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Seven new Y-STRs haplotypes of Chinese Han ethnic group

Announcement of Population Data

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Abstract

Seven new Y-chromosome STRs loci (DYS456, DYS460, DYS461, DYS462, DYS459, DYS438 and DYS439) have been amplified in 105 healthy unrelated males of Chinese Han population, in order to investigate allele and haplotype frequencies of them, to evaluate their usefulness in forensic casework, and to compare with other groups. © 2005 Elsevier Ireland Ltd. All rights reserved.

Keywords: Y-chromosome STR; Haplotype; Chinese Han population

Population: The studied samples were obtained from 105 unrelated, healthy, male individuals of Chinese Han population living in Shaanxi province of China.

DNA Extraction: The whole blood was obtained by venipuncture and collected into EDTA tubes. Genomic DNA was Chelex-extracted from peripheral blood samples as previously described [1].

PCR: Single PCR amplification for new seven Y-chromosome STRs loci was performed in a final volume of 20 μ l. The primer sequences and PCR conditions of DYS456, DYS459 used were described by Alan J. Redd et al. [2]. The primer sequences and PCR cycling reaction of DYS460, DYS461, DYS462, DYS438, and DYS439 were obtained from Genbank (http://www.gdb.org/).

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Typing: Detection and genotyping of seven Y-STRs loci PCR Products were carried out on polyacrylamide denaturing gel electrophoresis by using silver staining.

Results: See Tables 1 and 2.

Data analysis: Haplotypes and allele frequencies were estimated by counting method. Haplotypes and gene diversities were estimated according to Nei [3].

Access to the data: Available upon request: cmshen@ tom.com.

Other remarks: As shown in Tables 1 and 2, 30 alleles and 7 phenotypes (DYS459) were observed from 105 males of Chinese Han population. The allele 10 of DYS438 locus had the highest frequency (0.7078). DYS460 locus showed the highest gene diversity (0.7338). Out of a total of 105 individuals 96 showed different haplotypes. 88 were unique. Seven were found two times. One was found three times. The most common hapoltype was 16-8-10-11-(9-10)-10-12 (DYS456-DYS460-DYS461-DYS462-DYS459-DYS438-DYS439). The haplotype diversity of group was calculated as 0.9981. Due to the fact that population data on these new Y-STRs are scarce, there are no Chinese minorities' data

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Table 1 Y-STR haplotypes in 105 unrelated males of Chinese Han population^a

Haplotypes	n	F	DYS456	DYS460	DYS461	DYS462	DYS459	DYS438	DYS439
H1	1	0.0095	14	7	10	11	8–9	10	10
H2	1	0.0095	14	8	9	10	9-10	10	11
H3	1	0.0095	14	8	10	12	10-10	12	10
H4	1	0.0095	14	9	10	10	10-10	10	11
H5	1	0.0095	14	9	10	11	8–9	10	10
H6	1	0.0095	14	9	10	11	9–9	10	10
H7	1	0.0095	14	10	9	10	9-10	11	10
H8	1	0.0095	14	10	9	12	8–9	10	10
H9	1	0.0095	14	10	10	11	8–9	9	13
H10	1	0.0095	14	10	10	12	9–9	10	11
H11	1	0.0095	15	7	10	10	9–10	10	12
H12	1	0.0095	15	7	10	11	8–9	10	12
H13	1	0.0095	15	7	10	14	8–9	10	12
H14	1	0.0095	15	7	11	10	9–10	10	10
H15	1	0.0095	15	8	10	10	9–10	10	13
H16	1	0.0095	15	8	10	10	9–10	11	12
H17	2	0.0190	15	8	10	11	9-10	10	12
H18	1	0.0095	15	8	10	11	8–9	10	12
H19	1	0.0095	15	8	11	10	9-10	10	12
H20	1	0.0095	15	9	9	11	9-10	10	10
H21	1	0.0095	15	9	9	11	9–10	10	13
H22	1	0.0095	15	9	10	10	9-10	10	10
H23	1	0.0095	15	9	10	10	9-10	10	11
H24	1	0.0095	15	9	10	10	9-10	11	12
H25	1	0.0095	15	9	10	11	8-10	9	11
H26	1	0.0095	15	9	10	11	9_9	10	9
H27	1	0.0095	15	9	10	12	8–9	10	11
H28	1	0.0095	15	9	11	11	9-10	9	12
H29	1	0.0095	15	9	11	12	10-10	10	11
H30	1	0.0095	15	9	12	12	10-10	10	11
H31	1	0.0095	15	10	10	11	9-10	10	11
H32	1	0.0095	15	10	10	11	8–9	10	10
H33	1	0.0095	15	10	10	11	10-10	11	11
H34	1	0.0095	15	10	10	11	9_9	10	13
H35	1	0.0095	15	10	11	11	9–10	9	10
H36	1	0.0095	15	10	11	11	9–10	10	11
H37	1	0.0095	16	7	10	9	9–10	11	11
H38	2	0.0190	16	7	10	10	9–10	10	11
H39	1	0.0095	16	7	11	10	9–10	9	12
H40	1	0.0095	16	8	8	10	8–9	11	12
H41	1	0.0095	16	8	8	11	9–10	10	11
H42	1	0.0095	16	8	9	11	9–10	10	12
H43	1	0.0095	16	8	10	10	8-9	10	12
H44	1	0.0095	16	8	10	10	8-9	11	10
H45	2	0.0190	16	8	10	11	9–10	9	11
H46	3	0.0285	16	8	10	11	9–10	10	12
H47	1	0.0095	16	8	10	12	9–10	9	11
H48	2	0.0190	16	8	11	10	9_9	10	10
H49	1	0.0095	16	8	11	11	9–10	10	11
H50	1	0.0095	16	9	8	11	9–10	10	12
H51	1	0.0095	16	9	8	11	9–10	10	12
H52	1	0.0095	16	9	9	11	9_10	11	12
H53	1	0.0095	16	9	10	10	9_10	9	11
H54	1	0.0095	16	9	10	10	9_10	11	11
H55	1	0.0095	16	9	10	11	9_10	0	13
H56	1	0.0095	16	9	10	11	9_10	10	12
H57	1	0.0095	16	9	10	11	9_10	11	11
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