

Genetic Structure of Tibeto-Burman Populations of Bangladesh: Evaluating the Gene Flow along the Sides of Bay-of-Bengal

Nurun Nahar Gazi^{1,9}, Rakesh Tamang^{2,9}, Vipin Kumar Singh², Ahmed Ferdous¹, Ajai Kumar Pathak^{3,4}, Mugdha Singh², Sharath Anugula², Pandichelvam Veeraiah², Subburaj Kadarkaraisamy², Brijesh Kumar Yadav², Alla G. Reddy², Deepa Selvi Rani², Syed Saleheen Qadri¹, Lalji Singh^{2,5,6}, Gyaneshwer Chaubey⁴, Kumarasamy Thangaraj^{2*}

1 Center for Advanced Research in Physical, Chemical, Biological and Pharmaceutical Sciences, University of Dhaka, Dhaka, Bangladesh, **2** Centre for Cellular and Molecular Biology, Hyderabad, India, **3** Department of Evolutionary Biology, Institute of Molecular and Cell Biology, University of Tartu, Tartu, Estonia, **4** Estonian Biocentre, Tartu, Estonia, **5** Genome Foundation, Hyderabad, India, **6** Banaras Hindu University, Varanasi, India

Abstract

Human settlement and migrations along sides of Bay-of-Bengal have played a vital role in shaping the genetic landscape of Bangladesh, Eastern India and Southeast Asia. Bangladesh and Northeast India form the vital land bridge between the South and Southeast Asia. To reconstruct the population history of this region and to see whether this diverse region geographically acted as a corridor or barrier for human interaction between South Asia and Southeast Asia, we, for the first time analyzed high resolution uniparental (mtDNA and Y chromosome) and biparental autosomal genetic markers among aboriginal Bangladesh tribes currently speaking Tibeto-Burman language. All the three studied populations; Chakma, Marma and Tripura from Bangladesh showed strikingly high homogeneity among themselves and strong affinities to Northeast Indian Tibeto-Burman groups. However, they show substantially higher molecular diversity than Northeast Indian populations. Unlike Austroasiatic (Munda) speakers of India, we observed equal role of both males and females in shaping the Tibeto-Burman expansion in Southern Asia. Moreover, it is noteworthy that in admixture proportion, TB populations of Bangladesh carry substantially higher mainland Indian ancestry component than Northeast Indian Tibeto-Burmans. Largely similar expansion ages of two major paternal haplogroups (O2a and O3a3c), suggested that they arose before the differentiation of any language group and approximately at the same time. Contrary to the scenario proposed for colonization of Northeast India as male founder effect that occurred within the past 4,000 years, we suggest a significantly deep colonization of this region. Overall, our extensive analysis revealed that the population history of South Asian Tibeto-Burman speakers is more complex than it was suggested before.

Citation: Gazi NN, Tamang R, Singh VK, Ferdous A, Pathak AK, et al. (2013) Genetic Structure of Tibeto-Burman Populations of Bangladesh: Evaluating the Gene Flow along the Sides of Bay-of-Bengal. PLoS ONE 8(10): e75064. doi:10.1371/journal.pone.0075064

Editor: Dennis O'Rourke, University of Utah, United States of America

Received: January 31, 2013; **Accepted:** August 9, 2013; **Published:** October 9, 2013

Copyright: © 2013 Gazi et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Funding: K.T. was supported by the Council of Scientific and Industrial Research (GENESIS: BSC0121), Government of India. L.S. was supported by a Bose Fellowship from the Department of Science and Technology, Government of India and Bhatnagar fellowship from the Council of Scientific and Industrial Research, Government of India. G.C. was supported by the Centre of Excellence of the Estonian Biocentre and A.K.P. was supported by European Social Fund's Doctoral Studies and Internationalisation Programme DoRa. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

* E-mail: thangs@ccmb.res.in

⁹ These authors contributed equally to this work.

Introduction

Bangladesh is bordered by Eastern India in west, Northeastern India in north and by the Bay of Bengal in the south. It also shares a narrow boundary with Myanmar on the southeastern rim (Fig. 1). Its geographical placement epitomized it as an important linguistic contact zone. There are 32 tribal populations documented in Bangladesh representing 1% of the total population [1]. The tribal populations living in the coastal as well as Chittagong Hill Tract regions are poorly understood. Gaps in our knowledge are substantial with respect to population ecologies, habitat and phylogenetic relationships. As a consequence, these tribal people haven't been studied at molecular resolution to determine their

phylogenetic placement in terms of South Asia and East/Southeast (E/SE) Asian gene pool.

In the present study, we have carried out a detailed molecular analysis of three major tribal populations (Chakma, Marma and Tripura) living in Chittagong Hilly tract of Bangladesh. These populations are described as true aboriginal tribal populations of Bangladesh [2]. All the three populations analysed in this study speak a branch of Tibeto-Burman (TB) language. TB language family is considered as second largest language family in the world based on number of native speakers. In South Asia, TB language family is explicitly considered to have arrived from East and is mainly present in Nepal, Bhutan, Bangladesh, Northeast India and in some parts of Pakistan; where the Balti population from the

Karakoram Mountains speaks a TB branch [3]. It has been speculated that the TB language family originated in China and spread from the Yellow river of China into Myanmar and the greater Himalayan region [3]. The overwhelming majority of languages spoken in the greater Himalayan fringes belong to this language family. The internal classification of TB is still controversial [4] and needs a thorough vocabulary and lexical reconstructions. Genetic studies on limited populations of this group however, suggests their recent migration from East to Indian subcontinent [5–7].

The aim of this study was to trace footprints of initial Paleolithic colonization and the much later Neolithic expansion of populations among the aboriginal tribal populations living in Chittagong Hill Tract region of Bangladesh. We also assessed whether South Asian TB speaker's genetic variation was structured by the language or by their geographical placement. We also examined the relationships of the studied populations with Indian, Southeast Asian TB and other linguistic groups.

Results and Discussion

Highly permeable maternal boundaries

Marma and Tripura populations share high frequency of Indian and low frequency of East Asian specific maternal haplogroups, than Chakma (Table 1). East Asian specific Haplogroup F1 was observed highest among all the studied populations (Table 1 and Table S1), and shared their closest haplotypes with Northeast Indian populations. In contrast to the high endogamy observed among other Indian populations [8–12], the massive haplogroup sharing among all the three populations suggest that the maternal boundaries in this region is highly permeable (Table 1).

The haplotype based comparison with neighboring Indian and Southeast Asian populations showed a closest match with

Northeast India, implying their close genetic connection (Table S1). The haplotype diversity is highest among Marma, followed by Tripura and Chakma (Table 1). To see whether the Indian or the East Asian-specific haplogroups have higher diversity in this region, we have calculated the haplotype diversity of the HVS-I haplotypes from the aggregate data of the three populations. Indian-specific haplogroups have moderately higher haplotype diversity 0.989 (95% CI: 0.995, 0.983) than the East Asian-specific haplogroups 0.972 (95% CI: 0.975, 0.969), suggesting that the Indian-specific haplogroups were likely to be present before the geneflow from the East. However, high haplotype diversity may not always be a reflection of older lineages [13], and as this region share land borders from Northeastern as well as Eastern India, with a caution it could also be a consequence of repeated gene flow from two diverse sources and same explanation also applies to the East Asian maternal diversity of this region.

To learn more about the maternal relation of studied tribal populations with the neighboring populations, we performed Principal Component Analysis (PCA). PC1 was basically segregating Indian and E/SE Asian populations, while PC2 was setting apart loosely packed Indian and TB populations of Bangladesh from E/SE Asians and Indian groups (Fig. 2a). All the studied populations cluster tightly with one another and loosely with other Indian TB populations. In a geographical comparison, the Tibeto-Burman populations of Bangladesh remained closer to E/SE Asian cluster than Indian cluster.

Paternal Ancestry of Bangladeshi tribal populations

To gain insight into their paternal gene pool, we have analyzed Y chromosomal data from 89 Chakma, 60 Marma and 88 Tripura individuals. Over 35 biallelic markers and 17 short tandem repeats (STRs) loci were genotyped to produce a high-resolution dataset of

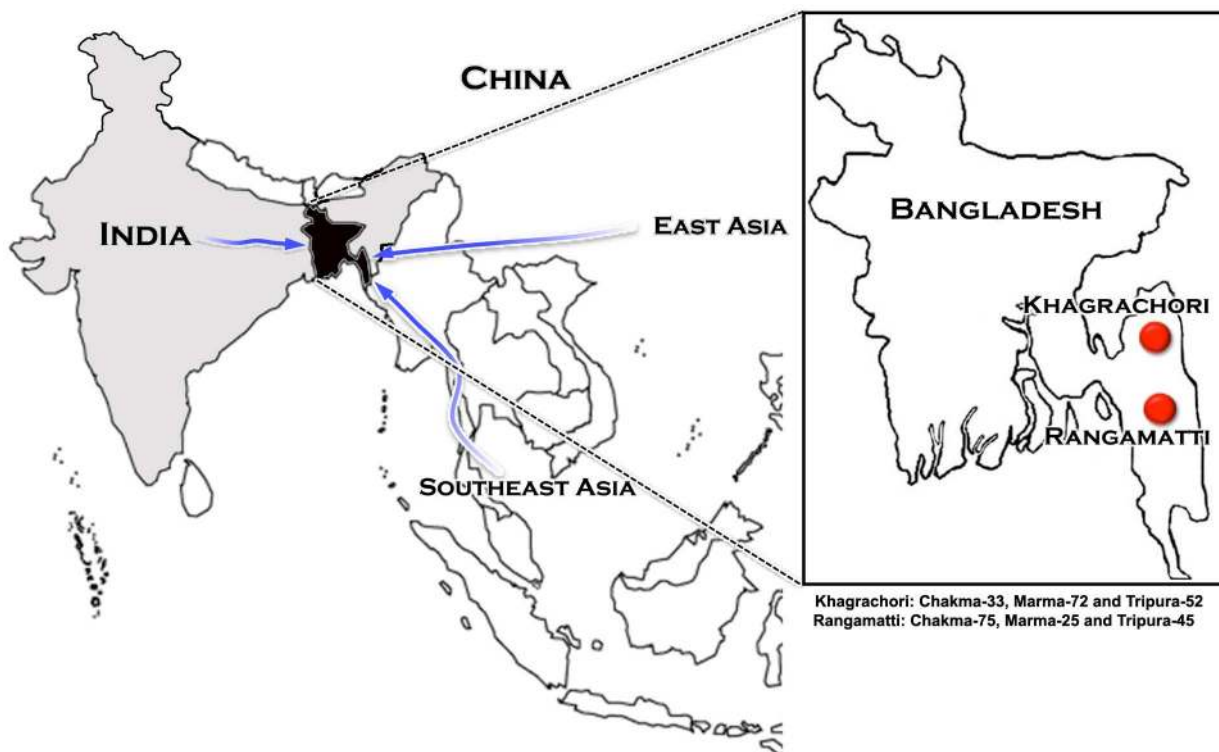


Figure 1. Map of Bangladesh showing the sampling area and suggested geneflow from different directions.

doi:10.1371/journal.pone.0075064.g001

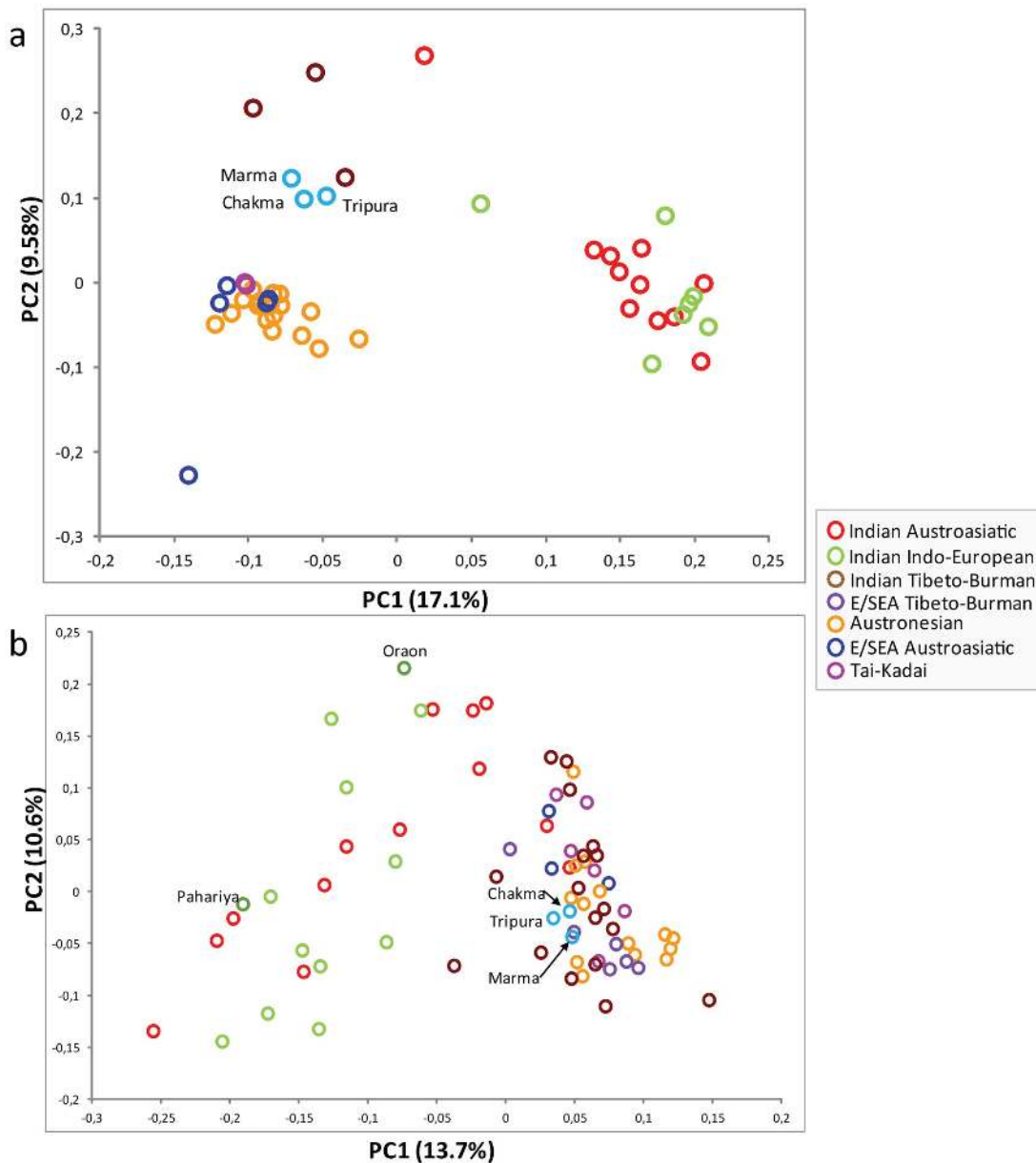


Figure 2. PCA plots constructed on the basis of (a) mtDNA haplogroup frequencies and (b) Y chromosome haplogroup frequencies.
doi:10.1371/journal.pone.0075064.g002

Y chromosomes from these groups. We observed considerable differences in Indian specific NRY haplogroup frequencies among the three groups, Chakma has the least, while Tripura has the highest Indian-specific haplogroups (Table 1). More than 60% of the individuals from all the three tribal populations are skewed towards Southeast Asian-specific haplogroups O2 and O3 (Table 1). All populations had high to moderate frequencies of C, D, O2a1, O3, P and R2 haplogroups.

Notably, none of the studied populations carry Indian-specific Paleolithic haplogroup H or any of its branches (Fig. S1), which is also reported in East and Southeast Asia among Balinese, Tibetans, Mongolians, Cambodians and Laotians [14,–17]. Unlike haplogroup H, haplogroup P that has unknown origin is substantially present among all the three studied populations (Table 1), and also reported in the adjoining regions [18]. A detailed phylogeographic study of haplogroup P would throw

more light about its origin and expansion in this region. In spite of sharing a larger gene pool with TB populations of Northeast India, in the wider geographical context, the paternal haplogroup frequency distribution among TB tribes of Bangladesh exhibits a unique trend of haplogroup composition, e.g., the occurrence of Indian specific haplogroups L and E/SE Asian specific haplogroup NO, which are completely absent among Northeast Indian populations (Fig. S1), thus indicating geneflow from three distinct directions (Fig. 1).

Similar to mtDNA PCA, in Y chromosome haplogroup based PCA, PC1 differentiates Indian with E/SE Asian clusters, while, PC2 sets apart Indian-Indian and E/SE Asian-E/SE Asian populations (Fig. 2b). The Bangladeshi TB populations cluster together with E/SE Asian specific group along with Indian TB speakers. This is due to overwhelming majority of East Asian-specific haplogroups in these populations (Table 1). Indian Indo-

European and Dravidian populations follow their geographical placement in the plot rather than their language affiliation. Unlike the Munda speakers of India where male mediated migration from Southeast Asia shaped the current landscape of their gene pool, among South Asian TB the presence of frequent East Asian maternal and paternal haplogroups suggest that both males and females played largely equal roles in TB expansion in Southern Asia.

To assess whether geography or linguistic affiliation was a better predictor of genetic variation, we conducted AMOVA analysis (Table 2). We noted that the variation among groups was not significant, and among population within-group variation was high. When the data were clustered by linguistic affiliation, among group variation rose to 18%, whereas the among population within-group value fell to about 4% (Table 2). This finding suggested that their paternal genetic history is structured along linguistic instead of geographic lines.

High Diversity and Deep coalescent expansion ages of founder haplogroups

Because variation accumulates with time, a relative chronology can be constructed by assessing haplogroup STR variance, haplotype diversity (HD), ρ (rho), and mean pairwise differences (MPD) (Table 3, and Tables S2 and S3). We noted the highest diversity of haplogroup O2a1 than N1a, NO and O3a2c1 haplogroups. Consistently Chakma had greater diversity than Marma and Tripura (Table 3). In the NETWORK analysis of 15 STRs, most of the haplotypes were unique and dispersed among longer branches of network, except three pairs of shared haplotypes of Tripura (Fig. S2).

To compare them with the surrounding populations, we have redone NETWORK analysis of O2a1 and O3a2c1 haplogroups based upon common STRs from published sources [14,19]. In haplogroup O2a1, the Bangladeshi TB populations form their own cluster and share some of their haplotypes with the Khasi population of Meghalaya, which speaks Khasi-Asialian branch of Austroasiatic language (Fig. 3a). The sharing of common haplotypes with Khasi advocates a recent geneflow beyond the borders of language. For a wider geographical coverage, we pulled all Bangladeshi TBs into a single group and reduced the number of common STRs to eight (Fig. S3). All the Bangladeshi individuals form their own cluster with Indian TB populations rooting out from Southeast Asian Island haplotype. In haplogroup O3a2c1, most of the Bangladeshi TB populations largely allocate their branches or haplotypes with Indian TB haplotypes (Fig. 3b).

The coalescent ages of haplogroups O2a1 and O3a2c1 were almost similar ranging between 14 and 18 Kya (Table S2), suggested that they arose before the differentiation of any language group and approximately at the same time. Contrary to the scenario proposed for colonization of northeast India as male founder effect have occurred within the past 4,000 years [6], we

suggest a significantly deep colonization of this region. STR haplotypes of haplogroups O2a1 and O3a2c1 showed the greatest variance and age estimates among Southeast Asians, moderate values among Bangladeshi aboriginal tribal and the lowest values in the Indians (Table S2), thus forming a east to west gradient of O2a1 and O3a2c1 diversity and determine the directionality of movement by bearers of O2a1 and O3a2c1 Y chromosomes. This trend of slightly decreasing values from east to west suggests an origin for O2a1 and O3a2c1 in the Southeast Asia and its dispersal through an westward expansion minimum with two different waves – first the Austroasiatic speakers carrying O2a1 (likely without O3 lineage) and second Tibeto-Burman containing O3 and O2a1 lineages.

Higher Indian ancestry component than Northeast Indian populations

To see the population structure and ancestry components among the studied population and surrounding groups, we have studied previously used 50 Ancestry Informative Markers (AIMs) [12,20] and combined them with the same numbers of markers extracted from the literature [21,22]. Four markers failed from the 99% quality control, therefore, we have used 46 AIMs for further analysis. The pairwise F_{st} among studied population showed a consistent pattern for all the studied loci (Table 4). Chakma and Tripura share the maximum genetic similarity while, Marma and Tripura were having highest F_{st} value. The Bangladeshi TB populations showed a closer affinity with Northeast Indian as well as East Asian populations (Fig. 4a and Table S4). The PCA with Indian and East Asian populations placed the Bangladeshi and Indian TB populations together with East Asians, however, there were some individuals of Tripura and Marma falling in India cluster (Fig. 4b). The STRUCTURE analysis of the studied populations in the context of rest of the world showed two major shared components among the studied populations (Fig. 4c). First shared component was higher among Indian populations, while the second was specific to East Asians. It was intriguing that the Bangladeshi TB populations were carrying substantially higher Indian ancestry component than the Northeast Indian TB populations, suggesting that the primary genetic structure of Bangladeshi populations was likely made up of the similar gene pool as Indian, which was further electroplated by the TB expansion.

In conclusions, our extensive analysis on uniparental and biparental markers led to the more precise identification of Indian and E/SE Asian haplogroups among Bangladeshi aboriginal tribal populations and a better understanding of the extent of ancient and recent admixtures. We present substantial evidence for multiple genetic strata that arose likely through a series of distinct migratory processes. In contrast to Indian context, where gene is highly correlated with geography, we found that the Northeast Indian and Bangladeshi landscape is associated with language. The post-Neolithic incursions make a major impact on the

Table 2. Analysis of molecular variance (AMOVA).

Grouping (number of groups)	Among groups	Among populations within groups	Within populations
Language (5)	17.9	3.8	78.3
Geography (5)	3.1	29.3	67.6

The language groups used for the analysis were Indo-European, Dravidian, Austroasiatic, Tibeto-Burman and Austronesian, while, geography was divided in to East Asia, Southeast Asia, Northeast India, East Bengal and West Bengal. All p-values were significant ($P < 0.05$) except for the Among groups-geography (3.1; $p = 0.12$).

doi:10.1371/journal.pone.0075064.t002

Table 3. Y-STR Diversity estimates of major haplogroups.

Haplogroup	Population(s)	<i>n</i>	<i>h</i>	HD	MPD	Variance	Age (Kya)	SD (Kya)
N1a	Chakma	4	4	1.000±0.177	7.500±4.441	0.35	11.47	2.42
N1a	Tripura	2	2	1.000±0.500	5.000±3.873	0.27	4.83	2.48
N1a	Chakma+Tripura	6	6	1.000±0.096	6.467±3.567	0.30	11.67	2.92
NO	Chakma+Marma+Tripura	3	3	1.000±0.272	7.667±4.928	0.29	9.66	1.75
O2a	Chakma	6	6	1.000±0.096	8.400±4.537	0.37	12.68	1.54
O2a	Marma	9	9	1.000±0.052	7.556±3.896	0.35	15.82	2.65
O2a	Tripura	10	10	1.000±0.045	7.889±4.011	0.38	15.22	2.52
O2a	Chakma+Marma+Tripura	25	25	1.000±0.011	7.717±3.720	0.38	16.23	2.01
O3a3c	Chakma	16	16	1.000±0.022	7.192±3.558	0.35	15.55	2.18
O3a3c	Marma	14	14	1.000±0.027	6.693±3.359	0.30	13.11	2.28
O3a3c	Tripura	15	12	0.971±0.033	6.715±3.355	0.35	15.30	2.84
O3a3c	Chakma+Marma+Tripura	45	42	0.997±0.006	7.188±3.4328	0.38	15.94	2.14

doi:10.1371/journal.pone.0075064.t003

composite gene pool of the studied tribal populations, consistent with the genetic impact of the language. In addition, by generating well resolved mtDNA and Y chromosomal lineages, we were able to detect the directional geneflow and their conglomeration from east and west of Bangladesh.

Methods

Sampling

About 5 ml blood samples were collected from each individual belonging to three tribes (108 Chakma, 97 Marma and 97 Tripura) from Rangamatti and Khagrachori regions of Chittagong Hill Tract in Bangladesh. All the three populations are contributed

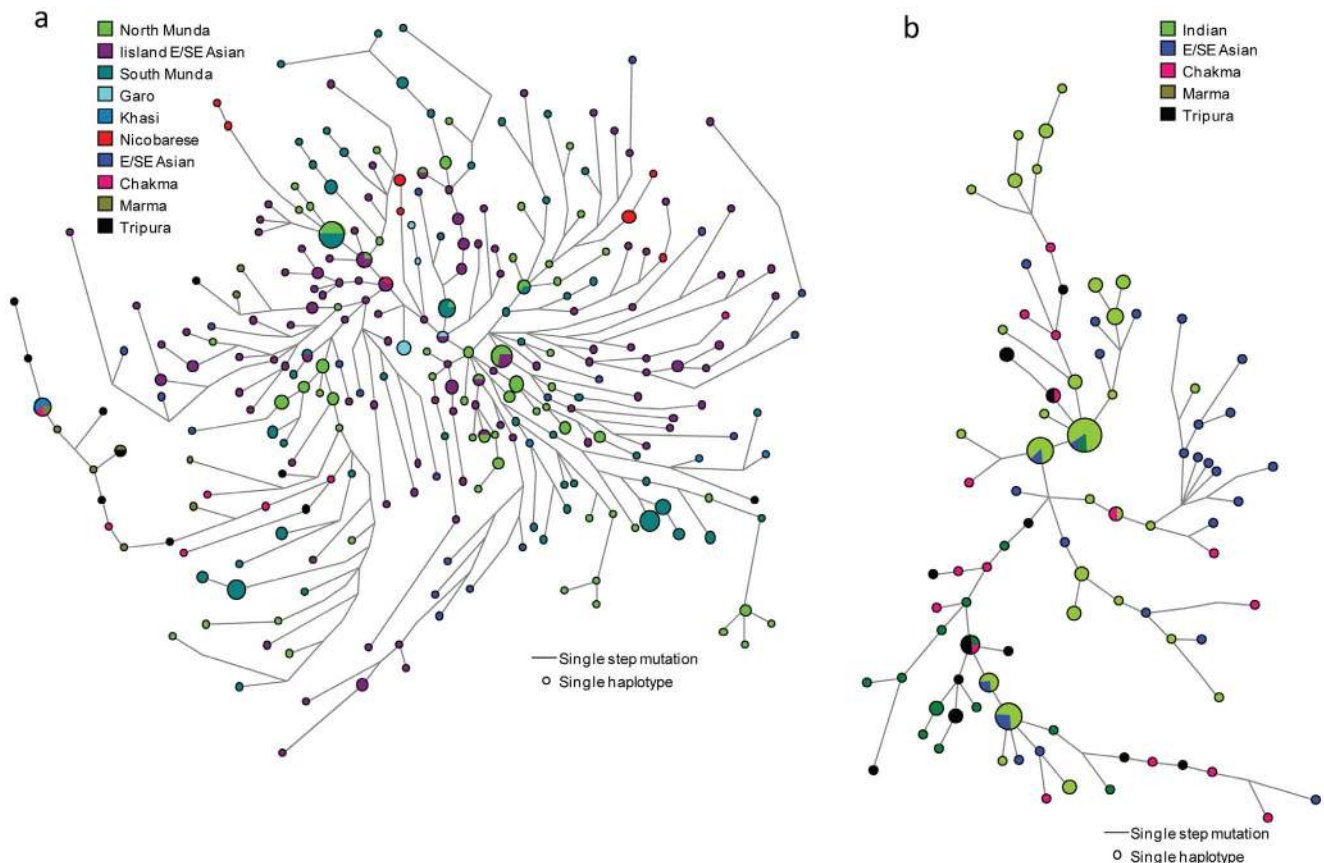


Figure 3. Unrooted phylogenetic network of a) haplogroups M95-O2a1; b) haplogroup M134-O3a2c1. The network was constructed using a median-joining algorithm as implemented in the Network 4.6.0 program. The size of the circles is proportional to the number of samples. doi:10.1371/journal.pone.0075064.g003

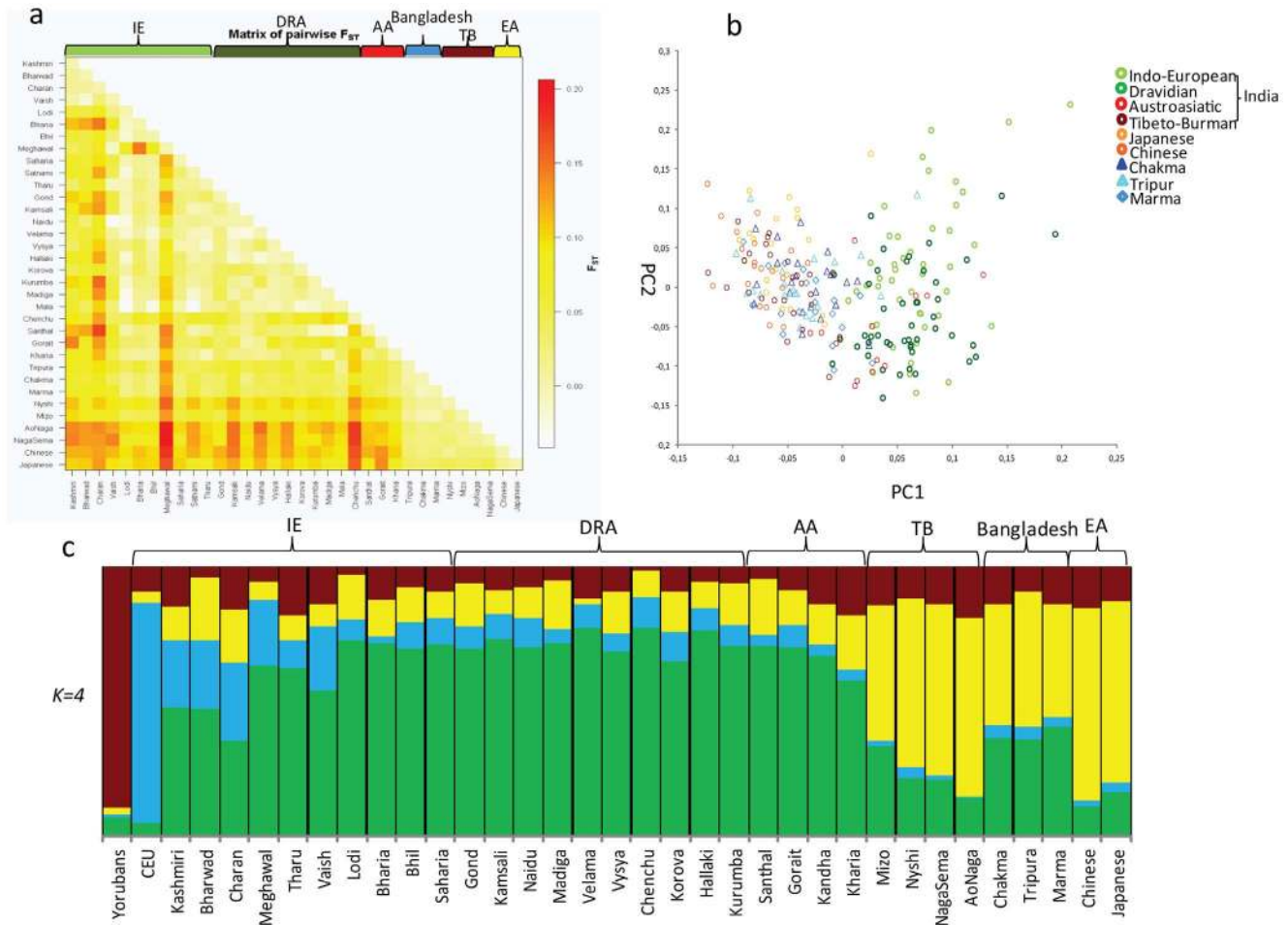


Figure 4. Autosomal Analysis. a) Heat map of pairwise F_{ST} of Bangladeshi tribal groups, in comparison with Indian and East Asian populations; b) PCA of Indian, East Asian and Bangladeshi groups. PC analysis was carried out using smartpca program (with default settings) of the EIGENSOFT package, PC1 represent 2.1%, while PC2 shows 1.7% of variations; c) Bar plot displays individual ancestry estimates for studied populations from a structure analysis by using STRUCTURE with $K=4$. doi:10.1371/journal.pone.0075064.g004

by these two places together (Fig. 1). These are major tribal groups inhabited in Bangladesh and represent approximately 90% of the total tribal population of Bangladesh. The sampling was done with an interview protocol that involved the queries pertaining to name of the tribe which they belonged, place of their ancestor, any oral history about their ancestry, etc. The related individuals with similar family background were avoided. This project was approved by the Institutional Ethical Committee of the Centre for Advanced Research in Sciences, University of Dhaka,

Bangladesh and the Centre for Cellular and Molecular Biology-CSIR, Hyderabad, India. The informed written consent was obtained from all the volunteers who participated in this study.

Genotyping

Over 32 Y chromosome biallelic markers from previously published dataset [23] were used in this study for assigning the haplogroup to each individual. A battery of 17 Y-STRs loci were amplified using Y-filer[®] kit (Applied Biosystems, Foster City, USA) in reaction volumes of 10 μ l with 1 U of AmpliTaq Gold[®] DNA polymerase (Applied Biosystems, Foster City, USA) with the manufacturer protocol. The PCR amplicons along with GS500 LIZ (as size standard) were analysed in the ABI 3730 DNA Analyzer (Applied Biosystems, Foster City, USA). GeneMapper v4.0 software program (Applied Biosystems, Foster City, US) was used to analyze the raw data.

We sequenced the hypervariable segment I (HVS-I) of mtDNA and the variations were scored against the Reconstructed Sapiens Reference Sequence (RSRS) [24]. Haplogroups were assigned based on HVS-I variations and are further confirmed by genotyping the coding region mutations published till date in PhyloTree (www.phylotree.org). Along with Y chromosome and

Table 4. Mean pairwise F_{ST} values for various loci between studied populations.

	mtDNA	Y chromosome	Autosomes
Chakma Vs. Marma	0.0095	0.0019	0.0035
Chakma Vs. Tripura	0.0051	0	0.0008
Marma Vs. Tripura	0.0155	0.0033	0.0104

doi:10.1371/journal.pone.0075064.t004

mtDNA markers, 50 AIMs published elsewhere [20], were also genotyped to infer the ancestry of Bangladesh population.

Statistical analysis

Fragment sizes of Y-STRs, were determined using the GeneMapper® Analysis Software v4.0 and allele designations were based on comparison with allelic ladders provided by the manufacturer. Out of 17 loci obtained, two DYS385 loci were excluded from the current analyses because they could not be distinguished using the typing method employed. DYS 389I (DYS 389cd) was subtracted from DYS389II and re-named DYS389ab. Thus, all the analysis linked with Y-STRs data were carried out with 15 loci. A median-joining network, resolved with the MP algorithm, was constructed using the Network package (version 4.5.0.2) (www.fluxus-engineering.com). The age of O2a1-M95 and O3a2c1-M134 was estimated from microsatellite variation within the haplogroup using the method described by Zhivotovsky et al. [25] and updated in Sengupta et al. [14].

Principal component analysis (PCA) for mtDNA and Y chromosomal haplogroups was performed using POPSTR, kindly provided by H. Harpending, and for autosomal SNP we used smartpca programme [26]. The analysis of molecular variance (AMOVA) was performed using Arlequin 3.5 [27]. For autosomal data, we filtered the combined data sets by using PLINK software 1.07 [28] to include only SNPs with a minor allele frequency >1% and genotyping success >99%. We calculated mean pairwise *F_{st}* values between populations for all autosomal SNPs using the approach of Cockerham and Weir [29]. We ran STRUCTURE [30] for the pruned data set (46 SNPs) from *K*=2 to *K*=8 (25 runs at each *K*) and selected the *K* (*K*=4) that maximizes the posterior probability of the data, as explained by the developers [31]. All structure runs performed 40,000 iterations after a burn-in of 50,000, following the default settings i.e. the admixture model, and assumed that allele frequencies were correlated.

References

- Bangladesh Bureau of Statistics. Available: <http://www.bbs.gov.bd/Home.aspx>. Accessed 2013 Aug 16.
- Maloney CT (1984) Tribes of Bangladesh and Synthesis of Bengali Culture. In: Mahmud S, Qureshi MS, editor. Tribal Cultures in Bangladesh. Rajshahi: Institute of Bangladesh Studies. pp. 5–52.
- van Driem G (2001) Languages of the Himalayas: An Ethnolinguistic Handbook of the Greater Himalayan Region, containing an Introduction to the Symbiotic Theory of Language, Leiden: Brill. 1401p.
- Blench R (2008) Re-evaluating the linguistic prehistory of South Asia. In: Toshiki Osada and Akinori Uesugi, editors. Kyoto: Indus Project, Research Institute for Humanity and Nature. pp. 159–178.
- Metspalu M, Kivisild T, Metspalu E, Parik J, Hudjashov G, et al. (2004) Most of the extant mtDNA boundaries in south and southwest Asia were likely shaped during the initial settlement of Eurasia by anatomically modern humans. *BMC Genet* 5: 26.
- Cordaux R, Weiss G, Saha N, Stoneking M (2004) The northeast Indian passageway: a barrier or corridor for human migrations? *Mol Biol Evol* 21: 1525–1533.
- Reddy BM, Langstich BT, Kumar V, Nagaraja T, Reddy ANS, et al. (2007) Austro-Asiatic tribes of Northeast India provide hitherto missing genetic link between South and Southeast Asia. *PLoS ONE* 2: e1141.
- Kivisild T, Rootsi S, Metspalu M, Mastana S, Kaldma K, et al. (2003) The genetic heritage of the earliest settlers persists both in Indian tribal and caste populations. *Am J Hum Genet* 72: 313–332.
- Chaubey G, Metspalu M, Kivisild T, Villesms R (2007) Peopling of South Asia: investigating the caste-tribe continuum in India. *Bioessays* 29: 91–100.
- Chaubey G, Metspalu M, Karmin M, Thangaraj K, Rootsi S, et al. (2008) Language shift by indigenous population: a model genetic study in South Asia. *International Journal of Human Genetics* 8: 41.
- Thangaraj K, Naidu BP, Crivellaro F, Tamang R, Upadhyay S, et al. (2010) The influence of natural barriers in shaping the genetic structure of Maharashtra populations. *PLoS one* 5: e15283.
- Sharma G, Tamang R, Chaudhary R, Singh VK, Shah AM, et al. (2012) Genetic affinities of the central Indian tribal populations. *PLoS one* 7: e32546.
- Tambets K, Tolk HV, Kivisild T, Metspalu E, Parik J, et al. (2003) Complex signals for population expansions in Europe and beyond. In: Bellwood P, Renfrew C, editors. McDonald Institute for Archaeological Research Monograph Series. Cambridge. pp. 449–458.
- Sengupta S, Zhivotovsky LA, King R, Mehdi SQ, Edmonds CA, et al. (2006) Polarity and temporality of high-resolution Y chromosome distributions in India identify both indigenous and exogenous expansions and reveal minor genetic influence of Central Asian pastoralists. *Am J Hum Genet* 78: 202–221.
- Underhill PA, Shen P, Lin AA, Jin L, Passarino G, et al. (2000) Y chromosome sequence variation and the history of human populations. *Nat Genet* 26: 358–361.
- Karafet TM, Lansing JS, Redd AJ, Reznikova S, Watkins JC, et al. (2005) Balinese Y-chromosome perspective on the peopling of Indonesia: genetic contributions from pre-neolithic hunter-gatherers, Austronesian farmers, and Indian traders. *Human biology* 77: 93–114.
- Hammer MF, Karafet TM, Park H, Omoto K, Harihara S, et al. (2006) Dual origins of the Japanese: common ground for hunter-gatherer and farmer Y chromosomes. *J Hum Genet* 51: 47–58.
- Sahoo S, Singh A, Himabindu G, Banerjee J, Sitalaximi T, et al. (2006) A prehistory of Indian Y chromosomes: evaluating demic diffusion scenarios. *Proc Natl Acad Sci U S A* 103: 843–848.
- Chaubey G, Metspalu M, Choi Y, Mägi R, Romero IG, et al. (2011) Population Genetic Structure in Indian Austroasiatic speakers: The Role of Landscape Barriers and Sex-specific Admixture. *Mol Biol Evol* 28: 1013–1024.
- Dhandapani PS, Sadayappan S, Xue Y, Powell GT, Rani DS, et al. (2009) A common MYBPC3 (cardiac myosin binding protein C) variant associated with cardiomyopathies in South Asia. *Nat Genet* 41: 187–191.
- Reich D, Thangaraj K, Patterson N, Price AL, Singh L (2009) Reconstructing Indian population history. *Nature* 461: 489–494.

Supporting Information

Figure S1 Y chromosome haplogroups observed among the studied populations with major Y chromosome biallelic markers. (TIF)

Figure S2 Unrooted phylogenetic network of a M214 derived individuals. (TIF)

Figure S3 Unrooted phylogenetic network Tree of all Bangladeshi Tibeto-Burmans with eight common Y-STRs. (TIF)

Table S1 mtDNA variations observed among the studied populations. (DOC)

Table S2 Y-chromosome age estimates for haplogroups O2a and O3a3c among population groups of India E/SE Asia and Bangladesh. (DOC)

Table S3 Y STR haplotype data of the studied populations. (DOC)

Table S4 Pairwise population *F_{st}* values for the autosomal analysis. (XLS)

Acknowledgments

We thank all the volunteers who donated their blood samples for this study. We are grateful to the anonymous reviewers for their constructive suggestions in improving the quality of the manuscript.

Author Contributions

Conceived and designed the experiments: NNG LS KT. Performed the experiments: NNG RT VKS AF AKP MS SA PV SK BKY AGR DSR. Analyzed the data: NNG RT GC. Contributed reagents/materials/analysis tools: KT SSQ LS. Wrote the paper: GC KT RT NNG.

22. Altshuler D, Gibbs R, Peltonen L, Dermitzakis E, Schaffner S, et al. (2010) Integrating common and rare genetic variation in diverse human populations. *Nature* 467: 52–58.
23. Karafet TM, Mendez FL, Meilerman MB, Underhill PA, Zegura SL, et al. (2008) New binary polymorphisms reshape and increase resolution of the human Y chromosomal haplogroup tree. *Genome Res.* 18: 830–838.
24. Behar DM, Van Oven M, Rosset S, Metspalu M, Loogväli E-L, et al. (2012) A “Copernican” reassessment of the human mitochondrial DNA tree from its root. *Am J Hum Genet* 90: 675–684.
25. Zhivotovsky LA, Underhill PA, Cinnioglu C, Kayser M, Morar B, et al. (2004) The effective mutation rate at Y chromosome short tandem repeats, with application to human population-divergence time. *Am J Hum Genet* 74: 50–61.
26. Patterson N, Price AL, Reich D (2006) Population structure and eigenanalysis. *PLoS Genet* 2: e190.
27. Excoffier L, Lischer HEL (2010) Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows. *Mol Ecol Resour* 10: 564–567.
28. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MAR, et al. (2007) PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am J Hum Genet* 81: 559–575.
29. Cockerham CC, Weir BS (1984) Covariances of relatives stemming from a population undergoing mixed self and random mating. *Biometrics* 40: 157–164.
30. Rosenberg NA, Pritchard JK, Weber JL, Cann HM, Kidd KK, et al. (2002) Genetic structure of human populations. *Science* 298: 2381–2385.
31. Falush D, Stephens M, Pritchard JK (2003) Inference of Population Structure Using Multilocus Genotype Data: Linked Loci and Correlated Allele Frequencies. *Genetics* 164: 1567–1587.