Distribution of Alpha-2-HS-glycoprotein Types in Four East Asian Populations

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Abstract The genetic polymorphism of alpha-2-HS-glycoprotein (AHSG) have been analyzed in Chinese, Korean and remaining Japanese orphan in China populations by isoelectric focusing and immunoblotting technique. Three new variants designated as *AHSG*C1*, *AHSG*C2* and *AHSG*C3* were found. The frequencies of common alleles (*AHSG*1* and *AHSG*2*) were approximately the same among East Asian populations.

Key Words Polymorphism, Serum alpha-2-HS-glycoprotein (AHSG), New variant, Asian populations

Introduction

Alpha-2-HS-glycoprotein (AHSG) is present in healthy human serum at concentrations of about 0.60 mg/ml and is known as negative acute-phase reactant. AHSG is synthesized in the liver and deposited in bone tissue. Its biological function is not yet entirely understood.

The three different types of AHSG were originally described by two-dimensional electrophoresis (ANDERSON and ANDERSON, 1979). Subsequently, one-dimensional isoelectric focusing (IEF) was introduced into AHSG phenotyping (COX and ANDREWS, 1983; UMETSU *et al.*, 1983). So far, 21 AHSG variants have been described (YUASA and UMETSU, 1988;

SALZANO *et al.*, 1990; FUKUMA *et al.*, 1990; FUKUMA *et al.*, 1991). The comparisons of the gene frequencies among the different populations are useful to solve the questions about the nature of migration and microevolution in the human.

This paper presents three new variants designated as *AHSG*C1*, *AHSG*C2* and *AHSG*C3*. In addition, the frequencies of AHSG types among population groups of Chinese, Koreans and remaining Japanese orphans in China are reported.

Materials and Methods

Serum or plasma samples were obtained from four populations: 431 Chinese in Shenyang, 510 Koreans in Seoul, 157 Koreans in Cheju island,

184 remaining Japanese orphans in China including 100 samples reported in a previous study (UMETSU *et al.*, 1988). Sialidase treatment of the samples was carried out by incubating the mixture of 5 μ l serum and 20 μ l sialidase from *Arthrobacter ureabaciens* (Nakarai tesque, 1 unit/ml, pH 5.0) overnight at room temperature. Desialyzed samples were phenotyped by polyacrylamide gel IEF and immunoblotting as described previously (UMETSU *et al.*, 1986, YUASA and UMETSU, 1988).

Results and Discussion

Six different alleles were found in the present populations. Among them, three alleles were new

variants designated as *AHSG**C1, *AHSG**C2 and *AHSG**C3 (Fig. 1). *AHSG**12 has already been reported previously (UMETSU *et al.*, 1988). In the desialyzed sample, *AHSG* C1 band located between *AHSG* 3 and *AHSG* 1 band; *AHSG* C2 band, between *AHSG* C1 and *AHSG* 1 band; and *AHSG* C3 band, slightly anodal of the minor *AHSG* 6 band. Family studies showing the inheritance patterns are illustrated in Fig. 2. The inheritance mode of the variants corresponds to Mendelian heredity. As shown in Fig. 1, desialyzed products of a *AHSG* allele includes three bands consisting of one anodal minor, one intermediate major and one cathodal minor band. There are some variants, such as *AHSG* C1 and

Fig. 1. Desialyzed *AHSG* patterns detected by immunoblotting followed to polyacrylamide gel IEF. Anode is at the top. Filled and empty triangles indicate major variant and minor variants bands, respectively. From left to right: *AHSG* 3-1, C1-2, C2-2, 1, 2-1, 2, C3-1, 6-1, 5-1, 12-1 and 15-1.

Fig. 2. Pedigrees of families possessing *AHSG* C1 (a), *AHSG* C2 (b) and *AHSG* 12 (c). The proband is indicated by the arrow.

AHSG 6, which have the exception to this general rule. They have one anodal major and two cathodal minor bands. The exception in the band pattern of these two variants could be explained by a stereochemical specificity of sialic acid or an abnormality of the processing of these variant molecules.

The distributions of the AHSG types and allele frequencies are given in Table 1. The observed numbers agreed with the expected values calculated on the basis of HARDY-WEINBERG equilibrium (Shenyang, $\chi^2=0.5527$, $df=1$, $0.30 < p < 0.50$; Seoul, $\chi^2=1.9536$, $df=1$, $0.10 < p < 0.20$; Cheju, $\chi^2=0.7873$, $df=1$, $0.70 < p < 0.80$; remaining Japanese orphan in China, $\chi^2=0.0011$, $df=1$, $0.95 < p < 0.98$). The allele frequencies among these four Mongoloid populations are almost the same.

AHSG allele frequencies in several East Asian populations are listed in Table 2. No significant differences of the allele frequencies have been

found among Japanese, Korean and Chinese populations ($\chi^2=9.4437$, $df=6$, $0.10 < p < 0.20$). However, the frequency of *AHSG*1* in Tsushima islands is a little lower than those obtained from the neighboring populations and that of Cheju island is somewhat higher than those found in other East Asian populations. Interestingly, the distribution of AHSG variants seems to be different from population to population in Japanese. Especially *AHSG*5* might be found only in Japanese and the frequency is higher in Okinawa.

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Table 1. Distribution of AHSG types and allele frequencies in four Mongoloid populations

Phenotype	Shenyang (Chinese)	Seoul (Korean)	Cheju is. (Korean)	Remaining Japanese orphan in China
1	216	274	93	100
2-1	182	191	53	69
2	32	45	11	12
12-1	0	0	0	1
C1-2	0	0	0	1
C2-2	1	0	0	0
C3-1	0	0	0	1
Total	431	510	157	184
Allele frequencies				
<i>AHSG*1</i>	0.7123	0.7245	0.7611	0.7365
<i>AHSG*2</i>	0.2865	0.2755	0.2389	0.2554
<i>AHSG*12</i>	—	—	—	0.0027
<i>AHSG*C1</i>	—	—	—	0.0027
<i>AHSG*C2</i>	0.0012	—	—	—
<i>AHSG*C3</i>	—	—	—	0.0027

Table 2. AHSG allele frequencies in the East Asian populations

Population (n)	Allele frequencies				References
	AHSG*1	AHSG*2	AHSG*5	Others	
Japanese					
Aomori (400)	0.7450	0.2475	—	0.0075	UMETSU <i>et al.</i> , 1987
Yamagata (2050)	0.7356	0.2639	0.0005	—	UMETSU <i>et al.</i> , 1984
Yamaguchi (400)	0.7325	0.2675	—	—	YUASA <i>et al.</i> , 1985
Fukuoka (1074)	0.7165	0.2817	0.0009	0.0010	FUKUMA <i>et al.</i> , 1990
Kochi (1366)	0.7218	0.2782	—	—	ISHIZU <i>et al.</i> , 1986
Okinawa (397)	0.7670	0.2065	0.0264	—	YUASA <i>et al.</i> , 1985
Tsushima (514)	0.6916	0.3045	0.0010	0.0029	FUKUMA <i>et al.</i> , 1990
Goto is. (655)	0.7221	0.2748	—	0.0032	FUKUMA <i>et al.</i> , 1991
Japanese ¹⁾ (184)	0.7365	0.2554	—	0.0081	The present study
Koreans					
Seoul (510)	0.7245	0.2755	—	—	The present study
Cheju is. (157)	0.7611	0.2389	—	—	The present study
Chinese					
Shenyang (431)	0.7123	0.2865	—	0.0012	The present study
Kaohsiung (199)	0.7286	0.2714	—	—	YUASA and UMETSU, 1988

1) Remaining Japanese orphan in China

抄 録

東アジア4集団における alpha-2-HS-glycoprotein 型の分布

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東アジアに属する中国人（瀋陽），韓国人（ソウル，済州島）および中国残留日本人孤児の4集団における alpha-2-HS-glycoprotein（AHSG）型の分布頻度を調査した。新しい変異型として，中国人より AHSG C2 型，中国残留日本人孤児から AHSG C1 型と AHSG C3 型を見出した。また AHSG * 1 と AHSG * 2 の頻度はいずれの集団においても基本的には他の近隣集団間とも大きな差異が見られなかったが，東アジア集団の変異型の出現頻度には集団によってかなり特徴的な差異があることが示唆された。

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