

Haplotypes and Mutations of 17 Y-STR Loci from Korean Father-Son Pairs

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Introduction

Short tandem repeat markers on the Y chromosome (Y-STRs) have been proved to be a valuable in male sibship analysis. Precise estimates of mutation rates at Y-STR loci provide an important basis for the correct interpretation of paternity tests using Y-STRs. Although several data on multiplex PCR analyses for Y-STRs have been reported in Korean population, Y-STR mutation study has never been performed. In this regard, we analyzed 17 Y-STR loci (DYS19, DYS385a/b, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439, DYS448, DYS456, DYS458, DYS635 (Y GATA C4), Y GATA H4) in 365 Korean father/son pairs of confirmed paternity with two multiplex PCR systems (multiplex I and multiplex II).

Materials and Methods

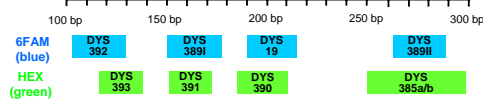
DNA samples

365 father/son pairs (6,205 meioses) of 355 families were obtained from a Korean population. DNA was extracted from buccal swab samples using QIAamp DNA Mini Kit (Qiagen).

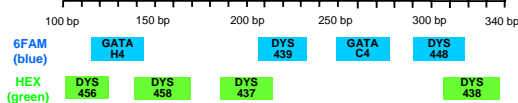
Multiplex PCR conditions

Amplification of two multiplex systems was performed in 10 µl PCR mixture containing 1 ng of DNA template. Thermal cycling was conducted under the conditions of 30 cycles of amplification with 55°C annealing temperature.

Multiplex I (minimal haplotype)



Multiplex II (additional 8 Y-STRs)



Allele typing

ABI prism 310 Genetic Analyzer (Applied Biosystems) and Gene Scan software 3.1 (Applied Biosystems) were used for sizing of each allele. The allele was designated using Genotyper 2.5 software (Applied Biosystems).

Mutation confirmation

Samples which showed mismatch between genotypes of father and son were subjected to autosomal STR analysis using PowerPlex16 System (Promega). In order to identify repetitive sequence differences between father/son pairs, cloning and sequencing were carried out.

Statistical analysis

Gene diversity and haplotype diversity values were calculated and exact test was performed using Arlequin version 2.0 software. The discriminatory capacity was determined by dividing the number of different haplotypes by the total number of samples in a Korean population. The average mutation rate was determined by dividing the number of mutated samples by the total number of meioses.

Results

Haplotype analysis

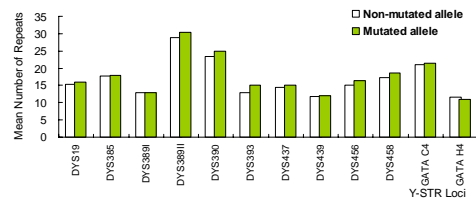
Y-STR marker	Number of haplotypes	Haplotype diversity	Discriminatory capacity
Multiplex I (minimal haplotype)	275	0.9972	77.46%
Multiplex II	275	0.9971	77.46%
17 Y-STRs	338	0.9996	95.21%

Average mutation rate: 0.34 %/meiosis (95% C.I. 0.21–0.52%)

Mutation rates of Y-STR loci

Y-STR marker	Motif	Allele range	No. of mutations	Mutation rate (x10 ⁻³)
DYS19	TAGA	13–17	2	5.48
DYS385	GAAA	8–23	2	5.48
DYS389I	(TCTG)(TCTA)	11–15	1	2.74
DYS389II	(TCTG)(TCTA)	27–32	2	5.48
DYS390	(TCTA)(TCTG)	21–26	1	2.74
DYS393	AGAT	12–16	1	2.74
DYS437	TCTA	13–16	2	5.48
DYS439	GATA	9–14	1	2.74
DYS456	AGAT	12–18	2	5.48
DYS458	GAAA	13–21	3	8.22
GATA C4	TCTA	19–24	3	8.22
GATA H4	TAGA	10–14	1	2.74

Mean number of repeats



**Gain : Loss = 8 : 13
One step mutation**

Mutation alleles

Locus	Allele		Repetitive sequence structure		type	No. of steps
	Father	Son	Non-mutated	Mutated		
DYS19	17	16	[TAGA] ₁₇ [TAGG][TAGA] ₁₄	[TAGA] ₁₇ [TAGG][TAGA] ₁₃	Loss	1
DYS19	15	16	[TAGA] ₁₅ [TAGG][TAGA] ₁₂	[TAGA] ₁₅ [TAGG][TAGA] ₁₃	Gain	1
DYS385	10-18	10-17	[GAAA] ₁₀	[GAAA] ₉	Loss	1
DYS385	13-20	13-19	[GAAA] ₁₃	[GAAA] ₁₂	Loss	1
DYS389I	14	13	[TCTG] ₁₄ [TCTA] ₁₁	[TCTG] ₁₃ [TCTA] ₁₀	Loss	1
DYS389II	29	30	[TCTG] ₂₉ [TCTA] ₂₆	[TCTG] ₃₀ [TCTA] ₂₇	Gain	1
DYS389II	32	31	[TCTG] ₃₂ [TCTA] ₂₉	[TCTG] ₃₁ [TCTA] ₂₈	Loss	1
DYS390	24	25	[TCTG] ₂₄ [TCTA] ₂₁	[TCTG] ₂₅ [TCTA] ₂₂	Gain	1
DYS393	16	15	[AGAT] ₁₆	[AGAT] ₁₅	Loss	1
DYS437	14	15	[TCTA] ₁₄ [TCTG] ₁₁ [TCTA] ₈	[TCTA] ₁₅ [TCTG] ₁₂ [TCTA] ₉	Gain	1
DYS439	13	12	[GATA] ₁₃	[GATA] ₁₂	Loss	1
DYS439	13	12	[GATA] ₁₃	[GATA] ₁₂	Loss	1
DYS456	18	17	[AGAT] ₁₈	[AGAT] ₁₇	Loss	1
DYS456	15	16	[AGAT] ₁₅	[AGAT] ₁₆	Gain	1
DYS458	18	19	[GAAA] ₁₈	[GAAA] ₁₉	Gain	1
DYS458	18	17	[GAAA] ₁₈	[GAAA] ₁₇	Loss	1
DYS458	19	20	[GAAA] ₁₉	[GAAA] ₂₀	Gain	1
GATA C4	21	22	[TCTA] ₂₁ [TGTAT] ₁₈ [TCTA] ₁₅ [TGTAT] ₁₂ [TCTA] ₉	[TCTA] ₂₂ [TGTAT] ₁₉ [TCTA] ₁₆ [TGTAT] ₁₃ [TCTA] ₁₀	Gain	1
GATA C4	22	21	[TCTA] ₂₂ [TGTAT] ₁₉ [TCTA] ₁₆ [TGTAT] ₁₃ [TCTA] ₁₀	[TCTA] ₂₁ [TGTAT] ₁₈ [TCTA] ₁₅ [TGTAT] ₁₂ [TCTA] ₉	Loss	1
GATA C4	22	21	[TCTA] ₂₂ [TGTAT] ₁₉ [TCTA] ₁₆ [TGTAT] ₁₃ [TCTA] ₁₀	[TCTA] ₂₁ [TGTAT] ₁₈ [TCTA] ₁₅ [TGTAT] ₁₂ [TCTA] ₉	Loss	1
GATA H4	12	11	[TAGA] ₁₂ [ATGGATAGAT] ₉ [GATG] ₆ [AATAGA] ₃	[TAGA] ₁₁ [ATGGATAGAT] ₈ [GATG] ₅ [AATAGA] ₂	Loss	1

Distribution of father's age

Age group	Father-son pairs	
	Non-mutated	Mutated
20-25	6	1
26-30	131	7
31-35	117	9
36-40	21	2
41-45	3	0
Unknown	66	2
Mean of age	31.0	31.1

➔ **No significant difference (p>0.05)**

Comparison of mutation rates

	Korea	Japan	Norway	Germany	Brazil
No. of mutations	21	5	5	14	8
Meiosis	6205	2254	1200	4999	2015
Mutation rate(%)	0.34	0.22	0.42	0.28	0.40
p-value	-	0.39	0.79	0.49	0.83

Summary

- ❖ In father's data obtained from 355 families, haplotype diversity of 17 Y-STRs was 0.9996, and the number of different haplotypes were 388.
- ❖ In 365 father/son pairs, 21 mutations were observed at 12 loci (0.34 %/meiosis).
- ❖ Mutation rate of Koreans did not show statistically significant difference from those of other populations.
- ❖ Simple repeats demonstrated more frequent mutations than complex repeats.
- ❖ All mutated samples showed a gain or loss mutation at each locus.
- ❖ Two mutations in the single germline transmission are unlikely to occur.
- ❖ Mutation rate and father's age were not in positive correlation.
- ❖ These results on the haplotypes and mutation patterns at 17 Y-STR loci in Koreans are expected to provide a valuable information for both forensic analysis and population genetics using Y-STR genetic profiling.

References

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