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Short Communication

Y-STR Polymorphism among Khandayat Community of Odisha, India

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Abstract

The study was conducted to determine the polymorphism and extent of genetic diversity at 9 Short Tandem Repeat (STR) loci of Y-chromosome among the Khandayat Community of Odisha. Blood samples were collected from 91 unrelated healthy individuals and genomic DNA was extracted by Organic Method. The DNA samples were amplified by multiplex-PCR followed by genotyping. Genotyping results of the 9 Y-STRs showed that all loci included in this study are highly polymorphic among the Khandayat population.

Keywords: Y-STR, multiplex-PCR, genotyping.

Introduction

After the discovery of DNA structure and successful completion of Human Genome Project, the major challenge for scientists is to decipher human genome variation[1-5]. Indian population is an amalgamation of various ethnic, cultural and geographical groups. DNA marker-based studies on Indian population have revealed the presence of large extent of human genetic variation in India[6-13]. Odisha is located on the southeast coastal region of India, which is inhabited by various population groups belonging to different strata of the hierarchical caste system like Brahmins, Khandayats, Karans and Gope. Khandayats belong to an ancient warrior group also known as Kshatriya and constituting over 35% of the state's population[14-19]. Genetic profiling is being widely used for the medico-legal purposes and it necessitates the study of the genetic polymorphism. Our study aims to understand the genetic diversity of 9 Y-STR loci of Khandayat Community of Odisha. The analyzed Y-STR loci include 8 tetra-nucleotide Y-STR markers DYS19, DYS385a/b, DYS389I/II, DYS390, DYS391, DYS393 and a tri-nucleotide marker DYS392. These Y-STR markers are known as Minimal Haplotype Loci (MHL)[20]. This study intends to estimate the genetic diversity among the Khandayat Community of Odisha using 9 Y-STR loci.

Material and Methods

Whole blood samples were collected in 2ml EDTA vacutainers (BD Biosciences, NJ, USA) from 91 healthy unrelated male individuals of Khandayat Community, Odisha (India) and stored at 4^0C till further analysis. Genomic DNA was isolated from by standard Organic (Phenol - Chloroform extraction) method[21]. The extracted DNA was quantified by spectrophotometer and quality of DNA was checked by agarose gel electrophoresis (0.8% agarose gel) and checked with the help of GelDoc System (AlphaImager, CA, USA). The DNA samples were amplified in Thermal Cycler (PTC 200, MJ Research Inc., USA) using AmpFL STR Yfiler® PCR Amplification Kit™ (Applied Biosystems, Foster City, CA, USA) for 9 STR loci simultaneously by Multiplex PCR (cycling conditions described in table-1) and then analyzed on ABI Prism 3130 Automated Genetic Analyzer (Applied Biosystems, Foster City, CA, USA)[22]. Allelic designations for different loci were obtained by Gene Mapper ID software (v. 3.2).

Table-1
Cycling conditions for Multiplex PCR

Pre-denaturation	95^0C	11 min
Denaturation	94^0C	1 min
Annealing	56^0C	1 min
Extension	72^0C	1 min
30 Cycles		
Final Extension	60^0C	40 min
Hold	4^0C	

Results and Discussion

The allelic frequencies (table-2) of the 9 Y-STR loci were calculated for DNA samples collected from 91 unrelated males of Khandayat Community of Odisha. The majority of haplotypes were unique (86/91). 7.69% samples showed mono-allelic condition for bi-allelic loci DYS385. 3 samples were unique which showed bi-allelic condition for DYS390 and DYS19. Highest polymorphism was shown by locus DYS393.

Conclusion

Forensic DNA Typing involves determining the DNA profiles of samples collected from the scene of crime and comparing them with the DNA profiles obtained from suspects and the victims. In case of a match, which includes the suspect as the potential source of sample collected at the scene of crime, the

last step is to find out the likelihood ratio, that someone else may have the same DNA profile as the studied sample. The likelihood ratio is determined by calculating the frequency of the suspect's profile in a relevant population.

The observed results indicate that 9 Y-STR loci used in the current study are highly polymorphic among Khandayat community. Thus, this set of Y-STRs can be used for the forensic purposes like paternity testing, individual identification, genetic mapping etc. Hence this will add to the databank of various studies conducted on Indian population.

Table-2
Haplotype Diversity of 9 Y-STR Loci

Sl. No.	Locus Designation	Range of Alleles
1	DYS19	14-18
2	DYS389I	10-16
3	DYS390	18-27
4	DYS389II	25-32
5	DYS391	9-17
6	DYS392	10-15
7	DYS393	12-16
8	DYS385 a/b	11-25

References

1. Wilkins M.H.F., Gosling R.G. and Seeds W.E., Physical studies of nucleic acid, *Nature*, **67(4254)**, 759–760 **(1951)**

2. Watson J.D. and Crick F.H., Molecular structure of nucleic acids; a structure for deoxyribose nucleic acid, *Nature*, **171(4356)**, 737–738 **(1953)**

3. Crick F.H.C., The Complementary Structure of DNA, *Proc Nat Acad Sci USA*, **40(8),** 756–758 **(1954)**

4. International Human Genome Sequencing Consortium, Finishing the euchromatic sequence of the human genome, *Nature*, **431**, 931-945 **(2004)**

5. The 1000 Genomes Project Consortium, A map of human genome variation from population-scale sequencing, *Nature*, **467**, 1061–1073 **(2010)**

6. Bhasin M.K. and Walter H., Genetics of Castes and Tribes of India, Kamla-Raj Enterprises, Delhi **(2001)**

7. Indian Genome Variation Consortium, Genetic landscape of the people of India: a canvas for disease gene exploration, *J. Genet.*, **87**, 3–20 **(2008)**

8. Cavalli-Sforza L.L., Menozzi P. and Piazza A., The history and geography of Human genes Princeton: Princeton University Press **(1994)**

9. Gadgil M., Joshi N.V., Shambu Prasad U.V., Manoharan S. and Patil S., Peopling of India, In The Indian Human Heritage, Universities Press, Hyderabad, India, 100-129 **(1997)**

10. Papiha S.S., Genetic variation in India, *Hum Biol*, **68,** 607-628 **(1996)**

11. Majumder P.P., People of India: Biological diversity and affinities, *Evol Anthropol*, **6,** 100-110 **(1998)**

12. Das K., Malhotra K.C., Mukherjee B.N., Walter H., Majumder P.P., and Papiha S.S., Population structure and genetic differentiation among 16 tribal population of Central India, *Hum Biol*, **68**, 679-705 **(1996)**

13. Basu A., Mukherjee N., Roy S., Sengupta S., Banerjee S., Chakraborty M., Dey B., Roy M., Roy B., Bhattacharya N.P., Roychoudhury S. and Majumder P.P., Ethnic India: A genomic view, with special reference to peopling and structure, *Genome Res*, **13**, 2277-2290 **(2003)**

14. Thapar R., Early India: From the origins to AD 1300, University of California Press; First Edition **(2004)**

15. Kosambi D.D., The Culture and Civilization of Ancient India in Historical Outline, Vikas Publishing House Pvt. Ltd, New Delhi **(1991)**

16. Cordaux R., Aunger R., Bentley G., Nasidze I., Sirajuddin S.M. and Stoneking M., Independent origins of Indian caste and tribal paternal lineages, *Curr Biol*, **14,** 231-235 **(2004)**

17. Singh K.S., People of India: An Introduction, Anthropological Survey of India, Calcutta **(1992)**

18. Reich, D., Thangaraj, K., Patterson, N., Price, A. L., and Singh, L., Reconstructing Indian population history, *Nature*, **461**, 489–495 **(2009)**

19. Bamshad, M., Kivisild, T., Scott Watkins, W., Dixon, M. E., Ricker, C. E., Rao, B. B., Mastan Naidu, J., Ravi Prasad, B. V., Govinda Reddy, P., Rasanayagam, A., Papiha, S. S., Villems, R., Redd, A. J., Hammer, M. F., Nguyen, S. V., Carroll, M. L., Batzer, M. A. and Jorde, L. B, Genetic evidence on the origins of Indian caste populations, *Genome Res*, **11,** 994-1004 **(2001)**

20. de Knijff, P., Kayser, M., Caglia, A., Corach, D., Fretwell, N., Gehrig, C., Graziosi, G., Heidorn, F., Herrmann, S., Herzog, B., Hidding, M., Honda, K., Jobling, M., Krawczak, M., Leim, K., Meuser, S., Meyer, E., Oesterreich, W., Pandya, A., Parson, W., Penacino, G., Perez-Lezaun, A., Piccinini, A., Prinz, M., Schmitt, C., Schneider, P. M., Szibor, R., Teifel-Greding, J., Weichhold, G. M. and Roewer, L., Chromosome Y microsatellites: population genetic and evolutionary aspects, *Int J Legal Med*, **110**(3), 134-149 **(1997)**

21. Sambrook, J., Maccallum, P. and Russel, D., Molecular Cloning: A Laboratory Manual, 3rd ed. Cold Springs Harbour Press, NY **(2001)**

22. Redd, A. J., Clifford, S. L. and Stoneking, M., Multiplex DNA typing of short-tandem-repeat loci on the Y chromosome, *Biol Chem*, **378**(8), 923-7 **(1997)**