



# Distribution of DYS385 genotypes in several Japanese subpopulations and a Korean population

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## Abstract

The distribution of DYS385 genotypes was studied in five Japanese subpopulations and a Korean population. Genotype 13–17 was the most frequently observed in the Japanese subpopulations except at Amami-oshima, but was not so frequent in the Korean population. Genotypes carrying the 10 allele were commonly observed in both the Japanese and the Korean populations.

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## 1. Introduction

The DYS385 locus, consisting of two linked short tandem repeat (STR) subloci, is the most polymorphic marker on the Y-chromosome. We have previously reported the distribution of DYS385 genotypes in two Japanese subpopulations, Miyazaki [1] and Kagoshima [2]. In this study, three more Japanese subpopulations in Tottori, Tanegashima (Tane) and Amami-oshima (Amami) and a Korean population in Seoul were added to the previous data set. Tottori, Miyazaki and Kagoshima are located in the southwestern part of Japan. Tane and Amami are islands in the East China Sea.

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## 2. Materials and methods

Genomic DNA was prepared from whole blood according to the standard protocols (116 samples in Tottori, 270 in Miyazaki, 117 in Kagoshima, 158 in Tane, 131 in Amami, and 94 in Seoul). PCR amplification was performed according to the procedure given by Kayser et al. [3]. Electrophoretic separation of the PCR products was carried out using 5% native polyacrylamide gel followed by silver staining.

## 3. Results and discussion

The frequencies of DYS385 genotypes in three Japanese subpopulations and a Korean population are shown in Table 1. The frequencies in Miyazaki and Kagoshima were previously reported [1,2]. Genotype numbers (GN) and Nei's gene diversity (GD) in each

Table 1  
Frequencies of DYS385 genotypes

Types	Amami	Tane	Tottori	Korea	Types	Amami	Tane	Tottori	Korea
9–15	0.015				13–13		0.013		0.043
9–16				0.011	13–14	0.015	0.025	0.034	
9–17			0.009		13–15	0.038	0.013	0.026	0.011
9–19	0.008			0.021	13–16	0.038	0.044	0.034	0.011
9–21				0.011	13–17	0.061	0.190	0.095	0.032
10–16		0.013	0.009		13–18	0.046	0.051	0.069	0.043
10–17	0.053	0.013	0.009	0.021	13–19	0.015	0.013	0.034	0.053
10–18	0.038	0.019	0.052	0.149	13–20		0.019	0.009	0.011
10–19	0.115	0.070	0.095	0.064	13–21		0.019		0.011
10–20	0.084	0.108	0.078	0.064	13–24			0.009	
10–21	0.023	0.006	0.026		14–14				0.011
10–22		0.006			14–15	0.015	0.006	0.026	0.011
11–11				0.011	14–16	0.069	0.006		
11–12	0.008	0.013	0.009	0.011	14–17	0.053	0.070	0.009	
11–13		0.006			14–18	0.053	0.025	0.009	0.032
11–15	0.008				14–19	0.015	0.013	0.009	0.032
11–17	0.008	0.013	0.017	0.043	14–20	0.031		0.009	0.011
11–18		0.019	0.060		14–21			0.026	
11–19		0.025	0.009	0.043	14–24				0.011
11–20		0.006		0.021	15–15	0.008		0.017	
11–21				0.011	15–18				0.011
12–12	0.023	0.006	0.017		15–19		0.006		0.011
12–13	0.008	0.006			15–20		0.025		0.011
12–14				0.032	15–21		0.006		0.021
12–15	0.031	0.006		0.011	15–22			0.009	0.011
12–16	0.023		0.034		16–16	0.008		0.009	
12–17	0.015	0.051	0.052	0.011	16–20			0.009	0.011
12–18	0.008	0.038	0.026	0.043	17–17	0.008	0.006		
12–19	0.008	0.006	0.017	0.032	18–18			0.009	
12–20	0.015	0.013	0.026		18–19	0.038	0.006		
12–21			0.009		<i>n</i>	131	158	116	94

population were as follows: GN=37, GD=0.95 in Tottori; GN=47, GD=0.96 in Miyazaki; GN=30, GD=0.92 in Kagoshima; GN=39, GD=0.93 in Tane; GN=34, GD=0.95 in Amami and GN=38, GD=0.95 in Seoul. The most frequently observed genotypes were as follows: 13–17 in Miyazaki, Kagoshima and Tane, 10–19 in Amami, both 13–17 and 10–19 in Tottori and 10–18 in Seoul. Previous reports by Schneider et al. [4,5] showed that genotypes carrying the 10 allele were rare in Chinese, Thai and European populations. However, such genotypes, especially 10–18, 10–19 and 10–20, were frequently observed in the Japanese and Korean populations studied here. The 13–17 genotype was not so common in the Korean population as in the Japanese population. A similarity in the distribution of genotypes carrying the 10 allele and a difference in that of the 13–17 genotype between Japanese and Korean populations should provide useful data for studies of the origin of the people of Japan.

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