Deposited research article

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Posted: 2 December 2004

Genome ***Biology*** 2004, **6:**P1

The electronic version of this article is the complete one and can be found online at http://genomebiology.com/2004/6/1/P1

Received: 18 November 2004

This is the first version of this article to be made available publicly.

Tracking The Genetic Imprints of Lost Jewish Tribes Among The Gene Pool of Kuki-Chin-Mizo Population of India

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Abstract

Background

The Kuki-Chin-Mizo population comprising traditionally endogamous tribal groups residing in the state of Mizoram, India claim their descent from the ten lost tribes of Israel that were exiled by the Assyrians. To ascertain their oral history, we analysed DNA markers comprising 15 autosomal microsatellite markers, 5 biallelic and 20 microsatellite markers on Y-chromosome and the maternally inherited mitochondrial DNA sequence variations on 414 individuals belonging to 5 tribal communities from Mizoram (Hmar, Kuki, Mara, Lai and Lusei). The genetic profiles obtained were compared either with populations sharing Jewish ancestry or with local populations along the probable route of migration of the Jewish ancestry claimant Mizoram tribes.

Results

Y-STR analyses showed absence of the Cohen Modal Haplotype, the genetic signature of Cohanim origin. Y-chromosomal biallelic marker analyses revealed the presence of East and Southeast Asian-specific lineages and absence of haplogroup J predominant among Jewish populations. The mitochondrial DNA sequence analyses however revealed traces of genetic relatedness between the Jewish ancestry claimant Mizoram tribes and Near Eastern lineages. Autosomal analyses showed moderate degree of genetic differentiation among the different Mizoram tribes.

Conclusions

Migration of the lost tribes through China resulting in subsequent genetic admixture over a long period of time has probably diluted the extant gene pool of the Kuki-Chin-Mizo population. Although their paternal lineages do not exhibit any trace of Jewish ancestry,

incidence of maternal Near Eastern lineages among the Mizoram tribals suggests their claim to Jewish ancestry cannot be excluded.

Background

Contemporary Jewish communities spread across Asia, Europe and North Africa trace their origins to ancient Judea and Israel. However, historical records that attribute these Jewish populations to the early dispersals from ancient Israel are often under dispute. Moreover, the origins of a number of minority populations that claim Jewish ancestry are seldom well documented. Prolonged geographic separation of these groups has led to variations in religious practices and languages that fail to throw up similarities that would indicate shared ancestries. Interactions with local populations have also contributed towards diluting the purported ancestry of these Jewish populations.

The Kuki-Chin-Mizo population inhabiting the northeastern state of Mizoram in India, claim to be descendants of one of the ten lost tribes of Israel. Although historical records attributing to their Jewish ancestry are absent, their oral traditions and socio-cultural procedures present striking parallelism with Judaism. According to their oral history, these tribes are said to have entered Mizoram, India from adjacent Myanmar. Although ethnically they are of Mongoloid descent and speak Tibeto-Burman languages, their tradition ascribes their origin to B'nai Menashe – a remnant of the ancient Israelite tribe of Menasseh. Further support arises from their socio-cultural and oral histories:

1. The tribes observe 3 festivals in a year similar to Jews.
2. Funeral rites, birth and marriage ceremonies of the tribes reflect analogy with ancient Judaism.

3. Local legend describes presence of scattered remnants of the lost Jewish tribe of Menashe more than 1,000 years ago in a cave in China that then made its way across Thailand into India.

According to Hranglien Songate [1], the tribes entered China after passing through Afganistan and Baluchistan. The ten lost tribes: Reuven, Dan, Naphtali, Gad, Asher, Issachar, Zebulun, Ephrain, Menasseh and Levi of ancient Israel were taken up as captives by Assyrians in 722 BC and taken to Persia following their exile in 457 BC. In 331 BC when Alexander the Great conquered Persia, Afghanistan and India, these tribes were sent away to Afganistan and other countries. The later migrations are said to have taken place eastwards through Hindukush until they reached the Tibetan region and China. In China, they were forced to serve as slaves. Thus the process of assimilation and subjugation had started and the forefathers of the Kuki-Chin-Mizo population are believed to be those who had resisted the assimilation and had made their way south through Thailand to Burma, India and Bangladesh. According to oral testimonies only a small part of the current Kuki people are originally related to the tribe of Menashe. The descendants of Menashe are supposed to have been assimilated by Kuki invaders at the end of 15^{th} century in northeastern India [2].

Recent genetic studies have tried to establish similarities among groups sharing Jewish ancestry [3,4].Analyses of the paternally inherited Y-chromosome have revealed the occurrence of a specific microsatellite haplotype, 'Cohen modal haplotype' (within haplogroup J) at high frequency in Jewish Cohanim [5], suggesting that it might be the genetic signature of ancient Hebrew population. The Cohen haplotype has been subsequently identified in both Jewish and non-Jewish Near Eastern populations [6,7] as well as in populations such as the Lemba [8], whose oral tradition suggested Jewish ancestry. Haplogroup J is reported to be the major haplogroup in Jewish populations [9]. Haplogroup R1a1 has been found to be predominant in Ashkenazi Levites [9], while haplogroups R1b and R* have been identified in

high frequencies among Sephardic Jews [10]. Mitochondrial DNA (mtDNA) analyses have also revealed population specific haplotypes [11,12] in different Jewish groups suggesting most Jewish communities were founded by relatively few women independently in different geographic areas.

Here we analyse tribes belonging to the Kuki-Chin-Mizo population from Mizoram using autosomal, Y-chromosomal and mitochondrial markers to ascertain their claims of Jewish ancestry. Given their marked East Asian appearance, we attempt to trace genetic signatures of Near Eastern origin in their maternal and paternal lineages amongst expected extensive East Asian admixture.

Results and Discussion

Y-chromosomal Analyses

Comparison of Y-chromosomal and mtDNA patterns of Kuki, Hmar and other Mizoram tribes revealed maternal and paternal lineages to have undergone different fates. Analyses at six Y-STR loci; DYS19, DYS388, DYS390, DYS391, DYS392 and DYS393 in 74 individuals reveals that all the alleles for the studied populations fall within the ranges 14-17, 8-11, 23-25, 9-11, 10-13 and 11-14 respectively (Table 1). On comparison of the Y-chromosomal haplotypes of Kuki, Hmar and other analysed Mizoram tribes with known Jewish communities (Ashkenazic Jews, Sephardic Jews and Lemba) [8], no shared haplotypes were observed. Furthermore, the Cohen modal haplotype found predominantly among Ashkenazic and Sephardic Cohanim[5], was also not observed in the Mizoram tribes suggesting absence of ancient Hebraic signature in the paternal lineage of contemporary Mizoram tribes. Further analyses with Y-chromosomal binary markers revealed the male samples falling into Y-chromosomal haplogroups K*, O2a, O2a1 and O3e. These haplogroups are found predominantly in populations of East and Southeast Asia [13-15]. Haplogroup J that is found in high frequencies among Jewish populations across the world [9] was absent among the Mizoram tribes indicating their extensive admixture with the local male population has probably eliminated any trace of Jewish ancestry. Other haplogroups such as R1a1 found in high frequency in Ashkenazic Levites [9], and haplogroups R1b and R* found among Jews of Sephardic ancestry [10] were also not observed in the Mizoram tribes. Haplogroups K* and O have been reported in high frequencies in populations inhabiting northeastern India [16,17] consistent with migrations to the area from East and Southeast Asia. Occurrence of these local paternal lineages in the Kuki, Hmar and other Mizoram tribes analysed reveals extensive

admixture with local populations, with absence of any traces of earlier paternal Jewish ancestry similar to Ethiopian Jews [10], who presented predominantly local African lineages, albeit single representations of J2e and K2 lineages.

Mitochondrial Analyses

A total of 46 mtDNA haplotypes were observed in 50 of the Mizoram individuals analysed. A neighbour-joining tree (Fig. 2) constructed based on the haplotypes revealed similarity of the Kuki and Lusei populations with the Jewish samples taken from literature [11] for the analysis. Further analysis of the mtDNA haplogroups revealed occurrence of predominantly East Asian specific lineages in the Mizoram tribes. However, incidence of haplogroup W in the Kuki population demonstrated presence of Near Eastern mtDNA lineage in this tribe. Interestingly, Near Eastern lineages have not been identified in other Jewish populations of India [11,18], where the local gene pool had probably overwhelmed the original maternal gene pool of Jewish migrants. The Central Asian contribution to the extant lineages of Mizoram tribes was also evident from presence of MG2a lineage amongst the Kuki. In addition, HVSI motif 129, 223 found in high frequency in Jews of Uzbekistan, occurred with additional mutations in the Mizoram tribes.

Autosomal Analyses

Population wise average heterozygosities and locuswise G_{ST} values reflecting the extent of population differentiation are given in Table 2. The average G_{ST} value (0.020) reveals moderate degree of genetic differentiation among the Mizoram tribes suggesting a common origin.

The genetic evidence from analyses of the Kuki-Chin-Mizo population suggests their paternal Jewish lineage has been lost through the gradual subjugation of the population by dominating local groups. The original maternal lineage on the other hand has been assimilated

into the local community and hence diluted over generations with only traces of Near Eastern ancestry currently discernible. The females of any population represent the torchbearers of their social tradition and more so among Jewish communities where Jewishness has been defined by maternal descent in absence of priestly approval. The genetic structure of the Kuki-Chin-Mizo population also draws parallelism to Ethiopian Jews [10] whose maternal lineage has also been overwhelmed by the local gene pool with only traces of Near Eastern ancestry still perceptible.

Conclusions

Although signatures of paternal inheritance of Jewish ancestry were not traceable, the genetic evidence revealed in this study is consistent with a plausible maternal Near Eastern contribution to the extant Kuki-Chin-Mizo gene pool. Haplogroup W has not been reported among other northeastern Indian tribal populations [19], hence its incidence among the Mizoram tribals suggests their claim to Jewish ancestry cannot be excluded. The presence of Central Asian-specific mtDNA haplogroups [20] further corroborates the oral tradition tracing their migration along the Silk Route. Studies across global Jewish populations have elucidated greater mtDNA differentiation than Y-chromosomal [10,11] while the opposite has been found true in other global communities [21,22]. The geographic structuring evident in mtDNA of Jewish populations signified different founding female lineages among diverse Jewish communities [10-12]. Since Talmudic times (circa 200 B.C. to 500 A.D.) Jewish identity in the absence of rabbinically authorized conversion has been determined through maternal descent [23]. It is likely that remnants of maternal founding lineages of the Kuki-Chin-Mizo population have survived while the original paternal gene pool has been obliterated by the overwhelming local contribution.

Methods

Sample collection and extraction of DNA

Blood samples of Kuki, Hmar and other tribes were collected by venipuncture from unrelated healthy volunteers of Mizoram. Individuals of all the populations present Mongoloid features. They form very distinct small groups and endogamy is practiced within each community. No comprehensive historical records about these populations are available. The samples belong to Kuki (60), Hmar (80), Mara (90), Lai 92) and Lusei (92) tribes. The Kuki and the Hmars are also found to be present in the neighbouring state of Manipur. DNA isolation was carried out by organic extraction method [24]. Quantity of the extracted DNA was estimated by slot blot technique using Quantiblot kit (Perkin Elmer, Foster City, CA, USA).

Genotyping

Y-Chromosomal Analyses

Haplotypes: We genotyped all the population samples for 20 STRs of which the data for six markers [DYS19, DYS388, DYS390, DYS391, DYS392, DYS393, CMH markers] are presented in this paper. All the markers were amplified with 25ng of template DNA in a multiplex PCR following conditions described elsewhere [25]. The standardization has been performed with NIST primers in our laboratory. The amplified samples were genotyped on Genetic Analyzer 3100 (Applied Biosystems, USA) and the fragment lengths were converted to repeat numbers by the use of allelic ladders for further statistical analysis.

Haplogroups: In all the population samples we have typed a set of thirty-five biallelic markars including one Alu insertion on hierarchical basis for defining the male genetic lineage. PCR protocols for detection of these polymorphisms were followed according to Underhill et al. 1997 [26] and haplogroups defined according to the Y Chromosome Consortium (2002) [27] nomenclature.

Mitochondrial DNA Sequence Analyses

The samples were amplified with primers L15997 and H16391 [28] for obtaining the sequence information in hypervariable segment I (HVSI). Amplicon sequence was determined using Genetic Analyzer ABI 3100 (Applied Biosystems, USA). A total of 100 samples from the 5 communities were sequenced for the HVSI region of the mtDNA. The final sequence information generated for each individual was a stretch of length of 390 nucleotides for base positions 16010 to 16400. The mtDNA sequences were aligned using the Clustal W program available in the software package - Bio Edit. For identifying the variable nucleotide positions the sequences were compared with the revised Anderson sequence [29]. The inter-population distances were calculated using AMOVA analysis option present in Arlequin software. Neighbour-joining tree was built using the software programme - Mega. The genetic relationship of the Kuki, Hmar and other Mizoram tribes with Jews or local populations along their probable route of migration was established from calculating the mean genetic distance D_A , defined as $D_A = d_{XY}-(d_X+d_Y)/2$, where d_{XY} is the mean pairwise difference between individuals from population X and Y and d_X (d_Y) is the mean pairwise difference between individuals within population X(or Y) [30].

Autosomal Microsatellite Analyses

Fifteen autosomal STR markers were amplified with PowerPlex 16 kit (Promega Corporation, USA) following the protocol provided by the manufacturer .The allele designation was carried out following electrophoresis in ABI 377 automated DNA sequencer (Applied Biosystems, USA) using Genotyper software. Average heterozygosity and G_{ST} values were estimated using DNA Type and Dispan softwares.

Authors' contributions

BM collected all the samples, carried out the molecular genetic studies, participated in the sequence alignment and drafted the manuscript. ST provided some critical new information and contributed significantly to editing of the manuscript. The contributions of BM & ST are equal. RT provided the technical support and coordinated the entire study. VKK conceived of the study, and participated in its design and manuscript preparation. All authors read and approved the final manuscript.

Acknowledgements

We thank Revathi Rajkumar and Sanghamitra Sahoo for providing extensive assistance in mt DNA & Y Chromosomal analysis. This work was supported by a grant under the Ninth Plan of Government of India, to Central Forensic Science Laboratory, Kolkata. This study would not have been possible without the voluntary participation of individuals of the studied populations**.** BM & ST were assisted with DFS and CSIR Research Fellowships respectively.

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Figures

Figure 1 - Cladogram of Y chromosomal lineages of Kuki, Hmar and other three Mizoram population

Figure 2 - Neighbour joining tree Based on mt. DNA haplotypes showing affinity between Kuki and Jewish population

Figure legend text:

Ti- Tibetan population, Zu- Zhuang population, Th-Thai Population, Tu- Tu Population, Tur-Turky Population, H-Hmar Population, Lu-Lusei Population, L-Lai Population, M-Mara Population, Kuki- Kuki Population, Jew- Jewish Population

Tables

Table 1 - Distribution of Y-Chromosome Haplotypes in Kuki,Hmar and other three Mizoram Populations

Table legend text:

KU: Kuki Population, LU : Lusei Population, LA:Lai Population, MA:Mara Population, HM:Hmar Population

Table 2 - Locus wise average Heterozygosity and G_{ST} values based on autosomal STR loci for Kuki, Hmar and other three Mizoram tribes

TABLE 1 : Distribution of Y-Chromosome Haplotypes in Kuki, Hmar and other three Mizoram populations

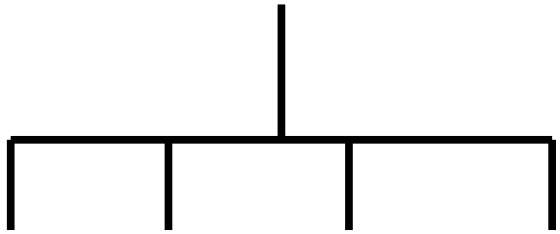
Haplotype index Number	No. of Microsatellite Repeats in						No. of Y Chromosomes in Populations				
	DYS19	DYS388	DYS390	DYS391	DYS392	DYS393	KU	LU	LA	MA	HM
1	14	9	23	10	11	12	2	*	*	*	*
2	14	9	23	10	10	12	2	*	*	*	*
3	15	9	22	10	13	11	1	*	*	*	*
4	15	9	24	9	13	13	1	*	*	*	*
5	16	11	24	9	13	12	1	*	*	*	*
6	16	11	24	10	13	13	1	*	*	*	*
7	14	11	23	10	11	13	1	*	*	*	*
8	14	9	24	10	11	12	*	1	*	*	*
9	14	9	24	10	10	11	*	1	*	*	*
10	14	11	23	9	13	11	*	1	*	*	*
11	14	9	23	10	13	12	*	2	*	*	*
12	14	11	24	10	13	11	*	1	*	*	*
13	15	9	24	10	13	12	*	1	*	*	*
14	15	11	24	9	10	12	*	1	*	*	*
15	15	11	24	10	13	13	*	2	*	*	*
16	15	11	24	9	13	11	*	1	*	*	*
17	16	11	24	9	13	12	*	3	*	*	*
18	16	11	24	10	13	12	*	1	*	*	*
19	14	9	24	9	13	11	*	*	*	2	*
20	14	11	24	9	13	13	*	*	*	1	*
21	14	9	24	9	13	12	*	*	*	1	*
22	15	9	24	9	13	11	*	*	*	2	*
23	15	11	24	9	13	11	*	*	*	2	*
24	15	11	24	9	13	12	*	*	*	3	*
25	15	11	24	9	13	13	*	*	*	1	*
26	16	11	24	9	13	11	*	*	*	1	*
27	16	11	24	9	13	12	*	*	*	2	*
28	15	9	25	9	13	11	*	*	*	*	2
29	15	9	24	9	13	12	*	*	*	*	4
30	15	9	24	11	11	13	*	*	*	*	3
31	16	9	24	11	11	12	*	*	*	*	2
32	16	9	24	9	13	13	*	*	*	*	5
33	17	9	24	9	13	12	*	*	*	*	2
34	14	9	24	9	13	12	*	*	1	*	*
35	14	9	24	9	13	11	*	*	3	*	*
36	14	9	24	9	13	12	*	*	1	*	*
37	15	8	24	9	13	14	*	*	1	*	*
38	15	9	24	9	13	11	*	*	1	*	*
39	15	9	24	9	13	12	*	*	1	*	*
40	15	11	24	9	13	12	*	*	2	*	*
41	15	11	24	9	13	11	*	*	1	*	*
42	16	9	24	9	13	12	*	*	5	*	*
43	16	11	24	9	13	12	*	*	1	*	*

Table- 2

Locus wise average Heterozygosity and G_{ST} values based on autosomal STR loci for Kuki,Hmar and other three Mizoram tribes

Locus	Hmar	Mara	Lai	Lusei	Kuki	G_{ST}
D18S51	0.850	0.822	0.826	0.848	0.895	0.012
D21S11	0.825	0.867	0.783	0.783	0.775	0.017
D5S818	0.825	0.778	0.783	0.783	0.834	0.012
D13S317	0.900	0.822	0.826	0.761	0.821	0.012
D7S820	0.875	0.844	0.826	0.783	0.709	0.012
vWA	0.800	0.778	0.608	0.804	0.834	0.018
D8S1179	0.850	0.822	0.761	0.674	0.792	0.019
FGA	0.900	0.800	0.913	0.848	0.542	0.012
D3S1358	0.700	0.733	0.652	0.609	0.874	0.069
Average Heterozygosity	0.814	0.819	0.808	0.808	0.824	0.020

Figure 1: Cladogram of Y chromosomal lineages of Kuki, Hmar and other three Mizoram population



		K	O2a	O2a1	O3e
Population Frequency	Mara	--	0.8	--	0.2
	Hmar	0.1	0.7	0.1	0.1
	Lai	--	0.5	--	0.5
	Lusei	--	0.823	--	0.167
	Kuki	0.1	0.143	--	0.857

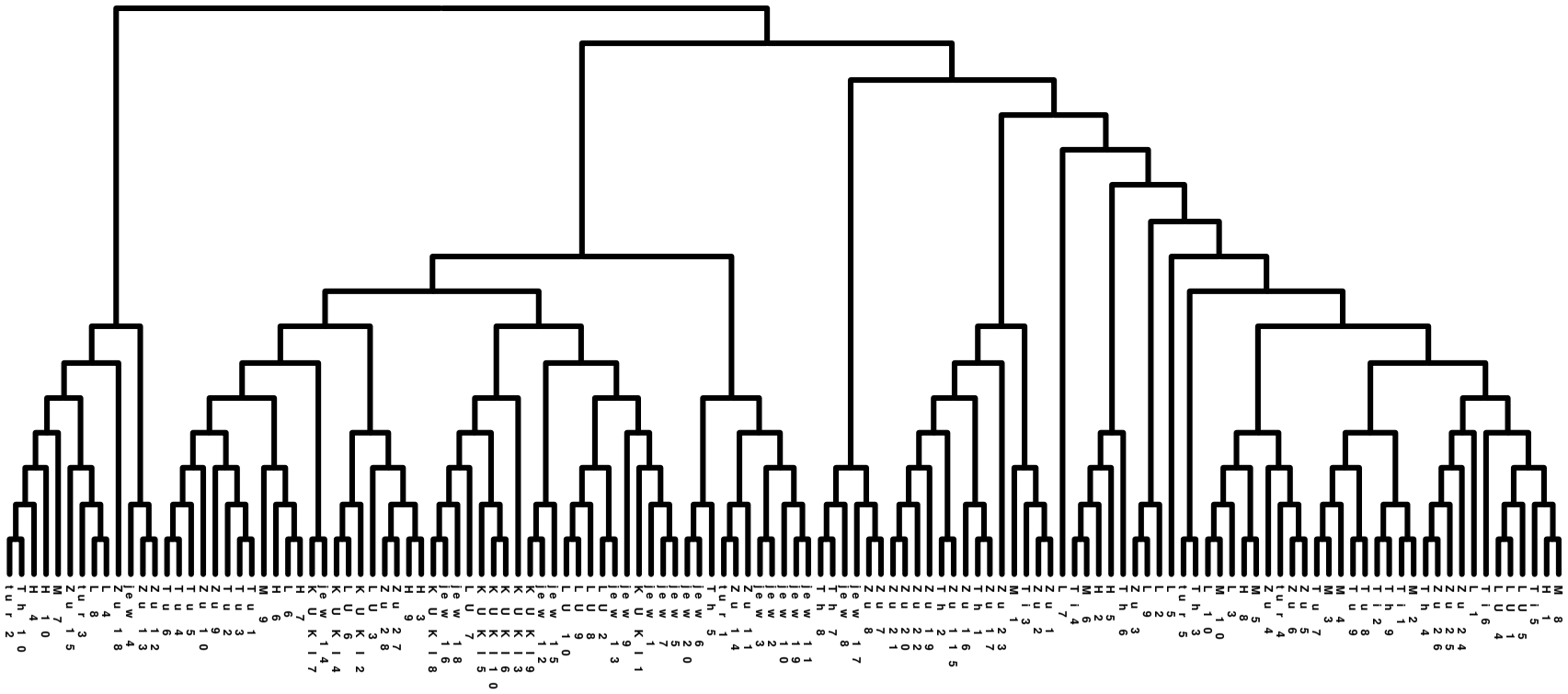


Figure-2

Neighbour joining tree Based on mt. DNA haplotypes showing affinity between Kuki and Jewish population