FOR THE RECORD

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Population Data for the Twelve Y-chromosome Short Tandem Repeat Loci from the Sample of Multinational Population in Bosnia and Herzegovina

POPULATION: We have analyzed the distribution of allele frequencies at 12 Y-chromosomal short tandem repeats loci (DYS19, DYS385a, DYS385b, DYS389I, DYS389I, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438 and DYS439) in the representative sample of Bosnian and Herzegovinians. A total of 100 unrelated male individuals (Caucasians) from different regions of Bosnia and Herzegovina have been sampled for the analysis. Samples were collected with a respect to the approximate proportional participation of three main ethnic groups in Bosnia and Herzegovina [Bosniacs-Muslim (35), Serbs (31), Croats (34)].

KEYWORDS: forensic science, Y-chromosome, DNA typing, short tandem repeats, DYS19, DYS385a, DYS385b, DYS389I, DYS389I, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438 and DYS439, population data, Bosnia and Herzegovina

All 100 tested males have been voluntary donors. Buccal swabs and blood samples (blood spots) have been used as the DNA source. All specimens were air dried, placed in 1.5-mL tubes, and immediately transported to the Laboratory for Forensic Genetics at the Institute for Genetic Engineering and Biotechnology, Sarajevo, B&H. The samples have been stored at -80° C until DNA was extracted. For extraction of DNA, the Qiagen DnaeasyTM Tissue Kit was used (1). The PowerPlex® Y System (Promega Corp., Madison, WI) has been used to simultaneously amplify by PCR 12 Y-STR loci. The STR loci are: DYS19, DYS385a, DYS385b, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438 and DYS439. Similar amounts of DNA have been used in all PCR reactions. Amplification was carried out as described previously (2). The total volume of each reaction was 10 µL. The PCR amplification has been carried out in PE Gene Amp PCR System Thermal Cycler (ABI, Foster City, CA) according to the manufacturer's recommendations. Electrophoresis of the amplification products was preformed on an ABI PRISM 377 genetic analyzer (ABI, Foster City, CA), using 5% bisacrilamide gel (Long Ranger[®] Single[®] Packs). Raw data have been compiled and analyzed using the accessory software: ABI PRISM[®] Data Collection Software and Gene Scan[®]. Numerical allele designations of the profiles were obtained by processing with PowertyperY Macro.

Eight one different Y-STR haplotypes: (from total number of 100 obtained) were detected: 69 of them were unique, 7 appeared twice, 4 appeared three and only 1 five times. Allele frequency distribution, the most frequent haplotypes and observed haplotype diversity (3) for the PowerPlex® Y System in examined sample of B&H population are presented in Tables 1 and 2. Major allele frequency and gene diversity for the PowerPlex® Y loci (4) are showed in Table 3. The entire data are available on http://www.ingeb.ba/edat/str/ystrbase.html.

Acknowledgments

We would like to thank to Dr. Bruce Budowle for providing us necessary information and literature.

References

- Qiagen Companies, QIAGEN Genomic DNA Handbook. Qiagen, Wiena, 2001
- Promega. PowerPlex[®] Y system–Technical Manual. Madison: Promega Corporation, 2003.

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TABLE 1—Allele frequency distribution and gene diversity for the PowerPlex® Y System STR loci in B&H population sample.

Locus	Allele	Num	%	Locus	Allele	Num	%	Locus	Allele	Num	%
DYS437	13			DYS438	8			DYS389I	10		
	14	44	44		9	7	7		11		
	15	48	48		10	72	72		12	8	8
	16	7	7		11	18	18		13	79	79
	17	1	1		12	3	3		14	13	13
									15		
DYS439	8			DYS393	8			DYS391	6		
	9			D10375	8 9			D 15371	8		
	10	8	8		10				9		
	11	20	20		11				10	54	54
	12	38	38		12	11	11		11	45	45
	13	27	27		13	82	82		12	1	1
	14	7	7		14	7	7		13	1	1
	15	/	/		15	/	/		13		
	13				13						
DVG200	10			DVC10	16			DMC200H	2.4		
DYS390	18			DYS19	10			DYS389II	24		
	19				11				25		
	20				12				26		
	21				13	15	15		27		
	22	3 9	3		14	17	17		28	5	5
	23	9	9		15	27	27		29	21	21
	24	61	61		16	37	37		30	27	27
	25	25	25		17	3	3 1		31	40	40
	26	2	25 2		18	1	1		32	6	6
	27				19				33	1	1
									34		
DYS385 (a and b)	7			DYS392	7						
	8				8						
	9				9						
	10	2	1		10						
	11	20	10		11	90	90				
	12	2	1		12	3	3				
	13	12	6		13	5	3 5 2				
	14	65	32,5		14	2	2				
	15	49	24,5		15	2	2				
	16	25	12,5		16						
	17	7	3,5		17						
	18	15	7,5		18						
	19	3	1,5								
	20										
	21										
	2.2.										
	23										
	23 24 25										
	25										
	23										

TABLE 2—PowerPlex $^{\circledR}$ Y haplotypes that have detected more than once in B&H population sample and observed haplotype diversity.

PowerPlex [®] Y Haplotypes	Number
10-13-12-30-10-14-13-11-13-24-16;18	5
10-13-11-29-11-14-16-11-13-25-11;14	3
11-13-13-30-10-15-16-11-13-24-14;15	3
11-13-13-31-10-15-16-11-13-24-14;15	3
11-13-14-31-10-15-15-11-13-24-14;15	3
10-12-12-29-10-16-15-11-13-22-14;14	2
10-14-11-31-10-14-13-11-13-24-16;18	2
11-13-11-29-11-14-15-11-13-25-11;14	2
11-13-12-31-10-15-16-11-13-24-13;15	2
11-13-12-31-10-15-16-11-13-24-14;15	2
11-13-13-31-10-15-14-11-13-24-14;15	2
11-13-14-31-10-15-16-11-13-24-14;15	2
Haplotype diversity (h)	0.9941 ± 0.0027

TABLE 3—Major allele frequency and gene diversity for the PowerPlex $^{\textcircled{R}}$ Y loci in examined sample of B&H population.

Locus	Major Allele Frequency	Gene Diversity
DYS391	0.5400	0.5058
DYS389I	0.7900	0.3526
DYS439	0.3800	0.7314
DYS389II	0.4000	0.7168
DYS438	0.7200	0.4434
DYS437	0.4800	0.5710
DYS19	0.3700	0.7378
DYS392	0.9000	0.1862
DYS393	0.8200	0.3106
DYS390	0.6100	0.5560
DYS385	0.3300	0.8492
		Average 0.5419

- 3. Nei M, Kumar S. Molecular evolution and phylogenetics. Oxford, New York: Oxford University Press, 2000.
- 4. Budowle B, Sinha SK, Lee HS, Chakraborty R. Utility of Y-chromosome STR haplotypes in forensic applications. Forens Sci Rev 2003;15(2):153-
- 5. Schneider S, Roessli D, Excoffier L. Arlequin ver. 2000: The software for population genetics data analysis. Switzerland: Genetics and Biometry Laboratory, University of Geneva, 2000.

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