



Evaluating the genetic impact of South and Southeast Asia on the peopling of Bangladesh



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ARTICLE INFO

Article history:

Received 14 April 2015

Received in revised form 21 September 2015

Accepted 30 September 2015

Available online 8 October 2015

Keywords:

Caste

Tribe

Bangladesh

Autosomal STR

South Asia

ABSTRACT

Despite rapidly growing understandings and dependency on single nucleotide polymorphisms (SNPs), highly variable autosomal short tandem repeats (STRs) are still regarded as the most established method to differentiate individuals at forensic level. Here with large number of various ethnic groups we undertook this study to reveal the genetic structure of the most densely populated part of South Asia i.e. the Bangladesh. The purpose of this work was to estimate population parameters based on the allele frequencies obtained for 15 polymorphic autosomal STR loci investigated in caste and tribal populations from Bangladesh ($n = 706$). We compared the results in a broader context by merging 24 different populations of Asia to pertain their affinity. Various statistical analyses suggested a clear cut demarcation of tribal and non-tribal in Bangladesh. Moreover, beside the phylogenetic structure of the studied populations, it is found that the mean heterozygosity value was highest among the populations of Bangladesh, likely because of gene flow from different directions. However, Tonchangya, Adi and Khumi showed sign of genetic isolation and reduced diversity, possibly as a result of genetic drift and/or strong founder effects working on small endogamous populations.

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1. Introduction

Bangladesh is geographically surrounded on three sides by India, joins a land bridge to Southeast Asia via Myanmar and in South it joins the Indian Ocean with the largest bay in the world, the Bay-of-Bengal. The alluvial deposits of the three major rivers form most of its land: the Ganges, the Brahmaputra and the Meghna. The populations of Bangladesh constitute mostly Bengali speakers (a branch of Indo-Aryan language), while the remaining are tribal groups affiliated with Dravidian, Indo-European, Austroasiatic and Tibeto-Burman language families [1–3]. The number of genetic studies of this region is very limited and mainly restricted to forensic markers for a few caste and tribal populations [4–8]. Several of the tribes are yet to be investigated and none of the study however, so far have analysed a large number of tribal and caste populations.

Therefore, in this study data from 15 autosomal polymorphic tetranucleotide STR loci were considered for analyzing eleven

ethnic groups of Bangladesh (Bangladesh Mixed, Bangladesh Muslim, Bom, Khumi, Khyang, Mro, Chakma, Marma, Tripura, Tonchangya and Bangladeshi Tibeto-Burman mixed). The generated data of present study was compared with twenty-four other populations: 8 from South Asia: Balochi, Brahui, Sindhi, Pathan, Burusho, Madiga, Kapu, Adi; and 16 from East and Southeast Asia: Cambodian, Han, Dai, Daur, Hezhen, Lahu, Miao, Oroqen, She, Tujia, Tu, Xibo, Yizu, Mongola, Naxi, Japanese (Supplementary Table 1). In the way to reveal the micro level genetic structure of Bangladeshi population, the purpose of this study was to evaluate the extent of diversity in Bangladeshi caste and tribal population in comparison to other related Asian populations.

2. Materials and methods

2–3 mL of peripheral blood was collected from each unrelated individuals. All individuals signed a written informed consent according to the ethical guidelines of the Helsinki Declaration. For some samples phenol–chloroform protocol and for others QIAamp[®] DNA blood mini kit (QIAGEN, Germany) were used to extract DNA from blood. DNA quantification was done with a Nanodrop 2000 spectrophotometer (Thermo Scientific, USA). Allele frequencies for the 15 short tandem repeats (STRs) loci included in

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Table 1
The mean heterozygosity values of the studied populations of Bangladesh.

Population	n	Heterozygosity	SD
Bangladeshi mix	197	0.81053	0.05379
Bom	24	0.78806	0.07138
Khumi	11	0.76075	0.09778
Khyang	17	0.81307	0.06686
Mro	28	0.79727	0.06416
Chakma	110	0.79999	0.05376
Marma	83	0.82814	0.03896
Tripura	81	0.83232	0.04445
Bangladesh_Muslim	109	0.80504	0.05545
Tonchangya	32	0.74312	0.09957
BDTB_Mix	14	0.81305	0.06501

n = number of samples.

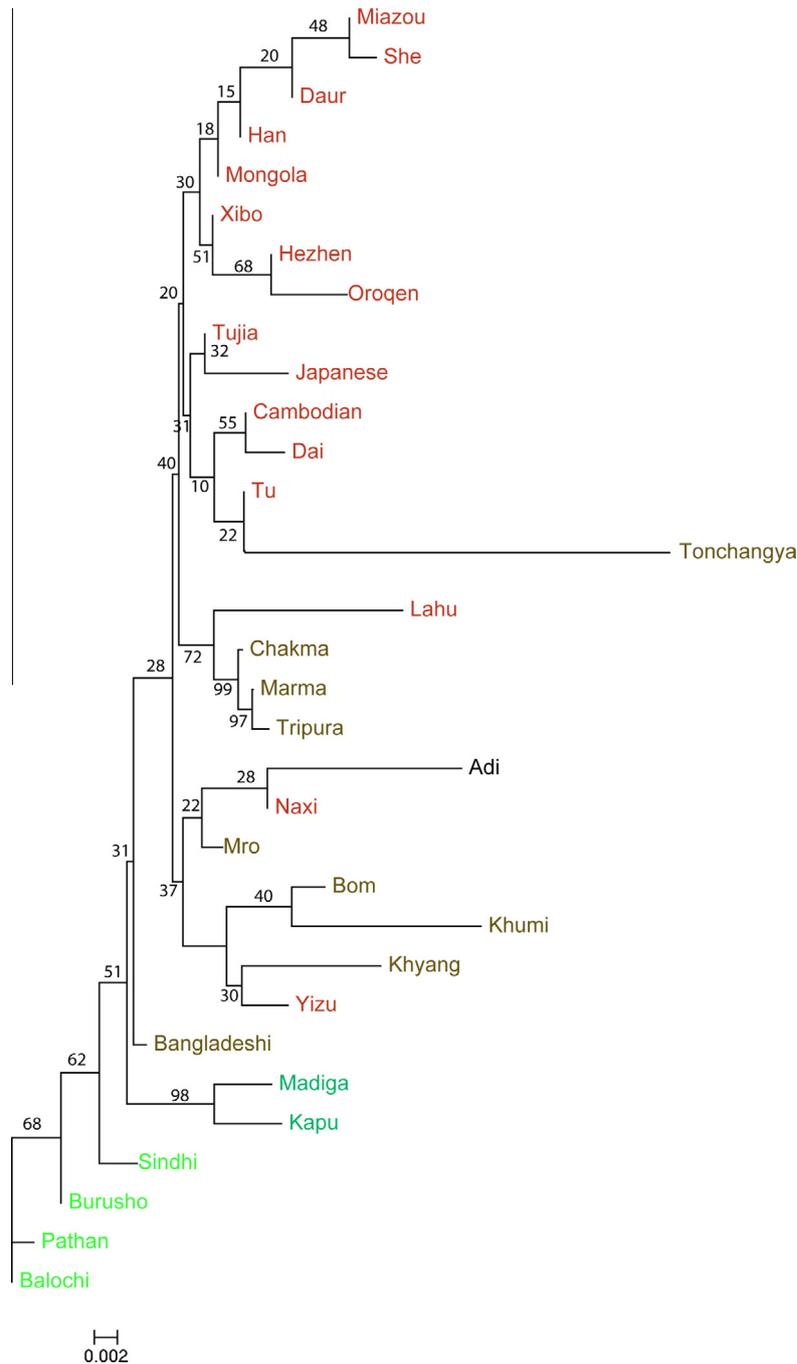


Fig. 1. Neighbor Joining Phylogenetic Tree showing the relatedness of 35 Asian populations from 15 loci autosomal STR data.

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