DISTRIBUTION OF Gm AND Km ALLOTYPES AMONG THE FIVE POPULATIONS IN THE PEOPLE'S REPUBLIC OF CHINA.

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INTRODUCTION

Inherited structural differences in human immunoglobulins are referred to as allotypes or genetic markers. So far, genetic markers have been found for the IgG heavy (H) chain (Gm), the IgA chain (Am), the IgE chain (Em) described recently by van Loghem et al. (1984), and the kappa type light chain (Km) common to all classes of immunoglobulins. The Gm system provides genetic markers which are unique in studies of human genetics, particularly in the characterization of different populations and in studies of gene flow and genetic drift determined by the presence of either a unique haplotype in a particular race or by differences in the frequencies of the same haplotypes in a given ethnic group.

This study of the five populations in Mainland China forms part of an extensive survey aimed at investigating the distribution of Gm and Km alleles among the Mongoloid populations acattered from Southeast Asia through East Asia into South America.

MATERIALS AND METHODS

Serum samples from a total of 806 unrelated individuals from five distinct regional populations in mainland China (173 from Inner Mongolia, 195 from Beijing, 131 from Anhui, 153 from Zhejiang and 152 from Guangzhou) were tested for G1m (a,x,f and z), G2m(n), G3m(b0,b1,b3,b4,b5, s,t, and u), and Km(l) allotypes. The reagents used for these tests and the methods were described previously (Matsumoto et al., 1979).

RESULTS AND DISCUSSION

Data of Gm phenotypes in five distinct Chinese populations are presented in table 1 and estimated frequencies of Gm haplotypes are presented in table 2. Haplotype frequencies and degree of fit with the Hardy-Weinberg distribution were determined using the computer program MAXIM. Nine to seven Gm phenotypes which are explained by the presence of four haplotypes, Gm a,z;..;g,u, Gm a,x,z;..;g,u, Gm a,z;..;b0,b3,b5,s,t and Gm a,f;n;b0,b1,b3,b4,b5,u, characteristic of Mongoloid populations were observed among these populations. Agreement was obtained for all five populations between the observed and the expected frequencies on the basis of the Hardy-Weinberg equilibrium of phenotypes.

To determine if significant heterogeneity in haplotypic distributions exists among the five Chinese populations, haplotype frequencies were analyzed using contingency chi-square test according to the methods of Snedecor (1956). Heterogeneities were not found between Inner Mongolia and Beijing (χ^2 =2.30 for 3 d.f., p=0.51) and also between Anhui and Zhejiang (χ^2=4.95 for 3 d.f., p=0.17). On the other hand, heterogeneities were observed between Inner Mongolia and Anhui (χ^2 =10.32 for 3 d.f., p=0.01), Inner Mongolia and Zhejiang (χ^2 =29.55 for 3 d.f., p=0.00), Inner Mongolia and Guangzhou (χ^2 =263.02 for 3 d.f., p=0.00), Beijing and Anhui (χ^2=9.62 for 3 d.f., p=0.02), Beijing and Zhejiang (χ^2 =25.13 for 3 d.f., p=0.00), Beijing and Guangzhou (χ^2 =262.88 for 3 d.f., p= 0.00), and between Zhejiang and Guangzhou (χ^2 =124.30 for 3 d.f., p= 0.00), respectively.

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As compared these results with the data of Chinese populations collected in Taiwan and in Ann Arbor, Michigan in the States and classified as to the province of origin by Schanfield (1972), heterogeneity was found between Beijing and north region (included Shantung, Hopei, Liaoning and Shansi) by Schanfield (χ^2 =12.45 for 3 d.f., p=0.00), whereas the result of Zhejiang is in accord with the central region by Schanfield (χ^2 =1.21 for 3 d.f., p=0.75) and also Guangzhou with south region by Schanfield (χ^2 =3.06 for 3 d.f., p=0.38), respectively. As shown in the results, clear genocline changing in a regular fashion is observed, i.e., a regular decrease from north to south in the frequencies of Gm a,z;..;g,u and Gm a,z;..;b0,b3,b5,s,t and on the contrary, a regular and remarkable increase from north to south in the frequency of Gm a,f;n;b0,b1,b3,b4, b5,u.

The haplotype frequencies determined for the 2,360 samples in the 11 Japanese populations from the various districts reported up to that time were tested for heterogeneity. The tests gave χ^2 =9.21 for 20 d.f., 0.97 > p > 0.95 (Matsumoto et al., 1977). Clearly the data showed Japanese to be homogenous. Pairwise comparison of the Gm phenotypes of Japanese from Osaka (haplotype frequencies: Gm a,z;..;g,u = 0.4503, Gm a,x,z; ..;g,u = 0.1590, Gm a,z;..;b0,b3,b5,s,t = 0.2609, and Gm a,f;n;b0,b1, b3,b4,b5,u = 0.1297) and each of the five populations in China revealed the differences to be statistically significant. Japanese samples differs significantly from all of the five regional populations in China (χ^2 =57.22 for 3 d.f., p=0.000 for Inner Mongolia; χ^2 =58.36 for 3 d.f., p=0.000 for Beijing; χ^2 =86.27 for 3 d.f., p=0.000 for Anhui; χ^2 =136.28 for 3 d.f., p=0.000 for Zhejiang; χ^2 =509.29 for 3 d.f., p=0.000 for Guangzhou, respectively). Thus, the differences between Japanese and each of the regional populations in China become greater from northern population to southern population.

In contrast to the significant and regular variation in the Gm haplotypes Km allele frequencies do not show any significant variation among the five Chinese populations as shown in table 3.

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TABLE 1. Gm phenotype frequencies among the five populations in China

Gm phenotype	Inner Mongolia		Beijing		Anhui		Zhejiang		Guangzhou	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
a,z;g,u	40	37.7	36	35.4	22	22.7	24	18.5	7	5.1
a,z;b0,b3,b5,s,t,g,u	19	15.5	21	19.3	8	9.2	7	8.4	1	1.8
a,x,z;g,u	39	39.4	43	44.2	23	22.6	26	24.5	4	3.5
a,f,z;n;b0,b1,b3,b4,b5,u	29	36.7	38	39.9	38	35.8	30	40.9	37	40.5
a,x,z;b0,b3,b5,s,t,g,u	4	6.7	7	9.6	5	3.8	4	4.4	0	0.5
a,f,z;n;b0,b1,b3,b4,b5,s,t,u	8	7.6	11	10.8	9	7.2	9	9.3	9	7.3
a,z;b0,b3,b5,s,t	1	1.6	3	2.6	0	0.9	2	1.0	0	0.2
a,x,f,z;n;b0,b1,b3,b4,b5,g,u	19	15.8	24	19.9	13	14.7	20	21.5	12	12.1
a,f;n;b0,b1,b3,b4,b5,u	11	8.9	10	11.2	13	14.1	29	22.7	82	81.1
Total	170	170.0	193	193.0	131	131.0	151	151.0	152	152.0
χ^2	4.98		2.03		1.63		7.35		1.68	
d.f.	5		5		4		4		3	
p	0.416		0.844		0.802		0.118		0.641	

TABLE 2. Gm haplotype frequencies among the five populations in China

Gm haplotype	Inner Mongolia		Beijing		Anhui		Zhejiang		Guangzhou	
	Freq.	S.E.	Freq.	S.E.	Freq.	S.E.	Freq.	S.E.	Freq.	S.E.
a,z;..;g,u	0.4708	0.0271	0.4285	0.0252	0.4163	0.0305	0.3496	0.0274	0.1825	0.0222
a,x,z;..;g,u	0.2027	0.0218	0.2140	0.0209	0.1715	0.0233	0.1835	0.0223	0.0543	0.0130
a,z;..;b0,b3,b5,s,t	0.0971	0.0161	0.1166	0.0163	0.0840	0.0171	0.0795	0.0156	0.0329	0.0102
a,f;n;b0,b1,b3,b4,b5,u	0.2294	0.0228	0.2409	0.0218	0.3282	0.0290	0.3874	0.0280	0.7303	0.0255

TABLE 3. Km phenotype and allele frequencies among the five populations in China

Km phenotype	Inner Mongolia	Beijing	Anhui	Zhejiang	Guangzhou
I+	106	114	73	77	82
I−	67	81	58	78	70
Total	173	195	131	155	152
Km allele frequency					
Km^1	0.3777	0.3555	0.3346	0.2906	0.3214

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