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BRIEF COMMUNICATION

Dissecting the paternal founders of Mundari (Austroasiatic) speakers associated with the language dispersal in South Asia

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Abstract

The phylogenetic analysis of Y chromosomal haplogroup O2a-M95 was crucial to determine the nested structure of South Asian branches within the larger tree, predominantly present in East and Southeast Asia. However, it had previously been unclear that how many founders brought the haplogroup O2a-M95 to South Asia. On the basis of the updated Y chromosomal tree for haplogroup O2a-M95, we analysed 1437 male samples from South Asia for various novel downstream markers, carefully selected from the extant phylogenetic tree. With this increased resolution of genetic markers, we were able to identify at least three founders downstream to haplogroup O2a-M95, who are likely to have been associated with the dispersal of Austroasiatic languages to South Asia. The fourth founder was exclusively present amongst Tibeto-Burman speakers of Manipur and Bangladesh. In sum, our new results suggest the arrival of Austroasiatic languages in South Asia during last 5000 years.

Introduction

Among the four major language families present in South Asia, the Austroasiatic language family has the smallest number of speakers. Nevertheless, its geographical location and exclusive distribution amongst tribal populations make Austroasiatic one of the most intriguing language families in the context of the Subcontinent [1–3] where it is represented by the major Mundari and minor Khasi branches [4]. The advancement in sequencing and genotyping technologies have helped to resolve the long standing debate about the arrival of Austroasiatic (Mundari) speakers to South Asia.

The three types of genetic markers (mtDNA, Y chromosome, and autosomes) revealed the extraordinary migratory phenomenon. Because of the incompatible histories of their paternal and maternal ancestries, the origin and dispersal of Austroasiatic language in these populations had remained a debatable issue for many years [5, 6]. For Mundari speakers, the exclusive South-Asian maternal ancestry pinpointed their origin in South Asia, whereas their overwhelming East/Southeast-Asian-specific paternal ancestry associated with haplogroup O2a-M95 suggested a dispersal from East to West [3, 6–8]. Another Austroasiatic branch, Khasi, evinced

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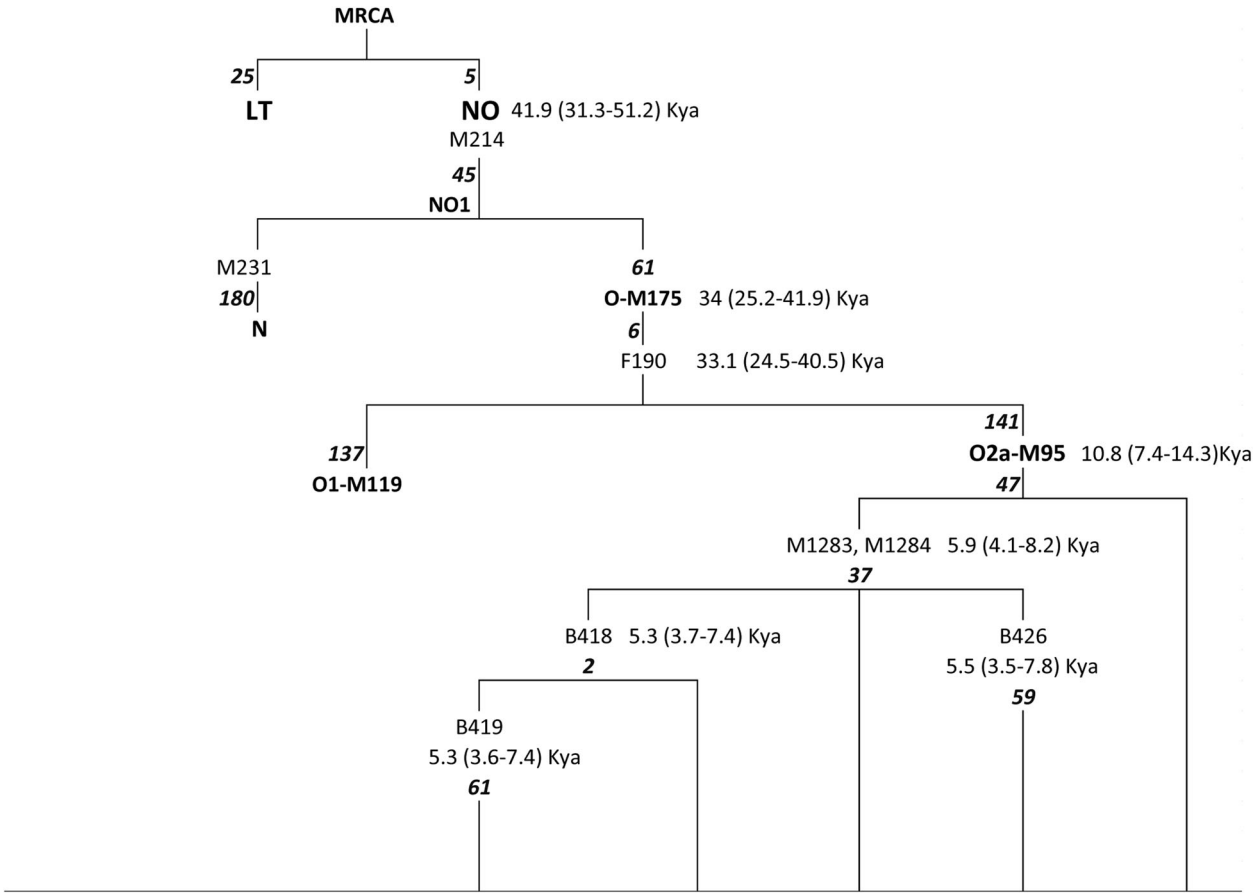

POPULATION	N	M95	B419	B418	M1284	B426	M95*
Asur	88	29	-	15 (0.17)	0 (0.0)	7 (0.07)	7 (0.07)
Birhar	62	24	-	6 (0.09)	4 (0.06)	4 (0.06)	10 (0.16)
Ho	45	9	-	4 (0.08)	2 (0.04)	1 (0.02)	2 (0.04)
Mahali	32	5	-	1 (0.031)	0 (0.0)	0 (0.0)	4 (0.12)
Mawasi	39	22	-	15 (0.38)	3 (0.07)	2 (0.05)	2 (0.05)
Santhal	20	5	-	4 (0.2)	0 (0.0)	1 (0.05)	0 (0.0)
Baiga	65	23	-	2 (0.03)	3 (0.04)	3 (0.04)	15 (0.23)
Total North Munda	**351**	**117**	-	**47 (0.13)**	**12 (0.03)**	**18 (0.05)**	**40 (0.11)**
Bonda	42	23	-	4 (0.09)	0 (0.0)	2 (0.04)	17 (0.40)
Gadaba	27	6	-	1 (0.03)	0 (0.0)	1 (0.03)	4 (0.14)
Juang	54	16	-	6 (0.11)	3 (0.05)	3 (0.05)	4 (0.07)
Kharia	37	3	-	0 (0.0)	0 (0.0)	1 (0.02)	2 (0.05)
Total South Munda	**160**	**48**	-	**11 (0.06)**	**3 (0.01)**	**7 (0.04)**	**27 (0.17)**
Khasi Maghalaya	21	8	-	3 (0.14)	1 (0.04)	1 (0.04)	3 (0.14)
Bangladesh	680	69	16 (0.02)	1 (0.001)	11 (0.01)	40 (0.05)	1 (0.001)
Manipur	225	153	3 (0.01)	0 (0.00)	8 (0.03)	141 (0.62)	1 (0.004)

Fig. 1 The updated phylogeography of haplogroup O2a-M95 in South Asia. The branch coalescent times were calculated according to Karmin et al. [18]. The number of variants of a branch is shown in bold italics. For each branch, the total number of individuals of a population as well as the frequencies are shown. The M95* is M95x (B418, B419, B426, M1284).

mixed ancestries for both the paternal and maternal lines [9]. Over a century of ethnographical and Indological scholarship had identified Austroasiatic language communities as representing the earliest settlers of South Asia, [3, 7, 9–12] so that this view represented the consensus [13]. Then, the increasing resolution of the

Y-chromosomal tree and Y-STR (short tendem repeat)-based coalescent calculations began to challenge our view of these populations. Despite the problems with STR-based coalescent calculations, the Y-STR variance for haplogroup O2a-M95 was consistently reported to be significantly higher in Southeast Asia [8, 14].

With the high resolution data of uniparental and biparental markers, a much clearer picture has now emerged, showing a strong association of largely male-mediated gene flow for the dispersal of Mundari speakers from Southeast Asia to South Asia [14–16]. The autosomal data showed a bidirectional gene flow between South and Southeast Asia [14]. In addition, the global distribution and internal phylogeny of Y-chromosomal haplogroup O2a-M95 decisively demonstrated that this language dispersal transpired from Southeast Asia to South Asia. In a recent genome-wide study on a large number of South and Southeast Asian populations, Dravidian speakers of Kerala and Lao speakers from Laos were found to be the best ancestral proxies for Mundari speakers [15]. The admixture dates for these ancestries were estimated to be between 2 and 3.8 kya. Moreover, this study also found clear-cut genetic differentiation between North and South Munda groups [15].

Based on the prevalence of haplogroup O2a-M95, the arrival of Mundari speakers to South Asia was shown to have been largely male-mediated [6, 8, 14]. However, it remained unclear how many paternal founders had brought this haplogroup to South Asia. Moreover, the recent admixture time estimated through autosomal data has now narrowed down the arrival of Mundari ancestors to South Asia [15]. Therefore, a marker such as M95, which originated >12 kya, would not help us to understand the most recent founding lineages. The association of haplogroup O2a-M95 with the arrival of Mundari speakers has been explored previously in detail [6, 8, 10, 14]. However, the lack of downstream markers made it impossible to discern the number of most recent founders who had originally borne the language to South Asia. Moreover, previous studies on Tibeto-Burman populations of Northeast India and Bangladesh also reported this haplogroup [6, 8, 10, 14, 17], giving rise to the contentious question as to whether the expansion of Tibeto-Burmans could have involved the assimilation of Austroasiatic populations? Therefore, we took advantage of recent Y-chromosome sequencing data and extracted the downstream Single Nucleotide Variants (SNVs) associated with Munda-related populations from one of our recent studies [18]. We genotyped these SNVs for large number of Mundari, Tibeto-Burman and Bangladeshi population groups (Supplementary Fig. 1) and reconstructed the phylogeographical distribution of downstream branches of haplogroup O2a-M95 in South Asia.

Methods

In our search to identify the founder branches of haplogroup O2a-M95 who are likely to have introduced Austroasiatic languages to South Asia, we first extracted the Y chromosome sequences from haplogroup O2a-M95-derived samples [18, 19]. We note that from South Asia, the 1000 genome samples and Karmin et al. [18], both had two South Asian individuals, however, both of the 1000 genome samples were falling in a single branch [19], whereas, Karmin et al. samples were present on two distinct branches [18]. Therefore, we used Karmin et al. data and reconstructed phylogenetic trees of haplogroup O2a-M95 based on the ~10MB region of the Y chromosome [18]. We extracted SNVs focussing on those branches where at least one South Asian sample was present (Supplementary text). Thereafter, we designed primers targeting selected SNVs and genotyped large number of samples either via RFLP (restriction fragment length polymorphism) or Sanger sequencing (Supplementary Table 1). We first genotyped the M95 marker among all the samples ($n = 1437$) and followed the hierarchal genotyping for the remaining SNVs among the M95-derived samples. The genomic positions and known equivalent marker of each new SNV genotyped have been incorporated in Supplementary Table 1. We used the data generated in the present study and reconstructed the phylogeny of haplogroup O2a-M95 with the frequency of each and every SNV among selected populations (Fig. 1).

For the coalescent age estimation of various nodes, we have used the mutation rate calibrations, 0.73×10^{-9}/bp/year (95% CI $0.63–0.95 \times 10^{-9}$/bp/year) published elsewhere [18]. By the inclusion of six new genetic markers downstream to O2a-M95, we were able to resolve the incompatible dates of the autosomal and Y-chromosomal studies [14, 15] as well as obtain a clearer picture of the phylogeography of haplogroup O2a-M95 specific to South Asia.

Results and discussion

The newly reconstructed South-Asian-specific phylogeny of haplogroup O2a-M95 is now defined by four new more recent branches showing a coalescent time in the range of 5 kya (kilo years ago) (Fig. 1). These four founders gave rise to ~77% of individuals carrying haplogroup O2a-M95 in South Asia, and the distribution of these four founders amongst the groups studied is intriguing. Founder one (represented by marker B419) is appears to be absent amongst Mundari speakers and is instead exclusively found amongst Tibeto-Burman speaking population in Manipur and Bangladesh (Fig. 1 and Supplementary Fig. 2). Conversely, founder two (marker B418) occurs most frequently in North Munda language communities and is absent among

Manipuri populations. Founder three (marker M1284) is infrequent, yet nevertheless present amongst all the groups studied here (Supplementary Fig. 2). Founder four (marker B426) is also present amongst all the groups and, most importantly, appears to be one of the leading founders of haplogroup O2a-M95 amongst those Tibeto–Burman populations where this paternal lineage is found (Fig. 1 and Supplementary Fig. 2). With these enhancements, we were able to assign 59% of Mundaris, 62% of the Khasis, and 99% of Manipuri and Bangladeshi individuals to the four well-defined downstream branches of haplogroup M95-O2a, which have originated in the course of last 5000 years (Fig. 1). We designated unclassified O2a-M95-derived samples as the M95* which is phylogenetically M95x (B418, B419, B426, and M1284).

Our current phylogenetic understanding suggests that haplogroup O2a-M95 originated >12 kya in East/Southeast Asia and expanded more recently into South Asia (Fig. 1). The frequency distribution and coalescent pattern of various founders amongst Mundari groups clearly show that the migration of Austroasiatics to South Asia was much later than the origin of O2a-M95 (Fig. 1). The diverse founders as well as the large number of unclassified samples (41% for Mundari, 38% for Khasi and 1% for Tibeto-Burmans) suggest that the dispersal of Austroasiatic speakers to South Asia was not associated with the migration of a single clan or a drifted population. Neither does the contrasting distribution of various founders discovered in this study amongst both Mundari and Tibeto-Burman populations support the assimilation of the former to the latter.

Thus, with the help of improved resolution, we have upgraded the phylogeography of haplogroup O2a-M95 and identified at least four founders in South Asia. Among the four founders identified by this study, one was exclusively present amongst Tibeto–Burman populations of Manipur and Bangladesh. The sequencing of a few representative samples from unresolved M95 samples would, it is hoped, be able to resolve this matter more fully in the near future.

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Compliance with ethical standards

Ethical approval This study was approved by the regional ethical committee of Institute of Science, Banaras Hindu University, India (I. Sc./ECM-XII/2018-19/06).

Conflict of interest The authors declare that they have no conflict of interest.

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