GENETIC DIVERSITY AMONG BANGALI AND SEVEN ETHNIC GROUPS OF BANGLADESH BASED ON Y-CHROMOSOME

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Certificate from supervisor

This is to certify that the research work embodied in this dissertation entitled **“Genetic diversity among Bangali and seven ethnic groups of Bangladesh based on Y-chromosome”** submitted by **Md. Mahamud Hasan** (Registration No.: 178/2014-15), has been carried out under my supervision. It is further certified that the research work presented here is original and suitable for submission for the partial fulfillment of the degree ‘Doctor of Philosophy (Ph.D) in Genetic Engineering and Biotechnology’ from University of Dhaka. The work on any part thereof has not been submitted elsewhere for any other degree.

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DECLARATION

I hereby declare that this thesis entitled **“Genetic diversity among Bangali and seven ethnic groups of Bangladesh based on Y-chromosome**” contains no material which has been accepted for the award of any other degree or diploma in any university or equivalent institution. To the best of my knowledge and belief, the thesis contains no material previously published or written by another person, except where due reference is made in the text of the thesis.

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DEDICATION

DEDICATED TO
MY PARENTS, MY WIFE AND MY BELOVED SON FOR THEIR UNCONDITIONAL LOVE, UNWAVERING SUPPORT AND ENCOURAGEMENT

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ABSTRACT

A comprehensive population genetic study was conducted using 17 Y-chromosome specific microsatellites to decipher genetic diversity of the Bangladeshi populations from a Y-chromosome perspective. Seven ethnic populations living in different parts of Bangladesh along with the mainstream Bangali population was included in this study. A total of 1,594 haplotypes were typed in 1,631 male subjects belonging to Bangali, Chakma, Tripura, Rakhine, Marma, Hajong, Manipuri, and Khasia with corresponding discrimination capacity of 97.301, 73.885, 65.563, 75.862, 77.536, 80.909, 74.809, and 81.250%, respectively. Overall, 1,359 different haplotypes were detected, of which 1,222 (89.919%) were each found in a single male-only. Observed haplotype diversity values were in a range between 0.982 (Manipuri) and 0.998 (Bangali). Bangalis have the highest average gene diversity value of 0.662 while tribal populations showed less. The pair-wise genetic distances R_{st} values between the studied populations and 32 worldwide reference populations revealed that the strong genetic relationship of Bangali with Nepalese (Kathmandu, Nepal), Irani (Central Iran, Iran), Iraqi (Iraq), Tamil (Tamil Nadu, India), and Bhil (Gujarat, India) populations. In addition, Chakma, Tripura, Rakhine, Marma, and Hajong were the most similar population to Tripuri (Tripura, India), Garo (Tangail, Bangladesh), Han (Beijing, China), Korean (Seoul, South Korea), Asian American (United States), and Japanese (Tokyo, Japan) populations, respectively. In contrast, Manipuri showed close genetic affinity with Tamil (Tamil Nadu, India) and Bhil (Gujarat, India) population. Moreover, Khasia lies closer to a clade consisting of Oraon (Chhattisgarh, India) and Santal (Dinajpur, Bangladesh). The studied samples analyzed were categorized into twenty different haplogroups. The Bangali showed greater frequency for haplogroups R1a, H, and L, whereas the studied seven ethnic populations exhibited higher frequency for haplogroups L, Q, R1a, and T. The Bangali contains paternal lineages from India, Pakistan, Afghanistan, and Iran of West Asia, whereas the ethnic populations contain paternal lineages from the northern and southern areas of East Asia. The study has also constructed haplotype and allele frequency data for 17 forensic identity markers and characterized the levels of populations sub-structure as well as genetic relationship within and between Bangladeshi populations.

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List of Abbreviations

AMOVA	Analysis of Molecular Variance
BBS	Bangladesh Bureau of Statistics
CE	Capillary Electrophoresis
ddH$_2$O	distilled deionized water
DNA	Deoxyribonucleic acid
DNase	Deoxyribonuclease
DYS	DNA-Y-chromosome-Segment (unique)
EDTA	Ethylene diamine tetra acetic acid
et al.	and others
F_{ST}	Fixation Index
FUH	Fraction of Unique Haplotypes
GD	Gene diversity
HD	Haplotype diversity
HID	Human Identification
Hi-Di	Highly deionized
HVR	Hypervariable region
ISFG	International Society of Forensic Genetics
ISOGG	International Society of Genetic Genealogy

Abbreviations

LRCA	Less recent common ancestor
Mb	Megabases
MDS	Multi-dimensional scaling
MEGA	Molecular Evolutionary Genetics Analysis
M-J Network	Median-Joining Network
MRCA	Most recent common ancestor
MSY	Male-specific region of the Y-chromosome
mtDNA	Mitochondrial DNA
NFDPL	National Forensic DNA Profiling Laboratory
N-J	Neighbor-Joining
NRY	Non-recombining region
OD	Optical Density
PAR	Pseudoautosomal region
PCR	Polymerase chain reaction
PD	Power of discrimination
PE	Power of exclusion paternity
PM	Match probability
POP	Performance Optimized Polymer
RNA	Ribonucleic acid
RNase	Ribonuclease
SNPs	Single nucleotide polymorphisms
ssDNA	Single-stranded DNA
STR	Short Tandem Repeat
Taq	*Thermus aquaticus*
TE	Tris EDTA
X-STRs	X-chromosome-specific STRs
Y-DNA	Y-chromosome deoxyribonucleic acid
YHRD	Y-chromosome Haplotype Reference Database
Y-STRs	Y-chromosome-specific-Short Tandem Repeats

Chapter One

INTRODUCTION

1.1 Background of the Present Study: Geography and Peoples

Bangladesh is a country in South Asia. It is bordered on the east, north, and west side with India and a short land with Myanmar in the southeast. The country occupies the water bodies formed by the Bay of Bengal on its southern side. Bangladesh is the 8th largest and densely populated country in the world. Bangladesh is inhabited by many different tribal groups. The total population of Bangladesh is 158.9 million [Bangladesh Statistics, 2017]. Historically, there are mainly four racial groups in Bangladesh: Bangali, Mongoloid, Dravidian, and Proto-Australoid. Being racially homogeneous, Bangali comprises 98% of the total population and belongs to the Bangali ethnolinguistic group. According to Asiatic Society of Bangladesh in 2007, overall 45 indigenous populations have been recorded. As stated by Bangladesh Bureau of Statistics in 2013, there are 32 tribal populations have been documented representing 1% of the total populations in Bangladesh. The remainder is mostly indigenous ethnic minorities living different pockets of the hilly zone in the southeastern, north-central, and northeastern regions as well as some areas of the plain lands of the country.

The Mongoloid group is confined to the hills beside the southern part of the Shillong plateau. This group then shuffled to the Sylhet hilly areas and in Chittagong Hill Tracts (Rangamati, Khagrachari, and Bandarban districts) along the eastern border of Bangladesh adjoining Myanmar and Indian states in Mizoram and Tripura. The Chittagong Hill Tracts host more than 13 tribes of which Chakma are the largest single tribe in Bangladesh. According to the population census carried out by the Government of Bangladesh in 2001, about 300,000 Chakmas and 90,000 Tripuras were inhabitants in Bangladesh [Ferdous *et al.*, 2010]. Chakma population is consisting of about 50% of the total tribal inhabitants of Bangladesh and belongs to the Tibeto-Burman lingual family [Hannan, 2015]. In the view of antropologists, the Chakmas are Mongoloid people and the largest indigenous group in Bangladesh. In 1998, as stated by H.H. Risely, the Chakmas bear 84.5% Mongolian characteristics on their bodily feature. Since ancient times, the Chakmas had lived in Tripura and Mizoram (in Lusai Hills). Anthropologist de Barros stated that this group had their settlement in the northeastern part of Chittagong Hill Tracts in the sixteenth century [Kamal *et al.*, 2007].

The Tripura community is one the largest ancient Tibeto-Burmese language ethnic groups living in the Chittagong Hill Tracts, comprises about 18% of the entire tribal populations of Bangladesh. This tribe is Mongoloid in respect of racial origin. The fact those five thousand years ago, their ancestors reached to the eastern states of India from Mongolia by crossing Tibet and Siberia of Central Asia. After the subcontinent had been divided in 1947, a significant number of the Tripuras acquired citizenship of East Pakistan, now Bangladesh. The Rakhine community is one of the tribe living in the Cox's Bazar, Patuakhali and Barguna of Bangladesh. They are Mongoloid in respect of racial origin. Their original homeland was Arakan province of Myanmar. In the eighteenth century, most of the Rakhines left Arakan due to political unrest and took their settlement at Ramu and its nearest regions of Chittagong. The Marmas are the second largest ethnic community living in the Chittagong Hill Tracts of Bangladesh. The Marma's are Mongoloid in respect of racial origin. Several historical sources confirm that Marmas were Myanmar's nationalism and in early seventeenth century, they lived in Pegu of Myanmar. During the time of Pegu war in early seventeenth century, most of the Marmas was forced to migrate to the Chittagong.

The Hajong community has been living in the northern areas of Sherpur, Netrokona, and Sunamganj districs of Bangladesh. Several historians stated that the Hanjongs are also descendants of the Tibeto-Burmese people of Indo-Mongoloid race. Many Hajongs believe that their original home was in Abantinagar (Malab) near Bihar. Many anthropologists, researchers and writers stated that the Hajongs migrated to Bangladesh from Hajo region of the district of Kamrup in Assam, India. During the fear of communal riots in 1964, a significant number of the Hajongs left their villages for India and forced to migrate to Bangladesh. The Manipuri community is one of the indigenous groups living in Maulvibazar, Sylhet, Habiganj and Sunamganj of Bangladesh. They are mainly inhabitants of Manipur state of India. During the war between Manipur and Myanmar in 1741, a greater number of Manipuris left their homeland and forced to migrate to Bangladesh. Bishnupriya Manipuri has originated from Magadhian Prakrit language group and its structural similarities with Assamese and Bengali. In contrast, Meithei Manipuri has originated from the Kuki-Chinese of dialects of the Tibetan-Burmese family of languages. It is also known from the ancient text that Meithei Manipuris came to Manipur state of India from Mongolia. The Khasia, also called Khasi, community is one of the small ethnic groups residing mainly in some hilly regions of Maulvibazar and

Habiganj district of Bangladesh. According to the anhropologists, the Khasis were originated from the Mon-Khem tribe of Thailand and Cambodia. They are mainly cultivators of betel-leaf and betel-nut by profession. According to the anthropologists, Khasias were originated from the Mon-Khem tribe who had come from the vast regions of Thailand and Cambodia. Although historians and anthropologists agree that the all tribes are not the original inhabitants of Bangladesh. Some historians have established their argument that Dravidian and Austro-Asiatic speaking groups have evolved from an older original substrate of proto-Australoids, while the Tibeto-Burman speaking groups are later immigrants from Tibet plateau and Myanmar to the Indian subcontinent [Guha, 1935].

This study is the first in-depth large study on genetic diversity of Bangladeshi population based on Y-chromosome short tandem repeats (Y-STRs) haplotypes which engaged the mainstream Bangali and seven major tribal populations (Chakma, Tripura, Rakhine, Marma, Hajong, Manipuri, and Khasia) living in Bangladesh. Y-chromosomal STR markers are very informative tools in understanding the human origin, paternal lineage, human migration, patrilineal affinities among populations as well as a powerful tool for criminal investigations. The present molecular genetic study presented a comprehensive genetic portrait of Bangladeshi population with respect to the Y-chromosome distributions in the country. Previous studies based on autosomal and Y-chromosomal STR markers focused on few indigenous groups with small sample size in Bangladesh. Several studies reported genetic affinities between Bangladeshi populations and global reference population groups, supporting the migration of the Bangali mainstream population and other castes into the Bangladesh [Alam *et al.,* 2010; Hasan *et al.,* 2015; Hasan *et al.,* 2016; Hasan *et al.,* 2018]. An extensive study of Y-chromosome diversity within the sub-continent found that the Central Asian population's influence in India is more cultural than genetic [Sengupta *et al.,* 2006].

1.2 Why study the Y-chromosome

For the past three decades, short tandem repeats (STRs) have been the most powerful tools in most of the genetic testing labs all over the world. Autosomal STR markers, also caled bi-parentally inherited markers, has become the gold standard in forensic investigations. The Y-chromosome markers are inherited from the non-recombining part of the Y-chromosome (NRY) transferred to the paternal germline. Due to its longer repeat units, lack of recombination and a lower rate of mutation, in some cases making them better suited for population genetic studies than other marker systems. For these chracteristics, the Y-chromosome is extremely sensitive to genetic drift. Y-chromosome is therefore a unique record of paternal inheritance a male child should share the Y-haplotypes with the father. Human genetic and ancestry studies throughout the male-specific region of the Y-chromosome (MSY) have assisted to understand human migration and evolution to uncover the roots during their spreading out on earth as well as will help to forensic investigations [Ambers *et al.*, 2018].

Comparable to the Y-chromosome, mitochondrial DNA (mtDNA), also called matrilineal lineage markers have lack of recombination followed by lower rate of mutation, and polymorphism has been remarkably hard to find. In contrast, the extraordinary characteristics with excessive mutation rate in the high variation region (HVR) in mtDNA and potential possibility of recombination may lead to frequent change in the DNA sequence and could cause bias [Arctander, 1999]. Recently several studies revealed that mtDNA can also be inherited from father i.e. father also occasionally contribute mtDNA to his child [Luo *et al.*, 2018; McWilliams and Suomalainen, 2019]. Nowadays, the X-chromosomes have been left out of many genome-wide studies and most of the geneticist declares that Y-chromosome microsatellite haplotypes are the storyteller and evolutionary markers for global human evolution. Unlike autosomal markers, analysis of sex-specific Y-chromosome and mtDNA markers has been quite extensive and these two genetic systems have smaller effective population sizes, they are more susceptible to gene variation in a population and, hence, more likely to vary in frequency among populations [Wood *et al.*, 2005].

1.3 Describing Genetic Diversity

Genetic diversity, also called genetic variation, can be quantified and interpreted from allele frequency distributions across the genome. Haplotypes, which is a sequence of physically linked alleles along a chromosome, can also be informative about diversity and human evolutionary history. A number of statistics and methodologies that use genetic differentiation have been developed to understand population demographic history. In addition, genetic diversity denotes the total number of genetic landscapes in the whole genome of a species. The genetic diversity is also differentiated from genetic variability, which explains the trend of genetic features to vary. It serves as a way for inhabitants to adjust to changing environments. With more dissimilarity, it is more likely that some species in a population will retain changes of alleles that are compatible with the environment. In 2006, geneticist Groom and his co-workers reported that the individuals were more likely to survive to produce offspring bearing those alleles and the population will continue for more generations because of the success of these individuals.

The genetic variation or diversity of a population can also be evaluated by the number of distinct alleles and private allele a population carries [Kalinowski, 2004]. Private alleles can be useful to study population structure as well as human migration. We can use private shared alleles between populations as an indicator for gene-flow between the populations [Szpiech *et al.*, 2008]. The field of population genetics study includes a number of assumptions, theories, and hypotheses concerning the research on genetic diversity. The evolution neutral concept recommends that diversity is the effect of the accumulation of neutral interchanges. Diversifying selection is one of the most important theories that two different sub-populations of a species live in different locations and environments that choose for several alleles in a specific locus. On the other hand, the frequency-dependent selection is the hypothesis that as alleles become more common, they become more vulnerable.

There are many different methods to evaluate genetic diversity and it can be determined in a) within populations and b) between populations. In 2007, a study was performed by the National Science Foundation and found that genetic diversity and biodiversity are dependent upon each other and that diversity inside a species is essential to retain diversity among other species, and the other way around. As we know, genotypic and phenotypic variation and diversity have been observed in all species at the molecular along with organism levels. In 2002, evolutionary geneticist Frankham and colleagues' reported that the genetic diversity can be influenced by many factors like the size of the population, natural selection, mutation rates, gene flow between populations, introgression from hybridization and historical effects on these factors (e.g., population bottlenecks). He also reported that genome-phenome organization in nature is non-random, heavily structured, and correlated with abiotic and environmental diversity and stress.

Genetic diversity is also essential for a species to expand their biological characteristics. From the molecular basis, species that have a less genetic variation or diversity are at a greater risk. In addition, with an insignificant amount of genetic variation within the species, healthy reproduction becomes gradually more difficult, and the descendant is more likely to deal with troubles such as inbreeding. The reduction of genetic diversity or genomic variations, as a result, can also increase for the certain types of inherited diseases of a species or a population.

1.4 The Y-chromosome STR Markers and the Paternal Transmission

Due to the unique biology of the Y-chromosome, Y-chromosomal polymorphisms and its genomic markers have been used in forensic investigation, medical genetics and human evolutionary studies to determine human ancestry or patrilineal associations within and among populations (Figure 1.1). It has been recommended that, due to diverse dissemination of region-specific allele frequencies, Y-STRs can be used to evaluate genetically close related human populations. It is proved that the Y-chromosome is inherited without changed from father to son to grandson, except for mutations (changes in the genetic code). But, it is the observation of a match of a Y-chromosome profile with another profile does not bring the power of discrimination as well as weight into court. The lack of recombination within the Y-chromosome markers signifies that Y-chromosomal repeat markers results have to be combined into a haplotype for investigating to available databases as well as estimating the rarity of a specific haplotype.

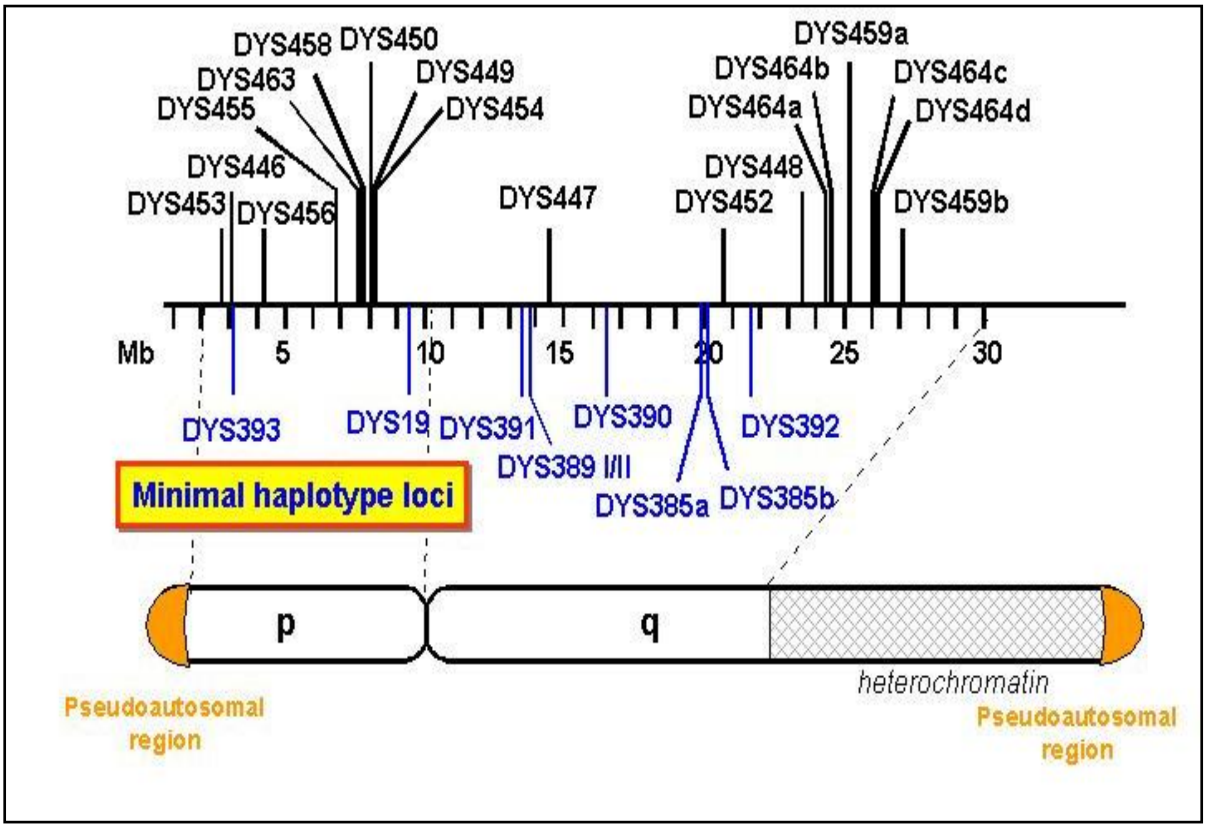

Figure 1.1: Relative positions for commonly used Y-STR markers (Redd *et. al.*, 2002).

DNA databases like as Autosomal STR database, Y-chromosomal STR database, X-chromosomal STR database, and mtDNA databases are important for comparison purposes and suspect identification to understand how frequent or how rare a crime-scene DNA profile may be in a particular population. Within the last several years, a number of Y-STR haplotype databases are developed by a different organization. The Y-Chromosome Haplotype Reference Database (YHRD), one of the largest organized and annotated human population databases in the world, and also most widely used and worldwide popular Y-STR database was constructed by population geneticist Prof. Dr. Lutz Roewer and co-scientists at Humbolt University, Berlin, Germany and has been available online since 2000. As of Release Version 59; November 01, 2018, more than 205,059 haplotypes from 932 populations around the world can be searched via the internet at the following websites: http://www.yhrd.org.

1.5 The Y-chromosome: A Storyteller for Studying Human Evolution and Migration

The human Y-chromosome DNA typing has become one of the major powerful bio-molecular tools for human identification in forensic investigations, genealogical mapping and the study of human evolutionary and ancestry history from a patrilineal lineage perspective given that it does not undergo meiotic recombination with the exception of the pseudoautosomal regions [Underhill *et al.*, 2000; Jobling and Tyler-Smith, 2003]. In the small portions of DNA, about 0.1% or one million nucleotide of whole genome, differs between people and makes us unique individuals and also have two hypervariable polymorphic regions (HV1 and HV2) which provide the capability of using DNA information for human identity as well as genealogical purposes [Butler *et al.*, 2002]. Short tandem repeats, STRs (Autosomal STRs, Y-STRs, and X-STRs), and single nucleotide polymorphisms, SNPs (Y-SNPs and mitochondrial SNPs) analyses are major classes of markers that will play a significant role in the forensic investigation as well as the study of the population genetics. It is a fact that the analysis of genetic variation, in the short tandem repeats of Y-Chromosomal DNA, provides unique information on the genetic diversity of the population. In view of that, the allele combination of a series of unique Y-STR loci has thus been considered a haplotype.

Besides this, the Y-chromosome STR and mitochondrial DNA markers are also known as ‘lineage markers’. These markers are passed down from parent to child without changing any paternal or maternal information, except for mutational events. Paternal lineages can be sketched with Y-chromosomal DNA sequence information while maternal lineages can be followed with mitochondrial DNA sequences. With respect to paternal or maternal lineage markers, the biological genetic information from each marker is mentioned to as a haplotype rather than a genotype because there is only one allele per locus in an individual. Because the Y-chromosome STR or SNP markers are associated on the same chromosome and the markers are not mixed up with each generation. Therefore, it is not effective for a haplotype in distinguishing between two or more individuals while genotypes obtained from autosomal STR markers that are unlinked and isolate separately from generation to generation. For that reason, short tandem repeat (STR) markers obtained from the X and/or Y-chromosome have been very convenient not only forensic application, but also use in the studies of human migration as well as human ancestry investigations [Jobling *et al.*, 1997; Roewer *et al.*, 2000]. Hence, the frequencies of unique markers cannot combine into one probability statement using the product rule [Butler, 2001].

A DNA profile is formed with a set of genetic markers which are found at different frequencies along with locus or gene diversity in a population. These collections of the same type of genetic markers are known as a population genetic database or DNA database. If the frequencies of the genetic markers making up a DNA profile are very high and found in half of the population, the statistical strength or discrimination power of the particular DNA profile is not strong. On the contrary, if the genetic markers of the DNA profile are found only in one in a million individuals, then the statistical discrimination power of the DNA profile is very strong. It is therefore important that the DNA databases of a population are statistically analyzed before the data are used to determine the incidence rate of a particular DNA profile in forensic casework. If the statistical analysis of the data shows significant value, it can exaggerate the strength of the evidence against the suspect [Balding *et al.*, 1996]. On the other hand, it is now widely accepted to the forensic scientists that mtDNA is maternally inherited and the population genetic characteristics of mtDNA are similar to the NRY. For this reason, population geneticists also use mtDNA as a tool for forensic investigation, mapping of population genetic diversity, and for studying human evolution [Ding *et al.*, 2011].

1.6 Population Genetics: A Study on Population Evolution

Population genetics is the study of the organization of any biological populations, and changes in genetic structure that result from a process of different types of factors including natural selection, genetic drift, transformation or mutation, and gene flow. For this basis, population geneticists engaged themselves with their aims by developing mathematical hypotheses or models of gene frequency and genetic diversity. Then they are trying to draw conclusions from those hypotheses about the likely configurations of genetic variance in the ancient populations and testing the conclusions against observed data.

By studying formal approaches of allele frequency change, forensic DNA scientists, human evolutionary investigators, and population geneticists, therefore, hope to make it easier understanding on the human evolutionary procedure and to permit the effect of different evolutionary hypotheses to be investigated in a quantitatively particular way. It is a fact that a sexual inhabitant is a set of species or organisms in which any pair of individuals can inter-breed together. This mentioned that all members belong to the same species and live close to each other. The field of theoretical population genetics came into being between the 1920s and 1930s, great thanks to the endless research of R.A. Fisher, J.B.S. Haldane and Sewall Wright for their contribution on population genetics [Provine, 1971]. Gradually with the development of biology and genetics, modern physical anthropology began to apply genetics and biochemistry to study the ancestry and diversity of human populations. According to molecular biology, population genetics is the study of the frequency and interchange of genes and alleles in population samples.

As long as the modern human being race existed, humans wondered about whom they are and where they came from. The human evolutionary study also developed to answer those questions. At the very beginning, population genetics deals with humans from a biological viewpoint and phenotypic characteristics like body size, skin colour, iris colour, hair structure, and form were the initial markers used to study populations. Hair, skin and iris colours are highly transmissible and visible characteristics or traits in humans. Several studies were conducted to evaluate the scope of the possible genetic consequences on the inter-individual variation of a number of body configuration indices, human skin and hair pigmentation genes differentiation as well as iris color through an examination of worldwide gene diversity patterns [Ginsburg *et al.*, 1998; Anno *et al.*, 2008; Kayser *et al.*, 2008].

For studying population genetics, Y chromosome STR diversity was measured by means of the analysis of molecular variance (AMOVA). Almost, genetic diversity and genetic relationship between and among populations can be visualized by a phylogenetic tree or Neighbor-Joining tree; an illustration that represents evolutionary relationships among organisms, using pair-wise R_{st} genetic distances. In this tree, two species are more genetically related if they have a more recent common ancestor (MRCA) and less related if they have a less recent common ancestor (LRCA).

1.7 The Y-chromosome: Powerful Tools for Forensic Sciences

More than three decades ago, in 1993, after the invention of polymerase chain reaction (PCR) technology by Dr. Karry Banks Mullis, short tandem repeats (STRs) become most powerful molecular techniques for human identification in forensic sciences and the investigation of human evolutionary history. Autosomal STRs, X-chromosomal STRs (both are bi-parental markers), Y-chromosomal STRs (patrilineal markers), and mitochondrial DNA (matrilineal markers) are the major molecular tools for playing a significant role in the forensic examination.

For these unique features of the Y-chromosome, most of the geneticist have been choosen Y-chromosomal STR markers for criminal identification, genealogical studies and investigation of genetic ancestry history of populations [Betranpetit, 2000; Kayser *et al.*, 2001; Jobling and Tyler-Smith, 2003; Purps *et al.*, 2014; Karmin *et al.*, 2015; Kayser, 2017]. Due to high power of exclusion, the Y-STR markers are routinely used in deficient paternity cases, missing person investigations or sibling testing, where the biological father is not present or dead, Y-chromosome STR or SNP analysis can be done in this situation [Roewer *et al.*, 2000]. On the other hand, Y-chromosome keeps an excellent potential in identifying the real offender from the male/female mixed sample, sample mixtures with multiple contributors and even from oligospermic or azoospermic perpetrators sample [Tsuji *et al.*, 2001; Purps *et al.*, 2015]. In addition, unlike autosomal and X-chromosome, 95% of its part does not undergo recombination and pass on clonally from father to son (except mutation), it has isolationist property as considered the best source to study the demographic and migratory history as well as the anthropology of human around the globe. In 2015, population geneticist Doğan and co-scientists reported on 21 European population and other 27 world-wide reference populations with Y-chromosome analyses. They reported that Y-STRs analyzed in this study were more informative and enabled regional clustering in addition to continental clustering. They also reported that the application of a larger amount of loci supports a more detailed insight into the relationships between European populations, compared to other reference populations.

1.8 Objectives of the Present Study

- To study the Y-chromosomal polymorphisms, genetic structure, genetic distances and genetic affinities of Bangali and seven ethnic populations in Bangladesh.
- To analyze 17 Y-STR loci in order to establish the genetic relationship between populations of Bangladesh and the neighboring populations to identify their origin or ancestral roots. This study could provide molecular genetic evidence for human settlement of the Asia Pacific.
- To know the historical and genealogical relationships particularly for surname investigation.
- To establish Y-chromosomal haplogroups in order to know the ancestry history and the migration history of the populations of Bangladesh.
- To construct allele frequencies along with gene diversity values for use in the calculation of DNA match statistics in the forensic investigations.
- To create a Y-chromosome DNA database for calculating forensic efficiency parameters in judiciary systems.
- To know the Y-chromosomal mutation rate in the populations of Bangladesh.

1.9 Importance of the Present Study

Until recently, the autosomal STR and Y-chromosome STR DNA data for Bangali and ethnic populations of Bangladesh are limited. In this study, we have gathered 1,594 Y-STR haplotypes from 1,631 individuals from the studied populations. The haplotype data have been submitted to YHRD (www.yhrd.org) and received the following accession numbers: Dhaka, Bangladesh [Bangladeshi] (YA003445), Khagrachari, Bangladesh [Chakma] (YA004320), Khagrachari, Bangladesh [Tripura] (YA004321), Cox's Bazar, Bangladesh [Rakhine] (YA004284), Bandarban, Bangladesh [Marma] (YA004285), Netrokona, Bangladesh [Hajong] (YA004283), Sylhet, Bangladesh [Manipuri] (YA004173) and Sylhet, Bangladesh [Khasia] (YA004172). Previously, we have submitted two populations Y-STR genetic data to YHRD and achieved the accession numbers: Dinajpur, Bangladesh [Santal] (YA003851) and Tangail, Bangladesh [Garo] (YA003852). These small quantities of genetic data are inadequate for population genetics study as well as forensic examinations. Therefore, to fill the void, for the first time here we report the Y-STR genetic data of Bangali and seven ethnic populations in Bangladesh based on evolutionary study and forensically importance. However, the Y-DNA database could be of great utility in determining the geographic origin and in investigating the genetic diversity of male individuals as well as in judiciary system. Because the Y-chromosomal component has remained unchanged and not to transfer to the next generation, this database can be used for determining the ancestor of different closely-related populations and contribute to a better understanding of geographic effects and human migration. It is also very important that the reduction of genetic diversity or genomic variations, as a result, can also increase for the certain types of inherited diseases of a species or a population.

Chapter Two

MATERIALS AND METHODS

2 Materials

2.1 Study Populations

A total of 1,631 subjects comprising 667 peripheral blood samples from Bangali population while 157 buccal swab samples from Chakma, 151 samples from Tripura, 152 samples from Rakhine, 144 samples from Marma, 112 samples from Hajong, 136 samples from Manipuri and 112 samples from Khasia were engaged in Y-chromosome genetic study (Table 2.1). Bangali samples were collected from routine paternity testing and suspect identification testing service of National Forensic DNA Profiling Laboratory, Dhaka Medical College, Bangladesh. All tribal male participants were healthy and unrelated of the respective population. The buccal swab samples from the tribal populations were collected with the help of the local authorities in different places like schools, colleges, temples, tea shops, garments factories, etc to avoid the sampling bias. Buccal swab samples were collected from unrelated male individuals of Chakma, Tripura, Rakhine, and Marma residing in Khagrachari, Bandarban and Cox's Bazar districts, the southern mountainous territory of Bangladesh, respectively. In addition, Manipuri and Khasia samples were collected from the border of the east of Sylhet district. The Hajong samples were collected from the border of the northern region of Netrokona district in Bangladesh. All participants were acknowledged with the informed consent and provided information about birthplace, age, and parents. The geographic distribution of the studied populations is shown in Figure 2.1.

2.2 Sample Size

The sample size was calculated based on the below formula [Daniel, 1999; Naing *et al.*, 2006; Pourhoseingholi *et al.*, 2013]:

$N = Z^2 P\ (1-P)\ /\ d^2$

Here,

N = Sample size;

Z = Statistic corresponding to the level of confidence (Z value is 1.96 for 95% confidence intervals);

P = Expected incidence or prevalence or proportion (in proportion of one; if 20%, P = 0.2); d = Acceptable error or precision in the estimate of "P" (in proportion of one; if 5%, d = 0.05).

Sample size calculation for the studied total populations in Bangladesh:

$Z = 1.96$; $P = 50\% = 0.5$; $d = 5.0\% = 0.05$

So, $N = Z^2 P\ (1-P)\ /\ d^2$

$= (1.96)^2 \times 0.5 \times 0.5\ /\ (0.05)^2$

$= 384.16 \approx 384$

According to the above formula, minimum sample size should be 384 individuals for a study purpose. In this study, we have collected 1,631 biological samples from the studied male populations.

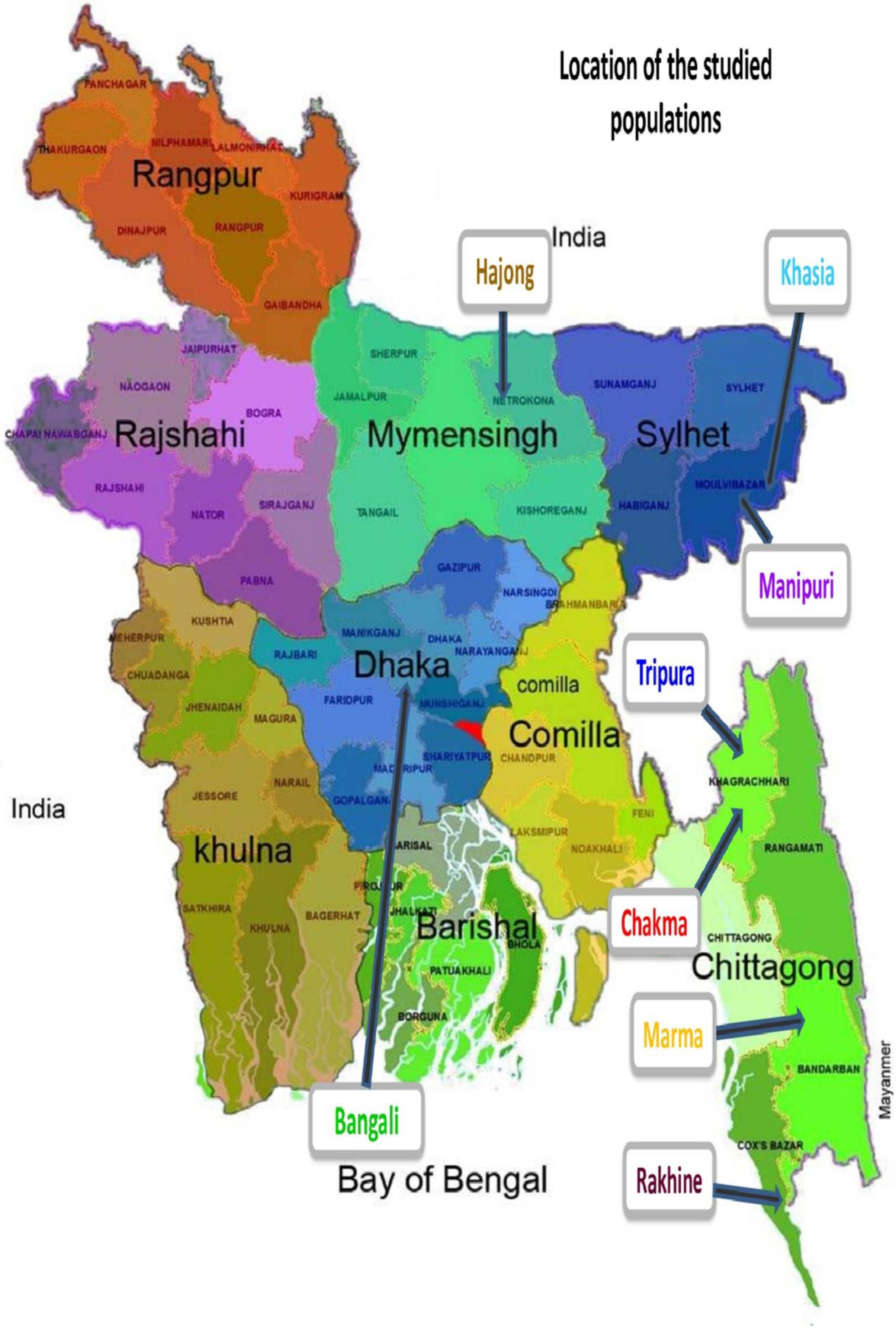

Figure 2.1: A map showing geographical location of the studied populations of Bangladesh.

2.3 Ethical Consideration

Every potential participant was explained about the study work. Cheek swab samples were collected from all healthy unrelated male participants with written informed consent. Ethical considerations for the study was approved by the Ethical Review Committee, Faculty of Biological Sciences, University of Dhaka, Dhaka-1000, Bangladesh (Reference number: 24/Biology Faculty:/2016-17; Dated: 16/05/2017) (Appendix-I) and each collection technique to control for intra and inter-individual differences in collection quality and quantity. All participants abstained from eating or drinking for at least 20 minutes prior to sample collection. Two buccal samples of the whole saliva were collected from each participant using the Sterile Swab Stick^{TM} DNA collection kit (Shenzhen Cleanmo, China). A copy of informed consent was provided to each sample donor (Appendix-II). This study follows the recommendations of the International Society of Forensic Genetics (ISFG) on the use of Y-chromosomal microsatellite markers in forensic analysis and population genetics study [Gusmão *et al.*, 2006].

2.4 The Studied Populations and Previously Reported Y-STR Data

The Y-chromosome STR data from our studied populations and previously published 32 geographically targeted populations were nominated for comparison across the 17 Y-STR loci (DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385a/b, DYS393, DYS391, DYS439, DYS635, DYS392, YGATAH4, DYS437, DYS438, and DYS448). To examine and portray the genetic affinities between and among the studied populations as well as neighboring populations, here we included most of the Asian reference populations. Furthermore, to know the genetic relationships between the studied populations and other than Asian populations, we also included one reference population from Australia, two from Europe, one from Africa, and two from North America. Depending on YHRD, the targeted populations including their geographical locations, designations, number of male participants, accession number and references are represented in Table 2.1.

Table 2.1: Y-chromosomal haplotypes data of the studied populations and 32 reference populations fromYHRD for investigating genetic diversity.

SL. No.	Population	Sample Size	Accession number in YHRD	Reference
	South Asia			
1	Dhaka, Bangladesh [Bangali]	667	YA003445	*Present study*
2	Khagrachari, Bangladesh [Chakma]	157	YA004320	*Present study*
3	Khagrachari, Bangladesh [Tripura]	151	YA004321	*Present study*
4	Cox's Bazar, Bangladesh [Rakhine]	152	YA004284	*Present study*
5	Bandarban, Bangladesh [Marma]	144	YA004285	*Present study*
6	Netrokona, Bangladesh [Hajong]	112	YA004283	*Present study*
7	Sylhet, Bangladesh [Manipuri]	136	YA004173	*Present study*
8	Sylhet, Bangladesh [Khasia]	112	YA004172	*Present study*
9	Tangail, Bangladesh [Garo]	120	YA003852	Hasan *et al.*, 2015
10	Dinajpur, Bangladesh [Santal]	139	YA003851	Hasan *et al.*, 2015
11	Gujarat, India [Bhil]	179	YA003762	Ramesh, 2012 contributed to YHRD
12	Madhya Pradesh, India [Gond]	75	YA003619	Ghosh *et al.*, 2011
13	Jharkhand, India [Munda]	68	YA003617	Ghosh *et al.*, 2011
14	Chhattisgarh, India [Oraon]	65	YA004113	Shrivastava *et al.*, 2016
15	West Bengal, India [Rajbanshi]	39	YA003630	Roy *et al.*, 2012
16	Tamil Nadu, India [Tamil]	400	YA003312	Raghunath *et al.*, 2016
17	Tripura, India [Tripuri]	65	YA003627	Ghosh *et al.*, 2011
18	Kathmandu, Nepal [Nepalese]	77	YA003656	Gayden *et al.*, 2009
19	Pakistan [Pathan]	270	YA003846	Lee *et al.*, 2014
	South Central Asia			
20	Afghanistan [Afghan]	169	YA003842	Älgenäs and Tillmar, 2014
	Central Asia			
21	Central Iran, Iran [Iranian]	154	YA003782	Ghaderi *et al.*, 2013 contributed to YHRD
22	Iraq [Iraqi]	124	YA003858	Purps *et al.*, 2014
	Tibetian Plateau			
23	Tibet, China [Tibetan]	348	YA004005	Ou *et al.*, 2015

SL. No.	Population	Sample Size	Accession number in YHRD	Reference
	Northeast Asia			
24	Beijing, China [Han]	961	YA004160	Nothnagel *et al.*, 2017
25	Taiwan [Paiwan]	237	YA003500	Wu *et al.*, 2011
	Southeast Asia			
26	Tokyo, Japan [Japanese]	156	YA003459	Mizuno *et al.*, 2008
27	Seoul, South Korea [Korean]	603	YA003406	Park *et al.*, 2005
28	Singapore [Malay]	556	YA004367	Yong *et al.*, 2006
29	Thailand [Thai]	140	YA004250	Herrera and Gayden, 2017 contributed to YHRD
30	Philippines [Filipino]	629	YA003892	Angustia, 2013 contributed to YHRD
31	Ulaanbaatar, Mongolia [Mongolian]	261	YA004127	Kim *et al.*, 2015 contributed to YHRD
32	Hanoi, Vietnam [Vietnamese]	48	YA003201	Kwak *et al.*, 2005
33	Java, Indonesia [Indonesian]	100	YA003770	Purnomo, 2013 contributed to YHRD
34	East Timor, Timor-Leste [Melanesian]	100	YA003306	Souto *et al.*, 2006
	Australia & Micronesia			
35	Australia [Aboriginal]	785	YA003697	Taylor and Henry, 2012
	Europe			
36	Cologne, Germany [German]	652	YA002963	Hidding *et al.*, 2000
37	Central Portugal, Portugal [Portuguese]	386	YA003145	González-Neira *et al.*, 2000; Carvalho *et al.*, 2003
	Africa			
38	Rio de Janeiro, Brazil [African]	100	YA003267	Domingues *et al.*, 2007
	North America			
39	Minnesota, United States [Asian American]	96	YA004088	Gross, 2015 contributed to YHRD
40	Minnesota, United States [Native American]	63	YA004091	Gross, 2015 contributed to YHRD

2.5 Methodology

2.5.1 Extraction of Genomic DNA by Chelex-100 Method

At first 1 mL of TE buffer was taken into an autoclaved and sterile 1.5 mL microcentrifuge tube. Approximately 3µL of peripheral blood or buccal swab was added to the tube and mixed gently. The mixture was incubated at room temperature for 30 minutes and mixed occasionally by inversion or gentle vortexing. Then the swab stick removed from the tube. The tube was centrifuged at 13,000 rpm for 3 minutes. The supernatant was removed as much as possible. About 50 µL of residual supernatant was left in the tube.

Then 60 µL of 20% Chelex was added to reach a final volume of 200 µL with ddH_2O. For saliva samples, added 4 µL of Proteinase K. It was taken for vortex at high speed for 5-10 seconds. The sample mixture was incubated at 56°C for 30 minutes in a heat block. After complete incubation, the sample was taken for vortexing at high speed for 5 to 10 seconds. Then the sample was incubated at 100°C in a heat block for 8 minutes. The sample was taken for vortexing at high speed for 5 to 10 seconds and centrifuged at 13,000 rpm for 3 minutes at room temperature. The sample was then ready for DNA quantitation and the PCR amplification process. For a better understanding, the complete workflow for Y-chromosome-specific-microsatellite analysis is shown in Figure 2.2.

2.5.2 DNA Quality and Quantification Tests

To check the purity and quantify the amount of nucleic acid in the Spectroscopy method, the absorbance reading was taken at wavelength of 260 nm and 280 nm using NanoDrop™ 1000 Spectrophotometer (Thermo Scientific, USA). At first, one (01) µL of deionized distilled water/ TE buffer was used as blank and subsequently read the optical density (OD) at 260/280 nm. After setting the blank as zero, wipe the water/TE buffer by soft tissue from lower and upper pedestal. In this system, about 1µL of aqueous nucleic acid sample is sufficient to ensure accurate and reproducible results. Due to highly concentrated DNA obtained from saliva, about 1 µL of genomic DNA was diluted 100 X with ddH_2O (1:99 µL ddH_2O) prior to the spectroscopy measurement. From spectrophotometer measurement, more than 2 ng/µL concentrations were found for all the saliva samples. After completion of each measurement, the lower and upper pedestal were washed through PCR grade water and wipe out by soft tissues. If the $OD_{260/280}$ ration of the nucleic acid is approximately 1.8, it is accepted as “pure DNA”.

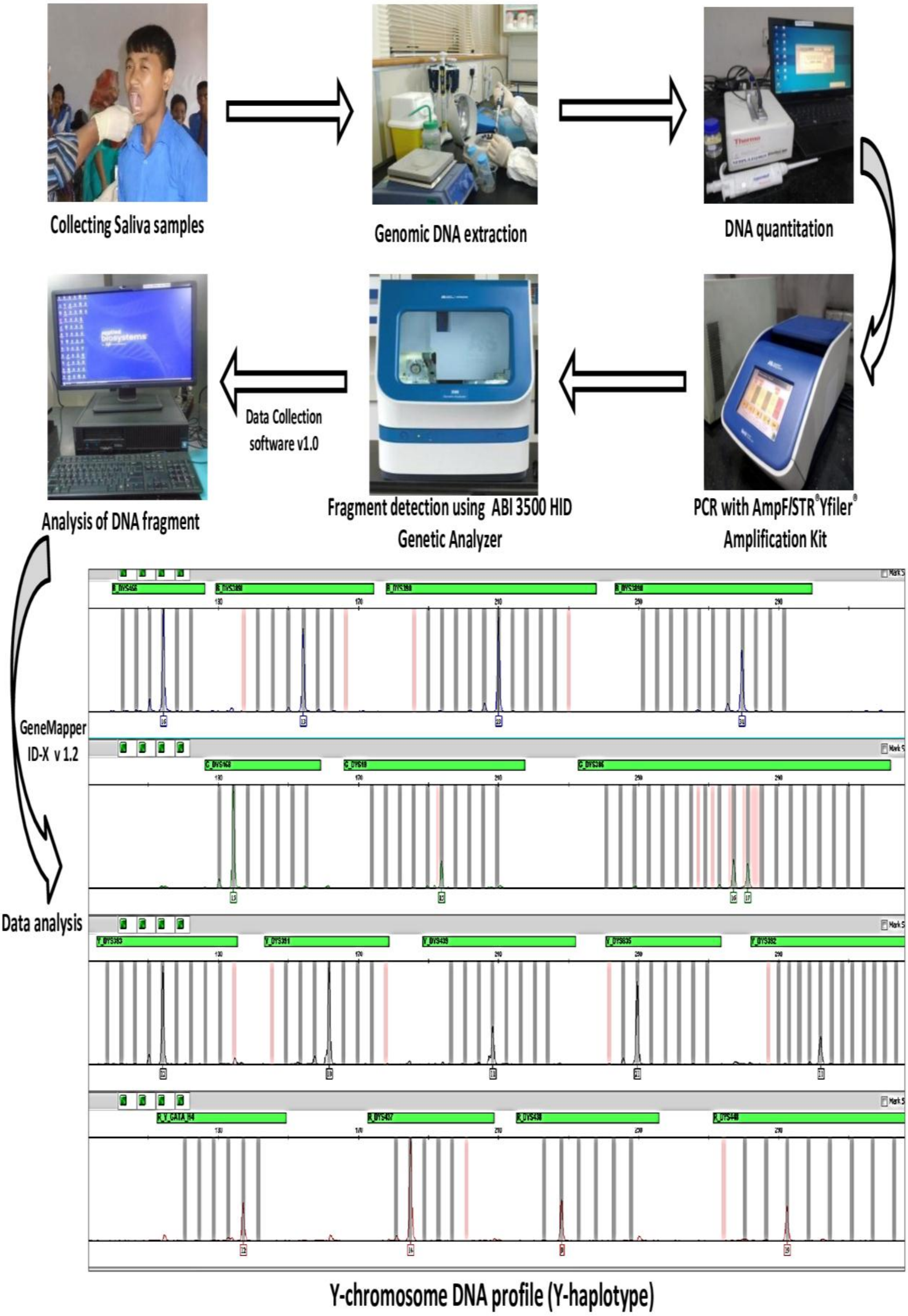

Fig 2.2 The complete workflow for Y-chromosome-specific-microsatellite analysis.

In order to check the presence of any PCR inhibitor, concentration and actual human genome copy number in extracted DNA samples, real-time polymerase chain reaction was also performed with a small portion of DNA samples. DNA concentrations and quality were determined with the instruments 7500 HID Real Time PCR System using Quantifiler® Y Human Male DNA Quantification Kit as per manufacturer's recommendations (ThermoFisher Scientific, USA).

All the extracted genomic DNA samples were stored in a -20°C freezer until used for PCR amplification process.

2.5.3 Materials for PCR of Y-STR Loci Amplification

The fluorescence-based AmpF*l*STR® Yfiler® PCR Amplification Kit (ThermoFisher Scientific, USA) is a Y-chromosome short tandem repeat (Y-STR) multiplex assay kit that amplifies 17 Y-STR loci (DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385a/b, DYS393, DYS391, DYS439, DYS635, DYS392, Y-GATA-H4, DYS437, DYS438, and DYS448) in a single PCR reaction [Mulero *et al.* 2006]. In this study, we have used this most popular Y-chromosomal STR detection kit. In this kit, the male specific 17 Y-chromosomal STR markers details shown in Table 2.2.

This Yfiler kit contains the following components:

- AmpF*l*STR® Yfiler™ PCR Reaction Mix
- AmpF*l*STR® Yfiler™ Primer Set
- Ampli*Taq* Gold® DNA Polymerase
- AmpF*l*STR® Yfiler™ Allelic Ladder
- AmpF*l*STR®DNA Control 007
- AmpFlSTR® Yfiler™ Control DNA 9947A

Table 2.2: Seventeen Y-Chromosomal STR markers details using AmpF*l*STR® Yfiler® PCR Amplification Kit.

STR Marker	Repeat Motif	ChrY Position (Mb)	Allelic Ladder Alleles	Mutation Rate	Dye Label
DYS456	AGAT	4.33	13, 14, 15, 16, 17, 18	0.42%	6-FAM™
DYS389I	[TCTG] [TCTA]	13.12	10, 11, 12, 13, 14, 15	0.25%	
DYS390	[TCTA] [TCTG]	15.78	18, 19, 20, 21, 22, 23, 24, 25, 26, 27	0.21%	
DYS389II	[TCTG] [TCTA]	13.12	24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34	0.36%	
DYS458	GAAA	7.93	14, 15, 16, 17, 18, 19, 20	0.64%	VIC®
DYS19	TAGA	10.13	10, 11, 12, 13, 14, 15, 16, 17, 18, 19	0.23%	
DYS385a/b	GAAA	19.26	7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20,21, 22, 23, 24, 25	0.21%	
DYS393	AGAT	3.19	8, 9, 10, 11, 12, 13, 14, 15, 16	0.10%	NED™
DYS391	TCTA	12.61	7, 8, 9, 10, 11, 12, 13	0.26%	
DYS439	AGAT	13.03	8, 9, 10, 11, 12, 13, 14, 15	0.52%	
DYS635	TSTA	12.89	20, 21, 22, 23, 24, 25, 26	0.35%	
DYS392	TAT	21.04	7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18	0.04%	PET®
YGATAH4	TAGA	17.25	8, 9, 10, 11, 12, 13	0.24%	
DYS437	TCTR	12.98	13, 14, 15, 16, 17	0.12%	
DYS438	TTTTC	13.38	8, 9, 10, 11, 12, 13	0.03%	
DYS448	AGAGAT	22.78	17, 18, 19, 20, 21, 22, 23, 24	0.16%	

2.5.4 Preparing the PCR Reactions

At first, thaw the AmpF*l*STR® Yfiler® PCR Reaction Mix, AmpF*l*STR®Yfiler® Primer Set and Ampli*Taq* Gold® DNA polymerase (ThermoFisher Scientific, USA) in room temperature for 5 minutes, then gently vortex 5 to 8 seconds and spin briefly before opening the tubes. The master mix was prepared by adding recommended volumes of reagents to a 0.2 mL PCR tube as follows in Table 2.3. Then vortex the PCR master mix for 5 to 8 seconds, then spin briefly. After thorough mixing and momentary spin 7.5 µL of PCR master mix was dispensed into each PCR tubes. Then added 1µL of genomic DNA (about 1-2 ng), control (AmpF*l*STR® Control DNA 007) (0.1ng/µL) and 4 µL of ddH$_2$O to the appropriate tubes. Finally, the tubes were subjected to momentary spin and transferred to Thermal Cycler for the amplification reaction.

Table 2.3: Master Mix preparation for PCR reaction

Component	**Volume per reaction (µL)**
AmpF*l*STR® Yfiler Kit PCR Reaction Mix	4.6
AmpF*l*STR® Yfiler Kit Primer Set	2.5
Ampli*Taq* Gold® DNA Polymerase	0.4
UltraPure™ DNase/RNase-Free Distilled Water	4.0
Genomic DNA	1.0
Total volume	**12.5**

The thermal cycling profiles programmed in PCR machine according to AmpF*l*STR® Yfiler® PCR Amplification Kit User's Manual to amplify the Y-STR markers/gene by polymerase chain reaction (PCR) for 28 cycles are as follows in Table 2.4.

Table 2.4: Thermal cycling profile for PCR amplification

Initial Incubation Step	**Cycle (28 cycles)**			**Final Extension**	**Final Hold**
	Denaturation	**Annealing**	**Extension**		
95°C	94°C	61°C	72°C	60°C	4°C
11 minute	1 minute	1 minute	1 minute	80 minutes	Infinite

2.5.5 Reagents Required for Fragment Analysis

The highly deionized formamide (Hi-Di™ Formamide) is used to stabilize denatured DNA samples for fluorescence detection before electrokinetic injection in capillary electrophoresis systems. During the time of separation of amplicons by capillary electrophoresis, the amplicons are subject to run along with internal size standards (GeneScan™ 600 LIZ® Size Standard v2.0), sets of DNA fragments with known size, so that the precise size of the amplicons can be computed relative to the internal size standard. The Y-STR genotyping was performed by comparison of the size of a sample's alleles to the size of alleles in AmpF*l*STR® Yfiler™ Allelic Ladder for the same loci being tested in the sample.

2.5.6 Samples Preparation for Capillary Electrophoresis

Allele sizing of the amplified PCR product was performed using the ABI 3500 Genetic Analyzer according to the AmpF*l*STR® Yfiler® PCR Amplification Kit User's Manual, 2014. Prior to loading the samples onto the Genetic Analyzer, the loading cocktail was prepared by combining and mixing the Hi-Di™ Formamide and GeneScan™ 600 LIZ® internal size standard as follows:

Table 2.5: Formamide: Size Standard cocktail preparation

Component name	**Volume per reaction (µL)**
Hi-Di™ Formamide	8.5
GeneScan™ 600 LIZ® Size Standard	0.5
Total volume	**9.0**

At first pipette the required volumes of components into a 1.5 mL microcentrifuge tube. Then vortex the tube and gently spin. In total, 09 µL of the Hi-Di Formamide: Size Standard mixture cocktail was dispensed to samples well of a MicroAmp® 96-Well reaction plate. Then 01µL of PCR product was added to the samples well and 01µL of Allelic Ladder for standard well. The reaction plates was sealed with septa, and then briefly centrifuge the plate to ensure that the contents of each well are mixed and collected at the bottom. The mixture was denatured by heating 95°C in a thermal cycler for 3 minutes. After completed the denaturation, the reaction plate immediately placed on PCR cooler box for 3 minutes. Finally, the reaction plate was placed into the ABI® 3500 Genetic Analyzer.

2.5.7 Running the Plate into Genetic Analyzer

The amplified PCR products (amplicons) were separated and detected electrophoretically with the liquid polymer (Performance Optimized Polymer, POP-4^{TM}) using 36 cm capillary array on the ABI$^{®}$ 3500 HID Genetic Analyzer, an 8-capillary array electrophoresis system. The G5 matrix filter was used to detect the five dyes 6-FAM$^{®}$ (Blue), VIC$^{®}$ (Green), NED$^{®}$ (Yellow), PET$^{®}$ (Red) and LIZ$^{®}$ (Orange). The samples were injected electrokinetically for 22 s at 3 kV. The Y-STR alleles were then separated at 15 kV for 25 minutes with a run temperature of 60°C and detection cell temperature of 50°C.

2.5.8 Data Collection and Analysis for Y-STR Genotyping

The samples run data were collected using Data Collection Software v1.0. The raw data as electrophoresis results were analyzed with GeneMapper ID-X^{TM} Software v1.2 together with an Allelic Ladder as well as controls. The GeneMapper ID-X^{TM} Software v1.2 was employed to determine fragment sizes and for genotype assignment. All loci were designated according to the number of repeat units present as latest recommended by the International Society of Forensic Genetics (ISFG) Y-chromosome STR polymorphisms [Gusmão *et al.*, 2006]. A peak detection threshold of 50 RFU's was used for allele designation. Allele designations were determined by comparison of the sample fragments to an allelic ladder supplied by the manufacturer. Panel and bin files for these 17 Y-STRs were programmed using allelic ladders, respectively.

2.5.9 Quality Control for Y-STR Genotyping

The experimental techniques were guided in keeping with laboratory internal control standards and kit controls. The study was carried out strictly in accordance with the guidelines of DNA Commission of the ISFG on the analysis of Y-chromosome STR polymorphisms, using AmpF*l*STR$^{®}$ Control DNA 007 as positive controls, and AmpF*l*STR$^{®}$ Control DNA 9947A or UltraPure™ DNase/RNase-Free Distilled Water as negative controls and these controls were run concurrently with each sample batch.

2.5.10 Confirmation of Abnormal Alleles

The off-ladder alleles, intermediate alleles, partial alleles, null alleles, and duplicate alleles were confirmed by re-amplified using the AmpF*l*STR$^{®}$ Yfiler$^{®}$ PCR Amplification Kit with the same amount of genomic DNA template. In order to check a possible mutation in the primer binding site, the samples were also retyped with PowerPlex® Y23 System (Promega Corporation, USA).

2.5.11 Re-genotyping

Randomly chosen about 4-5% of the total samples were re-genotyped to confirm the reproducibility of the DNA profile. Our laboratory has participated and passed in the Y-Chromosome Haplotype Reference Database (YHRD) quality assurance exercise for typing the YHRD core loci as well as additional loci DYS437, DYS448, DYS456, DYS458, DYS635 and Y-GATA-H4 (Certificate date: September 11, 2008). The haplotypes obtained from each population in this study have been submitted to YHRD and received accession numbers. The populations described herein can be searched by population name, contributor or accession number at http://www.yhrd.org.

2.6 Statically Analysis of Y-STR Haplotype Data

Different types of calculation methods and online software’s were used for statistical analysis of the Y-chromosome STR haplotype data.

2.6.1 Calculation of the Fraction of Unique Haplotypes

The fraction of unique haplotypes (FUH) was calculated as the percentage proportion of unique haplotypes in each group. Fraction of unique haplotypes was calculated as $D=N_{uniq}/N$, where N_{uniq} is the total number of unique haplotypes and N is the total number of haplotypes obtained in a population.

2.6.2 Calculation of Haplotype Discrimination Capacity

Haplotype discrimination capacity (DC) means that the number of haplotypes observed only once in the population. Discrimination capacity was calculated as $D=N_{diff}/N$, where N_{diff} is the total number of different haplotypes (not unique haplotype) and N is the total number of haplotypes obtained in a population.

2.6.3 Estimation of Allele or Gene Frequency

The allele frequency represents the prevalence of gene polymorphism in a population. An allele frequency is computed by dividing the number of times the allele of interest is detected in a population sample by the overall number of copies of all the alleles at that specific genetic marker or locus in the population. The genotyping data were then transformed into allele frequencies by computing the number of times each allele was found.

Allele frequencies and haplotype frequencies were estimated using PowerStat v1.2 Microsoft Excel spreadsheet [Tereba, 1999]. Multi-copy locus DYS385a/b was treated as allelic combinations. Statistics proved that closely related populations are likely to have similar frequencies of each type; more distantly related populations are expected to show progressively greater differences.

2.6.4 Estimation of the Haplotype Diversity

Haplotype diversity (HD) is the measure of the uniqueness of a particular haplotype in a given population. Haplotype diversity was calculated as an analogous to the gene diversity. Haplotype diversity (HD) of a population was calculated as HD = $1-\sum (x_i / N_x)^2$. Here x_i is the absolute frequency of the i-th haplotype and h is the total number of different haplotypes in the N_x samples [Nei, 1987].

2.6.5 Determination of the Allele or Gene Diversity

Gene diversity (GD) is a measure of the uniqueness of a particular locus or gene in a given population. Gene diversity (GD), power of matching or match probability (PM), power of discrimination (PD), and power of exclusion (PE) were calculated as GD = $n/(n-1)(1-\sum pi^2)$; PM= $\sum pi^2$; PD= 1-PM; and PE= $1-\sum pi^2$, respectively. Here for GD, n is the total number of haplotypes and pi is the allelic frequency of the ith haplotype. Power of matching or match probability (PM) was calculated as the sum of squared haplotype frequencies [Nei, 1987].

2.6.6 Calculation of Y-STR Haplotype Match Probability

There are two probabilities or possibilities of a Y-STR haplotype to match in a database [Decker, 2009].

One, if a haplotype has been found in a database, calculated using the below formula:

$$p+1.96\sqrt{\{p(1-p)\}/N}$$

Here, p indicates the profile’s frequency i.e. a particular number of times (x) in a database containing total haplotypes (N) and 1.96 indicates the 95% confidence interval value.

Another, if a haplotype has not been found in a database, the formula will be as below:

$$1-\alpha^{1/N} \text{ or } 3/N$$

Here, α is the confidence coefficient (0.05 for a 95% confidence interval).

2.6.7 Determination of Diversity Parameters

Diversity parameters including the minimum diversity within the population (dw_{min}), the maximum diversity between two populations (db_{max}), the maximum matching probability within the population (mw_{max}), the minimum matching probability within the population (mw_{min}), and the minimum matching probability between two populations (mb_{min}) were calculated for the Bangladeshi populations as described previously [Brinkmann *et al.*,1999; Lacau *et al.*,2011].

The ratio mw_{max}/mb_{min} gives an estimate for the upper limit of how many times more probable it is to find a match within a population rather than between two populations. On the other hand, the ratio mw_{min}/mb_{min} then yields a lower estimate of how much more probable it is to obtain a match within a population than between two populations.

Simple haplotype diversity dw_{min} within a population, i.e. the probability of unlike haplotypes when sampling two males, was calculated as-

$$dw_{min} = 1-\sum_{i=1}^{h} (x_i / N_x)^2$$

where x_i is the absolute frequency of the *i*-th haplotype and *h* the total number of different haplotypes in the *Nx* samples [Nei M, 1987].

When comparing between populations, the formula for the probability db_{max} of obtaining different haplotypes when sampling two individuals from two different populations simplify to-

$$db_{max} = 1-\sum_{i=1}^{m} (x_i y_i) / (N_x N_y)$$

where only the m sequence matches between populations X and Y need to be considered. Both formulas assume that the absolute frequency of each haplotype in a sample reflects its relative frequency in the population, which may be an overestimate in small, highly diverse samples. Thus the ratio $(1–dw_{min})/(1– db_{max})$ or its equivalent expression mw_{max}/mb_{min} is an overestimate of the probability ratio of obtaining a match when sampling a pair of individuals from the same population versus from two different populations. In order to obtain a lower bound for this interpopulation comparison, we assume that at the extreme all unique haplotypes in the sample reflect close to zero relative frequency.

Then the within population matching pair probability mw_{min} equals.

$$mw_{min} = \sum_{i=1;\, x_i>1}^{h} [x_i!/2(x_i-2)!] \,/\, [N_x!/2(N_x-2)!]$$

2.6.8 Estimation of Pairwise Genetic Distances

Population pairwise values were calculated to measure the genetic distance corresponding to 17 Y-STR loci of the studied population as well as other populations of whose most of them are a neighbour to Bangladesh geographically. The interpopulation comparison was carried out based on the sum of the squared allele size differences (R_{st}) values and the significance tested with 10,000 permutations using the online Analysis of Molecular Variance (AMOVA) tools in the YHRD. The genetic distances were also visualized in two-dimensional space using the multi-dimensional scaling (MDS) analysis included in the YHRD website [Willuweit and Roewer, 2007].

2.6.9 Construction of Phylogenetic Tree

To portray the genetic association among the populations, a Neighbor-Joining (NJ) or Phylogenetic tree was constructed and visualized based on the R_{st} value using the Molecular Evolutionary Genetics Analysis (MEGA) Software version 7.0.21 available at https://www.megasoftware.net [Cavalli-Sforza and Feldman, 2003].

2.6.10 Configuration of Pairwise Matrixes

Matrix of pairwise F_{st}, co-ancestry coefficient, pairwise differences and measurement of ancestral population sizes were generated by Arlequin Software version 3.5.2.2 program available at http://cmpg.unibe.ch/software/arlequin35/ [Excoffier and Lischer, 2010]. Microsatellite-based study would be to say $F_{st}<0.1$ represents low differentiation, populations with F_{st} = 0.15-0.2 are moderately differentiation and $F_{st}>0.25$ represents strongly differtiation.

The coefficient of co-ancestry designates the probability that one allele, derived from the same common ancestor, is identical by descent in two individuals.

2.6.11 Distribution of Haplogroup Frequencies

The Y-chromosomal haplogroup frequencies distribution were investigated from Y-STR data and calculated by direct counting. The haplogroup predictions were generated using Whit Athey's Haplogroup Predictor assignment algorithms on the web (http://www.hprg.com/hapest5/hapest5a/hapest5.htm) [Athey, 2011]. Pie charts of haplogroup frequency were constructed in Microsoft Excel. Y-chromosomal haplogroups were classified based on the International Society of Genetic Genealogy phylogenetic tree at January 28, 2015 (http://www.isogg.org/).

2.6.12 Haplotypes Networking

The Median-Joining networks projections of Y-STR haplotypes were produced with the assistance of the programme NETWORK 5.0.0.3 using the reduced median algorithm with the reduction threshold set to 1 and visualized with Network Publisher version 1.2.0.0 in order to assess the genetic relationships between the haplotypes, available at www.fluxus-engineering.com (Fluxus Engineering, Clare, UK) [Bandelt *et al.*, 1999]. In this network, each haplotype is shown as a node and the position of each mutation is shown a line connecting two nodes. The network tree is not rooted because the ancestral state of each polymorphism is not known. The genetic relationships between haplotypes inside of specific haplogroups were analyzed using NETWORK 5.0.1.1. Moreover, haplotype which had a bi-allelic marker (DYS385a/b), microvariants or null alleles were excluded in this study.

Chapter Three

RESULTS AND DISCUSSION

A total of 1,594 distinct haplotypes were obtained from 1,631 unrelated males in Bangali and seven ethnic populations (Chakma, Tripura, Rakhine, Marma, Hajong, Manipuri, and Khasia) in Bangladesh (Supplementary Table 01-08). We examined 17 Y-chromosome Short Tandem Repeat (Y-STR) markers using Y-filer panel and report a comprehensive statistical analysis of data on these markers. The allele/gene frequency, haplotype distribution, haplotype frequency, gene diversity, forensic efficiency parameters, phylogenetic tree, haplotype networking and distribution of haplogroup were determined from the Y-chromosome genetic data of the studied populations.

In this present study, a total of 121 alleles and 77 genotypes were determined. The number of observed alleles varied: 8 alleles for DYS456, 8 alleles for DYS389I, 8 alleles for DYS390, 11 alleles for DYS389II, 13 alleles for DYS458, 7 alleles for DYS19, 7 alleles for DYS393, 5 alleles for DYS391, 7 alleles for DYS439, 12 alleles for DYS63, 9 alleles for DYS392, 7 alleles for YGATAH4, 5 alleles for DYS437, 7 alleles for DYS438, 7 alleles for DYS448, and 77 genotypes for DYS385a/b. The distributions of alleles and genotypes for every above-mentioned DYS loci among the studied populations are given in Table 3.1-3.8. We also observed locus-specific differences in both intra- and interpopulation genetic variance.

3.1 Bangali Population

Peripheral blood samples were collected from 667 unrelated, healthy Bangali male individuals from routine casework analysis at National Forensic DNA Profiling Laboratory (NFDPL), Dhaka Medical College, Bangladesh. All participants signed on to the informed consent and provided the information about their age, parents and birthplaces during sample collection. Seventeen Y-chromosomal microsatellite markers were analyzed in all collected Bangali males and identified a total of 667 haplotypes (Supplementary Table 01). The number of alleles and frequencies of alleles were calculated of 17 Y-STRs loci for determining genetic diversity within Bangali population. A total of 649 different haplotypes were detected of which 633 were unique (accounting 97.534%), 14 were shared in two individuals and 2 were shared in three individuals

(Table 3.9). In total, 649 singletones haplotypes among 667 individuals which correspond to a discrimination capacity (DC) was 97.301% (Supplementary Table 10). The most frequent haplotypes were observed 16 times (2.398%). One hundred and seven different alleles (8 alleles for DYS456, 7 alleles for DYS389I, 8 alleles for DYS390, 8 alleles for DYS389II, 12 alleles for DYS458, 5 alleles for DYS19, 6 alleles for DYS393, 5 alleles for DYS391, 6 alleles for DYS439, 11 alleles for DYS635, 8 alleles for DYS392, 6 alleles for YGATAH4, 5 alleles for DYS437, 6 alleles for DYS438, 6 alleles for DYS448), and 60 genotypes or allele classes for DYS385a/b were detected in Bangali population. The most common alleles of the 17 Y-chromosomal STR loci were DYS456*15, DYS389I*13, DYS390*25, DYS389II*30, DYS458*16, DYS19*15, DYS393*13, DYS391*10, DYS439*10, DYS635*23, DYS392*11, YGATAH4*12, DYS437*14, DYS438*11, DYS448*19, and DYS385a/b*11/14 (Supplementary Table 09).

The off-ladder alleles and microvariants or partial alleles were presented in Supplementary Table 09. In total, twelve distinct off-ladder alleles or rare alleles were detected in Bangali population samples and were not present in the AmpF*l*STR® Yfiler™ Allelic Ladder. A number of off-ladder alleles were observed: allele 12 (five times) and allele 19 (once) at the locus DYS456; allele 9 (once) and allele 18 (once) at the locus DYS389I; allele 12 (once), allele 13 (twice) and allele 22 (once) at the locus DYS458; allele 17 (three times), allele 18 (twelve times), allele 19 (twenty-three times) and allele 27 (once) at the locus DYS635, and allele 14 (eleven times) at the locus YGATAH4.

Based on fragment size, a total of two specific microvariants or partial alleles or intermediate alleles typed as 18.2 (twice) and 19.2 (once) were observed at DYS458 in three individuals of Bangali population. Null allele or duplicate alleles (multiple peaks) were reproducibly obtained at a number of loci. Four null alleles were observed at three loci: DYS389II, DYS391 and DYS392 and carried by three individuals. Two duplicate alleles typed as (17, 18) and (15, 17) were found at DYS458 locus in two individuals (Supplementary Table 01). Haplotypes bearing double alleles and null alleles were excluded from allele frequency, gene diversity and AMOVA calculations.

Haplotypes sharing were observed within Bangali population. The most frequent haplotypes in Bangali population study revealed by 17 Y-STR loci system. According to YHRD order, two haplotypes (Bn98: 16-13-24-30-17-15-12,12-14-10-11-19-11-12-14-

11-19 and Bn316: 15-14-25-32-16-15-11,14-13-10-10-23-11-13-14-11-20) were shared in three individuals within Bangali males (0.899%). In addition, fourteen haplotypes were shared between two individuals. We also searched for all Y-STR profiles from Bangali population in the YHRD, the most popular and widely used Y-STR database. Out of 649 haplotypes from Bangali population, 53 haplotypes were found to have a match, 247 haplotypes were shown once and 349 haplotypes demonstrated no sharing among 205,059 haplotypes from 932 world-wide reference populations in a set of 17 Y-STR loci in YHRD (Release version R59; November 01, 2018). The most common and frequent haplotype Bn476, Bn228, Bn96, 518, and Bn371 were shared in 26, 25, 17, 17, and 16 individuals, respectively (Supplementary Table 01).

The analyzed Bangali population exhibited significant allele frequency variation. The observed alleles and gene diversity for 15 single-copy loci and 1 multi-copy locus in Bangali population are summarized in Table 3.1. For Bangali males, the allele frequencies of single-copy DYS loci ranged from minimum 0.002 to maximum 0.744, while the frequencies of genotypes of bi-allelic DYS marker (DYS385a/b) ranged from 0.002 to 0.199. DYS458, DYS635 and DYS385a/b loci were observed to be the most polymorphic out of all 17 Y-STR markers. Single-copy locus DYS458 exhibited the highest polymorphism having twelve alleles followed by locus DYS635 having eleven alleles whereas multi-copy loci DYS385a/b exhibited sixty genotypes. The genotype 11/14 observed standing out with a frequency of 0.199. On the other hand, DYS19, DYS391, and DYS437 loci showed the lowest polymorphism with five alleles, respectively. Among all alleles detected in Bangali males, allele 10 of DYS391 locus was found with the highest frequency of 0.744.

The gene diversity values were estimated from the allele frequencies at each Y-STR markers (Table 3.1). The highest gene diversity value was found at DYS385a/b (0.938), the most diverse marker within the Y-STR set, followed by DYS635 (0.821) and DYS390 (0.775). On the other hand, the lowest gene diversity value was observed at DYS391 (0.376). This result indicated that DYS385a/b and DYS635 were the most informative loci, but DYS391 and DYS437 were the less informative loci with gene diversity below 0.500. This result exhibited a high level of genetic polymorphisms in the Bangali population (Supplementary Table 11).

Table 3.1 Allele/genotype frequencies and gene diversity for 17 Y-STR markers in 667 unrelated Bangali males

DYS456		**DYS389I**		**DYS390**		**DYS389II**		**DYS458**		**DYS19**		**DYS393**	
A*	**F***	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
12	0.008	9	0.002	20	0.002	25	0.002	12	0.002	13	0.017	11	0.037
13	0.046	11	0.005	21	0.028	27	0.015	13	0.003	14	0.268	12	0.325
14	0.086	12	0.154	22	0.198	28	0.148	14	0.032	15	0.504	13	0.424
15	0.581	13	0.516	23	0.257	29	0.228	15	0.128	16	0.183	14	0.192
16	0.217	14	0.308	24	0.228	30	0.320	16	0.322	17	0.028	15	0.020
17	0.057	15	0.013	25	0.259	31	0.194	17	0.304	-	-	16	0.002
18	0.003	18	0.002	26	0.026	32	0.082	18	0.141	-	-	-	-
19	0.002	-	-	27	0.002	33	0.101	18.2	0.002	-	-	-	-
-	-	-	-	-	-	-	-	19	0.051	-	-	-	-
-	-	-	-	-	-	-	-	19.2	0.002	-	-	-	-
-	-	-	-	-	-	-	-	20	0.101	-	-	-	-
-	-	-	-	-	-	-	-	22	0.002	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD*	**0.603**		**0.616**		**0.775**		**0.770**		**0.755**		**0.641**		**0.677**
DYS391		**DYS439**		**DYS635**		**DYS392**		**YGATAH4**		**DYS437**		**DYS438**	
A	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
8	0.002	9	0.005	17	0.005	8	0.003	9	0.002	13	0.006	8	0.035
9	0.023	10	0.356	18	0.018	9	0.005	10	0.023	14	0.683	9	0.266
10	0.744	11	0.342	19	0.035	10	0.131	11	0.298	15	0.186	10	0.153
11	0.266	12	0.219	20	0.185	11	0.678	12	0.461	16	0.123	11	0.524
12	0.005	13	0.069	21	0.162	12	0.042	13	0.199	17	0.002	12	0.020
-	-	14	0.009	22	0.079	13	0.063	14	0.017	-	-	13	0.002
-	-	-	-	23	0.302	14	0.067	-	-	-	-	-	-
-	-	-	-	24	0.115	15	0.011	-	-	-	-	-	-
-	-	-	-	25	0.083	-	-	-	-	-	-	-	-
-	-	-	-	26	0.014	-	-	-	-	-	-	-	-
-	-	-	-	27	0.002	-	-	-	-	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD	**0.376**		**0.705**		**0.821**		**0.514**		**0.659**		**0.484**		**0.631**
DYS448		**DYS385a/b**											
A	**F**	**Gt***	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**
17	0.009	9,14	0.002	11,15	0.054	12,17	0.011	13,18	0.051	14,19	0.029	15,21	0.003
18	0.077	9,15	0.002	11,16	0.008	12,18	0.028	13,19	0.049	14,20	0.009	15,22	0.002
19	0.459	9,16	0.003	11,17	0.006	12,19	0.006	13,20	0.015	14,21	0.005	16,16	0.015
20	0.381	9,18	0.002	11,18	0.003	12,20	0.003	13,21	0.005	14,23	0.002	16,17	0.023
21	0.072	10,14	0.009	11,20	0.002	12,21	0.003	13,22	0.003	15,15	0.009	16,18	0.011
22	0.002	10,15	0.002	12,12	0.015	13,13	0.006	14,14	0.006	15,16	0.043	16,19	0.004
-	-	11,11	0.006	12,13	0.009	13,14	0.011	14,15	0.008	15,17	0.057	16,20	0.004
-	-	11,12	0.005	12,14	0.023	13,15	0.014	14,16	0.014	15,18	0.026	17,17	0.004
-	-	11,13	0.012	12,15	0.003	13,16	0.015	14,17	0.023	15,19	0.022	17,18	0.002
-	-	11,14	0.199	12,16	0.008	13,17	0.058	14,18	0.015	15,20	0.011	19,21	0.002
Total	**1**												**1**
GD	**0.634**												**0.938**

A: Allele; F: Frequency; Gt: Genotype; GD: Gene diversity

A Median-joining network analysis showed the Y-chromosome relationship of each haplotype within Bangali population (Figure 3.1). The network was constructed with 15 Y-chromosome microsatellite loci of AmpF*l*STR® Yfiler™ PCR Amplification Kit except for the multi-copy loci DYS385a/b. The network projections of 649 Y-STR haplotypes of Bangali population showed very high compactness in their clusters. The reason for that some loci were highly uninformative with low levels of polymorphism in the Bangali population. In the haplotype network analysis tree showed that there were two major clusters and two minor branches which also indicated a certain degree of polymorphisms or mutations between these haplotypes. Large quantities of haplotypes have resided in the major two clusters and few haplotypes have existed in the two minor branches. Haplotype Bn73 and Bn98 were the most frequent haplotypes and each haplotype contained four analogue haplotypes, respectively, followed by Bn341 was the second most frequent haplotype and consisted of three identical haplotypes in the center of a cluster. Haplotypes networking between Bn73 and Bn467 had the most compact clustering which was shown by relative time estimate value represented in an age of 4,036 years. Similarly, the networking tree also showed that the most frequent haplotype Bn98 had a strong affinity with Bn295, Bn446, and Bn537, respectively and the relative time estimate value between the haplotypes was represented in an age of 4,036 years. Haplotype Bn73 was observed at the center of the network and haplotype Bn325 had a long distance linkage relationship with it.

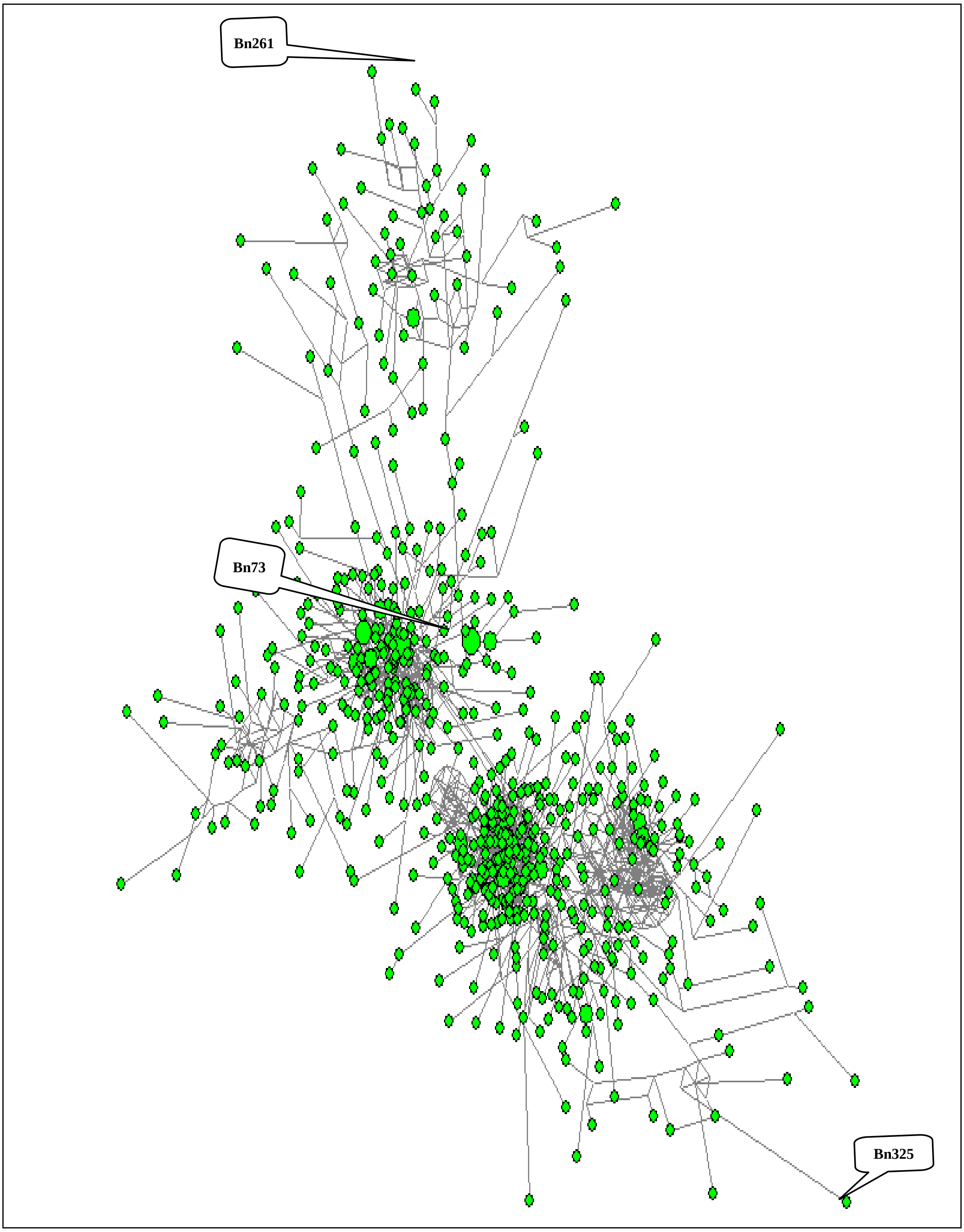

Figure 3.1 The Median-joining (MJ) networks of Y-STR haplotypes network of Bangali individuals (649 haplotypes) reported in this study based on 15 Y-STRs. *Circles* represent haplotypes with areas proportional to frequencies; the smallest area is equivalent to one individual. Branch length is proportional to the number of mutations between haplotypes.

3.2 Chakma Population

In this population, 17 Y-STRs were analyzed in 157 unrelated healthy Chakma males and identified a total of 150 haplotypes (Supplementary Table 02). The number of alleles and frequencies of alleles were calculated of 17 Y-STRs loci within Chakma population.

Overall 116 different haplotypes were observed of which 94 were individual-specific (accounting 81.034%). Moreover, 14, 5, 2 and 1 haplotypes were shared in 2, 3, 4 and 5 individuals, respectively (Table 3.9). In total, 116 different haplotypes among 157 individuals which correspond to a discrimination capacity were 73.885% (Supplementary Table 10). The most frequent haplotypes occured 22 times, accounting 14.666%. The most common haplotype (DYS456:16, DYS389I:13, DYS390:24, DYS389II:29, DYS458:16, DYS19:17, DYS385a/b:15/20, DYS393:14, DYS391:10, DYS439:12, DYS635:22, DYS392:14, YGATAH4:13, DYS437:14, DYS438:10, and DYS448:18) was found in five individuals within Chakma males (3.333%). Seventy five alleles (5 alleles for DYS456, 4 alleles for DYS389I, 4 alleles for DYS390, 7 alleles for DYS389II, 8 alleles for DYS458, 5 alleles for DYS19, 5 alleles for DYS393, 3 alleles for DYS391, 5 alleles for DYS439, 7 alleles for DYS635, 6 alleles for DYS392, 5 alleles for YGATAH4, 3 alleles for DYS437, 3 alleles for DYS438, 5 alleles for DYS448), and 32 genotypes or allele classes for DYS385a/b were detected in Chakmas. The most common alleles of the 17 Y-chromosomal STR loci were DYS456*15, DYS389I*12, DYS390*24, DYS389II*28, DYS458*18, DYS19*14, DYS393*12, DYS391*10, DYS439*11, DYS635*20, DYS392*14, YGATAH4*12, DYS437*15, DYS438*11, DYS448*20, DYS385a/b*13/19 and DYS385a/b*13/20 (Supplementary Table 09).

A total of three specific rare alleles or off-ladder alleles at different loci were detected in this population sample which were not present in the AmpF*l*STR® Yfiler™ Allelic Ladder. Some off-ladder alleles have been observed: allele 21 (twice) at the loci DYS458; allele 19 (eight times) at the locus DYS635 and allele 14 (once) at the locus YGATAH4 (Supplementary Table 09).

The most frequent haplotypes in this population study revealed by 17 Y-STR loci system. According to YHRD order, the most common haplotype Ck3 (16-13-24-29-16-17-15,20-14-10-12-22-14-13-14-10-18) was shared in five individuals within this group (accounting 3.333%). In addition, two, five, and fourteen haplotypes were shared between four, three, and two individuals, respectively. We also searched for all Y-STR profiles from Chakma population in the YHRD (Release version R59; November 01, 2018). Out of 116 different haplotypes, 18 haplotypes were found a match and 98 haplotypes occurred only once with the global populations of the 205,059 haplotypes. The most common and frequent haplotype Ck22 was shared between 10 individuals followed by haplotype Ck62 and Ck84 were shared between 6 and 5 individuals, respectively (Supplementary Table 02).

The analyzed Chakma tribe exhibited remarkable allele frequency variation. The observed alleles and gene diversity for 15 single-copy loci and 1 multi-copy locus in Chakma population are summarized in Table 3.2. For Chakma male samples, the allele frequencies of single-copy DYS loci ranged from minimum 0.009 to maximum 0.733, while the frequencies of genotypes of bi-allelic marker DYS385a/b ranged from 0.009 to 0.129. The DYS458 and DYS385a/b were observed to be the most polymorphic loci out of all 17 Y-STR markers. Single-copy locus DYS458 exhibited the highest polymorphism having eight alleles followed by loci DYS389II and DYS635 having seven alleles, whereas multi-copy loci DYS385a/b exhibited thirty-two genotypes. The observed genotypes 13/19 and 13/20 showed the highest frequency of 0.129, respectively. In contrast, DYS391, DYS437, and DYS438 loci showed the lowest polymorphism with three alleles, respectively. Among all the alleles identified in Chakma males, allele 10 of DYS391 locus was found with the highest frequency of 0.733.

The locus-wise gene diversities were also estimated from the allele frequencies at each Y-STR markers (Table 3.2). The highest gene diversity value was found at DYS385a/b (0.946) followed by DYS458 (0.761) and DYS635 (0.700). In contrast, the lowest gene diversity value was observed at DYS391 (0.400). This result indicated that DYS385a/b and DYS458 were the most informative loci, whereas DYS391, DYS437, and DYS438 were the less informative loci with gene diversity below 0.560. This result exhibited a high level of genetic polymorphisms in the Chakma population (Supplementary Table 11).

Table 3.2: Allele/genotype frequencies and gene diversity for 17 Y-STR markers in 157 unrelated Chakma males

DYS456		DYS389I		DYS390		DYS389II		DYS458		DYS19		DYS393	
A*	**F***	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
14	0.129	11	0.026	21	0.009	26	0.017	14	0.034	13	0.017	12	0.638
15	0.716	12	0.647	23	0.397	27	0.095	15	0.043	14	0.552	13	0.138
16	0.060	13	0.224	24	0.414	28	0.500	16	0.112	15	0.310	14	0.155
17	0.078	14	0.103	25	0.182	29	0.234	17	0.310	16	0.103	15	0.060
18	0.017	-	-	-	-	30	0.103	18	0.353	17	0.017	16	0.009
-	-	-	-	-	-	31	0.034	19	0.078	-	-	-	-
-	-	-	-	-	-	32	0.017	20	0.052	-	-	-	-
-	-	-	-	-	-	-	-	21	0.017	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD*	**0.465**		**0.524**		**0.443**		**0.680**		**0.761**		**0.593**		**0.551**

DYS391		DYS439		DYS635		DYS392		YGATAH4		DYS437		DYS438	
A	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
10	0.733	10	0.060	19	0.069	10	0.043	10	0.009	14	0.293	10	0.101
11	0.258	11	0.405	20	0.448	11	0.147	11	0.233	15	0.655	11	0.242
12	0.009	12	0.388	21	0.284	12	0.103	12	0.654	16	0.052	12	0.616
-	-	13	0.121	22	0.129	13	0.112	13	0.095	-	-	-	-
-	-	14	0.026	23	0.052	14	0.526	14	0.009	-	-	-	-
-	-	-	-	24	0.009	15	0.069	-	-	-	-	-	-
-	-	-	-	25	0.009	-	-	-	-	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD	**0.400**		**0.672**		**0.700**		**0.678**		**0.513**		**0.487**		**0.557**

DYS448		DYS385a/b											
A	**F**	**Gt***	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**
17	0.009	10,16	0.052	12,12	0.026	13,18	0.094	14,18	0.009	15,17	0.017	16,21	0.009
18	0.112	11,12	0.017	12,13	0.026	13,19	0.129	14,19	0.026	15,19	0.017	17,20	0.009
19	0.361	11,14	0.026	12,16	0.034	13,20	0.129	14,20	0.017	15,20	0.017	-	-
20	0.440	11,16	0.009	12,17	0.026	13,21	0.034	14,21	0.009	15,21	0.017	-	-
21	0.078	11,17	0.034	12,19	0.026	13,22	0.052	14,22	0.009	15,22	0.009	-	-
-	-	11,18	0.017	13,17	0.060	14,16	0.009	15,16	0.026	16,20	0.009	-	-
Total	**1**												**1**
GD	**0.663**												**0.946**

A: Allele; F: Frequency; Gt: Genotype; GD: Gene diversity

A Median-joining network analysis showed the genetic relationships of each haplotype within Chakma population (Figure 3.2). The network projections of 116 Y-STR haplotypes of this population showed very high compactness in their clusters. The reason for that some loci were highly uninformative with low levels of polymorphism in the Chakma population. In the haplotype network analysis tree showed that there was one major cluster and one minor branch which indicated a certain degree of polymorphisms or mutations between these haplotypes. Most of the haplotypes were resided in the major cluster and the few haplotypes stayed in the minor branch. Haplotype Ck21 was the most frequent and consisted of six identical haplotypes resided in the center of the cluster followed by haplotype Ck3 was the second most frequent and consisted of sfive analogue haplotypes which existed in the minor branch. Additionally, the most frequent haplotype Ck21 showed closely related to Ck14 and Ck93, respectively, and the relative time estimate value between the haplotypes was represented in as of 2,883 years. Another most frequent haplotype Ck28 showed the close affinity with haplotypes Ck18, Ck52 and Ck74, respectively, and the relative time estimate value between the haplotypes was represented in as of 4,036 years. Haplotype Ck30 was observed at the center of the network and haplotype Ck69 had a distance linkage relationship with it.

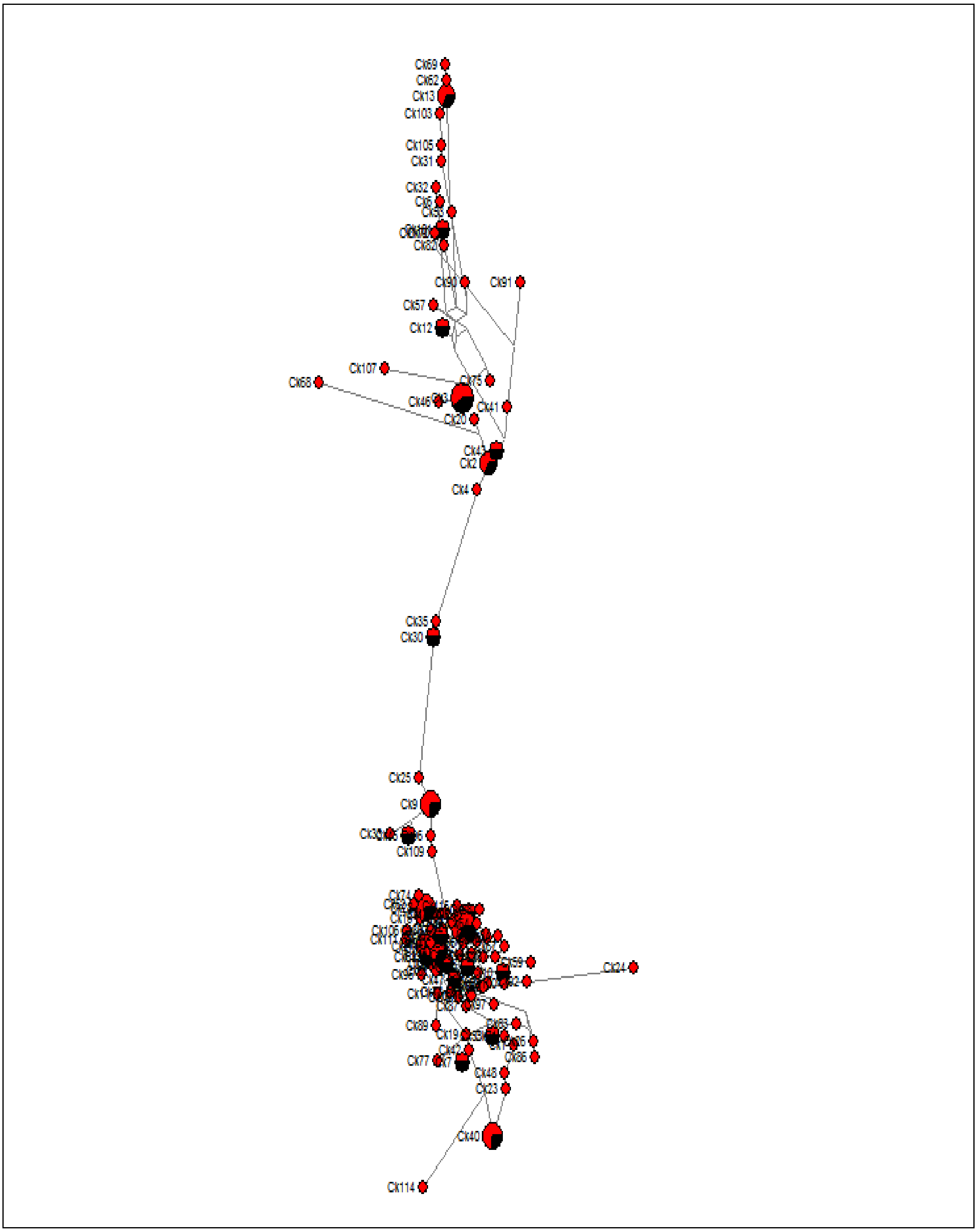

Fig. 3.2: The Median-joining (MJ) networks of Y-STR haplotypes network of Chakma individuals (116 haplotypes) reported in this study based on 15 Y-STRs. *Circles* represent haplotypes with areas proportional to frequencies; the smallest area is equivalent to one individual. Branch length is proportional to the number of mutations between haplotypes.

3.3 Tripura Population

In total of 151 unrelated healthy Chakma males were recruited in this study and identified 144 haplotypes (Supplementary Table 03). The number of alleles and frequencies of alleles were calculated of 17 Y-STRs loci within Tripura population.

In total 99 different haplotypes were detected of which 77 were unique, 12 were shared in two individuals, 4 were shared in three individuals, 3 were shared in four individuals, 2 were shared in six individuals and 1 were shared in seven individuals (Table 3.9). In total, 99 different haplotypes among 151 individuals which correspond to a discrimination capacity were 65.563% (Supplementary Table 10). The most frequent haplotype occurs 22 times (accounting 15.277%). On the other hand, the most common haplotype (DYS456:15, DYS389I:12, DYS390:23, DYS389II:28, DYS458:17, DYS19:14, DYS385a/b:13/18, DYS393:12, DYS391:10, DYS439:12, DYS635:20, DYS392:14, YGATAH4:12, DYS437:14, DYS438:11, and DYS448:20) was found in five individuals (3.333%). Seventy one alleles (4 alleles for DYS456, 4 alleles for DYS389I, 5 alleles for DYS390, 8 alleles for DYS389II, 5 alleles for DYS458, 5 alleles for DYS19, 5 alleles for DYS393, 3 alleles for DYS391, 5 alleles for DYS439, 6 alleles for DYS635, 5 alleles for DYS392, 4 alleles for YGATAH4, 2 alleles for DYS437, 5 alleles for DYS438, 5 alleles for DYS448), and 18 genotypes or allele classes for DYS385a/b were detected in Tripura males. The most common alleles of the 17 Y-chromosomal STR loci were DYS456*15, DYS389I*12, DYS390*24, DYS389II*28, DYS458*17, DYS19*14, DYS393*12, DYS391*10, DYS439*12, DYS635*20, DYS392*14, YGATAH4*11, DYS437*15, DYS438*11, DYS448*20, and DYS385a/b*14/19 (Supplementary Table 09).

The off-ladder alleles and Microvariants or partial alleles were presented in Supplementary Table 09. In the Tripura population samples, we found only one distinct rare or off-ladder allele (allele 19) at DYS635 locus which was not present in the AmpF*l*STR® Yfiler™ Allelic Ladder.

Haplotypes sharing were observed within Tripura males. According to YHRD order, the most prominent haplotype Tr37 (15-12-23-28-17-14-13,18-12-10-12-20-14-12-14-11-20) was shared in seven individuals in this population (4.861%). In addition, other two most frequent haplotypes (Tr18: 14-14-23-30-17-14-14,19-13-10-12-23-11-11-14-9-21 and Tr22: 15-12-24-27-18-14-13,18-12-10-12-21-14-11-15-11-20) were shared between six individuals in this population (8.333%), respectively. Furthermore, three, four, and twelve haplotypes were shared between four, three, and two individuals, respectively.

We also searched for all Y-STR profiles from Tripura population in the YHRD (Release version R59; November 01, 2018). Out of 99 different haplotypes, 13 haplotypes were found a match and 98 haplotypes occurred only once for each with the global population along with 205,059 haplotypes. The most common and frequent haplotype Tr34 was shared between 41 individuals followed by haplotype Tr10 and Tr29 were shared in 8 individuals, respectively (Supplementary Table 03).

The analyzed Tripura population exhibited significant allele frequency variation. The observed alleles and gene diversity for 15 single-copy loci and 1 multi-copy locus in Tripura population are summarized in Table 3.3. For Tripura male samples, the allele frequencies of single-copy DYS loci ranged from minimum 0.010 to maximum 0.828, while the frequencies of genotypes of DYS385a/b marker ranged from 0.010 to 0.212. The DYS389II and DYS385a/b loci were observed to be the most polymorphic out of all 17 Y-STR markers. Single-copy locus DYS389II exhibited the highest polymorphism having eight alleles followed by locus DYS635 with six alleles while DYS385a/b exhibited eighteen genotypes. The genotype 14/19 was observed standing out with a frequency of 0.212. In contrast, locus DYS437 showed less polymorphism with two alleles. Among all alleles detected in Tripura males, allele 10 of DYS391 was found with the highest frequency of 0.828.

The gene diversity values were estimated from the allele frequencies at each Y-STR markers (Table 3.3). The highest gene diversity value was found at DYS385a/b (0.882) followed by DYS389II (0.716) and DYS458 (0.705). In contrast, the lowest gene diversity value was observed at DYS391 (0.301). This result indicated that DYS385a/b and DYS389II were the most informative loci; however, DYS437 and DYS391 were less informative with gene diversity below 0.500. This result exhibited a high level of genetic polymorphisms in the Tripura population (Supplementary Table 11).

Table 3.3 Allele/genotype frequencies and gene diversity for 17 Y-STR markers in 151 unrelated Tripura males

DYS456		**DYS389I**		**DYS390**		**DYS389II**		**DYS458**		**DYS19**		**DYS393**	
A*	**F***	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
14	0.141	12	0.566	21	0.030	24	0.020	16	0.141	13	0.010	11	0.010
15	0.525	13	0.323	22	0.030	27	0.162	17	0.424	14	0.747	12	0.788
16	0.273	14	0.081	23	0.343	28	0.455	18	0.303	15	0.162	13	0.121
17	0.061	15	0.030	24	0.485	29	0.222	19	0.101	16	0.030	14	0.071
-	-	-	-	25	0.111	30	0.081	20	0.030	17	0.051	15	0.010
-	-	-	-	-	-	31	0.040	-	-	-	-	-	-
-	-	-	-	-	-	32	0.010	-	-	-	-	-	-
-	-	-	-	-	-	33	0.010	-	-	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD*	**0.633**		**0.574**		**0.639**		**0.716**		**0.705**		**0.416**		**0.363**
DYS391		**DYS439**		**DYS635**		**DYS392**		**YGATAH4**		**DYS437**		**DYS438**	
A	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
9	0.061	10	0.101	19	0.010	11	0.242	10	0.030	14	0.414	9	0.101
10	0.828	11	0.263	20	0.545	12	0.071	11	0.434	15	0.586	10	0.242
11	0.111	12	0.505	21	0.232	13	0.111	12	0.364	-	-	11	0.616
-	-	13	0.111	22	0.040	14	0.505	13	0.172	-	-	12	0.030
-	-	14	0.020	23	0.162	15	0.071	-	-	-	-	13	0.010
-	-	-	-	24	0.010	-	-	-	-	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD	**0.301**		**0.660**		**0.627**		**0.671**		**0.655**		**0.490**		**0.556**
DYS448		**DYS385a/b**											
A	**F**	**Gt***	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**				
17	0.071	8,13	0.010	13,18	0.162	14,16	0.010	15,20	0.061				
18	0.121	12,15	0.010	13,19	0.152	14,18	0.030	16,17	0.020				
19	0.101	12,19	0.010	13,20	0.141	14,19	0.212	16,18	0.010				
20	0.566	12,20	0.051	13,21	0.010	14,20	0.030	-	-				
21	0.141	13,17	0.061	13,22	0.010	15,18	0.010	-	-				
Total	**1**								**1**				
GD	**0.636**								**0.882**				

A: Allele; F: Frequency; Gt: Genotype; GD: Gene diversity

A Median-joining network analysis showed the Y-chromosome relationships of each haplotype within Tripuras (Figure 3.3). The network projections of 99 Y-STR haplotypes of Tripura population showed very high compactness in its clusters. The reason for that some loci were highly uninformative with low levels of polymorphism in this tribe. In the haplotype network analysis tree showed that the tree consisted of one cluster and one minor branch which indicated a certain degree of polymorphisms or mutations between these haplotypes. A large number of haplotypes have resided in the cluster and few haplotypes have existed in the minor branch. Haplotypes Tr3, Tr18, and Tr29 were the most frequent haplotypes and each haplotype contained seven identical haplotypes, respectively, followed by Tr21 was the second most frequent haplotype and consisted of six analogue haplotypes in the center of a cluster. The most abundant haplotype Tr3 showed closely genetic affinity with haplotype Tr5 and the relative time estimate value between the two haplotypes represented in an age of 2,523 years. The most prominent haplotype Tr18 showed a close relationship with Tr94 and the relative time estimate value between the two haplotypes represented in an age of 2,523 years. Another most abundant haplotype Tr29 exhibited close affinity with haplotypes Tr55 and Tr67, respectively, and the relative time estimate value between the two haplotypes represented in an age of 2,523 years. The second most dominant haplotype Tr21 showed the close genetic similarity with Tr26, Tr40, and Tr56, respectively, and the relative time estimate value between the two haplotypes represented in an age of 2,883 years. Furthermore, haplotypes Tr16 and Tr46 were observed the long distance Y-chromosome relationships.

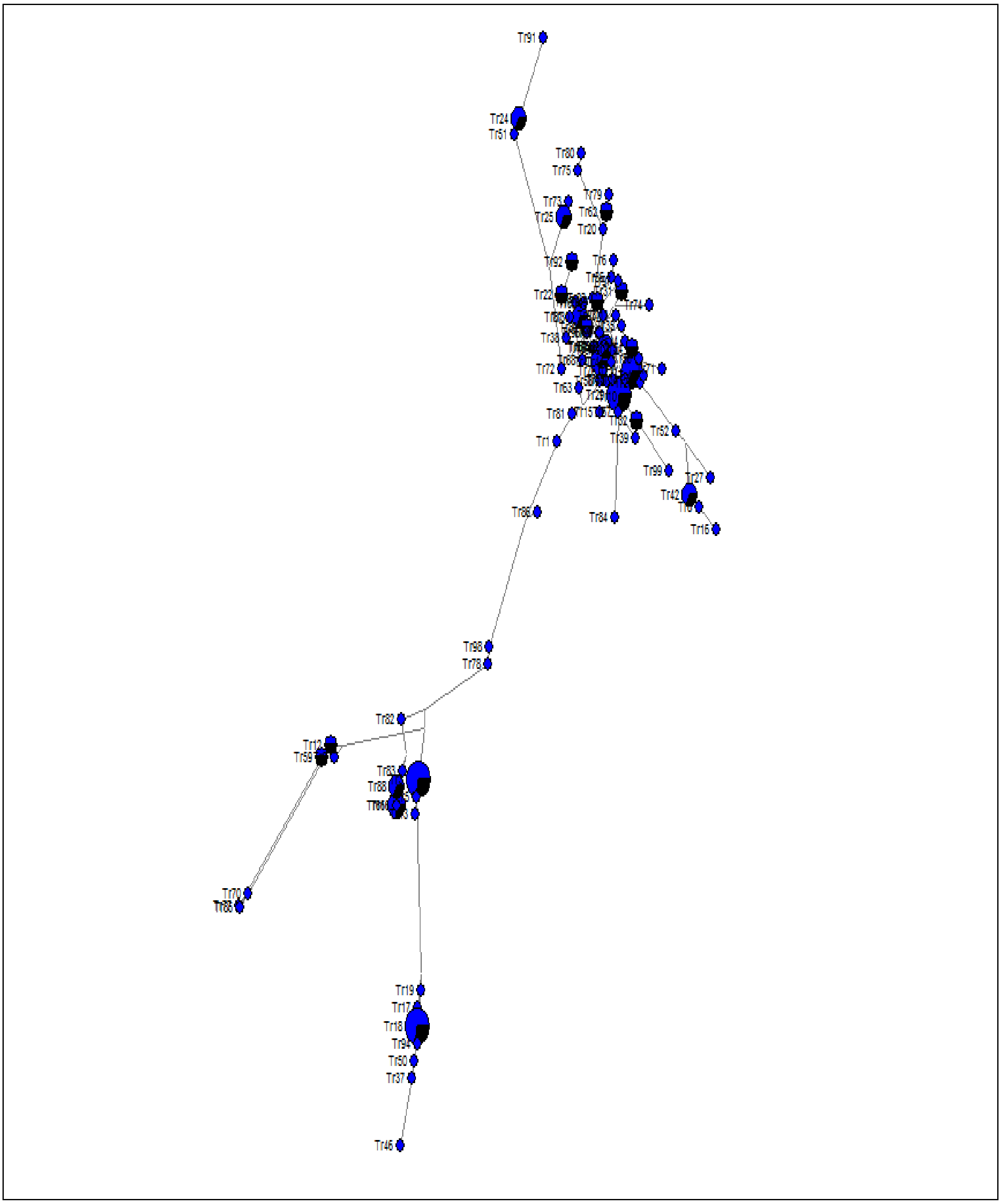

Figure 3.3 The Median-joining (MJ) networks of Y-STR haplotypes network of Tripura individuals (99 haplotypes) reported in this study based on 15 Y-STRs. *Circles* represent haplotypes with areas proportional to frequencies; the smallest area is equivalent to one individual. Branch length is proportional to the number of mutations between haplotypes.

3.4 Rakhine Population

In this genetic study, 17 Y-STRs were analyzed in 152 unrelated healthy Rakhine males and identified a total of 145 haplotypes (Supplementary Table 04). The number of alleles and frequencies of alleles were calculated of 17 Y-STRs loci within Rakhine population.

A total of 110 different haplotypes were detected of which 95 were unique, 9 were shared in two individuals, 2 were shared in three individuals, 1 was shared in four individuals, 2 were shared in six individuals and 1 was shared in seven individuals (Table 3.9). In total, 110 different haplotypes among 152 individuals which correspond to a discrimination capacity were 75.862% (Supplementary Table 10). The most frequent haplotypes occurred 15 times (10.245%). The most common haplotype (DYS456:15, DYS389I:14, DYS390:25, DYS389II:31, DYS458:16, DYS19:15, DYS385a/b: 11/14, DYS393:13, DYS391:10, DYS439:10, DYS635:23, DYS392:11, YGATAH4:13, DYS437:14, DYS438:11, and DYS448:20) was found in seven individuals in Rakhine males (4.762%). Eighty-four alleles (6 alleles for DYS456, 3 alleles for DYS389I, 5 alleles for DYS390, 7 alleles for DYS389II, 7 alleles for DYS458, 5 alleles for DYS19, 6 alleles for DYS393, 4 alleles for DYS391, 6 alleles for DYS439, 9 alleles for DYS635, 6 alleles for DYS392, 6 alleles for YGATAH4, 3 alleles for DYS437, 5 alleles for DYS438, 6 alleles for DYS448), and 35 allele classes for DYS385a/b were observed in Rakhine population. The most common alleles of the 17 Y-chromosomal STR loci were DYS456*15, DYS389I*12, DYS390*24, DYS389II*28, DYS458*16, DYS19*14, DYS393*12, DYS391*10, DYS439*11, DYS635*21, DYS392*14, YGATAH4*12, DYS437*14, DYS438*11, DYS448*20, and DYS385a/b*13/19 (Supplementary Table 09).

The off-ladder alleles and microvariants or partial alleles of the Rakhine groups were presented in Supplementary Table 09. Overall, four distinct off ladder or rare alleles at different loci were detected in this population samples which were not present in the AmpF*l*STR$^{®}$ Yfiler^{TM} Allelic Ladder. The off-ladder alleles were observed: allele 18 (once), allele 19 (once) at the locus DYS635, and allele 14 (seven times), allele 15 (once) at the locus YGATAH4. Three null alleles were observed at the locus DYS389II and carried by three male samples. Haplotypes bearing null alleles were excluded from allele frequency, gene diversity and AMOVA calculations.

Y-chromosomal haplotypes sharing were observed within Rakhine males. According to YHRD order, the most frequent haplotype RK22 (15-14-25-31-16-15-11,14-13-10-10-23-

11-13-14-11-20) was shared between seven individuals in this population group (4.828%). Another two most frequent haplotypes (Rk6: 15-12-24-27-18-14-13,19-12-10-13-21-14-12-15-11-20 and Rk7: 15-12-24-29-18-14-14,20-12-10-11-20-14-14-14-11-20) were shared between six individuals in this population group (8.276%), respectively. In addition, one, two, and nine haplotypes were shared between four, three, and two individuals, respectively.

We also searched for all Y-STR profiles from Rakhine population in YHRD (Release version R59; November 01, 2018). Out of 110 different haplotypes, 22 haplotypes were found a match and 88 haplotypes occurred only once for each among the global population of the 205,059 haplotypes. The most common and frequent haplotype Rk22 was shared between 12 individuals followed by haplotype Rk106 shared between 10 individuals and haplotype Rk62 was shred between 8 individuals, respectively (Supplementary Table 04).

This analyzed population exhibited a significant level of allele frequency variation. The observed alleles and gene diversity for 15 single-copy and one 1 multi-copy locus in Rakhine population are summarized in Table 3.4. For Rakhine males, allele frequencies of single-copy DYS loci varied from 0.009 to 0.791, while the frequencies of genotypes of bi-allelic DYS385a/b loci ranged from 0.009 to 0.127. DYS635 and DYS385a/b loci were observed to be the most polymorphic out of all 17 Y-STR markers. Single-copy locus DYS635 was exhibited highest polymorphism having 9 alleles and multi-copy loci DYS385a/b exhibited 35 genotypes. The genotype 13/19 was observed the highest value with a frequency of 0.127. DYS389I, DYS391, and DYS437 loci were observed with the lowest polymorphism. Among all alleles detected in Rakhine males, allele 10 of DYS391 was found the highest frequency of 0.791.

The gene diversity values were estimated from the allele frequencies at each Y-STR markers (Table 3.4). The highest gene diversity value was found at DYS385a/b (0.950) followed by DYS389II (0.809) and DYS458 (0.793). On the other hand, the lowest gene diversity value was observed at DYS391 (0.391). This result indicated that DYS385a/b and DYS458 were the most informative loci, whereas DYS391 and DYS456 were less informative with gene diversity below 0.450. This result exhibited a high level of genetic polymorphism in the Rakhine population (Supplementary Table 11).

Table 3.4 Allele/genotype frequencies and gene diversity for 17 Y-STR markers in 152 unrelated Rakhine males

DYS456		**DYS389I**		**DYS390**		**DYS389II**		**DYS458**		**DYS19**		**DYS393**	
A*	**F***	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
13	0.036	12	0.491	22	0.109	27	0.118	14	0.009	13	0.009	10	0.009
14	0.064	13	0.236	23	0.209	28	0.291	15	0.091	14	0.536	11	0.009
15	0.736	14	0.273	24	0.427	29	0.227	16	0.273	15	0.400	12	0.555
16	0.136	-	-	25	0.236	30	0.182	17	0.227	16	0.036	13	0.245
17	0.018	-	-	26	0.018	31	0.091	18	0.255	17	0.018	14	0.155
18	0.009	-	-	-	-	32	0.082	19	0.118	-	-	15	0.027
-	-	-	-	-	-	33	0.009	20	0.027	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD*	**0.438**		**0.634**		**0.713**		**0.809**		**0.793**		**0.556**		**0.613**
DYS391		**DYS439**		**DYS635**		**DYS392**		**YGATAH4**		**DYS437**		**DYS438**	
A	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
9	0.009	8	0.027	18	0.009	10	0.036	10	0.009	14	0.518	8	0.009
10	0.791	9	0.009	19	0.009	11	0.373	11	0.291	15	0.445	9	0.127
11	0.191	10	0.164	20	0.264	12	0.036	12	0.473	16	0.036	10	0.209
12	0.009	11	0.355	21	0.382	13	0.109	13	0.155	-	-	11	0.645
-	-	12	0.345	22	0.064	14	0.427	14	0.064	-	-	13	0.009
-	-	13	0.100	23	0.200	15	0.018	15	0.009	-	-	-	-
-	-	-	-	24	0.045	-	-	-		-	-	-	-
-	-	-	-	25	0.018	-	-	-		-	-	-	-
-	-	-	-	26	0.009	-	-	-		-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD	**0.341**		**0.724**		**0.744**		**0.670**		**0.669**		**0.537**		**0.529**
DYS448		**DYS385a/b**											
A	**F**	**Gt***	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**
17	0.018	9,14	0.009	11,14	0.109	12,17	0.027	14,16	0.018	15,15	0.018	15,21	0.009
18	0.118	9,17	0.009	11,15	0.009	13,16	0.018	14,17	0.018	15,16	0.009	16,18	0.018
19	0.227	9,18	0.018	11,17	0.027	13,17	0.055	14,18	0.027	15,17	0.045	16,19	0.009
20	0.573	11,11	0.027	11,21	0.009	13,18	0.064	14,19	0.018	15,18	0.027	16,20	0.009
21	0.055	11,12	0.009	12,14	0.009	13,19	0.127	14,20	0.055	15,19	0.027	17,21	0.009
22	0.009	11,13	0.018	12,15	0.009	13,20	0.100	14,24	0.009	15,20	0.027	-	-
Total	1												1
GD	0.608												0.950

A: Allele; F: Frequency; Gt: Genotype; GD: Gene diversity

A Median-joining network showed the Y-chromosome relationships of each haplotype within Rakhine population (Figure 3.4). The network projections of 110 Y-STR haplotypes of Rakhine population showed moderate compactness in their clusters. The reason for that some loci were highly uninformative with low levels of polymorphism in the Rakhine population. In the haplotype network analysis tree showed that there was one major cluster and three minor sub-clusters which indicated a certain degree of polymorphisms or mutations between these haplotypes. Most of the haplotypes were resided in the major cluster and the few haplotypes existed in the minor branches. A number of haplotypes were scattered in the network analysis tree. Haplotype Rk22 was the most frequent haplotype and contained seven analogue haplotypes and showed close genetic relationship with haplotype Rk90. Besides, haplotypes Rk6 and Rk7 were the second most frequent haplotypes and each haplotype consist of six analogues, respectively. The second most prominent haplotype Rk6 was shown the close relationship with Rk85. Another most dominant haplotype Rk7 was shown the close affinity with Rk23, Rk35, and Rk37, respectively. Haplotypes networking between Rk7, Rk23, and Rk37 had been observed the closest affinity which was shown by relative time estimate value represented in an age of 2,883 years, respectively. Furthermore, haplotypes Rk59 and Rk98 were observed the long distance Y-chromosome linkage relationship.

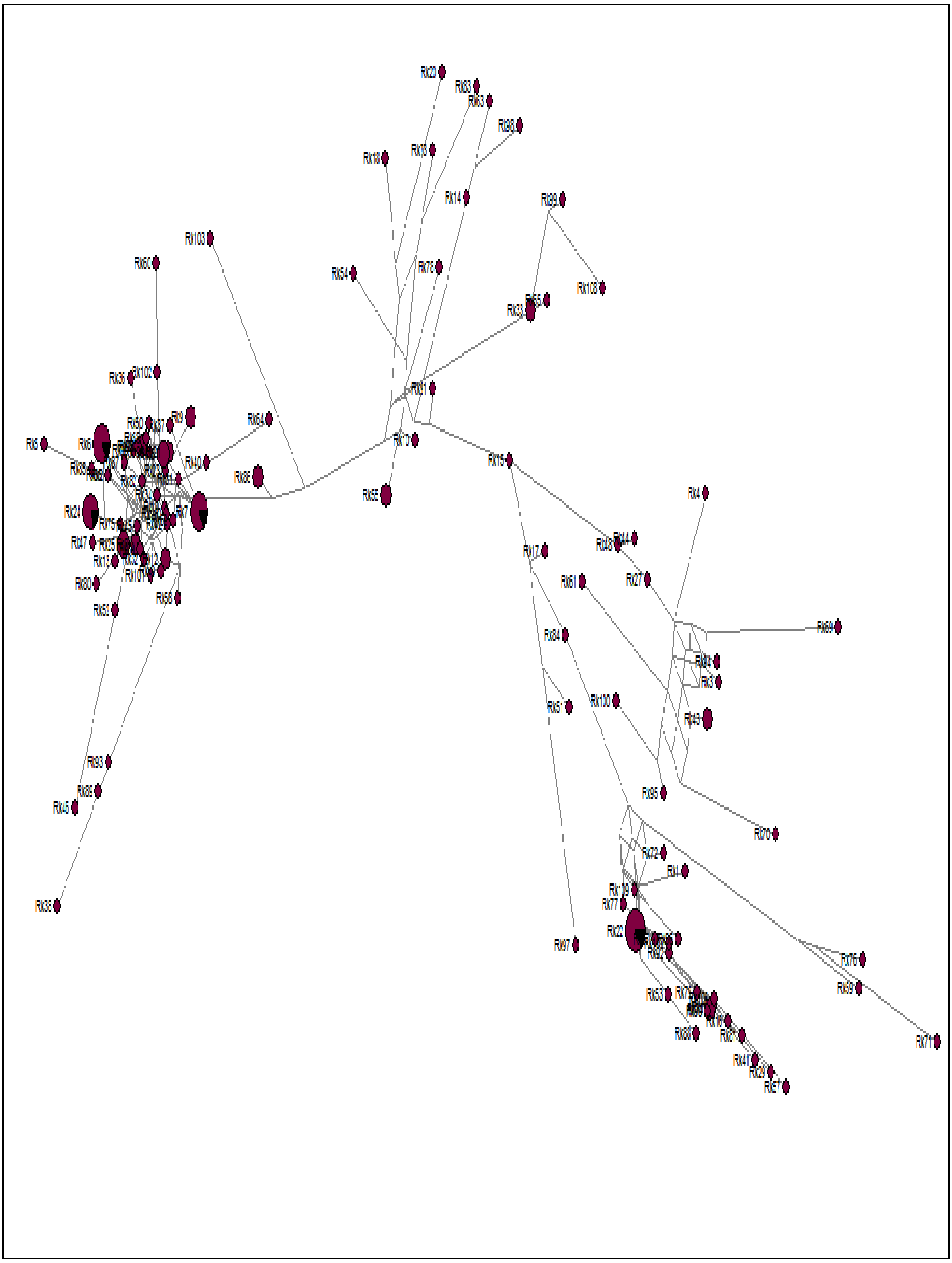

Figure 3.4 The Median-joining (MJ) networks of Y-STR haplotypes network of Rakhine individuals (110 haplotypes) reported in this study based on 15 Y-STRs. *Circles* represent haplotypes with areas proportional to frequencies; the smallest area is equivalent to one individual. Branch length is proportional to the number of mutations between haplotypes.

3.5 Marma Population

In this population genetics study, 17 Y-chromosomal STRs markers were analyzed in 144 unrelated healthy Marma males and identified a total of 138 haplotypes (Supplementary Table 05). The number of alleles and frequencies of alleles were calculated of 17 Y-STRs loci within Marma population.

In total 107 different haplotypes were detected of which 91 were unique, 11 were shared in two individuals, 2 were shared in three individuals, 1 was shared in four individuals, 1 was shared in seven individuals and 1 was shared in eight individuals (Table 3.9). In total, 107 different haplotypes within 144 individuals which correspond to a discrimination capacity were 77.536% (Supplementary Table 10). The most common haplotype (DYS456:15, DYS389I:12, DYS390:24, DYS389II:28, DYS458:19, DYS19:14, DYS385a/b: 13/21, DYS393:12, DYS391:10, DYS439:12, DYS635:21, DYS392:14, YGATAH4:12, DYS437:15, DYS438:11, and DYS448:20) was found in eight individuals (5.797%) while another haplotype (15-12-24-27-17-14-13/19-12-10-12-23-14-13-15-11-20) comprises 5.072% of Y-chromosomes in this population. Seventy-five alleles (7 alleles for DYS456, 4 alleles for DYS389I, 4 alleles for DYS390, 7 alleles for DYS389II, 7 alleles for DYS458, 3 alleles for DYS19, 5 alleles for DYS393, 3 alleles for DYS391, 5 alleles for DYS439, 7 alleles for DYS635, 6 alleles for DYS392, 5 alleles for YGATAH4, 3 alleles for DYS437, 5 alleles for DYS438, 4 alleles for DYS448), and 33 allele classes for DYS385a/b were observed in Marma. The most frequent haplotypes were detected 16 times i.e. 11.594%. The most common alleles of the 17 Y-chromosomal STR loci were DYS456*15, DYS389I*12, DYS390*24, DYS389II*28, DYS458*17, DYS19*14, DYS393*12, DYS391*10, DYS439*12, DYS635*20, DYS392*14, YGATAH4*12, DYS437*15, DYS438*11, DYS448*20, and DYS385a/b*13/19 (Supplementary Table 09).

The off-ladder alleles of the Marma population were presented in Supplementary Table 09. A total of five particular off-ladder rare alleles at different loci were detected in this population samples which were not present in the AmpF*l*STR® Yfiler™ Allelic Ladder. The off-ladder alleles have been observed: allele 12 (once) at the locus DYS456; allele 22 (once) at the locus DYS458, allele 19 (three times) at the locus DYS635; allele 14 (six times) at the locus YGATAH4, and allele 7 (twice) at the locus DYS438.

Y-chromosome haplotypes sharing were observed at intra-population level. The most frequent haplotype Mr37 (15-12-24-28-19-14-13,21-12-10-12-21-14-12-15-11-20) was shared between eight individuals in this population group (5.797%). Furthermore, the second most frequent haplotype Mr1 (15-12-24-27-17-14-13,19-12-10-12-23-14-13-15-11-20) was shared in seven individuals (5.072%). In addition, one, two, and eleven haplotypes were shared between four, three, and two individuals, respectively.

We also searched for all Y-STR profiles from Marma population in the YHRD (Release version R59; November 01, 2018). Out of 107 different haplotypes, 18 haplotypes were found a match and 89 haplotypes occurred only once for each among the global population of the 205,059 haplotypes. The most common and frequent haplotype Mr72 was shared between 12 individuals followed by haplotype Mr11 and Mr87 were shared between 10 and 8 individuals, respectively (Supplementary Table 05).

The analyzed group exhibited significant allele frequency variation. The observed alleles and gene diversity for 15 single-copy and 1 multi-copy locus in Marma population are summarized in Table 3.5. For Marma males, the allele frequencies of single-copy DYS loci ranged from minimum 0.009 to maximum 0.850 (DYS391), while the frequencies of genotypes of bi-allelic DYS385a/b marker ranged from 0.009 to 0.131. DYS635 and DYS3853a/b loci were observed to be the most polymorphic out of all 17 Y-STR markers. Single-copy locus DYS635 was exhibited highest polymorphism having 8 alleles and multi-copy loci DYS385a/b was exhibited with 33 genotypes. The genotype 13/19 was observed standing out with a frequency of 0.131. DYS19, DYS391, and DYS437 loci were observed with the lowest polymorphisms with 3 alleles. Among all alleles detected in Marma males, allele 10 of DYS391 was found the highest frequency of 0.850.

The gene diversity values were estimated from the allele frequencies at each Y-STR markers (Table 3.5). The highest gene diversity value was found at DYS385a/b (0.952) followed by DYS458 (0.807), DYS389II (0.763), and DYS635 (0.763). In contrast, the lowest gene diversity value was observed at DYS391 (0.265). This result indicated that DYS458, DYS389II, and DYS635 were the most informative loci whereas DYS391 was less informative with gene diversity below 0.270. This result demonstrated a high level of genetic polymorphism in the Marma population (Supplementary Table 11).

Table 3.5 Allele/genotype frequencies and gene diversity for 17 Y-STR markers in 144 unrelated Marma males

DYS456		**DYS389I**		**DYS390**		**DYS389II**		**DYS458**		**DYS19**		**DYS393**	
A*	**F***	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
12	0.009	10	0.009	22	0.037	27	0.187	15	0.084	14	0.514	11	0.037
13	0.019	12	0.579	23	0.243	28	0.364	16	0.187	15	0.364	12	0.645
14	0.009	13	0.131	24	0.514	29	0.234	17	0.234	16	0.121	13	0.131
15	0.701	14	0.280	25	0.206	30	0.140	18	0.271	-	-	14	0.140
16	0.196	-	-	-	-	31	0.047	19	0.168	-	-	15	0.047
17	0.056	-	-	-	-	32	0.009	20	0.047	-	-	-	-
18	0.009	-	-	-	-	33	0.019	22	0.009	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD*	**0.471**		**0.574**		**0.639**		**0.763**		**0.807**		**0.594**		**0.549**
DYS391		**DYS439**		**DYS635**		**DYS392**		**YGATAH4**		**DYS437**		**DYS438**	
A	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
9	0.028	8	0.009	19	0.027	10	0.084	10	0.028	14	0.420	7	0.019
10	0.850	10	0.093	20	0.318	11	0.252	11	0.336	15	0.533	9	0.075
11	0.121	11	0.383	21	0.290	12	0.037	12	0.383	16	0.047	10	0.280
-	-	12	0.393	22	0.178	13	0.187	13	0.196	-	-	11	0.579
-	-	13	0.121	23	0.159	14	0.402	14	0.056	-	-	12	0.047
-	-	-	-	25	0.009	15	0.037	-	-	-	-	-	-
-	-	-	-	26	0.019	-	-	-	-	-	-	-	-
-	-	-	-	27	0.027	-	-	-	-	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD	**0.265**		**0.682**		**0.763**		**0.737**		**0.705**		**0.542**		**0.584**
DYS448		**DYS385a/b**											
A	**F**	**Gt***	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**
18	0.121	9,13	0.009	11,17	0.047	13,16	0.019	14,16	0.065	15,16	0.019	16,17	0.009
19	0.262	9,17	0.009	11,20	0.028	13,17	0.009	14,18	0.009	15,17	0.019	16,18	0.009
20	0.542	10,16	0.009	12,16	0.009	13,18	0.056	14,19	0.037	15,18	0.009	17,18	0.009
21	0.075	11,12	0.009	12,17	0.028	13,19	0.131	14,20	0.037	15,20	0.037	-	-
-	-	11,14	0.093	12,19	0.028	13,20	0.084	14,21	0.037	15,21	0.009	-	-
-	-	11,16	0.009	13,13	0.037	13,21	0.056	14,22	0.009	16,16	0.009	-	-
Total	**1**												**1**
GD	**0.623**												**0.952**

A: Allele; F: Frequency; Gt: Genotype; GD: Gene diversity

A Median-joining network showed the Y-chromosome relationships of each haplotype within the Marma tribe (Figure 3.5). The network projections of 107 Y-STR haplotypes of Marma population showed very high compactness in their clusters. The reason for that some loci were highly uninformative with low levels of polymorphism in the Marma population. In this network analysis, the haplotype network tree exhibited two clusters which indicated a certain degree of polymorphisms or mutations between these haplotypes. Haplotypes Mr1 and Mr37 were the most frequent haplotypes and each haplotype consist of eight analogues, respectively. The most prominent haplotype Mr1 showed the close affinity with Mr50 which was shown by relative time estimate value represented in an age of 2,242 years. Similarly, the network also showed that the another most frequent haplotype Mr37 had a close genetic relation with Mr82 and the relative time estimate value between the haplotypes was represented in an age of 2,242 years. Furthermore, haplotypes Mr4 and Mr94 were observed the long distance Y-chromosome relationships.

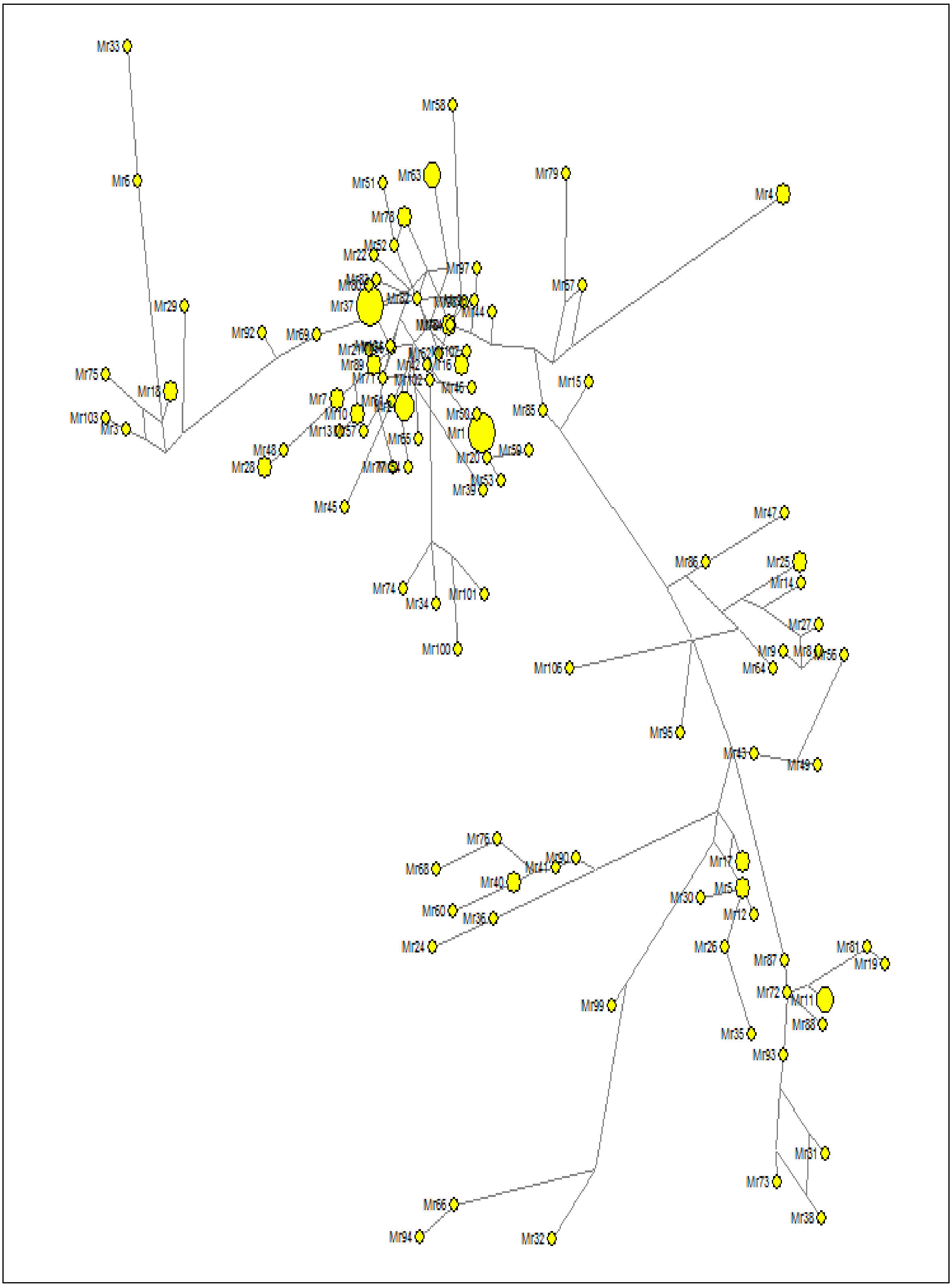

Figure 3.5 The Median-joining (MJ) networks of Y-STR haplotypes network of Marma individuals (107 haplotypes) reported in this study based on 15 Y-STRs. *Circles* represent haplotypes with areas proportional to frequencies; the smallest area is equivalent to one individual. Branch length is proportional to the number of mutations between haplotypes.

3.6 Hajong Population

Overall 112 unrelated healthy Hajong males were recruited in this study and identified a total of 109 Y-chromosomal STR haplotypes (Supplementary Table 06). The number of alleles and frequencies of alleles were calculated of 17 Y-STRs loci within Hajong population.

A total of 89 different haplotypes were monitored of which 71 were unique, 16 were shared in two individuals and 2 were shared in three individuals (Table 3.9). In total, 89 different haplotypes among 112 individuals which correspond to a discrimination capacity was 80.909% (Supplementary Table 10). The most frequent haplotype occurred 18 times, accounting 16.363%. Seventy-eight alleles (5 alleles for DYS456, 3 alleles for DYS389I, 5 alleles for DYS390, 8 alleles for DYS389II, 7 alleles for DYS458, 4 alleles for DYS19, 5 alleles for DYS393, 3 alleles for DYS391, 5 alleles for DYS439, 8 alleles for DYS635, 7 alleles for DYS392, 5 alleles for YGATAH4, 3 alleles for DYS437, 4 alleles for DYS438, 6 alleles for DYS448), and 29 allele classes for DYS385a/b were observed in Hajong. The most common alleles of the 17 Y-chromosomal STR loci were DYS456*15, DYS389I*12, DYS390*24, DYS389II*28, DYS458*17, DYS19*14, DYS393*12, DYS391*10, DYS439*12, DYS635*20, DYS392*14, YGATAH4*12, DYS437*15, DYS438*11, DYS448*20, and DYS385a/b*13/18 (Supplementary Table 09).

The off-ladder or rare alleles and microvariants of Hajong population were presented in Supplementary Table 09. A total of four unique off-ladder or rare alleles at different loci were detected in the Hajong population samples and not present in the AmpF*l*STR® Yfiler™ Allelic Ladder. The off-ladder alleles have been observed: allele 23 (once) at the locus DYS389II; allele 19 (four times) at the locus DYS635; allele 14 (once) at the locus YGATAH4, and allele 16 (once) at the locus DYS448. Only one microvariant or partial allele typed as 13.2 based on fragment size was observed once at DYS385a/b locus in one individual of Hajong tribe [Hasan *et al.*, 2018].

Y-chromosome haplotypes sharing were observed within Hajong inhabitants. The most frequent haplotypes in this population study depicted by 17 Y-STR loci system. According to YHRD order, two haplotypes (Hj3: 15-13-24-29-17-14-12,18-14-10-10-24-10-13-16-11-19 and Hj48: 15-12-23-28-18-14-13,20-12-10-11-20-14-12-15-11-20) were shared in three individuals in Hajong population (5.455%), respectively. On the other hand, sixteen haplotypes were shared between two individuals.

We also searched for all Y-chromosomal STR profiles from Hajong population in the YHRD (Release version R59; November 01, 2018). Out of 89 different haplotypes, 12 haplotypes were found a match and 77 haplotypes were occurred once for each among the global populations with 205,059 haplotypes. The most common and frequent haplotype Hj49 was shared between 15 individuals followed by haplotype Hj33 was shared between 14 individuals (Supplementary Table 06).

This analyzed population exhibited a significant level of allele frequency variation. The observed alleles and gene diversity for 15 single-copy loci and 1 multi-copy locus in Hajong population were summarized in Table 3.6. For Hajong males, the allele frequencies of single-copy DYS loci ranged from minimum 0.011 to maximum 0.685, while the frequencies of genotypes of bi-allelic DYS385a/b marker ranged from 0.011 to 0.169. DYS389II, DYS635, and DYS385a/b loci were observed to be the most polymorphic out of all 17 Y-STR markers. Single-copy loci DYS389II and DYS635 were exhibited highest polymorphism with 8 alleles and multi-copy loci DYS385a/b exhibited 29 genotypes. The genotype 13/18 was observed the highest frequency of 0.169. DYS389I, DUS391, and DYS437 loci were showed the lowest polymorphism with 3 alleles. Among all alleles detected in Hajong males, allele 11 of DYS438 was found the highest frequency of 0.685.

The gene diversity values were estimated from the allele frequencies at each Y-STR markers (Table 3.6). The highest gene diversity value was found at DYS385a/b (0.932) followed by DYS458 (0.803) and DYS635 (0.754). On the other hand, the lowest gene diversity value was observed at DYS438 (0.477). This result indicated that DYS385a/b, DYS458 and DYS635 were the most informative loci, whereas DYS438 was observed less informative with gene diversity below 0.480. This result exhibited a high level of genetic polymorphism in the Hajong population (Supplementary Table 11).

Table 3.6 Allele/genotype frequencies and gene diversity for 17 Y-STR markers in 112 unrelated Hajong males

DYS456		**DYS389I**		**DYS390**		**DYS389II**		**DYS458**		**DYS19**		**DYS393**	
A*	**F***	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
13	0.056	12	0.539	21	0.011	23	0.011	14	0.067	14	0.483	10	0.011
14	0.079	13	0.315	22	0.101	25	0.011	15	0.091	15	0.427	11	0.113
15	0.573	14	0.146	23	0.348	27	0.034	16	0.202	16	0.079	12	0.551
16	0.225	-	-	24	0.371	28	0.416	17	0.303	17	0.011	13	0.213
17	0.067	-	-	25	0.169	29	0.258	18	0.236	-	-	14	0.112
-	-	-	-	-	-	30	0.191	19	0.056	-	-	-	-
-	-	-	-	-	-	31	0.067	20	0.045	-	-	-	-
-	-	-	-	-	-	32	0.011	-	-	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD*	**0.614**		**0.596**		**0.710**		**0.726**		**0.803**		**0.585**		**0.633**
DYS391		**DYS439**		**DYS635**		**DYS392**		**YGATAH4**		**DYS437**		**DYS438**	
A	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
10	0.146	10	0.112	19	0.045	7	0.011	10	0.056	14	0.281	9	0.045
11	0.674	11	0.348	20	0.393	10	0.034	11	0.281	15	0.618	10	0.236
12	0.180	12	0.371	21	0.270	11	0.236	12	0.483	16	0.101	11	0.685
-	-	13	0.146	22	0.056	12	0.045	13	0.169	-	-	12	0.034
-	-	14	0.022	23	0.135	13	0.169	14	0.011	-	-	-	-
-	-	-	-	24	0.045	14	0.483	-	-	-	-	-	-
-	-	-	-	25	0.022	15	0.022	-	-	-	-	-	-
-	-	-	-	26	0.034	-	-	-	-	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD	**0.498**		**0.715**		**0.754**		**0.686**		**0.663**		**0.535**		**0.477**
DYS448		**DYS385a/b**											
A	**F**	**Gt***	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**
16	0.011	9,16	0.011	12,14	0.011	13,18	0.169	14,15	0.011	15,16	0.034		
17	0.011	10,14	0.011	12,16	0.034	13,19	0.135	14,19	0.011	15,18	0.022		
18	0.101	11,13	0.011	12,18	0.022	13,20	0.079	14,20	0.011	15,19	0.034		
19	0.214	11,13.2	0.011	13,15	0.011	13,21	0.079	14,21	0.034	16,17	0.011		
20	0.618	11,14	0.089	13,16	0.034	13,22	0.011	14,22	0.011	16,19	0.011		
21	0.045	11,15	0.011	13,17	0.045	13,23	0.022	15,15	0.011	-	-		
Total	**1**										**1**		
GD	**0.566**										**0.932**		

A: Allele; F: Frequency; Gt: Genotype; GD: Gene diversity

A Median-joining network showed the Y-chromosome relationships of each haplotype within Hajong population (Figure 3.6). The network projections of 89 Y-STR haplotypes of Hajong tribe showed very high compactness in their clusters. The reason for that some loci were highly uninformative with low levels of polymorphism in the Hajong population. In the haplotype network analysis tree showed that there was one cluster and one minor branch which indicated a certain degree of polymorphisms or mutations between these haplotypes. Most of the haplotypes have resided in the clusters and few haplotypes have existed in the minor branch. Haplotype Hj48 was the most frequent haplotype and consisted of four analogue haplotypes which resided in the center of a cluster and also close genetic similarity with haplotypes Hj51 and Hj59, respectively. Haplotypes networking between Hj30 and Hj34 had the most compact relationship which was shown by relative time estimate value represented in an age of 6,726 years. Similarly, haplotypes Hj37 and Hj66 had the most compact relationship which was shown by relative time estimate value represented in an age of 6,726 years. Besides, haplotypes Hj56 and Hj59 were observed the long distance Y-chromosome relationship.

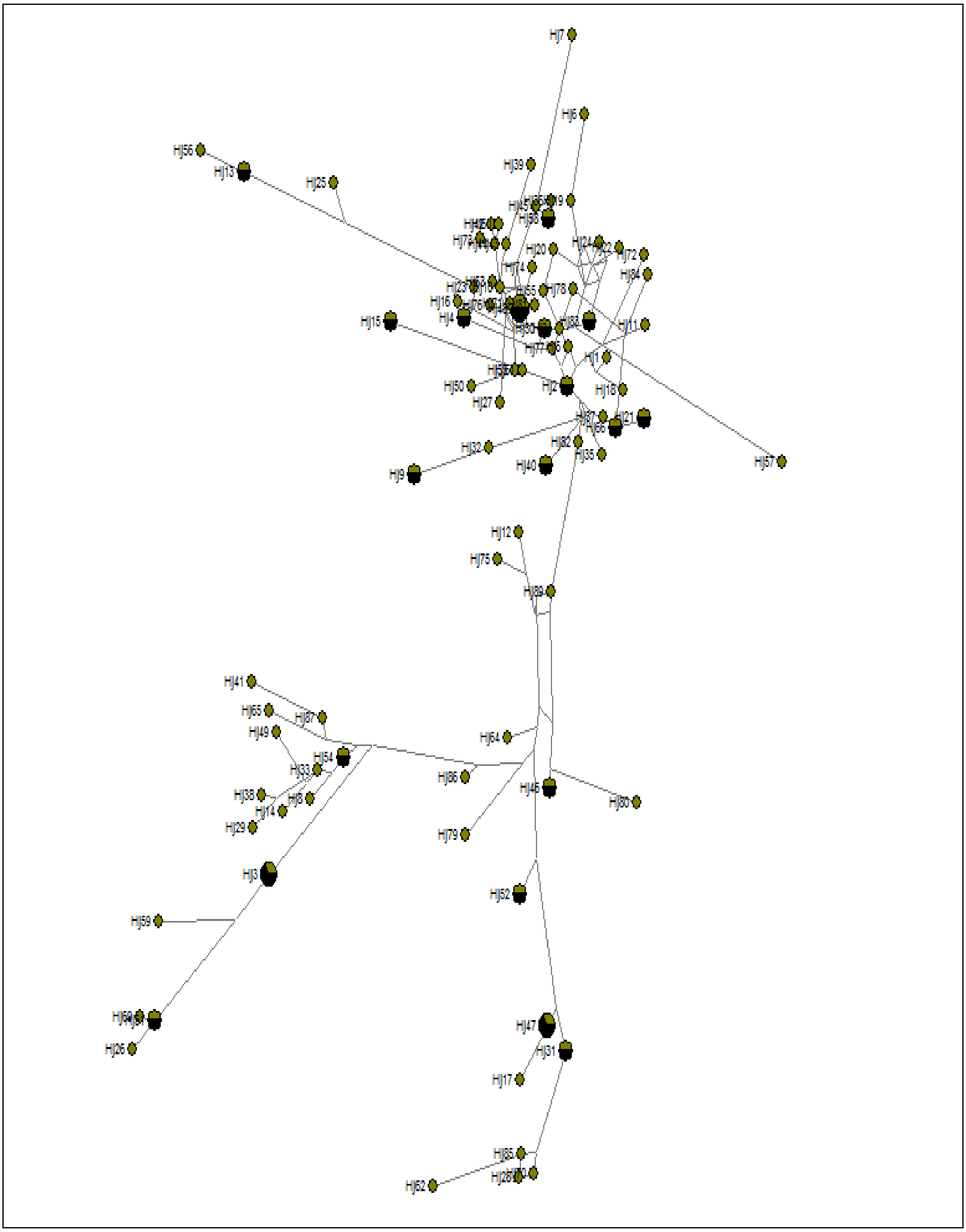

Figure 3.6 The Median-joining (MJ) networks of Y-STR haplotypes network of Hajong individuals (89 haplotypes) reported in this study based on 15 Y-STRs. *Circles* represent haplotypes with areas proportional to frequencies; the smallest area is equivalent to one individual. Branch length is proportional to the number of mutations between haplotypes.

3.7 Manipuri Population

Seventeen Y-STRs were analyzed in 136 unrelated healthy Manipuri males and identified a total of 131 haplotypes (Supplementary Table 07). The number of alleles and frequencies of alleles were calculated of 17 Y-STRs loci within Manipuri population.

A total of 98 different haplotypes were identified of which 83 were unique, 11 were shared in two individuals, 1 was shared in four individuals, 1 was shared in five individuals, 1 was shared in eight individuals, and 1 was shared in nine individuals (Table 3.9). In total, 98 different haplotypes among 136 individuals which correspond to a discrimination capacity were 74.809% (Supplementary Table 10). Seventy-two alleles (4 alleles for DYS456, 4 alleles for DYS389I, 5 alleles for DYS390, 7 alleles for DYS389II, 5 alleles for DYS458, 6 alleles for DYS19, 5 alleles for DYS393, 4 alleles for DYS391, 5 alleles for DYS439, 9 alleles for DYS635, 6 alleles for DYS392, 5 alleles for YGATAH4, 3 alleles for DYS437, 4 alleles for DYS438, 4 alleles for DYS448), and 20 allele classes for DYS385a/b were observed in Bangali. The most frequent haplotype occurs 15 times (11.450%). The most common alleles of the 17 Y-chromosomal STR loci were DYS456*15, DYS389I*13, DYS390*23, DYS389II*30, DYS458*16, DYS19*14, DYS393*13, DYS391*10, DYS439*10, DYS635*23, DYS392*11, YGATAH4*12, DYS437*14 &15, DYS438*11, DYS448*20, and DYS385a/b*11/14 (Supplementary Table 09).

The off-ladder or rare alleles and microvariants of Manipuri population were presented in Supplementary Table 09. In general, three distinct rare alleles or off-ladder alleles at different loci were detected in the Manipuri population samples which were not present in the AmpF*l*STR® Yfiler™ Allelic Ladder. The off-ladder alleles have been found: allele 19 (four times), allele 32 (once) at the locus DYS635, and allele 14 (once) at the locus YGATAH4. Only one microvariant or partial allele typed as 13.2 based on fragment size was monitored once at DYS19 locus in one individual of Manipuri tribe samples [Hasan *et al.*, 2018].

Y-chromosomal haplotype sharing was observed at the intra-population level in Manipuri males. According to YHRD order, the most frequent haplotype Mn36 (15-14-23-30-16-14-20,20-13-10-11-24-12-12-15-11-19) was shared between nine individuals in this population group (6.870%). Furthermore, the second most frequent haplotype Mn37 (16-13-25-30-15-15-11,14-13-10-10-21-11-13-14-11-20) was shared in eight individuals

(5.344%). In contrast, one, one, and eleven haplotypes were shared between five, four, and two individuals, respectively. Interestingly, no Manipuri male chromosome shared among the studied population samples.

We also searched for all Y-STR profiles from Manipuri population in the YHRD (Release version R59; November 01, 2018). Out of 98 different haplotypes, 5 haplotypes were found a match, 31 haplotypes occurred once and 62 haplotypes demonstrated no haplotype sharing among the global populations with 205,059 haplotypes. The most common and frequent haplotype Mn71 was shared between 7 individuals followed by haplotype Mn14 was shared between 3 individuals (Supplementary Table 07).

The analyzed Manipuri population exhibited significant allele frequency variation. The observed alleles and gene diversity for 15 single-copy and 1 multi-copy locus in Manipuri population were summarized in Table 3.7. For Manipuri males, the allele frequencies of single-copy DYS loci ranged from minimum 0.010 to maximum 0.929 (DYS391), while the frequencies of genotypes of bi-allelic DYS385a/b marker ranged from 0.010 to 0.327. The DYS635 and DYS385a/b loci were observed to be the most polymorphic out of all 17 Y-STR markers. Single-copy loci DYS635 exhibited the highest polymorphism with 8 alleles and multi-copy loci DYS385a/b was exhibited with 20 genotypes. The genotype 11/14 was observed the highest frequency of 0.327. In contrast, the locus DYS437 demonstrated the lowest polymorphism with 3 alleles. Among all alleles detected in Manipuri males, allele 10 of DYS391 was found the highest frequency of 0.929.

The gene diversity values were estimated from the allele frequencies at each Y-STR markers (Table 3.7). The highest gene diversity value was found at DYS385a/b (0.848) followed by DYS635 (0.824) and DYS389II (0.818). In contrast, the lowest gene diversity value was found at DYS391 (0.136). This result indicated that DYS385a/b, DYS635, and DYS389II were the most informative loci whereas DYS391 was observed less informative with gene diversity below 0.140. This result exhibited a high level of genetic polymorphism in the Manipuri population (Supplementary Table 11).

Table 3.7 Allele/genotype frequencies and gene diversity for 17 Y-STR markers in 136 unrelated Manipuri males

DYS456		**DYS389I**		**DYS390**		**DYS389II**		**DYS458**		**DYS19**		**DYS393**	
A*	**F***	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
14	0.051	12	0.296	22	0.061	27	0.031	15	0.122	13.2	0.010	10	0.010
15	0.786	13	0.367	23	0.327	28	0.204	16	0.541	14	0.520	12	0.388
16	0.153	14	0.327	24	0.306	29	0.204	17	0.204	15	0.265	13	0.540
17	0.010	15	0.010	25	0.265	30	0.234	18	0.102	16	0.122	14	0.031
-	-	-	-	26	0.041	31	0.184	19	0.031	17	0.071	15	0.031
-	-	-	-	-	-	32	0.133	-	-	18	0.010	-	-
-	-	-	-	-	-	33	0.010	-	-	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD*	**0.360**		**0.678**		**0.731**		**0.818**		**0.646**		**0.646**		**0.562**
DYS391		**DYS439**		**DYS635**		**DYS392**		**YGATAH4**		**DYS437**		**DYS438**	
A	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
9	0.020	9	0.010	20	0.041	10	0.061	10	0.020	14	0.479	9	0.122
10	0.929	10	0.429	21	0.204	11	0.378	11	0.102	15	0.479	10	0.041
11	0.041	11	0.316	22	0.142	12	0.276	12	0.490	16	0.041	11	0.816
12	0.010	12	0.204	23	0.041	13	0.071	13	0.378	-	-	12	0.020
-	-	13	0.041	24	0.276	14	0.194	14	0.010	-	-	-	-
-	-	-	-	25	0.204	15	0.020	-	-	-	-	-	-
-	-	-	-	26	0.041	-	-	-	-	-	-	-	-
-	-	-	-	32	0.010	-	-	-	-	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD	**0.136**		**0.680**		**0.824**		**0.742**		**0.612**		**0.545**		**0.320**
DYS448		**DYS385a/b**											
A	**F**	**Gt***	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**		
18	0.031	11,13	0.031	12,17	0.041	13,19	0.153	14,20	0.051	18,20	0.010		
19	0.316	11,14	0.327	12,19	0.010	13,20	0.010	15,17	0.051	19,20	0.031		
20	0.643	11,15	0.010	12,20	0.020	14,17	0.031	16,19	0.010	19,21	0.010		
21	0.010	11,18	0.010	13,18	0.031	14,19	0.020	16,20	0.010	20,20	0.133		
Total	**1**										**1**		
GD	**0.491**										**0.848**		

A: Allele; F: Frequency; Gt: Genotype; GD: Gene diversity

A Median-joining network showed the Y-chromosome relationships of each haplotype within Manipuri population (Figure 3.7). The network projections of 98 Y-STR haplotypes of Manipuri population showed very high compactness in their clusters. The reason for that some loci were highly uninformative with low levels of polymorphism in the Manipuri population. In the haplotype network analysis tree showed that the tree was composed of three isolated branches which indicated a certain degree of polymorphisms or mutations between these haplotypes. Among the 98 haplotypes of Manipuri tribes, the most frequent haplotype Mn9 consisted of twelve analogue haplotypes in the centre of the network tree and also exhibited the strong genetic affinity with Mn17, Mn28, Mn39, and Mn83, respectively. The second most prominent haplotype Mn37 consisted of eight analogue haplotypes and showed the close affinity with Mn81, Mn92, and Mn97, respectively. Haplotypes networking between Mn37 and Mn97 had the most compact clustering which was shown by relative time estimate value represented in an age of 2,242 years. Moreover, haplotypes Mn5 and Mn42 were observed the long distance Y-chromosome relationships.

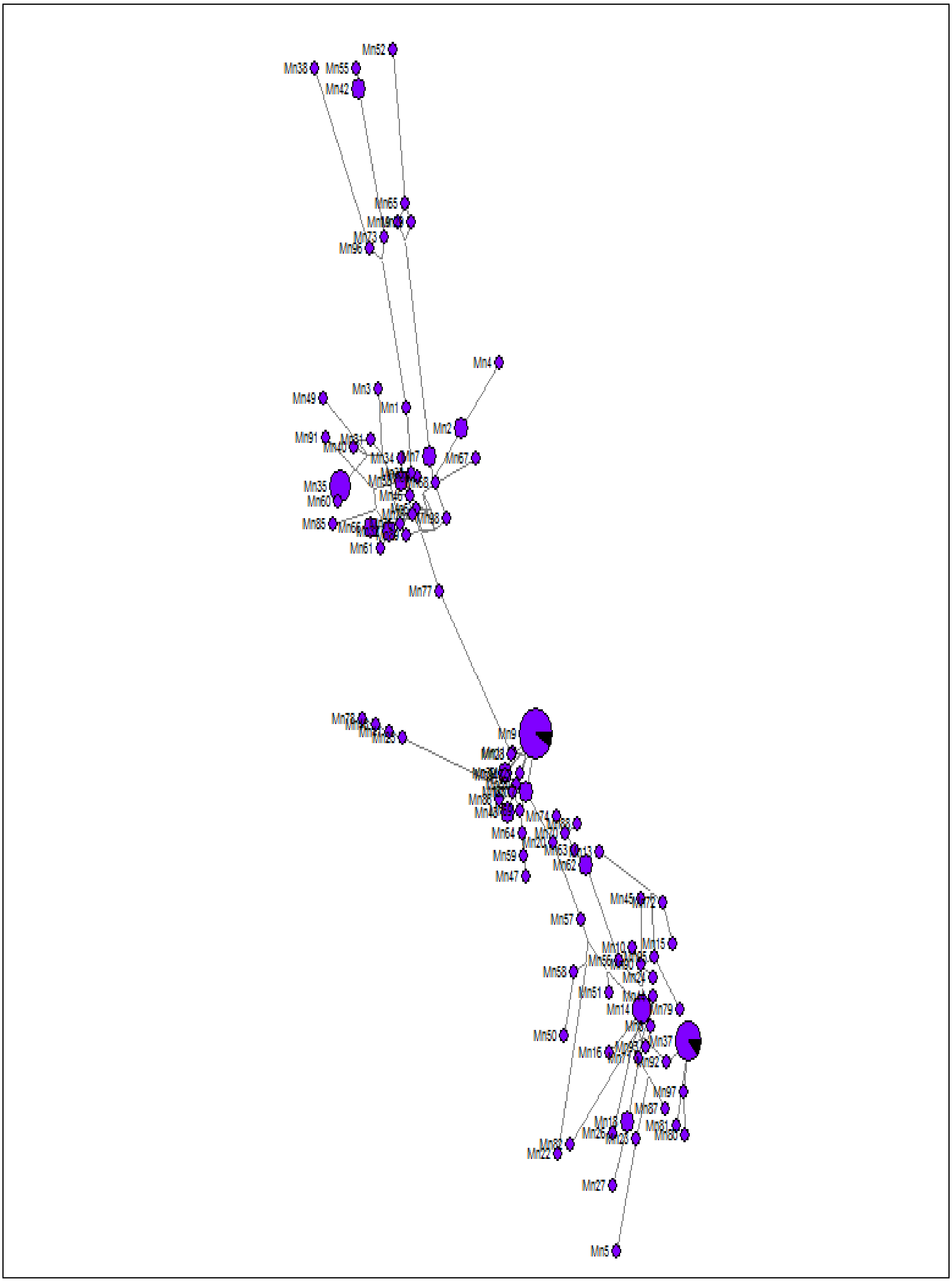

Figure 3.7 The Median-Joining (MJ) networks of Y-STR haplotypes network of Manipuri individuals (98 haplotypes) reported in this study based on 15 Y-STRs. *Circles* represent haplotypes with areas proportional to frequencies; the smallest area is equivalent to one individual. Branch length is proportional to the number of mutations between haplotypes.

3.8 Khasia Population

Overall 112 unrelated healthy Khasia males were employed in this study and identified a total of 110 haplotypes (Supplementary Table 08). The number of alleles and frequencies of alleles were calculated of 17 Y-STRs loci within Khasia population.

A total of 91 different haplotypes were observed of which 78 were unique, 10 were shared in two individuals, 2 were shared in three individuals, and 1 was shared in six individuals (Figure 3.9). In total, 91 different haplotypes among 112 individuals which correspond to a discrimination capacity were 81.250% (Supplementary Table 10). Seventy-two alleles (4 alleles for DYS456, 4 alleles for DYS389I, 5 alleles for DYS390, 6 alleles for DYS389II, 5 alleles for DYS458, 4 alleles for DYS19, 5 alleles for DYS393, 3 alleles for DYS391, 5 alleles for DYS439, 8 alleles for DYS635, 6 alleles for DYS392, 4 alleles for YGATAH4, 3 alleles for DYS437, 4 alleles for DYS438, 6 alleles for DYS448), and 32 allele classes for DYS385a/b were observed in Khasia. The most frequent haplotype occurs 13 times (11.818%). The most common alleles of the 17 Y-chromosomal STR loci were DYS456*15, DYS389I*13, DYS390*25, DYS389II*30, DYS458*16, DYS19*15, DYS393*14, DYS391*10, DYS439*11, DYS635*21, DYS392*13, YGATAH4*11, DYS437*14, DYS438*10, DYS448*18, and DYS385a/b*12/17 (Supplementary Table 09).

The off-ladder or rare alleles of Manipuri population were presented in Supplementary Table 09. A total of two specific rare alleles or off-ladder alleles were detected in the Khasia population samples and not present in the AmpF*l*STR® Yfiler™ Allelic Ladder. These two rare alleles have been found: allele18 (three times), and allele 19 (eleven times) at the locus DYS635.

Y-chromosome haplotype sharing was observed with Khasia population. According to YHRD order, the most frequent haplotype Kh16 (15-13-25-29-17-15-15,19-14-10-11-21-13-10-14-10-18) was shared in six individuals in this population (5.455%). In addition, two and ten haplotypes were shared between three and two individuals, respectively.

We also searched for all Y-STR profiles from Khasia population in the YHRD (Release version R59; November 01, 2018). Out of 91 different haplotypes, 3 haplotypes were found a match, 29 haplotypes occurred once for each and rest of the 59 haplotypes demonstrated no haplotype sharing among the global populations with 205,059 haplotypes. The most common and frequent haplotype Kh11 was shared between 8 individuals among the worldwide populations (Supplementary Table 08).

This analyzed population exhibited significant allele frequency variation. The observed alleles and gene diversity for 15 single-copy and 1 multi-copy locus in Khasia population were summarized in Table 3.8. For Khasia males, the allele frequencies of single-copy DYS loci ranged from minimum 0.011 to maximum 0.725 (maximum values for DYS19 and DYS437), while the frequencies of genotypes of DYS385a/b marker ranged from 0.011 to 0.098. The loci DYS635 and DYS385a/b were observed to be the most polymorphic out of all 17 Y-STR markers. Single-copy loci DYS635 exhibited the highest polymorphism with 8 alleles and multi-copy loci DYS385a/b exhibited 32 genotypes. The genotype 12/17 was observed the highest frequency of 0.098. Then again, the loci DYS391 and DYS437 were observed with the lowest polymorphism with 3 alleles. Among all alleles detected in Khasia males, allele 14 of DYS437 was found the highest frequency of 0.725.

The gene diversity values were estimated from the allele frequencies at each Y-STR markers (Table 3.8). The highest gene diversity value was found at multi-copy loci DYS385a/b (0.964) followed by DYS635 (0.784) and DYS392 (0.746). On the other hand, the lowest gene diversity value was at DYS437 (0.414). This result indicated that DYS385a/b and DYS635 were the most informative loci. On the other hand, DYS19 and DYS437 were less informative loci with gene diversity below 0.450. This result exhibited a high level of genetic polymorphism in the Khasia population (Supplementary Table 11).

Table 3.8 Allele/genotype frequencies and gene diversity for 17 Y-STR markers in 110 unrelated Khasia males

DYS456		**DYS389I**		**DYS390**		**DYS389II**		**DYS458**		**DYS19**		**DYS393**	
A*	**F***	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
14	0.088	12	0.099	22	0.055	27	0.033	15	0.154	13	0.011	12	0.143
15	0.582	13	0.659	23	0.296	28	0.209	16	0.417	14	0.154	13	0.340
16	0.286	14	0.231	24	0.187	29	0.253	17	0.352	15	0.725	14	0.396
17	0.044	15	0.011	25	0.429	30	0.395	18	0.055	16	0.110	15	0.110
-	-	-	-	26	0.033	31	0.066	19	0.022	-	-	16	0.011
-	-	-	-	-	-	32	0.044	-	-	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD*	**0.576**		**0.508**		**0.697**		**0.737**		**0.682**		**0.443**		**0.703**
DYS391		**DYS439**		**DYS635**		**DYS392**		**YGATAH4**		**DYS437**		**DYS438**	
A	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**	**A**	**F**
10	0.659	10	0.132	18	0.033	10	0.055	10	0.121	14	0.725	9	0.077
11	0.319	11	0.483	19	0.121	11	0.264	11	0.527	15	0.253	10	0.604
12	0.022	12	0.286	20	0.132	12	0.198	12	0.220	16	0.022	11	0.297
-	-	13	0.088	21	0.395	13	0.374	13	0.132	-	-	12	0.022
-	-	14	0.011	22	0.088	14	0.099	-	-	-	-	-	-
-	-	-	-	23	0.154	15	0.011	-	-	-	-	-	-
-	-	-	-	24	0.022	-	-	-	-	-	-	-	-
-	-	-	-	25	0.055	-	-	-	-	-	-	-	-
Total	**1**		**1**		**1**		**1**		**1**		**1**		**1**
GD	**0.469**		**0.667**		**0.784**		**0.746**		**0.649**		**0.414**		**0.547**
DYS448		**DYS385a/b**											
A	**F**	**Gt***	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**	**Gt**	**F**
17	0.022	10,14	0.044	12,14	0.011	13,17	0.044	14,18	0.033	15,19	0.077	17,17	0.011
18	0.385	11,12	0.033	12,16	0.044	13,18	0.044	14,19	0.033	15,20	0.055	18,18	0.011
19	0.297	11,14	0.022	12,17	0.098	13,19	0.055	14,20	0.022	15,21	0.044	-	-
20	0.209	11,15	0.022	12,18	0.011	13,22	0.011	15,16	0.011	15,22	0.011	-	-
21	0.077	11,17	0.033	13,15	0.011	14,14	0.011	15,17	0.022	15,23	0.033	-	-
22	0.011	11,18	0.011	13,16	0.022	14,16	0.011	15,18	0.022	16,19	0.077	-	-
Total	**1**												**1**
GD	**0.721**												**0.964**

A: Allele; F: Frequency; Gt: Genotype; GD: Gene diversity

A Median-joining network showed the Y-chromosome relationships of each haplotype within Khasia tribe (Figure 3.8). The network projections of 91 Y-STR haplotypes of Khasia population showed moderate compactness in their clusters. The reason for that some loci were highly uninformative with low levels of polymorphism in the Khasia population. In the haplotype network analysis tree showed that there were one cluster and four branches which indicated a certain degree of polymorphisms or mutations between these haplotypes. Most of the haplotypes have resided in the cluster and a number of haplotypes have scattered within branches. The most abundant haplotype Kh16 consisted of 6 analogue haplotypes and it showed a strong genetic relationship with haplotypes Kh46, Kh65, and Kh88, respectively. The second most prominent haplotype Kh31 consisted of 4 analogue haplotypes and showed a close affinity with Kh50. Networking revealed that haplotypes Kh46, Kh65, and Kh88 have the most compact clustering which was shown by relative time estimate value represented in an age of 2,883 years. Besides, haplotypes Kh41 and Kh52 were observed the long distance Y-chromosome relationships.

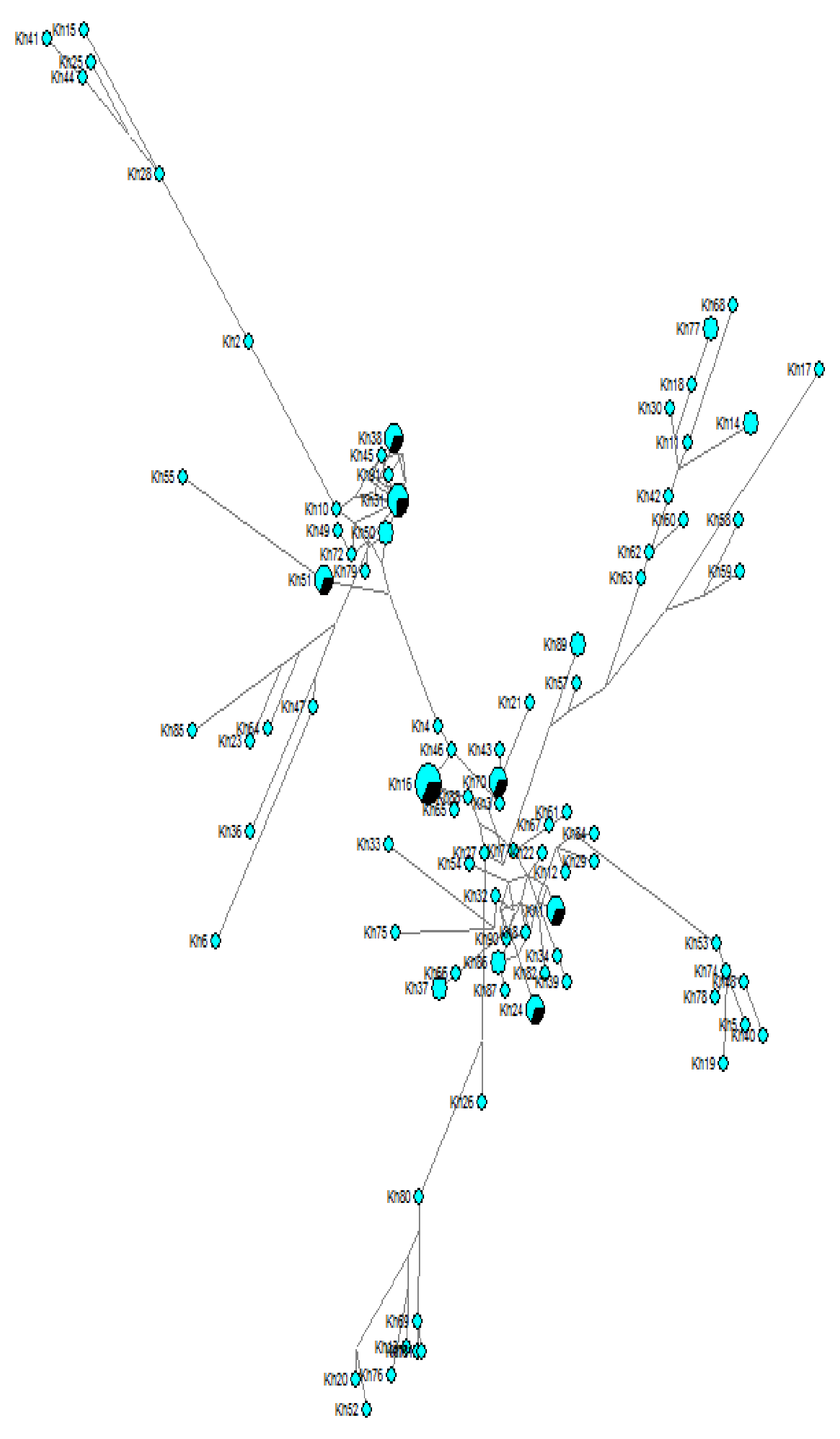

Figure 3.8 The Median-Joining (MJ) networks of Y-STR haplotypes network of Khasia individuals (91 haplotypes) reported in this study based on 15 Y-STRs. *Circles* represent haplotypes with areas proportional to frequencies; the smallest area is equivalent to one individual. Branch length is proportional to the number of mutations between haplotypes.

3.9 Y-chromosomal Haplotypes Analysis of the Studied Populations

In this study, 1,631 unrelated male samples of the studied populations from Bangladesh were genotyped for Y-chromosome haplotypes and haplogroup defining markers. We successfully obtained 1,594 distinct haplotypes for the total 17 Y-STRs loci. In total, 1,359 different haplotypes were identified of which 1,222 were unique (accounting 89.919%) with observing a little number of off-ladder alleles, null alleles, partial alleles or duplicate alleles. High levels of genetic polymorphisms were detected for all 17 Y-STRs markers of the Y-filer panels. Among the studied population samples, 667 haplotypes were detected in the Bangali (accounting 41.844%). A number of haplotypes were detected from the major seven ethnic groups in Bangladesh seemed to be existent to a smaller extent in the following style: 150 haplotypes from Chakma (9.410%), 145 haplotypes from Rakhine (9.096), 144 haplotypes from Tripura (9.033%), 138 haplotypes from Marma (8.657%), 131 haplotypes from Manipuri (8.218%), 110 haplotypes from Khasia (6.900%), and 109 haplotypes from Hajong (6.838%).

Y-chromosomal haplotypes sharing were monitored among the studied populations (Table 3.9). We found that high level of haplotypes were shared within the same population groups and signifying a high level of endogamy with people marrying within the community at the same locality or in close relatives. We also searched for the all 1,359 different haplotypes among the studied populations including Garo and Santal [Hasan *et al.,* 2015] and a total of 36 haplotypes were shared between individuals. In Manipuris, the most frequent haplotype Mn36 and Mn37 were shared between nine and eight individuals within this population, respectively. In contrast, in Marmas, the most common haplotype Mr37 and Mn1 were shared between eight and seven individuals, respectively. In total, 1,222 haplotypes out of 1,359 haplotypes (89.919%) were shared in single individuals, 97 haplotypes were shared by two individuals. Furthermore, the numbers of haplotypes shared by larger numbers of individuals i.e. 19, 8, 2, 5, 3, 2, 1 haplotype were shared by 3, 4, 5, 6, 7, 8, and 9 individuals, respectively.

Table 3.9: Number of haplotypes observed for the 17 Y-STRs markers within the population

No. of haplotypes observed	**Studied populations**								**Grand Total**
	Bangali	**Chakma**	**Tripura**	**Rakhine**	**Marma**	**Hajong**	**Manipuri**	**Khasia**	
n = 1	633 (97.534%)	94 (81.034%)	77 (77.777%)	95 (86.363%)	91 (85.046%)	71 (79.775%)	83 (84.693%)	78 (85.714%)	1,222 (89.919%)
n = 2	14	14	12	9	11	16	11	10	97
n = 3	2	5	4	2	2	2	-	2	19
n = 4	-	2	3	1	1	-	1	-	8
n = 5	-	1	-	-	-	-	1	-	2
n = 6	-	-	2	2	-	-	-	1	5
n = 7	-	-	1	1	1	-	-	-	3
n = 8	-	-	-	-	1	-	1	-	2
n = 9	-	-	-	-	-	-	1	-	1
Different haplotypes	**649**	**116**	**99**	**110**	**107**	**89**	**98**	**91**	**1,359**
Total haplotypes	**667**	**150**	**144**	**145**	**138**	**109**	**131**	**110**	**1,594**
Total individuals	**667**	**157**	**151**	**152**	**144**	**112**	**136**	**112**	**1,631**

Comparisons of haplotypes sharing of Y-STR profiles among the studied populations were represented in Table 3.10. Out of 649 different haplotypes from Bangali males, five haplotypes were shared with six individuals across the four ethnic groups i.e. two haplotypes with Rakhine: Bn138 was identical to Rk22 and Bn485 was identical to Rk106; two haplotypes with Marma: Bn138 was identical to Mr72 and Bn237 was identical to Mr88. Furthermore, one haplotype shared with Santal male: Bn265 was identical to Sn87 as well as one haplotype with Garo male: Bn365 was identical to Gr83 [Hasan *et al.*, 2015].

Four haplotypes from Chakma individuals were shared with five individuals from two tribal groups i.e. three haplotypes with Rakhine: Ck14 was identical to Rk101, Ck16 was identical to Rk66 and Ck54 was identical to Rk12; two haplotypes with Marma: Ck16 was identical to Mr10 and Ck115 was identical to Mr70. Moreover, one haplotype Tr57 from Tripura males was shared with one haplotype Rk96 from Rakhine males. Twelve haplotypes from Rakhine male samples were shared between fourteen individuals from five tribal groups i.e. two haplotypes with Bangali: Rk22 was identical to Bn138 and Rk106 was identical to Bn485; three haplotypes with Chakma: Rk12 was identical to Ck54, Rk66 was identical to Ck16 and Rk101 was identical to Ck14; one haplotype with Tripura: Rk96 was identical to Tr57; seven haplotypes with Marma: Rk6 was identical to Mr55, Rk22 was identical to Mr72, Rk35 was identical to Mr52, Rk38 was identical to Mr4, Rk66 was identical to Mr10, Rk91 was identical to Mr41 and Rk103 was identical to Mr103 and one haplotype with Hajong: Rk82 was identical to Hj30.

Table 3.10 Y-chromosome haplotypes sharing among the studied populations in Bangladesh

DYS 456-389I-390-389II-458-19-385a/b-393-391 -439-635-392-YGATAH4-437-438-448	Studied populations							
	Bn	**Ck**	**Tr**	**Rk**	**Mr**	**Hj**	**Mn**	**Kh**
15-14-25-31-16-15-11,14-13-10-10-23-11-13-14-11-20	√	-	-	√	√	-	-	-
15-13-24-31-16-15-11,14-13-10-10-23-11-13-14-11-20	√	-	-	-	√	-	-	-
15-13-25-31-16-16-11,15-13-11-10-23-11-12-14-11-20	√	-	-	-	-	-	-	-
15-13-23-30-15-14-14,19-13-10-11-21-11-12-14-9-20	√	-	-	-	-	-	-	-
15-13-25-31-16-16-11,14-13-11-10-23-11-13-14-11-20	√	-	-	√	-	-	-	-
15-12-23-28-19-14-13,17-12-10-11-21-14-12-15-11-20	-	√	-	√	-	-	-	-
15-12-24-27-18-14-13,20-12-10-12-21-14-12-15-11-18	-	√	-	√	√	-	-	-
15-12-23-28-18-14-13,17-12-10-11-21-14-12-15-11-20	-	√	-	√	-	-	-	-
15-12-23-28-19-14-13,20-12-10-11-20-14-12-15-11-20	-	√	-		√	-	-	-
15-12-24-28-18-14-13,19-12-10-12-20-14-13-15-11-20	-	-	√	√	-	-	-	-
15-12-24-27-18-14-13,19-12-10-13-21-14-12-15-11-20	-	-	-	√	√	-	-	-
15-12-24-28-18-14-14,20-12-10-11-20-14-14-14-11-20	-	-	-	√	√	-	-	-
15-12-22-30-15-15-9,17-12-10-8-21-14-11-16-10-19	-	-	-	√	√	-	-	-
15-12-24-28-18-14-13,18-12-10-12-20-14-12-15-11-20	-	-	-	√		√	-	-
16-14-23-30-16-15-14,16-12-10-12-20-11-12-15-9-20	-	-	-	√	√	-	-	-
17-12-24-28-20-15-15,16-11-10-11-20-10-11-14-10-19	-	-	-	√	√	-	-	-
15-14-25-31-16-15-11,14-13-10-10-23-11-12-14-11-20	-	-	-	-	√	-	-	√

Note: Bn= Bangali, Ck= Chakma, Tr= Tripura, Rk= Rakhine, Mr= Marma, Hj= Hajong, Mn= Manipuri, Kh= Khasia

Furthermore, out of 107 different haplotypes from Marma, ten haplotypes were shared between twelve individuals from four tribal groups i.e. two haplotypes with Bangali: Mr72 was identical to Bn138 and Mr88 was identical to Bn237; two haplotypes with Chakma: Mr10 was identical to Ck16 and Mr70 was identical to Ck115; seven haplotypes with Rakhine: Mr4 was identical to Rk38, Mr10 was identical to Rk66, Mr41 was identical to Rk91, Mr52 was identical to Rk35, Mr55 was identical to Rk6, Mr72 was identical to Rk22, and Mr103 was identical to Rk103 and one haplotype with Khasia: Mr87 was identical to Kh11. Moreover, one haplotype Hj30 from Hajong males was shared with one haplotype Rk82 from Rakhine male samples and one haplotype Kh11 from Khasia individual was shared with one haplotype Mr87 from Marma male samples. Interestingly, no Manipuris Y-chromosome shared with the other studied populations.

In addition, thirteen most frequent haplotypes were detected among the studied population samples which shared by more than four individuals within the population (Table 3.11). The most frequent haplotype Mn36 was shared between nine individuals followed by haplotype Mn37 and Mr37 were shared in eight individuals within the Manipuri and Marma populations, respectively. On the other hand, the most frequent haplotype Ck3 was shared between five individuals in Chakma population samples. These results indicated that high levels of endogamy featured within the tribal groups or the haplotypes were duplicated when sampling from paternally related male relatives. The study also revealed that male individuals from isolated ethnic populations shared chromosomes mainly wth male individuals from their own population.

Table 3.11 The Y-chromosome haplotype shared by more than four individuals within population.

DYS 456-389I-390-389II-458-19-385a/b-393-391 -439-635-392-YGATAH4-437-438-448	***n***	**Population (Number of haplotypes)**
16-13-24-29-16-17-15,20-14-10-12-22-14-13-14-10-18	5	Chakma (150)
15-12-23-28-18-14-14,20-12-10-11-19-15-13-15-11-20	5	Manipuri (131)
14-14-23-30-17-14-14,19-13-10-12-23-11-11-14-9-21	6	Tripura (144)
15-12-24-27-18-14-13,18-12-10-12-21-14-11-15-11-20	6	Tripura (144)
15-12-24-27-18-14-13,19-12-10-13-21-14-12-15-11-20	6	Rakhine (145)
15-12-24-29-18-14-14,20-12-10-11-20-14-14-14-11-20	6	Rakhine (145)
15-13-25-29-17-15-15,19-14-10-11-21-1310-14-10-18	6	Khasia (110)
15-12-23-28-17-14-13,18-12-10-12-20-14-12-14-11-20	7	Tripura (144)
15-14-25-31-16-15-11,14-13-10-10-23-11-13-14-11-20	7	Rakhine (145)
15-12-24-27-17-14-13,19-12-10-12-23-14-13-15-11-20	7	Marma (138)
15-12-24-28-19-14-13,21-12-10-12-21-14-12-15-11-20	8	Marma (138)
16-13-25-30-15-15-11,14-13-10-10-21-11-13-14-11-20	8	Manipuri (131)
15-14-23-30-16-14-20,20-13-10-11-24-12-12-15-11-19	9	Manipuri (131)

We searched for all 1,359 different haplotypes from the studied populations in the YHRD (Release version R59; November 01, 2018) with 205,059 haplotypes from the worldwide 932 reference populations. A number of haplotypes were identical and found match with global population samples in a set of 17 Y-STR markers. The most frequent haplotype Tr34 of Tripuras was shared between 41 individuals followed by haplotype Bn476 and haplotype Bn228 of Bangalis were found match with 26 and 25 individuals, respectively. In addition, haplotype Hj49 of Hajong, haplotype Rk22 of Rakhine, haplotype Mr72 of

Marma, haplotype Ck22 of Chakma, haplotype Kh11 of Khasia, and haplotype Mn71 of Manipuri were found match with 15, 12, 12, 10, 8, and 7 individuals in the global populations, respectively. One haplotype Bn11 from Bangali was identical to the Tripuri male samples of Tripura, India [Ghosh *et al.*, 2011]; two haplotypes (Bn86 and Bn610) were identical to the Tamil males of Tamil Nadu, India [Balamurugan *et al.,* 2010]; three haplotypes (Bn307, Bn371, and Bn476) were identical to the Pakistani males [Perveen *et al.,* 2014]; one haplotype (Bn96) was identical to the Pathan males of Pakistan [Lee *et al.,* 2014]; one haplotype (Bn371) was identical to the Iranian males [Tabrizi *et al.,* 2015]; haplotype Bn314 and Bn476 were identical to the Croatian males [Pokupčić *et al.,* 2008]. Five haplotypes from Tripura males of Bangladesh (Tr1, Tr22, Tr29, Tr41, and Tr50) were identical to the Tripuri population of Tripura, India [Ghosh *et al.,* 2011]. According to the Y-chromosome allele frequency distribution, Tripura population of Bangladesh exhibited features of Indian Tripuri gene pools. One haplotype Rk50 from Rakhine was identical to the Tripuri population of Tripura, India [Ghosh *et al.,* 2011]. In addition, one haplotype Mr87 from Marma, one haplotype Hj33 from Hajong, one haplotype Mn73 and one haplotype Kh11 from Khasia were shared between four individuals from the Pakistani male samples (Perveen *et al.,* 2014).

A total of 121 different alleles were detected in 15 single-copy Y-STR loci as well as 77 genotypes or allelic classes were observed in the multi-copy locus DYS385a/b. In total, 107 different alleles and 60 genotypes or allelic classes for DYS385a/b were detected in Bangali population samples. The second most abundant different alleles (n=84) and genotypes (n=35) were found in Rakhine population samples. In contrast, a minimum number of different alleles (n=71) and genotypes (n=18) were investigated in Tripura males.

Microvariant alleles included a) null alleles, likely due to a deletion or primer site mutation, b) partial or intermediate alleles comprising fractional repeats, and c) copy-number variants such as duplications and triplications of the whole locus. On the other hand, the allele or alleles were out of an allelic range in a locus, represented as off-ladder allele(s). In Bangali, four null alleles were observed at three loci: DYS389II, DYS391, and DYS392 and carried by three individuals while three null alleles were detected at DYS389II in three individuals in Rakhine males [Hasan *et al.,* 2018]. Null types of alleles may result due to a mutation at a primer building site or large deletion in the Y-chromosome [Budowle *et al.,* 2008]. Null alleles have been primarily reported in Asian populations [Chang *et al.*, 2007; Park *et al.*, 2008]. In total, five intermediate or partial alleles, typed as allele 18.2 (twice) and allele 19.2 (once) based on fragment size were detected at DYS458 locus in three individuals of Bangali population; allele 13.2 (once) was found at DYS385a/b locus in one individual of Hajong and allele 13.2 (once) was monitored at DYS19 locus in one individual of Manipuri tribe. Two duplicate alleles typed as (17, 18) and (15, 17) were found at DYS458 locus in two individuals in Bangali males [Hasan *et al.*, 2018]. In total, eighteen distinct rare alleles or off-ladder alleles were detected of which five alleles were found in locus DYS635 (27.777%) followed by locus DYS458 with four alleles (22.222%). Overall, twelve rare alleles were detected in Bangalis, with DYS635 showing the highest (n = 4) followed by locus DYS458 (n=3) while YGATAH4 showing the lowest (n = 1). Interestingly, a number of off-ladder alleles were detected in the locus DYS635 (n=14) for all the studied populations. The second most frequent locus was YGATAH4 which was carried seven off-ladder alleles. Here, five off-ladder alleles were detected in Marma followed by four were monitored in Rakhine and Hajong population samples, respectively. In addition, only one rare allele was observed in Tripura population and this rare allele was found in locus DYS635.

In order to check a possible mutation in the primer binding site, the sample was retyped with AmpF*l*STR® Yfiler® PCR amplification kit (Applied Biosystems, USA) and PowerPlex® Y23 system (Promega Corporation, USA). The two Bangali male samples bearing duplicate alleles were also analyzed with AmpF*l*STR® Identifiler® PCR amplification kit (Applied Biosystems, USA) and showed a clean, single source DNA profile with no evidence of contamination.

The obtained Y-chromosome haplotype data strongly supports the idea that these are excellent forensic tools. The forensic statistical parameters like allele/gene frequency, power of matching, power of discrimination, and power of exclusion are represented in Supplementary Table 10. The allele or gene frequency of single-copy DYS loci ranged from minimum 0.002 in Bangali to maximum 0.929 in Khasias, while the frequencies of genotypes of bi-allelic DYS marker (DYS385a/b) ranged from 0.002 in Bangalis to 0.327 in Manipuris. The DYS458, DYS635, and DYS385a/b loci were observed to be the most polymorphic loci in Bangalis. Single-copy locus DYS458 exhibited the highest polymorphism with 12 alleles followed by locus DYS635 with 11 alleles in Bangali, while locus DYS437 showed the lowest polymorphisms with 2 alleles in Tripura. On the contrary, multi-copy loci DYS385a/b exhibited 60 genotypes in Bangali, while 18 genotypes observed in Tripura. The genotype 11/14 observed with the highest frequency of 0.327 in Manipuri population. Overall, the least polymorphic loci DYS389I, DYS19, DYS391, DYS437, and DYS438 were observed in the studied populations. The results also showed that significant differences between the populations were apparent in almost every locus. Furthermore, the allele frequencies for the single-copy loci showed a more similar distribution in Bangali, whereas the studied ethnic groups being somewhat different. These results indicated that the studied ethnic groups may have a greater anthropological affinity to each other than to tha Bangalis.

The haplotype diversity values of the 17 Y-STR loci were calculated 0.998 for Bangali, 0.988 for Chakma, 0.984 for Tripura, 0.986 for Rakhine, 0.985 for Marma, 0.987 for Hajong, 0.982 for Manipuri, and 0.985 for Khasia populations (Supplementary Table 10). Results showed that the haplotype diversity in all the studied population was high; the highest being in the Bangali (0.998), followed by the Chakma (0.988) and the Hajong (0.987). Among all the studied populations, the lowest haplotype diversity value was observed in the Manipuri population (0.982). Natably, the higher values indicate the increased discrimination capacity of the 17 Y-STR haplotypes and therefore their forensic utility.

The locus-wise gene diversity values were also estimated from allele frequencies. Whilst the multi-copy locus DYS385a/b showed the greatest gene diversity across all the studied populations, the greatest gene diversity in single-copy locus for each population were different (Supplementary Table 10). Among the studied populations, the highest gene diversity value was found in the Khasia (0.964), while the lowest value was observed in the Manipuri (0.848). In contrast, the Y-STR data showed that the Manipuri population had less genetic diversity than the other populations. Across all the studied populations, the average gene diversity values for the each loci were determined and the multy-copy locus DYS385a/b possessed the highest gene diversity value (0.927), whereas the single-copy loci possessed as follows: DYS389II (0.752), DYS458 (0.744), DYS635 (0.733), DYS439 (0.688), DYS392 (0.681), DYS390 (0.668), YGATAH4 (0.641), DYS448 (0.618), DYS389I (0.588), DYS393 (0.581), DYS19 (0.559), DYS438 (0.525), DYS456 (0.520), and DYS437 (0.504). The gene diversity analyses also revealed the values greater than 0.500, exhibiting a high level of genetic polymorphisms in the total populations. Among the 17 Y-STR loci, only DYS391 showed a minimum level of gene diversity, which accounts for a total value of 0.348. The population-wise average gene diversity values were also calculated and found that Bangali population showed the highest gene diversity value of 0.662 while all the seven other tribal populations showed less gene diversity values.

The comparison of locus-wise gene diversity among Bangali and seven others tribal populations (Chakma, Tripura, Rakhine, Marma, Hajong, Manipuri and Khasia) in Bangladesh is represented in the Figure 3.9.

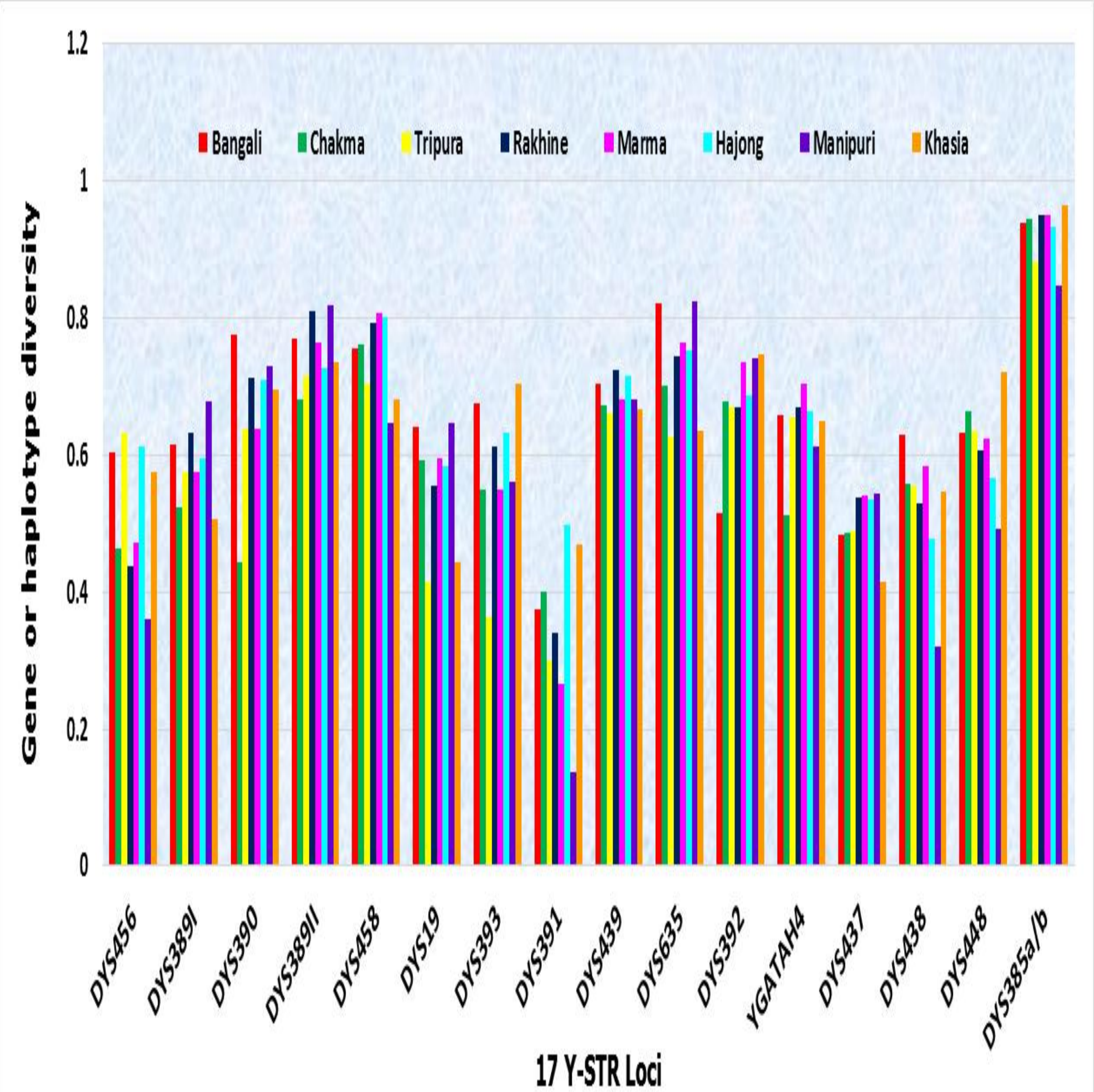

Figure 3.9 The comparison of gene diversity values for each genetic loci among the studied populations based on Y-chromosomal short tandem repeats.

We also analyzed haplotype matching probability for the 1,359 different haplotypes from studied populations. For a better assessment, 99 and 129 different haplotypes were included from Garo and Santal population, respectively. Out of 1,587 different haplotypes, 5 haplotypes from Bangali males were observed among the studied populations. Furthermore, 4 haplotypes from Chakma, 1 haplotype from Tripura, 12 haplotypes from Rakhine, 10 haplotypes from Marma, 1 haplotype from Hajong, and 1 haplotype from Khasia were found among the studied populations. Therefore, if a haplotype has been or has not been observed in a database, haplotype matching probabilities for the respective population were summarized in Table 3.12. Interestingly, no Manipuri haplotype shared among the studied populations.

Table 3.12: Y-chromosome haplotype matching probabilities among the studied populations in Bangladesh

Population	**If a profile has been observed in a database (N=1,587) Formula: $p+1.96\sqrt{p(1-p)}/N$**	**If a profile has not been observed in a database (N=1,551) Formula: $1-\alpha^{1/N}$ or 3/N**
Bangali	0.005907731 (~1 in 169)	0.001934236 (~1 in 518)
Chakma	0.004987335 (~1 in 202)	0.001934236 (~1 in 518)
Tripura	0.001864724 (~1 in 535)	0.001934236 (~1 in 518)
Rakhine	0.011823457 (~1 in 85)	0.001934236 (~1 in 518)
Marma	0.010194345 (~1 in 99)	0.001934236 (~1 in 518)
Hajong	0.001864724 (~1 in 535)	0.001934236 (~1 in 518)
Manipuri	ND*	ND*
Khasia	0.001864724 (~1 in 535)	0.001934236 (~1 in 518)

ND*= Not detected

3.10 Estimation of Diversity Parameters

The Y-chromosome STR matching probabilities within and between the nine Bangladeshi populations were represented in Table 3.13. Consistent with the haplotype diversity values, Manipuri exhibited the maximum probability of finding a match within the population (mw_{max}) (0.018239) followed by Tripura (0.015914) and Marma (0.014808). On the other hand, Bangali (0.001589) demonstrated the bottommost maximum probability within the population.

When compared among the studied populations, the maximum diversity (db_{max}) of obtaining two different haplotypes when sampling a pair of individuals. In this study, there were observed twenty-eight pairs of individuals with the maximum diversity values i.e. from Bangali and Chakma (100%), Bangali and Tripura (100%), Bangali and Rakhine (99.991%), Bangali and Marma (99.996%), Bangali and Hajong (100%), Bangali and Manipuri (100%), Bangali and Khasia (100%), Chakma and Tripura (100%), Chakma and Rakhine (99.981%), Chakma and Marma (99.980%), Chakma and Hajong (100%), Chakma and Manipuri (100%), Chakma and Khasia (100%), Tripura and Rakhine (99.995%), Tripura and Marma (100%), Tripura and Hajong (100%), Tripura and Manipuri (100%), Tripura and Khasia (100%), Rakhine and Marma (99.890%), Rakhine and Hajong (99.987%), Rakhine and Manipuri (100%), Rakhine and Khasia (100%), Marma and Hajong (100%), Marma and Manipuri (100%), Marma and Khasia (99.993%), Hajong and Manipuri (100%), Hajong and Khasia (100%), and Manipuri and Khasia (100%). These values are supported by the observed haplotype sharing between populations in the above-mentioned pairs.

The elevated db_{max} values for each population pair indicated genetic uniqueness not only within the Bangali population but also among them. As suggested by the ratio mw_{max}/mb_{min}, it was more probable to find a match within each studied populations than between any two of these populations. Particularly, it was about 454 times more likely to find a match within Marma followed by 332 times within Tripura and 283 times within Rakhine, than between either of these populations and rest of the studied populations. These particular ratios were also prominent at the lower estimate of the parameter (mw_{min}/mb_{min}) and these values were about 234, 189 and 144 times for Marma, Tripura, and Rakhine, respectively. These ratios designated a greater degree of genetic heterogeneity and distinctiveness in Bangali, Hajong, and Manipuri than in Chakma, Tripura, Rakhine, Marma or Khasia. The high power of discriminations emphasizes the genetic heterogeneity and uniqueness of the studied populations and the need for independent databases for forensic applications and studies in population genetics.

The highest haplotype sharing occurs between Rakhine and Marma, which have seven different 17 Y-STRs haplotypes in common. On the contrary, Tripura, Hajong, and Khasia were more unique, as these populations shared only one distinct haplotype with Rakhine and Marma, respectively. Interestingly, Manipuri population did not share any haplotype with the other seven studied populations.

Table 3.13 Y-STR haplotype matching probabilities within and between the studied populations in Bangladesh.

Diversity parameters	**Bangali (Bn)**	**Chakma (Ck)**	**Tripura (Tr)**	**Rakhine (Rk)**	**Marma (Mr)**	**Hajong (Hj)**	**Manipuri (Mn)**	**Khasia (Kh)**
Number of total haplotypes (*N**)	667	150	144	145	138	109	131	110
dw_{min} (haplotype diversity)	0.998411	0.988800	0.984086	0.986397	0.985192	0.987122	0.981761	0.985537
$mw_{max} = (1\text{-}dw_{min})$	0.001589	0.011200	0.015914	0.013603	0.014808	0.012878	0.018239	0.014463
mw_{min}	20/222,111	51/11,175	93/10,296	72/10,440	72/9,453	22/5,886	91/8,515	31/5,995
$mb_{min} = (1\text{-}db_{max})$	Bn/Ck 0.000 Bn/Tr 0.000 Bn/Rk 0.00008 Bn/Mr 0.00003 Bn/Hj 0.000 Bn/Mn 0.000 Bn/Kh 0.000	Ck/Bn 0.000 Ck/Tr 0.000 Ck/Rk 0.00018 Ck/Mr 0.00019 Ck/Hj 0.000 Ck/Mn 0.000 Ck/Kh 0.000	Tr/Bn 0.000 Tr/Ck 0.000 Tr/Rk 0.00004 Tr/Mr 0.000 Tr/Hj 0.000 Tr/Mn 0.000 Tr/Kh 0.000	Rk/Bn 0.00008 Rk/Ck 0.00018 Rk/Tr 0.00004 Rk/Mr 0.00109 Rk/Hj 0.00012 Rk/Mn 0.000 Rk/Kh 0.000	Mr/Bn 0.00003 Mr/Ck 0.00019 Mr/Tr 0.000 Mr/Rk 0.00109 Mr/Hj 0.000 Mr/Mn 0.000 Mr/Kh 0.00006	Hj/Bn 0.000 Hj/Ck 0.000 Hj/Tr 0.000 Hj/Rk 0.00012 Hj/Mr 0.000 Hj/Mn 0.000 Hj/Kh 0.000	Mn/Bn 0.000 Mn/Ck 0.000 Mn/Tr 0.000 Mn/Rk 0.000 Mn/Mr 0.000 Mn/Hj 0.000 Mn/Kh 0.000	Kh/Bn 0.000 Kh/Ck 0.000 Kh/Tr 0.000 Kh/Rk 0.000 Kh/Mr 0.00006 Kh/Hj 0.000 Kh/Mn 0.000
$db_{max} = (1\text{-}mb_{min})$	Bn/Ck 1.000 Bn/Tr 1.000 Bn/Rk 0.99991 Bn/Mr 0.99996 Bn/Hj 1.000 Bn/Mn 1.000 Bn/Kh 1.000	Ck/Bn 1.000 Ck/Tr 1.000 Ck/Rk 0.99981 Ck/Mr 0.99980 Ck/Hj 1.000 Ck/Mn 1.000 Ck/Kh 1.000	Tr/Bn 1.000 Tr/Ck 1.000 Tr/Rk 0.99995 Tr/Mr 1.000 Tr/Hj 1.000 Tr/Mn 1.000 Tr/Kh 1.000	Rk/Bn 0.99991 Rk/Ck 0.99981 Rk/Tr 0.99995 Rk/Mr 0.99890 Rk/Hj 0.99987 Rk/Mn 1.000 Rk/Kh 1.000	Mr/Bn 0.99996 Mr/Ck 0.99980 Mr/Tr 1.000 Mr/Rk 0.99890 Mr/Hj 1.000 Mr/Mn 1.000 Mr/Kh 0.99993	Hj/Bn 1.000 Hj/Ck 1.000 Hj/Tr 1.000 Hj/Rk 0.99987 Hj/Mr 1.000 Hj/Mn 1.000 Hj/Kh 1.000	Mn/Bn 1.000 Mn/Ck 1.000 Mn/Tr 1.000 Mn/Rk 1.000 Mn/Mr 1.000 Mn/Hj 1.000 Mn/Kh 1.000	Kh/Bn 1.000 Kh/Ck 1.000 Kh/Tr 1.000 Kh/Rk 1.000 Kh/Mr 0.99993 Kh/Hj 1.000 Kh/Mn 1.000
mw_{max}/mb_{min}	Bn/Ck *ND Bn/Tr ND Bn/Rk 19.1908 Bn/Mr 48.7423 Bn/Hj ND Bn/Mn ND Bn/Kh ND	Ck/Bn ND Ck/Tr ND Ck/Rk 60.8695 Ck/Mr 57.9410 Ck/Hj ND Ck/Mn ND Ck/Kh ND	Tr/Bn ND Tr/Ck ND Tr/Rk 332.233 Tr/Mr ND Tr/Hj ND Tr/Mn ND Tr/Kh ND	Rk/Bn 164.287 Rk/Ck 73.9619 Rk/Tr 283.987 Rk/Mr 12.3719 Rk/Hj 107.448 Rk/Mn ND Rk/Kh ND	Mr/Bn 454.233 Mr/Ck 76.6063 Mr/Tr ND Mr/Rk 13.4679 Mr/Hj ND Mr/Mn ND Mr/Kh 224.704	Hj/Bn ND Hj/Ck ND Hj/Tr ND Hj/Rk 101.721 Hj/Mr ND Hj/Mn ND Hj/Kh ND	Mn/Bn ND Mn/Ck ND Mn/Tr ND Mn/Rk ND Mn/Mr ND Mn/Hj ND Mn/Kh ND	Kh/Bn ND Kh/Ck ND Kh/Tr ND Kh/Rk ND Kh/Mr 219.468 Kh/Hj ND Kh/Mn ND
mw_{min}/mb_{min}	Bn/Ck ND Bn/Tr ND Bn/Rk 1.08750 Bn/Mr 2.76211 Bn/Hj ND Bn/Mn ND Bn/Kh ND	Ck/Bn ND Ck/Tr ND Ck/Rk 24.8030 Ck/Mr 23.6097 Ck/Hj ND Ck/Mn ND Ck/Kh ND	Tr/Bn ND Tr/Ck ND Tr/Rk 188.572 Tr/Mr ND Tr/Hj ND Tr/Mn ND Tr/Kh ND	Rk/Bn 83.2916 Rk/Ck 37.4812 Rk/Tr 143.978 Rk/Mr 6.27244 Rk/Hj 54.4751 Rk/Mn ND Rk/Kh ND	Mr/Bn 233.638 Mr/Ck 39.4031 Mr/Tr ND Mr/Rk 6.92735 Mr/Hj ND Mr/Mn ND Mr/Kh 115.578	Hj/Bn ND Hj/Ck ND Hj/Tr ND Hj/Rk 29.5235 Hj/Mr ND Hj/Mn ND Hj/Kh ND	Mn/Bn ND Mn/Ck ND Mn/Tr ND Mn/Rk ND Mn/Mr ND Mn/Hj ND Mn/Kh ND	Kh/Bn ND Kh/Ck ND Kh/Tr ND Kh/Rk ND Kh/Mr 78.4670 Kh/Hj ND Kh/Mn ND

* N= Excludes samples carrying null alleles and duplicated loci

*ND= No data. If, no haplotype match between two populations, the value of the db_{max} will be 1 and the value of the mb_{min} will be 0. Any value cannot be divided by Zero (0).

3.11 Phylogenetic Tree Analysis

The Phylogenetic tree, also called Neighbor-Joining (N-J) tree and multidimensional scaling (MDS) plot was constructed based on pair-wise genetic distances R_{st} values between the studied populations and 32 reference populations from YHRD database. To examine the genetic affinities between neighboring populations, pair-wise genetic distances (R_{st}) and associated probability values (p-values; 10,000 permutations) were calculated using the analysis of molecular variance (AMOVA) tools, which is available in the YHRD (http://www.yhrd.org/amova). A total of 9,580 haplotypes from the studied populations from 32 world-wide reference population samples were included in the phylogenetic tree analysis. To portray the genetic relationship between populations, the phylogenetic tree was constructed based on R_{st} value using AMOVA tool and the tree was visualized using radiation style of the MEGA 7.0.21 software (Figure 3.10). Comparative analysis for the Bangali population showed statistically significant different from Tripura population (R_{st} = 0.249, p = 0.000). In addition, Bangalis were considered significantly different from Chakma (R_{st} = 0.199, p = 0.000), Hajong (R_{st} = 0.145, p = 0.000), Marma (R_{st} = 0.134, p = 0.000), Khasia (R_{st} = 0.106, p = 0.000), Rakhine (R_{st} = 0.087, p = 0.000), and Manipuri (R_{st} = 0.046, p = 0.000) populations, respectively (Supplementary Table 12).

Phylogenetic analysis also showed the strong genetic relationship of Bangali population with Nepalese (Kathmandu, Nepal), Iranian (Central Iran, Iran), Iraqi (Iraq), Tamil (Tamil Nadu, India), and Bhil (Gujarat, India) populations. A previous study of Y-chromosomal STRs also revealed a difference in distribution between Bangali and the other published reference population [Hasan *et al.*, 2016]. In addition, Chakma, Tripura, Rakhine, Marma, and Hajong populations were the most similar population to Tripuri (Tripura, India), Garo (Tangail, Bangladesh), Han (Beijing, China), Korean (Seoul, South Korea), Asian American (United States), and Japanese (Tokyo, Japan) populations, respectively. On the other hand, the Manipuri population has a close genetic affinity with Tamil (Tamil Nadu, India) and Bhil (Gujarat, India) population. In addition, the Khasia population lies closer to a clade consisting Oraon (Chhattisgarh, India) and Santal (Dinajpur, Bangladesh).

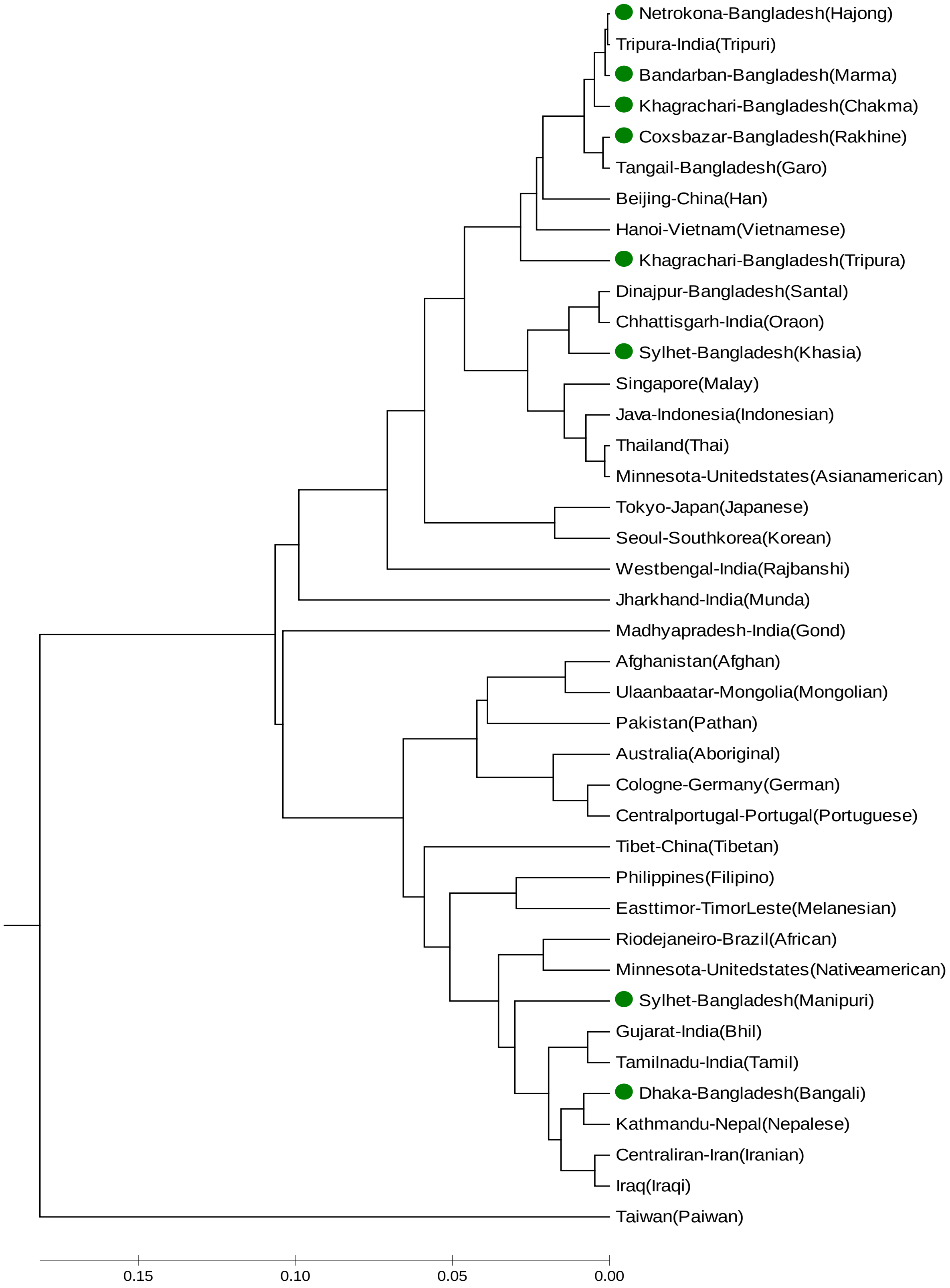

Figure 3.10 The Neighbour-Joining Tree constructed a relationship among the studied populations (*marked with green symbol*) and 32 reference populations from YHRD.

To demonstrate the relationship between and among populations, a Multidimensional Scaling (MDS) plot was generated using "population analysis" tools of the YHRD (Figure 3.11). The MDS plot showed that the Bangali population lies closer to a clade consisting Nepalese (Kathmandu, Nepal), Iranian (Central Iran, Iran), Tamil (Tamil Nadu, India), and Bhil (Gujarat, India) populations.

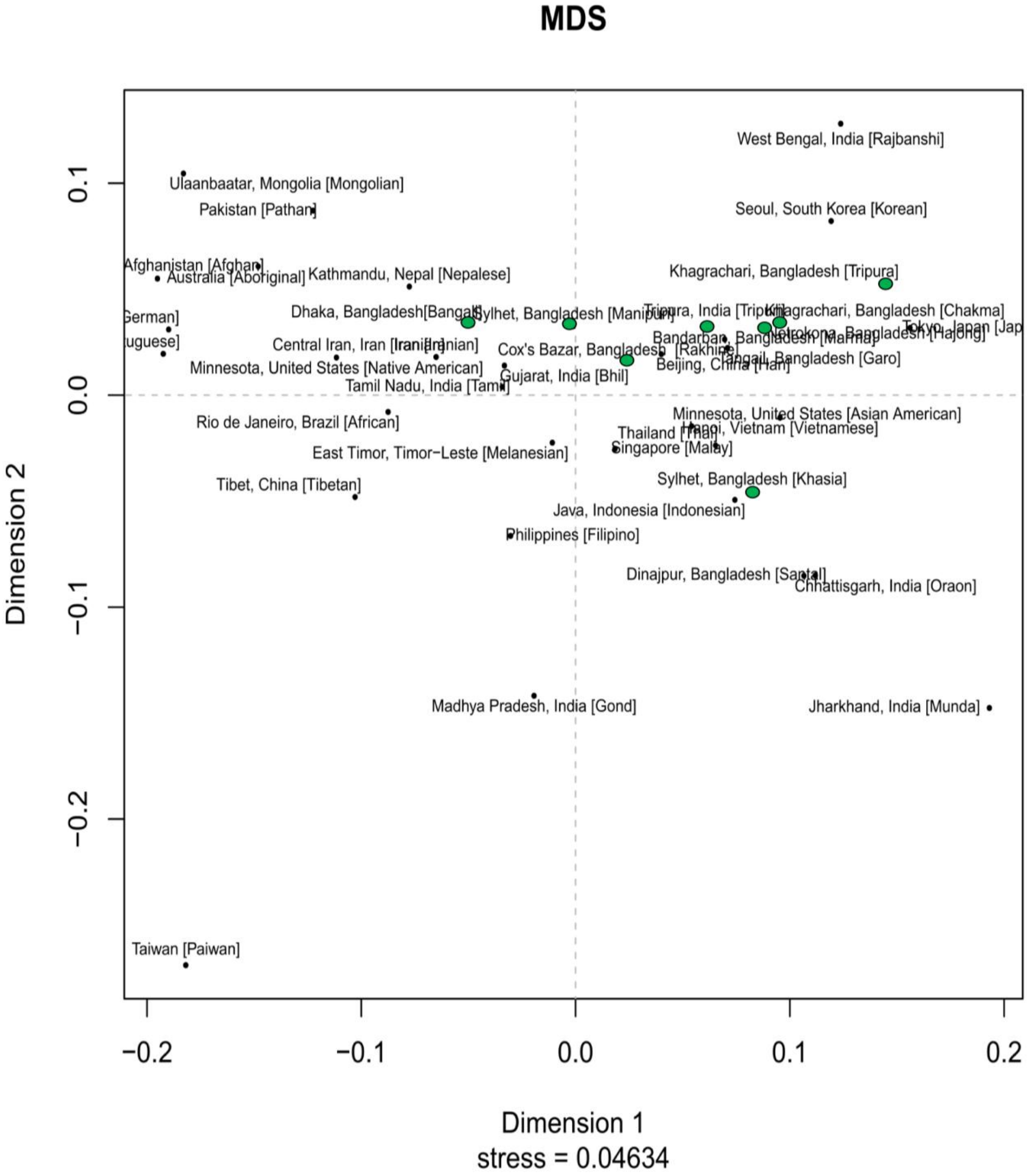

Fig. 3.11 The Mulltidimensional Scaling (MDS) plot based on pairwise R_{st} values between studied populations (marked with green symbol) and 32 reference populations from YHRD.

Moreover, the AMOVA analysis also revealed strong genetic relationship of Chakmas (Khagrachari, Bangladesh) with Han (Beijing, China), Tripura (Khagrachari, Bangladesh), Rakhine (Cox's Bazar, Bangladesh), Garo (Tangail, Bangladesh), Marma (Bandarban, Bangladesh), Hajong (Netrokona, Bangladesh), Tripuri (Tripura, India), Korean (Seoul, South Korea), and Japanese (Tokyo, Japan) populations. On the other hand, Manipuri (Sylhet, Bangladesh) showed close genetic affinity with Tamil (Tamil Nadu, India) population followed by Bhil (Gujarat, India) population. In addition, Khasia (Sylhet, Bangladeshi) population lies closer to a clade consisting Oraon (Chhattisgarh, India), Santal (Dinajpur, Bangladesh), Indonesian (Java, Indonesia), Munda (Jharkhand, India), and Thai (Thailand) populations.

3.12 Population Comparisons Analysis

Subsequent analysis of every Y-chromosomal STR data from the studied populations, it was found that there was great dissimilarity or gene variation between the data. Moreover, pairwise values of R_{st} were calculated to measure the genetic distance corresponding to 17 Y-STR loci of the studied populations as well as from other 32 reference populations published in YHRD whose most of them are neighbor to Bangladesh geographically (Table 3.14). Using online AMOVA tool including significance tests for all pairwise comparisons indicated that the genetic makeup among these population groups was almost different. This study was consistent with previous analyses of the Bangladeshi male population which demonstrating the strong effect of population substructures in this region. This study also showed the inhomogeneity of the Bangladeshi populations which were widely dispersed across the Asian population.

Table 3.14 Y-chromosome haplotypes genetic data from the studied populations and others reference population used for analysis and constructing correlation coefficients

Population	Abbreviation	Number of different haplotypes	References
South Asia			
Bangali (Bangladesh)	BAN	649	*Present study*
Chakma (Bangladesh)	CHA	116	*Present study*
Tripura (Bangladesh)	TRI	99	*Present study*
Rakhine (Bangladesh)	RAK	110	*Present study*
Marma (Bangladesh)	MAR	107	*Present study*
Hajong (Bangladesh)	HAJ	89	*Present study*
Manipuri (Bangladesh)	MAN	98	*Present study*
Khasia (Bangladesh)	KHA	91	*Present study*
Garo (Bangladesh)	GAR	99	Hasan *et al.*, 2015
Santal (Bangladesh)	SAN	129	Hasan *et al.*, 2015
Balmiki (India)	BAL	62	Ghosh *et al.*, 2011
Dhimal (India)	DHI	25	Roy *et al.*, 2012
Gond (India)	GON	75	Ghosh *et al.*, 2011
Munda (India)	MUN	68	Ghosh *et al.*, 2011
Paliya (India)	PAL	45	Roy *et al.*, 2012
Rajbanshi (India)	RAJ	35	Roy *et al.*, 2012
Tamil (India)	TAM	151	Balamurugan *et al.*, 2010
Tripuri (India)	TR-IND	65	Ghosh *et al.*, 2011
Riang (India)	RIA	67	Ghosh *et al.*, 2011
Pakistani (Pakistan)	PAK	274	Perveen *et al.*, 2014
Pathan (Pakistan)	PAT	270	Lee *et al.*, 2014
South Central Asia			
Afgan (Afganistan)	AFG	155	Älgenäs and Tillmar, 2014
Central Asia			
Iranian (Iran)	IRN	259	Tabrizi *et al.*, 2015
Iraqi (Iraq)	IRQ	119	Purps *et al.*, 2014
Kuwaiti (Kuwait)	KUW	248	Taqi *et al.*, 2015
Tibetian Plateau			
Tibetan (Tibet, China)	TIB	163	Zhang *et al.*, 2006
Northeast Asia			
Han (China)	HAN	424	Bing *et al.*, 2013
Taiwanese (Taiwan)	TAI	200	Huang *et al.*, 2008
Southeast Asia			
Japanese (Japan)	JAP	896	Mizuno *et al.*, 2008
Korean (Korea)	KOR	471	Kim *et al.*, 2010
Mongolian (Mongolia)	MON	282	Fu *et al.*, 2016
Vietnamese (Vietnam)	VIE	198	Miranda-Barros *et al.*, 2016
Australia and Micronesia			
Australian (Australia)	AUS	761	Taylor and Henry, 2012
Central Europe			
Croatian (Croatia)	CRO	146	Pokupčić *et al.*, 2008
South America			
Brazilian (Brazil)	BRA	481	Pereira *et al.*, 2007

3.13 Correlation Coefficients Values for the Y-chromosome Genetic Data

To know about better genetic affinities, we have analyzed the studied populations and compared with other 27 reference populations from different published articles shown in Table 3.14. We have also drowned the matrix of co-ancestry coefficients, the matrix of pairwise F_{st} values, the average number of pairwise differences, the Slatkins Linearized F_{st}, the number of alleles at different loci, the Garza-Williamson index at different loci, and the molecular distance at different loci (θ_H) from the Y-chromosome haplotypes genetic data. The intensity of colour represents the relationship between and among the populations. Light colour represents more genetic relationship while the dark colour represents a distant relationship.

3.13.1 Matrix of Co-ancestry Coefficients

Matrix of co-ancestry coefficients indicated the relationship between different populations (Figure 3.12). Small genetic distances represent as lower values indicated close genetic affinity between the two populations. The co-ancestry coefficients results showed that among Bangali, Afgan, Tamil, Pakistani, Iranian and Iraqi populations ranged from about 0.00 to 0.03, which signified the populations were closely related to each other and had features of Asian Y-chromosome gene pool. On the other hand, Chakma, Tripura, Rakhine, Marma, Hajong, Garo, Dhimal, Tripuri-India, and Taiwanese population ranged from about 0.00 to 0.04, indicated the aforementioned populations were closely related to each other. In addition, the analyses revealed the strong genetic relationship of Manipuris with Garos with ranged from 0.05 to 0.08. Similarly, Khasias exhibited close genetic affinity with Santal population and have ranged from 0.00 to 0.04.

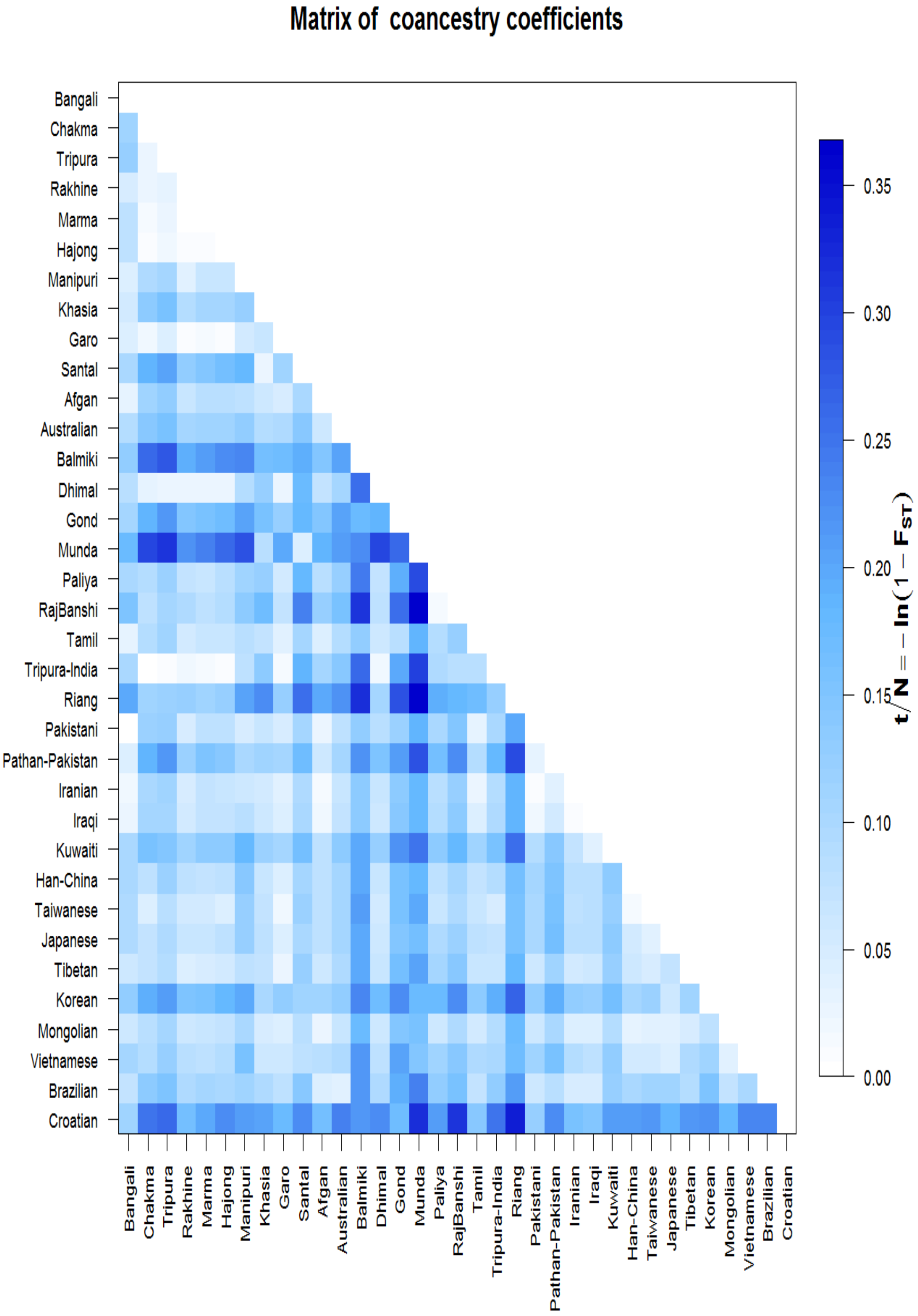

Figure 3.12: Matrix of co-ancestry coefficients indicates the relationship between populations

3.13.2 Matrix of Pairwise F_{st}

The Matrix of pairwise F_{st} values is near similar to the matrix of co-ancestry coefficients and indicated the relationship between different populations (Figure 3.13). Small genetic distances represent as lower values of the matrix of pairwise F_{st} indicated the close genetic affinity between the two populations. The results showed that the matrix of pairwise F_{st} among Bangali, Afgan, Tamil, Pakistani, Iranian and Iraqi populations ranged from about 0.00 to 0.03, which indicated the aforesaid populations were closely related to each other and had features of Asian Y-chromosome gene pool. On the other hand, Chakma, Tripura, Rakhine, Marma, Hajong, Garo, Dhimal, Tripuri-India, and Taiwanese populations ranged from about 0.00 to 0.04, indicated the abovementioned populations were closely related to each other. In addition, Manipuris displayed the strong genetic relationship with Garos and ranged from 0.05 to 0.08. Similarly, Khasias showed a close genetic relationship with Santal population and ranged from 0.00 to 0.04.

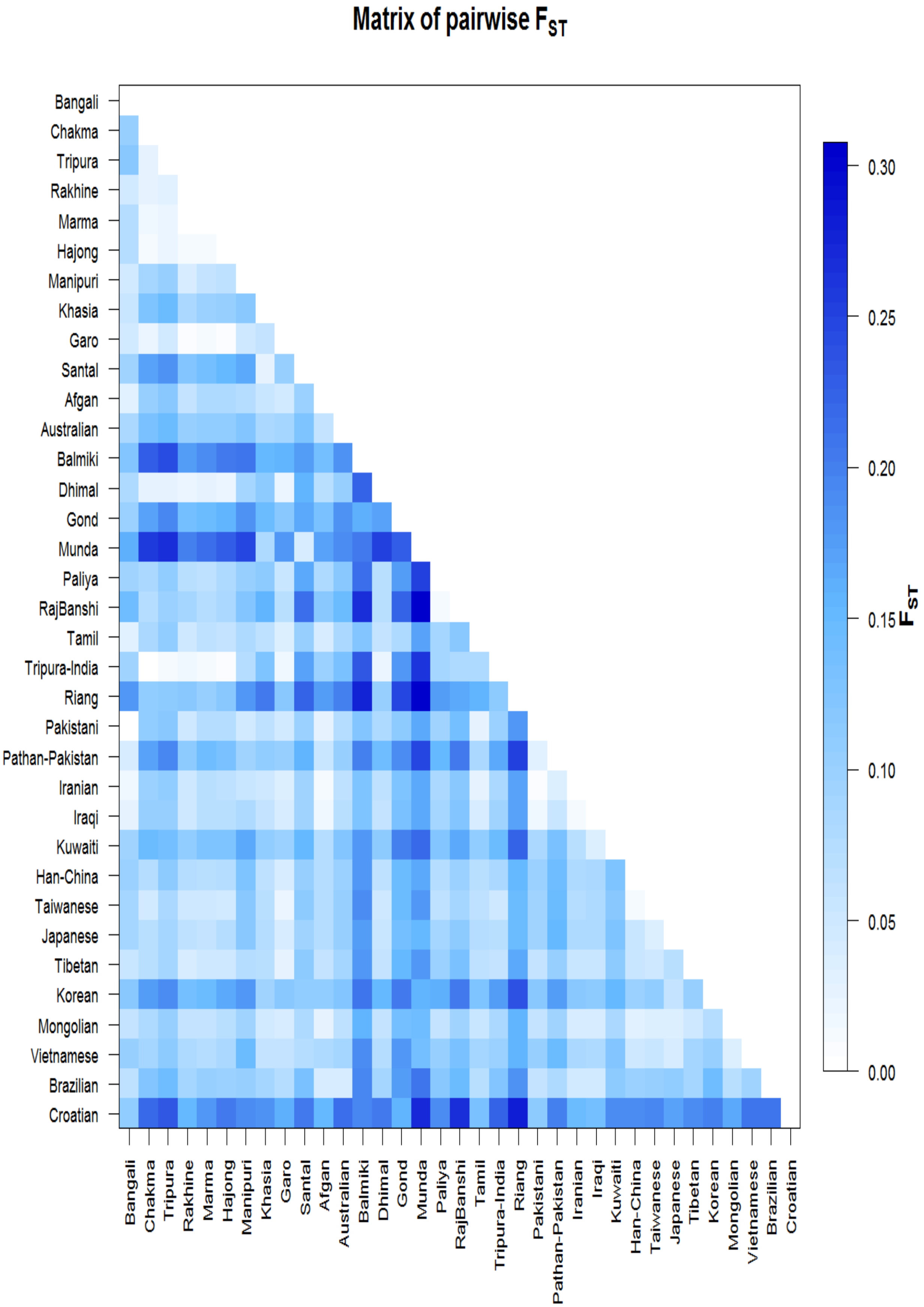

Figure 3.13 Matrix of pairwise F_{st} values indicates short-term genetic distances between populations.

3.13.3 Average Number of Pairwise Differences

The average number of pairwise differences is correlated with the matrix of pairwise F_{st} values and indicates the relationship between different populations (Figure 3.14). Small genetic distances represent as lower values of the average number of pairwise differences indicated close genetic affinity between two populations. The Nei's genetic distances (d) also showed that among Bangali, Afgan, Tamil, Pakistani, Iranian and Iraqi populations ranged from about 0.0 to 0.5, which indicated for the abovementioned populations were closely related to each other and exhibited features of Asian Y-chromosome gene pool. On the other hand, Chakma, Tripura, Rakhine, Marma, Hajong, Garo, Dhimal, Tripuri-India, and Taiwanese population ranged from about 0.0 to 0.4, indicated these populations were closely related to each other. In addition, Manipuris showed close genetic relationship with Garos ranged from 0.0 to 0.4. Similarly, Khasias displayed a strong genetic affinity with Santal population ranged from 0.0 to 0.3 (below diagonal).

On the other hand, the average number of pairwise differences results (above diagonal) also showed that Bangali population displayed a close genetic affinity with Afgan, Balmiki from India, Pakistani, Pathan from Pakistan, Iranian, and Iraqi populations and have ranged from 11.0 to 11.5. Likewise, Bangalis showed no genetic affinities with Australian, Riang and Rajbanshi populations. In addition, Chakmas showed a close genetic relationship with Tripura from Bangladesh (ranged from 10.8 to 11.0) and Tripuri from India (ranged from 10.3 to 10.5). Interestingly, Tripura from Bangladesh exhibited a close genetic relationship with Tripuri population from India (ranged from 9.5 to 10.0) and also Riang population from India (ranged from 11.0 to 11.3). Moreover, Tripuras indicated a strong genetic bonding with Rakhine, Marma, and Hajong population ranged from 10.5 to 10.7. Other major tribal populations like Rakhine, Marma, Hajong, and Manipuri displayed strong genetic relationship with some Mongoloid populations similar to Chinese Han, Taiwanese, Japanese, Tibetan, Korean, Mongolian, and Vietnamese populations, respectively. Surprisingly, Khasias showed a close genetic relationship with Santal from Bangladesh and Munda from India, respectively.

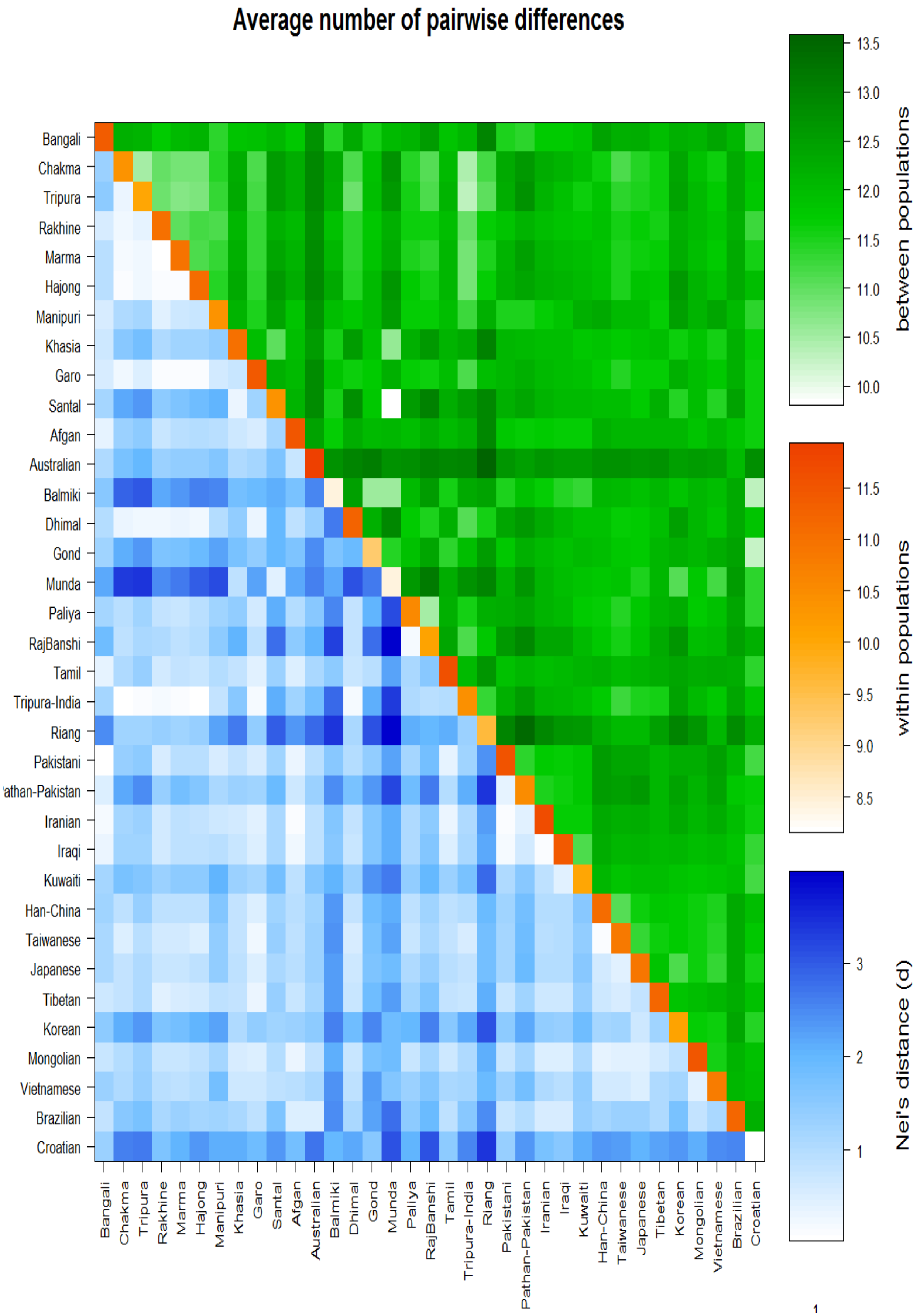

Figure 3.14: Average number of pairwise differences indicates the relationship between populations.

3.13.4 Slatkin's Linearized *Fst*

Slatkin's Linearized F_{st} values are near similar to the matrix of co-ancestry coefficients and matrix of pairwise genetic distance F_{st} values and also demonstrated the chromosomal relationship between populations (Figure 3.15). Small genetic distances represent as lower values of the Slatkin's Linearized F_{st} indicated a strong genetic relationship between the two populations. Results showed that Slatkin's Linearized F_{st} among Bangali, Afgan, Tamil, Pakistani, Iranian and Iraqi populations ranged from about 0.00 to 0.05, which means that these populations are closely related to each other and exhibited features of Asian Y-chromosome gene pool. On the other hand, Chakma, Tripura, Rakhine, Marma, Hajong, Garo, Dhimal, Tripuri-India, and Taiwanese population ranged from about 0.00 to 0.03 means these nine populations are closely related to each other. In addition, Manipuris were closely genetic relation with Garos ranged from 0.08 to 0.1. Similarly, Khasias were the closest genetic relationship with Santal population ranged from 0.00 to 0.04.

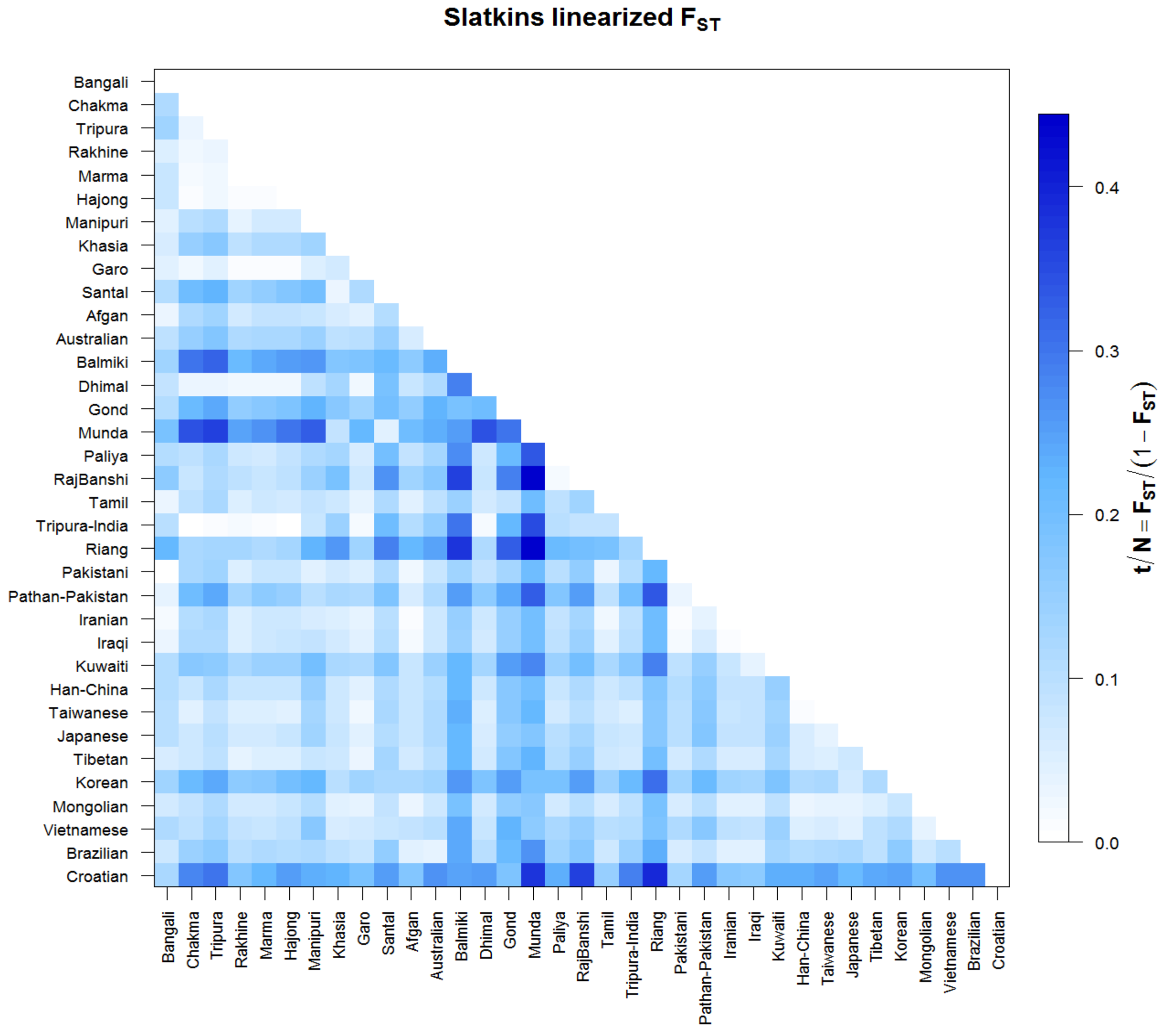

Figure 3.15 Slatkins Linearized F_{st} value indicates short-term genetic distances between populations.

3.13.5 Number of Alleles at Different Loci

The number of alleles at different loci showed the polymorphisms of alleles in the studied populations and 27world-wide reference populations shown in Figure 3.16. The number of alleles per locus was compared between different populations. Allele distribution in different loci indicated that Bangalis had most divergence alleles in their chromosome and showed a similar allocation from Tamil, Pakistani, Iranian, Iraqi, and Kuwaiti population. On the other hand, the allele distribution of Bangladeshi tribal were near similar and also analogous with Han, Japanese, Korean, Mongolian, Vietnamese populations.

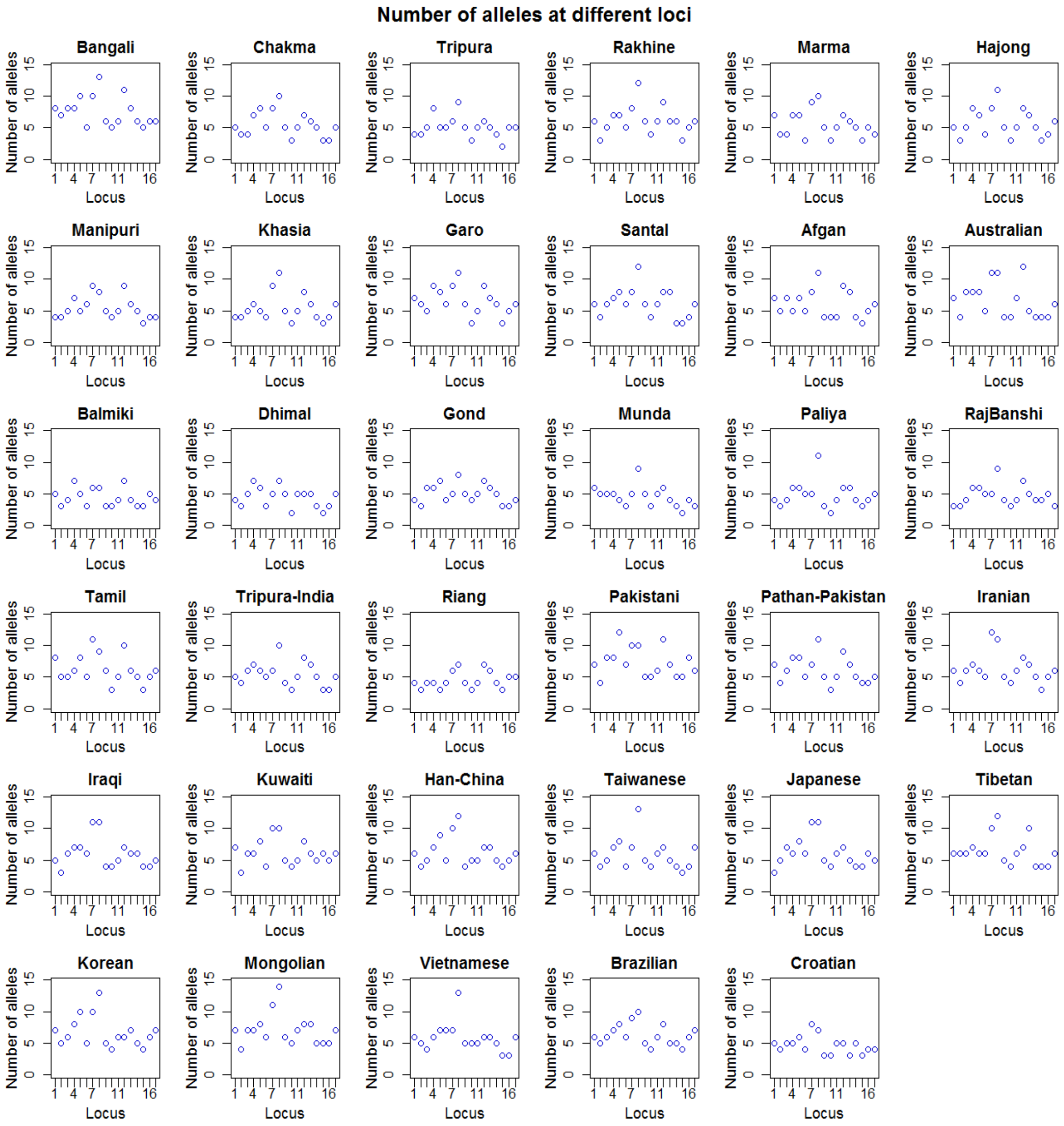

Figure 3.16 Number of alleles at the set of 17 Y-STR loci showed the polymorphisms of alleles in the studied populations and 27 reference populations

3.13.6 Alleles Size Range at Different Loci

Allele size range at different loci showed the variations of alleles in the studied populations and 27 world-wide reference populations shown in Figure 3.17. Allele size range for each locus was compared among different populations. Allele size range distribution in different loci indicated that Bangalis had most divergence alleles in their chromosome and showed a similar allocation from Tamil, Pakistani, Iranian, Iraqi, and Kuwaiti population. On the contrary, allele size range distribution of Bangladeshi tribal were near similar and also analogous with Han, Japanese, Korean, Mongolian, and Vietnamese populations.

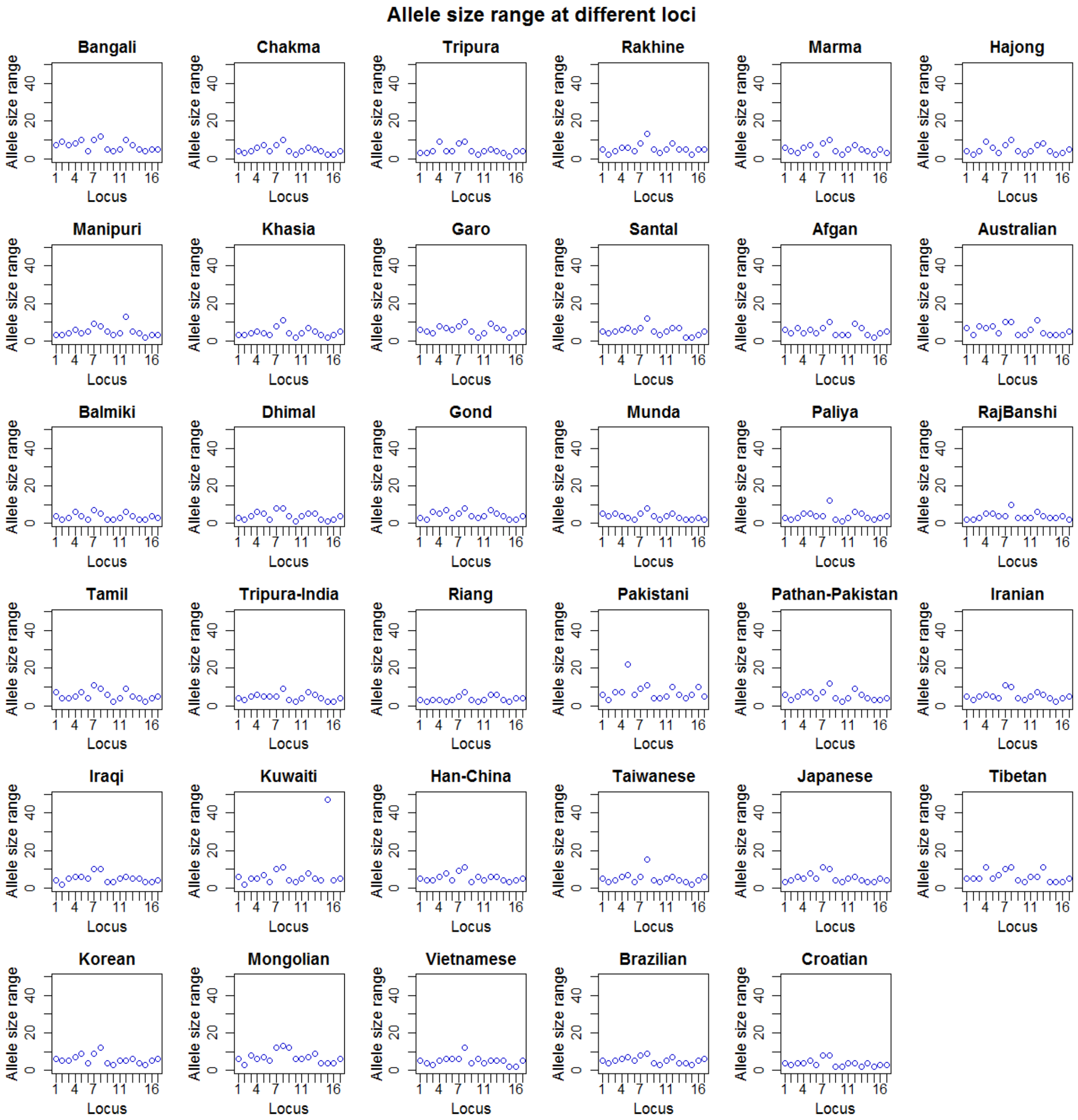

Figure 3.17 Allele size range at the set of 17 Y-STR loci showed the distribution of alleles in the studied populations and 27 reference populations.

3.13.7 Expected Heterozygosity

Expected heterozygosity of a set of 17 Y-STR loci exhibited the genetic relationship among the studied population and 27 different reference populations. Expected heterozygosity of most of the loci showed that Pakistani, Pakistani Pathan, Tamil, Iranian, Iraqi, and Kuwaiti populations had a close genetic affinity to Bangali population. Results also indicated that Chakma, Tripura, Rakhine, Marma, Hajong, Manipuri, Khasia tribes were near similar genetic affinities and also analogous with Chinese Han, Tibetan, Japanese, Korean, Mongolian, and Vietnamese populations, respectively (Figure 3.18).

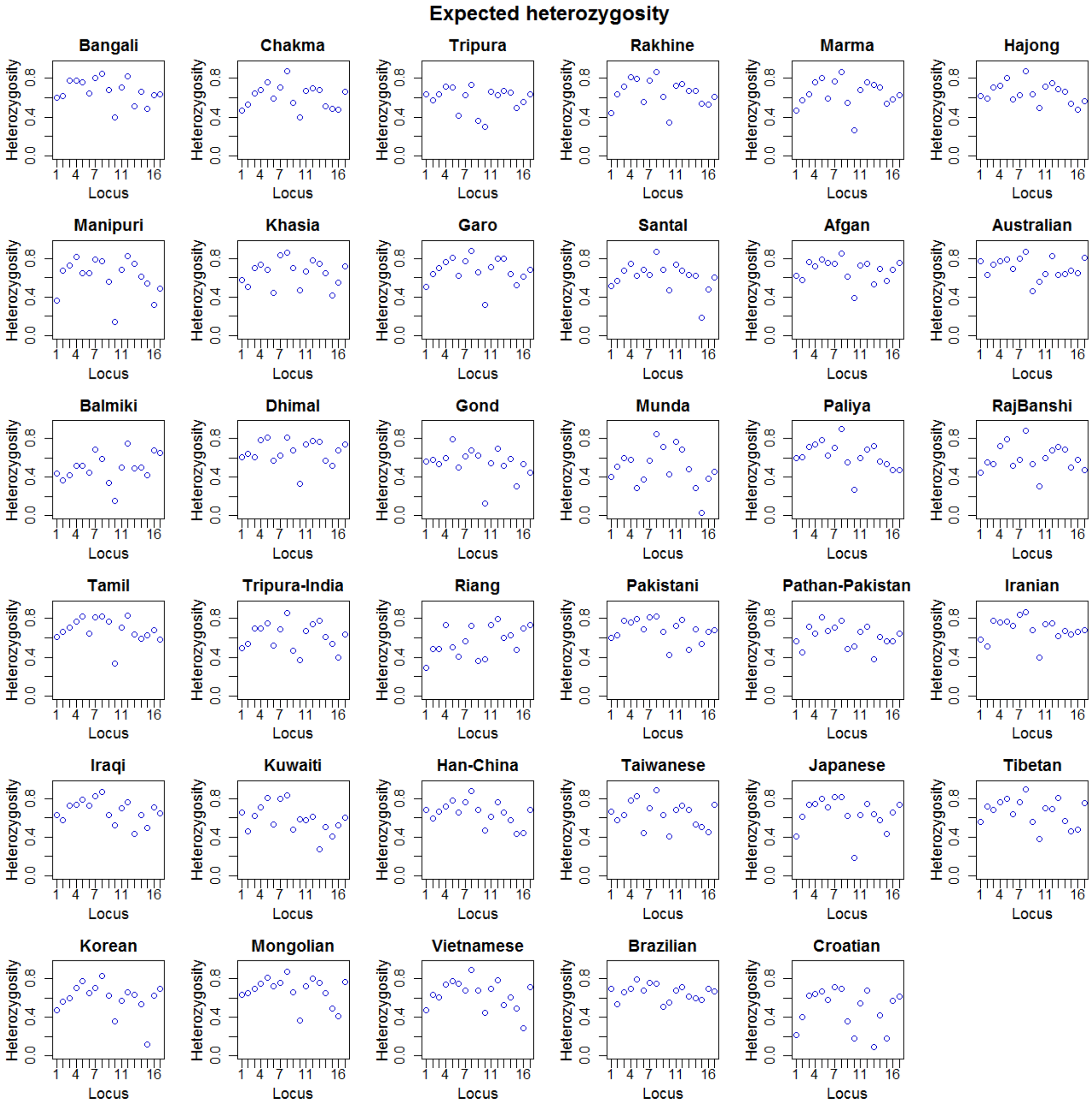

Figure 3.18 Expected heterozygosity of a set of 17 Y-STR loci exhibited the genetic affinity among the studied populations and 27 different reference populations.

3.13.8 Garza-Williamson Index at Different Loci

Garza-Williamson Index at different loci showed the divergences of alleles in the studied populations and 27 reference populations shown in Figure 3.19. Garza-Williamson Index for each locus was compared among different populations. The Garza-Williamson Index dissemination in different loci indicated that Bangalis had most divergence alleles in their chromosome and showed a similar allocation from Tamil, Pakistani, Iranian, Iraqi, and Kuwaiti population. In contrast, The Garza-Williamson Index distribution of the studied tribals was near similar and also associated with Tibetan, Han, Japanese, Korean, Mongolian, and Vietnamese populations.

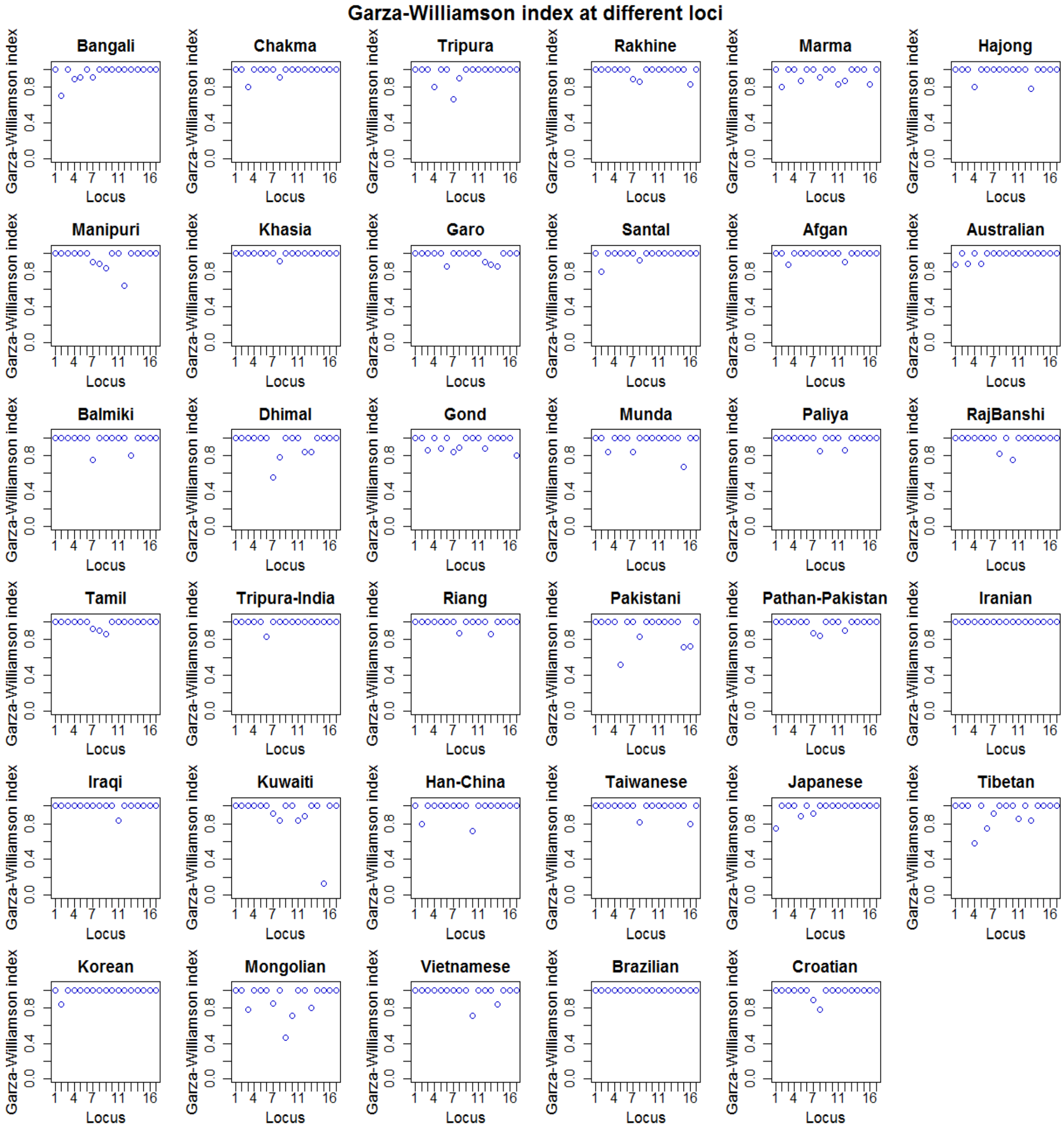

Figure 3.19 Garza-Williamson Index of a set of 17 Y-STR loci exhibited the genetic affinity among the studied populations and 27 global reference populations.

3.13.9 Molecular Distance (θ_H) at Different Loci

Molecular distance (θ_H) at different loci indicates the genetic distance among various populations based on expected heterozygosity. Molecular distance (θ_H) values of the set of 17-Y-STRs loci showed that Bangalis appeared least molecular distance with Tamil, Pakistani, Iranian, Iraqi, and Kuwaiti populations. In contrast, the studied tribal populations showed insignificant genetic distance with Tibetan, Han, Japanese, Korean, Mongolian, and Vietnamese populations (Figure 3.20).

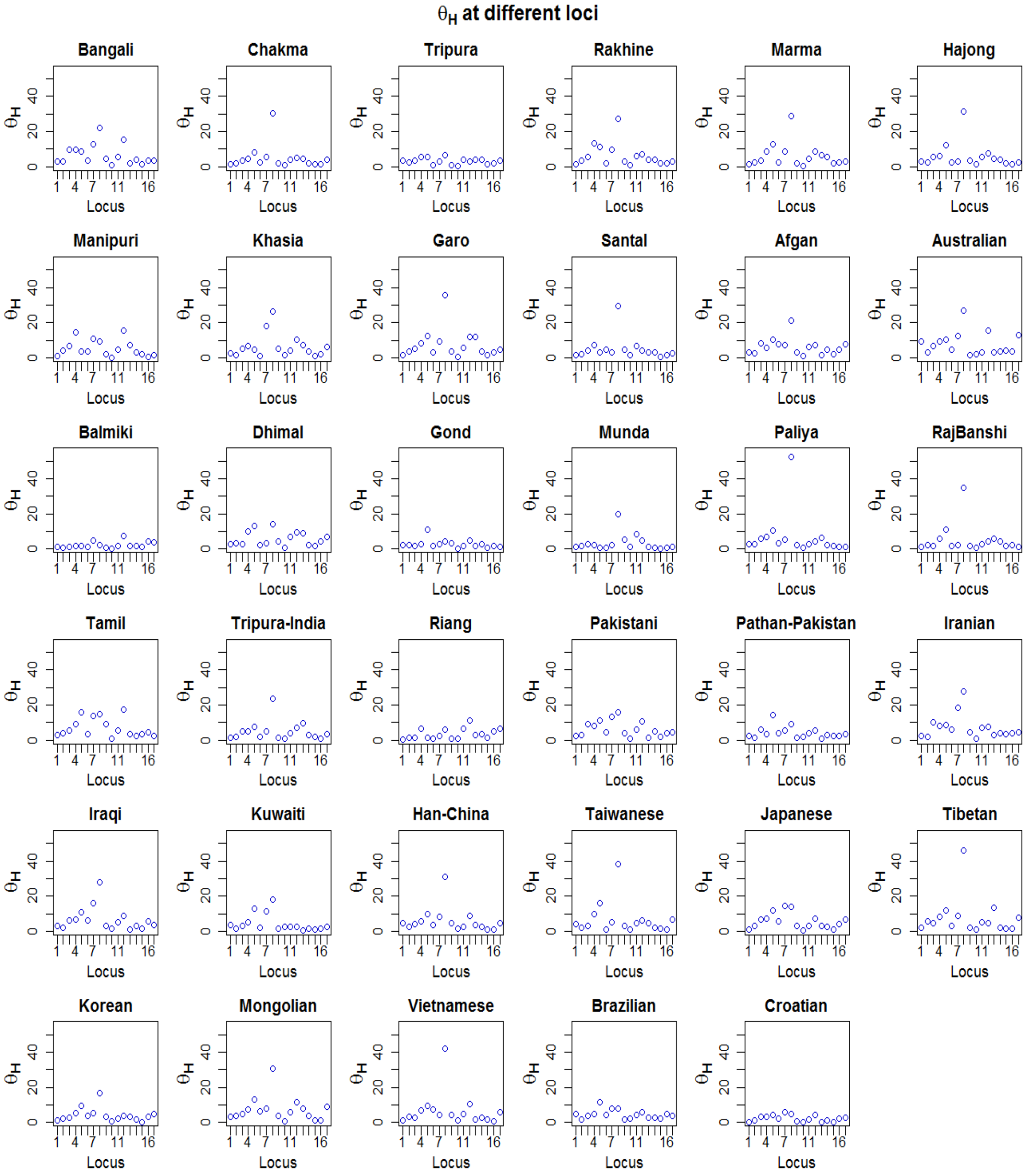

Figure 3.20 Molecular distance (θ_H) at 17 Y-STR loci indicates the genetic distance among the studied populations based on expected heterozygosity.

3.14 Y-chromosomal Haplogroup Studies

A total of 1,594 Y-chromosome haplotypes out of 1,631 individuals were assigned to haplogroups based on 17 Y-STRs using Whit Athey's Haplogroup Predictor algorithm, and the frequency for each haplogroup was determined (Figure 3.21 and Supplementary Table 21). Overall 20 haplogroups (E1b1a, E1b1b, G2a, H, I1, I2a (xI2a1), I2a1, I2b (xI2b1), I2b1, J1, J2a1b, J2a1h, J2a1 x J2a1-bh, J2b, L, N, Q, R1a, R1b, and T) were detected in this study, whereas haplogroup G2c mentioned in the haplogroup assigning tool was not observed in the studied population samples. The highest ancestry proportions of a majority of individuals match the highest average continental-ancestry proportions in 424 haplotypes for L, 275 haplotypes for R1a, and 146 haplotypes for H and Q, respectively. In contrast, the low consistencies have been found in the following style: J1 (53), J2a1xJ2a1-bh (52), T (46), J2b (39), J2a1b (32), E1b1b (29), G2a (24), I2b1 (23), E1b1a (15), I2a1 (14), I2a(xI2a1) (11), J2a1h (10), N (10), R1b (5), I1 (4), and I2b(xI2b1) (1).

In Bangali population, the analyzed male samples were categorized into twenty different haplogroups and the major haplogroups were R1a (31.587%), H (19.720%) and L (17.411%). Besides, haplogroup R1a, H, and L were found in 205, 115, and 113 of the total 649 Y-chromosomes with carrying the allele's characteristics, respectively. In contrast, the minor haplogroups Q, J2a1 x J2a1-bh, J2b, J2a1b, I2a1, I2b1, J1, T, E1b1b, E1b1a, G2a, J2a1h, R1b, and N were observed in 45, 32, 32, 20, 12, 12, 12, 11, 9, 8, 7, 6, 4, and 3 individuals, respectively. Haplogroups I1, I2a(xI2a1), and I2b(xI2b1) were represented by only one individual in the Bangali males.

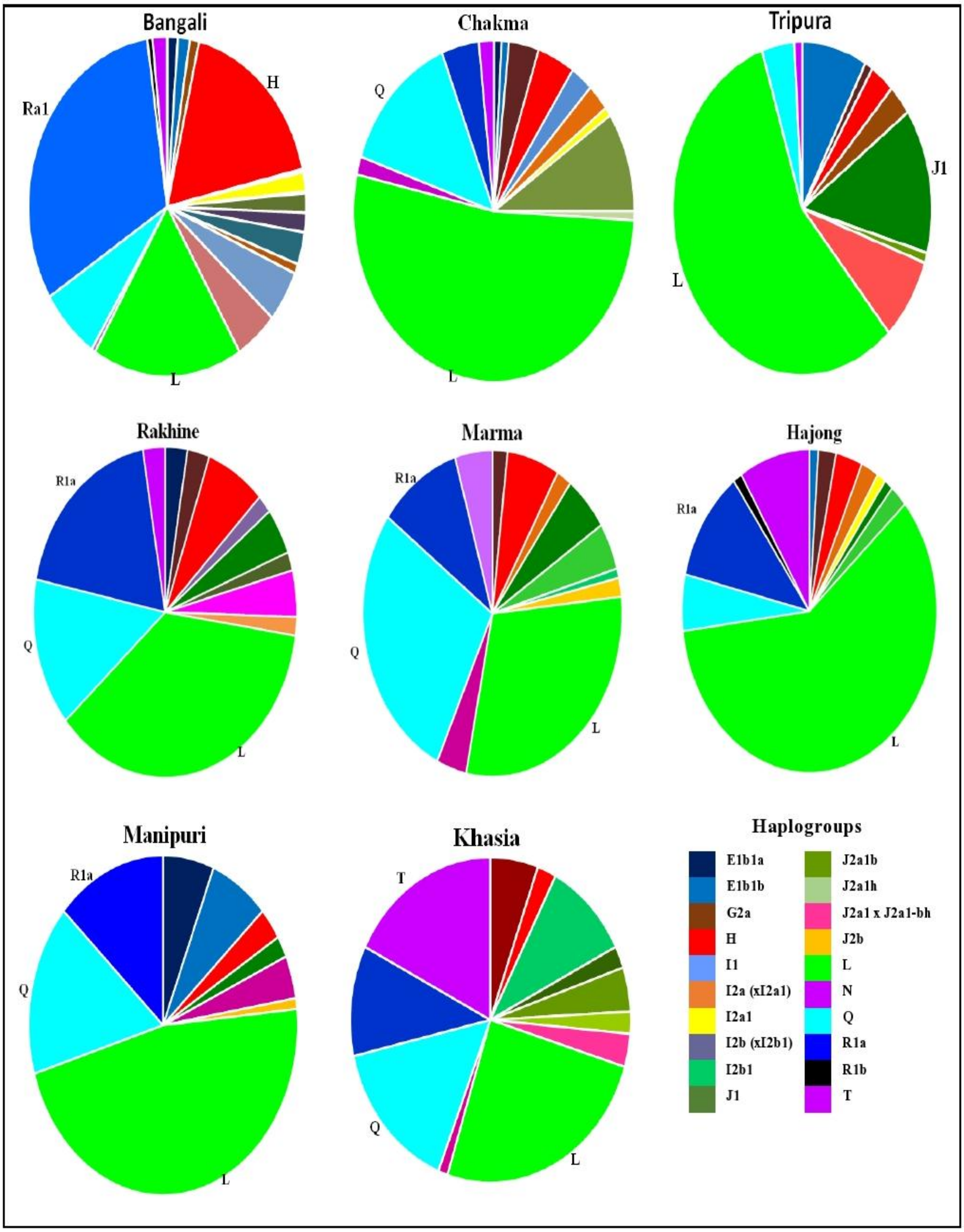

Figure 3.21 The frequency distribution of Y-chromosome haplogroups among the studied populations of Bangladesh.

In Chakma population, the analyzed male samples were classified into fourteen different haplogroups and the most abundant haplogroups were L (52.586%) and Q (13.793%). Besides, haplogroup L and Q were found on 61 and 16 of the total 116 Y-chromosomes, respectively. The remaining twelve haplogroups seem to be existent to a smaller extent in the following style: J1 (9.483%), H (4.310%), R1a (4.310%), G2a (3.448%), I1 (2.586%), I2a(xI2a1) (2.586%), N (1.724%), T (1.724%), E1b1a (0.862%), E1b1b (0.862%), I2a1 (0.862%) and J2a1h (0.862%). Haplogroup J1, H, R1a, G2a, I1, I2a(xI2a1), N, and T were monitored in 11, 5, 5, 4, 3, 3, 2, and 2 individuals, respectively. Besides, haplogroups E1b1a, E1b1b, I2a1, and J2a1h were represented by only one individual. Interestingly, haplogroups I2b(xI2b1), I2b1, J2a1b, J2a1xJ2a1-bh, J2b, and R1b were not detected in the Chakma population.

In Tripura population, ten haplogroups have been detected and the most abundant haplogroups were L (56.566%) and J1 (14.141%). Besides, haplogroup L and J1 were found on 56 and 14 of the total 99 Y-chromosomes, respectively. The remaining eight haplogroups seem to be existent to a smaller extent in the following style: E1b1b (8.081%), J2a1xJ2a1-bh (8.081%), Q (4.040%), H (3.030%), I2a1(xI2a1) (3.030%), G2a (1.010%), J2a1b (1.010%), and T (1.010%). Haplogroups E1b1b, J2a1xJ2a1-bh, Q, H, and I2a1(xI2a1) were observed in 8, 8, 4, 3 and 3 individuals, respectively. Besides, haplogroups G2a, J2a1b, and T were represented by only one individual. Furthermore, haplogroups E1b1a, I1, I2a1, I2b(xI2b1), I2b1, J2a1h, J2b, N, R1a, and R1b were not detected in the Tripura population.

In total, twelve haplogroups have been detected in Rakhine population samples. Haplogroup L, R1a, and Q were being the most abundant haplogroups with a frequency account for a total of 36.364%, 19.091%, and 14.545%, respectively. Besides, haplogroup L, R1a, and Q were found on 40, 21, and 16 of the total 110 Y-chromosomes, respectively. The remaining seven haplogroups seem to be existent to a smaller extent in the following style: H (7.273%), J1 (4.545%), J2a1xJ2a1-bh (4.545%), E1b1b (2.727%), G2a (2.727%), T (2.727%), I2b1 (1.818%), J2a1b (1.818%), and J2b (1.818%). Haplogroups H, J1, J2a1xJ2a1-bh, E1b1b, G2a, T, I2b1, J2a1b, and J2b were observed in 8, 5, 5, 3, 3, 3, 2, 2, and 2 individuals, respectively. Interestingly, haplogroups E1b1a, I1, I2a(xI2a1), I2a1, I2b(xI2b1), J2a1h, N, and R1b were not observed.

Overall, twelve haplogroups have been detected in Marma population samples. Haplogroup L, Q, and R1a were being the most abundant haplogroups with a frequency account for a total of 29.907%, 28.037%, and 10.280%, respectively. Furthermore, haplogroup L, Q, and R1a were found on 32, 30, and 11 of the total 107 Y-chromosomes, respectively. The remaining ten haplogroups seem to be existent to a smaller extent in the following style: H (6.542%), J1 (5.607%), J2a1b (4.673%), T (4.673%), N (3.738%), G2a (1.869%), I2a(xI2a1) (1.869%), J2b (1.869%), and J2a1h (0.935%). Haplogroups H, J1, J2a1b, T, N, G2a, I2a(xI2a1), and J2b were observed in 7, 6, 5, 5, 4, 2, 2, and 2 individuals, respectively. Furthermore, haplogroup J2a1h was observed once. In contrast, haplogroups E1b1a, E1b1b, I1, I2a1, I2b(xI2b1), J2a1xJ2a1-bh, and R1b were not monitored.

In total, eleven haplogroups have been detected in Hajong population samples. Haplogroup L and R1a were being the most frequent haplogroups with a frequency account for a total of 59.551% and 11.236%, respectively. Besides, haplogroup L and R1a were found on 53 and 10 of the total 89 Y-chromosomes, respectively. The remaining nine haplogroups seemed to be existent to a smaller extent in the following style: T (8.989%), Q (5.618%), H (3.371%), G2a (2.247%), I2a(xI2a1) (2.247%), E1b1b (1.124%), I2a1 (1.124%), J1 (1.124%), and R1b (1.124%). Haplogroups T, Q, H, G2a, and I2a(xI2a1) were observed in 8, 5, 3, 2, and 2 individuals, respectively. Furthermore, haplogroups E1b1b, I2a1, J1, and R1b were represented by only one individual. In contrast, haplogroups E1b1a, I1, I2b(xI2b1), I2b1, J2a1b, J2a1h, J2a1xJ2a1-bh, J2b, and N were not detected.

In this study, nine haplogroups have been detected in Manipuri population samples. Haplogroups L, Q, and R1a were being the most abundant haplogroups with a frequency account for a total of 46.939%, 16.327%, and 13.265%, respectively. Additionally, haplogroup L, Q, and R1a were found on 46, 16, and 13 of the total 98 Y-chromosomes, respectively. The remaining five haplogroups seemed to be existent to a smaller extent in the following style: E1b1b (7.143%), E1b1a (6.122%), J2a1xJ2a1-bh (4.082%), H (3.061%), J1 (2.041%), and J2b (1.020%). Haplogroups E1b1b, E1b1a, J2a1xJ2a1-bh, H, and J1 were detected in 7, 6, 5, 4, 3, and 2 individuals, respectively. In contrast, haplogroup J2b was represented by only one individual. In addition, haplogroups G2a, I1, I2a (xI2a1), I2a1, I2b (xI2b1), I2b1, J2a1b, J2a1h, N, R1b and T were not detected.

In Khasia population, the analyzed male samples were categorized into twelve different haplogroups and the most abundant haplogroups were L (25.275%), T (17.582%), and Q (15.385%). Furthermore, haplogroup L, T, and Q were found on 23, 16, and 14 of the total 91 Y-chromosomes. The remaining nine haplogroups seemed to be existent to a smaller extent in the following method: R1a (10.989%), I2b1 (9.890%), G2a (5.495%), J2a1b (4.496%), J2a1 x J2a1-bh (3.297%), H (2.198%), J1 (2.198%), J2a1h (2.198%) and N (1.099%). Haplogroups R1a, I2b1, G2a, J2a1b, J2a1 xJ2a1-bh, H, J1, and J2a1h were detected in 10, 9, 5, 3, 3, 2, 2 and 2 individuals, respectively. Also, haplogroup N was represented by only one individual. Interestingly, haplogroups E1b1a, E1b1b, I1, I2a (xI2a1), I2a1, I2b (xI2b1), J2b, and R1b were not detected.

The haplogroup analysis showed that the Bangali had the greater frequency for haplogroups R1a, H, and L. The R1a haplogroup was reported to be the most frequent haplogroup present in Eurasia [Trivedi *et al.,* 2008; Karafet *et al.*, 2008]. The R1a haplogroup was observed to be the most abundant haplogroup in Afghanistan [Älgenäs and Tillmar, 2014], in Pakistan [Perveen *et al.*, 2014], in Iran [Tabrizi *et al.*, 2015], and all the major geographic regions of India [Sahoo *et al.*, 2006; Singh *et al.*, 2018]. Another study revealed that haplogroup L, R, and Q were three largest haplogroups in Jat population from India with the frequency of 36.8, 28.5, and 15.6%, respectively [Mahal and Matsoukas, 2017]. Interestingly, the haplogroup R, including its subhaplogroups R1a, R1b, and R2 as well as haplogroup H were found the significant frequency of 20 and 3% in the Tibetan population from China, respectively. R1b was the second most frequent haplogroup in the Turkish population living in Sarajevo, Bosnia and Herzegovina, with a prevalence of 15% [Doğan *et al.*, 2016] and this haplogroup was originated in West Asia [Myres *et al.*, 2011].

The studied ethnic populations exhibited higher frequency for haplogroups L, Q, R1a, and T. The haplogroup L had a significant frequency of approximately 28% in Western Pakistan and Baluchistan male samples, respectively [Qamar *et al.,* 2002]. A study revealed that haplogroup L detected in the Indian male samples with a total frequency of about 7 to 15% [Basu *et al.*, 2003; Cordaux *et al.*, 2004]. The haplogroup Q was observed at the moderate frequency of 13.2% in Hui, 3.0% in Han and 3% in the Mongolian population from China [Wang *et al.*, 2015]. Haplogroup G2a was found at extremely low frequency in the studied populations, whereas this haplogroup present at the moderate frequency in the West Asian males. In 2010, Indian biologist Eaaswarkhanth and his co-workers studied on the Muslims in India and found 2.3% of 129 Indian Sunni males in Uttar Pradesh and 8% of 161 Indian Shia males were G, and also found that in Andhra Pradesh in southern India, 8% of 25 Iranian Shia were haplogroup G. The ancestor of the haplogroup I, G, and E can be traced to different part of Africa, Middle East, South Central Asia, and also in Europe [ISOGG, 2015]. Another study revealed that G2a was one of the largest haplogroups within a recently settled Turkish population in Sarajevo, Bosnia and Herzegovina, and it had been observed a frequency of about 12% [Doğan *et al.*, 2016]. Haplogroup J along including its sublineages J1, J2a1b, J2a1h, J2a1xJ2a1-bh, and J2b were found at the moderate frequency in Bangali population. A study revealed that haplogroup J present in the Jat population at a total frequency of about 9.6% [Mahal and Matsoukas, 2017]. In 2013, genetic genealogist Kerchner reported that the ancestor of haplogroup J was born in the Middle East and believed that the Middle Eastern merchants carried this genetic marker to the Indian-Subcontinent. Haplogroup J showed a significant frequency of about 6% in the Tibetan population from China [Wang *et al.*, 2015]. In 2016, geneticist Doğan and co-scientists reported that J2 was the largest haplogroup in Turkish population living in Sarajevo, Bosnia and Herzegovina with a frequency of about 29% including its sublineage haplogroups J2a and J2b. Haplogroup N was found at extremely low frequency in the studied populations. In 2013, Shi and co-scientists reported that haplogroup N was prevalent (>5%) in East Asia (e.g., among Han Chinese, Tibeto-Burman and Austro-Asiatic language groups), as well as in Northern or Central Asia. In contrast, it was relatively rare in Southeastern, Southern and Western Asia.

Haplogroup E (sublineages E1b1a and E1b1b) and haplogroup I (sublineages I1, I2a(xI2a1), I2a1, I2b(xI2b1) and I2b1) were found the low frequency in Bangali but these haplogroups were not found in the studied ethnic groups. A study revealed that E1b1b was the second dominant with a frequency of 17% in Bosnian- Herzegovinian population samples and forth dominant haplogroup with the frequency of 6.7% and 2.7% for Croatian and Slovenian population, respectively. This study also showed that I2a was the largest haplogroup with a frequency of 49% in Bosnian- Herzegovinian population and 32.6% in Croatian population [Doğan *et al.*, 2016; Šehović *et al.*, 2017].

3.15 Asian Paternal Ancestry and Evidence for Migration from Y-chromosome

In the studied populations, the analyzed male samples were categorized into twenty different haplogroups and their geographic distribution across the country as well as Asia and Australia is illustrated in Figure 3.22. We also investigated the possible origins of the major haplogroups R1a, L, Q, and H chromosomes in more detail by using information from the Y-chromosomal STR haplotypes. R1a, H, and L were the most frequent Y-chromosome haplogroup found in Bangali. R1a, H, and L were the major haplogroups with the frequency of 51.5, 16.2, and 15.8% present throughout India, respectively and accounted for more than three-fourths of the Y lineages [Singh *et al.*, 2018]. R1a, L, H, and J2a1xJ2a1-bh were the most common haplogroup found in Pakistan and accounted for 34.307, 17.518, 9.854 and 9.489% of Pakistani Y-chromosomes, respectively [Perveen *et al.*, 2014]. I2a1, R1a, R1b, I2a(xI2a1), and L were the most frequent haplogroup observed in Afghanistan, and account for 15.924, 14.013, 10.191, 8.280 and 7.643% of Afghani Y-chromosomes [Älgenäs and Tillmar, 2014]. In addition, R1a, L and J2a1b were the most common haplogroup detected in Iranian population, and account for 24.710, 21.236 and 9.653% of Iranian Y-chromosomes [Tabrizi *et al.*, 2015]. R1a, H and L were the most prominent Bangali Y-chromosome haplogroups, and these were shared with Indian, Pakistani, Afghanistani and Iranian populations. Also, these haplogroups had predominately West Asian ancestry. It is suggesting that R1a including H and L haplogroups presence in Bangali may originate from demic diffusion by way of west-to-east migration. Interestingly, haplogroup I2b(xI2b1) belongs to one individual in Bangalis, whereas it was not found in the studied ethnic populations. Haplogroup T was also found at low frequency in Bangalis, whereas it was found in Khasia, Santal, Tibet, Mongolia, China, Thailand and Malaysian population at moderate frequencies. Besides, we found the moderate frequency of J2a1b to be characteristics of Bangali, India, Iran, and Australian populations, but its distribution elsewhere in the Northeastern and Southeastern Asian populations was very insignificant.

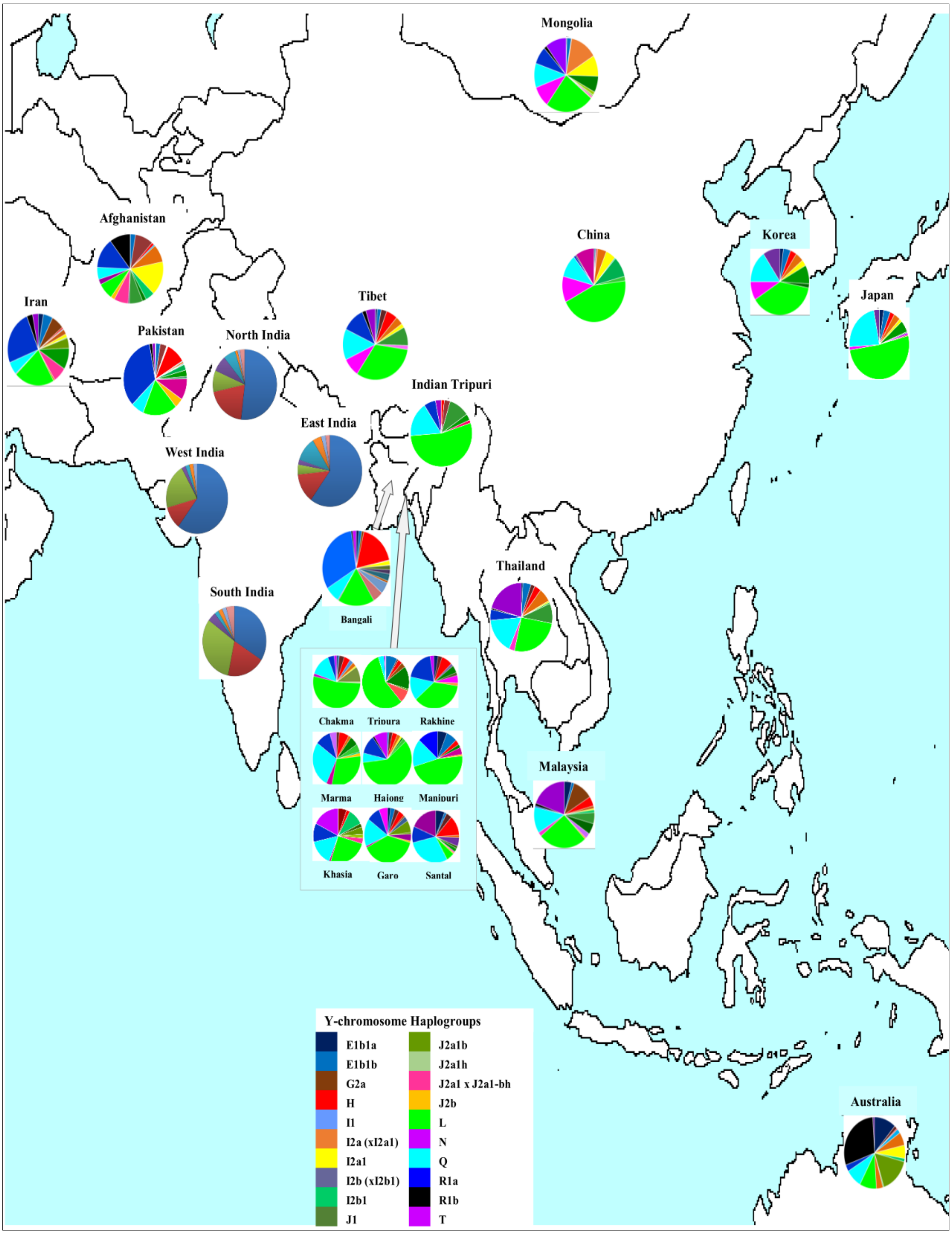

Figure 3.22 The frequency distribution of Y-chromosomal haplogroups in Asian and Australian populations. The data used were from the current and published studies (Chang *et al.*, 2007; Kang *et al.*, 2007; Mizuno *et al.*, 2008; Kim *et al.*, 2010; Ghosh *et al.*, 2011; Taylor and Henry, 2012; Bing *et al.*, 2013; Älgenäs and Tillmar, 2014; Perveen *et al.*, 2014; Tabrizi *et al.*, 2015; Hasan *et al.*, 2015; Fu *et al.*, 2016; Singh *et al.*, 2018; Li *et al.*, 2019).

On the whole, we found the studied ethnic population groups of Bangladesh to be characterized by male haplogroup homogeneity, showing mostly expansions of haplogroup L, Q, and R1a. L and Q were the most frequent Y-chromosome haplogroups found in the studied ethnic populations, and these were shared primarily with populations in eastern including Indian Tripuri, Tibet, China, Mongolia, Thailand, Malaysia, Korea, and Japan. The Northeastern and Southeastern Asian network and diversity analyses of haplogroup L and Q may support an eastern origin that migrated into Bangladesh via the eastern route. Haplogroup L and Q were found to be distributed widely across both Northeastern and Southeastern Asia. In addition, most of the South-East Asian population groups seemed to have L, Q, T, and J1 chromosomes, whereas haplogroup R1a and H were not present. Haplogroup T, J1, and H were present in the studied ethnic populations at moderate frequencies, suggesting that these populations may have shared a common origin with Mongoloid stock populations in the South-East Asian regions. Haplogroup I2a(xI2a1) and I2a1 were found at extremely low frequencies in the studied ethnic populations, whereas these haplogroups present at high frequency in the Mongolian males.

Based on the result of the Y-chromosomal haplogroup prediction analysis, the Bangali population contains paternal lineages from India, Pakistan, Afghanistan, and Iran of West Asia. In contrast, the studied ethnic populations contain paternal lineages from the northern and southern areas of East Asia.

3.16 Analysis of Individual Major Haplogroups of the Studied Populations

The Median-Joining networks showed the genetic affinity for the most frequent haplotypes among the studied populations. Several haplotypes of the studied populations screened from Whit Athey's Haplogroup Predictor. At the same time, most common haplotypes were appointed for a sketch of each haplogroup and these haplotypes were assigned for network analysis i.e. 64 haplotypes for R1a, 80 for L, 69 for Q, and 40 for H. The abundance of these four haplogroups are also shown in the Network analysis (Figure 3.23).

The most common Y-chromosome haplotypes from the studied populations were spread all around the haplogroup R1a network and form a cluster. The Y-STR pattern thus showed that haplogroup R1a was genetically diverse and widespread. The Bangali haplotypes have resided in the centre of the cluster and other seven tribal haplotypes scattered around the cluster indicated a certain degree of differences between haplotypes. The haplogroup L cluster showed the highest degree of relative compactness out of the analyzed haplogroups indicating a high degree of intrahaplogroup similarity between the haplotypes. In contrast, the haplogroup Q cluster has the least degree of compactness as it forms two minor clusters within it. This indicates that there is a low level of intrahaplogroup similarity between the haplotypes. The haplogroup H clustering is not as compact as the R1a, L, and Q median-joining tree and it contains two minor clusters. The H network, which was prevalent in the Bangali population, represented a relatively simple pattern with fewer haplotypes. Notably, most Y-chromosomes in this population were clustered into the same haplotype or closely related haplotypes.

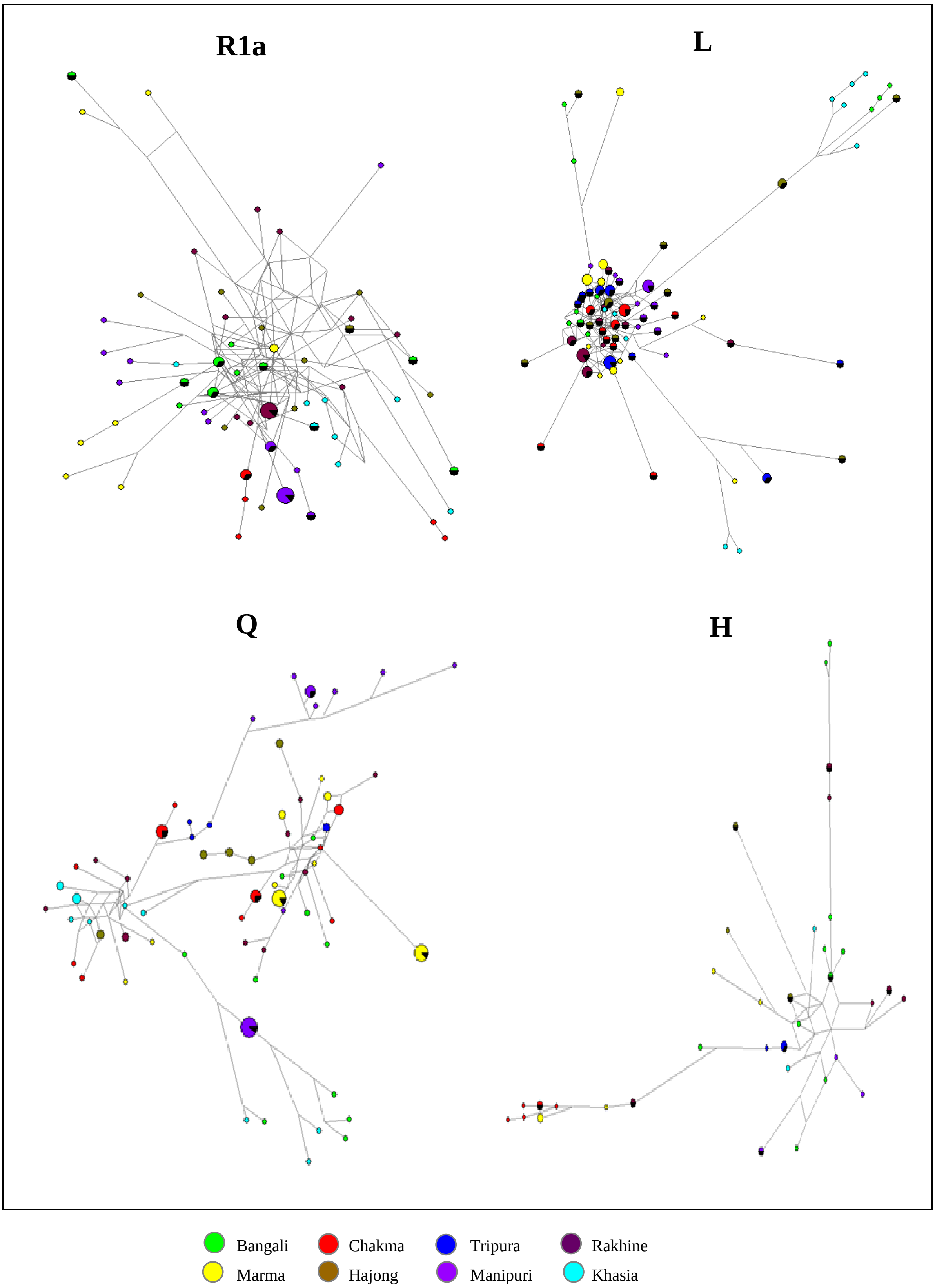

Figure 3.23 The Median-joining (MJ) networks of Y-STR haplotypes within haplogroups R1a, L, Q, and H reported in this study based on 15 Y-STRs. *Circles* represent haplotypes with areas proportional to frequencies; the smallest area is equivalent to one individual. *Colours* indicate the population of origin, as listed at the bottom of the figure. Branch length is proportional to the number of mutations between haplotypes.

3.17 Metapopulation Analysis using Y-chromosomal Haplotypes

We also searched for the most frequent Y-chromosomal haplotypes from the studied populations with the metapopulations in the YHRD, and have drawn their gene pool relationship to the metapopulations of the world (Supplementary Fig. 01 to Fig.08). Ancestry information showed that the Y-chromosomes of Bangali population belong to the Dravidian, Altaic, Indian, Indo-Iranian, and Admixed metapopulations culture, which correspondence with its history, ethnicity, customs, and geographical distribution. The three most prominent haplotypes of Chakma population be possessed by the Chinese (Han), Tibeto-Burman, Japanese, Tai-Kadai, and Indian metapopulations. Metapopulation analysis showed that the haplotypes of Tripura population genetically close relationship with the Chinese (Han), Tibeto-Burman, Tai-Kadai, and Altaic metapopulations. The haplotypes of Rakhine population belong to the Chinese (Han), Tibeto-Burman, and Indian metapopulations. Furthermore, the haplotypes of Marma population belong to the Chinese (Han), Tibeto-Burman, and Indian metapopulations. Besides, the haplotypes of Hajong population belong to the Chinese (Han), Tibeto-Burman, and Indian metapopulations. The haplotypes of the Manipuri population be affiliated with the European, Altaic, and Indian metapopulations. In contrast, the Y-chromosomal haplotypes of the Khasia population belong to the Sino-Tibetan, Altaic, and Indian metapopulations.

Chapter Four

CONCLUSION

This study represents one of the most comprehensive reports of Y-chromosome distribution in Bangladesh to date. Advances in molecular genetics, both in terms of sequencing and fragment analyses of short tendem repeats has enhanced our understanding of human genetic diversity and migration of the peoples worldwide. Nowadays, Y-chromosome data is vastly using for establishing the genetic diversity and human evolution history among the populations of a country. In this study, Y-chromosome haplotype data of the mainstream Bangali and seven other ethnic populations were compared with the published data in YHRD by means of AMOVA. Based on pairwise R_{st} comparisons indicated that Bangali population lies closer to a clade consisting Nepalese, Iranian, Iraqi, Tamil, and Bhil populations. Moreover, the comparative analysis showed that Bangalis were significantly different from the tribal populations living in Bangladesh. According to statistical analyses the investigated tribal populations are genetically heterogeneous, closely related to other Mongoloid populations from East Asia. The Bangali males presented greater frequency for haplogroups R1a, H, and L of the total Y-chromosome. Whereas L and Q were the most frequent haplogroups found in the studied ethnic populations. Based on the result of the Y-chromosomal STR data, the Bangali population contains paternal lineages originating from either India, Pakistan, Afghanistan or Iran. Rest of the ethnic populations contains paternal lineages from the northern and southern areas of East Asia. These findings also indicate that the Bangali and the studied ethnic groups are separate populations with different paternal lineage and migration.

Chapter Five

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Supplementary Table 1. A list of Y-chromosome STR haplotypes detected in 667 unrelated males in Bangali (Bn) population

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Bn1	15	13	25	28	19	13	14,15	13	10	13	21	11	11	14	10	20	1	0.0015	MF-1
Bn2	15	13	23	29	17	13	14,14	14	10	10	25	10	11	16	11	19	1	0.0015	MF-1
Bn3	15	14	22	30	18	13	12,16	14	11	11	23	15	10	15	11	19	1	0.0015	MF-1
Bn4	16	11	22	27	15	14	13,17	11	10	13	24	14	12	15	10	19	1	0.0015	MF-1
Bn5	15	12	24	27	18	14	13,19	12	10	12	22	14	12	15	11	20	1	0.0015	MF-2
Bn6	15	12	22	28	15	14	13,17	11	10	12	23	14	12	15	10	19	1	0.0015	MF-1
Bn7	15	12	24	28	18	14	13,19	12	9	11	20	14	12	15	11	20	1	0.0015	MF-1
Bn8	13	12	24	28	15	14	13,18	12	10	12	22	11	11	15	9	19	1	0.0015	MF-1
Bn9	15	12	24	28	18	14	13,18	12	10	12	20	14	11	15	11	20	1	0.0015	MF-5
Bn10	16	12	24	28	19	14	13,18	12	10	12	20	14	13	15	11	20	1	0.0015	MF-1
Bn11	15	12	24	28	16	14	14,19	12	10	12	20	14	11	15	11	20	2	0.0029	MF-2
Bn12	15	12	24	28	16	14	13,19	13	10	11	20	14	11	14	11	20	1	0.0015	MF-1
Bn13	16	12	24	28	17	14	14,17	13	10	12	20	14	13	15	11	20	1	0.0015	MF-1
Bn14	15	12	24	28	17	14	13,19	12	11	12	23	14	12	15	11	20	1	0.0015	MF-1
Bn15	15	12	26	28	19	14	13,19	12	10	13	20	13	11	15	11	20	1	0.0015	MF-1
Bn16	17	12	23	29	17	14	13,18	14	10	12	25	10	12	16	11	19	1	0.0015	MF-1
Bn17	17	12	23	29	18	14	13,19	14	10	13	25	10	11	16	11	19	1	0.0015	MF-1
Bn18	17	12	23	29	18	14	13,19	14	10	13	25	10	12	16	11	19	1	0.0015	MF-1
Bn19	16	12	23	29	19	14	12,21	12	10	12	21	14	13	14	11	20	1	0.0015	MF-1
Bn20	15	12	24	29	19	14	14,15	14	10	14	18	11	12	14	10	19	1	0.0015	MF-1
Bn21	15	13	22	29	17	14	13,22	14	10	10	25	10	12	16	11	20	1	0.0015	MF-1
Bn22	15	13	22	29	18	14	14,17	12	10	11	20	11	12	14	9	19	1	0.0015	MF-1
Bn23	15	13	23	29	17	14	15,20	13	10	10	25	10	14	16	11	19	1	0.0015	MF-1
Bn24	15	13	23	29	15	14	13,15	14	10	12	25	10	12	16	11	19	1	0.0015	MF-1
Bn25	15	13	23	29	19.2	14	12,18	12	10	13	20	11	11	14	10	20	1	0.0015	MF-1
Bn26	15	13	23	29	17	14	15,19	12	10	11	23	11	11	14	9	21	1	0.0015	MF-1
Bn27	15	13	23	29	17	14	12,18	14	11	11	25	10	12	16	11	19	1	0.0015	MF-1
Bn28	15	13	23	29	17	14	13,17	12	11	11	20	11	14	16	11	19	1	0.0015	MF-1
Bn29	15	13	24	29	16	14	11,20	14	10	10	26	10	12	16	11	19	1	0.0015	MF-1
Bn30	15	13	24	29	17	14	13,18	14	10	10	25	10	12	16	11	20	1	0.0015	MF-1
Bn31	15	13	24	29	15	14	15,16	13	10	11	20	13	11	14	10	18	1	0.0015	MF-1
Bn32	15	13	25	29	16	14	14,17	14	11	13	18	12	12	14	10	19	1	0.0015	MF-1
Bn33	15	13	22	30	15	14	14,18	13	10	13	21	11	12	14	9	20	1	0.0015	MF-1
Bn34	15	13	23	30	16	14	14,15	14	9	10	18	11	12	14	10	19	1	0.0015	MF-1
Bn35	16	13	23	30	17	14	11,18	14	10	10	25	10	13	16	11	19	1	0.0015	MF-1
Bn36	15	13	23	30	18	14	14,15	12	10	11	21	11	11	15	9	19	1	0.0015	MF-1
Bn37	15	13	24	30	14	14	11,14	11	11	12	24	13	12	15	12	19	1	0.0015	MF-1
Bn38	16	13	25	30	16	14	12,18	13	10	11	23	13	11	15	11	19	1	0.0015	MF-1
Bn39	15	13	23	31	17	14	11,14	13	10	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn40	15	13	23	31	15	14	14,20	13	11	11	21	11	12	14	9	20	1	0.0015	MF-1
Bn41	14	14	23	29	16	14	13,19	14	10	10	25	10	12	14	11	19	1	0.0015	MF-2
Bn42	14	14	24	29	17	14	13,16	13	9	11	22	11	12	14	10	20	1	0.0015	MF-1
Bn43	15	14	23	30	17	14	14,19	14	10	10	25	10	12	14	11	19	1	0.0015	MF-1
Bn44	14	14	23	30	17	14	16,18	12	10	11	23	11	11	14	9	21	1	0.0015	MF-1
Bn45	15	14	23	30	16	14	12,17	13	10	11	23	11	11	16	9	21	1	0.0015	MF-1
Bn46	15	14	23	30	16	14	13,20	13	10	11	25	12	11	14	11	19	1	0.0015	MF-1
Bn47	15	14	24	30	18	14	13,14	14	10	11	25	10	12	16	11	19	1	0.0015	MF-1
Bn48	15	14	23	31	16	14	13,19	14	10	12	26	10	12	16	11	19	1	0.0015	MF-1
Bn49	16	14	23	31	17	14	12,18	15	10	11	24	10	12	16	11	19	1	0.0015	MF-1

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Bn50	15	14	23	31	16	14	16,17	13	10	11	18	11	12	14	10	19	1	0.0015	MF-1
Bn51	15	14	23	32	15	14	14,19	12	10	11	21	11	13	14	9	20	1	0.0015	MF-1
Bn52	15	12	22	28	17	15	15,16	12	10	11	20	11	11	14	8	19	1	0.0015	MF-1
Bn53	18	12	22	28	20	15	15,16	12	10	11	20	11	12	14	9	19	1	0.0015	MF-2
Bn54	16	12	22	28	16	15	15,18	13	10	11	21	11	12	14	9	19	1	0.0015	MF-1
Bn55	16	12	22	28	17	15	14,17	12	10	12	22	12	12	14	9	20	1	0.0015	MF-1
Bn56	15	12	22	28	16	15	13,17	11	10	13	23	14	11	15	10	19	1	0.0015	MF-1
Bn57	16	12	22	28	16	15	15,17	12	11	10	21	11	12	14	9	19	1	0.0015	MF-1
Bn58	15	12	23	28	17	15	13,22	12	10	12	21	13	11	14	11	20	1	0.0015	MF-1
Bn59	15	12	23	28	17	15	14,20	12	10	12	21	14	11	15	11	20	1	0.0015	MF-1
Bn60	13	12	24	28	19	15	11,16	12	10	11	20	11	11	15	9	18	1	0.0015	MF-1
Bn61	15	12	24	28	17	15	12,16	14	10	12	22	14	12	14	11	19	1	0.0015	MF-1
Bn62	13	12	24	28	17	15	13,17	13	11	11	24	11	11	15	9	19	1	0.0015	MF-1
Bn63	13	12	24	29	16	15	13,16	12	10	13	21	11	10	15	9	19	1	0.0015	MF-1
Bn64	13	12	24	29	16	15	13,17	12	11	13	22	11	10	14	9	19	1	0.0015	MF-1
Bn65	15	12	25	30	15	15	12,14	13	10	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn66	15	13	23	28	20	15	13,18	14	10	10	24	10	12	16	11	19	1	0.0015	MF-1
Bn67	15	13	23	28	16	15	11,18	15	10	13	21	11	11	14	10	21	1	0.0015	MF-1
Bn68	16	13	23	28	16	15	13,20	13	11	13	25	10	11	15	12	21	1	0.0015	MF-1
Bn69	16	13	24	28	17	15	15,19	14	10	12	21	14	11	14	10	18	1	0.0015	MF-2
Bn70	15	13	21	29	17	15	15,16	12	10	11	20	11	11	14	8	19	2	0.0029	MF-3
Bn71	15	13	22	29	17	15	14,16	12	10	11	21	11	13	14	9	19	1	0.0015	MF-1
Bn72	17	13	22	29	17	15	14,17	12	10	12	21	11	13	14	9	19	1	0.0015	MF-1
Bn73	15	13	22	29	17	15	15,16	12	10	11	20	11	11	14	8	19	2	0.0029	MF-2
Bn74	15	13	22	29	17	15	15,16	12	10	11	21	11	11	14	8	19	1	0.0015	MF-1
Bn75	17	13	22	29	19	15	15,16	12	10	11	20	11	11	14	9	19	1	0.0015	MF-1
Bn76	16	13	22	29	18	15	15,17	12	10	11	20	11	11	14	9	19	1	0.0015	MF-1
Bn77	15	13	22	29	17	15	15,17	12	10	12	20	11	12	14	9	19	1	0.0015	MF-1
Bn78	16	13	22	29	16	15	14,17	12	11	12	20	11	13	14	9	18	1	0.0015	MF-1
Bn79	15	13	22	29	17	15	15,17	12	11	11	20	11	12	14	9	19	1	0.0015	MF-1
Bn80	15	13	22	29	18	15	15,17	12	11	11	20	11	12	14	9	19	1	0.0015	MF-1
Bn81	15	13	23	29	20	15	13,17	14	10	10	25	10	12	14	11	19	1	0.0015	MF-1
Bn82	15	13	23	29	17	15	15,18	12	11	12	23	11	11	15	9	21	1	0.0015	MF-1
Bn83	17	13	24	29	16	15	12,12	14	10	11	19	11	12	14	11	19	1	0.0015	MF-1
Bn84	15	13	24	29	14	15	11,17	15	10	13	23	11	11	14	10	21	1	0.0015	MF-1
Bn85	16	13	24	29	17	15	15,21	14	11	12	21	13	11	14	10	18	1	0.0015	MF-1
Bn86	14	13	25	29	16	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn87	15	13	25	29	16	15	11,14	13	10	10	23	11	12	14	11	19	1	0.0015	MF-1
Bn88	16	13	25	29	15	15	16,18	14	11	12	21	13	10	14	10	18	1	0.0015	MF-1
Bn89	15	13	21	30	17	15	15,15	12	10	11	21	11	11	14	8	19	1	0.0015	MF-1
Bn90	12	13	22	30	18	15	13,17	12	10	11	22	11	11	14	9	20	1	0.0015	MF-1
Bn91	17	13	22	30	18	15	15,17	12	10	11	20	11	12	14	9	19	1	0.0015	MF-1
Bn92	15	13	22	30	19	15	9,15	12	11	12	22	14	11	16	10	21	1	0.0015	MF-1
Bn93	15	13	23	30	18	15	16,17	12	10	11	20	11	13	14	9	19	1	0.0015	MF-1
Bn94	15	13	23	30	15	15	14,19	13	10	12	23	11	12	14	9	20	1	0.0015	MF-2
Bn95	15	13	23	30	17	15	15,16	12	10	11	21	12	11	14	8	19	1	0.0015	MF-1
Bn96	15	13	24	30	15	15	11,14	13	10	10	23	11	12	14	11	20	1	0.0015	MF-17
Bn97	14	13	24	30	16	15	10,14	14	10	11	22	11	11	14	12	20	1	0.0015	MF-1
Bn98	16	13	24	30	17	15	12,12	14	10	11	19	11	12	14	11	19	3	0.0045	MF-3
Bn99	17	13	24	30	17	15	12,12	14	10	11	19	11	12	14	11	19	2	0.0029	MF-2
Bn100	15	13	24	30	16	15	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	MF-7

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Bn101	15	13	24	30	16	15	11,15	13	11	9	23	11	13	14	11	20	1	0.0015	MF-1
Bn102	15	13	25	30	17	15	11,13	13	10	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn103	15	13	25	30	17	15	11,14	13	10	10	23	11	12	14	11	20	2	0.0029	MF-5
Bn104	15	13	25	30	14	15	11,15	13	10	10	24	11	12	14	11	20	1	0.0015	MF-1
Bn105	15	13	25	30	16	15	12,14	13	10	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn106	15	13	26	30	16	15	11,14	13	10	10	24	11	12	14	11	20	1	0.0015	MF-1
Bn107	16	13	22	31	16	15	15,16	12	11	14	20	11	11	14	9	19	1	0.0015	MF-1
Bn108	15	13	23	31	15	15	15,17	12	10	11	20	11	12	14	9	19	1	0.0015	MF-1
Bn109	15	13	24	31	16	15	11,14	13	11	10	24	11	12	14	11	20	1	0.0015	MF-1
Bn110	15	13	25	31	16	15	11,14	11	10	11	23	11	12	14	11	20	1	0.0015	MF-1
Bn111	15	13	25	31	17	15	10,14	13	10	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn112	15	13	25	31	16	15	16,20	13	10	12	21	13	11	14	10	18	1	0.0015	MF-1
Bn113	15	13	25	31	16	15	10,14	13	11	10	23	11	12	14	11	21	1	0.0015	MF-1
Bn114	15	13	25	31	16	15	11,15	13	11	10	23	11	13	14	11	21	1	0.0015	MF-1
Bn115	15	13	25	31	18	15	11,15	13	11	10	23	11	11	14	11	21	1	0.0015	MF-1
Bn116	15	13	25	31	17	15	15,19	14	12	11	17	13	11	14	10	18	1	0.0015	MF-1
Bn117	15	13	26	31	15	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	MF-3
Bn118	16	13	24	32	17	15	11,14	13	10	10	23	11	12	14	11	21	1	0.0015	MF-1
Bn119	14	14	23	29	16	15	13,19	14	10	10	25	10	12	14	11	19	1	0.0015	MF-1
Bn120	16	14	24	29	16	15	12,20	13	10	11	24	10	12	16	11	19	1	0.0015	MF-1
Bn121	15	14	21	30	17	15	16,17	12	10	11	20	11	11	14	9	19	1	0.0015	MF-1
Bn122	15	14	21	30	16	15	15,18	12	11	11	22	11	12	14	9	19	1	0.0015	MF-1
Bn123	15	14	22	30	19	15	15,17	12	9	11	20	11	12	14	9	19	1	0.0015	MF-1
Bn124	15	14	22	30	19	15	15,16	12	10	11	20	11	12	15	9	19	1	0.0015	MF-1
Bn125	15	14	22	30	15	15	15,17	12	10	12	20	11	12	14	9	20	1	0.0015	MF-1
Bn126	15	14	22	30	18	15	16,17	12	10	11	20	11	12	14	9	19	1	0.0015	MF-7
Bn127	15	14	22	30	18	15	14,18	12	11	12	20	11	12	14	9	19	1	0.0015	MF-1
Bn128	16	14	22	30	16	15	15,20	12	11	11	20	11	12	14	9	20	1	0.0015	MF-1
Bn129	16	14	23	30	18	15	15,19	13	10	12	24	10	11	16	11	20	1	0.0015	MF-1
Bn130	14	14	23	30	17	15	13,17	14	10	11	26	10	12	15	11	19	1	0.0015	MF-2
Bn131	15	14	24	30	16	15	11,15	13	10	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn132	15	14	22	31	17	15	15,18	12	10	11	20	11	12	14	9	19	1	0.0015	MF-1
Bn133	16	14	22	31	16	15	15,18	12	10	11	20	11	12	14	9	19	1	0.0015	MF-1
Bn134	15	14	23	31	19	15	13,18	14	10	11	25	10	13	16	11	19	1	0.0015	MF-1
Bn135	15	14	23	31	15	15	13,18	14	11	10	25	10	12	16	11	19	1	0.0015	MF-1
Bn136	15	14	24	31	16	15	11,15	14	11	10	23	11	13	14	11	21	1	0.0015	MF-1
Bn137	15	14	25	31	16	15	10,14	13	10	11	23	11	12	14	11	20	1	0.0015	MF-1
Bn138	15	14	25	31	16	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	MF-12
Bn139	15	14	25	31	17	15	11,14	13	10	10	23	11	13	14	11	19	1	0.0015	MF-1
Bn140	15	14	25	31	16	15	11,14	13	10	10	23	11	13	14	12	20	1	0.0015	MF-2
Bn141	15	14	25	31	17	15	11,15	13	10	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn142	15	14	25	31	18	15	11,14	13	10	10	23	13	13	14	11	20	1	0.0015	MF-1
Bn143	15	14	25	31	16	15	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn144	15	14	27	31	17	15	11,15	13	10	10	24	11	13	14	11	20	1	0.0015	MF-1
Bn145	15	14	23	32	18	15	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn146	15	14	24	32	17	15	11,14	13	10	10	23	11	12	14	11	20	1	0.0015	MF-3
Bn147	16	14	25	32	17	15	11,14	13	9	10	24	11	11	14	11	20	1	0.0015	MF-1
Bn148	15	14	25	32	14	15	11,14	13	10	10	23	11	14	14	11	20	1	0.0015	MF-1
Bn149	15	14	25	32	15	15	11,14	13	10	10	23	11	13	14	11	20	2	0.0029	MF-5
Bn150	15	14	25	32	16	15	11,14	14	11	11	23	11	12	14	11	20	1	0.0015	MF-1
Bn151	13	15	22	29	16	15	14,16	12	10	11	20	11	11	14	9	19	1	0.0015	MF-1

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Bn152	15	15	22	31	19	15	16,16	12	10	12	19	11	13	14	9	19	1	0.0015	MF-1
Bn153	15	15	22	31	18	15	9,18	12	10	12	21	15	11	16	10	20	1	0.0015	MF-1
Bn154	17	15	22	32	17	15	15,19	12	10	10	20	11	11	14	9	19	1	0.0015	MF-1
Bn155	15	15	25	33	17	15	12,13	13	10	12	23	11	12	14	11	20	1	0.0015	MF-1
Bn156	15	12	22	28	17	16	16,17	12	10	11	21	12	12	14	9	19	1	0.0015	MF-1
Bn157	13	12	24	28	16	16	13,16	12	10	12	21	11	11	15	9	19	1	0.0015	MF-1
Bn158	16	12	24	28	18	16	13,17	13	11	11	20	11	12	15	10	19	1	0.0015	MF-1
Bn159	13	12	25	28	18	16	11,16	12	10	11	20	11	11	15	9	19	1	0.0015	MF-1
Bn160	16	12	23	29	14	16	15,18	14	10	11	21	12	10	15	10	20	1	0.0015	MF-1
Bn161	15	13	23	28	16	16	11,17	14	10	11	23	11	11	14	10	20	1	0.0015	MF-1
Bn162	16	13	23	28	17	16	13,18	14	10	11	24	11	12	15	11	19	1	0.0015	MF-1
Bn163	15	13	22	29	17	16	15,17	12	10	12	21	11	13	14	9	19	1	0.0015	MF-1
Bn164	13	13	24	29	16	16	13,15	12	10	11	21	11	11	15	9	19	1	0.0015	MF-1
Bn165	13	13	24	29	16	16	13,19	13	10	12	22	11	11	16	9	19	1	0.0015	MF-1
Bn166	15	13	24	29	15	16	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn167	15	13	24	29	16	16	11,14	13	11	10	23	11	12	14	11	20	1	0.0015	MF-2
Bn168	15	13	25	29	15	16	11,13	13	10	10	23	11	12	14	12	20	1	0.0015	MF-1
Bn169	15	13	25	29	16	16	16,18	14	11	12	21	13	11	14	10	18	1	0.0015	MF-1
Bn170	15	13	26	29	18	16	16,20	14	10	12	22	13	12	14	10	17	1	0.0015	MF-1
Bn171	14	13	22	30	16	16	16,17	12	10	11	21	11	11	14	8	19	1	0.0015	MF-1
Bn172	17	13	24	30	18	16	11,15	13	10	12	23	11	13	14	11	19	1	0.0015	MF-1
Bn173	13	13	24	30	18	16	13,13	13	10	11	21	11	12	14	9	19	1	0.0015	MF-1
Bn174	16	13	24	30	16	16	11,14	13	11	10	24	11	12	14	11	20	1	0.0015	MF-1
Bn175	15	13	24	30	14	16	11,15	13	11	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn176	15	13	25	30	17	16	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	MF-5
Bn177	16	13	25	30	14	16	12,13	14	10	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn178	15	13	25	30	15	16	11,14	13	11	10	23	11	13	14	11	21	1	0.0015	MF-1
Bn179	17	13	25	30	16	16	12,14	13	11	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn180	15	13	24	31	17	16	11,14	13	10	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn181	16	13	24	31	18	16	11,14	13	10	10	23	11	12	14	11	21	1	0.0015	MF-1
Bn182	15	13	24	31	16	16	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	MF-4
Bn183	15	13	24	31	16	16	11,14	13	11	10	24	11	12	14	11	20	1	0.0015	MF-2
Bn184	15	13	25	31	16	16	11,14	13	10	10	23	11	12	14	11	21	1	0.0015	MF-1
Bn185	15	13	25	31	17	16	11,14	13	10	10	24	11	12	14	11	20	1	0.0015	MF-1
Bn186	15	13	25	31	17	16	11,15	13	10	10	23	11	13	14	11	20	1	0.0015	MF-2
Bn187	15	13	25	31	16	16	11,14	14	10	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn188	15	13	26	31	16	16	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	MF-2
Bn189	15	13	25	32	17	16	11,14	13	10	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn190	15	13	25	32	18	16	11,14	14	11	11	23	9	12	14	11	20	1	0.0015	MF-1
Bn191	16	13	25	33	17	16	11,15	13	10	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn192	16	14	22	30	16	16	15,17	12	10	11	20	11	12	14	9	20	1	0.0015	MF-1
Bn193	15	14	23	30	15	16	13,18	13	10	10	25	10	12	16	11	19	1	0.0015	MF-1
Bn194	15	14	23	30	17	16	14,19	13	10	10	25	10	12	16	11	19	1	0.0015	MF-1
Bn195	13	14	25	30	15	16	13,17	13	10	12	21	11	11	14	9	20	1	0.0015	MF-1
Bn196	15	14	23	31	17	16	15,17	12	10	12	20	11	12	14	9	19	1	0.0015	MF-1
Bn197	15	14	25	31	16	16	11,14	13	10	10	25	11	12	14	11	20	1	0.0015	MF-1
Bn198	16	14	22	32	18	16	15,17	14	10	10	24	10	12	14	9	19	1	0.0015	MF-1
Bn199	14	14	23	32	15	16	10,15	13	11	11	25	8	12	14	11	20	1	0.0015	MF-1
Bn200	16	14	25	32	15	16	11,14	13	10	10	24	11	13	14	11	19	1	0.0015	MF-1
Bn201	15	14	25	32	16	16	11,15	13	10	10	23	11	11	14	11	20	1	0.0015	MF-1
Bn202	16	14	25	32	16	16	11,14	14	11	10	23	11	12	14	11	20	1	0.0015	MF-1

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Bn203	16	14	25	32	15	16	11,15	14	11	11	23	11	12	13	11	20	1	0.0015	MF-1
Bn204	15	14	25	33	15	16	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn205	15	14	25	33	16	16	11,14	13	11	10	24	11	13	14	11	21	1	0.0015	MF-1
Bn206	16	13	22	29	18	17	16,16	12	11	11	22	11	11	14	9	19	1	0.0015	MF-1
Bn207	13	13	23	30	16	17	13,17	12	10	12	21	11	11	15	9	20	1	0.0015	MF-1
Bn208	17	13	25	31	14	17	11,14	13	10	11	23	11	13	14	11	20	1	0.0015	MF-2
Bn209	18	13	25	31	16	17	11,14	13	12	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn210	15	14	25	31	17	17	11,14	13	10	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn211	15	14	25	32	19	17	9,14	14	11	13	20	11	12	14	11	19	1	0.0015	MF-1
Bn212	15	14	25	30	15	16	14,17	14	9	13	24	10	12	15	11	19	1	0.0015	MF-1
Bn213	17	13	23	28	18	14	13,18	15	10	10	24	10	12	16	11	18	1	0.0015	MF-1
Bn214	16	13	24	30	17	14	16,17	13	10	11	18	11	12	14	10	19	1	0.0015	MF-1
Bn215	15	13	25	31	16	16	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn216	17	14	21	30	17	17	15,17	12	10	12	23	11	12	14	10	19	1	0.0015	MF-2
Bn217	14	14	24	30	17	15	15,19	14	10	12	21	13	11	14	10	18	1	0.0015	MF-1
Bn218	15	14	23	31	13	14	14,21	13	10	11	21	12	11	14	9	20	1	0.0015	MF-1
Bn219	14	12	23	28	16	15	13,17	13	11	11	21	11	11	14	9	19	1	0.0015	MF-1
Bn220	15	13	25	30	16	15	12,14	13	10	10	23	11	13	14	12	20	1	0.0015	MF-1
Bn221	15	13	23	30	14	14	14,20	13	10	11	21	11	12	14	9	20	1	0.0015	NMF
Bn222	15	13	24	31	15	16	12,14	13	11	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn223	15	13	23	28	16	15	14,16	12	10	13	21	11	11	14	10	20	1	0.0015	MF-1
Bn224	15	14	24	32	16	15	11,14	13	10	10	24	11	13	14	11	20	1	0.0015	MF-1
Bn225	15	14	22	30	16	15	17,17	12	10	11	20	11	11	14	10	19	1	0.0015	NMF
Bn226	15	14	24	30	18	16	12,13	12	10	13	21	11	12	14	10	19	1	0.0015	MF-1
Bn227	15	12	22	28	18	17	14,16	14	10	11	21	11	12	15	10	21	1	0.0015	MF-1
Bn228	15	13	25	30	16	16	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	MF-25
Bn229	15	14	25	31	15	15	11,14	13	10	10	23	11	11	14	11	20	1	0.0015	MF-2
Bn230	16	12	25	29	15	14	13,18	13	10	12	24	14	11	15	11	18	1	0.0015	NMF
Bn231	16	13	25	29	18	15	15,17	12	10	12	20	11	12	14	9	19	1	0.0015	NMF
Bn232	16	14	23	31	17	14	13,18	15	10	11	25	10	11	16	11	19	1	0.0015	MF-1
Bn233	15	14	23	30	17	15	13,15	14	10	11	24	10	12	16	11	19	1	0.0015	MF-1
Bn234	15	13	25	31	17	16	11,14	13	11	11	23	11	14	14	11	20	1	0.0015	MF-1
Bn235	16	13	24	29	14	15	12,17	12	9	12	22	11	12	14	9	21	1	0.0015	NMF
Bn236	15	13	25	30	17	16	11,14	13	11	11	23	11	12	14	11	20	2	0.0029	MF-1
Bn237	15	13	24	31	16	15	11,14	13	10	10	23	11	13	14	11	20	2	0.0029	MF-3
Bn238	15	13	25	31	17	16	11,14	12	11	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn239	16	14	22	30	17	14	13,17	12	10	12	20	11	13	14	9	19	1	0.0015	NMF
Bn240	16	13	23	33	18	14	13,17	13	10	10	26	10	12	16	11	19	1	0.0015	MF-1
Bn241	15	14	25	32	16	16	11,13	13	10	10	23	11	12	15	11	20	1	0.0015	MF-1
Bn242	16	13	23	30	17	14	12,18	13	10	12	25	10	12	16	11	19	1	0.0015	MF-1
Bn243	13	14	23	30	16	15	13,17	12	10	12	23	11	12	15	9	18	1	0.0015	MF-1
Bn244	15	13	24	29	15	16	13,17	12	10	12	21	11	11	15	9	19	1	0.0015	MF-1
Bn245	15	12	25	29	20	14	13,14	12	10	12	23	13	12	15	10	20	1	0.0015	MF-1
Bn246	15	13	22	30	17	14	15,19	13	10	13	21	11	12	14	9	21	1	0.0015	MF-1
Bn247	15	14	22	31	18	15	15,18	12	10	11	20	11	12	14	9	19	1	0.0015	MF-2
Bn248	15	13	23	31	16	14	14,20	13	10	11	23	12	13	14	9	19	1	0.0015	NMF
Bn249	16	13	24	28	17	15	12,14	13	10	10	23	11	11	14	11	20	1	0.0015	MF-1
Bn250	15	13	23	29	18	14	13,14	14	10	11	25	13	11	16	11	19	1	0.0015	NMF
Bn251	15	12	24	30	17	15	13,17	14	10	11	22	14	12	14	11	19	1	0.0015	NMF
Bn252	15	14	25	32	16	15	10,14	13	10	10	24	11	13	14	11	20	1	0.0015	MF-1
Bn253	16	14	22	28	16	15	15,18	12	10	11	21	11	11	14	9	19	1	0.0015	MF-1

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Bn254	15	14	25	31	17	15	11,14	13	11	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn255	16	13	25	30	16	14	12,18	13	10	11	23	13	11	14	11	19	1	0.0015	MF-1
Bn256	15	12	24	27	17	14	13,18	12	10	12	21	14	12	15	11	20	1	0.0015	MF-7
Bn257	15	13	24	30	15	14	14,19	13	10	13	21	11	11	15	9	19	1	0.0015	MF-1
Bn258	16	14	25	31	16	15	11,14	13	10	10	23	11	12	14	11	20	1	0.0015	MF-7
Bn259	15	13	23	30	14	14	14,14	13	10	11	21	11	13	15	9	19	1	0.0015	NMF
Bn260	15	13	21	29	18	15	15,16	12	10	11	20	11	11	14	8	19	1	0.0015	MF-1
Bn261	17	11	22	27	15	15	13,17	11	10	12	24	14	12	15	10	19	1	0.0015	MF-1
Bn262	19	13	25	32	16	15	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	NMF
Bn263	15	12	22	28	15	15	13,17	11	10	12	25	14	12	15	10	19	1	0.0015	MF-1
Bn264	14	12	23	28	17	17	15,16	13	11	11	21	10	11	15	8	21	1	0.0015	MF-1
Bn265	15	13	25	31	16	16	11,15	13	11	10	23	11	12	14	11	20	1	0.0015	MF-2
Bn266	17	13	24	30	17	15	12,12	14	10	11	19	8	12	14	11	19	1	0.0015	NMF
Bn267	15	13	24	29	17	15	16,16	13	10	11	18	11	12	14	10	20	1	0.0015	MF-1
Bn268	16	13	23	30	18	14	15,15	14	10	12	18	12	11	14	10	19	1	0.0015	NMF
Bn269	15	14	23	30	16	14	13,19	14	9	12	24	10	11	16	11	19	1	0.0015	NMF
Bn270	14	14	22	32	17	14	14,19	12	10	10	18	11	12	14	10	19	1	0.0015	NMF
Bn271	15	13	24	30	16	15	12,14	13	10	10	23	12	13	14	11	20	1	0.0015	NMF
Bn272	15	14	24	28	15	15	11,15	13	10	11	23	12	13	14	11	20	1	0.0015	NMF
Bn273	16	13	24	30	16	15	12,12	14	10	11	19	13	12	14	11	19	1	0.0015	NMF
Bn274	15	13	24	30	17	16	11,14	13	11	10	23	9	12	14	11	20	1	0.0015	NMF
Bn275	14	14	25	28	19	13	11,13	13	10	10	23	13	12	14	11	18	1	0.0015	NMF
Bn276	13	14	24	30	16	15	13,19	12	10	12	22	11	11	15	9	18	1	0.0015	NMF
Bn277	15	14	21	30	17	15	16,18	12	10	11	20	11	11	14	9	19	1	0.0015	MF-1
Bn278	16	13	23	29	16	15	13,19	13	10	10	24	10	12	16	11	19	2	0.0029	MF-1
Bn279	15	13	22	30	15	14	13,19	13	10	11	21	11	12	14	9	20	1	0.0015	MF-1
Bn280	14	12	24	28	20	14	14,19	12	10	11	21	14	12	15	11	20	1	0.0015	MF-1
Bn281	15	13	25	31	16	15	11,13	13	10	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn282	14	13	23	29	18	15	13,19	15	10	11	25	10	12	16	11	19	1	0.0015	MF-1
Bn283	13	12	24	28	18	17	11,15	12	10	12	20	11	11	15	9	19	1	0.0015	NMF
Bn284	15	13	25	30	16	15	15,17	14	10	11	22	13	11	14	10	18	1	0.0015	MF-1
Bn285	15	14	23	31	17	14	13,19	15	10	11	25	10	12	16	11	19	1	0.0015	MF-1
Bn286	15	14	23	30	19	14	13,21	14	10	10	24	10	12	16	11	20	1	0.0015	MF-1
Bn287	16	12	25	30	17	15	11,14	13	11	10	23	11	12	14	11	20	1	0.0015	NMF
Bn288	13	12	24	28	17	15	13,17	13	11	12	20	11	11	15	9	19	1	0.0015	MF-1
Bn289	17	13	24	30	15	16	11,15	13	10	10	23	11	13	14	11	20	1	0.0015	MF-1
Bn290	15	13	22	29	18	14	15,17	12	10	11	21	11	12	14	9	19	1	0.0015	MF-1
Bn291	15	13	25	30	16	15	11,11	13	10	10	23	12	13	14	11	20	1	0.0015	NMF
Bn292	15	12	24	28	16	14	13,19	12	10	11	21	14	11	15	11	20	1	0.0015	MF-1
Bn293	15	13	21	29	17	15	16,16	13	10	11	20	11	11	14	8	19	1	0.0015	NMF
Bn294	16	13	24	30	16	15	11,15	12	10	10	23	11	12	14	11	20	1	0.0015	NMF
Bn295	16	13	24	30	17	15	12,12	14	10	12	19	11	12	14	11	19	1	0.0015	MF-1
Bn296	15	13	24	32	15	16	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	NMF
Bn297	16	12	23	28	18	14	13,21	12	10	11	20	12	13	15	11	20	1	0.0015	NMF
Bn298	15	14	26	32	16	15	11,15	12	10	11	23	11	13	14	11	20	1	0.0015	NMF
Bn299	15	14	23	30	16	14	15,20	12	10	13	22	11	11	14	9	20	1	0.0015	NMF
Bn300	17	13	24	29	16	16	12,12	14	10	11	19	11	12	14	11	19	1	0.0015	NMF
Bn301	15	12	22	27	15	14	13,17	11	11	13	24	13	12	15	10	19	1	0.0015	NMF
Bn302	16	13	25	31	16	15	11,14	13	10	11	23	12	12	14	11	20	1	0.0015	NMF
Bn303	15	13	23	30	17	14	13,13	12	10	12	26	13	12	14	11	19	1	0.0015	NMF
Bn304	16	14	24	31	16	15	11,14	13	10	11	23	12	12	14	11	20	1	0.0015	NMF

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Bn305	13	15	24	30	16	16	11,11	13	11	10	23	11	12	14	11	19	1	0.0015	NMF
Bn306	15	14	23	30	17	14	13,20	14	10	12	24	12	11	14	11	19	1	0.0015	NMF
Bn307	15	13	25	30	17	16	11,14	13	11	10	23	11	13	14	11	19	1	0.0015	MF-2
Bn308	15	14	23	30	19	15	13,18	14	10	12	25	10	12	17	11	19	1	0.0015	NMF
Bn309	15	14	24	31	15	14	16,17	13	11	11	24	11	12	14	9	20	1	0.0015	NMF
Bn310	16	12	22	28	16	14	14,17	11	10	12	24	14	11	15	11	19	1	0.0015	NMF
Bn311	16	13	22	28	17	15	14,18	13	10	11	21	11	12	14	9	19	1	0.0015	NMF
Bn312	16	14	23	32	19	14	13,19	15	10	11	25	10	12	16	12	19	1	0.0015	NMF
Bn313	15	13	21	29	17	15	15,16	12	10	12	20	11	11	14	8	19	1	0.0015	NMF
Bn314	15	14	25	32	16	15	11,14	13	10	10	23	11	13	14	11	20	3	0.0045	MF-8
Bn315	14	13	25	30	16	15	15,19	14	11	11	21	13	10	14	10	18	1	0.0015	NMF
Bn316	16	13	23	29	22	14	12,17	12	10	12	24	11	12	14	10	21	1	0.0015	NMF
Bn317	14	13	24	30	16	16	11,14	13	11	10	23	11	12	14	11	20	1	0.0015	NMF
Bn318	16	13	24	29	14	15	12,18	13	10	11	21	11	11	14	10	19	1	0.0015	NMF
Bn319	15	14	25	31	15	15	11,14	13	10	10	23	11	12	14	11	20	1	0.0015	NMF
Bn320	15	14	23	30	15	14	11,12	12	11	11	23	14	13	14	11	20	1	0.0015	NMF
Bn321	16	12	23	30	15	15	13,13	13	10	12	21	15	12	14	10	18	1	0.0015	NMF
Bn322	16	13	25	30	14	16	11,14	13	11	10	23	11	12	14	11	20	1	0.0015	MF-2
Bn323	16	14	22	29	17	16	15,17	12	10	11	21	11	12	14	9	19	1	0.0015	NMF
Bn324	15	15	22	31	17	15	16,16	12	10	12	21	12	11	14	9	19	1	0.0015	NMF
Bn325	14	13	23	31	12	14	14,17	15	10	12	19	11	11	14	10	19	1	0.0015	NMF
Bn326	15	14	25	31	18	16	11,14	13	11	10	23	11	12	14	11	20	1	0.0015	NMF
Bn327	16	14	24	29	16	15	15,18	14	10	12	23	13	11	14	10	18	1	0.0015	NMF
Bn328	15	13	23	29	**18.2**	14	12,18	12	10	13	20	11	11	14	10	20	1	0.0015	NMF
Bn329	15	14	22	30	17	15	16,16	12	10	9	21	11	11	13	9	20	1	0.0015	NMF
Bn330	15	14	25	32	16	15	11,14	14	10	10	24	11	12	14	11	20	1	0.0015	NMF
Bn331	15	14	23	30	17	14	13,19	14	10	10	25	10	14	15	11	19	1	0.0015	NMF
Bn332	15	9	25	25	15	15	11,15	13	10	10	23	11	13	14	11	20	1	0.0015	NMF
Bn333	15	13	25	32	15	16	11,14	13	11	9	23	11	12	13	11	20	1	0.0015	NMF
Bn334	17	14	22	30	17	14	14,17	12	10	11	21	11	12	14	9	19	1	0.0015	NMF
Bn335	16	14	22	29	15	15	15,16	12	10	11	20	11	12	14	9	19	1	0.0015	NMF
Bn336	15	13	25	30	17	16	11,14	13	11	12	23	11	12	14	11	20	1	0.0015	NMF
Bn337	15	13	25	30	16	15	11,13	13	11	11	23	11	13	14	11	20	1	0.0015	NMF
Bn338	15	13	25	30	16	16	13,14	13	11	10	23	11	13	14	11	20	1	0.0015	NMF
Bn339	17	14	22	33	18	15	15,16	12	10	11	20	11	12	15	9	19	1	0.0015	NMF
Bn340	13	12	23	29	16	15	12,17	13	10	12	20	11	11	15	9	20	2	0.0029	NMF
Bn341	15	14	22	31	16	15	15,16	12	10	11	20	11	12	14	9	19	1	0.0015	NMF
Bn342	15	13	21	29	15	15	17,18	12	10	12	20	11	12	14	8	19	1	0.0015	NMF
Bn343	15	13	25	31	16	15	11,15	13	10	10	24	11	13	14	11	20	1	0.0015	NMF
Bn344	14	13	24	28	17	14	13,16	12	10	11	21	11	13	15	9	20	1	0.0015	NMF
Bn345	14	13	25	31	16	16	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	NMF
Bn346	15	12	24	27	19	15	13,19	12	10	11	20	14	13	15	11	20	1	0.0015	NMF
Bn347	16	13	25	32	15	15	11,14	13	11	10	24	11	13	14	11	20	1	0.0015	NMF
Bn348	12	13	21	29	17	15	15,16	12	10	11	20	11	11	14	8	19	1	0.0015	NMF
Bn349	15	13	25	31	16	15	11,16	13	10	12	24	11	12	14	11	20	1	0.0015	NMF
Bn350	14	13	25	31	16	16	12,13	13	10	10	23	11	12	14	11	20	1	0.0015	NMF
Bn351	16	13	25	28	16	16	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	NMF
Bn352	15	13	22	30	18	14	15,16	12	10	10	21	12	12	14	11	19	1	0.0015	NMF
Bn353	13	14	22	30	18	13	15,15	12	10	11	20	11	11	14	10	20	1	0.0015	NMF
Bn354	15	14	24	30	17	15	11,15	13	10	10	23	11	12	14	11	19	1	0.0015	NMF
Bn355	15	13	23	30	15	14	13,19	13	10	11	21	12	12	14	9	20	1	0.0015	NMF

Haplotype/ Locus	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a/b	DYS393	DYS391	DYS439	DYS635	DYS392	YGATAH4	DYS437	DYS438	DYS448	*Individual (N)*	*Frequency (F)*	*Searched in YHRD*
Bn356	15	13	23	28	17	14	13,17	14	10	10	24	10	12	16	8	19	1	0.0015	NMF
Bn357	15	15	24	32	17	15	12,12	14	10	11	19	11	12	14	11	19	1	0.0015	NMF
Bn358	17	13	25	30	15	15	11,14	14	11	10	23	12	12	14	11	20	1	0.0015	NMF
Bn359	15	13	23	29	17	13	14,19	14	10	10	25	10	11	16	11	19	1	0.0015	NMF
Bn360	15	13	24	29	16	14	14,20	14	10	10	24	10	12	16	11	18	1	0.0015	NMF
Bn361	15	14	22	30	18	15	15,19	12	10	11	21	11	11	14	9	19	1	0.0015	NMF
Bn362	15	13	23	30	15	14	14,14	13	10	11	21	11	12	15	9	20	1	0.0015	MF-1
Bn363	14	13	26	30	16	15	11,14	13	10	11	23	11	11	14	11	20	1	0.0015	NMF
Bn364	15	14	23	30	17	15	12,21	13	10	11	24	10	12	15	11	19	1	0.0015	NMF
Bn365	15	13	23	30	15	14	14,19	13	10	11	21	11	12	14	9	20	1	0.0015	MF-1
Bn366	15	14	24	32	17	15	11,14	13	10	10	24	11	13	13	11	20	1	0.0015	NMF
Bn367	16	14	22	30	17	15	13,17	12	10	12	20	11	13	14	9	19	1	0.0015	NMF
Bn368	14	14	22	30	16	15	15,17	12	10	10	23	11	12	14	9	19	1	0.0015	NMF
Bn369	15	13	25	31	17	15	11,15	13	11	10	23	11	12	15	11	21	1	0.0015	NMF
Bn370	16	13	25	29	16	16	11,14	13	11	11	23	11	13	14	11	19	1	0.0015	NMF
Bn371	15	13	23	29	17	14	12,18	14	10	10	24	10	12	16	11	19	1	0.0015	MF-16
Bn372	16	14	22	30	17	15	15,18	12	10	11	20	11	12	14	9	19	1	0.0015	MF-1
Bn373	15	14	24	30	17	14	14,18	12	10	10	20	11	11	14	10	17	1	0.0015	NMF
Bn374	15	13	23	29	18	15	11,17	14	11	10	24	10	12	16	11	19	1	0.0015	NMF
Bn375	15	13	25	30	16	16	11,14	13	11	11	23	11	14	14	11	20	1	0.0015	NMF
Bn376	16	13	22	29	18	15	15,17	12	10	12	20	11	12	14	9	19	1	0.0015	NMF
Bn377	15	13	22	30	17	15	15,19	12	10	10	20	11	12	14	9	19	1	0.0015	NMF
Bn378	14	14	25	32	16	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	MF-2
Bn379	15	14	25	32	17	15	12,14	13	10	10	23	11	13	14	11	20	1	0.0015	NMF
Bn380	16	13	25	30	15	15	15,21	14	11	13	22	13	11	14	10	18	1	0.0015	NMF
Bn381	15	14	23	31	15	15	14,19	13	11	10	25	10	12	16	11	19	1	0.0015	NMF
Bn382	13	12	23	28	17	15	13,18	12	10	12	22	11	10	15	9	19	1	0.0015	NMF
Bn383	16	12	23	29	18	14	12,18	14	10	11	25	10	12	16	11	19	1	0.0015	NMF
Bn384	15	12	22	28	16	15	12,16	14	10	11	21	11	12	16	10	21	1	0.0015	NMF
Bn385	15	14	25	32	16	15	11,14	13	10	11	23	11	12	14	11	20	1	0.0015	NMF
Bn386	14	13	24	28	17	14	13,15	13	10	11	20	11	11	14	10	18	1	0.0015	NMF
Bn387	15	14	24	30	17	14	13,15	14	10	10	25	10	12	15	12	19	1	0.0015	NMF
Bn388	16	13	21	30	17	15	13,17	13	11	13	22	11	11	14	10	19	1	0.0015	NMF
Bn389	16	12	23	28	19	14	13,19	12	10	11	20	14	13	15	11	20	1	0.0015	NMF
Bn390	16	13	25	29	15	15	12,15	12	11	13	23	13	12	15	12	19	1	0.0015	NMF
Bn391	16	12	23	28	19	14	13,21	12	10	12	20	14	13	15	11	20	1	0.0015	NMF
Bn392	15	13	22	29	17	15	15,17	12	10	11	20	11	12	14	9	19	1	0.0015	MF-4
Bn393	16	13	22	29	19	15	14,17	12	10	12	20	11	12	14	9	19	1	0.0015	NMF
Bn394	16	13	25	31	16	15	11,14	13	11	14	21	11	12	14	11	18	1	0.0015	NMF
Bn395	14	12	24	29	15	15	12,18	12	10	12	22	11	10	15	9	19	1	0.0015	NMF
Bn396	15	14	23	29	20	14	13,20	14	11	11	24	10	12	16	11	19	1	0.0015	NMF
Bn397	15	13	25	30	16	13	13,16	13	10	12	22	13	13	15	11	19	1	0.0015	NMF
Bn398	16	14	22	31	17	15	16,17	12	11	13	20	11	12	14	9	19	1	0.0015	NMF
Bn399	14	13	23	29	17	14	15,16	13	11	12	21	11	11	14	10	18	1	0.0015	NMF
Bn400	15	13	22	29	17	15	15,15	12	10	11	20	11	11	14	8	19	1	0.0015	NMF
Bn401	16	13	25	29	15	15	15,18	16	11	12	22	13	11	14	10	18	1	0.0015	NMF
Bn402	16	14	25	31	16	15	19,21	14	10	13	22	13	11	14	10	18	1	0.0015	NMF
Bn403	15	12	23	28	18	14	12,20	12	10	11	20	14	12	16	11	20	1	0.0015	NMF
Bn404	16	14	22	32	18	15	16,17	12	10	12	20	11	12	14	9	19	1	0.0015	NMF
Bn405	13	12	26	28	16	14	14,16	13	11	13	21	11	11	15	9	19	1	0.0015	NMF
Bn406	15	13	23	28	16	15	11,17	14	10	11	22	11	12	14	10	21	1	0.0015	NMF

Haplotype/ Locus	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a/b	DYS393	DYS391	DYS439	DYS635	DYS392	YGATAH4	DYS437	DYS438	DYS448	*Individual (N)*	*Frequency (F)*	*Searched in YHRD*
Bn407	15	13	25	31	16	15	11,14	13	11	10	23	11	13	14	11	19	1	0.0015	MF-1
Bn408	15	14	25	28	17	15	15,19	14	10	12	21	13	11	14	10	18	1	0.0015	NMF
Bn409	16	12	22	28	14	14	13,16	11	10	14	25	14	13	15	10	19	1	0.0015	NMF
Bn410	16	13	23	30	17	14	13,18	13	10	12	25	10	12	16	11	19	1	0.0015	NMF
Bn411	15	13	25	29	15	16	11,14	13	11	10	23	11	12	14	11	20	1	0.0015	MF-5
Bn412	15	13	26	31	16	16	11,15	13	11	10	23	11	13	14	11	20	1	0.0015	NMF
Bn413	15	13	26	31	16	16	12,13	13	10	12	23	11	13	14	11	20	1	0.0015	NMF
Bn414	16	13	23	29	17	15	15,17	12	10	11	20	11	12	14	9	19	1	0.0015	NMF
Bn415	15	14	23	30	17	14	13,20	15	11	12	26	10	11	16	11	19	1	0.0015	NMF
Bn416	17	13	22	31	16	16	15,16	13	9	11	20	11	12	14	9	19	1	0.0015	NMF
Bn417	15	14	22	31	18	15	15,17	12	10	12	20	11	12	14	9	19	1	0.0015	NMF
Bn418	15	14	25	33	16	15	11,14	13	10	10	24	11	13	14	11	19	2	0.0029	NMF
Bn419	15	13	25	30	17	16	11,14	13	11	10	23	11	12	14	11	20	1	0.0015	MF-2
Bn420	17	14	23	31	16	15	15,16	12	10	11	22	11	13	14	9	19	1	0.0015	NMF
Bn421	15	13	24	30	16	13	13,19	13	10	12	22	13	12	15	11	19	1	0.0015	NMF
Bn422	12	12	23	28	18	16	11,16	12	10	12	20	11	11	15	9	19	1	0.0015	NMF
Bn423	15	14	25	31	16	15	11,15	13	11	10	23	11	12	14	11	20	1	0.0015	NMF
Bn424	16	14	25	31	16	16	12,14	14	12	10	23	11	13	14	11	20	1	0.0015	NMF
Bn425	15	14	24	32	17	15	11,14	13	10	10	24	11	13	14	11	20	1	0.0015	NMF
Bn426	16	14	22	30	17	14	15,16	12	10	10	20	11	12	14	9	19	1	0.0015	NMF
Bn427	14	13	25	29	17	15	13,15	14	8	11	21	11	12	14	9	21	1	0.0015	NMF
Bn428	14	14	25	32	18	15	11,14	13	10	10	23	11	12	14	11	19	1	0.0015	NMF
Bn429	16	13	24	29	17	16	11,14	13	11	11	23	11	12	14	11	20	1	0.0015	NMF
Bn430	15	13	25	30	14	16	11,14	13	10	10	23	11	12	14	11	20	1	0.0015	NMF
Bn431	15	12	23	29	18	14	13,20	12	10	11	20	14	12	15	11	20	1	0.0015	NMF
Bn432	15	14	26	31	15	16	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	NMF
Bn433	15	13	24	30	13	14	13,16	14	10	11	18	11	11	14	10	17	1	0.0015	NMF
Bn434	15	12	24	29	17	15	13,18	14	10	11	22	14	12	14	11	19	1	0.0015	NMF
Bn435	13	12	23	30	14	15	15,17	13	9	12	21	11	11	15	9	18	1	0.0015	NMF
Bn436	15	13	25	31	15	15	11,15	13	10	10	23	11	13	14	11	20	1	0.0015	NMF
Bn437	16	13	23	30	16	14	14,19	12	9	10	22	11	11	14	10	17	1	0.0015	NMF
Bn438	15	13	23	29	18	14	15,16	12	10	12	20	11	11	14	9	19	1	0.0015	NMF
Bn439	16	13	24	28	17	15	13,20	14	10	12	24	11	11	16	11	22	1	0.0015	NMF
Bn440	14	13	25	32	16	16	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	NMF
Bn441	15	14	23	29	17	14	13,18	14	10	11	24	10	12	14	11	19	1	0.0015	NMF
Bn442	13	12	24	28	15	16	13,17	12	10	13	20	11	10	15	9	19	1	0.0015	NMF
Bn443	15	13	23	28	17	14	12,19	14	10	10	24	10	12	16	11	19	1	0.0015	NMF
Bn444	16	14	22	30	18	15	16,18	12	10	11	20	11	13	14	9	19	1	0.0015	NMF
Bn445	15	13	23	28	16	15	13,18	14	10	10	24	10	11	16	11	19	1	0.0015	NMF
Bn446	16	13	24	30	17	15	12,14	14	10	10	19	11	12	14	11	19	1	0.0015	NMF
Bn447	13	12	25	29	19	16	13,17	12	10	13	21	11	11	15	9	18	1	0.0015	NMF
Bn448	16	13	24	30	15	14	10,14	13	10	10	23	11	13	14	11	20	1	0.0015	NMF
Bn449	15	13	22	31	16	15	11,14	13	11	14	23	11	13	14	11	21	1	0.0015	NMF
Bn450	15	13	24	32	17	16	11,13	13	11	11	24	11	13	14	11	20	1	0.0015	NMF
Bn451	15	12	23	27	19	14	13,20	12	10	11	20	15	12	15	11	19	1	0.0015	NMF
Bn452	14	13	23	32	15	14	16,20	13	11	11	21	11	13	16	9	20	1	0.0015	NMF
Bn453	16	13	22	29	16	14	13,20	14	10	12	24	10	12	16	11	20	1	0.0015	NMF
Bn454	15	12	23	28	18	14	12,17	12	10	12	19	12	12	15	10	19	1	0.0015	MF-7
Bn455	15	13	25	29	16	16	11,14	13	11	10	22	11	13	14	11	20	1	0.0015	NMF
Bn456	16	13	24	28	16	15	15,22	14	10	12	21	13	11	14	11	18	1	0.0015	NMF
Bn457	17	14	24	31	17	15	12,12	14	10	11	19	11	12	14	11	19	2	0.0029	NMF

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Bn458	15	13	23	30	18	14	12,18	14	10	10	26	10	12	16	11	19	1	0.0015	NMF
Bn459	15	14	22	31	16	15	15,18	12	10	11	20	11	12	14	9	19	1	0.0015	NMF
Bn460	16	13	22	29	17	15	16,16	12	11	11	19	11	12	16	9	18	1	0.0015	NMF
Bn461	15	14	25	31	16	15	11,14	13	11	10	23	11	11	14	10	20	1	0.0015	NMF
Bn462	15	14	22	30	17	15	15,17	12	10	12	22	11	12	14	9	19	1	0.0015	NMF
Bn463	15	13	23	31	18	14	14,16	14	10	12	19	11	12	14	10	19	1	0.0015	NMF
Bn464	16	12	23	29	18	14	13,19	14	10	13	25	10	12	16	11	19	1	0.0015	MF-1
Bn465	15	13	25	29	17	16	15,20	14	10	12	21	14	13	14	10	17	1	0.0015	NMF
Bn466	15	14	23	30	18	15	12,18	14	10	11	25	10	13	16	11	19	1	0.0015	NMF
Bn467	15	13	22	29	16	15	15,16	12	10	11	20	11	11	14	8	19	1	0.0015	MF-1
Bn468	15	14	22	30	17	15	16,17	12	10	11	20	11	11	14	9	19	1	0.0015	MF-2
Bn469	15	12	24	28	18	14	13,19	12	11	11	20	13	11	15	11	20	1	0.0015	NMF
Bn470	15	14	22	30	16	15	17,17	12	10	11	20	11	11	14	9	19	1	0.0015	NMF
Bn471	16	14	22	30	17	15	15,17	12	11	12	20	11	11	14	9	19	1	0.0015	NMF
Bn472	16	13	25	29	15	16	11,14	13	10	10	23	11	14	14	11	19	1	0.0015	NMF
Bn473	13	13	24	29	16	15	13,18	13	10	13	20	11	11	15	9	19	2	0.0029	NMF
Bn474	15	13	25	32	16	15	11,14	13	11	11	23	12	12	14	11	20	1	0.0015	NMF
Bn475	16	13	25	30	16	14	13,18	13	10	11	23	13	11	15	11	18	1	0.0015	NMF
Bn476	15	13	25	31	16	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	MF-26
Bn477	15	14	22	30	17	15	15,17	12	11	10	20	11	11	15	9	19	1	0.0015	NMF
Bn478	16	13	24	30	17	15	12,13	14	10	11	19	11	12	14	11	19	1	0.0015	NMF
Bn479	15	13	23	28	17	16	11,16	15	10	12	20	11	11	14	10	21	1	0.0015	NMF
Bn480	16	13	22	29	18	15	15,17	13	10	11	20	11	12	14	9	19	1	0.0015	NMF
Bn481	15	14	22	31	16	15	15,19	12	10	11	20	11	12	14	9	19	1	0.0015	NMF
Bn482	17	12	23	28	18	14	13,19	14	10	13	25	10	12	16	11	19	1	0.0015	NMF
Bn483	14	12	24	29	16	15	13,18	12	10	12	21	11	11	14	9	19	1	0.0015	NMF
Bn484	17	11	23	28	15	15	11,12	13	10	12	22	14	12	14	11	19	1	0.0015	NMF
Bn485	15	13	25	31	16	16	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	MF-10
Bn486	15	14	25	31	16	16	11,14	13	11	10	23	11	14	14	11	20	1	0.0015	NMF
Bn487	14	13	23	29	14	14	16,18	12	10	11	23	11	11	14	9	21	1	0.0015	NMF
Bn488	17	14	25	31	16	15	11,11	13	10	10	23	11	12	14	11	20	1	0.0015	NMF
Bn489	16	13	21	29	18	15	15,17	12	10	11	21	11	12	14	9	19	1	0.0015	NMF
Bn490	16	14	24	31	17	15	11,15	13	10	10	23	11	13	14	11	20	1	0.0015	NMF
Bn491	15	13	22	29	19	15	9,16	12	10	11	22	14	11	16	10	20	1	0.0015	NMF
Bn492	15	14	26	31	17	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	NMF
Bn493	15	12	24	28	18	14	14,16	14	10	13	19	11	12	14	10	19	1	0.0015	NMF
Bn494	15	13	24	29	19	14	14,19	13	10	12	24	11	12	15	9	21	1	0.0015	NMF
Bn495	17	13	22	29	16	15	12,17	13	11	10	19	12	13	15	10	18	1	0.0015	NMF
Bn496	15	13	23	29	17	14	14,17	13	11	10	24	10	12	16	11	19	1	0.0015	NMF
Bn497	14	14	24	30	15	15	13,15	13	10	12	22	11	11	14	9	19	1	0.0015	NMF
Bn498	16	14	21	29	17	16	12,19	14	10	11	26	10	11	16	12	18	1	0.0015	NMF
Bn499	15	13	24	29	18	14	13,20	12	10	13	20	14	12	15	11	20	1	0.0015	NMF
Bn500	14	12	23	28	17	17	14,17	12	11	12	21	10	13	15	11	20	1	0.0015	NMF
Bn501	15	13	24	31	16	16	13,14	14	11	10	23	11	13	14	11	20	1	0.0015	NMF
Bn502	15	13	25	30	19	15	11,14	14	10	13	21	11	12	15	11	19	1	0.0015	NMF
Bn503	16	13	23	30	16	14	14,15	14	10	11	18	12	11	14	10	19	1	0.0015	NMF
Bn504	15	13	24	30	15	14	15,15	12	10	11	21	11	11	15	9	19	1	0.0015	NMF
Bn505	14	14	23	30	17	14	15,17	12	11	11	23	11	11	14	9	21	1	0.0015	NMF
Bn506	15	13	23	29	15	14	13,17	13	10	10	24	10	12	16	11	19	1	0.0015	NMF
Bn507	16	13	23	29	17	14	13,14	13	10	11	19	11	12	14	10	21	1	0.0015	NMF
Bn508	17	13	22	28	17	15	16,17	12	10	10	20	11	11	14	9	20	1	0.0015	NMF

Haplotype/ Locus	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a/b	DYS393	DYS391	DYS439	DYS635	DYS392	YGATAH4	DYS437	DYS438	DYS448	*Individual (N)*	*Frequency (F)*	*Searched in YHRD*
Bn509	16	14	22	31	17	15	15,15	12	10	11	20	11	12	14	9	19	1	0.0015	NMF
Bn510	15	12	24	28	18	14	13,19	12	10	11	20	13	11	15	11	20	1	0.0015	NMF
Bn511	15	13	25	31	16	16	15,20	13	11	13	22	14	11	14	10	18	1	0.0015	NMF
Bn512	16	13	22	29	17	15	16,18	12	10	11	19	11	12	14	10	20	1	0.0015	NMF
Bn513	15	14	24	32	16	15	11,13	13	10	10	23	11	13	14	12	20	1	0.0015	NMF
Bn514	16	14	25	31	16	15	11,14	13	10	10	23	11	12	15	12	21	1	0.0015	NMF
Bn515	15	13	25	30	16	14	13,18	13	10	11	23	14	11	15	11	18	1	0.0015	NMF
Bn516	15	13	23	30	15	14	14,19	13	10	11	22	11	11	14	9	20	1	0.0015	NMF
Bn517	14	13	23	29	16	14	12,18	14	10	11	24	10	12	16	11	19	1	0.0015	NMF
Bn518	15	13	25	30	16	15	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	MF-17
Bn519	15	13	24	30	15	15	11,14	13	10	10	23	11	13	14	11	19	1	0.0015	NMF
Bn520	16	12	24	28	17	14	15,18	12	10	12	20	15	12	15	11	20	1	0.0015	NMF
Bn521	15	13	25	31	16	17	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	NMF
Bn522	17	12	24	28	18	14	13,19	14	10	13	25	10	11	16	11	19	1	0.0015	NMF
Bn523	14	13	23	29	17	15	15,16	12	10	12	20	11	11	14	8	19	1	0.0015	NMF
Bn524	15	13	22	30	19	15	16,19	12	10	11	22	11	11	14	9	19	1	0.0015	NMF
Bn525	16	13	25	31	16	16	11,11	13	10	10	23	11	13	14	11	19	1	0.0015	NMF
Bn526	17	13	25	29	15	16	14,23	14	11	12	22	13	11	14	10	18	1	0.0015	NMF
Bn527	16	13	22	30	18	15	13,18	12	9	10	19	11	13	14	10	17	1	0.0015	NMF
Bn528	15	14	23	31	16	15	13,19	13	10	10	25	10	12	16	11	19	1	0.0015	NMF
Bn529	15	12	25	28	16	15	11,14	13	11	12	24	11	13	14	11	20	1	0.0015	NMF
Bn530	16	13	25	31	16	16	12,14	14	11	10	23	11	13	14	11	20	1	0.0015	NMF
Bn531	15	13	22	29	18	15	16,16	11	11	11	21	11	13	14	9	19	1	0.0015	NMF
Bn532	15	12	23	27	19	17	13,15	11	10	12	21	14	12	15	11	21	1	0.0015	NMF
Bn533	16	13	20	29	17	15	12,19	13	9	12	24	11	11	16	10	19	1	0.0015	NMF
Bn534	15	14	23	30	17	15	13,18	13	10	10	25	10	12	16	11	19	1	0.0015	NMF
Bn535	15	12	22	28	16	14	13,17	11	10	13	23	14	11	15	10	19	1	0.0015	NMF
Bn536	15	13	25	29	17	15	15,18	14	10	12	22	13	11	14	10	18	1	0.0015	MF-1
Bn537	16	13	24	29	17	15	12,12	14	10	11	19	11	12	14	11	19	1	0.0015	NMF
Bn538	16	14	23	31	18	14	13,19	14	10	11	25	10	12	16	13	19	1	0.0015	NMF
Bn539	15	14	22	30	17	15	15,18	11	10	11	20	9	12	14	9	19	1	0.0015	NMF
Bn540	15	13	23	30	18	14	13,17	13	11	10	24	10	11	16	11	19	1	0.0015	NMF
Bn541	16	14	22	30	17	16	14,16	12	10	10	23	11	10	14	10	19	1	0.0015	NMF
Bn542	16	13	21	29	17	15	15,17	12	10	11	20	11	11	14	8	19	1	0.0015	NMF
Bn543	15	14	23	30	18	14	12,18	14	10	10	24	10	12	16	11	19	1	0.0015	NMF
Bn544	15	14	24	31	16	15	11,14	13	11	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn545	15	14	26	31	16	16	11,14	12	11	11	23	11	12	14	11	20	2	0.0029	NMF
Bn546	15	13	25	30	17	16	11,14	12	10	10	25	11	12	14	11	21	1	0.0015	NMF
Bn547	15	12	23	29	18	15	12,16	12	10	12	19	12	12	15	10	19	1	0.0015	MF-3
Bn548	13	14	24	30	16	14	13,18	12	10	11	22	11	10	15	9	18	1	0.0015	NMF
Bn549	14	13	26	30	14	15	11,14	13	10	10	24	11	13	14	11	19	1	0.0015	NMF
Bn550	14	13	26	29	16	14	15,17	13	11	10	20	11	11	14	10	18	1	0.0015	NMF
Bn551	15	14	25	32	16	15	11,14	13	10	10	24	11	13	14	10	20	1	0.0015	NMF
Bn552	15	13	24	30	16	16	11,15	13	11	10	23	11	13	14	11	20	1	0.0015	NMF
Bn553	14	13	26	30	16	14	15,17	13	10	10	20	11	12	14	10	18	1	0.0015	NMF
Bn554	15	14	22	30	14	15	14,17	12	10	11	18	11	11	14	9	19	1	0.0015	NMF
Bn555	12	13	24	30	16	17	13,16	12	10	12	21	11	10	15	9	19	1	0.0015	NMF
Bn556	14	13	24	30	15	15	11,15	13	10	10	24	11	12	14	11	20	1	0.0015	NMF
Bn557	16	12	23	28	18	14	12,18	14	10	10	25	10	12	16	11	19	1	0.0015	NMF
Bn558	15	14	25	32	17	15	11,14	13	10	11	23	11	12	14	11	20	1	0.0015	MF-1
Bn559	15	12	24	29	18	15	12,16	14	10	11	21	11	12	14	11	19	1	0.0015	NMF

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Bn560	16	13	25	28	17	14	13,15	13	11	11	21	11	11	14	10	20	1	0.0015	NMF
Bn561	16	14	24	32	15	15	11,14	13	10	10	25	11	11	14	9	20	1	0.0015	NMF
Bn562	15	13	23	29	15	14	13,17	13	10	11	21	11	11	14	9	20	1	0.0015	MF-1
Bn563	14	14	25	32	17	15	11,14	13	10	10	23	11	12	14	11	20	1	0.0015	MF-1
Bn564	15	13	23	31	15	14	14,18	13	10	12	21	11	12	14	9	20	1	0.0015	NMF
Bn565	17	13	22	29	18	15	15,17	12	10	12	20	11	12	14	9	19	1	0.0015	NMF
Bn566	15	13	26	31	16	16	11,15	13	11	11	23	11	12	14	11	20	1	0.0015	NMF
Bn567	15	13	23	29	17	15	14,18	14	10	10	24	10	11	16	11	19	1	0.0015	NMF
Bn568	15	13	23	30	16	14	14,18	12	10	11	21	11	12	14	9	21	1	0.0015	NMF
Bn569	15	13	25	30	15	16	11,15	13	11	10	23	11	12	14	11	20	1	0.0015	NMF
Bn570	15	13	25	31	16	15	11,15	13	9	10	23	11	12	14	11	20	1	0.0015	NMF
Bn571	15	14	24	32	17	15	11,14	13	10	10	23	11	14	14	11	20	1	0.0015	NMF
Bn572	15	13	23	30	17	16	11,14	12	10	10	25	11	12	14	11	21	1	0.0015	NMF
Bn573	15	13	22	30	16	15	17,17	12	10	11	20	11	12	14	9	19	1	0.0015	NMF
Bn574	16	13	25	30	16	15	13,18	13	10	11	23	13	11	15	11	18	1	0.0015	NMF
Bn575	15	13	23	28	16	14	13,17	12	10	12	22	11	11	15	9	21	1	0.0015	NMF
Bn576	15	13	24	31	16	15	11,14	13	11	10	23	11	13	14	11	20	1	0.0015	MF-5
Bn577	14	13	23	29	16	15	13,17	14	10	11	25	10	11	15	11	19	1	0.0015	NMF
Bn578	15	13	24	28	19	15	13,18	14	10	10	24	10	12	16	11	19	1	0.0015	NMF
Bn579	16	13	23	29	15	14	14,19	11	10	11	21	12	12	15	9	19	1	0.0015	NMF
Bn580	15	14	23	30	17	14	14,19	11	10	13	22	11	11	14	9	21	1	0.0015	NMF
Bn581	15	14	21	31	17	15	12,18	12	10	10	21	11	12	15	10	18	1	0.0015	NMF
Bn582	15	13	22	30	16	15	15,16	13	10	11	20	11	11	15	8	19	1	0.0015	NMF
Bn583	15	14	22	30	17	15	15,18	12	10	11	20	11	11	14	9	19	1	0.0015	NMF
Bn584	15	13	23	28	17	14	14,19	12	10	12	22	11	11	14	9	21	1	0.0015	NMF
Bn585	14	12	24	28	18.2	15	13,17	12	10	11	21	11	11	15	9	18	1	0.0015	NMF
Bn586	15	13	24	30	18	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	NMF
Bn587	14	13	23	30	17	15	12,15	11	10	12	22	11	12	14	10	19	1	0.0015	NMF
Bn588	15	14	25	31	16	17	11,15	12	10	10	23	11	13	14	11	20	1	0.0015	NMF
Bn589	14	13	22	31	18	15	14,18	11	10	10	17	11	12	14	10	19	1	0.0015	NMF
Bn590	15	13	24	30	16	15	12,14	12	11	10	23	11	13	14	11	21	1	0.0015	NMF
Bn591	15	13	22	28	18	15	9,16	11	10	12	20	14	11	16	10	19	1	0.0015	NMF
Bn592	14	13	25	31	15	15	11,14	13	10	10	25	11	12	14	11	20	1	0.0015	NMF
Bn593	16	13	25	30	16	15	11,14	13	10	10	23	11	13	14	9	20	1	0.0015	NMF
Bn594	17	13	24	30	15	15	12,14	13	11	10	23	11	12	14	11	20	1	0.0015	NMF
Bn595	16	14	25	31	16	15	14,21	15	11	12	21	13	11	14	10	18	1	0.0015	NMF
Bn596	15	18	22	29	16	16	15,17	14	10	10	21	11	12	15	10	21	1	0.0015	NMF
Bn597	15	12	22	28	17	14	15,17	11	10	12	24	15	12	15	11	19	1	0.0015	NMF
Bn598	14	14	23	30	17	14	16,19	12	11	12	23	11	13	14	9	21	1	0.0015	NMF
Bn599	17	12	22	28	14	14	13,17	11	10	12	22	14	12	15	10	19	1	0.0015	NMF
Bn600	14	14	24	32	15	15	11,14	13	10	10	23	11	12	14	11	20	1	0.0015	NMF
Bn601	15	14	22	30	17	13	12,19	13	10	10	24	15	10	15	11	19	1	0.0015	NMF
Bn602	15	14	24	32	16	17	11,14	13	10	10	23	11	12	14	11	19	1	0.0015	NMF
Bn603	15	13	23	30	14	14	12,18	12	10	12	22	11	12	14	9	21	1	0.0015	NMF
Bn604	16	12	22	28	20	15	13,19	13	10	11	25	10	12	15	11	19	1	0.0015	NMF
Bn605	12	12	24	29	17	15	13,17	13	10	12	21	11	11	15	9	19	1	0.0015	NMF
Bn606	15	14	23	30	16	14	13,18	11	11	11	21	11	11	15	9	20	1	0.0015	NMF
Bn607	16	14	23	30	18	15	14,19	13	10	12	24	10	11	16	11	20	1	0.0015	NMF
Bn608	15	13	22	30	19	14	14,18	12	10	11	17	11	12	14	11	19	1	0.0015	NMF
Bn609	14	14	23	30	17	14	15,20	12	10	12	24	11	11	14	9	21	1	0.0015	NMF
Bn610	15	14	25	30	16	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0015	MF-1

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Bn611	13	12	24	28	19	16	13,18	12	10	10	20	11	11	15	10	18	1	0.0015	NMF
Bn612	14	14	22	30	17	15	16,17	12	10	13	22	11	12	14	9	19	1	0.0015	NMF
Bn613	15	14	22	30	17	15	16,17	12	10	13	22	11	12	14	9	19	1	0.0015	MF-1
Bn614	17	14	23	30	19	14	13,18	13	10	12	26	10	12	16	11	19	1	0.0015	NMF
Bn615	15	14	24	31	18	15	14,16	11	10	11	21	11	11	15	10	19	1	0.0015	NMF
Bn616	15	13	22	30	18	14	15,19	12	10	10	18	11	11	14	10	20	1	0.0015	NMF
Bn617	13	12	24	29	16	14	13,17	12	10	14	21	11	11	15	9	19	1	0.0015	NMF
Bn618	14	15	23	30	17	14	13,17	14	10	11	27	10	12	15	11	19	1	0.0015	NMF
Bn619	16	12	25	28	17	15	14,21	14	10	13	21	13	11	14	10	18	1	0.0015	NMF
Bn620	16	13	24	30	17	15	14,18	12	10	12	20	11	12	14	9	19	1	0.0015	NMF
Bn621	17	13	22	30	16	16	15,16	13	10	11	20	11	9	14	9	19	1	0.0015	NMF
Bn622	16	13	25	31	16	15	11,15	13	11	10	23	11	11	14	11	20	1	0.0015	NMF
Bn623	15	12	23	27	16	16	12,17	13	10	12	20	11	11	14	11	21	1	0.0015	NMF
Bn624	15	13	21	30	17	15	15,16	12	10	11	20	11	11	14	8	19	1	0.0015	NMF
Bn625	15	12	23	29	16	14	13,14	15	10	11	21	12	10	15	10	20	1	0.0015	NMF
Bn626	15	14	25	31	17	15	12,14	14	10	10	23	11	14	14	11	20	1	0.0015	NMF
Bn627	15	13	22	29	17	15	16,16	12	10	11	20	11	11	14	8	19	1	0.0015	NMF
Bn628	15	14	25	32	16	15	11,14	13	10	10	24	11	12	14	11	19	1	0.0015	NMF
Bn629	15	12	25	29	16	17	12,14	13	11	10	23	11	12	14	11	20	1	0.0015	NMF
Bn630	14	13	23	29	17	14	16,19	12	10	12	22	11	11	14	9	21	1	0.0015	NMF
Bn631	14	13	22	30	16	15	16,16	12	10	11	21	11	11	14	8	19	1	0.0015	NMF
Bn632	17	14	22	31	17	15	15,17	12	10	11	20	11	12	14	9	19	1	0.0015	NMF
Bn633	15	14	23	30	18	15	15,19	13	10	13	24	10	11	16	11	19	1	0.0015	NMF
Bn634	15	13	24	28	19	13	13,16	13	10	12	22	11	11	14	10	20	1	0.0015	NMF
Bn635	15	13	25	29	17	14	13,18	13	11	11	23	13	11	15	12	18	1	0.0015	NMF
Bn636	15	14	25	32	16	15	11,14	12	9	10	24	11	11	14	11	20	1	0.0015	NMF
Bn637	16	13	25	31	15	16	11,14	13	11	10	24	11	13	14	11	20	1	0.0015	MF-3
Bn638	15	14	22	30	18	15	15,18	12	10	12	20	11	12	14	9	19	1	0.0015	NMF
Bn639	16	14	22	30	18	16	14,14	11	10	10	25	11	10	15	10	19	1	0.0015	NMF
Bn640	15	13	23	29	17	13	14,20	14	11	10	25	10	11	16	11	19	1	0.0015	NMF
Bn641	15	12	21	28	16	15	16,17	12	10	11	21	11	11	14	8	18	1	0.0015	MF-1
Bn642	15	12	23	27	16	17	14,17	12	10	12	21	14	11	15	11	20	1	0.0015	NMF
Bn643	16	14	24	31	18	15	13,13	12	10	12	21	11	11	15	9	19	1	0.0015	NMF
Bn644	13	12	24	28	17	16	13,16	12	10	12	21	11	11	15	9	19	1	0.0015	NMF
Bn645	16	14	23	30	15	14	11,12	12	11	11	23	14	13	14	11	20	1	0.0015	NMF
Bn646	16	13	23	29	17	15	15,20	14	10	12	21	13	11	14	10	18	1	0.0015	NMF
Bn647	16	14	23	30	18	15	14,19	13	10	12	24	10	11	15	11	19	1	0.0015	NMF
Bn648	15	14	25	32	16	15	11,14	13	10	10	23	11	12	14	11	20	1	0.0015	MF-7
Bn649	15	13	25	31	15	15	11,14	13	11	10	23	11	14	14	11	20	1	0.0015	NMF
Bn650*	15	13	22	29	17	13	12,16	13	10	11	23	-	10	15	11	19	1	-	-
Bn651*	15	13	22	29	17,18	15	15,16	12	10	11	19	11	10	14	8	19	1	-	-
Bn652*	15	14	25	-	17	15	15,19	14	10	12	21	-	11	14	10	18	1	-	-
Bn653*	16	13	25	31	16	15	11,15	13	-	10	23	11	11	14	11	20	1	-	-
Bn654*	12	13	24	29	**15,17**	14	12,18	13	10	14	20	11	11	15	9	19	1	-	-

N= Number of individual; *F:* Frequency of each haplotype in 667 Bangali males; YHRD: Y-Chromosome Haplotype Reference Database; MF: Match Found; NMF: No Match Found

*Note: Haplotypes bearing double alleles and null alleles were excluded from allele frequency, gene diversity, AMOVA calculations and haplogroup analysis.

Supplementary Table 2. A list of Y-chromosome STR haplotypes detected in 150 unrelated males in Chakma (Ck) population

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Ck1	15	12	23	29	17	16	10,16	12	10	13	19	12	12	15	10	19	1	0.0066	MF-1
Ck2	15	14	23	30	16	15	11,18	14	10	11	22	11	11	14	10	21	3	0.0200	MF-2
Ck3	16	13	24	29	16	17	15,20	14	10	12	22	14	13	14	10	18	5	0.0333	MF-1
Ck4	15	14	23	32	16	15	11,18	14	10	11	22	11	11	14	10	21	1	0.0066	MF-1
Ck5	15	12	24	28	16	14	13,20	12	10	12	21	14	12	15	11	20	3	0.0200	MF-1
Ck6	15	11	23	28	14	14	12,13	16	11	12	24	11	12	16	10	20	1	0.0066	MF-1
Ck7	15	12	23	26	18	15	12,16	13	10	13	20	13	13	15	10	19	2	0.0133	MF-1
Ck8	15	12	25	29	20	15	15,16	12	10	11	20	10	11	14	10	19	1	0.0066	MF-1
Ck9	14	12	24	28	17	14	13,20	12	10	11	22	15	12	15	11	19	4	0.0267	MF-1
Ck10	15	12	24	27	19	14	13,19	12	10	14	21	14	12	15	11	20	2	0.0133	MF-1
Ck11	15	12	24	28	18	14	13,19	13	10	13	20	14	12	15	11	19	1	0.0066	MF-1
Ck12	15	13	24	29	15	15	13,19	14	11	11	21	13	11	14	10	18	2	0.0133	MF-1
Ck13	17	13	25	30	15	15	11,14	13	10	10	23	11	13	14	11	20	3	0.0200	MF-3
Ck14	15	12	23	28	19	14	13,17	12	10	11	21	14	12	15	11	20	1	0.0066	MF-2
Ck15	15	12	23	28	17	14	13,21	12	10	11	20	14	11	15	11	21	1	0.0066	MF-1
Ck16	15	12	24	27	18	14	13,20	12	10	12	21	14	12	15	11	18	1	0.0066	MF-3
Ck17	15	12	23	28	17	14	13,22	12	10	11	20	14	12	15	11	20	1	0.0066	MF-1
Ck18	15	12	23	28	17	15	13,22	12	10	11	20	14	12	15	11	20	1	0.0066	MF-1
Ck19	15	12	23	27	18	15	12,16	13	10	13	20	13	12	15	10	19	1	0.0066	MF-1
Ck20	15	14	23	30	18	15	11,17	15	10	11	22	11	11	14	10	21	1	0.0066	MF-1
Ck21	15	12	23	28	18	14	13,19	12	10	11	21	14	12	15	11	20	3	0.0200	MF-3
Ck22	15	12	24	28	17	14	13,17	12	10	12	20	14	12	15	11	20	3	0.0200	MF-10
Ck23	15	12	23	30	17	16	10,16	13	10	12	19	12	12	15	10	19	1	0.0066	MF-1
Ck24	15	13	24	29	19	14	14,18	12	11	11	21	11	11	14	11	17	1	0.0066	MF-1
Ck25	14	12	24	30	17	14	13,20	12	10	11	22	15	12	15	11	19	1	0.0066	MF-1
Ck26	15	12	23	28	20	14	12,17	12	10	12	19	12	11	15	10	19	1	0.0066	MF-1
Ck27	15	12	25	28	18	15	13,21	12	10	12	20	14	12	15	11	20	2	0.0133	MF-1
Ck28	14	12	23	28	17	15	14,21	12	10	11	20	14	12	15	11	20	1	0.0066	MF-1
Ck29	14	12	23	28	17	15	14,22	12	10	11	20	14	12	15	11	20	1	0.0066	MF-1
Ck30	15	14	23	31	16	14	11,12	13	10	11	22	14	12	14	11	19	2	0.0133	MF-1
Ck31	17	13	25	30	17	15	12,12	14	10	11	19	11	12	14	11	19	1	0.0066	MF-1
Ck32	15	13	25	31	18	16	15,20	15	10	13	21	13	10	14	10	18	1	0.0066	MF-1
Ck33	14	12	24	28	17	14	13,20	13	10	11	21	15	11	16	11	19	1	0.0066	MF-1
Ck34	15	13	24	29	18	14	13,18	12	10	13	21	14	11	15	11	20	1	0.0066	MF-1
Ck35	15	14	23	32	16	14	11,12	13	10	11	22	14	12	14	11	19	1	0.0066	MF-1
Ck36	15	12	23	29	17	14	13,22	12	10	11	20	14	12	15	11	20	1	0.0066	MF-1
Ck37	14	13	24	29	17	14	12,19	12	10	12	20	14	12	15	11	20	1	0.0066	MF-1
Ck38	16	12	24	27	18	14	13,20	12	10	12	21	14	12	15	11	20	1	0.0066	MF-1
Ck39	16	12	24	27	17	14	13,20	12	10	12	21	14	12	15	11	20	1	0.0066	MF-1
Ck40	15	12	23	30	17	16	10,16	13	10	12	20	12	12	15	10	19	4	0.0267	MF-1
Ck41	15	14	23	28	16	15	11,17	15	10	11	21	11	11	14	10	21	1	0.0066	MF-1
Ck42	15	12	23	27	18	15	12,16	13	10	13	20	13	13	15	10	19	1	0.0066	MF-1
Ck43	15	14	23	30	16	15	11,17	14	10	11	21	11	11	14	10	21	1	0.0066	MF-2
Ck44	15	13	24	29	18	14	13,20	12	10	12	20	14	12	15	11	20	1	0.0066	MF-3
Ck45	14	12	24	27	17	14	13,20	12	10	11	21	15	12	16	11	19	2	0.0133	MF-1
Ck46	14	13	24	29	16	17	15,21	14	10	12	22	14	13	14	10	14	1	0.0066	MF-1
Ck47	15	12	24	29	18	14	13,19	12	10	13	20	14	12	15	11	19	2	0.0133	MF-2
Ck48	15	12	23	29	17	16	10,16	13	10	12	19	12	12	15	10	19	1	0.0066	MF-1
Ck49	15	12	24	27	18	14	13,20	12	10	12	21	14	12	15	11	20	2	0.0133	MF-1

Haplotype/ Locus	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a/b	DYS393	DYS391	DYS439	DYS635	DYS392	YGATAH4	DYS437	DYS438	DYS448	*Individual (N)*	*Frequency (F)*	*Searched in YHRD*
Ck50	15	12	24	28	18	14	13,19	12	10	12	20	14	12	15	11	19	2	0.0133	MF-2
Ck51	15	12	24	28	17	14	13,18	12	10	11	20	14	12	15	11	20	1	0.0066	MF-2
Ck52	14	12	23	28	17	15	13,21	12	10	11	20	14	12	15	12	20	1	0.0066	MF-1
Ck53	17	13	25	29	14	16	16,21	13	11	14	21	13	11	14	10	18	1	0.0066	MF-1
Ck54	15	12	23	28	18	14	13,17	12	10	11	21	14	12	15	11	20	1	0.0066	MF-2
Ck55	15	12	23	28	17	16	10,16	12	10	13	20	12	12	15	10	19	2	0.0133	MF-1
Ck56	15	12	23	28	18	14	14,19	12	10	11	21	14	12	15	11	20	1	0.0066	MF-1
Ck57	16	13	25	29	15	16	15,19	14	10	11	21	13	11	14	10	18	1	0.0066	MF-1
Ck58	15	13	24	29	18	14	13,19	13	11	12	20	15	12	15	11	20	1	0.0066	MF-1
Ck59	14	13	24	26	17	14	12,19	12	10	12	20	14	12	15	11	20	1	0.0066	MF-1
Ck60	14	12	23	28	17	15	13,22	12	10	11	20	14	12	15	11	20	2	0.0133	MF-1
Ck61	15	12	23	28	20	15	13,17	12	10	11	21	14	12	15	11	20	1	0.0066	MF-1
Ck62	17	13	25	29	15	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0066	MF-6
Ck63	15	12	24	28	16	14	13,20	12	10	12	20	14	12	15	11	20	2	0.0133	MF-1
Ck64	15	13	24	28	18	14	13,19	12	10	11	21	14	12	14	11	20	1	0.0066	MF-1
Ck65	15	12	24	29	19	14	13,18	12	10	12	21	14	12	15	11	20	1	0.0066	MF-1
Ck66	15	12	24	28	18	14	14,16	12	10	12	21	14	12	15	11	20	1	0.0066	MF-1
Ck67	14	13	24	29	17	13	12,19	12	10	12	20	14	12	15	11	20	1	0.0066	MF-1
Ck68	17	14	23	31	17	14	14,19	15	10	10	25	10	11	16	11	19	1	0.0066	MF-1
Ck69	17	13	25	28	15	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0066	MF-1
Ck70	15	11	23	28	14	14	12,13	15	11	12	23	11	12	16	10	20	1	0.0066	MF-1
Ck71	15	12	23	29	17	16	10,16	12	10	13	20	12	12	15	10	19	1	0.0066	MF-1
Ck72	15	12	23	28	18	14	13,18	12	10	11	21	14	12	15	11	20	1	0.0066	MF-2
Ck73	15	12	25	28	20	15	15,17	12	10	11	20	10	11	14	10	19	1	0.0066	MF-1
Ck74	14	12	23	28	17	15	13,22	12	10	11	20	13	12	15	11	20	1	0.0066	MF-1
Ck75	16	13	24	29	16	15	15,19	14	10	12	22	12	13	14	10	18	1	0.0066	MF-1
Ck76	15	12	25	29	20	15	15,16	12	10	12	20	10	11	14	10	19	1	0.0066	MF-1
Ck77	15	12	23	27	20	15	12,16	13	10	14	20	13	12	15	10	19	1	0.0066	MF-1
Ck78	15	12	24	27	18	14	13,19	12	10	13	20	14	12	15	11	19	1	0.0066	MF-1
Ck79	15	14	23	30	16	15	11,16	14	10	11	21	11	11	14	10	21	1	0.0066	MF-1
Ck80	15	12	23	28	19	14	13,18	12	10	11	21	14	12	15	11	20	1	0.0066	MF-1
Ck81	15	12	24	28	17	14	13,19	12	10	12	20	14	12	15	11	19	1	0.0066	MF-1
Ck82	18	13	25	28	17	16	16,20	14	10	12	22	13	11	14	10	18	1	0.0066	MF-1
Ck83	15	12	23	28	18	15	12,17	12	10	12	20	12	11	15	10	19	1	0.0066	MF-2
Ck84	15	12	24	28	18	14	13,19	12	11	12	20	14	12	15	11	19	1	0.0066	MF-5
Ck85	15	12	23	29	18	14	13,19	12	10	12	21	13	12	14	11	19	1	0.0066	MF-1
Ck86	15	12	23	28	19	14	12,17	12	10	12	19	12	11	15	10	19	1	0.0066	MF-1
Ck87	15	12	24	29	18	14	13,19	12	10	13	20	12	12	15	11	19	1	0.0066	MF-1
Ck88	15	12	23	28	19	14	13,18	12	10	11	22	14	12	15	11	20	1	0.0066	MF-1
Ck89	15	12	24	28	18	14	13,18	14	10	13	20	14	12	15	11	20	1	0.0066	MF-1
Ck90	17	13	25	30	16	15	15,22	14	10	12	21	14	11	14	10	18	1	0.0066	MF-1
Ck91	15	14	23	28	17	13	11,17	15	11	11	22	12	13	14	10	21	1	0.0066	MF-1
Ck92	15	12	25	29	21	15	15,16	12	11	11	20	11	11	14	10	19	1	0.0066	MF-1
Ck93	15	12	23	28	18	14	13,17	12	11	11	21	14	12	15	11	20	1	0.0066	MF-1
Ck94	15	12	24	28	17	14	13,17	12	11	12	20	14	12	15	11	20	1	0.0066	MF-4
Ck95	15	12	24	28	19	14	13,19	12	11	11	20	14	12	15	11	19	1	0.0066	MF-1
Ck96	14	12	24	28	17	14	13,20	12	11	10	22	15	12	15	11	19	1	0.0066	MF-1
Ck97	15	12	24	27	18	14	13,20	12	11	12	21	14	11	15	11	18	1	0.0066	MF-1
Ck98	15	12	24	29	18	14	13,18	12	11	12	20	14	13	15	11	20	1	0.0066	MF-1
Ck99	15	12	24	28	18	14	13,18	12	11	12	20	14	12	15	11	19	1	0.0066	MF-1
Ck100	15	12	25	28	21	15	15,17	12	11	11	20	10	11	14	10	19	1	0.0066	MF-1

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Ck101	18	13	25	28	17	16	17,20	14	11	12	22	13	11	14	10	18	2	0.0133	MF-1
Ck102	15	12	24	28	18	14	13,18	12	11	12	20	14	12	15	11	20	2	0.0133	MF-1
Ck103	17	13	25	28	17	15	12,12	14	11	11	19	11	12	14	11	19	1	0.0066	MF-1
Ck104	15	13	25	29	18	14	14,20	12	11	12	20	14	12	15	11	20	1	0.0066	MF-1
Ck105	17	13	25	30	17	15	12,12	14	11	11	19	11	12	14	11	19	1	0.0066	MF-1
Ck106	15	12	24	28	18	15	14,19	12	11	12	20	14	11	15	12	20	1	0.0066	MF-1
Ck107	16	14	24	31	18	16	15,21	14	11	12	23	14	13	14	10	18	1	0.0066	MF-1
Ck108	15	12	24	28	18	14	13,18	12	11	10	21	14	12	15	11	20	1	0.0066	MF-1
Ck109	14	12	24	28	17	14	13,21	12	11	10	21	15	12	15	11	19	1	0.0066	MF-1
Ck110	15	11	23	28	14	14	12,13	15	12	11	23	11	12	16	10	20	1	0.0066	MF-1
Ck111	15	12	25	28	18	14	13,19	12	11	13	20	14	12	15	11	21	1	0.0066	MF-1
Ck112	15	13	24	29	18	14	14,20	12	11	11	20	15	12	15	11	20	1	0.0066	MF-1
Ck113	15	12	24	28	18	14	13,20	12	11	12	20	14	12	11	11	19	1	0.0066	MF-1
Ck114	16	14	21	30	18	15	13,17	14	11	12	20	13	14	15	10	19	1	0.0066	MF-1
Ck115	15	12	23	28	19	14	13,20	12	10	11	20	14	12	15	11	20	1	0.0066	MF-3
Ck116	15	12	25	28	18	15	13,22	12	10	12	20	14	12	15	11	20	1	0.0066	MF-1

N= Number of individual; *F:* Frequency of each haplotype in 150 Chakma males; YHRD: Y-Chromosome Haplotype Reference Database; MF: Match Found; NMF: No Match Found

Supplementary Table 3. A list of Y-chromosome STR haplotypes detected in 144 unrelated males in Tripura (Tr) population

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Tr1	15	12	25	28	18	14	13,17	12	11	12	20	14	12	15	11	21	1	0.0069	MF-3
Tr2	16	13	25	29	17	14	15,20	14	9	12	21	12	11	14	10	18	1	0.0069	MF-1
Tr3	15	13	24	29	17	15	13,20	12	10	10	23	11	11	14	10	18	1	0.0069	MF-1
Tr4	15	12	24	28	17	14	13,17	12	10	12	20	14	13	15	11	19	4	0.0277	MF-1
Tr5	15	13	24	28	17	15	14,19	12	10	10	23	11	11	14	10	18	1	0.0069	MF-1
Tr6	14	13	24	27	19	14	13,19	12	10	12	20	14	12	15	11	21	1	0.0069	MF-1
Tr7	16	12	23	28	19	14	13,20	12	10	11	20	14	11	15	11	20	1	0.0069	MF-1
Tr8	15	12	24	27	18	17	14,19	12	10	13	23	13	11	15	12	20	1	0.0069	MF-1
Tr9	16	12	23	28	17	14	12,20	12	10	11	20	13	13	15	11	20	1	0.0069	MF-1
Tr10	15	12	23	29	17	14	13,18	12	10	11	20	14	12	14	11	20	1	0.0069	MF-10
Tr11	15	12	24	28	17	14	13,18	12	10	11	21	14	12	15	11	20	1	0.0069	MF-1
Tr12	16	13	25	29	16	14	15,20	14	10	12	21	12	11	14	10	18	2	0.0138	MF-1
Tr13	15	13	24	28	17	15	14,19	12	10	10	23	12	11	14	10	18	1	0.0069	MF-1
Tr14	15	12	24	27	17	14	13,20	12	10	12	21	13	12	15	11	20	1	0.0069	MF-1
Tr15	15	13	23	27	17	14	13,18	12	10	12	20	14	12	14	11	20	1	0.0069	MF-1
Tr16	15	12	24	27	18	17	14,19	12	10	14	22	13	11	15	12	20	1	0.0069	MF-1
Tr17	15	15	23	27	17	14	14,19	13	10	12	23	11	11	14	9	21	1	0.0069	MF-1
Tr18	14	14	23	30	17	14	14,19	13	10	12	23	11	11	14	9	21	6	0.0416	MF-1
Tr19	14	14	23	28	17	14	14,19	13	10	12	23	11	11	14	9	21	1	0.0069	MF-1
Tr20	16	13	24	28	19	14	13,19	12	11	12	20	15	11	15	11	20	1	0.0069	MF-1
Tr21	15	12	24	27	18	14	13,18	12	10	12	21	14	11	15	11	20	6	0.0416	MF-2
Tr22	15	12	23	28	20	14	13,19	12	10	11	20	14	12	15	11	20	2	0.0138	MF-3
Tr23	15	13	24	28	19	14	13,20	12	10	12	20	14	12	15	11	20	1	0.0069	MF-1
Tr24	16	14	21	29	18	15	13,17	14	10	12	20	13	10	15	10	19	3	0.0208	MF-1
Tr25	17	13	22	29	18	15	16,18	12	10	11	20	11	12	14	9	19	2	0.0138	MF-1
Tr26	15	12	24	27	18	15	13,18	12	10	12	21	14	11	15	11	20	1	0.0069	MF-1
Tr27	15	12	24	28	17	17	14,16	12	10	11	22	13	12	15	11	20	1	0.0069	MF-1
Tr28	15	12	24	28	17	14	13,19	12	10	12	20	14	13	15	11	20	3	0.0208	MF-3
Tr29	15	12	23	28	17	14	13,18	12	10	12	20	14	12	14	11	20	7	0.0486	MF-8
Tr30	16	12	23	28	19	14	13,20	12	10	11	20	14	12	15	11	20	2	0.0138	MF-1
Tr31	15	12	24	29	18	14	13,18	13	10	12	21	14	12	15	10	20	2	0.0138	MF-1
Tr32	15	12	23	28	17	14	13,18	12	10	13	20	14	11	14	11	20	2	0.0138	MF-1
Tr33	14	14	23	30	17	14	14,20	13	10	12	23	11	11	14	9	21	1	0.0069	MF-1
Tr34	15	12	23	28	17	14	13,18	12	10	11	20	14	12	14	11	20	1	0.0069	MF-41
Tr35	15	12	24	28	17	14	13,20	12	10	12	21	13	12	15	11	20	1	0.0069	MF-1
Tr36	14	13	24	28	19	14	13,19	12	10	12	20	14	12	15	11	21	1	0.0069	MF-1
Tr37	15	15	23	31	17	14	14,19	13	10	12	23	11	11	14	9	21	1	0.0069	MF-1
Tr38	17	12	23	27	18	14	13,20	12	10	11	20	14	12	15	11	20	1	0.0069	MF-1
Tr39	15	12	23	29	17	14	13,18	12	10	13	20	14	11	14	11	20	1	0.0069	MF-1
Tr40	15	12	25	27	18	14	13,18	12	10	12	21	14	11	15	11	20	1	0.0069	MF-1
Tr41	15	13	24	29	17	15	14,19	12	10	10	23	11	11	14	10	18	4	0.0277	MF-2
Tr42	15	12	24	28	18	17	14,19	12	10	13	23	13	11	15	12	20	3	0.0208	MF-1
Tr43	15	13	24	29	17	15	14,20	12	10	10	23	11	11	14	10	18	2	0.0138	MF-1
Tr44	15	12	23	28	17	14	12,20	12	10	12	20	14	13	15	11	20	1	0.0069	MF-1
Tr45	15	12	24	28	17	14	13,17	12	10	12	20	14	12	15	11	19	1	0.0069	MF-1
Tr46	15	14	23	31	16	15	12,19	15	10	11	21	11	11	14	10	21	1	0.0069	MF-3
Tr47	17	13	22	29	18	15	16,17	12	10	11	20	11	12	14	9	19	1	0.0069	MF-1
Tr48	15	12	23	28	18	14	13,20	12	10	11	20	14	13	15	11	20	1	0.0069	MF-1
Tr49	16	12	24	28	17	14	15,18	12	10	11	20	14	12	15	11	20	2	0.0138	MF-1

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Tr50	14	15	23	31	17	14	14,19	13	10	12	23	11	11	14	9	21	1	0.0069	MF-2
Tr51	16	14	21	29	18	15	13,17	14	10	11	20	13	10	15	10	19	1	0.0069	MF-1
Tr52	15	12	24	28	18	17	14,19	12	10	12	21	13	11	15	11	20	1	0.0069	MF-1
Tr53	16	12	23	28	19	14	13,21	12	10	11	20	14	12	15	11	20	1	0.0069	MF-1
Tr54	16	12	24	27	17	14	14,18	12	10	12	21	14	11	15	11	20	2	0.0138	MF-1
Tr55	15	12	23	28	17	14	14,18	12	10	12	20	14	13	14	11	20	1	0.0069	MF-1
Tr56	14	12	24	27	18	14	13,18	12	10	12	21	14	11	15	11	20	1	0.0069	MF-1
Tr57	15	12	24	28	18	14	13,19	12	10	12	20	14	13	15	11	20	1	0.0069	MF-1
Tr58	15	12	25	28	16	14	13,19	12	10	12	20	14	13	15	11	20	1	0.0069	MF-1
Tr59	16	13	25	30	16	14	15,20	14	10	12	21	12	11	14	10	18	1	0.0069	MF-1
Tr60	14	12	24	28	17	14	13,20	12	10	11	20	15	12	15	11	19	1	0.0069	MF-1
Tr61	14	13	24	33	16	14	14,19	12	9	10	21	11	11	14	10	17	4	0.0277	MF-1
Tr62	16	13	24	29	19	14	13,19	12	11	12	20	15	11	15	11	20	2	0.0138	MF-1
Tr63	15	12	25	27	16	14	13,18	12	10	12	20	14	12	15	11	21	1	0.0069	MF-1
Tr64	16	12	23	28	18	14	12,20	12	10	11	20	14	13	14	11	20	1	0.0069	MF-1
Tr65	16	13	25	30	16	14	13,20	14	10	12	21	12	11	14	10	18	1	0.0069	MF-1
Tr66	14	13	24	32	16	14	14,20	12	9	10	22	11	11	14	10	17	1	0.0069	MF-1
Tr67	15	12	23	29	17	14	13,18	12	10	12	20	14	12	14	11	20	1	0.0069	MF-1
Tr68	17	12	23	28	18	15	13,20	12	10	11	20	14	12	15	11	20	1	0.0069	MF-1
Tr69	15	12	24	28	17	14	14,18	12	10	12	20	14	12	15	11	20	1	0.0069	MF-6
Tr70	16	13	24	29	16	16	15,20	13	10	13	23	14	13	14	10	18	1	0.0069	MF-1
Tr71	15	12	24	30	17	14	8,13	12	10	12	20	11	13	15	11	20	1	0.0069	MF-1
Tr72	17	12	23	28	18	14	13,20	12	10	11	20	12	12	15	11	20	1	0.0069	MF-1
Tr73	17	13	22	29	19	15	16,17	12	10	11	20	11	12	14	9	19	1	0.0069	MF-1
Tr74	15	12	24	27	20	14	13,19	13	10	12	21	14	12	15	10	20	1	0.0069	MF-1
Tr75	16	13	24	24	19	14	13,19	12	11	12	20	15	11	15	11	20	1	0.0069	MF-1
Tr76	16	13	23	28	17	14	12,20	12	10	11	20	14	13	15	11	20	1	0.0069	MF-2
Tr77	16	13	24	30	16	16	15,20	13	10	13	23	14	13	14	10	18	1	0.0069	MF-1
Tr78	15	13	24	29	18	14	14,19	12	11	13	21	11	11	14	11	17	1	0.0069	MF-1
Tr79	16	13	24	29	18	14	13,19	12	11	12	20	15	11	15	11	20	1	0.0069	MF-1
Tr80	16	13	24	24	18	14	13,19	12	11	12	20	15	11	15	11	20	1	0.0069	MF-1
Tr81	15	12	25	28	16	14	13,18	12	11	12	20	14	12	15	11	21	1	0.0069	MF-1
Tr82	14	13	24	29	17	14	14,19	12	9	10	21	11	11	14	10	17	1	0.0069	MF-1
Tr83	14	13	24	30	16	14	14,19	12	9	10	22	11	11	14	10	17	1	0.0069	MF-1
Tr84	15	12	23	29	17	15	12,15	12	10	12	19	12	12	15	10	20	1	0.0069	MF-1
Tr85	16	13	24	29	16	16	15,20	13	10	13	24	14	13	14	10	18	1	0.0069	MF-1
Tr86	15	12	25	28	18	14	13,19	12	11	14	20	11	11	15	11	21	1	0.0069	MF-1
Tr87	14	12	24	28	18	13	13,19	12	10	12	20	14	12	15	11	19	1	0.0069	MF-1
Tr88	15	13	24	31	16	14	14,19	12	9	10	21	11	11	14	10	17	3	0.0208	MF-1
Tr89	15	12	24	28	17	14	13,18	12	10	13	20	14	12	15	11	20	2	0.0138	MF-1
Tr90	16	12	23	28	17	14	12,20	12	10	11	20	14	13	14	11	20	1	0.0069	MF-2
Tr91	16	14	21	27	18	14	13,17	14	10	12	20	15	10	15	10	19	1	0.0069	MF-1
Tr92	15	12	23	27	20	14	14,19	12	10	12	20	14	12	15	11	20	2	0.0138	MF-1
Tr93	16	12	23	28	18	14	13,20	12	10	11	21	14	13	15	11	20	1	0.0069	MF-1
Tr94	14	14	23	30	17	14	14,19	13	11	12	23	11	11	14	9	21	1	0.0069	MF-1
Tr95	16	12	24	28	17	14	13,19	12	10	12	20	14	13	15	11	20	1	0.0069	MF-1
Tr96	16	12	23	28	18	14	13,20	12	10	11	20	14	12	15	11	20	1	0.0069	MF-1
Tr97	15	12	24	28	18	15	14,19	12	10	11	20	14	12	15	13	20	1	0.0069	MF-1
Tr98	15	13	25	29	18	14	14,19	12	11	13	21	11	11	14	11	17	1	0.0069	MF-1
Tr99	15	12	23	28	17	15	13,22	11	10	13	21	13	11	14	11	20	1	0.0069	MF-1

N= Number of individual; *F:* Frequency of each haplotype in 144 Tripura males; YHRD: Y-Chromosome Haplotype Reference Database; MF: Match Found; NMF: No Match Found

Supplementary Table 4. A list of Y-chromosome STR haplotypes detected in 145 unrelated males in Rakhine (Rk) population

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Rk1	15	14	26	31	18	15	11,15	13	10	10	23	11	12	14	11	20	1	0.0069	MF-1
Rk2	15	12	24	29	18	14	13,20	12	10	13	21	14	12	15	11	20	1	0.0069	MF-1
Rk3	15	13	25	30	16	15	13,17	14	11	12	22	13	11	14	10	19	1	0.0069	MF-1
Rk4	16	13	25	29	15	15	15,15	14	10	11	24	13	11	14	10	18	1	0.0069	MF-1
Rk5	15	12	24	27	18	14	13,19	12	10	13	21	13	12	15	13	18	1	0.0069	MF-1
Rk6	15	12	24	27	18	14	13,19	12	10	13	21	14	12	15	11	20	6	0.0414	MF-2
Rk7	15	12	24	29	18	14	14,20	12	10	11	20	14	14	14	11	20	6	0.0414	MF-1
Rk8	15	12	24	28	19	14	15,20	12	10	11	20	14	12	15	11	19	2	0.0138	MF-1
Rk9	15	12	24	28	15	14	13,19	12	10	11	20	14	12	15	11	20	2	0.0138	MF-2
Rk10	15	14	22	30	17	15	16,18	12	10	11	20	11	12	14	8	19	1	0.0069	MF-1
Rk11	15	13	25	32	16	16	11,14	14	11	10	23	11	13	14	11	20	1	0.0069	MF-1
Rk12	15	12	23	28	18	14	13,17	12	10	11	21	14	12	15	11	20	2	0.0138	MF-2
Rk13	16	12	24	27	19	14	13,19	12	10	12	21	14	12	15	11	20	1	0.0069	MF-1
Rk14	14	14	23	30	17	14	14,18	12	10	12	23	11	11	14	9	20	1	0.0069	MF-1
Rk15	16	14	23	30	16	15	11,17	14	10	12	21	11	11	14	10	20	1	0.0069	MF-1
Rk16	15	12	25	29	16	15	9,14	13	11	10	23	11	12	14	11	20	1	0.0069	MF-1
Rk17	15	14	23	30	16	15	11,17	14	11	11	21	11	11	14	10	21	1	0.0069	MF-1
Rk18	15	13	24	30	16	14	14,17	10	10	11	21	11	12	15	9	19	1	0.0069	MF-1
Rk19	15	12	24	29	19	14	14,20	12	10	11	20	14	13	14	11	20	1	0.0069	MF-1
Rk20	15	13	24	30	17	14	16,18	12	9	11	21	11	11	14	10	17	1	0.0069	MF-1
Rk21	15	12	24	29	17	14	13,19	12	10	12	20	14	12	15	11	20	2	0.0138	MF-3
Rk22	15	14	25	31	16	15	11,14	13	10	10	23	11	13	14	11	20	7	0.0483	MF-12
Rk23	15	12	24	29	19	14	14,20	12	10	11	20	14	14	14	11	20	1	0.0069	MF-1
Rk24	15	12	24	27	19	14	15,19	12	10	13	21	14	11	15	11	20	4	0.0276	MF-1
Rk25	15	12	24	28	20	14	13,18	12	10	12	21	14	12	15	11	20	3	0.0207	MF-2
Rk26	15	12	24	27	19	14	16,19	12	10	13	21	14	11	15	11	20	1	0.0069	MF-1
Rk27	16	13	24	29	16	14	15,17	14	10	12	22	13	11	14	10	18	1	0.0069	MF-1
Rk28	15	12	24	27	17	14	13,19	12	10	12	21	14	13	15	11	20	2	0.0138	MF-1
Rk29	15	12	24	29	16	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0069	MF-1
Rk30	15	12	24	28	17	14	13,18	12	10	13	21	15	12	15	11	20	1	0.0069	MF-1
Rk31	15	12	24	28	17	14	13,17	13	10	12	21	14	12	15	11	20	1	0.0069	MF-1
Rk32	16	12	23	28	18	14	14,24	12	10	11	20	14	12	15	11	20	1	0.0069	MF-1
Rk33	15	12	22	28	16	15	15,18	12	11	12	21	11	11	14	9	19	2	0.0138	MF-1
Rk34	15	12	24	28	18	14	13,20	12	10	11	20	14	12	15	11	20	1	0.0069	MF-3
Rk35	15	12	24	28	18	14	14,20	12	10	11	20	14	14	14	11	20	3	0.0207	MF-2
Rk36	15	12	25	27	16	14	13,19	12	10	12	21	14	13	15	11	20	1	0.0069	MF-1
Rk37	15	12	24	29	18	14	14,20	12	10	11	20	14	14	14	11	19	1	0.0069	MF-1
Rk38	15	12	22	30	15	15	9,17	12	10	8	21	14	11	16	10	19	1	0.0069	MF-2
Rk39	15	12	23	28	19	14	13,19	12	10	11	20	14	12	15	11	20	1	0.0069	MF-5
Rk40	15	14	24	30	18	14	13,18	12	10	12	20	14	12	15	11	20	1	0.0069	MF-1
Rk41	15	14	25	29	16	15	11,14	13	12	10	23	11	12	14	11	19	1	0.0069	MF-1
Rk42	15	12	24	28	18	14	13,20	12	10	11	21	14	12	15	11	20	1	0.0069	MF-1
Rk43	16	13	25	29	18	15	15,21	15	11	12	22	13	11	14	10	18	2	0.0138	MF-1
Rk44	16	14	24	30	16	14	15,17	14	10	13	22	13	11	14	10	18	1	0.0069	MF-1
Rk45	15	12	24	28	19	14	13,20	12	10	12	21	14	12	15	11	20	1	0.0069	MF-1
Rk46	13	13	24	29	17	14	14,17	12	11	12	23	14	12	15	11	20	1	0.0069	MF-1
Rk47	15	12	23	28	19	14	13,17	13	10	12	20	15	12	15	11	20	1	0.0069	MF-1
Rk48	16	14	24	30	16	14	15,17	14	10	12	22	13	11	14	10	18	1	0.0069	MF-1
Rk49	15	12	24	28	19	14	13,20	12	10	11	22	14	12	15	11	20	1	0.0069	MF-1

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Rk50	15	12	23	28	18	14	13,20	12	10	11	19	14	14	15	11	20	1	0.0069	MF-2
Rk51	15	13	23	29	18	15	11,17	15	10	11	21	11	11	14	10	21	1	0.0069	MF-2
Rk52	14	12	24	27	18	14	13,19	12	10	12	23	14	12	15	11	20	1	0.0069	MF-1
Rk53	15	14	25	32	17	15	11,14	13	10	10	23	11	13	14	11	19	1	0.0069	MF-1
Rk54	16	14	22	30	14	15	15,17	12	10	11	18	11	12	14	9	19	1	0.0069	MF-1
Rk55	15	14	22	31	17	15	15,18	12	10	11	20	11	12	14	9	18	1	0.0069	MF-1
Rk56	14	13	25	31	16	15	11,14	13	10	10	24	11	12	14	11	20	1	0.0069	MF-1
Rk57	14	13	23	31	16	16	11,14	13	11	11	23	11	12	14	11	20	1	0.0069	MF-1
Rk58	15	12	24	29	18	14	14,20	12	10	11	20	14	10	14	11	20	1	0.0069	MF-1
Rk59	15	13	23	31	17	14	13,17	15	10	12	25	10	11	16	11	19	1	0.0069	MF-1
Rk60	16	12	23	28	17	14	13,18	12	10	11	21	14	15	15	11	20	1	0.0069	MF-1
Rk61	18	12	25	27	16	15	16,21	14	11	12	21	13	11	14	10	17	1	0.0069	MF-1
Rk62	15	13	23	29	18	14	13,18	12	10	12	20	14	12	15	11	20	1	0.0069	MF-8
Rk63	14	14	23	30	17	14	14,18	12	10	12	23	11	12	14	9	22	1	0.0069	MF-1
Rk64	16	14	24	30	18	14	13,20	13	10	13	20	14	13	15	11	20	1	0.0069	MF-1
Rk65	15	12	22	28	17	15	15,18	12	11	12	21	11	11	14	9	19	1	0.0069	MF-1
Rk66	15	12	24	27	18	14	13,20	12	10	12	21	14	12	15	11	18	1	0.0069	MF-3
Rk67	15	14	25	32	16	15	11,11	13	10	10	23	12	12	14	11	20	1	0.0069	MF-1
Rk68	14	12	24	28	17	14	13,19	12	10	13	21	14	12	15	11	20	1	0.0069	MF-1
Rk69	13	13	25	29	15	14	12,15	13	10	11	22	12	11	14	10	20	1	0.0069	MF-1
Rk70	17	13	24	30	18	17	15,20	13	11	11	21	13	11	14	10	18	1	0.0069	MF-1
Rk71	15	14	23	29	19	14	13,19	14	10	10	25	10	12	14	11	21	1	0.0069	MF-1
Rk72	15	14	25	33	16	15	11,11	14	10	11	23	11	12	14	11	20	1	0.0069	MF-1
Rk73	15	13	22	30	15	14	14,19	13	10	11	21	12	12	14	9	20	1	0.0069	MF-1
Rk74	15	14	22	32	17	15	11,14	13	11	11	23	11	13	14	11	20	2	0.0138	MF-1
Rk75	15	12	24	27	18	14	13,19	12	10	12	21	14	11	15	11	20	1	0.0069	MF-1
Rk76	15	14	23	31	18	14	13,19	14	11	11	26	10	13	16	11	19	1	0.0069	MF-1
Rk77	15	14	25	32	15	15	11,14	13	10	11	23	11	13	14	11	20	1	0.0069	MF-1
Rk78	15	14	23	30	16	17	15,15	12	11	12	20	11	12	14	10	19	1	0.0069	MF-1
Rk79	15	13	25	32	16	15	11,12	13	11	10	24	11	12	14	11	19	1	0.0069	MF-1
Rk80	15	13	24	29	20	14	13,20	12	10	12	21	14	12	15	11	20	1	0.0069	MF-1
Rk81	15	13	24	29	16	15	11,14	13	11	10	23	11	12	14	11	19	1	0.0069	MF-2
Rk82	15	12	24	28	18	14	13,18	12	10	12	20	14	12	15	11	20	1	0.0069	MF-7
Rk83	15	13	23	29	15	14	14,18	14	10	11	21	11	13	15	9	19	1	0.0069	MF-1
Rk84	15	14	25	30	15	15	11,21	14	10	11	21	11	11	14	10	21	1	0.0069	MF-1
Rk85	15	12	24	27	18	14	13,20	12	10	13	21	14	12	15	11	18	1	0.0069	MF-1
Rk86	15	13	25	29	18	15	12,17	12	10	11	20	12	12	15	10	19	2	0.0138	MF-1
Rk87	15	12	24	28	19	14	14,19	12	10	12	20	14	13	15	11	20	1	0.0069	MF-1
Rk88	15	14	25	32	17	15	12,14	13	10	10	23	11	14	15	11	19	1	0.0069	MF-1
Rk89	15	12	22	28	17	15	9,18	12	10	8	21	14	11	16	10	19	1	0.0069	MF-1
Rk90	15	14	25	28	16	13	11,14	13	10	10	23	11	13	14	11	20	1	0.0069	MF-1
Rk91	16	14	23	30	16	15	14,16	12	10	12	20	11	12	15	9	20	1	0.0069	MF-2
Rk92	15	13	25	32	16	15	11,13	13	11	10	23	11	12	14	11	20	1	0.0069	MF-1
Rk93	15	12	22	28	17	15	9,18	12	10	8	21	14	11	15	10	19	1	0.0069	MF-1
Rk94	16	13	25	29	17	15	17,21	14	10	12	21	13	11	14	10	19	1	0.0069	MF-1
Rk95	16	13	25	29	15	15	15,20	14	11	10	21	13	11	14	10	18	1	0.0069	MF-1
Rk96	15	12	24	28	18	14	13,19	12	10	12	20	14	13	15	11	20	1	0.0069	MF-2
Rk97	15	12	23	27	17	16	13,16	13	10	12	20	11	11	14	11	21	1	0.0069	MF-1
Rk98	14	14	23	30	18	14	15,19	12	10	13	24	11	11	14	9	21	1	0.0069	MF-1
Rk99	13	12	22	28	16	15	13,16	12	10	12	21	11	11	15	9	19	1	0.0069	MF-1
Rk100	15	13	24	29	16	15	15,17	14	11	9	21	13	11	14	10	18	1	0.0069	MF-1

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Rk101	15	12	23	28	19	14	13,17	12	10	11	21	14	12	15	11	20	1	0.0069	MF-2
Rk102	16	12	23	28	17	14	13,18	12	10	12	21	14	13	15	11	20	1	0.0069	MF-1
Rk103	17	12	24	28	20	15	15,16	11	10	11	20	10	11	14	10	19	1	0.0069	MF-2
Rk104	15	14	22	31	17	15	15,19	12	10	11	20	11	12	14	9	18	1	0.0069	MF-1
Rk105	15	12	25	28	17	15	13,20	12	10	12	20	14	12	15	11	20	1	0.0069	MF-1
Rk106	15	13	25	31	16	16	11,14	13	11	10	23	11	13	14	11	20	1	0.0069	MF-10
Rk107	15	14	26	32	16	15	11,11	13	10	11	23	11	14	14	11	20	1	0.0069	MF-1
Rk108	13	12	24	28	16	15	14,16	13	11	12	20	11	11	15	9	19	1	0.0069	MF-1
Rk109	15	14	25	31	15	15	11,13	13	10	10	24	11	12	14	11	20	1	0.0069	MF-2
Rk110	15	12	24	28	17	15	12,17	12	10	12	21	14	12	15	11	20	1	0.0069	MF-1
Rk111*	15	14	23	-	16	14	13,19	14	10	11	25	10	12	15	12	19	1	-	-
Rk112*	15	12	24	-	16	14	13,19	12	10	12	20	14	12	15	11	20	1	-	-
Rk113*	15	12	20	-	18	15	13,19	12	10	12	20	14	12	15	12	20	1	-	-

N= Number of Individual; *F:* Frequency of each haplotype in 145 Rakhine males; YHRD: Y-Chromosome Haplotype Reference Database; MF: Match Found; NMF: No Match Found

*Note: Haplotypes bearing null alleles were excluded from allele frequency, gene diversity and AMOVA calculations.

Supplementary Table 5. A list of Y-chromosome STR haplotypes detected in 138 unrelated males in Marma (Mr) population.

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Mr1	15	12	24	27	17	14	13,19	12	10	12	23	14	13	15	11	20	7	0.0507	MF-1
Mr2	15	12	24	28	16	14	13,19	12	10	12	20	14	12	15	11	20	4	0.029	MF-4
Mr3	16	12	24	28	20	15	15,16	11	10	11	20	10	11	14	10	19	1	0.0072	MF-1
Mr4	15	12	22	30	15	15	9,17	12	10	8	21	14	11	16	10	19	2	0.0145	MF-2
Mr5	15	14	23	30	16	15	11,17	14	11	11	22	11	11	14	10	21	2	0.0145	MF-1
Mr6	13	12	24	28	19	15	13,16	12	11	13	22	11	11	15	7	18	1	0.0072	MF-1
Mr7	15	12	24	27	18	14	14,19	12	10	13	22	14	12	15	11	18	2	0.0145	MF-1
Mr8	16	13	24	28	18	16	13,20	14	11	12	21	13	11	14	10	19	1	0.0072	MF-1
Mr9	16	13	24	30	18	16	13,19	14	11	12	21	13	11	14	10	19	1	0.0072	MF-1
Mr10	15	12	24	27	18	14	13,20	12	10	12	21	14	12	15	11	18	2	0.0145	MF-3
Mr11	15	14	25	32	17	15	11,14	13	10	10	23	11	13	14	11	20	3	0.0217	MF-10
Mr12	15	14	23	30	16	15	11,16	15	11	11	22	11	11	14	10	21	1	0.0072	MF-1
Mr13	15	12	24	27	19	14	13,20	12	10	12	21	14	12	15	11	18	1	0.0072	MF-1
Mr14	16	13	25	29	19	15	15,21	15	11	12	21	13	11	14	10	18	1	0.0072	MF-1
Mr15	15	12	25	28	17	15	12,17	12	10	11	19	12	12	15	10	19	1	0.0072	MF-1
Mr16	15	12	23	28	19	14	13,19	12	10	11	22	14	12	15	11	21	2	0.0145	MF-1
Mr17	15	14	23	30	17	15	11,17	14	10	11	21	11	11	14	10	21	2	0.0145	MF-1
Mr18	15	12	24	28	20	15	16,18	12	10	11	21	10	10	14	10	19	1	0.0072	MF-1
Mr19	15	14	24	33	15	16	11,14	13	10	10	23	11	13	14	11	20	1	0.0072	MF-1
Mr20	15	12	24	29	17	14	13,19	12	10	12	23	14	13	15	11	20	1	0.0072	MF-1
Mr21	15	12	24	28	18	14	13,18	12	10	12	21	15	12	15	11	20	1	0.0072	MF-2
Mr22	16	12	24	27	19	14	13,18	12	10	12	21	14	11	15	11	20	1	0.0072	MF-1
Mr23	15	12	24	28	20	15	16,17	12	10	11	21	10	10	14	10	19	1	0.0072	MF-1
Mr24	15	14	22	29	18	15	15,17	11	10	12	20	11	10	14	9	19	1	0.0072	MF-1
Mr25	16	14	25	29	17	15	17,18	14	11	13	22	13	11	14	10	18	2	0.0145	MF-1
Mr26	15	14	23	30	17	16	11,17	14	11	11	22	11	11	14	10	21	1	0.0072	MF-1
Mr27	16	13	24	29	18	14	9,13	14	11	12	21	13	11	14	10	19	1	0.0072	MF-1
Mr28	15	12	24	27	17	14	14,19	12	9	12	22	14	12	14	11	18	2	0.0145	MF-1
Mr29	16	12	24	27	22	15	16,16	12	11	11	21	10	11	14	10	20	1	0.0072	MF-1
Mr30	15	14	23	28	16	15	11,17	14	11	11	22	11	11	14	10	21	1	0.0072	MF-1
Mr31	15	14	25	28	17	15	11,14	13	10	10	23	13	13	14	11	20	1	0.0072	MF-1
Mr32	14	14	22	29	17	14	12,17	13	10	11	25	13	11	16	11	19	1	0.0072	MF-1
Mr33	13	12	24	28	15	15	13,16	12	11	13	22	11	11	15	7	18	1	0.0072	MF-1
Mr34	17	12	24	28	15	14	13,13	12	10	12	22	14	11	15	12	20	1	0.0072	MF-1
Mr35	15	13	23	29	17	16	11,17	14	11	12	22	11	11	14	10	21	1	0.0072	MF-1
Mr36	16	14	22	29	18	15	15,17	12	10	12	20	11	11	14	9	19	1	0.0072	MF-1
Mr37	15	12	24	28	19	14	13,21	12	10	12	21	14	12	15	11	20	8	0.0579	MF-2
Mr38	15	14	25	27	15	16	11,14	13	10	10	23	13	13	14	11	20	1	0.0072	MF-1
Mr39	15	13	24	30	17	15	13,18	12	10	12	20	14	12	16	11	20	1	0.0072	MF-1
Mr40	16	14	23	30	16	15	14,16	12	10	12	20	11	14	15	9	20	2	0.0145	MF-1
Mr41	16	14	23	30	16	15	14,16	12	10	12	20	11	12	15	9	20	1	0.0072	MF-2
Mr42	15	12	24	27	17	14	14,19	12	10	12	21	14	13	15	11	20	1	0.0072	MF-1
Mr43	15	14	25	30	16	15	11,20	15	10	11	21	11	11	14	10	20	1	0.0072	MF-1
Mr44	15	12	24	30	18	14	14,21	12	10	11	20	13	12	15	11	19	1	0.0072	MF-1
Mr45	15	12	24	27	18	15	13,20	12	10	13	20	11	12	15	11	20	1	0.0072	MF-1
Mr46	16	12	23	28	17	14	13,19	12	10	12	20	15	12	15	11	20	1	0.0072	MF-1
Mr47	15	13	25	27	17	16	15,20	14	10	11	21	15	11	14	10	18	1	0.0072	MF-1
Mr48	15	12	24	27	17	14	14,19	12	9	13	22	14	12	14	11	18	1	0.0072	MF-1
Mr49	15	14	25	27	16	15	11,20	15	10	11	21	11	11	14	10	20	1	0.0072	MF-1

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Mr50	15	12	23	27	17	14	13,19	12	10	12	23	14	13	15	11	20	1	0.0072	MF-1
Mr51	15	12	24	29	18	14	14,20	12	10	11	20	13	14	14	11	20	1	0.0072	MF-1
Mr52	15	12	24	28	18	14	14,20	12	10	11	20	14	14	14	11	20	1	0.0072	MF-2
Mr53	15	12	24	29	17	14	13,20	12	10	12	23	14	13	15	11	19	1	0.0072	MF-1
Mr54	15	13	24	29	18	14	13,19	12	10	13	20	14	13	15	11	20	1	0.0072	MF-1
Mr55	15	12	24	27	18	14	13,19	12	10	13	21	14	12	15	11	20	1	0.0072	MF-2
Mr56	15	14	25	28	16	15	11,20	15	10	11	21	15	11	14	10	20	1	0.0072	MF-1
Mr57	15	12	24	29	18	14	13,19	12	10	13	21	14	12	14	11	20	1	0.0072	MF-1
Mr58	12	14	25	28	19	14	14,21	12	10	11	20	14	12	15	11	19	1	0.0072	MF-1
Mr59	15	12	24	30	17	14	13,19	12	10	12	23	13	13	15	11	20	1	0.0072	MF-1
Mr60	16	14	23	30	16	15	14,16	12	10	12	20	14	14	15	9	20	1	0.0072	MF-1
Mr61	15	12	24	28	18	15	13,20	12	10	13	20	14	12	15	11	20	1	0.0072	MF-1
Mr62	15	12	23	28	18	14	13,18	12	10	11	20	14	12	15	11	20	1	0.0072	MF-3
Mr63	15	10	24	27	19	14	14,18	12	10	11	20	14	13	15	11	20	3	0.0217	MF-1
Mr64	16	13	25	27	16	15	14,20	14	10	12	21	13	11	14	10	18	1	0.0072	MF-1
Mr65	15	12	25	28	18	14	13,18	12	10	12	20	14	11	15	11	21	1	0.0072	MF-1
Mr66	17	13	23	29	15	14	12,19	14	10	11	26	11	12	16	11	19	1	0.0072	MF-1
Mr67	15	12	23	29	17	16	10,16	12	10	12	20	13	12	15	10	19	1	0.0072	MF-1
Mr68	16	14	23	27	16	15	14,16	12	10	12	20	13	13	15	9	20	1	0.0072	MF-1
Mr69	15	12	24	28	19	14	13,21	12	10	12	21	10	12	15	11	20	1	0.0072	MF-1
Mr70	15	12	23	28	19	14	13,20	12	10	11	20	14	12	15	11	20	2	0.0145	MF-3
Mr71	15	12	24	28	18	14	13,20	13	10	13	20	14	12	15	11	20	1	0.0072	MF-1
Mr72	15	14	25	31	16	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0072	MF-12
Mr73	15	14	25	28	15	16	11,14	13	10	10	23	11	13	14	11	19	1	0.0072	MF-1
Mr74	18	12	24	28	18	14	13,13	12	10	12	22	14	11	15	12	20	1	0.0072	MF-1
Mr75	15	12	25	29	20	15	14,16	12	10	11	20	10	11	14	10	19	1	0.0072	MF-1
Mr76	16	14	23	28	16	15	14,16	12	10	12	20	11	13	15	9	20	1	0.0072	MF-1
Mr77	15	12	23	29	18	14	13,19	12	10	13	21	13	12	15	11	20	1	0.0072	MF-1
Mr78	15	12	24	28	19	14	14,20	12	10	11	20	14	14	14	11	20	1	0.0072	MF-1
Mr79	15	12	23	29	18	16	12,16	12	9	12	19	12	11	15	10	19	1	0.0072	MF-2
Mr80	15	12	24	29	19	14	13,21	12	10	12	21	13	12	15	11	20	1	0.0072	MF-1
Mr81	15	14	25	33	15	16	11,14	13	10	10	23	11	13	14	11	20	1	0.0072	MF-1
Mr82	15	12	24	28	19	14	13,21	12	10	11	21	14	12	15	11	20	1	0.0072	MF-1
Mr83	15	12	24	29	19	14	13,21	12	10	11	21	14	12	15	12	20	1	0.0072	MF-1
Mr84	15	12	24	28	18	14	14,22	12	10	11	20	14	12	15	11	19	1	0.0072	MF-1
Mr85	15	12	25	29	18	15	12,17	12	10	11	19	13	12	15	10	19	1	0.0072	MF-1
Mr86	15	13	25	29	17	16	15,20	14	10	11	21	13	11	14	10	18	1	0.0072	MF-1
Mr87	15	14	25	31	16	15	11,14	13	10	10	23	11	12	14	11	20	1	0.0072	MF-8
Mr88	15	13	24	31	16	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0072	MF-3
Mr89	15	12	24	27	18	14	13,19	12	10	13	21	14	12	15	11	19	2	0.0145	MF-1
Mr90	16	14	23	30	16	15	14,16	12	10	12	20	11	11	15	9	20	1	0.0072	MF-1
Mr91	15	12	24	27	17	14	12,19	12	10	12	23	14	13	15	11	20	1	0.0072	MF-1
Mr92	16	12	23	28	19	14	13,18	12	10	11	21	10	12	15	11	20	1	0.0072	MF-1
Mr93	15	14	25	29	16	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0072	MF-1
Mr94	17	13	23	29	15	14	12,19	14	10	11	26	10	12	16	11	19	1	0.0072	MF-1
Mr95	15	14	25	31	18	15	15,18	14	10	11	22	13	11	14	10	19	1	0.0072	MF-1
Mr96	15	12	24	28	18	14	14,21	12	10	11	20	12	12	15	11	19	1	0.0072	MF-1
Mr97	16	12	24	28	18	14	14,21	12	10	11	20	12	12	15	11	19	1	0.0072	MF-1
Mr98	15	12	23	29	19	14	13,20	12	10	11	20	14	12	15	11	20	1	0.0072	MF-1
Mr99	15	14	23	30	16	14	11,12	13	10	11	22	14	11	14	11	19	1	0.0072	MF-1
Mr100	17	12	24	31	17	14	13,13	12	10	12	22	13	11	15	12	20	1	0.0072	MF-1

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Mr101	17	12	24	28	17	14	13,13	12	10	12	22	11	11	15	12	20	1	0.0072	MF-1
Mr102	16	12	24	28	17	14	13,17	12	10	12	20	14	12	15	11	20	1	0.0072	MF-2
Mr103	17	12	24	28	20	15	15,16	11	10	11	20	10	11	14	10	19	1	0.0072	MF-2
Mr104	15	12	24	28	18	14	13,21	12	10	12	21	14	12	15	11	20	1	0.0072	MF-2
Mr105	15	12	24	28	19	14	15,20	12	10	11	20	14	14	14	11	20	1	0.0072	MF-1
Mr106	16	13	24	29	16	16	15,20	13	10	12	23	14	13	14	10	18	1	0.0072	MF-1
Mr107	15	12	23	28	19	14	13,19	11	10	11	22	14	12	15	11	20	1	0.0072	MF-1

N= Number of Individual; *F:* Frequency of each haplotype in 138 Marma males; YHRD: Y-Chromosome Haplotype Reference Database; MF: Match Found; NMF: No Match Found

Supplementary Table 6. A list of Y-chromosome STR haplotypes detected in 109 unrelated males in Hajong (Hj) population

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Hj1	16	12	24	29	17	15	13,15	12	10	12	21	14	12	15	11	19	1	0.0091	MF-1
Hj2	15	12	24	28	17	15	13,18	12	10	12	21	14	11	15	11	20	2	0.0183	MF-2
Hj3	15	13	24	29	17	14	12,18	14	10	10	24	10	13	16	11	19	3	0.0275	MF-1
Hj4	15	12	24	28	20	14	13,18	13	11	13	20	14	11	15	11	20	2	0.0183	MF-1
Hj5	15	12	24	28	17	15	13,19	12	10	12	20	14	12	15	11	20	1	0.0091	MF-2
Hj6	15	14	24	27	18	14	13,19	12	10	13	21	15	12	15	11	20	1	0.0091	MF-1
Hj7	14	12	23	23	15	14	13,19	12	11	11	20	10	13	15	11	20	1	0.0091	MF-1
Hj8	15	13	24	32	16	16	11,14	13	11	10	23	11	12	14	11	20	1	0.0091	MF-1
Hj9	13	13	24	29	17	15	13,17	12	10	14	21	11	11	15	9	19	2	0.0183	MF-1
Hj10	16	12	23	28	18	14	13,21	12	10	11	20	14	13	15	11	20	1	0.0091	MF-1
Hj11	15	12	25	28	18	14	13,20	12	10	12	21	14	12	15	12	19	1	0.0091	MF-1
Hj12	15	12	23	30	19	15	12,16	13	10	12	19	12	12	14	10	19	1	0.0091	MF-1
Hj13	16	14	22	30	14	14	13,17	11	10	13	24	14	12	15	11	19	2	0.0183	MF-1
Hj14	15	13	25	30	16	16	11,13	12	10	11	23	11	12	14	11	20	1	0.0091	MF-1
Hj15	16	14	22	30	18	16	9,16	12	10	12	22	14	11	16	10	20	2	0.0183	MF-1
Hj16	15	12	23	28	19	15	13,18	11	9	12	21	14	12	15	11	20	1	0.0091	MF-1
Hj17	15	13	25	29	14	15	15,18	12	9	12	21	13	11	14	10	18	1	0.0091	MF-1
Hj18	15	12	24	29	17	15	13,19	11	9	12	21	14	12	15	11	19	1	0.0091	MF-1
Hj19	15	14	24	27	18	14	13,19	11	9	12	20	15	12	15	11	20	1	0.0091	MF-1
Hj20	16	12	24	28	17	14	13,18	11	9	13	20	14	12	15	11	20	1	0.0091	MF-1
Hj21	15	12	25	28	17	15	14,21	11	9	12	23	13	11	16	11	20	2	0.0183	MF-1
Hj22	14	13	24	28	16	15	14,22	11	9	12	20	14	12	15	11	20	1	0.0091	MF-1
Hj23	15	12	23	28	18	15	13,18	11	9	12	22	14	12	15	11	20	1	0.0091	MF-1
Hj24	16	13	24	29	16	14	13,19	11	9	12	20	14	12	15	11	20	1	0.0091	MF-1
Hj25	15	12	22	28	15	14	15,15	10	9	13	24	14	12	15	10	19	1	0.0091	MF-1
Hj26	13	13	23	30	16	14	13,16	13	9	11	26	11	12	16	11	19	1	0.0091	MF-1
Hj27	14	12	22	28	18	15	13,20	13	9	11	20	14	12	15	11	20	1	0.0091	MF-1
Hj28	17	13	24	30	16	15	15,19	14	10	13	21	13	10	14	10	18	1	0.0091	MF-1
Hj29	15	14	25	31	15	15	11,14	13	11	11	23	11	12	14	11	20	1	0.0091	MF-1
Hj30	15	12	24	28	18	14	13,18	12	10	12	20	14	12	15	11	20	2	0.0183	MF-7
Hj31	16	13	25	29	15	15	14,20	14	11	12	21	13	11	14	10	18	2	0.0183	MF-1
Hj32	13	12	24	28	17	15	13,17	12	10	12	22	11	11	15	9	19	1	0.0091	MF-1
Hj33	15	13	25	30	16	16	11,14	13	11	10	23	11	12	14	11	20	1	0.0091	MF-14
Hj34	15	12	24	28	17	14	13,18	12	10	12	20	14	12	15	11	20	1	0.0091	MF-8
Hj35	15	12	24	28	17	17	14,15	12	10	12	21	13	11	14	11	20	1	0.0091	MF-1
Hj36	14	12	23	28	15	14	13,18	12	10	11	20	14	13	15	11	21	1	0.0091	MF-1
Hj37	15	12	25	28	17	15	14,21	12	10	12	22	13	11	16	11	20	1	0.0091	MF-1
Hj38	15	13	25	31	15	15	11,14	13	11	10	23	11	12	14	11	21	1	0.0091	MF-1
Hj39	17	12	23	27	16	14	13,20	12	10	11	21	14	12	15	11	20	1	0.0091	MF-1
Hj40	15	12	24	28	16	15	13,20	12	11	14	21	13	11	15	11	20	2	0.0183	MF-1
Hj41	15	14	25	31	17	15	11,14	13	10	10	25	11	14	14	11	20	1	0.0091	MF-1
Hj42	16	12	23	29	18	14	13,23	12	10	11	20	14	13	15	10	21	1	0.0091	MF-1
Hj43	16	12	23	28	17	14	13,18	12	10	11	21	14	13	15	11	20	1	0.0091	MF-1
Hj44	16	12	23	29	18	14	13,22	12	10	11	20	14	13	15	10	20	1	0.0091	MF-1
Hj45	14	12	23	28	15	14	13,18	12	10	11	20	14	13	15	11	20	1	0.0091	MF-1
Hj46	15	13	22	29	18	14	15,16	12	10	11	20	11	11	14	9	19	2	0.0183	MF-1
Hj47	15	13	25	29	14	15	15,18	13	11	12	21	13	11	14	10	18	1	0.0091	MF-1
Hj48	15	12	23	28	18	14	13,20	12	10	11	20	14	12	15	11	20	3	0.0275	MF-3
Hj49	16	13	25	30	16	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0091	MF-15

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Hj50	17	12	23	28	20	14	13,20	12	10	11	20	14	11	15	11	20	1	0.0091	MF-1
Hj51	13	13	23	30	16	14	13,16	14	10	11	26	11	12	16	11	19	2	0.0183	MF-1
Hj52	14	13	23	29	16	14	15,16	13	11	11	20	11	11	14	10	18	2	0.0183	MF-1
Hj53	17	12	23	28	19	14	13,21	12	10	12	20	14	12	15	11	20	1	0.0091	MF-1
Hj54	15	13	24	30	17	16	**11,13.2**	13	11	10	23	11	12	14	11	20	2	0.0183	MF-1
Hj55	16	12	24	28	17	14	13,18	12	10	13	20	14	12	15	11	20	1	0.0091	MF-3
Hj56	16	14	22	30	14	14	13,17	11	10	13	24	11	12	15	11	19	1	0.0091	MF-1
Hj57	15	13	24	25	17	14	10,14	12	10	12	19	7	12	15	11	16	1	0.0091	MF-1
Hj58	14	12	23	29	15	14	13,19	12	10	11	20	14	13	15	11	20	2	0.0183	MF-1
Hj59	16	14	23	29	19	15	13,19	14	10	11	25	10	13	16	11	19	1	0.0091	MF-1
Hj60	16	12	23	29	19	14	13,23	12	10	11	20	14	13	15	10	20	1	0.0091	MF-1
Hj61	15	13	24	29	18	15	13,18	12	10	12	21	14	11	15	11	20	1	0.0091	MF-2
Hj62	15	14	24	30	16	15	16,19	14	11	10	21	13	10	14	10	18	1	0.0091	MF-1
Hj63	15	12	23	28	17	15	13,20	12	10	11	20	14	12	15	11	21	1	0.0091	MF-1
Hj64	15	14	22	28	17	15	14,19	13	10	12	20	11	11	15	10	19	1	0.0091	MF-1
Hj65	15	14	24	31	16	15	11,14	13	10	10	23	11	10	14	11	20	1	0.0091	MF-1
Hj66	15	12	25	28	17	15	14,21	12	10	12	23	13	11	16	11	20	2	0.0183	MF-1
Hj67	15	13	25	29	14	15	16,17	13	11	12	21	13	11	14	10	18	2	0.0183	MF-1
Hj68	15	12	23	28	18	14	13,21	12	10	11	20	14	12	15	11	20	1	0.0091	MF-2
Hj69	13	13	23	30	16	14	13,16	14	10	11	26	11	12	16	11	20	1	0.0091	MF-1
Hj70	17	13	24	29	16	15	15,19	14	10	13	21	13	10	14	10	18	1	0.0091	MF-1
Hj71	16	12	23	28	18	14	13,19	12	10	12	20	14	13	15	11	20	1	0.0091	MF-1
Hj72	15	12	24	28	20	16	13,19	12	10	11	22	14	12	15	11	19	1	0.0091	MF-1
Hj73	16	12	23	30	18	14	13,21	12	10	11	20	14	13	15	10	20	1	0.0091	MF-1
Hj74	15	12	23	28	18	14	13,21	12	11	11	21	14	12	15	11	20	1	0.0091	MF-1
Hj75	16	12	23	31	18	15	12,16	13	10	13	19	12	12	14	10	19	1	0.0091	MF-1
Hj76	16	12	23	28	18	14	13,19	12	10	11	20	14	12	14	11	20	1	0.0091	MF-1
Hj77	15	12	24	28	17	14	13,18	12	10	12	20	14	11	15	11	20	1	0.0091	MF-6
Hj78	15	12	24	28	16	14	13,18	12	10	12	20	14	12	15	12	20	1	0.0091	MF-1
Hj79	15	13	22	29	17	16	11,14	14	10	11	21	12	11	15	10	17	1	0.0091	MF-1
Hj80	16	14	22	30	20	15	15,16	12	9	11	20	11	11	14	9	19	1	0.0091	MF-1
Hj81	15	12	23	29	18	14	13,21	12	10	11	20	14	12	15	11	20	1	0.0091	MF-1
Hj82	15	12	23	28	17	15	13,21	12	10	13	21	13	11	15	11	20	1	0.0091	MF-1
Hj83	15	13	24	29	17	14	13,19	12	10	12	20	14	12	15	11	20	1	0.0091	MF-1
Hj84	15	12	25	28	14	14	11,15	12	10	13	23	13	12	15	12	20	1	0.0091	MF-1
Hj85	17	13	24	30	16	15	15,19	14	10	12	21	13	10	14	10	18	1	0.0091	MF-1
Hj86	15	13	21	30	17	15	12,18	13	11	11	21	11	11	15	10	20	1	0.0091	MF-1
Hj87	15	14	24	31	17	15	12,14	13	11	10	23	11	13	14	11	20	1	0.0091	MF-1
Hj88	15	13	24	29	17	14	13,18	12	10	12	20	14	12	15	11	20	1	0.0091	MF-4
Hj89	15	12	23	29	18	15	12,16	12	10	13	19	12	11	15	10	19	1	0.0091	MF-1

N= Number of Individual; *F:* Frequency of each haplotype in 109 Hajong males; YHRD: Y-Chromosome Haplotype Reference Database; MF: Match Found; NMF: No Match Found

Supplementary Table 7. A list of Y-chromosome STR haplotypes detected in 131 unrelated males in Manipuri (Mn) population.

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Mn1	15	12	24	29	17	14	13,19	12	10	12	20	11	13	14	11	20	1	0.0076	MF-1
Mn2	15	12	25	27	17	15	16,20	12	10	12	20	13	11	15	11	20	2	0.0153	MF-1
Mn3	16	12	23	28	18	14	12,20	12	10	11	20	14	14	15	11	20	1	0.0076	MF-1
Mn4	15	12	25	28	17	15	16,19	10	10	12	20	12	11	15	11	20	1	0.0076	MF-1
Mn5	16	14	24	30	15	16	14,20	14	10	13	23	11	13	14	10	18	1	0.0076	MF-1
Mn6	15	12	23	28	16	14	13,20	12	10	12	20	14	12	15	11	19	1	0.0076	MF-1
Mn7	15	12	25	27	16	14	13,19	12	10	12	21	14	11	15	11	20	2	0.0153	MF-1
Mn8	15	13	25	32	16	15	11,14	13	10	10	23	10	13	14	11	20	1	0.0076	MF-1
Mn9	15	14	23	30	16	14	19,21	13	10	11	24	12	12	15	11	19	1	0.0076	MF-1
Mn10	15	13	24	33	16	16	11,14	13	10	10	23	11	13	14	11	20	1	0.0076	MF-1
Mn11	15	14	23	30	16	15	19,20	13	10	11	24	13	12	15	11	19	1	0.0076	MF-1
Mn12	15	14	23	30	16	14	19,20	13	10	11	24	12	12	15	11	19	1	0.0076	MF-1
Mn13	15	13	24	27	16	14	11,13	13	10	10	23	12	13	14	11	20	1	0.0076	MF-1
Mn14	15	13	25	32	16	15	11,14	13	10	10	23	11	13	14	11	20	4	0.0305	MF-3
Mn15	15	13	24	28	16	17	11,14	13	10	9	23	11	12	14	11	20	1	0.0076	MF-1
Mn16	15	13	25	32	16	15	11,14	13	10	10	23	12	13	14	11	18	1	0.0076	MF-1
Mn17	15	14	23	30	16	14	20,20	13	10	10	24	12	12	15	11	19	2	0.0153	MF-1
Mn18	16	13	25	31	15	16	11,14	13	10	10	23	11	10	14	11	20	2	0.0153	MF-1
Mn19	14	12	26	28	16	14	14,17	13	11	12	22	12	11	15	9	19	1	0.0076	MF-1
Mn20	15	14	23	30	16	14	20,20	13	10	10	24	11	12	14	11	20	1	0.0076	MF-1
Mn21	15	14	23	31	16	15	20,20	13	10	11	24	12	12	15	11	19	1	0.0076	MF-1
Mn22	15	13	25	29	16	15	11,14	13	10	10	32	12	13	14	11	20	1	0.0076	NMF
Mn23	16	13	24	30	15	16	11,14	13	10	11	23	12	13	14	11	20	1	0.0076	MF-1
Mn24	15	13	24	32	16	16	11,14	12	10	10	23	11	13	14	11	20	1	0.0076	MF-1
Mn25	15	13	23	29	17	14	12,17	14	10	10	26	10	12	16	11	19	1	0.0076	MF-2
Mn26	17	13	25	31	16	15	11,14	12	11	11	23	11	13	14	11	20	1	0.0076	MF-1
Mn27	16	13	24	31	15	16	11,18	12	10	10	24	12	10	14	10	20	1	0.0076	MF-1
Mn28	15	14	23	30	16	14	19,20	12	10	11	24	12	12	15	11	19	1	0.0076	MF-1
Mn29	14	12	26	28	16	14	14,17	12	11	12	22	11	11	15	9	19	1	0.0076	MF-1
Mn30	15	12	24	29	17	14	13,19	12	10	11	21	14	13	15	11	20	1	0.0076	NMF
Mn31	15	12	23	30	18	14	13,19	12	10	11	20	14	13	15	11	20	1	0.0076	NMF
Mn32	15	13	23	29	17	14	13,19	12	10	12	20	14	12	15	11	20	2	0.0153	NMF
Mn33	15	12	24	29	17	14	13,19	12	10	12	20	14	13	14	11	20	1	0.0076	NMF
Mn34	15	12	24	28	18	**13.2**	13,19	12	10	11	21	14	12	15	11	20	1	0.0076	NMF
Mn35	15	12	23	28	18	14	14,20	12	10	11	19	15	13	15	11	20	5	0.0382	NMF
Mn36	15	14	23	30	16	14	20,20	13	10	11	24	12	12	15	11	19	9	0.0687	NMF
Mn37	16	13	25	30	15	15	11,14	13	10	10	21	11	13	14	11	20	8	0.0611	NMF
Mn38	14	14	23	31	17	15	14,19	12	10	12	22	11	11	14	9	21	1	0.0076	NMF
Mn39	15	14	23	30	16	14	20,20	14	10	11	24	12	12	15	11	19	2	0.0153	NMF
Mn40	15	12	23	29	19	14	14,20	12	10	11	19	14	13	15	11	20	1	0.0076	NMF
Mn41	15	13	23	29	17	14	12,17	15	10	10	26	10	12	16	11	19	1	0.0076	NMF
Mn42	16	13	22	29	17	14	15,17	12	10	13	21	11	12	14	10	19	2	0.0153	NMF
Mn43	15	14	23	31	16	14	20,20	13	10	11	24	12	12	14	11	19	2	0.0153	NMF
Mn44	15	13	25	32	15	15	11,14	13	10	10	23	11	13	14	11	20	1	0.0076	NMF
Mn45	14	13	24	32	16	18	11,13	13	10	10	23	11	13	14	11	20	1	0.0076	NMF
Mn46	15	12	24	28	18	14	13,19	12	10	11	20	14	12	15	11	20	1	0.0076	MF-1
Mn47	15	14	23	32	16	14	20,20	13	10	11	24	11	12	15	11	19	1	0.0076	NMF
Mn48	15	13	22	29	17	14	12,17	15	10	10	26	10	12	16	11	19	1	0.0076	NMF
Mn49	15	12	23	30	18	14	14,20	12	9	11	19	12	13	15	11	20	1	0.0076	NMF

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Mn50	15	14	25	28	16	16	11,14	13	10	10	25	13	13	14	11	20	1	0.0076	NMF
Mn51	16	14	25	32	16	15	11,14	13	10	10	25	11	13	14	11	20	1	0.0076	NMF
Mn52	15	12	24	28	19	15	15,17	13	10	12	21	11	11	15	9	18	1	0.0076	NMF
Mn53	15	12	24	28	18	14	13,19	12	10	11	21	14	12	15	11	20	2	0.0153	MF-2
Mn54	15	14	23	29	16	14	12,20	13	10	11	24	13	12	15	11	19	1	0.0076	NMF
Mn55	16	13	22	29	17	14	15,17	12	10	13	21	12	12	14	10	19	1	0.0076	NMF
Mn56	15	14	24	32	16	15	11,15	13	10	10	23	11	12	14	11	20	1	0.0076	NMF
Mn57	15	14	25	30	16	15	11,14	13	10	10	25	11	12	14	11	20	1	0.0076	MF-1
Mn58	15	14	25	28	16	15	11,14	13	10	10	25	11	13	14	11	20	1	0.0076	NMF
Mn59	15	14	23	32	16	14	20,20	13	10	10	24	11	12	15	11	19	1	0.0076	NMF
Mn60	15	12	23	28	18	14	14,20	12	9	11	19	15	13	15	11	20	1	0.0076	NMF
Mn61	15	13	23	29	17	14	13,19	12	10	12	20	14	11	15	11	20	1	0.0076	MF-2
Mn62	15	14	25	32	16	17	11,14	13	10	10	23	11	12	14	9	20	2	0.0153	NMF
Mn63	15	14	25	31	16	17	11,14	13	10	10	23	11	12	14	9	20	1	0.0076	NMF
Mn64	15	14	23	32	16	14	20,20	13	10	10	24	12	12	15	11	19	1	0.0076	NMF
Mn65	14	12	26	28	16	14	14,17	13	11	12	22	11	11	15	9	19	2	0.0153	NMF
Mn66	15	12	24	30	19	14	13,18	12	10	12	20	14	12	15	11	20	1	0.0076	NMF
Mn67	15	12	24	29	17	14	13,19	12	10	12	20	12	12	15	12	19	1	0.0076	NMF
Mn68	15	12	24	28	17	14	13,19	12	10	12	20	14	12	15	12	19	1	0.0076	NMF
Mn69	15	14	23	31	16	14	20,20	13	10	10	24	12	12	15	11	19	1	0.0076	NMF
Mn70	15	14	25	30	16	17	11,14	13	10	10	23	11	12	14	9	20	1	0.0076	NMF
Mn71	16	13	25	31	15	16	11,14	13	10	10	23	11	13	14	11	20	1	0.0076	MF-7
Mn72	15	13	24	28	16	17	11,13	13	10	10	23	11	13	14	11	20	1	0.0076	NMF
Mn73	15	13	22	29	17	15	15,17	12	10	11	20	11	13	14	9	19	1	0.0076	MF-1
Mn74	15	14	25	30	16	17	11,14	13	10	10	23	12	12	14	9	20	1	0.0076	NMF
Mn75	15	12	24	29	17	14	13,18	12	10	12	20	14	12	15	11	20	1	0.0076	NMF
Mn76	15	12	24	29	17	14	13,19	12	10	12	20	14	11	15	11	20	1	0.0076	MF-1
Mn77	15	12	24	29	16	14	13,19	12	10	11	20	12	12	15	11	20	1	0.0076	NMF
Mn78	15	13	22	30	17	14	12,17	15	10	10	26	10	12	16	11	19	1	0.0076	NMF
Mn79	15	14	24	31	16	16	11,14	13	10	10	23	13	13	14	11	20	1	0.0076	NMF
Mn80	16	13	24	28	15	15	11,14	13	10	10	21	11	13	14	11	20	1	0.0076	NMF
Mn81	16	13	25	30	15	15	11,14	13	10	10	21	13	13	14	11	20	1	0.0076	NMF
Mn82	15	13	25	29	16	15	11,14	13	12	11	23	12	12	14	11	20	1	0.0076	NMF
Mn83	15	14	23	31	16	14	20,20	13	10	11	24	12	12	15	11	19	1	0.0076	NMF
Mn84	15	14	23	30	16	14	18,20	13	10	11	24	12	12	15	11	19	1	0.0076	NMF
Mn85	15	14	24	30	18	14	13,18	12	10	13	21	14	12	15	11	20	1	0.0076	NMF
Mn86	15	15	23	31	16	14	20,20	13	10	11	24	12	12	15	11	19	1	0.0076	NMF
Mn87	16	13	26	31	15	16	11,14	13	10	10	23	13	13	14	11	20	1	0.0076	NMF
Mn88	15	14	25	29	16	17	11,14	13	10	10	23	11	12	14	9	20	1	0.0076	NMF
Mn89	15	12	23	28	16	15	14,19	12	10	12	20	14	12	15	11	20	1	0.0076	NMF
Mn90	15	13	24	32	16	16	11,14	13	10	10	23	11	13	14	11	20	1	0.0076	NMF
Mn91	15	12	24	31	18	14	12,19	12	10	11	21	11	12	15	11	20	1	0.0076	NMF
Mn92	16	13	25	31	15	15	11,14	13	10	10	21	11	13	14	11	20	1	0.0076	NMF
Mn93	15	13	25	31	16	15	11,14	13	10	10	23	10	13	14	11	20	1	0.0076	NMF
Mn94	15	14	23	31	16	14	20,20	12	10	11	24	12	12	15	11	19	1	0.0076	NMF
Mn95	15	13	24	31	16	16	11,14	13	10	10	23	11	13	14	11	20	1	0.0076	MF-1
Mn96	15	13	22	30	17	15	15,17	12	10	11	20	11	13	14	9	20	1	0.0076	NMF
Mn97	16	13	24	30	15	15	11,14	13	10	10	21	11	13	14	11	20	1	0.0076	NMF
Mn98	15	12	25	28	16	14	13,19	12	10	12	20	14	12	15	11	20	1	0.0076	NMF

N= Number of Individual; *F:* Frequency of each haplotype in 131 Manipuri males; YHRD: Y-Chromosome Haplotype Reference Database; MF: Match Found; NMF: No Match Found

Supplementary Table 8. A list of Y-chromosome STR haplotypes detected in 110 unrelated males in Khasia (Kh) population

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Kh1	15	13	25	29	16	15	15,22	14	11	13	21	13	11	14	10	18	2	0.0181	MF-1
Kh2	14	14	23	30	16	14	18,18	14	11	10	20	12	11	15	11	19	1	0.0091	MF-1
Kh3	15	13	25	29	16	15	15,18	12	10	11	21	12	10	14	10	18	1	0.0091	MF-1
Kh4	15	13	25	30	17	15	15,19	14	10	11	21	12	10	14	10	18	1	0.0091	MF-1
Kh5	15	13	23	28	16	15	12,17	15	10	13	20	11	11	14	10	21	1	0.0091	MF-1
Kh6	14	14	24	30	17	14	15,19	12	10	13	23	11	11	14	9	20	1	0.0091	MF-1
Kh7	16	13	25	29	16	15	15,19	14	11	11	21	13	11	14	10	18	1	0.0091	MF-1
Kh8	16	13	24	30	16	15	15,20	14	11	12	21	13	11	14	10	18	1	0.0091	MF-1
Kh9	15	13	25	29	16	15	15,23	14	11	13	21	13	11	14	10	18	1	0.0091	MF-1
Kh10	15	14	23	30	16	15	12,17	13	10	11	19	12	11	15	10	19	1	0.0091	MF-1
Kh11	15	14	25	31	16	15	11,14	13	10	10	23	11	12	14	11	20	1	0.0091	MF-8
Kh12	15	13	25	28	17	15	14,18	15	11	12	21	13	11	14	10	18	1	0.0091	MF-1
Kh13	14	12	24	28	17	14	14,18	12	10	12	21	14	12	15	10	20	1	0.0091	MF-1
Kh14	17	14	25	31	16	15	11,15	13	10	10	23	11	13	14	12	19	2	0.0181	MF-1
Kh15	15	13	23	30	17	14	14,19	15	10	10	25	10	11	16	11	19	1	0.0091	MF-1
Kh16	15	13	25	29	17	15	15,19	14	10	11	21	13	10	14	10	18	6	0.0545	MF-2
Kh17	15	14	22	30	18	13	12,16	13	10	12	23	15	10	15	11	19	1	0.0091	MF-1
Kh18	15	14	25	32	16	16	11,14	13	11	10	23	11	13	14	11	20	1	0.0091	MF-1
Kh19	16	12	23	27	15	15	11,17	15	10	12	20	11	11	14	10	21	1	0.0091	MF-1
Kh20	15	12	23	28	17	15	13,22	12	10	13	21	13	11	14	11	20	1	0.0091	MF-1
Kh21	16	13	26	29	15	15	16,19	14	10	13	21	13	10	14	10	18	1	0.0091	MF-1
Kh22	17	13	25	29	16	15	15,21	14	11	12	21	13	11	14	10	18	1	0.0091	MF-1
Kh23	16	13	22	30	17	15	15,17	12	11	11	20	12	11	14	9	19	1	0.0091	MF-1
Kh24	15	14	25	30	16	16	15,20	14	11	11	21	13	11	14	10	18	1	0.0091	MF-1
Kh25	14	14	23	29	16	14	13,19	15	10	10	25	10	12	14	11	19	1	0.0091	MF-1
Kh26	15	12	25	29	17	16	13,16	14	10	11	22	14	12	14	12	19	1	0.0091	MF-1
Kh27	16	13	25	29	17	15	16,19	14	10	11	22	13	11	14	10	18	1	0.0091	MF-1
Kh28	14	14	23	30	16	14	13,18	14	11	10	25	10	11	15	11	19	1	0.0091	MF-1
Kh29	15	13	26	28	16	15	13,18	15	11	11	21	13	11	14	10	18	1	0.0091	MF-1
Kh30	15	14	25	32	16	15	11,12	13	10	10	24	11	13	14	11	20	1	0.0091	MF-1
Kh31	15	13	23	30	17	15	12,18	13	10	11	19	12	11	15	10	19	1	0.0091	MF-1
Kh32	16	13	24	29	16	15	16,19	14	10	12	21	13	12	14	10	18	1	0.0091	NMF
Kh33	16	13	24	28	16	16	14,20	14	10	14	22	14	13	14	10	18	1	0.0091	NMF
Kh34	15	13	25	29	16	16	16,19	14	11	12	22	13	11	14	10	18	1	0.0091	NMF
Kh35	15	13	23	30	17	15	12,17	13	10	11	19	12	11	15	10	19	2	0.0181	NMF
Kh36	15	13	23	30	15	14	14,14	13	12	11	22	11	13	14	9	19	1	0.0091	NMF
Kh37	16	14	25	32	17	15	15,20	14	10	12	21	13	11	14	10	18	2	0.0181	NMF
Kh38	16	14	23	30	18	15	12,16	13	10	11	19	12	11	15	10	19	3	0.0273	NMF
Kh39	15	13	25	29	15	16	17,17	14	11	12	22	13	11	14	10	18	1	0.0091	NMF
Kh40	15	13	23	28	15	15	12,17	14	10	12	20	11	10	14	10	22	1	0.0091	NMF
Kh41	14	13	23	28	17	15	13,17	14	10	10	25	10	12	15	11	19	1	0.0091	NMF
Kh42	15	14	25	31	16	15	10,14	13	10	11	23	11	13	14	11	20	1	0.0091	NMF
Kh43	15	13	25	29	16	15	15,21	14	10	12	21	13	10	14	10	18	1	0.0091	NMF
Kh44	14	13	23	28	17	14	13,17	14	11	10	25	10	12	15	11	19	1	0.0091	NMF
Kh45	15	13	23	30	18	15	12,17	13	11	11	19	12	11	15	10	19	1	0.0091	NMF
Kh46	15	13	25	29	17	15	15,19	14	10	11	21	12	10	14	10	18	1	0.0091	NMF
Kh47	15	13	23	30	16	14	14,20	13	10	11	22	12	11	14	9	20	1	0.0091	NMF
Kh48	15	13	23	28	15	15	11,18	14	10	12	20	11	11	14	10	21	1	0.0091	NMF
Kh49	15	13	24	30	16	15	12,17	13	10	12	19	12	11	15	10	19	1	0.0091	NMF

Haplotype/ Locus	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a/b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**YGATAH4**	**DYS437**	**DYS438**	**DYS448**	***Individual (N)***	***Frequency (F)***	***Searched in YHRD***
Kh50	15	13	23	30	17	15	12,17	13	10	11	19	12	11	14	10	19	2	0.0181	NMF
Kh51	15	13	24	30	17	15	15,16	14	10	11	18	11	12	14	10	19	2	0.0181	NMF
Kh52	17	13	23	29	17	15	13,15	12	10	13	22	11	11	16	10	20	1	0.0091	NMF
Kh53	15	13	23	28	15	15	12,17	15	10	12	21	11	11	14	10	21	1	0.0091	NMF
Kh54	16	13	25	29	15	15	16,19	15	11	12	21	13	12	14	10	18	1	0.0091	NMF
Kh55	15	13	22	31	19	14	14,16	13	10	11	18	11	12	14	10	20	1	0.0091	NMF
Kh56	15	14	25	30	16	16	15,21	14	11	11	21	13	11	14	10	18	2	0.0181	NMF
Kh57	17	13	25	30	16	15	13,17	13	10	11	23	13	12	15	11	18	1	0.0091	NMF
Kh58	16	14	23	29	15	14	11,12	13	11	11	23	14	13	14	11	19	1	0.0091	NMF
Kh59	16	13	23	30	15	14	11,12	13	11	11	24	14	12	14	11	20	1	0.0091	NMF
Kh60	15	13	25	30	18	15	10,14	13	10	11	23	11	13	14	11	20	1	0.0091	NMF
Kh61	16	13	25	28	16	15	14,19	13	12	11	21	13	11	14	10	18	1	0.0091	NMF
Kh62	15	13	25	30	16	15	10,14	13	10	11	23	11	13	14	11	20	1	0.0091	NMF
Kh63	15	13	25	30	16	15	10,14	13	10	11	23	11	13	14	11	19	1	0.0091	NMF
Kh64	15	14	22	30	15	15	15,18	12	10	11	21	13	11	14	9	19	1	0.0091	NMF
Kh65	15	14	25	29	17	15	15,19	14	10	11	21	13	10	14	10	18	1	0.0091	NMF
Kh66	16	14	25	31	17	15	15,20	14	10	12	21	13	11	14	10	18	1	0.0091	NMF
Kh67	16	13	25	28	16	15	14,19	13	11	11	21	13	11	14	10	18	1	0.0091	NMF
Kh68	16	13	25	31	17	15	11,15	13	11	10	23	11	12	14	11	21	1	0.0091	NMF
Kh69	16	12	24	28	17	15	13,19	12	10	11	20	14	11	15	11	20	1	0.0091	NMF
Kh70	16	13	25	29	16	15	16,19	14	10	12	21	13	10	14	10	18	3	0.0273	NMF
Kh71	16	12	24	28	17	15	13,19	12	10	11	20	13	11	15	11	20	1	0.0091	NMF
Kh72	15	13	24	30	16	15	12,17	13	10	11	19	12	11	15	10	19	1	0.0091	NMF
Kh73	15	13	24	30	17	15	13,16	14	10	11	18	11	12	14	10	19	1	0.0091	NMF
Kh74	15	13	23	28	15	15	11,17	15	10	12	20	11	11	14	10	21	1	0.0091	NMF
Kh75	15	13	24	29	19	16	16,19	14	10	12	21	13	12	14	10	17	1	0.0091	NMF
Kh76	15	12	24	27	17	14	13,19	12	10	12	20	14	13	15	11	20	1	0.0091	MF-2
Kh77	14	15	25	32	16	16	12,14	13	11	10	23	11	13	14	11	20	2	0.0181	NMF
Kh78	15	13	23	28	15	15	11,17	16	10	12	20	11	11	14	10	21	1	0.0091	NMF
Kh79	15	13	24	30	17	15	12,16	13	10	11	19	12	11	15	9	19	1	0.0091	NMF
Kh80	15	12	25	28	17	15	13,18	12	10	11	21	14	12	15	11	20	1	0.0091	NMF
Kh81	16	12	24	27	17	15	13,19	12	10	11	20	14	11	15	11	20	1	0.0091	NMF
Kh82	16	13	25	30	15	16	15,21	14	11	13	21	13	11	14	10	18	1	0.0091	NMF
Kh83	15	13	23	30	17	15	12,16	13	10	11	19	12	11	15	10	19	1	0.0091	NMF
Kh84	15	13	24	28	16	15	14,18	15	11	12	21	13	11	14	11	18	1	0.0091	NMF
Kh85	15	13	22	29	18	15	15,17	12	10	11	21	11	12	14	9	18	1	0.0091	NMF
Kh86	15	14	25	30	16	15	15,23	14	11	12	21	13	12	14	10	18	2	0.0181	NMF
Kh87	15	14	25	30	16	15	15,23	14	11	12	21	12	12	14	10	18	1	0.0091	NMF
Kh88	16	13	25	29	17	15	15,19	14	10	11	21	13	10	14	10	18	1	0.0091	NMF
Kh89	16	13	26	30	16	14	13,18	13	10	11	23	13	11	15	11	17	2	0.0181	NMF
Kh90	16	13	24	30	16	15	15,20	14	11	12	21	13	12	14	10	18	1	0.0091	NMF
Kh91	16	13	23	30	17	15	13,17	13	11	11	19	12	11	15	10	19	1	0.0091	NMF

N= Number of Individual; *F:* Frequency of each haplotype in 110 Khasia males; YHRD: Y-Chromosome Haplotype Reference Database; MF: Match Found; NMF: No Match Found

Supplementary Table 9. The distribution of alleles for every 17 Y-STRs loci among the studied populations.

STR Loci	Alleles	Studied populations							
		Bangali	**Chakma**	**Tripura**	**Rakhine**	**Marma**	**Hajong**	**Manipuri**	**Khasia**
DYS456	12	***5***	-	-	-	**1**	-	-	-
	13	30	-	-	4	2	5	-	-
	14	56	15	14	7	1	7	5	8
	15	377	83	52	81	75	51	77	53
	16	141	7	27	15	21	20	15	26
	17	37	9	6	2	6	6	1	4
	18	2	2	-	1	1	-	-	-
	19	***1***	-	-	-	-	-	-	-
DYS389I	9	***1***	-	-	-	-	-	-	-
	10	-	-	-	-	1	-	-	-
	11	3	3	-	-	-	-	-	-
	12	100	75	56	54	62	48	29	9
	13	335	26	32	26	14	28	36	60
	14	200	12	8	30	30	13	32	21
	15	9	-	3	-	-	-	1	1
	18	***1***	-	-	-	-	-	-	-
DYS390	20	1	-	-	-	-	-	-	-
	21	18	1	3	-	-	1	-	-
	22	129	-	3	12	4	9	6	5
	23	167	46	34	23	26	31	32	27
	24	148	48	48	47	55	33	30	17
	25	168	21	11	26	22	15	26	39
	26	17	-	-	2	-	-	4	3
	27	1	-	-	-	-	-	-	-
DYS389II	23	-	-	-	-	-	***1***	-	-
	24	-	-	2	-	-	-	-	-
	25	1	-	-	-	-	1	-	-
	26	-	2	-	-	-	-	-	-
	27	10	11	16	13	20	3	3	3
	28	96	58	45	32	39	37	20	19
	29	148	27	22	25	25	23	20	23
	30	208	12	8	20	15	17	23	36
	31	126	4	4	10	5	6	18	6
	32	53	2	1	9	1	1	13	4
	33	7	-	1	1	2	-	1	-
DYS458	12	***1***	-	-	-	-	-	-	-
	13	***2***	-	-	-	-	-	-	-
	14	21	4	-	1	-	6	-	-
	15	83	5	-	10	9	8	12	14
	16	209	13	14	30	20	18	53	38
	17	197	36	42	25	25	27	20	32
	18	92	41	30	28	29	21	10	5
	18.2	***2***	-	-	-	-	-	-	-
	19	33	9	10	13	18	5	3	2
	19.2	***1***	-	-	-	-	-	-	-
	20	7	6	3	3	5	4	-	-
	21	-	***2***	-	-	-	-	-	-
	22	***1***	-	-	-	***1***	-	-	-

STR Loci	**Alleles**	**Studied populations**							
		Bangali	**Chakma**	**Tripura**	**Rakhine**	**Marma**	**Hajong**	**Manipuri**	**Khasia**
DYS19	13	11	2	1	1	-	-	-	1
	13.2	-	-	-	-	-	-	**1**	-
	14	174	64	74	59	55	43	51	14
	15	327	36	16	44	39	38	26	66
	16	119	12	3	4	13	7	12	10
	17	18	2	5	2	-	1	7	-
	18	-	-	-	-	-	-	1	-
DYS393	10	-	-	-	1	-	1	1	-
	11	24	-	1	1	4	10	-	-
	12	211	74	78	61	69	49	38	13
	13	275	16	12	27	14	19	53	31
	14	125	18	7	17	15	10	3	36
	15	13	7	-	3	5	-	3	10
	16	1	1	1	-	-	-	-	1
DYS391	8	1	-	-	-	-	-	-	-
	9	15	-	6	1	3	13	2	-
	10	483	85	82	87	91	60	91	60
	11	147	30	11	21	13	16	4	29
	12	3	1	-	1	-	-	1	2
DYS439	8	-	-	-	3	1	-	-	-
	9	3	-	-	1	-	-	1	-
	10	231	7	10	18	10	10	42	12
	11	222	47	26	39	41	31	31	44
	12	142	45	50	38	42	33	20	26
	13	45	14	11	11	13	13	4	8
	14	6	3	2	-	-	2	-	1
DYS635	17	***3***	-	-	-	-	-	-	-
	18	***12***	-	-	***1***	-	-	-	***3***
	19	***23***	***8***	***1***	***1***	***3***	***4***	***4***	***11***
	20	120	52	54	29	34	35	20	12
	21	105	33	23	42	31	24	14	36
	22	51	15	4	7	19	5	4	8
	23	196	6	16	22	17	12	27	14
	24	75	1	1	5	-	4	20	2
	25	54	1	-	2	1	2	4	5
	26	9	-	-	1	2	3	4	-
	27	***1***	-	-	-	-	-	-	-
	32	-	-	-	-	-	-	***1***	-
DYS392	7	-	-	-	-	-	1	-	-
	8	2	-	-	-	-	-	-	-
	9	3	-	-	-	-	-	-	-
	10	85	5	-	4	9	3	6	5
	11	440	17	24	41	27	21	37	24
	12	27	12	7	4	4	4	27	18
	13	41	13	11	12	20	15	7	34
	14	44	61	50	47	43	43	19	9
	15	7	8	7	2	4	2	2	1

STR Loci	**Alleles**	**Studied populations**							
		Bangali	**Chakma**	**Tripura**	**Rakhine**	**Marma**	**Hajong**	**Manipuri**	**Khasia**
YGATAH4	9	1	-	-	-	-	-	-	-
	10	15	1	3	1	3	5	2	11
	11	194	27	43	32	36	25	10	48
	12	299	76	36	52	41	43	48	20
	13	129	11	17	17	21	15	37	12
	14	***11***	***1***	-	***7***	***6***	***1***	***1***	-
	15	-	-	-	***1***	-	-	-	-
DYS437	13	4	-	-	-	-	-	-	-
	14	443	34	41	57	45	25	47	66
	15	121	76	58	49	57	55	47	23
	16	80	6	-	4	5	9	4	2
	17	1	-	-	-	-	-	-	-
DYS438	7	-	-	-	-	***2***	-	-	-
	8	23	-	-	1	-	-	-	-
	9	173	-	10	14	8	4	12	7
	10	99	40	24	23	30	21	4	55
	11	340	74	61	71	62	61	80	27
	12	13	2	3	-	5	3	2	2
	13	1	-	1	1	-	-	-	-
DYS448	16	-	-	-	-	-	***1***	-	-
	17	6	1	7	2	-	1	-	2
	18	50	13	12	13	13	9	3	35
	19	298	42	10	25	28	19	31	27
	20	247	51	56	63	58	55	63	19
	21	47	9	14	6	8	4	1	7
	22	1	-	-	1	-	-	-	1
Total number of alleles		107	75	71	84	71	78	72	72
Specific off-ladder alleles and microvariants		***14***	***4***	***1***	***4***	***5***	***4***	***4***	***2***

Supplementary Table 10. Forensic statistical parameters of the studied populations using 17 Y-STRs loci haplotypes.

17-loci Y-STR haplotypes		Studied populations								Total
		Bangali	Chakma	Tripura	Rakhine	Marma	Hajong	Manipuri	Khasia	
Number of individuals		667	157	151	152	144	112	136	112	1,631
Number of total haplotypes		667	150	144	145	138	109	131	110	1,594
Number of different haplotypes		649	116	99	110	107	89	98	91	1,359
Number of unique haplotypes		633	94	77	95	91	71	83	78	1,222
Fraction of unique haplotypes (%)		94.902	62.666	53.472	65.517	65.942	65.137	63.358	70.909	-
Discrimination capacity (%)		97.301	73.885	65.563	75.862	77.536	80.909	74.809	81.250	-
Number of alleles (%)		88.429	61.983	58.677	69.421	58.677	64.462	59.504	59.504	-
Haplotype diversity		0.998	0.988	0.984	0.986	0.985	0.987	0.982	0.985	-
Allele/Gene Frequency	Max^m	0.744	0.733	0.828	0.791	0.850	0.685	0.929	0.725	-
	Min^m	0.002	0.009	0.010	0.009	0.009	0.011	0.010	0.011	-
Allele/Gene diversity	Max^m	0.938	0.946	0.882	0.950	0.952	0.932	0.848	0.964	-
	Min^m	0.376	0.400	0.301	0.341	0.265	0.477	0.136	0.414	-
	Avg. With *sd*	0.662 *±0.137*	0.599 *±0.140*	0.595 *±0.145*	0.646 *±0.149*	0.641 *±0.157*	0.656 *±0.118*	0.602 *±0.197*	0.644 *±0.144*	-
Power of matching	Max^m	0.625	0.604	0.702	0.662	0.738	0.528	0.865	0.590	-
	Min^m	0.063	0.062	0.127	0.059	0.057	0.078	0.160	0.047	-
	Avg.	0.338	0.391	0.411	0.358	0.366	0.351	0.404	0.363	-
Power of discrimination	Max^m	0.937	0.938	0.873	0.941	0.943	0.922	0.840	0.953	-
	Min^m	0.375	0.396	0.298	0.338	0.262	0.472	0.135	0.410	-
	Avg.	0.662	0.607	0.589	0.640	0.635	0.649	0.596	0.637	-
Power of exclusion	Max^m	0.937	0.938	0.873	0.941	0.943	0.922	0.840	0.953	-
	Min^m	0.375	0.396	0.298	0.338	0.262	0.472	0.135	0.410	-
	Avg.	0.662	0.607	0.589	0.640	0.635	0.649	0.596	0.637	-

Supplementary Table 11. Comparison of gene diversity values for the 17 Y-STRs of Bangali and seven studied populations in Bangladesh.

17 Y-STR loci	Gene diversity values of the studied populations								Locus-wise average GD values
	Bangali	Chakma	Tripura	Rakhine	Marma	Hajong	Manipuri	Khasia	
DYS456	0.603[13]	0.465[14]	0.633[9]	0.438[15]	0.471[15]	0.614[10]	0.360[14]	0.576[11]	0.520[14]
DYS389I	0.616[12]	0.524[11]	0.574[11]	0.634[9]	0.574[12]	0.596[11]	0.678[7]	0.508[13]	0.588[10]
DYS390	0.775[3]	0.443[15]	0.639[8]	0.713[6]	0.639[8]	0.710[6]	0.731[5]	0.697[6]	0.668[7]
DYS389II	0.770[4]	0.680[4]	0.716[2]	0.809[2]	0.763[3]	0.726[4]	0.818[3]	0.737[3]	0.752[2]
DYS458	0.755[5]	0.761[2]	0.705[3]	0.793[3]	0.807[2]	0.803[2]	0.646[8]	0.682[7]	0.744[3]
DYS19	0.641[9]	0.593[10]	0.416[14]	0.556[12]	0.594[10]	0.585[12]	0.646[9]	0.443[15]	0.559[12]
DYS393	0.677[7]	0.551[9]	0.363[15]	0.613[10]	0.549[13]	0.633[9]	0.562[11]	0.703[5]	0.581[11]
DYS391	0.376[16]	0.400[16]	0.301[16]	0.341[16]	0.265[16]	0.498[15]	0.136[16]	0.469[14]	0.348[16]
DYS439	0.705[6]	0.672[6]	0.660[6]	0.724[5]	0.682[7]	0.715[5]	0.680[6]	0.667[8]	0.688[5]
DYS635	0.821[2]	0.700[3]	0.627[10]	0.744[4]	0.763[4]	0.754[3]	0.824[2]	0.635[10]	0.733[4]
DYS392	0.514[14]	0.678[5]	0.671[4]	0.670[7]	0.737[5]	0.686[7]	0.742[4]	0.746[2]	0.681[6]
YGATAH4	0.659[8]	0.513[12]	0.655[7]	0.669[8]	0.705[6]	0.663[8]	0.612[10]	0.649[9]	0.641[8]
DYS437	0.448[15]	0.487[13]	0.490[13]	0.537[13]	0.542[14]	0.535[14]	0.545[12]	0.414[16]	0.504[15]
DYS438	0.631[11]	0.557[8]	0.556[12]	0.529[14]	0.584[11]	0.477[16]	0.320[15]	0.547[12]	0.525[13]
DYS448	0.634[10]	0.663[7]	0.663[5]	0.608[11]	0.623[9]	0.566[13]	0.491[13]	0.721[4]	0.618[9]
DYS385a/b	0.938[1]	0.946[1]	0.882[1]	0.950[1]	0.952[1]	0.932[1]	0.848[1]	0.964[1]	0.927[1]
Population-wise average GD values	0.6624[1]	0.5995[7]	0.5952[8]	0.6455[3]	0.6406[5]	0.6558[2]	0.6024[6]	0.6441[4]	-

Note: The numbers in parentheses correspond to the rank order by gene diversity values.

Supplementary Table 12. R_{st} genetic distances (below diagonal) and *p*-values (above diagonal) for pair-wise comparisons of the studied populations and 32 reference populations available in YHRD based on 10,000 repetitions at significance level 0.01.

Pop^{n}	**BAN**	**MAN**	**KHA**	**AFG**	**AUS**	**RAK**	**CHA**	**GAR**	**HAJ**	**MAR**	**SAN**	**TRI**	**AFR**	**HAN**	**TIB**	**GER**	**BHI**	**GON**	**MUN**	**ORA**
BAN	-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MAN	0.046	-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KHA	0.106	0.076	-	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0	0	0	0.015
AFG	0.087	0.168	0.258	-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AUS	0.164	0.216	0.299	0.070	-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RAK	0.087	0.045	0.056	0.201	0.233	-	0.001	0.159	0.059	0.162	0	0	0	0	0	0	0	0	0	0
CHA	0.199	0.146	0.108	0.315	0.318	0.034	-	0.001	0.034	0.041	0	0.002	0	0	0	0	0	0	0	0
GAR	0.092	0.069	0.046	0.200	0.246	0.004	0.030	-	0.079	0.072	0	0	0	0	0	0	0	0	0	0
HAJ	0.145	0.083	0.081	0.261	0.277	0.012	0.013	0.008	-	0.170	0	0.001	0	0	0	0	0	0	0	0
MAR	0.134	0.086	0.076	0.248	0.269	0.004	0.012	0.008	0.004	-	0	0	0	0	0	0	0	0	0	0
SAN	0.168	0.123	0.024	0.331	0.369	0.118	0.160	0.105	0.142	0.135	-	0	0	0	0	0	0	0	0.001	0.144
TRI	0.249	0.179	0.152	0.400	0.384	0.077	0.025	0.066	0.034	0.037	0.188	-	0	0	0	0	0	0	0	0
AFR	0.069	0.087	0.171	0.089	0.142	0.134	0.239	0.126	0.177	0.179	0.215	0.309	-	0	0	0	0	0	0	0
HAN	0.109	0.121	0.086	0.151	0.204	0.033	0.054	0.028	0.045	0.041	0.151	0.115	0.133	-	0	0	0	0	0	0
TIB	0.096	0.158	0.168	0.084	0.185	0.152	0.221	0.141	0.193	0.174	0.219	0.273	0.110	0.153	-	0	0	0	0	0
GER	0.131	0.215	0.306	0.048	0.037	0.253	0.361	0.257	0.309	0.305	0.376	0.438	0.111	0.195	0.149	-	0	0	0	0
BHI	0.018	0.082	0.106	0.116	0.183	0.094	0.198	0.079	0.142	0.134	0.163	0.263	0.078	0.091	0.079	0.167	-	0	0	0
GON	0.133	0.154	0.196	0.256	0.329	0.166	0.250	0.137	0.203	0.189	0.193	0.298	0.156	0.151	0.159	0.336	0.113	-	0	0
MUN	0.297	0.240	0.115	0.463	0.466	0.233	0.246	0.201	0.234	0.233	0.046	0.268	0.354	0.234	0.302	0.498	0.304	0.349	-	0
ORA	0.161	0.112	0.028	0.339	0.377	0.113	0.162	0.094	0.132	0.129	0.007	0.184	0.213	0.149	0.216	0.394	0.156	0.172	0.075	-
RAJ	0.226	0.188	0.185	0.311	0.335	0.096	0.074	0.069	0.076	0.071	0.261	0.119	0.288	0.096	0.228	0.391	0.222	0.291	0.362	0.257
TAM	0.023	0.054	0.106	0.119	0.185	0.082	0.181	0.076	0.119	0.121	0.155	0.219	0.056	0.103	0.127	0.163	0.014	0.080	0.274	0.133
I-TRI	0.176	0.109	0.101	0.297	0.302	0.017	0.004	0.016	0.001	0.001	0.150	0.016	0.206	0.053	0.204	0.344	0.178	0.226	0.254	0.149
IND	0.150	0.104	0.028	0.293	0.312	0.085	0.121	0.074	0.092	0.096	0.029	0.152	0.183	0.099	0.208	0.322	0.141	0.182	0.099	0.036
IRN	0.031	0.051	0.124	0.074	0.122	0.084	0.194	0.087	0.124	0.132	0.190	0.257	0.037	0.092	0.112	0.092	0.045	0.164	0.321	0.186
IRQ	0.026	0.069	0.162	0.047	0.110	0.128	0.255	0.131	0.185	0.179	0.222	0.324	0.034	0.133	0.089	0.080	0.052	0.171	0.364	0.221
JAP	0.174	0.175	0.108	0.290	0.298	0.111	0.123	0.081	0.109	0.109	0.167	0.182	0.242	0.096	0.176	0.329	0.154	0.282	0.244	0.186
KOR	0.195	0.199	0.137	0.276	0.279	0.091	0.073	0.068	0.076	0.076	0.215	0.128	0.244	0.061	0.228	0.308	0.176	0.276	0.284	0.219
MON	0.150	0.229	0.300	0.028	0.093	0.250	0.351	0.256	0.314	0.289	0.373	0.429	0.167	0.192	0.118	0.103	0.184	0.308	0.485	0.382
NEP	0.016	0.059	0.162	0.049	0.096	0.102	0.228	0.115	0.168	0.154	0.237	0.319	0.074	0.104	0.078	0.088	0.054	0.205	0.398	0.245
PAT	0.058	0.132	0.252	0.054	0.081	0.204	0.331	0.216	0.271	0.259	0.330	0.407	0.122	0.186	0.134	0.078	0.114	0.294	0.471	0.338
FIL	0.134	0.176	0.154	0.148	0.181	0.130	0.183	0.119	0.157	0.158	0.203	0.261	0.145	0.059	0.179	0.151	0.117	0.190	0.304	0.220
POR	0.143	0.219	0.315	0.063	0.034	0.243	0.349	0.248	0.302	0.288	0.378	0.432	0.112	0.181	0.138	0.014	0.177	0.338	0.507	0.403
MAL	0.077	0.086	0.052	0.148	0.204	0.067	0.123	0.057	0.089	0.093	0.086	0.174	0.094	0.049	0.144	0.171	0.058	0.114	0.177	0.091
TAI	0.339	0.396	0.406	0.331	0.321	0.389	0.434	0.363	0.412	0.408	0.409	0.519	0.344	0.242	0.284	0.320	0.365	0.401	0.514	0.458
THA	0.131	0.089	0.026	0.256	0.279	0.042	0.069	0.040	0.053	0.049	0.052	0.108	0.165	0.053	0.191	0.298	0.122	0.170	0.135	0.054
MEL	0.081	0.097	0.108	0.133	0.171	0.080	0.151	0.071	0.115	0.109	0.147	0.216	0.069	0.062	0.137	0.177	0.054	0.096	0.265	0.143
AAM	0.095	0.059	0.032	0.186	0.219	0.023	0.061	0.020	0.034	0.038	0.069	0.112	0.102	0.028	0.150	0.226	0.079	0.139	0.159	0.071
NAM	0.093	0.084	0.204	0.086	0.076	0.127	0.244	0.138	0.176	0.176	0.264	0.334	0.042	0.123	0.131	0.058	0.128	0.263	0.424	0.289
VIE	0.159	0.103	0.052	0.295	0.318	0.049	0.049	0.037	0.035	0.045	0.084	0.084	0.197	0.058	0.198	0.359	0.150	0.205	0.159	0.078

Pop^{n}	**RAJ**	**TAM**	**I-TRI**	**IND**	**IRN**	**IRQ**	**JAP**	**KOR**	**MON**	**NEP**	**PAT**	**FIL**	**POR**	**MAL**	**TAI**	**THA**	**MEL**	**AAM**	**NAM**	**VIE**
BAN	0	0	0	0	0	0	0	0	0	0.012	0	0	0	0	0	0	0	0	0	0
MAN	0	0	0	0	0	0	0	0	0	0.001	0	0	0	0	0	0	0	0	0	0
KHA	0	0	0	0.002	0	0	0	0	0	0	0	0	0	0	0	0.003	0	0.003	0	0.002
AFG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AUS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RAK	0	0	0.042	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0.002
CHA	0	0	0.648	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001
GAR	0	0	0.025	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.008	0	0.002
HAJ	0	0	0.447	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002	0	0.005
MAR	0	0	0.321	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001
SAN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TRI	0	0	0.031	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AFR	0	0	0	0	0	0.002	0	0	0	0	0	0	0	0	0	0	0	0	0.004	0
HAN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TIB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GER	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BHI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GON	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MUN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ORA	0	0	0	0.001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RAJ	-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TAM	0.210	-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
I-TRI	0.082	0.151	-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001	0	0
IND	0.236	0.120	0.109	-	0	0	0	0	0	0	0	0	0	0	0	0.053	0	0.004	0	0.001
IRN	0.224	0.026	0.163	0.144	-	0.041	0	0	0	0.001	0	0	0	0	0	0	0	0	0.001	0
IRQ	0.273	0.035	0.222	0.188	0.009	-	0	0	0	0.007	0	0	0	0	0	0	0	0	0.001	0
JAP	0.167	0.179	0.133	0.145	0.197	0.246	-	0	0	0	0	0	0	0	0	0	0	0	0	0
KOR	0.107	0.194	0.088	0.165	0.202	0.258	0.035	-	0	0	0	0	0	0	0	0	0	0	0	0
MON	0.340	0.197	0.338	0.338	0.156	0.117	0.327	0.308	-	0	0	0	0	0	0	0	0	0	0	0
NEP	0.243	0.056	0.206	0.202	0.039	0.028	0.199	0.200	0.093	-	0.008	0	0	0	0	0	0	0	0	0
PAT	0.340	0.108	0.315	0.294	0.078	0.052	0.286	0.279	0.101	0.021	-	0	0	0	0	0	0	0	0	0
FIL	0.229	0.120	0.178	0.133	0.098	0.133	0.180	0.166	0.195	0.124	0.189	-	0	0	0	0	0	0	0	0
POR	0.388	0.167	0.331	0.323	0.104	0.097	0.327	0.296	0.109	0.107	0.114	0.149	-	0	0	0	0	0	0.001	0
MAL	0.186	0.059	0.110	0.039	0.058	0.088	0.117	0.134	0.204	0.091	0.162	0.032	0.169	-	0	0	0	0.011	0	0
TAI	0.486	0.326	0.440	0.346	0.319	0.351	0.408	0.376	0.346	0.378	0.409	0.139	0.324	0.192	-	0	0	0	0	0
THA	0.176	0.107	0.061	0.008	0.124	0.168	0.114	0.112	0.298	0.164	0.263	0.109	0.292	0.034	0.339	-	0	0.215	0	0.036
MEL	0.191	0.045	0.128	0.098	0.063	0.079	0.157	0.153	0.183	0.086	0.165	0.059	0.162	0.034	0.262	0.071	-	0.001	0	0
AAM	0.138	0.072	0.047	0.022	0.070	0.111	0.089	0.091	0.239	0.103	0.202	0.066	0.217	0.013	0.284	0.003	0.038	-	0	0.026
NAM	0.296	0.093	0.212	0.207	0.035	0.047	0.259	0.238	0.144	0.071	0.117	0.120	0.045	0.101	0.342	0.178	0.089	0.103	-	0
VIE	0.149	0.134	0.051	0.046	0.162	0.208	0.084	0.077	0.335	0.191	0.301	0.162	0.363	0.072	0.423	0.017	0.110	0.023	0.239	-

Note: BAN= Dhaka, Bangladesh [Bangali] (YA003445); MAN= Sylhet, Bangladesh [Manipuri] (YA004173); KHA= Sylhet, Bangladesh [Khasia] (YA004172); AFG= Afghanistan [Afghan] (YA003842); AUS= Australia [Aboriginal] (YA003697); RAK= Cox's Bazar, Bangladesh [Rakhine] (YA004284); CHA= Khagrachari, Bangladesh [Chakma] (YA004320); GAR= Tangail, Bangladesh [Garo] (YA003852); HAJ= Netrokona, Bangladesh [Hajong] (YA004283); MAR= Bandarban, Bangladesh [Marma] (YA004285); SAN= Dinajpur, Bangladesh [Santal] (YA003851); TRI= Khagrachari, Bangladesh [Tripura] (YA004321); AFR= Rio de Janeiro, Brazil [African] (YA003267); HAN= Beijing, China [Han] (YA004160); TIB=Tibet, China [Tibetan] (YA004005); GER= Cologne, Germany [German] (YA002963); BHI= Gujarat, India [Bhil] (YA003762); GON= Madhya Pradesh, India [Gond] (YA003619); MUN= Jharkhand, India [Munda] (YA003617); ORA= Chhattisgarh, India [Oraon] (YA004113); RAJ= West Bengal, India [Rajbanshi] (YA003630); TAM= Southern India, India [Tamil] (YA003312); I-TRI= Tripura, India [Tripuri] (YA003312); IND=Java, Indonesia [Indonesian] (YA003770); IRN= Central Iran, Iran [Iranian] (YA003782); IRQ= Iraq [Iraqi] (YA003858); JAP= Tokyo, Japan [Japanese] (YA003459); KOR= Seoul, South Korea [Korean] (YA003406); MON= Ulaanbaatar, Mongolia [Mongolian] (YA004127); NEP= Kathmandu, Nepal [Nepalese] (YA003656); PAT= Pakistan [Pathan] (YA003846); FIL= Philippines [Filipino] (YA003892); POR= Central Portugal, Portugal [Portuguese] (YA003145); MAL= Singapore [Malay] (YA004367); TAI= Taiwan [Paiwan] (YA003500); THA= Thailand [Thai] (YA004250); MEL=East Timor, Timor-Leste [Melanesian] (YA003306); AAM=Minnesota, United States [Asian American] (YA004088); NAM=Minnesota, United States [Native American] (YA004091); VIE=Hanoi, Vietnam [Vietnamese] (YA003201).

Supplementary Table 13. Y-chromosomal haplogroup assignments for each haplotype in Bangali (Bn) population using Whit Athey's algorithm.

Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)
Bn1	E1b1b	74.3	Bn49	L	100	Bn97	R1a	99.9	Bn145	R1a	100
Bn2	Q	98.3	Bn50	E1b1a	93.5	Bn98	I2a1	97.1	Bn146	R1a	100
Bn3	Q	98.9	Bn51	J2a1	92.4	Bn99	I2a1	74.7	Bn147	R1a	100
Bn4	L	100	Bn52	H	100	Bn100	R1a	100	Bn148	R1a	100
Bn5	Q	89.6	Bn53	H	100	Bn101	R1a	100	Bn149	R1a	100
Bn6	L	100	Bn54	H	100	Bn102	R1a	100	Bn150	R1a	100
Bn7	L	98.6	Bn55	J2a1	92.9	Bn103	R1a	100	Bn151	H	100
Bn8	J2b	100	Bn56	L	100	Bn104	R1a	100	Bn152	H	99.3
Bn9	L	98.6	Bn57	H	100	Bn105	R1a	100	Bn153	L	100
Bn10	L	99.9	Bn58	J1	94.8	Bn106	R1a	100	Bn154	H	100
Bn11	L	90.9	Bn59	L	76.5	Bn107	H	100	Bn155	R1a	99.7
Bn12	Q	86.5	Bn60	J2b	100	Bn108	H	99.9	Bn156	H	97.5
Bn13	Q	86.5	Bn61	Q	99.9	Bn109	R1a	100	Bn157	J2b	100
Bn14	Q	97.7	Bn62	J2b	99.8	Bn110	R1a	100	Bn158	I2b1	99.8
Bn15	L	95	Bn63	J2b	100	Bn111	R1a	100	Bn159	J2b	77
Bn16	L	87.5	Bn64	J2b	100	Bn112	E1b1b	44.8	Bn160	I2b1	100
Bn17	L	80.4	Bn65	R1a	100	Bn113	R1a	100	Bn161	I2a	96.1
Bn18	L	91.1	Bn66	L	99.5	Bn114	R1a	100	Bn162	L	90.3
Bn19	Q	95.4	Bn67	J2a1h	38.8	Bn115	R1a	100	Bn163	H	100
Bn20	J2a1b	77.1	Bn68	Q	87.7	Bn116	E1b1a	80.5	Bn164	J2b	100
Bn21	Q	98.9	Bn69	T	59.5	Bn117	R1a	100	Bn165	J2b	100
Bn22	H	99.9	Bn70	H	100	Bn118	R1a	100	Bn166	R1a	100
Bn23	L	89.5	Bn71	H	95.3	Bn119	L	79.3	Bn167	R1a	100
Bn24	L	98.6	Bn72	H	98.8	Bn120	L	99.9	Bn168	R1a	100
Bn25	J1	100	Bn73	H	100	Bn121	H	100	Bn169	T	76.2
Bn26	J2a1	87.7	Bn74	H	100	Bn122	H	100	Bn170	Q	96.4
Bn27	L	99.9	Bn75	H	100	Bn123	H	100	Bn171	H	99.9
Bn28	J1	53.6	Bn76	H	100	Bn124	H	94.6	Bn172	R1a	99.4
Bn29	R1b	60.2	Bn77	H	100	Bn125	H	100	Bn173	T	97
Bn30	L	67.9	Bn78	H	100	Bn126	H	100	Bn174	R1a	100
Bn31	T	99.6	Bn79	H	100	Bn127	H	100	Bn175	R1a	100
Bn32	I2b1	99.4	Bn80	H	100	Bn128	H	100	Bn176	R1a	100
Bn33	J2a1	59.1	Bn81	Q	64.9	Bn129	L	95.5	Bn177	R1a	100
Bn34	J2a1b	98	Bn82	J2a1	83.3	Bn130	L	98.9	Bn178	R1a	100
Bn35	L	89.2	Bn83	I2a1	97.8	Bn131	R1a	100	Bn179	R1a	100
Bn36	J2a1b	93.7	Bn84	J2a1h	99.8	Bn132	H	100	Bn180	R1a	100
Bn37	R1b	100	Bn85	Q	96.7	Bn133	H	100	Bn181	R1a	100
Bn38	Q	98.5	Bn86	R1a	100	Bn134	L	99.6	Bn182	R1a	100
Bn39	R1a	100	Bn87	R1a	100	Bn135	L	99.8	Bn183	R1a	100
Bn40	J2a1	99.3	Bn88	T	80	Bn136	R1a	100	Bn184	R1a	100
Bn41	Q	51.8	Bn89	H	99.2	Bn137	R1a	100	Bn185	R1a	100
Bn42	E1bab	87.8	Bn90	J2a1b	43.5	Bn138	R1a	100	Bn186	R1a	100
Bn43	Q	99.5	Bn91	H	100	Bn139	R1a	100	Bn187	R1a	100
Bn44	J2a1	51	Bn92	L	100	Bn140	R1a	100	Bn188	R1a	100
Bn45	J2a1b	50.5	Bn93	H	99.9	Bn141	R1a	100	Bn189	R1a	100
Bn46	Q	99.9	Bn94	J2a1	98.5	Bn142	R1a	100	Bn190	R1a	100
Bn47	L	89.1	Bn95	I2b1	54.7	Bn143	R1a	100	Bn191	R1a	100
Bn48	L	96.2	Bn96	R1a	100	Bn144	R1a	100	Bn192	H	100

Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)
Bn193	L	100	Bn244	J2a1h	33.8	Bn295	I2a1	95.8	Bn346	L	100
Bn194	L	99.9	Bn245	J1	39.2	Bn296	R1a	100	Bn347	R1a	100
Bn195	J2b	95.8	Bn246	E1b1a	70.6	Bn297	L	61.3	Bn348	H	99.9
Bn196	H	100	Bn247	H	100	Bn298	R1a	100	Bn349	R1a	100
Bn197	R1a	100	Bn248	J2a1	98.2	Bn299	J2a1	71.7	Bn350	R1a	100
Bn198	E1b1a	84.5	Bn249	R1a	99.9	Bn300	L	100	Bn351	R1a	100
Bn199	R1a	100	Bn250	L	67.6	Bn301	R1a	100	Bn352	Q	49
Bn200	R1a	100	Bn251	Q	100	Bn302	Q	96.1	Bn353	H	57.3
Bn201	R1a	100	Bn252	R1a	100	Bn303	R1a	100	Bn354	R1a	100
Bn202	R1a	100	Bn253	H	100	Bn304	R1a	100	Bn355	J2a1	53
Bn203	R1a	100	Bn254	R1a	100	Bn305	R1a	100	Bn356	L	99.6
Bn204	R1a	100	Bn255	Q	96.4	Bn306	Q	99.8	Bn357	I2a1	94.8
Bn205	R1a	100	Bn256	L	93.7	Bn307	R1a	100	Bn358	R1a	100
Bn206	H	99.9	Bn257	J2a1	95.7	Bn308	L	99.7	Bn359	Q	98.9
Bn207	J2b	99.4	Bn258	R1a	100	Bn309	E1b1b	99.5	Bn360	Q	80.8
Bn208	R1a	100	Bn259	J2a1	95.5	Bn310	L	99.9	Bn361	H	100
Bn209	R1a	100	Bn260	H	100	Bn311	H	99	Bn362	J2a1	82.5
Bn210	R1a	100	Bn261	L	100	Bn312	L	99.9	Bn363	R1a	100
Bn211	R1a	99.6	Bn262	R1a	100	Bn313	H	100	Bn364	L	80.6
Bn212	L	94.1	Bn263	L	100	Bn314	R1a	100	Bn365	J2a1	92.8
Bn213	L	99.5	Bn264	I2b1	100	Bn315	I2b1	62.3	Bn366	R1a	100
Bn214	E1b1b	97.6	Bn265	R1a	100	Bn316	J2a1h	60.5	Bn367	H	99.8
Bn215	R1a	100	Bn266	R1a	92.2	Bn317	R1a	100	Bn368	H	81
Bn216	E1b1a	99.8	Bn267	I2b1	78.9	Bn318	J2a1h	66.7	Bn369	R1a	100
Bn217	T	91.2	Bn268	I2b1	99.1	Bn319	R1a	100	Bn370	R1a	100
Bn218	J2a1	78.3	Bn269	L	98.2	Bn320	N	98.8	Bn371	L	99.9
Bn219	H	60.8	Bn270	J2a1b	48.4	Bn321	T	98.6	Bn372	H	100
Bn220	R1a	100	Bn271	R1a	100	Bn322	R1a	100	Bn373	J1	79.1
Bn221	J2a1	99.9	Bn272	R1a	99.9	Bn323	H	100	Bn374	L	82.3
Bn222	R1a	100	Bn273	T	95.4	Bn324	H	96.3	Bn375	R1a	100
Bn223	J2a1b	35.2	Bn274	R1a	100	Bn325	I2b1	90.3	Bn376	H	100
Bn224	R1a	100	Bn275	N	94.8	Bn326	R1a	100	Bn377	H	100
Bn225	H	100	Bn276	J2b	100	Bn327	T	87.9	Bn378	R1a	100
Bn226	I2a1	55.4	Bn277	H	100	Bn328	J1	100	Bn379	R1a	100
Bn227	G2a	100	Bn278	L	99.9	Bn329	H	98.6	Bn380	Q	99.8
Bn228	R1a	100	Bn279	J2a1	63.1	Bn330	R1a	100	Bn381	L	99.2
Bn229	R1a	100	Bn280	L	95	Bn331	L	66.2	Bn382	J2b	100
Bn230	Q	92.5	Bn281	R1a	100	Bn332	R1a	100	Bn383	L	99.9
Bn231	H	100	Bn282	L	100	Bn333	R1a	100	Bn384	G2a	100
Bn232	L	100	Bn283	J2b	99.5	Bn334	H	99.9	Bn385	R1a	100
Bn233	L	54.4	Bn284	I2b1	46.7	Bn335	H	100	Bn386	J1	60.6
Bn234	R1a	100	Bn285	L	100	Bn336	R1a	100	Bn387	R1b	94.8
Bn235	J2a1h	100	Bn286	L	88.4	Bn337	R1a	100	Bn388	E1b1a	98.5
Bn236	R1a	100	Bn287	R1a	100	Bn338	R1a	100	Bn389	L	100
Bn237	R1a	100	Bn288	J2b	99.6	Bn339	H	99.9	Bn390	R1b	100
Bn238	R1a	100	Bn289	R1a	100	Bn340	J2b	94.7	Bn391	L	96.3
Bn239	H	94.7	Bn290	H	100	Bn341	H	100	Bn392	H	100
Bn240	E1b1b	94.2	Bn291	R1a	100	Bn342	H	95	Bn393	H	99.9
Bn241	R1a	100	Bn292	L	91.1	Bn343	R1a	100	Bn394	R1a	99.8
Bn242	L	99.8	Bn293	H	94.4	Bn344	J2a1b	83.9	Bn395	J2b	94.1
Bn243	J2b	94.4	Bn294	R1a	100	Bn345	R1a	100	Bn396	L	99.9

Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)
Bn397	Q	100	Bn448	R1a	100	Bn499	L	96.8	Bn550	H	100
Bn398	H	100	Bn449	R1a	98.2	Bn500	J2a1	51.4	Bn551	R1a	100
Bn399	H	86.7	Bn450	R1a	100	Bn501	R1a	100	Bn552	R1a	100
Bn400	H	100	Bn451	L	100	Bn502	R1a	100	Bn553	H	97.9
Bn401	I2b1	84.3	Bn452	J2a1	46.4	Bn503	I2b1	99.9	Bn554	J2a1b	84.3
Bn402	E1b1b	80.9	Bn453	L	96.4	Bn504	J2a1b	76.5	Bn555	J2b	100
Bn403	L	100	Bn454	L	99.1	Bn505	J2a1	89.2	Bn556	R1a	100
Bn404	H	100	Bn455	R1a	100	Bn506	L	99.9	Bn557	L	100
Bn405	J2b	92.3	Bn456	Q	99.8	Bn507	J1	72	Bn558	R1a	100
Bn406	G2a	77.9	Bn457	I2a1	82.9	Bn508	H	100	Bn559	G2a	33.6
Bn407	R1a	100	Bn458	L	92.8	Bn509	H	100	Bn560	J1	58.7
Bn408	T	98.7	Bn459	H	100	Bn510	J1	66.2	Bn561	R1a	100
Bn409	L	100	Bn460	L	41.9	Bn511	Q	99.4	Bn562	J2a1b	79.6
Bn410	L	98.8	Bn461	R1a	100	Bn512	H	66.3	Bn563	R1a	100
Bn411	R1a	100	Bn462	H	100	Bn513	R1a	100	Bn564	J2a1	64.8
Bn412	R1a	100	Bn463	E1b1b	31.7	Bn514	R1a	1200	Bn565	H	100
Bn413	R1a	100	Bn464	L	99	Bn515	Q	100	Bn566	R1a	100
Bn414	H	100	Bn465	Q	87.3	Bn516	J2a1	83.4	Bn567	L	86.2
Bn415	L	99.9	Bn466	L	99.9	Bn517	L	100	Bn568	J2a1	62.6
Bn416	H	100	Bn467	H	100	Bn518	R1a	100	Bn569	R1a	100
Bn417	H	100	Bn468	H	100	Bn519	R1a	100	Bn570	R1a	100
Bn418	R1a	100	Bn469	J1	56.9	Bn520	L	95.8	Bn571	R1a	100
Bn419	R1a	100	Bn470	H	100	Bn521	R1a	100	Bn572	R1a	100
Bn420	H	82.2	Bn471	H	100	Bn522	L	54.8	Bn573	H	100
Bn421	Q	100	Bn472	R1a	100	Bn523	H	100	Bn574	Q	95.5
Bn422	J2b	99.9	Bn473	J2b	100	Bn524	H	59.7	Bn575	J2a1b	59.5
Bn423	R1a	100	Bn474	R1a	100	Bn525	R1a	100	Bn576	R1a	100
Bn424	R1a	100	Bn475	Q	99.4	Bn526	Q	99.7	Bn577	L	96.6
Bn425	R1a	100	Bn476	R1a	100	Bn527	J2a1b	98.4	Bn578	L	99.5
Bn426	H	100	Bn477	H	99.8	Bn528	L	99.9	Bn579	L	60.5
Bn427	J2a1	91.6	Bn478	I2a1	56	Bn529	R1a	100	Bn580	J2a1	97.2
Bn428	R1a	100	Bn479	I2a1	50.5	Bn530	R1a	100	Bn581	J2a1b	51
Bn429	R1a	100	Bn480	H	100	Bn531	H	100	Bn582	H	85.9
Bn430	R1a	100	Bn481	H	100	Bn532	L	100	Bn583	H	100
Bn431	L	98.1	Bn482	L	95.8	Bn533	L	93.1	Bn584	J2a1	92.5
Bn432	R1a	100	Bn483	J2b	99.6	Bn534	L	100	Bn585	J2b	97.8
Bn433	J2a1b	99.9	Bn484	Q	99.9	Bn535	L	100	Bn586	R1a	100
Bn434	Q	100	Bn485	R1a	100	Bn536	Q	81.4	Bn587	I2a1	46.1
Bn435	J2b	97.1	Bn486	R1a	100	Bn537	I2a1	99.8	Bn588	R1a	100
Bn436	R1a	100	Bn487	J2a1	92.7	Bn538	L	64.9	Bn589	E1b1a	99.7
Bn437	J2a1b	57.9	Bn488	R1a	100	Bn539	H	99.8	Bn590	R1a	99.9
Bn438	H	99.7	Bn489	H	100	Bn540	L	98.6	Bn591	L	100
Bn439	G2a	52.7	Bn490	R1a	100	Bn541	J2a1b	51.3	Bn592	R1a	100
Bn440	R1a	100	Bn491	L	100	Bn542	H	100	Bn593	R1a	100
Bn441	Q	83.6	Bn492	R1a	100	Bn543	L	100	Bn594	R1a	100
Bn442	J2b	100	Bn493	E1b1b	43.8	Bn544	R1a	100	Bn595	Q	80.2
Bn443	L	99.8	Bn494	J2a1	98.5	Bn545	R1a	100	Bn596	G2a	89.5
Bn444	H	100	Bn495	I2a1	52.3	Bn546	R1a	100	Bn597	L	99.9
Bn445	L	99.6	Bn496	L	97.6	Bn547	L	96.3	Bn598	J2a1	99.5
Bn446	R1a	82.7	Bn497	T	45.7	Bn548	J2b	99.7	Bn599	L	100
Bn447	J2b	100	Bn498	L	63.6	Bn549	R1a	100	Bn600	R1a	100

Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)
Bn601	Q	88.8	-	-	-	-	-	-	-	-	-
Bn602	R1a	100	-	-	-	-	-	-	-	-	-
Bn603	J2a1	68.9	-	-	-	-	-	-	-	-	-
Bn604	L	99.8	-	-	-	-	-	-	-	-	-
Bn605	J2b	100	-	-	-	-	-	-	-	-	-
Bn606	J2a1b	73.8	-	-	-	-	-	-	-	-	-
Bn607	L	96	-	-	-	-	-	-	-	-	-
Bn608	E1b1a	99.7	-	-	-	-	-	-	-	-	-
Bn609	J2a1	99.9	-	-	-	-	-	-	-	-	-
Bn610	R1a	100	-	-	-	-	-	-	-	-	-
Bn611	J2b	97.7	-	-	-	-	-	-	-	-	-
Bn612	H	99.9	-	-	-	-	-	-	-	-	-
Bn613	H	100	-	-	-	-	-	-	-	-	-
Bn614	L	99.1	-	-	-	-	-	-	-	-	-
Bn615	L	64.8	-	-	-	-	-	-	-	-	-
Bn616	J2a1b	97.7	-	-	-	-	-	-	-	-	-
Bn617	J2b	100	-	-	-	-	-	-	-	-	-
Bn618	L	87.9	-	-	-	-	-	-	-	-	-
Bn619	Q	98.4	-	-	-	-	-	-	-	-	-
Bn620	H	98.7	-	-	-	-	-	-	-	-	-
Bn621	H	98.9	-	-	-	-	-	-	-	-	-
Bn622	R1a	100	-	-	-	-	-	-	-	-	-
Bn623	G2a	85.9	-	-	-	-	-	-	-	-	-
Bn624	H	99.7	-	-	-	-	-	-	-	-	-
Bn625	I1	64.6	-	-	-	-	-	-	-	-	-
Bn626	R1a	100	-	-	-	-	-	-	-	-	-
Bn627	H	100	-	-	-	-	-	-	-	-	-
Bn628	R1a	100	-	-	-	-	-	-	-	-	-
Bn629	R1a	100	-	-	-	-	-	-	-	-	-
Bn630	J1	97.1	-	-	-	-	-	-	-	-	-
Bn631	H	100	-	-	-	-	-	-	-	-	-
Bn632	H	100	-	-	-	-	-	-	-	-	-
Bn633	L	99.8	-	-	-	-	-	-	-	-	-
Bn634	E1b1b	99.5	-	-	-	-	-	-	-	-	-
Bn635	Q	76.4	-	-	-	-	-	-	-	-	-
Bn636	R1a	100	-	-	-	-	-	-	-	-	-
Bn637	R1a	100	-	-	-	-	-	-	-	-	-
Bn638	H	100	-	-	-	-	-	-	-	-	-
Bn639	L	98.8	-	-	-	-	-	-	-	-	-
Bn640	Q	99.4	-	-	-	-	-	-	-	-	-
Bn641	H	100	-	-	-	-	-	-	-	-	-
Bn642	L	99.2	-	-	-	-	-	-	-	-	-
Bn643	J2a1b	92.3	-	-	-	-	-	-	-	-	-
Bn644	J2b	100	-	-	-	-	-	-	-	-	-
Bn645	N	90	-	-	-	-	-	-	-	-	-
Bn646	Q	79.5	-	-	-	-	-	-	-	-	-
Bn647	L	52.3	-	-	-	-	-	-	-	-	-
Bn648	R1a	100	-	-	-	-	-	-	-	-	-
Bn649	R1a	100	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-

Supplementary Table 14. Y-chromosomal haplogroup assignments for each haplotype in Chakma (Ck) population using Whit Athey’s algorithm.

Haplotype	**Predicted Y-haplogroup**	**Probability (%)**	**Haplotype**	**Predicted Y-haplogroup**	**Probability (%)**	**Haplotype**	**Predicted Y-haplogroup**	**Probability (%)**	**Haplotype**	**Predicted Y-haplogroup**	**Probability (%)**
Ck1	L	99	Ck49	L	75.4	Ck97	Q	81.6	-	-	-
Ck2	G2a	64.3	Ck50	L	99.5	Ck98	L	99.1	-	-	-
Ck3	Q	66.9	Ck51	L	99.3	Ck99	L	99.8	-	-	-
Ck4	E1b1a	60.1	Ck52	L	99	Ck100	H	99.8	-	-	-
Ck5	L	84.5	Ck53	Q	93.7	Ck101	Q	94.1	-	-	-
Ck6	I1	86.1	Ck54	L	98.7	Ck102	L	99.6	-	-	-
Ck7	L	98.8	Ck55	L	99.1	Ck103	I2a1	93.1	-	-	-
Ck8	H	99.6	Ck56	L	89.8	Ck104	L	83.5	-	-	-
Ck9	Q	69.6	Ck57	T	83.4	Ck105	R1a	76.9	-	-	-
Ck10	L	97.6	Ck58	Q	67.2	Ck106	L	82.9	-	-	-
Ck11	L	93.6	Ck59	L	99.9	Ck107	Q	99.7	-	-	-
Ck12	T	98.5	Ck60	J1	68.1	Ck108	L	97.3	-	-	-
Ck13	R1a	100	Ck61	L	99.8	Ck109	L	50.8	-	-	-
Ck14	L	99.6	Ck62	R1a	100	Ck110	I1	90.6	-	-	-
Ck15	J1	53.1	Ck63	L	99.1	Ck111	L	85.4	-	-	-
Ck16	Q	68.6	Ck64	J1	63.4	Ck112	L	68.7	-	-	-
Ck17	J1	62.3	Ck65	L	95.4	Ck113	L	99.1	-	-	-
Ck18	J1	49.8	Ck66	Q	68.2	Ck114	L	80.5	-	-	-
Ck19	L	98.9	Ck67	L	84.2	Ck115	L	99.8	-	-	-
Ck20	G2a	78.7	Ck68	L	94.5	Ck116	Q	87.3	-	-	-
Ck21	L	98.5	Ck69	R1a	100	-	-	-	-	-	-
Ck22	L	98.8	Ck70	I1	89.2	-	-	-	-	-	-
Ck23	I2a	85.5	Ck71	L	99	-	-	-	-	-	-
Ck24	J1	75.9	Ck72	L	99.4	-	-	-	-	-	-
Ck25	Q	93.9	Ck73	H	99.9	-	-	-	-	-	-
Ck26	L	82.4	Ck74	J1	99.2	-	-	-	-	-	-
Ck27	L	93.6	Ck75	E1b1b	64.4	-	-	-	-	-	-
Ck28	L	98.3	Ck76	H	99.4	-	-	-	-	-	-
Ck29	J1	42.9	Ck77	L	99.8	-	-	-	-	-	-
Ck30	N	91.6	Ck78	L	99.9	-	-	-	-	-	-
Ck31	R1a	56.6	Ck79	G2a	97.6	-	-	-	-	-	-
Ck32	J1	31.6	Ck80	L	99.8	-	-	-	-	-	-
Ck33	L	94.3	Ck81	L	99.4	-	-	-	-	-	-
Ck34	L	85.3	Ck82	Q	92	-	-	-	-	-	-
Ck35	N	94	Ck83	L	99.8	-	-	-	-	-	-
Ck36	J1	78.9	Ck84	L	99.6	-	-	-	-	-	-
Ck37	L	96.1	Ck85	J1	58.5	-	-	-	-	-	-
Ck38	L	75.4	Ck86	L	95.9	-	-	-	-	-	-
Ck39	L	73.2	Ck87	L	96	-	-	-	-	-	-
Ck40	I2a	88.6	Ck88	L	93.5	-	-	-	-	-	-
Ck41	J2a1h	91	Ck89	L	88.4	-	-	-	-	-	-
Ck42	L	98.8	Ck90	Q	100	-	-	-	-	-	-
Ck43	G2a	89.7	Ck91	Q	96.4	-	-	-	-	-	-
Ck44	L	93.2	Ck92	H	91.7	-	-	-	-	-	-
Ck45	L	100	Ck93	L	99	-	-	-	-	-	-
Ck46	Q	93.8	Ck94	L	99	-	-	-	-	-	-
Ck47	L	99.6	Ck95	L	99.9	-	-	-	-	-	-
Ck48	I2a	63.8	Ck96	Q	61	-	-	-	-	-	-

Supplementary Table 15. Y-chromosomal haplogroup assignments for each haplotype in Tripura (Tr) population using Whit Athey's algorithm.

Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)
Tr1	L	75.5	Tr49	L	99.3	Tr97	L	77.7	-	-	-
Tr2	E1b1b	95	Tr50	J2a1	98.8	Tr98	J1	95.2	-	-	-
Tr3	J1	91.4	Tr51	T	50.7	Tr99	J1	80.5	-	-	-
Tr4	L	99	Tr52	L	98.8	-	-	-	-	-	-
Tr5	I2a	88.3	Tr53	L	98.6	-	-	-	-	-	-
Tr6	L	89.3	Tr54	Q	62.7	-	-	-	-	-	-
Tr7	L	99.8	Tr55	L	65.9	-	-	-	-	-	-
Tr8	L	48.3	Tr56	L	98.2	-	-	-	-	-	-
Tr9	L	99.9	Tr57	L	98.7	-	-	-	-	-	-
Tr10	J1	94.1	Tr58	L	99.7	-	-	-	-	-	-
Tr11	L	96.1	Tr59	E1b1b	97.4	-	-	-	-	-	-
Tr12	E1b1b	84	Tr60	L	99.8	-	-	-	-	-	-
Tr13	I2a	83	Tr61	E1b1b	73.4	-	-	-	-	-	-
Tr14	L	73.7	Tr62	L	96.7	-	-	-	-	-	-
Tr15	J1	72.6	Tr63	L	95.1	-	-	-	-	-	-
Tr16	L	84	Tr64	L	97.8	-	-	-	-	-	-
Tr17	J2a1	93.9	Tr65	E1b1b	94	-	-	-	-	-	-
Tr18	J2a1	99.2	Tr66	E1b1b	69.9	-	-	-	-	-	-
Tr19	J2a1	97.8	Tr67	J1	88.2	-	-	-	-	-	-
Tr20	L	97.2	Tr68	L	99.7	-	-	-	-	-	-
Tr21	L	86.8	Tr69	L	96.2	-	-	-	-	-	-
Tr22	L	96.2	Tr70	Q	99.5	-	-	-	-	-	-
Tr23	L	98.7	Tr71	J2a1	98.1	-	-	-	-	-	-
Tr24	L	73.9	Tr72	L	57.5	-	-	-	-	-	-
Tr25	H	100	Tr73	H	100	-	-	-	-	-	-
Tr26	L	97	Tr74	L	99.2	-	-	-	-	-	-
Tr27	L	87.3	Tr75	L	95.3	-	-	-	-	-	-
Tr28	L	98.5	Tr76	L	99.9	-	-	-	-	-	-
Tr29	J1	62.2	Tr77	Q	99.5	-	-	-	-	-	-
Tr30	L	99.9	Tr78	J1	85.4	-	-	-	-	-	-
Tr31	L	96.3	Tr79	L	89.2	-	-	-	-	-	-
Tr32	J1	82.1	Tr80	L	85.3	-	-	-	-	-	-
Tr33	J2a1	100	Tr81	L	94.9	-	-	-	-	-	-
Tr34	J1	77.4	Tr82	J1	96.4	-	-	-	-	-	-
Tr35	L	63.6	Tr83	E1b1b	73.7	-	-	-	-	-	-
Tr36	L	81.1	Tr84	J2a1b	44.5	-	-	-	-	-	-
Tr37	J2a1	96.6	Tr85	Q	74.3	-	-	-	-	-	-
Tr38	L	99	Tr86	J1	99.5	-	-	-	-	-	-
Tr39	J1	95.5	Tr87	L	87.3	-	-	-	-	-	-
Tr40	L	92.8	Tr88	E1b1b	48.6	-	-	-	-	-	-
Tr41	I2a	45.3	Tr89	L	99.7	-	-	-	-	-	-
Tr42	L	57	Tr90	L	97.4	-	-	-	-	-	-
Tr43	J1	57.1	Tr91	L	96.4	-	-	-	-	-	-
Tr44	L	99.9	Tr92	L	99.3	-	-	-	-	-	-
Tr45	L	99.4	Tr93	L	96.4	-	-	-	-	-	-
Tr46	G2a	85.1	Tr94	J2a1	99.7	-	-	-	-	-	-
Tr47	H	100	Tr95	L	98.5	-	-	-	-	-	-
Tr48	L	99.8	Tr96	L	99.8	-	-	-	-	-	-

Supplementary Table 16. Y-chromosomal haplogroup assignments for each haplotype in Rakhine (Rk) population using Whit Athey's algorithm.

Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)
Rk1	R1a	100	Rk49	Q	73.6	Rk97	G2a	78.7	-	-	-
Rk2	L	79	Rk50	L	97.7	Rk98	J2a1	58.1	-	-	-
Rk3	Q	72.1	Rk51	G2a	75	Rk99	J2b	100	-	-	-
Rk4	I2b1	99.3	Rk52	Q	82.1	Rk100	T	75	-	-	-
Rk5	Q	89.2	Rk53	R1a	100	Rk101	L	99.6	-	-	-
Rk6	L	95.6	Rk54	H	99.1	Rk102	L	98.3	-	-	-
Rk7	J1	94.4	Rk55	H	100	Rk103	H	99.4	-	-	-
Rk8	L	99.4	Rk56	R1a	100	Rk104	H	100	-	-	-
Rk9	L	99.9	Rk57	R1a	100	Rk105	L	99.7	-	-	-
Rk10	H	100	Rk58	J1	98.2	Rk106	R1a	100	-	-	-
Rk11	R1a	100	Rk59	L	98.7	Rk107	R1a	100	-	-	-
Rk12	L	98.7	Rk60	L	98.5	Rk108	J2b	99.4	-	-	-
Rk13	L	95.8	Rk61	Q	99.4	Rk109	R1a	100	-	-	-
Rk14	J2a1	82.8	Rk62	L	98.6	Rk110	L	99.2	-	-	-
Rk15	E1b1b	30.9	Rk63	J2a1	98.9	-	-	-	-	-	-
Rk16	R1a	100	Rk64	L	74.4	-	-	-	-	-	-
Rk17	G2a	92.9	Rk65	H	100	-	-	-	-	-	-
Rk18	J2a1b	89.1	Rk66	Q	68.6	-	-	-	-	-	-
Rk19	Q	82.8	Rk67	R1a	100	-	-	-	-	-	-
Rk20	J1	50	Rk68	L	99	-	-	-	-	-	-
Rk21	L	94.9	Rk69	I2b1	64.8	-	-	-	-	-	-
Rk22	R1a	100	Rk70	T	37.9	-	-	-	-	-	-
Rk23	J1	95.6	Rk71	Q	97.6	-	-	-	-	-	-
Rk24	L	88.5	Rk72	R1a	100	-	-	-	-	-	-
Rk25	L	97.9	Rk73	J2a1	80.1	-	-	-	-	-	-
Rk26	L	99.2	Rk74	R1a	100	-	-	-	-	-	-
Rk27	Q	79.1	Rk75	L	72.1	-	-	-	-	-	-
Rk28	L	78.7	Rk76	L	97.6	-	-	-	-	-	-
Rk29	R1a	100	Rk77	R1a	100	-	-	-	-	-	-
Rk30	L	93.2	Rk78	H	99.7	-	-	-	-	-	-
Rk31	Q	89.9	Rk79	R1a	100	-	-	-	-	-	-
Rk32	Q	67.5	Rk80	L	75.3	-	-	-	-	-	-
Rk33	H	100	Rk81	R1a	100	-	-	-	-	-	-
Rk34	L	98.7	Rk82	L	99.5	-	-	-	-	-	-
Rk35	J1	88.5	Rk83	J2a1	75.7	-	-	-	-	-	-
Rk36	L	94.6	Rk84	E1b1b	40.8	-	-	-	-	-	-
Rk37	Q	73.5	Rk85	L	60.4	-	-	-	-	-	-
Rk38	L	100	Rk86	L	99.5	-	-	-	-	-	-
Rk39	L	99.8	Rk87	L	96.3	-	-	-	-	-	-
Rk40	L	99.1	Rk88	R1a	100	-	-	-	-	-	-
Rk41	R1a	100	Rk89	L	100	-	-	-	-	-	-
Rk42	L	85	Rk90	R1a	100	-	-	-	-	-	-
Rk43	Q	100	Rk91	J2a1b	75	-	-	-	-	-	-
Rk44	Q	55.2	Rk92	R1a	100	-	-	-	-	-	-
Rk45	L	89.8	Rk93	L	100	-	-	-	-	-	-
Rk46	Q	98.8	Rk94	Q	96	-	-	-	-	-	-
Rk47	L	95.8	Rk95	E1b1b	45	-	-	-	-	-	-
Rk48	T	54.6	Rk96	L	98.7	-	-	-	-	-	-

Supplementary Table 17. Y-chromosomal haplogroup assignments for each haplotype in Marma (Mr) population using Whit Athey's algorithm.

Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)
Mr1	Q	98.7	Mr49	R1a	40.7	Mr97	Q	93.9	-	-	-
Mr2	L	99.6	Mr50	Q	90.8	Mr98	L	99.3	-	-	-
Mr3	H	97.3	Mr51	J1	99.9	Mr99	N	98.5	-	-	-
Mr4	L	100	Mr52	J1	88.5	Mr100	Q	99.9	-	-	-
Mr5	G2a	71.4	Mr53	Q	99.6	Mr101	Q	58.8	-	-	-
Mr6	J2b	94.3	Mr54	L	99	Mr102	L	99	-	-	-
Mr7	Q	99.4	Mr55	L	95.6	Mr103	H	99.4	-	-	-
Mr8	L	37.4	Mr56	N	98.8	Mr104	Q	93.1	-	-	-
Mr9	T	73	Mr57	J1	51.1	Mr105	J1	62.6	-	-	-
Mr10	Q	68.6	Mr58	L	99.8	Mr106	Q	99.7	-	-	-
Mr11	R1a	100	Mr59	Q	89.8	Mr107	L	99.8	-	-	-
Mr12	J2a1h	42.4	Mr60	T	80.3	-	-	-	-	-	-
Mr13	L	61.7	Mr61	L	99.9	-	-	-	-	-	-
Mr14	Q	94.4	Mr62	L	99.8	-	-	-	-	-	-
Mr15	L	99.9	Mr63	L	100	-	-	-	-	-	-
Mr16	Q	92.9	Mr64	Q	93.3	-	-	-	-	-	-
Mr17	G2a	55.8	Mr65	L	61	-	-	-	-	-	-
Mr18	H	82.7	Mr66	L	75.4	-	-	-	-	-	-
Mr19	R1a	100	Mr67	L	100	-	-	-	-	-	-
Mr20	Q	99.5	Mr68	T	97.4	-	-	-	-	-	-
Mr21	L	82.3	Mr69	L	46.7	-	-	-	-	-	-
Mr22	L	95.9	Mr70	L	99.8	-	-	-	-	-	-
Mr23	H	95.6	Mr71	L	81.1	-	-	-	-	-	-
Mr24	H	100	Mr72	R1a	100	-	-	-	-	-	-
Mr25	T	53.7	Mr73	R1a	100	-	-	-	-	-	-
Mr26	N	99.9	Mr74	Q	100	-	-	-	-	-	-
Mr27	Q	100	Mr75	H	85.6	-	-	-	-	-	-
Mr28	J1	75.7	Mr76	J2a1b	95.7	-	-	-	-	-	-
Mr29	I2a	87.7	Mr77	L	68.7	-	-	-	-	-	-
Mr30	R1a	100	Mr78	J1	88.7	-	-	-	-	-	-
Mr31	L	100	Mr79	J2a1b	51.5	-	-	-	-	-	-
Mr32	J2b	90.8	Mr80	Q	69.3	-	-	-	-	-	-
Mr33	L	99.8	Mr81	R1a	100	-	-	-	-	-	-
Mr34	Q	100	Mr82	Q	62.7	-	-	-	-	-	-
Mr35	I2a	93.9	Mr83	Q	99.5	-	-	-	-	-	-
Mr36	H	100	Mr84	Q	99.8	-	-	-	-	-	-
Mr37	Q	79.4	Mr85	L	99.9	-	-	-	-	-	-
Mr38	R1a	100	Mr86	Q	46.7	-	-	-	-	-	-
Mr39	L	99.7	Mr87	R1a	100	-	-	-	-	-	-
Mr40	J2a1b	90.6	Mr88	R1a	100	-	-	-	-	-	-
Mr41	J2a1b	75	Mr89	L	97.2	-	-	-	-	-	-
Mr42	Q	73.1	Mr90	J2a1b	93.5	-	-	-	-	-	-
Mr43	N	40.1	Mr91	Q	92.2	-	-	-	-	-	-
Mr44	Q	88.3	Mr92	L	98.3	-	-	-	-	-	-
Mr45	L	74.5	Mr93	R1a	100	-	-	-	-	-	-
Mr46	L	99.6	Mr94	L	98.9	-	-	-	-	-	-
Mr47	Q	90	Mr95	T	46.8	-	-	-	-	-	-
Mr48	Q	100	Mr96	Q	93.8	-	-	-	-	-	-

Supplementary Table 18. Y-chromosomal haplogroup assignments for each haplotype in Hajong (Hj) population using Whit Athey's algorithm.

Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)
Hj1	L	91.3	Hj49	R1a	100	-	-	-	-	-	-
Hj2	L	95.9	Hj50	L	83.3	-	-	-	-	-	-
Hj3	L	97.6	Hj51	L	89.8	-	-	-	-	-	-
Hj4	L	98	Hj52	H	99.3	-	-	-	-	-	-
Hj5	L	99.7	Hj53	L	81	-	-	-	-	-	-
Hj6	L	99.8	Hj54	R1a	100	-	-	-	-	-	-
Hj7	L	92.3	Hj55	L	99.8	-	-	-	-	-	-
Hj8	R1a	100	Hj56	L	100	-	-	-	-	-	-
Hj9	J2b	100	Hj57	I2a1	66.8	-	-	-	-	-	-
Hj10	L	94.5	Hj58	L	100	-	-	-	-	-	-
Hj11	L	57.8	Hj59	L	99.9	-	-	-	-	-	-
Hj12	I2a	62.9	Hj60	L	98	-	-	-	-	-	-
Hj13	L	100	Hj61	L	91	-	-	-	-	-	-
Hj14	R1a	100	Hj62	T	93.3	-	-	-	-	-	-
Hj15	L	100	Hj63	L	94.1	-	-	-	-	-	-
Hj16	L	100	Hj64	L	96.8	-	-	-	-	-	-
Hj17	T	57.7	Hj65	R1a	100	-	-	-	-	-	-
Hj18	L	99.9	Hj66	Q	99.1	-	-	-	-	-	-
Hj19	L	100	Hj67	T	98.7	-	-	-	-	-	-
Hj20	L	100	Hj68	L	93.5	-	-	-	-	-	-
Hj21	Q	73.4	Hj69	E1b1b	73.6	-	-	-	-	-	-
Hj22	L	56.4	Hj70	T	56.4	-	-	-	-	-	-
Hj23	L	99.7	Hj71	L	99.8	-	-	-	-	-	-
Hj24	L	100	Hj72	L	98.7	-	-	-	-	-	-
Hj25	L	100	Hj73	L	99.7	-	-	-	-	-	-
Hj26	L	65.4	Hj74	L	59.8	-	-	-	-	-	-
Hj27	L	99.9	Hj75	I2a	76.5	-	-	-	-	-	-
Hj28	T	48.9	Hj76	J1	54.4	-	-	-	-	-	-
Hj29	R1a	100	Hj77	L	98	-	-	-	-	-	-
Hj30	L	99.5	Hj78	L	99.1	-	-	-	-	-	-
Hj31	Q	94.4	Hj79	G2a	95.7	-	-	-	-	-	-
Hj32	J2b	100	Hj80	H	100	-	-	-	-	-	-
Hj33	R1a	100	Hj81	L	80.8	-	-	-	-	-	-
Hj34	L	99.4	Hj82	L	53.3	-	-	-	-	-	-
Hj35	T	88.1	Hj83	L	90.2	-	-	-	-	-	-
Hj36	L	100	Hj84	R1b	99.7	-	-	-	-	-	-
Hj37	Q	96	Hj85	T	63.4	-	-	-	-	-	-
Hj38	R1a	100	Hj86	G2a	44.4	-	-	-	-	-	-
Hj39	L	92.3	Hj87	R1a	100	-	-	-	-	-	-
Hj40	L	95.6	Hj88	L	95.9	-	-	-	-	-	-
Hj41	R1a	100	Hj89	L	87.9	-	-	-	-	-	-
Hj42	Q	81	-	-	-	-	-	-	-	-	-
Hj43	L	99.2	-	-	-	-	-	-	-	-	-
Hj44	L	76.6	-	-	-	-	-	-	-	-	-
Hj45	L	100	-	-	-	-	-	-	-	-	-
Hj46	H	100	-	-	-	-	-	-	-	-	-
Hj47	T	94.3	-	-	-	-	-	-	-	-	-
Hj48	L	99.5	-	-	-	-	-	-	-	-	-

Supplementary Table 19. Y-chromosomal haplogroup assignments for each haplotype in Manipuri (Mn) population using Whit Athey's algorithm.

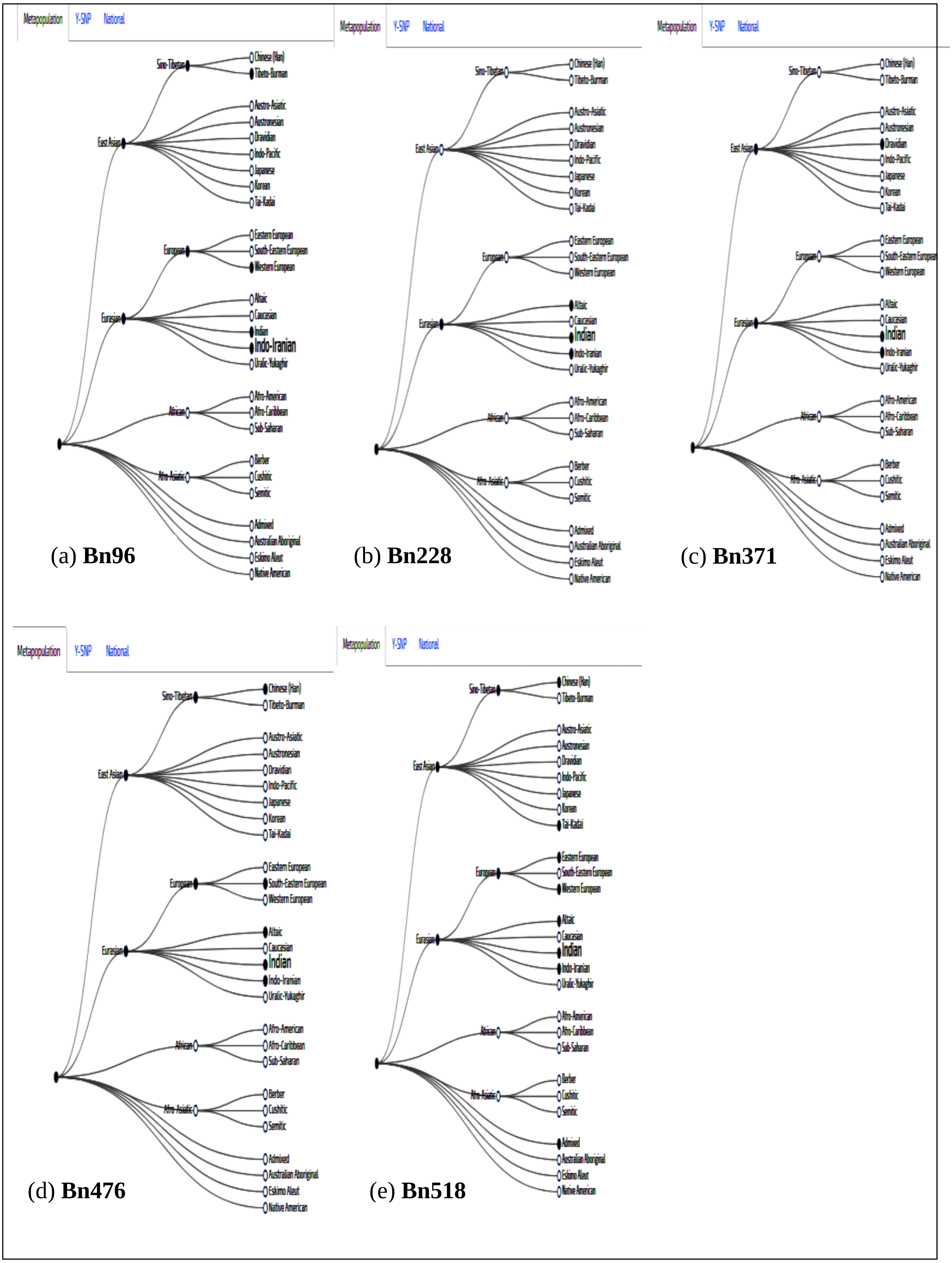
Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)
Mn1	J1	46.2	Mn49	L	44.4	Mn97	L	100	-	-	-
Mn2	L	99.2	Mn50	Q	100	Mn98	L	99.8	-	-	-
Mn3	L	99.4	Mn51	R1a	100	-	-	-	-	-	-
Mn4	L	100	Mn52	J2b	88.2	-	-	-	-	-	-
Mn5	E1b1b	89	Mn53	L	91.9	-	-	-	-	-	-
Mn6	L	99.9	Mn54	L	91.7	-	-	-	-	-	-
Mn7	L	91.7	Mn55	L	67.4	-	-	-	-	-	-
Mn8	R1a	100	Mn56	Q	100	-	-	-	-	-	-
Mn9	Q	80.1	Mn57	Q	100	-	-	-	-	-	-
Mn10	Q	100	Mn58	L	99.9	-	-	-	-	-	-
Mn11	L	90.3	Mn59	E1b1a	85.2	-	-	-	-	-	-
Mn12	E1b1b	68.2	Mn60	L	99.5	-	-	-	-	-	-
Mn13	R1a	99.3	Mn61	L	79.6	-	-	-	-	-	-
Mn14	Q	100	Mn62	L	100	-	-	-	-	-	-
Mn15	Q	100	Mn63	L	100	-	-	-	-	-	-
Mn16	L	99.8	Mn64	E1b1a	51	-	-	-	-	-	-
Mn17	E1b1b	44.2	Mn65	J2a1	50.4	-	-	-	-	-	-
Mn18	R1a	100	Mn66	L	98.5	-	-	-	-	-	-
Mn19	J2a1	65	Mn67	L	59.1	-	-	-	-	-	-
Mn20	E1b1b	95	Mn68	L	96.7	-	-	-	-	-	-
Mn21	E1b1a	99.7	Mn69	E1b1b	53.7	-	-	-	-	-	-
Mn22	L	100	Mn70	L	100	-	-	-	-	-	-
Mn23	Q	100	Mn71	R1a	100	-	-	-	-	-	-
Mn24	R1a	100	Mn72	R1a	100	-	-	-	-	-	-
Mn25	L	99.5	Mn73	H	100	-	-	-	-	-	-
Mn26	L	100	Mn74	R1a	100	-	-	-	-	-	-
Mn27	E1b1b	46.8	Mn75	L	97.9	-	-	-	-	-	-
Mn28	L	84.3	Mn76	L	84.2	-	-	-	-	-	-
Mn29	J2a1	86.7	Mn77	L	59.3	-	-	-	-	-	-
Mn30	L	75.9	Mn78	L	100	-	-	-	-	-	-
Mn31	L	99.4	Mn79	R1a	100	-	-	-	-	-	-
Mn32	L	94	Mn80	R1a	100	-	-	-	-	-	-
Mn33	Q	64.3	Mn81	L	100	-	-	-	-	-	-
Mn34	L	75.4	Mn82	L	99.8	-	-	-	-	-	-
Mn35	L	99.7	Mn83	E1b1a	69.5	-	-	-	-	-	-
Mn36	Q	61.4	Mn84	Q	58.7	-	-	-	-	-	-
Mn37	R1a	100	Mn85	L	97.7	-	-	-	-	-	-
Mn38	J2a1	96.5	Mn86	Q	39.9	-	-	-	-	-	-
Mn39	E1b1a	48.4	Mn87	L	100	-	-	-	-	-	-
Mn40	L	99.9	Mn88	L	100	-	-	-	-	-	-
Mn41	L	100	Mn89	L	99.9	-	-	-	-	-	-
Mn42	H	99.9	Mn90	L	100	-	-	-	-	-	-
Mn43	E1b1b	48.3	Mn91	J1	66.1	-	-	-	-	-	-
Mn44	L	100	Mn92	Q	100	-	-	-	-	-	-
Mn45	Q	100	Mn93	R1a	100	-	-	-	-	-	-
Mn46	L	98.8	Mn94	L	61.3	-	-	-	-	-	-
Mn47	E1b1a	97.8	Mn95	R1a	100	-	-	-	-	-	-
Mn48	L	100	Mn96	H	95.6	-	-	-	-	-	-

Supplementary Table 20. Y-chromosomal haplogroup assignments for each haplotype in Khasia (Kh) population using Whit Athey's algorithm.

Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)	Haplotype	Predicted Y-haplogroup	Probability (%)
Kh1	L	93.1	Kh49	L	62.4	-	-	-	-	-	-
Kh2	Q	52.8	Kh50	I2b1	82	-	-	-	-	-	-
Kh3	L	92.2	Kh51	I2b1	94.7	-	-	-	-	-	-
Kh4	L	89.1	Kh52	J1	71.3	-	-	-	-	-	-
Kh5	G2a	85	Kh53	J2a1h	99.5	-	-	-	-	-	-
Kh6	J2a1	97.5	Kh54	L	83.9	-	-	-	-	-	-
Kh7	T	92.3	Kh55	J2a1b	76.4	-	-	-	-	-	-
Kh8	T	71.6	Kh56	I2b1	53.1	-	-	-	-	-	-
Kh9	T	87.2	Kh57	Q	98	-	-	-	-	-	-
Kh10	I2b1	86.9	Kh58	N	83.6	-	-	-	-	-	-
Kh11	R1a	100	Kh59	R1a	76	-	-	-	-	-	-
Kh12	T	80.1	Kh60	R1a	100	-	-	-	-	-	-
Kh13	L	99.6	Kh61	T	98.8	-	-	-	-	-	-
Kh14	R1a	100	Kh62	R1a	100	-	-	-	-	-	-
Kh15	L	97.6	Kh63	R1a	100	-	-	-	-	-	-
Kh16	T	71.8	Kh64	T	93.2	-	-	-	-	-	-
Kh17	T	99.8	Kh65	T	99.1	-	-	-	-	-	-
Kh18	R1a	100	Kh66	Q	86.5	-	-	-	-	-	-
Kh19	G2a	91.7	Kh67	T	99.5	-	-	-	-	-	-
Kh20	J1	97.6	Kh68	R1a	100	-	-	-	-	-	-
Kh21	L	58.2	Kh69	L	99.6	-	-	-	-	-	-
Kh22	L	99.1	Kh70	T	75.5	-	-	-	-	-	-
Kh23	H	99.5	Kh71	Q	87.5	-	-	-	-	-	-
Kh24	L	43.3	Kh72	I2b1	88.4	-	-	-	-	-	-
Kh25	L	98.1	Kh73	I2b1	57.8	-	-	-	-	-	-
Kh26	L	98	Kh74	J2a1h	59.4	-	-	-	-	-	-
Kh27	Q	82	Kh75	T	42.9	-	-	-	-	-	-
Kh28	L	98.3	Kh76	L	98.8	-	-	-	-	-	-
Kh29	T	87.9	Kh77	Q	100	-	-	-	-	-	-
Kh30	R1a	100	Kh78	G2a	83.8	-	-	-	-	-	-
Kh31	Q	39.7	Kh79	J2a1b	72.1	-	-	-	-	-	-
Kh32	T	52.9	Kh80	Q	99.5	-	-	-	-	-	-
Kh33	L	99.9	Kh81	L	99.8	-	-	-	-	-	-
Kh34	Q	54	Kh82	Q	57	-	-	-	-	-	-
Kh35	I2b1	53.3	Kh83	I2b1	78.9	-	-	-	-	-	-
Kh36	J2a1	80.4	Kh84	T	95.8	-	-	-	-	-	-
Kh37	Q	83.8	Kh85	H	100	-	-	-	-	-	-
Kh38	L	48.9	Kh86	Q	77.3	-	-	-	-	-	-
Kh39	T	64.5	Kh87	L	91.5	-	-	-	-	-	-
Kh40	G2a	68.6	Kh88	L	91.4	-	-	-	-	-	-
Kh41	L	97.5	Kh89	L	99.8	-	-	-	-	-	-
Kh42	R1a	100	Kh90	Q	62.6	-	-	-	-	-	-
Kh43	Q	81.1	Kh91	J2a1b	34.6	-	-	-	-	-	-
Kh44	L	91.6	-	-	-	-	-	-	-	-	-
Kh45	J2a1b	35.6	-	-	-	-	-	-	-	-	-
Kh46	I2b1	96.7	-	-	-	-	-	-	-	-	-
Kh47	J2a1	91.5	-	-	-	-	-	-	-	-	-
Kh48	G2a	64.9	-	-	-	-	-	-	-	-	-

Supplementary Table 21. Frequency distribution of Y-chromosomal haplogroups in the studied populations of Bangladesh.

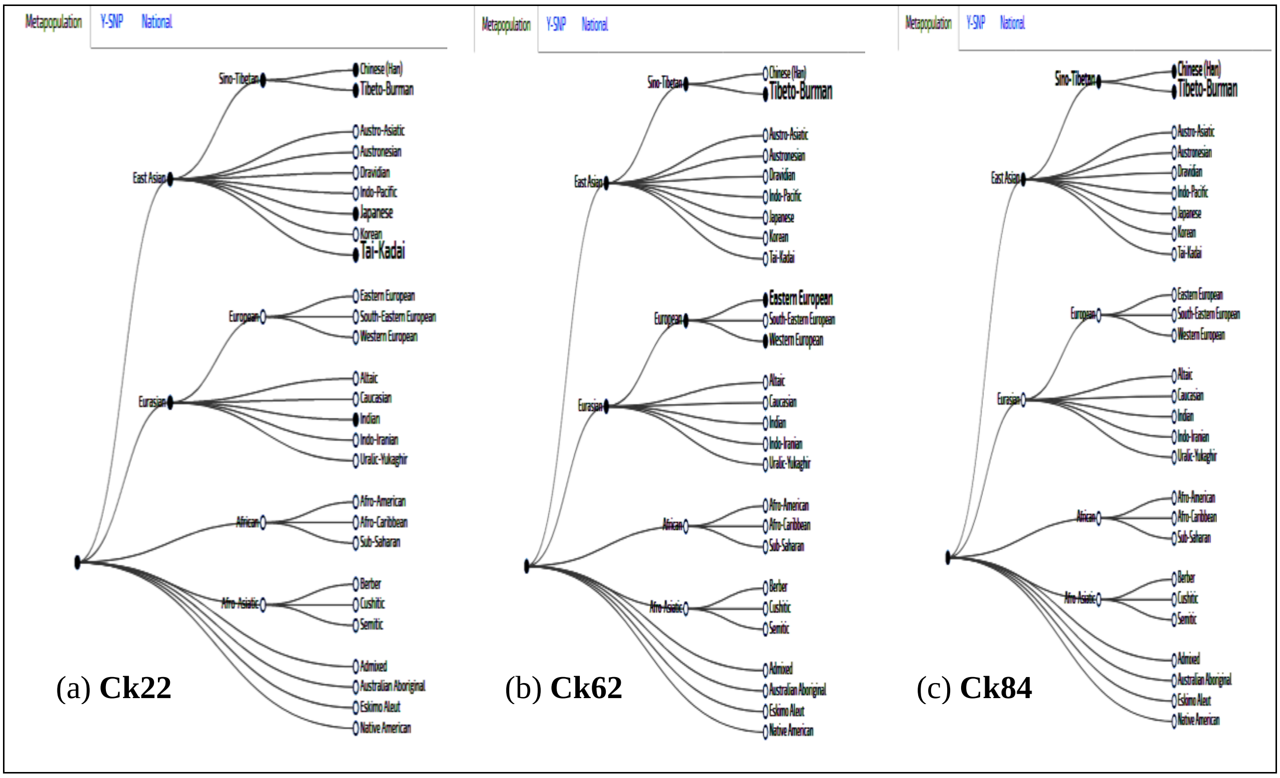
Haplogroups		**Studied populations**							
		Bangali	**Chakma**	**Tripura**	**Rakhine**	**Marma**	**Hajong**	**Manipuri**	**Khasia**
E1b1a	Number of haplotypes (Frequency in %)	8 (1.233)	1 (0.862)	-	-	-	-	6 (6.122)	-
E1b1b		9 (1.387)	1 (0.862)	8 (8.081)	3 (2.727)	-	1 (1.124)	7 (7.143)	-
G2a		7 (1.079)	4 (3.448)	1 (1.010)	3 (2.727)	2 (1.869)	2 (2.247)	-	5 (5.494)
H		115 (17.720)	5 (4.310)	3 (3.030)	8 (7.273)	7 (6.542)	3 (3.371)	3 (3.061)	2 (2.198)
I1		1 (0.154)	3 (2.586)	-	-	-	-	-	-
I2a (xI2a1)		1 (0.154)	3 (2.586)	3 (3.030)	-	2 (1.869)	2 (2.247)	-	-
I2a1		12 (1.849)	1 (0.862)	-	-	-	1 (1.124)	-	-
I2b (xI2b1)		1 (0.154)	-	-	-	-	-	-	-
I2b1		12 (1.849)	-	-	2 (1.818)	-	-	-	9 (9.890)
J1		12 (1.849)	11 (9.483)	14 (14.141)	5 (4.545)	6 (5.607)	1 (1.124)	2 (2.041)	2 (2.198)
J2a1b		20 (3.082)	-	1 (1.010)	2 (1.818)	5 (4.673)	-	-	4 (4.395)
J2a1h		6 (0.924)	1 (0.862)	-	-	1 (0.935)	-	-	2 (2.198)
J2a1 x J2a1-bh		32 (4.931)	-	8 (8.081)	5 (4.545)	-	-	4 (4.082)	3 (3.297)
J2b		32 (4.931)	-	-	2 (1.818)	2 (1.869)	2 (2.247)	1 (1.020)	-
L		113 (17.410)	61 (52.586)	56 (56.566)	40 (36.364)	32 (29.907)	53 (59.550)	46 (46.939)	23 (25.275)
N		3 (0.462)	2 (1.724)	-	-	4 (3.738)	-	-	1 (1.099)
Q		45 (6.934)	16 (13.793)	4 (4.040)	16 (14.545)	30 (28.037)	5 (5.618)	16 (16.327)	14 (15.385)
R1a		205 (31.587)	5 (4.310)	-	21 (19.091)	11 (10.280)	10 (11.235)	13 (13.265)	10 (10.989)
R1b		4 (0.616)	-	-	-	-	1 (1.124)	-	-
T		11 (1.695)	2 (1.724)	1 (1.010)	3 (2.727)	5 (4.673)	8 (8.989)	-	16 (17.582)
Number of different haplotypes		**649 (100%)**	**116 (100%)**	**99 (100%)**	**110 (100%)**	**107 (100%)**	**89 (100%)**	**98 (100%)**	**91 (100%)**



(a) **Bn96** (b) **Bn228** (c) **Bn371**

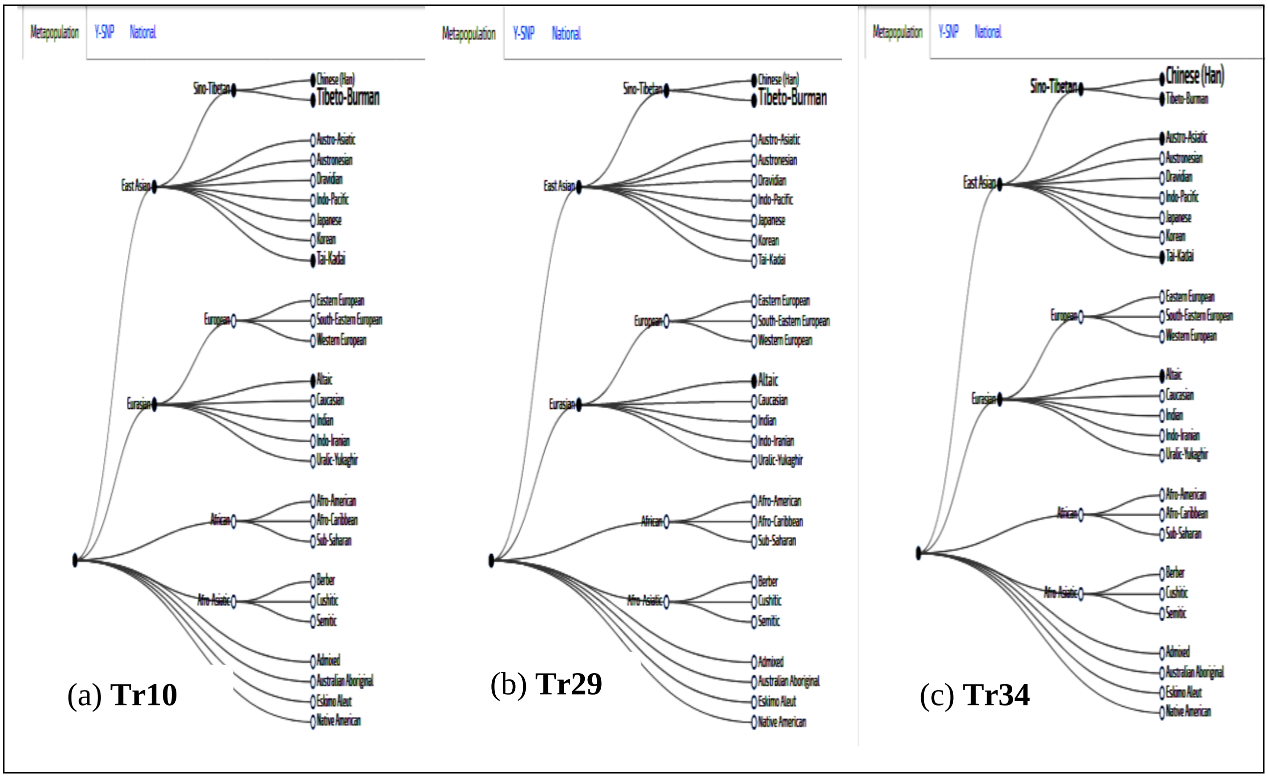
(d) **Bn476** (e) **Bn518**

Supplementary Fig. 01. The most frequent haplotypes of Bangali (Bn) population searched in 205,059 haplotypes of YHRD metapopulation database (Release version R59; November 01, 2018). ***Bold Circles*** **represent the respective haplotype matched with the metapopulation.**



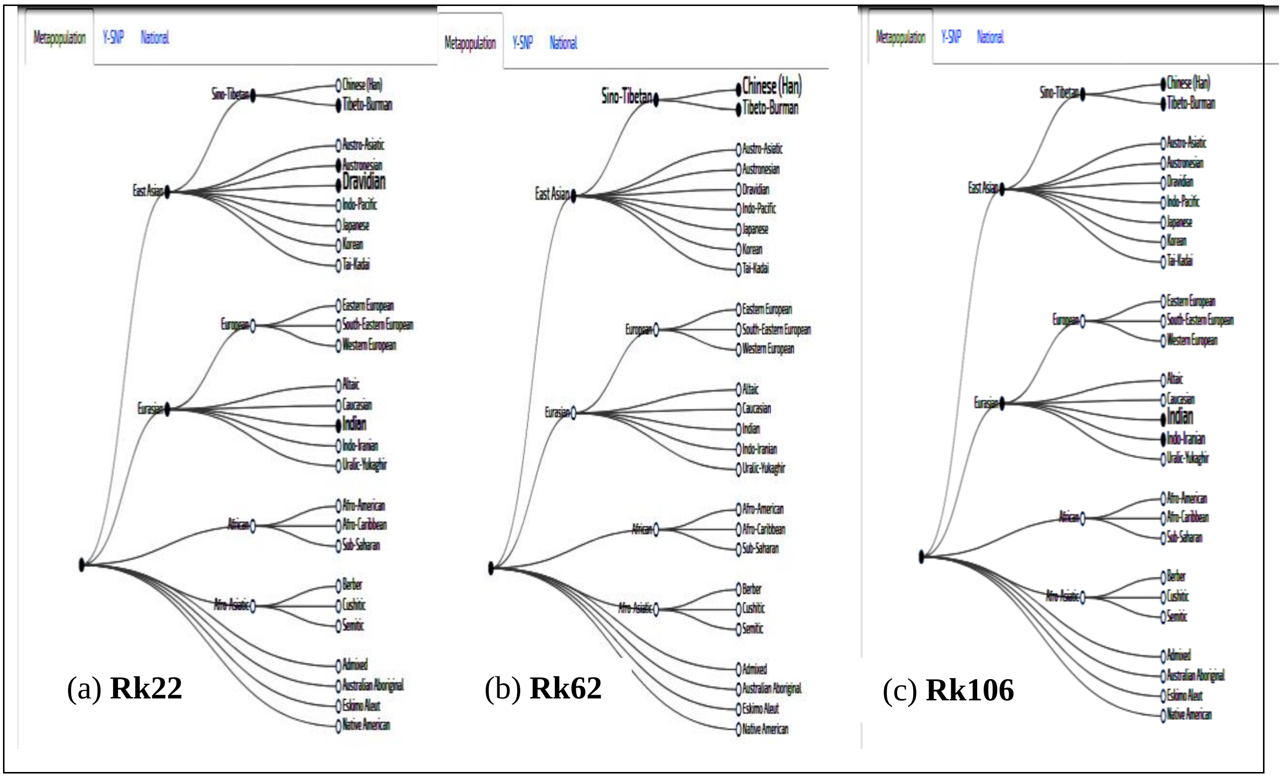
(a) **Ck22** (b) **Ck62** (c) **Ck84**

Supplementary Fig. 02. The most frequent haplotypes of Chakma (Ck) population searched in 205,059 haplotypes of YHRD metapopulation database (Release version R59; November 01, 2018). *Bold Circles* represent the respective haplotype match with the metapopulation.



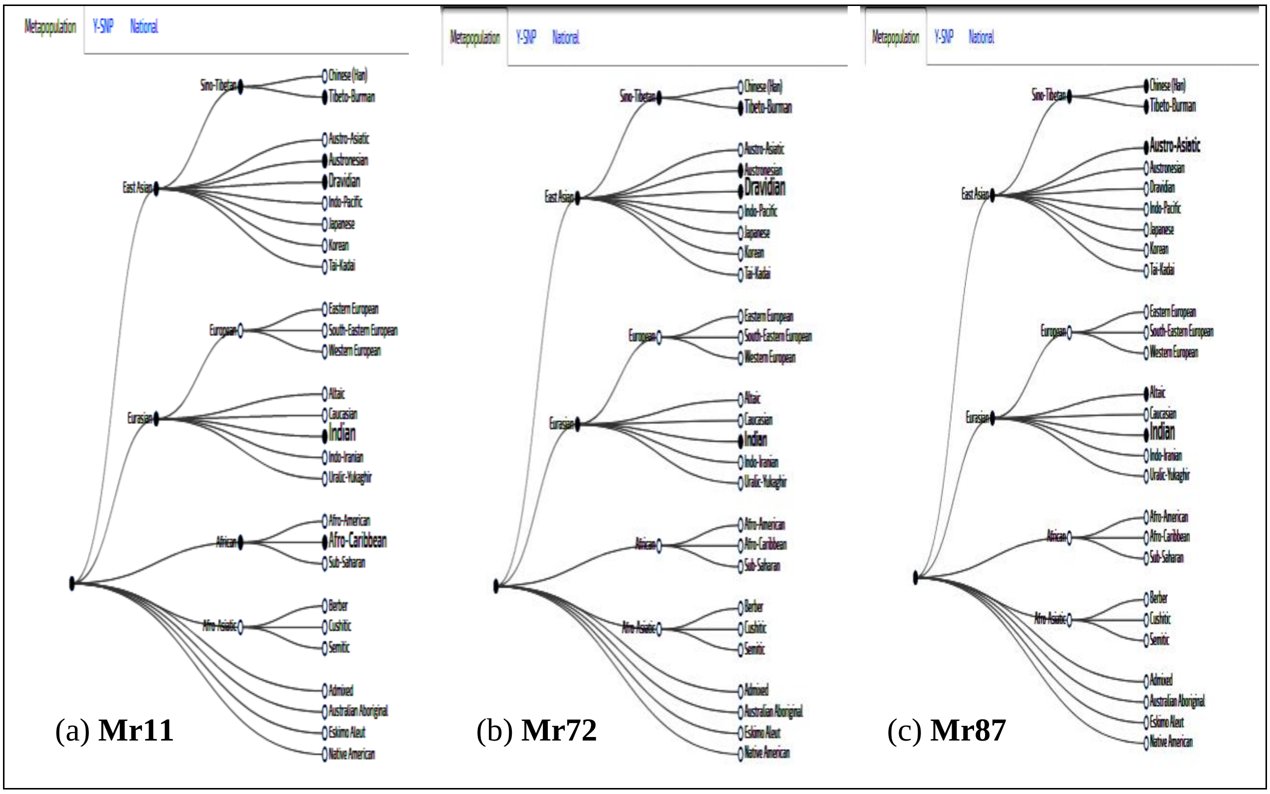
(a) **Tr10** (b) **Tr29** (c) **Tr34**

Supplementary Fig. 03. The most frequent haplotypes of Tripura (Tr) population searched in 205,059 haplotypes of YHRD metapopulation database (Release version R59; November 01, 2018). *Bold Circles* represent the respective haplotype match with the metapopulation.



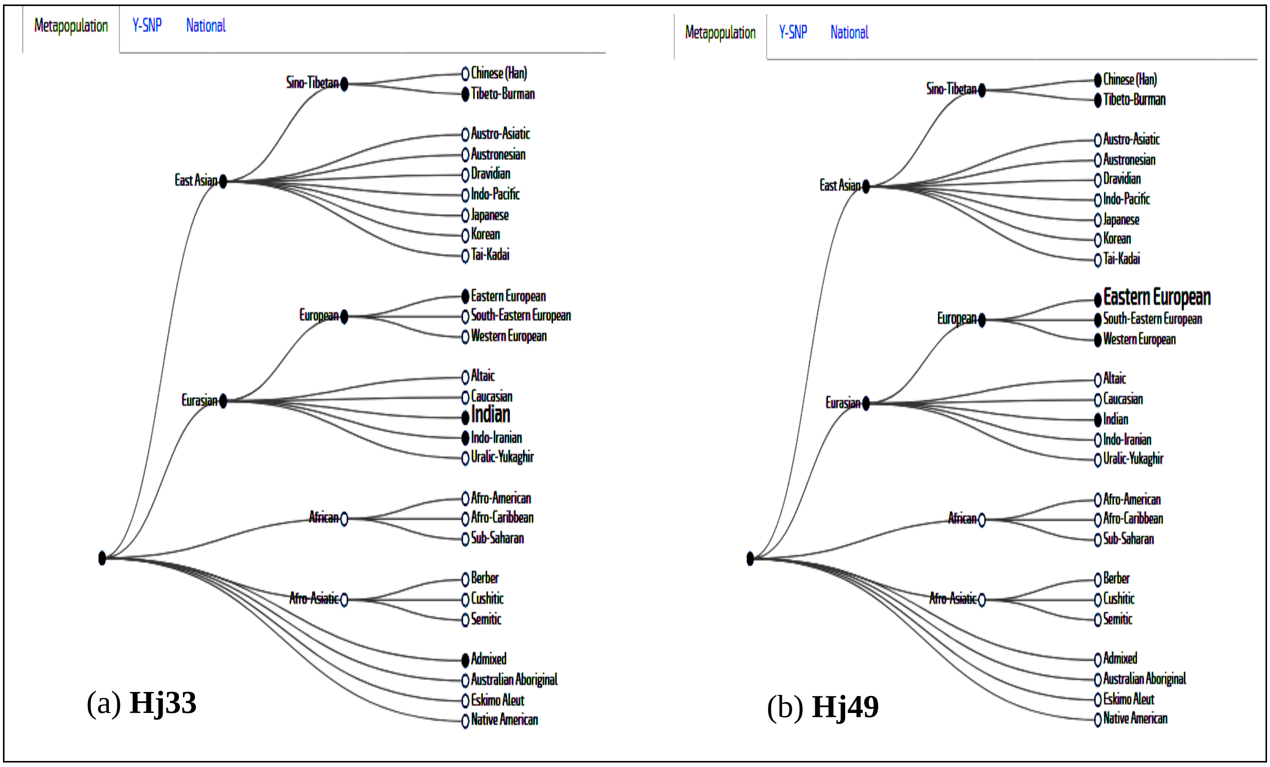
(a) **Rk22** (b) **Rk62** (c) **Rk106**

Supplementary Fig. 04. The three most frequent haplotypes of Rakhine (Rk) population searched in 205,059 haplotypes of YHRD metapopulation database (Release version R59; November 01, 2018). *Bold Circles* represent the respective haplotype match with the metapopulation.



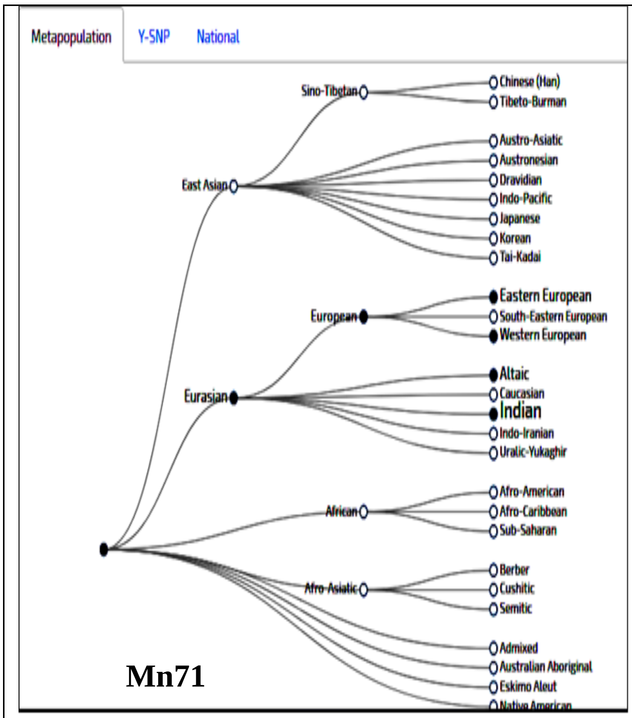
(a) **Mr11** (b) **Mr72** (c) **Mr87**

Supplementary Fig. 05. The three most frequent haplotypes of Marma population searched in 205,059 haplotypes of YHRD metapopulation database (Release version R59; November 01, 2018). *Bold Circles* represent the respective haplotype match with the metapopulation.

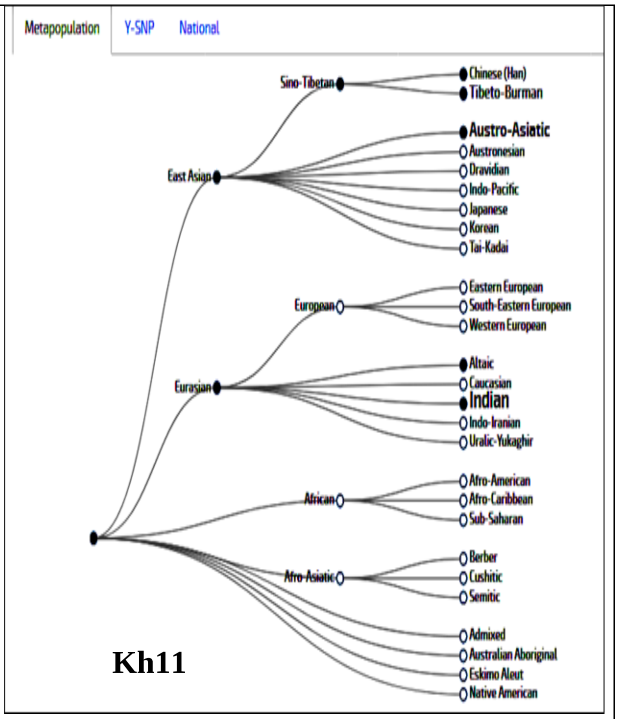


(a) **Hj33** (b) **Hj49**

Supplementary Fig. 06. The two most frequent haplotypes of Hajong(Hj) population searched in 205,059 haplotypes of YHRD metapopulation database (Release version R59; November 01, 2018). *Bold Circles* represent the respective haplotype match with the metapopulation.



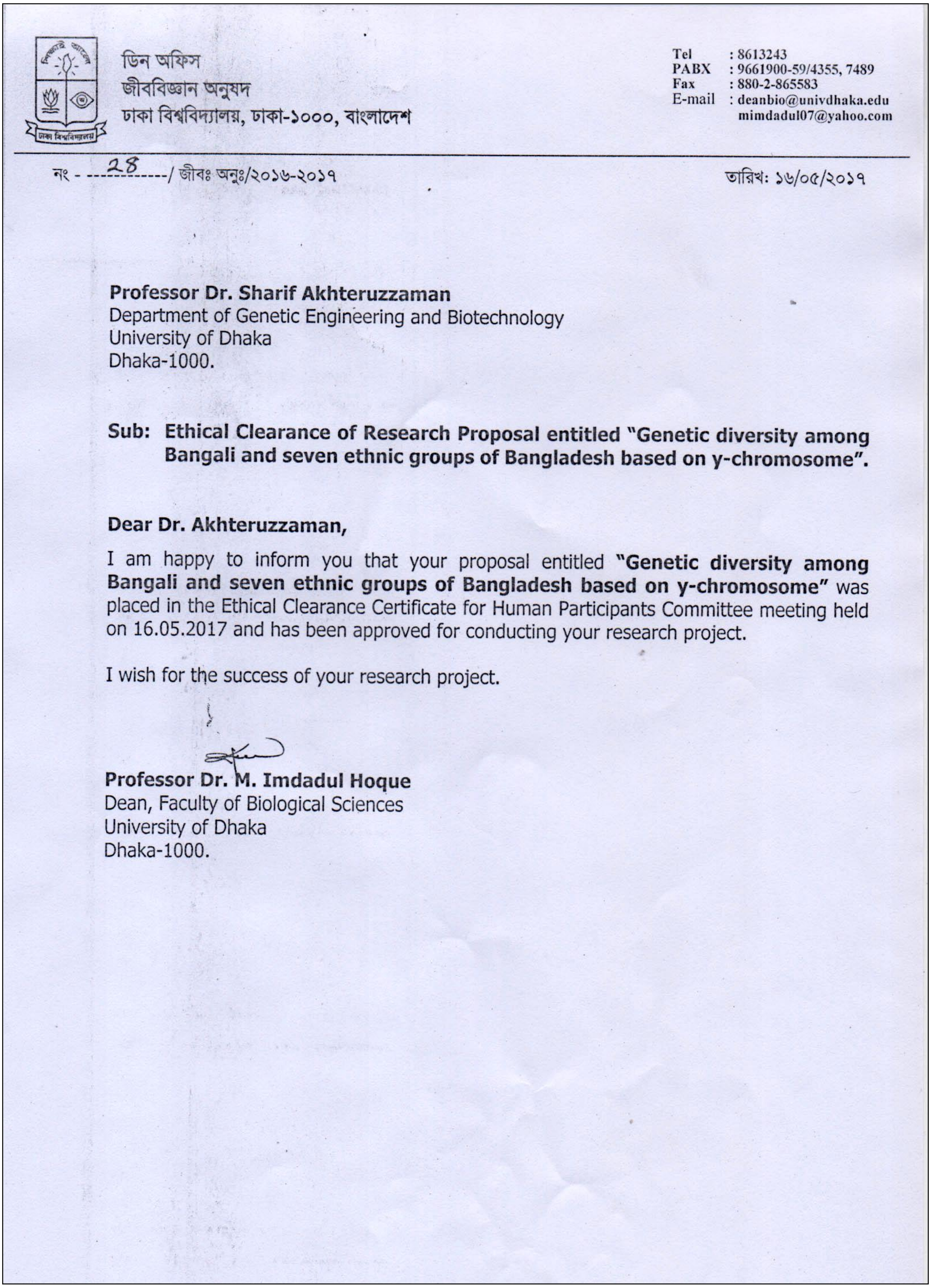
Mn71



Kh11

Supplementary Fig. 07. The most frequent haplotype of Manipuri (Mn) population searched in 205,059 haplotypes of YHRD metapopulation database (Release version R59; November 01, 2018). *Bold Circles* represent the respective haplotype match with the metapopulations.

Supplementary Fig. 08. The most frequent haplotype of Khasia (Kh) population searched in 205,059 haplotypes of YHRD metapopulation database (Release version R59; November 01, 2018). *Bold Circles* represent the respective haplotype match with the metapopulation.



ডিন অফিস
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নং - 28/ জীবঃ অনুঃ/২০১৬-২০১৭

তারিখ: ১৬/০৫/২০১৭

Professor Dr. Sharif Akhteruzzaman
Department of Genetic Engineering and Biotechnology
University of Dhaka
Dhaka-1000.

Sub: Ethical Clearance of Research Proposal entitled "Genetic diversity among Bangali and seven ethnic groups of Bangladesh based on y-chromosome".

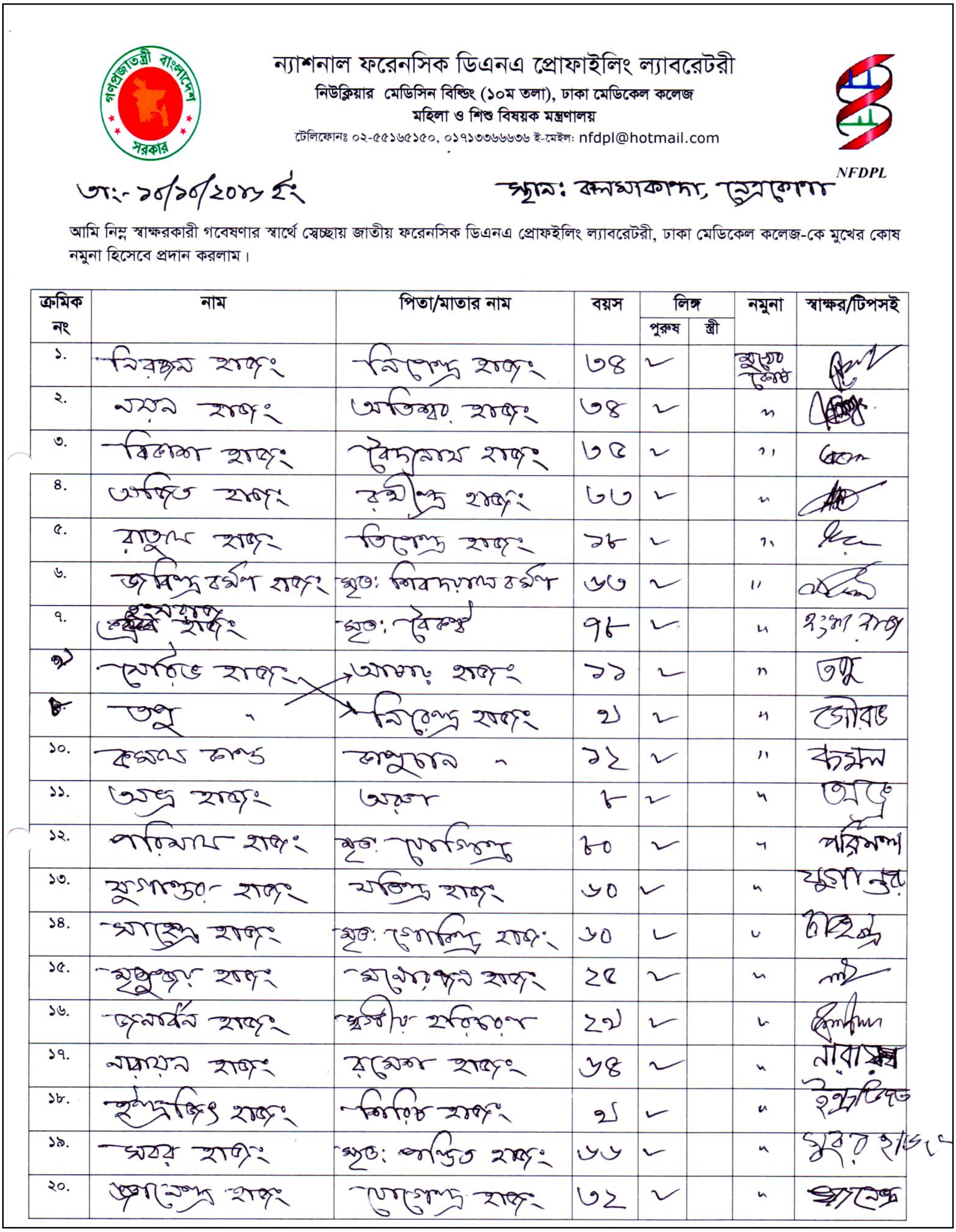
Dear Dr. Akhteruzzaman,

I am happy to inform you that your proposal entitled **"Genetic diversity among Bangali and seven ethnic groups of Bangladesh based on y-chromosome"** was placed in the Ethical Clearance Certificate for Human Participants Committee meeting held on 16.05.2017 and has been approved for conducting your research project.

I wish for the success of your research project.

Professor Dr. M. Imdadul Hoque
Dean, Faculty of Biological Sciences
University of Dhaka
Dhaka-1000.

Appendix-I. Ethical Clearance Certificate for Human Participants, Faculty of Biological Sciences, University of Dhaka, Dhaka-1000, Bangladesh.



ন্যাশনাল ফরেনসিক ডিএনএ প্রোফাইলিং ল্যাবরেটরী
নিউক্লিয়ার মেডিসিন বিল্ডিং (১০ম তলা), ঢাকা মেডিকেল কলেজ
মহিলা ও শিশু বিষয়ক মন্ত্রণালয়
টেলিফোনঃ ০২-৫৫১৬৫১৫০, ০১৭১৩৩৬৬৬৩৬ ই-মেইল: nfdpl@hotmail.com

NFDPL

তাং- ১০/১০/২০১৯ ইং

স্থান: কলমাকান্দা, নেত্রকোণা

আমি নিম্ন স্বাক্ষরকারী গবেষণার স্বার্থে স্বেচ্ছায় জাতীয় ফরেনসিক ডিএনএ প্রোফাইলিং ল্যাবরেটরী, ঢাকা মেডিকেল কলেজ-কে মুখের কোষ নমুনা হিসেবে প্রদান করলাম।

ক্রমিক নং	নাম	পিতা/মাতার নাম	বয়স	লিঙ্গ		নমুনা	স্বাক্ষর/টিপসই
				পুরুষ	স্ত্রী		
১.	নিরঞ্জন হাজং	নিপেন্দ্র হাজং	৩৪	✓		মুখের কোষ	
২.	নয়ন হাজং	অতিশ্বর হাজং	৩৪	✓		〃	
৩.	বিকাশ হাজং	বৈদ্যনাথ হাজং	৩৫	✓		〃	
৪.	অজিত হাজং	রবীন্দ্র হাজং	৬৩	✓		〃	
৫.	রাতুল হাজং	জিতেন্দ্র হাজং	১৮	✓		〃	
৬.	জগিন্দ্র বর্মণ হাজং	মৃত: শিবদয়াল বর্মণ	৬৩	✓		〃	
৭.	[illegible] হাজং	মৃত: বৈকুণ্ঠ	৭৮	✓		〃	হংসা হাজং
৯	সৌরভ হাজং	আনন্দ হাজং	১১	✓		〃	তনু
৮	তনু 〃	নিরেন্দ্র হাজং	৯	✓		〃	সৌরভ
১০.	কমল চন্দ	ভানুচরণ 〃	১২	✓		〃	কমল
১১.	অভ্র হাজং	অরুণ	৮	✓		〃	অভ্র
১২.	পরিমল হাজং	মৃত: সুরেন্দ্র	৮০	✓		〃	পরিমল
১৩.	যুগান্তর হাজং	যতীন্দ্র হাজং	৬০	✓		〃	যুগান্তর
১৪.	[illegible] হাজং	মৃত: গোবিন্দ্র হাজং	৬০	✓		〃	
১৫.	মৃত্যুঞ্জয় হাজং	মনমোহন হাজং	২৫	✓		〃	
১৬.	জনার্দন হাজং	স্বর্গীয় হরিচরণ	২৯	✓		〃	
১৭.	নারায়ন হাজং	রমেশ হাজং	৬৪	✓		〃	নারায়ন
১৮.	ইন্দ্রজিৎ হাজং	শিশির হাজং	৯	✓		〃	ইন্দ্রজিৎ
১৯.	সমর হাজং	মৃত: পন্ডিত হাজং	৬৬	✓		〃	সমর হাজং
২০.	জ্ঞানেন্দ্র হাজং	যোগেন্দ্র হাজং	৩২	✓		〃	জ্ঞানেন্দ্র

Appendix-II. A form of written informed consent by participants for population genetics research. Written consent was taken from Hajong ethnic community of different villages of Kalmakanda Upazilla under Netrokona District.