HUMAN ZN-ALPHA 2-GLYCOPROTEIN PHENOTYPING IN SEVERAL POPULATIONS

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Human Zn-alpha 2-glycoprotein (ZAG) is widely distributed in various body fluids such as plasma, semen, sweat, saliva, urine and tear, however, the biological function is still unknown. Lately, by means of isoelectric focusing (IEF) followed by immunoblotting, the genetic variation of plasma ZAG has been reported (Kamboh and Ferrell 1986; Nakayashiki and Katsura 1989; Ding et al. 1990). In this study, five new ZAG alleles and the distribution of ZAG alleles in the Japanese, Korean, Philippine, Thai, Brazilian Indian and Papua New Guinean popuations will be reported.

MATERIALS AND METHODS

Plasma or serum samples were obtained from following populations: 2180 Japanese composing of 182 Ainu individuals from Hokkaido, 1080 individuals from Iwate prefecture, 554 from Yamaguchi prefecture and 364 from Okinawa prefecture; 554 Koreans from Seoul city; 115 Philippines of 69 from Kadaklan and 46 from Bagbag village of Luzon island; 218 Thai from Tha-Keow-Pleuk village; 398 Brazilian Indians composing of three tribes, 205 from Pacaás Novos, 77 from Urubu-Kaapor and 116 from Parakanã; 52 Papua New Guineans from Lae city.

ZAG phenotyping for native and desialized samples were performed mostly according to the previous description (Nakayashiki and Katsura 1989). When separator IEF (SIEF) was applied to asialo ZAG typing, 1% HEPES was added to the IEF gel and the focusing time was prolonged.

RESULTS AND DISCUSSION

Figure 1 and 2 show eleven IEF phenotypes of native and asialo ZAG in plasma, respectively. Although the genetic background could not be examined, five new ZAG bands produced by ZAG*6 to ZAG*10, which tentatively named, were observed. The sequence of asialo ZAG band mobilities in IEF gel was as follows: ZAG 10 (pI about 5)→2→5→1 (common band, pI 5.15)→7→6→3→4→9→8 (pI about 5.3) in increasing order of pI.

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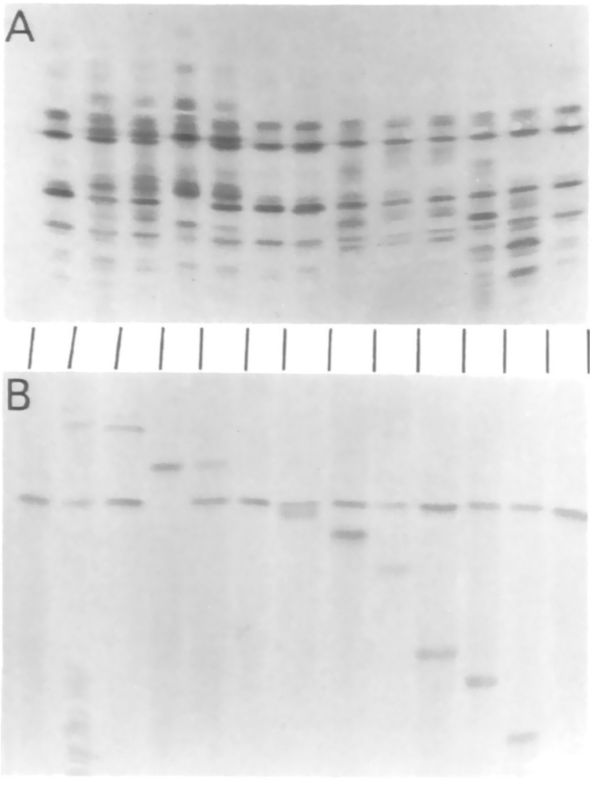

Fig. 1. Different phenotypes of plasma ZAG analyzed by immunoblotting after polyacrylamide gel IEF of native samples (A) and after SIEF of desialized samples (B). Anode at top. From left to right: ZAG 1, 10-1, 2-1, 5, 5-1, 1, 7-1, 6-1, 3-1, 4-1, 9-1, 8-1, 1

Table 1. Distribution of ZAG phenotypes in twelve populations

Population	n	Phenotype, n										
		1	2-1	3-1	4-1	5	5-1	6-1	7-1	8-1	9-1	10-1
JAPANESE com.	2180	2148	16	3	1	1	9	1			1	
Ainu (Hokkaido)	182	182										
Iwate	1080	1062	4	3	1	1	7	1			1	
Yamaguchi	554	543	9				2					
Okinawa	364	361	3									
KOREAN	525	517		4			2		1	1		
PHILIPPINE com.	115	115										
Kadaklan	69	69										
Bagbag	46	46										
THAI	218	217					1					
BRAZILIAN INDIAN com.	398	398										
Pacaás Novos	205	205										
Urubu-Kaapor	77	77										
Parakanã	116	116										
PAPUA NEW GUINEAN	52	47										5
Total	3488	3442	16	7	1	1	12	1	1	1	1	5

com., combined

Table 2. ZAG allele frequencies in different populations

Population	n	Allele frequencies										References
		ZAG*1	ZAG*2	ZAG*3	ZAG*4	ZAG*5	ZAG*6	ZAG*7	ZAG*8	ZAG*9	ZAG*10	Others	
JAPANESE													
Ainu	182	1.0000											This study
Iwate	1224	.9935	.0025	.0016	.0004	.0020							Reference 1
Iwate	1080	.9912	.0019	.0014	.0005	.0042	.0005			.0005			This study
Yamaguchi	554	.9901	.0081			.0018							This study
Okinawa	364	.9959	.0041										This study
CHINESE													
Shenyang	390	.9962				.0038							Reference 2
Kaohsiung	200	1.0000											Reference 2
KOREAN													
Cheju	350	.9929		.0071									Reference 2
Seoul	523	.9971		.0029									Reference 2
Seoul	525	.9923		.0038		.0019		.0010	.0010				This study
PHILIPPINE com.	115	1.0000											This study
THAI	218	.9977				.0023							This study
BRAZILIAN INDIAN com.	398	1.0000											This study
PAPUA NEW GUINEAN	52	.9519									.0481		This study
AMERICAN (The United States)													
Black	111	.9955										.0045[a]	Reference 3
Caucasian	228	1.0000											Reference 3
Eskimo	106	1.0000											Reference 3

a, not identified
Reference: 1, Nakayashiki and Katsura 1989; 2, Ding et al. 1990; 3, Kamboh and Ferrell 1986

Table 1 shows the distribution of ZAG phenotypes observed in this study and Table 2 summarizes the ZAG allele frequencies in the different populations up to now. In all of the populations, ZAG*1 was a predominant allele and the other alleles were seen less than polymorphic frequency (0.01) except for ZAG*10 (0.0481).

Ding et al. (1990) suggested the characteristic presence of ZAG*3 for the Koreans and ZAG*5 for the Chinese. We could not clarify this, however, the restricted distribution of some ZAG alleles might be possible, e.g., ZAG*2 for the Japanese and ZAG*10 for the Papua New Guineans. In addition, some ZAG alleles, e.g., the ZAG*10 in the Papua New Guinean population, might be distributed as a polymorphic marker. Therefore, further studies on ZAG phenotyping in various populations are necessary, to reveal its usefulness with regard to a genetic information in both fields of anthropology and forensic science.

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