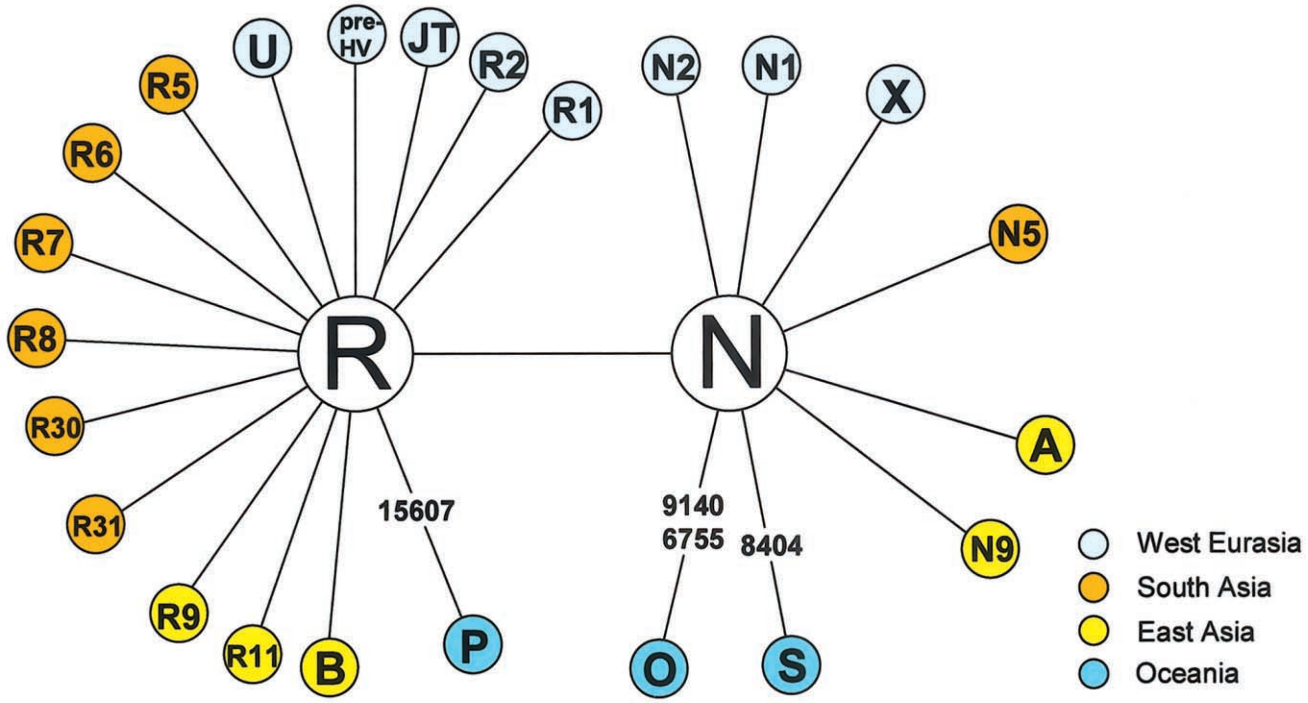

Figure 2 Subcontinental ancestry of the most basal Eurasian/Oceanian branches of the mtDNA phylogeny. South Asian and western Eurasian haplogroups are defined as described in the present study; for East Asian haplogroups, see Kong et al. (2003); for haplogroup P, see Forster et al. (2001); O and S are newly defined here on the basis of the data from Ingman and Gyllensten (2003). Potential coalescences based only on a single highly variable site are disregarded.

of the arrival of the predicted founder R haplotype in India by stipulating that all of the variation seen in this part of the phylogeny arose in situ. Then, we estimate the age of the root type of R on the basis of these lineages, in the same way as Kong et al. (2003), by assuming the rate of one substitution (other than a deletion or insertion) in the coding region per 5,140 years (Mishmar et al. 2003). This yields an age (mean ± SD) of 64,200 ± 6,300 years, so the actual entry of the R root has a point estimate of ~65 kya. The only other branch of macrohaplogroup N that could have arisen in India that early is haplogroup N5, but more data on the diversity and geographic distribution of this haplogroup are needed.

Haplogroup U2 as a subhaplogroup of haplogroup U is definitely younger than this early diversification of R in India. Taking the mtDNA lineages from the autochthonous subhaplogroups U2a, U2b, and U2c, we estimate a potential founder age of 49,900 ± 7,900 years for this part of the phylogeny. The age calculated here, however, depends on the relative frequency of U2a versus U2b, since the latter contributes to higher ages in view of the large number of coding-region mutations in the U2b stem of the phylogeny. Control-region estimates for the Indian U2 lineages are slightly higher (~50–55 kya [Kivisild et al. 1999*a*]). On the other hand, unless further screening of the Near Eastern mtDNA pool would exhibit early offshoots of U2a, U2b, or U2c, an entry of U2 in India more recent than 40 kya is not plausible. A recent estimate giving a very young age for U (25.6 kya [Baig et al., in press]), however, results from insufficient data, miscalculation (of ρ and σ), and an inadequate merging of U2 lineages with the other U lineages that came to India definitely much later.

Much later migrations, during the Holocene, from the Near East or Central Asia to India are well discernible in the Indian mtDNA pool and are believed to be related to the spread of agriculture and the Aryan invasion, respectively (Kivisild et al. 1999*a*, 1999*b*, 2000; McElreavey and Quintana-Murci 2002). Our analysis of the complete sequence variation supports the recent entry of those typical European haplogroups, at least for those haplogroups that have been widely sampled in western Eurasia, such as H, V, K, U5, J, and T. The entry time (calculated from the potentially private mutations) for members of these haplogroups is bounded by <11.5 kya (see Kivisild et al. [1999*a*] for an estimate based on HVS-I). The actual arrival times will be much more recent, since the Near Eastern mtDNA pool is insufficiently screened for the coding region.

South Asia as the Gate from Africa to Southeast Asia

In regard to the evolution and spread of modern humans, the genetic evidence obtained from high-resolution uniparental (i.e., mtDNA and Y chromosome) markers clearly supports the recent African origin of modern humans. Although this key feature of the Out-of-Africa scenario is widely accepted, the specific question of the routes used by modern humans to leave Africa is still being disputed. The traditional view, born out of the analysis of classic markers and the interpretation of population trees, is that there were two distinct exit routes: a southern route along the Asian coastline and a northern route through the Levant via Central Asia. The modernized variant of this model, however, suggests that both migrations stemmed from a single source in Africa (Cavalli-Sforza and Feldman 2003). Since the Eurasian/Oceanian mtDNA pool consists of two macrohaplogroups, a simplistic interpretation would tag one macrohaplogroup (M) to the southern root and the other (N) to the northern route (Maca-Meyer et al. 2001). This "one haplogroup–one migration" model, however, does not sit easily with the geographic distribution (fig. 2) and with estimated ages of the most basal branches of these macrohaplogroups and of R in particular. Moreover, the mtDNA record from Oceania indicates three autochthonous subhaplogroups of R and N (i.e., P, O, and S; see fig. 2) as well as two autochthonous M subhaplogroups (Ingman et al. 2000). Our analysis of the indigenous haplogroup R lineages in India points to a common first spread of the root haplotypes of M, N, and R along the southern route some 60–70 kya, since haplogroup M was estimated to be essentially of this age in India (Kivisild et al. 2003*a*) as well as in East Asia (Kong et al. 2003). The analysis further shows that the intrusion of haplogroup U2 (from the Near East ~50 kya) postdated the protosettlement along the southern route, thus giving further support to the migration scenario proposed by Kivisild et al. (1999*a*, 1999*b*). Equating these two events, as Cann (2001) apparently suggested in her figure 1, is then difficult to reconcile with the mtDNA data. At the other extreme, a very early protomigration along the southern Asian coast, before the Toba event (~74 kya), as proposed by Oppenheimer (2003), does not receive support from the complete sequence data, at least given the employed calibration of the molecular clock. It must be noted, however, that this calibration is inevitably fraught with uncertainty; calibrating mtDNA founder events directly against well documented archeological records may provide more precise estimates in the future.

Acknowledgments

We warmly thank Hui Pan, Guo-Dong Wang, Liang Xie and Yong-Yi Shen for technical assistance. We are also grateful to an anonymous reviewer for drawing our attention to the sister lineage of haplogroup W. The work was supported by National Natural Science Foundation of China grant 30021004, National Key Technologies R&D Program of China and Science and Technology Committee of Yunnan Province grant 2004BA901A07, and Chinese Academy of Sciences grant KSCX2-SW-2010.

Electronic-Database Information

Accession numbers and the URL for data presented herein are as follows:

GenBank, http://www.ncbi.nlm.nih.gov/Genbank/ (for accession numbers AY713976–AY714050)

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