Review

The origin of the Japanese race
based on genetic markers of immunoglobulin G

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Abstract: This review addresses the distribution of genetic markers of immunoglobulin G (Gm) among 130 Mongoloid populations in the world. These markers allowed the populations to be clearly divided into 2 groups, the northern and southern groups. The northern group is characterized by high frequencies of 2 marker genes, ag and ab3st, and an extremely low frequency of the marker gene afb1b3; and the southern group, in contrast, is indicated by a remarkably high frequency of afb1b3 and low frequencies of ag and ab3st. Based on the geographical distribution of the markers and gene flow of Gm ag and ab3st (northern Mongoloid marker genes) from northeast Asia to the Japanese archipelago, the Japanese population belongs basically to the northern Mongoloid group and is thus suggested to have originated in northeast Asia, most likely in the Baikal area of Siberia.

Keywords: population genetics, immunoglobulin allotype, gene flow, geno-cline, Mongoloid, Japanese

Introduction

Various theories as to the origin of the Japanese race have been advanced on the basis of the morphology of excavated bones. The most accepted theory at present is the "dual structure model" by Hanihara.[1] All of these theories are, however, dependent on morphometrical differences between bones, which are well known to be easily subject to nutrition.

In 1959, the ABO blood group system was first applied to human classification. Since then, polymorphic markers harbored in macromolecules such as proteins and glycoconjugates including blood group systems have been used for this purpose. The reason is based on the fact that the blood group system is inherited as a Mendelian trait and that the gene frequencies vary among different populations. As reviewed by Mourant *et al.*[2] no individual system except the genetic markers of immunoglobulin G (allotype; immunoglobulin G marker; Gm) was found to characterize human populations. Based on the study of Gm in Hungarian Gypsy populations, van Loghem *et al.*[3] stated that the Gm data contributed much to clarifying genetic differentiation of the populations and that Gm was thus applicable to the study of the origin and migration of populations, or to evaluate the extent of racial admixture within populations.

We found 2 novel Gm (s) and Gm (t) types in 1966,[4] which were then designated as the Gm ab3st gene; and further studies of the geographical distribution of this gene suggested to us that it is a northern Mongoloid marker. When I was invited to the USSR in 1983, about 1,000 serum samples collected from Mongoloid minorities in the Baikal area were given to me for study of Gm by Professor Rychkov of the then Soviet Scientific Academy. During the course of studying these samples, with our aim fixed on Gm genes that characterize Mongoloid populations, we obtained an unexpected result allowing us to approach the roots of Japanese people.[5,6] Based on further cooperative studies with the Russian labs on the dispersal of Mongoloids in Asia,[7] we confirmed the highest frequencies

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Abbreviations: Gm; immunoglobulin G marker, mtDNA; mitochondrial DNA, HLA; human leukocyte antigen.

of the Gm ab3st gene among the 3 Buryat populations in the Baikal area; and the geno-cline of Gm ab3st was shown to be in good order, leading to the conclusion that our hypothesis has validtiy.

Materials and methods

About 20,000 individual sera from 130 populations were tested for Gm types by using the agglutination inhibition test with the reagents described previously.[8] This test is based on classical antigen-antibody reaction and allows unequivocally the identification of 8 Gm types: a, b1, b3, f, g, s, t and x. A total of 9 different phenotypes, each of which comprises 2 to 6 types, were detected in Mongoloids and explained by 4 genes, as described below.

Each gene frequency (ratio of a gene in each population) was calculated by using the maximum likelihood method.[8] Phenotypic distribution in a population was tested for Hardy-Weinberg equilibrium by using a computer program through the courtesy of Kurcznsky and Steinberg.[9]

Results

A total of 9 different phenotypes, ag, axg, agb3st, agfb1b3, axgb3st, axgfb1b3, ab3st, afb1b3st, and afb1b3, could be well accounted for by 4 genes, i.e., ag, axg, ab3st, and afb1b3, through the segregation patterns among the offsprings of Japanese families. The populations studied were all in good Hardy-Weinberg equilibrium. The Gm gene frequencies of each of the 130 populations are presented in Tables 1 to 5, and the geographical distributions of the populations are shown with the ratios of the genes in each population as circle graphs in Figs. 1 and 2.

These results clarified that Mongoloid populations can be divided into 2 groups, the northern and southern groups. The northern group is characterized by high frequenies of the Gm ag (blue in the Figures) and Gm ab3st genes (yellow in the Figures) and a low frequency of the Gm afb1b3 gene (red in the Figures). On the contrary, the southern group is characterized by an extremely high frequency of the Gm afb1b3 gene and low frequencies of the Gm ag and ab3st genes. Of particular note is the frequent occurrence of the Gm ab3st gene exclusively in the northern group. Thus, Gm ag and ab3st are the northern genes and Gm afb1b3 is the southern gene.

Characteristics of the Japanese population.[10),11)] The results obtained from 26 Japanese populations living in Japan are shown in Table 1 and Fig. 1. The Ainu population[12] and the 8 island populations (Sadogashima, Kamishima, Tanegashima, Yakushima, Amamiohshima, Miyakojima, Ishigakijima, and Yonakunijima) were not included for the calculation of the mean frequencies in the general Japanese (17 populations, general Japanese), because the Ainu are indigenous Japanese people and the 8 islanders are isolated and small in number. The mean frequencies of the Gm genes observed among the 17 Japanese populations were 0.458 for Gm ag, 0.176 for Gm axg, 0.260 for Gm ab3st, and 0.106 for Gm afb1b3. These 17 Japanese populations were shown to be genetically homogeneous $(\chi^2 = 90.63, \text{ d.f.} = 136, \text{ p} > 0.999)$, when compared with each other. Heterogeneities, however, were found when the 17 Japanese populations were compared with the Ainu $(\chi^2 = 71.2, \text{d.f.} = 2, \text{p} < 0.001)$ and with the Miyakojima population $(\chi^2 = 37.2, \text{ d.f.} = 3, \text{ p} < 0.001)$; whereas homogeneity was observed between the Ainu and the Miyakojima populations $(\chi^2 = 3.15, \text{d.f.} = 3, \text{p} > 0.369)$. In other words, the Ainu and the Ryukyu islanders (Miyakojima, Ishigakijima, and Yonakunijima) differed from the general Japanese populations in Gm gene pattern. Both Ainu and Miyakojima populations showed a more remarkable northern type, characterized by a higher frequency of one of the northern genes, Gm ag (blue in the Figures), and by a lower frequency of the southern gene, Gm afb1b3 (red in Figures). In particular, the frequency of the other northern gene, Gm ab3st (yellow in the Figures), was much higher in the Ryukyu islanders than in the general Japanese populations. Another view of this is that the general Japanese populations have a higher frequency of the southern afb1b3 gene than the Ainu and the Ryukyu islanders, resulting from some admixture at rates as low as 7–8% with south Asian populations having the Gm afb1b3 gene in high frequency, but yet all of these Japanese populations studied had the Gm pattern of the northern Mongoloid.

On the other hand, in sharp contrast to the 3 Ryukyu Islanders, a native tribe in Taiwan, the Takasago,[13),14)] and a Taiwanese population (descendants of people who migrated from southern China about 300 years ago)[15] showed a typical southern Mongoloid pattern, as dipicted in Fig. 1,

Table 1　Gm gene frequencies in populations of Japan[10)–12)]

code	ethnic group	locality	sample	gene frequency			
				ag	axg	ab3st	afb1b3
J1	Ainu	Hidaka*	406	0.571	0.134	0.252	0.043
J2	Japanese	Shizunai	122	0.448	0.191	0.283	0.078
J3	Japanese	Akita	159	0.453	0.161	0.295	0.091
J4	Japanese	Sendai	205	0.476	0.166	0.246	0.112
J5	Japanese	Tokyo	405	0.460	0.168	0.263	0.109
J6	Japanese	Yokohama	184	0.477	0.166	0.251	0.106
J7	Japanese	Isehara	203	0.442	0.179	0.273	0.106
J8	Japanese	Niigata	196	0.488	0.145	0.250	0.117
J9	Japanese	Sadogasima*	153	0.480	0.207	0.251	0.062
J10	Japanese	Tsu	129	0.482	0.188	0.233	0.097
J11	Japanese	Kamishima*	152	0.453	0.182	0.276	0.089
J12	Japanese	Nara	481	0.464	0.161	0.252	0.123
J13	Japanese	Osaka	343	0.450	0.159	0.261	0.130
J14	Japanese	Matsue	208	0.444	0.181	0.260	0.115
J15	Japanese	Okayama	277	0.414	0.189	0.276	0.121
J16	Japanese	Hiroshima	328	0.456	0.186	0.265	0.093
J17	Japanese	Kohchi	200	0.440	0.200	0.255	0.105
J18	Japanese	Ohita	172	0.481	0.190	0.236	0.093
J19	Japanese	Nagasaki	198	0.454	0.200	0.255	0.091
J20	Japanese	Tanegashima*	200	0.448	0.193	0.254	0.105
J21	Japanese	Yakushima*	200	0.479	0.176	0.220	0.125
J22	Japanese	Amamiohshima*	200	0.492	0.202	0.247	0.059
J23	Japanese	Naha, Okinawa	348	0.434	0.221	0.262	0.083
J24	Ryukyuan	Miyakojima*	250	0.533	0.138	0.286	0.043
J25	Ryukyuan	Ishigakijima*	290	0.453	0.186	0.321	0.040
J26	Ryukyuan	Yonakunijima*	136	0.446	0.146	0.364	0.044
	mean in Japanese (*not included)		4158	0.458	0.176	0.260	0.106

in spite of the fact that there is only an 80-km distance between Taiwan and the southwestern-most inhabited island of Japan (Yonakunijima). This difference in pattern was reflected in heterogeneities observed between the Yonakunijima islanders and the Takasago population ($\chi^2 = 957.178$, p < 0.0001), and between the Ainu and Takasago populations ($\chi^2 = 1572.650$, p < 0.0001).
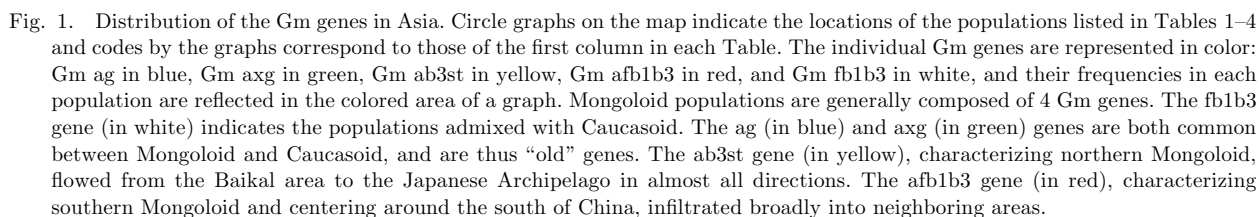
Based on these Gm results, it is hard to consider that peoples from the south migrated through the Ryukyu islands northwards to mainland Japan.

Characteristics of the Korean population.[16)] Seven Korean populations in Cheju Island, Pusan, Kwangju, Kongsan, Chonju, Wonju, and Kannung of South Korea, and 1 Korean population in Yanji of northeast China were tested

Table 2　Gm gene frequencies in Korean populations[16)]

code	locality	sample	gene frequency			
			ag	axg	ab3st	afb1b3
K1	Cheju Island	282	0.506	0.223	0.140	0.131
K2	Pusan	330	0.520	0.213	0.131	0.136
K3	Kwangju	394	0.486	0.207	0.141	0.166
K4	Kongsan	196	0.496	0.195	0.148	0.161
K5	Chonju	297	0.493	0.199	0.158	0.150
K6	Wonju	173	0.492	0.221	0.142	0.145
K7	Kannung	177	0.513	0.185	0.167	0.135
K8	Yanji, China	105	0.491	0.166	0.186	0.157
	mean in Korean	1954	0.501	0.207	0.145	0.147

for the Gm types (Table 2 and Fig. 1). These 7 Korean populations in different regions throughout South Korea showed homogeneity ($\chi^2 = 30.83$,

Fig. 1. Distribution of the Gm genes in Asia. Circle graphs on the map indicate the locations of the populations listed in Tables 1–4 and codes by the graphs correspond to those of the first column in each Table. The individual Gm genes are represented in color: Gm ag in blue, Gm axg in green, Gm ab3st in yellow, Gm afb1b3 in red, and Gm fb1b3 in white, and their frequencies in each population are reflected in the colored area of a graph. Mongoloid populations are generally composed of 4 Gm genes. The fb1b3 gene (in white) indicates the populations admixed with Caucasoid. The ag (in blue) and axg (in green) genes are both common between Mongoloid and Caucasoid, and are thus "old" genes. The ab3st gene (in yellow), characterizing northern Mongoloid, flowed from the Baikal area to the Japanese Archipelago in almost all directions. The afb1b3 gene (in red), characterizing southern Mongoloid and centering around the south of China, infiltrated broadly into neighboring areas.

d.f. = 48, p > 0.9). Homogeneity was also found between the 7 South Korean populations and the Korean population in Yanji, China ($\chi^2 = 4.9$, d.f. = 3, p > 0.179). In spite of the northern Mongoloid pattern in both Japanese and Korean groups, a highly significant heterogeneity was identified between these 2 groups ($\chi^2 = 288.7$, d.f. = 3, p < 0.001). The frequency of the Gm ab3st gene (yellow in the Figures) in the Korean population was 14.5% on average, which is intermediate between the mean frequency in the general Japanese (26%) and the highest frequency in a Han population (11.7%, Beijing in China). Similarly, the mean frequency of Gm afb1b3 (red in the Figures) among Koreans (14.7%) was intermediate between that of Gm afb1b3 in the general Japanese (10.6%) and the frequency of Gm afb1b3 in the Beijing Han (24.1%). The Korean populations showed the northern Mongoloid pattern, like the general Japanese, but higher frequencies of the southern marker gene, Gm afb1b3 (red in the Figures), than the Japanese populations. It seemed to be during the formation of the contemporary Korean population that such a Gm pattern intermediate between Japanese and the northern Han in China emerged. Japanese and Korean populations were originally identical or extremely close to each other. The difference in Gm pattern between contemporary Japanese and Korean populations resulted probably from frequent influxes of Chinese and/or northern populations into the Korean Peninsula.

Characteristics of the Chinese Han population.[10),11),17] The major ethnic group in the vast territory of China is the Han, making up 93% of the population, while the remaining 7% is composed of 55 minority ethnic groups. Chinese history has witnessed repeated ethnic movement, colonization, migration, and frequent dynastic changes. Such factors as mixed settlements and communal habitation on a finite scale are behind the multiracial but Han-dominative spread over the wide areas. The outcome is visible in both geographical distributions of the populations in China and distinctive geno-clines of the Gm genes among the populations, as described below.

The Han also have the 4 same Gm genes as the Japanese and Koreans (Table 3 and Fig. 1). The 17 Han populations tested for the Gm types are distributed from north to south in China. In sharp contrast to the Korean and the general Japanese,

Table 3 Gm gene frequencies in Han populations[10),11,17]

code	locality	sample	gene frequency			
			ag	axg	ab3st	afb1b3
H1	Haerbin	235	0.441	0.210	0.113	0.236
H2	Changchun	197	0.471	0.219	0.089	0.221
H3	Liaoyuan	199	0.466	0.237	0.083	0.214
H4	Dairen	154	0.384	0.266	0.094	0.256
H5	Beijing	195	0.428	0.214	0.117	0.241
H6	Shandong	133	0.431	0.190	0.116	0.263
H7	Kunsan	270	0.376	0.141	0.098	0.385
H8	Hefei	159	0.416	0.172	0.084	0.328
H9	Xian	159	0.405	0.183	0.113	0.299
H10	Chengdu	177	0.168	0.078	0.048	0.706
H11	Wuhan	360	0.290	0.131	0.055	0.524
H12	Hangzhou	151	0.350	0.184	0.079	0.387
H13	Changsha	139	0.204	0.066	0.054	0.676
H14	Gueiyang	151	0.226	0.085	0.043	0.646
H15	Guangzhou	127	0.183	0.054	0.033	0.730
H16	Fuzhou	211	0.188	0.077	0.043	0.692
H17	Taiwan	286	0.222	0.087	0.047	0.644

both of which are homogeneous for Gm, the Han clearly display latitudinal geno-clines extending from Haerbin in the northern area to Guangzhou in the southern area with reciprocal changes in frequencies of the northern and southern marker genes. One northern marker, Gm ag (blue in the Figures), decreased southwards in frequency from 0.471 to 0.168, together with another northern marker, Gm ab3st (yellow in the Figures) from 0.117 to 0.033; but the southern marker, Gm afb1b3 (red in the Figures), increased southwards in frequency from 0.214 to 0.730.

Eventually, the Han populations existent in northern Asia were more influenced by the northern Mongoloid; and the Han populations in southern Asia, more by the southern Mongoloid. Comparison of a Han population in Beijing with Korean and Japanese populations showed highly significant heterogeneities ($\chi^2 = 32.85$, d.f. = 3, p < 0.001 and $\chi^2 = 114.58$, d.f. = 3, p < 0.001, respectively). Such heterogeneities among the Han populations and between the Beijing Han and the 2 other populations are reflected in the distinctive reciprocal geno-clines.

Minority ethnic groups in the World. *Admixture populations with Caucasoid.* The distributions of the Gm genes among minority ethnic groups in Central and Southwest Asia and in North

and South America are shown in Tables 4 and 5 and in Figs. 1 and 2. As stated above, the Gm pattern of Mongoloid populations is characterized by the 4 Gm genes, i.e., ag, axg, ab3st, and afb1b3; and that of Caucasoid populations by 3 Gm genes, i.e., ag, axg, and fb1b3. Thus, the Gm ab3st and afb1b3 genes are specific to the Mongoloid, and the Gm fb1b3 gene (white in the Figures) is specific to the Caucasoid; whereas, the Gm ag and axg genes are found in common between the 2 groups[18] and are thus "old" genes.

A total of 5 Gm genes were found in 12 ethnic groups, and an irregular combination of the 2 common genes with the Mongoloid ab3st and Caucasoid fb1b3 genes was observed in a Uralian population. These combinations of the Gm genes indicate that the 13 ethnic groups are admixed populations of Caucasoid and Mongoloid. Similarly, judging from their Gm patterns, it is reasonable to assume that Huis are basically Mongoloid with some Caucasoid admixture; whereas Uighurs are basically Caucasoid with some Mongoloid admixture.

Indian populations in India and its neighboring regions are basically Caucasoid; however, many of them, e.g., Kalitas, Brahmin, Nepal, Tamil, Sinhalese, and Hindu, have admixed with the Mongoloid. Only a few populations, e.g., Muslim and Ahom, are basically Mongoloid admixed with Caucasoid. In the case of the Brahmins, which have the highest social status in the Hindu cast system, the fb1b3 gene frequency is 52% (white in the Figures), the highest in Indian populations. Two populations from westernmost locations in our study, Iranian and Uralian, are basically Caucasoid with a northern Mongoloid admixture.

Northern minority populations. A total of 17 populations among the Buryats, Yakut, Even, Evenki, Olunchun, Tungus, Dawoer, Udehe, Mongols, and Tibetans showed high frequencies of the ag and ab3st genes and a low frequency of the afb1b3 gene, i.e., the northern Mongoloid pattern. Among them, Buryat populations in the Baikal area are recognized as the most remarkable northern-type holder. A northernmost Buryat population (north Baikal) displayed the highest frequency of the Gm ab3st gene, which indicates gene flow from the Baikal area to the Japanese Archipelagos (Fig. 2).

The Buryats, numbering approximately 500,000, are the largest minority group in Siberia.

It is said that the Baikal area has always been suitable for human subsistence because of rich foods and mild climate even in winter, when it is 10 °C higher there than in the surrounding regions. It may thus be imagined that peoples in the Baikal area and around the upper neighborhood of the Yenisei River could certainly have survived even during the Last Glacial Maximum time.

The Yakut tribe originally lived in the Baikal area, migrated while mixing with Even and Evenki populations, and settled widely around north Asia. Now they comprise the Saha Republic (population, 380,000) that covers almost half of Asian Russia.

The Evenki (population, 30,000 in Russia) and Tungus (25,000 in China) are the same tribe. The Olunchun in China are supposedly like the Evenki in Russia. The Gm ab3st gene observed at high frequency of 44% in the Olunchun population is probably due to a bottle neck phenomenon because of their small population size of only 2,400 individuals.

Two Tibetan populations in Lasa and west Tibet have a more remarkable northern Mongoloid pattern than the 4 Mongolian populations, but a Tibetan population in Hezhue and the 4 Mongolian populations have higher frequencies of Gm afb1b3, which indicates admixture with the Han.

Southern minority populations. With regard to Southeast Asia, Chuang is the largest minority tribe (14 million) among minority groups there and has an extremely high frequency (94%) of Gm afb1b3 (the southern-type gene, red in the Figures). Gm afb1b3 was observed still at a high frequency in the populations of Micronesia, Melanesia, Indonesia, Cook Islands, and Hawaii in the Pacific Ocean.

Negritos in the Philippine islands, whose ethnic origin has been controversial, have the Gm ag, axg, and afb1b3 genes with the southern afb1b3 gene higher than the other 2 genes, but lack the Gm ab3st gene, characteristic of northern Mongoloid. Based on this Gm pattern, Negritos can be considered to be southern Mongoloid whose ancestors became dispersed to the archipelagos in fairly ancient times, similarly as did the Indonesians, Micronesians, and Polynesians.

Figure 2 allows us to conclude that the center of dispersal of the Gm afb1b3 gene is in the Yunnan and Guangxi area of southern China.

American Indians. The Gm data on the American Indians are shown in Table 5 and Fig. 2.

Table 4   Gm gene frequencies in Asian populations[10),11)]

code	ethnic group	locality	sample	gene frequency				
				ag	axg	ab3st	afb1b3	fb1b3
1	Buryat	north Baikal	137	0.473	0.162	0.307	0.058	—
2	Buryat	central Baikal	178	0.444	0.132	0.281	0.143	—
3	Buryat	south Baikal	81	0.492	0.125	0.272	0.111	—
4	Yakut	Siberia	89	0.552	0.087	0.267	0.094	—
5	Even	Siberia	204	0.569	0.12	0.299	0.012	—
6	Evenki	Siberia	194	0.59	0.103	0.227	0.08	—
7	Olunchun	Sibazhan	100	0.374	0.121	0.44	0.065	—
8	Tungus	northeast China	363	0.391	0.155	0.3	0.154	—
9	Dawoer	Qiqihaer	120	0.41	0.228	0.187	0.175	—
10	Udehe	Siberia	110	0.581	0.196	0.164	0.059	—
11	Mongol	Mongolia	61	0.431	0.102	0.229	0.238	—
12	Mongol	Wulanhoubu	103	0.325	0.209	0.194	0.272	—
13	Mongol	Huhahote	170	0.471	0.203	0.097	0.229	—
14	Mongol	west Mongolia	150	0.379	0.190	0.140	0.291	—
15	Tibetan	Hezhue	90	0.470	0.185	0.128	0.217	—
16	Tibetan	west Tibet	170	0.65	0.159	0.13	0.061	—
17	Tibetan	Lasa	87	0.57	0.148	0.213	0.069	—
18	Tujia	Yichang	148	0.42	0.114	0.071	0.395	—
19	Negritos	Mindanao	93	0.12	0.208	—	0.672	—
20	Negritos	Luzon	124	0.136	0.1	—	0.764	—
21	Philippinos	Luzon	321	0.098	0.039	0.027	0.836	—
22	Chuang	Guangxi	112	0.031	0.005	0.022	0.942	—
23	Shui	Sandu	104	0.024	0.005	0.019	0.952	—
24	Miao	Guizhou	100	0.095	0.015	0.015	0.875	—
25	Puyi	Duyun	105	0.062	0.010	0.014	0.914	—
26	Hani	Jinping	144	0.184	0.084	0.062	0.670	—
27	Bai	Xiaguan	150	0.256	0.147	0.057	0.540	—
28	Dai	Luxi	153	0.108	0.029	0.023	0.840	—
29	Thai	Thailand	198	0.044	0.042	0.015	0.899	—
30	Vietnamese	Vietnam	360	0.188	0.085	0.016	0.711	—
31	Laotian	Laos	116	0.013	0.009	0.008	0.970	—
32	Miao	Thailand	111	0.207	0.036	0.018	0.739	—
33	Karen	Thailand	161	0.108	0.048	0.021	0.823	—
34	Takasago	Taiwan	468	0.194	0.042	0.002	0.762	—
35	Hui	Changji	104	0.377	0.108	0.141	0.277	0.097
36	Uighur	Wulmuqi	258	0.331	0.120	0.113	0.095	0.341
37	Kacharis	Assam	84	0.024	0.024	0.143	0.809	—
38	Kalitas	Assam	91	0.118	0.063	0.066	0.366	0.387
39	Brahmin	Assam	76	0.180	0.089	0.086	0.127	0.518
40	Muslim	Bangladesh	114	0.265	0.195	0.044	0.356	0.140
41	Ahom	Assam	80	0.079	0.058	0.100	0.604	0.159
42	Nepalese	Nepal	128	0.284	0.177	0.090	0.199	0.250
43	Tamil	south India	258	0.415	0.252	0.048	0.083	0.202
44	Sinhalese	Sri Lanka	98	0.515	0.183	0.026	0.125	0.151
45	Hindu	India	200	0.324	0.134	0.042	0.074	0.426
46	Cambodian	Cambodia	200	0.142	0.054	0.037	0.767	—

Continued.

code	ethnic group	locality	sample	ag	axg	ab3st	afb1b3	fb1b3
47	Mazanderanian	Iran	280	0.143	0.007	0.085	0.026	0.739
48	Giranian	Iran	259	0.150	0.017	0.088	0.018	0.727
49	Uralian	Ural	316	0.279	0.085	0.029	—	0.608
50	Polynesian	Cook Islands	293	0.183	0.070	—	0.747	—

Table 5   Gm gene frequencies in the other populations[10),11)]

code	ethnic group	locality	ag	axg	ab3st	afb1b3
51	Inuit	Greenland	0.707	0.005	0.247	0.041
52	Inuit	Chaplin, Russia	0.795	—	0.205	—
53	Chukchi	northeast Kamchatka	0.731	0.109	0.153	0.007
54	Koryak	Kamchatka	0.714	0.055	0.200	0.031
55	Inuit	Alaska	0.683	0.011	0.254	0.052
56	Athabascan	Alaska	0.623	0.178	0.143	0.056
57	Algonquian	northeast Ontario	0.860	0.071	0.069	—
58	Apatch	New Mexico	0.598	0.133	0.197	0.072
59	Pima	Arizona	0.910	0.057	0.006	0.027
60	Mazatecos	Mexico	0.787	0.158	0.022	0.033
61	Quechua	Peru	0.865	0.093	0.016	0.026
62	Matigengua	Peru	0.735	0.253	0.008	0.004
63	Moroni	French Guyana	0.702	0.237	0.061	—
64	Kayapok	French Guyana	0.792	0.152	0.049	0.007
65	Wayana	Surinam	0.748	0.225	0.023	0.004
66	Torio	Surinam	0.649	0.328	0.021	0.002
67	Wapyshyna	south Guyana	0.611	0.352	0.025	0.012
68	Maxi	north Brazil	0.585	0.385	0.030	—
69	Cayapo	Brazil	0.712	0.288	—	—
70	Cayapo	Brazil	0.870	0.130	—	—
71	Xavante	Brazil	0.797	0.203	—	—
72	Aborigine	Australia	0.730	0.270	—	—
73	Polynesian	Hawaii	0.243	0.063	—	0.694
74	Micronesian	Micronesia	0.087	0.026	—	0.887
75	Melanesian	Melanesia	0.197	0.057	—	0.746
76	Celebes	Indonesia	0.156	0.078	—	0.766
77	Java	Indonesia	0.127	0.116	0.005	0.752
78	Malay	Malaysia	0.086	0.058	0.006	0.850
79	Kadazan	Borneo	0.015	0.012	—	0.973

American Indians are generally classified as Mongoloid. The most obvious specific place of departure of their ancestors was anywhere in Siberia. The South American Indians have only 2 Gm genes, ag and axg. They are considered to be ancestors to American Indians who crossed the Bering land bridge since they have the same Gm pattern as the Australian aborigines.[19)] Then the more specialized Mongoloid arrived later, carrying the Gm ab3st gene to North America.

Gm gene composition of the Mongoloid. Populations dispersed over broad areas of Asia and North and South America are regarded as Mongoloid characterized by 4 Gm genes, i.e., Gm ag, axg,
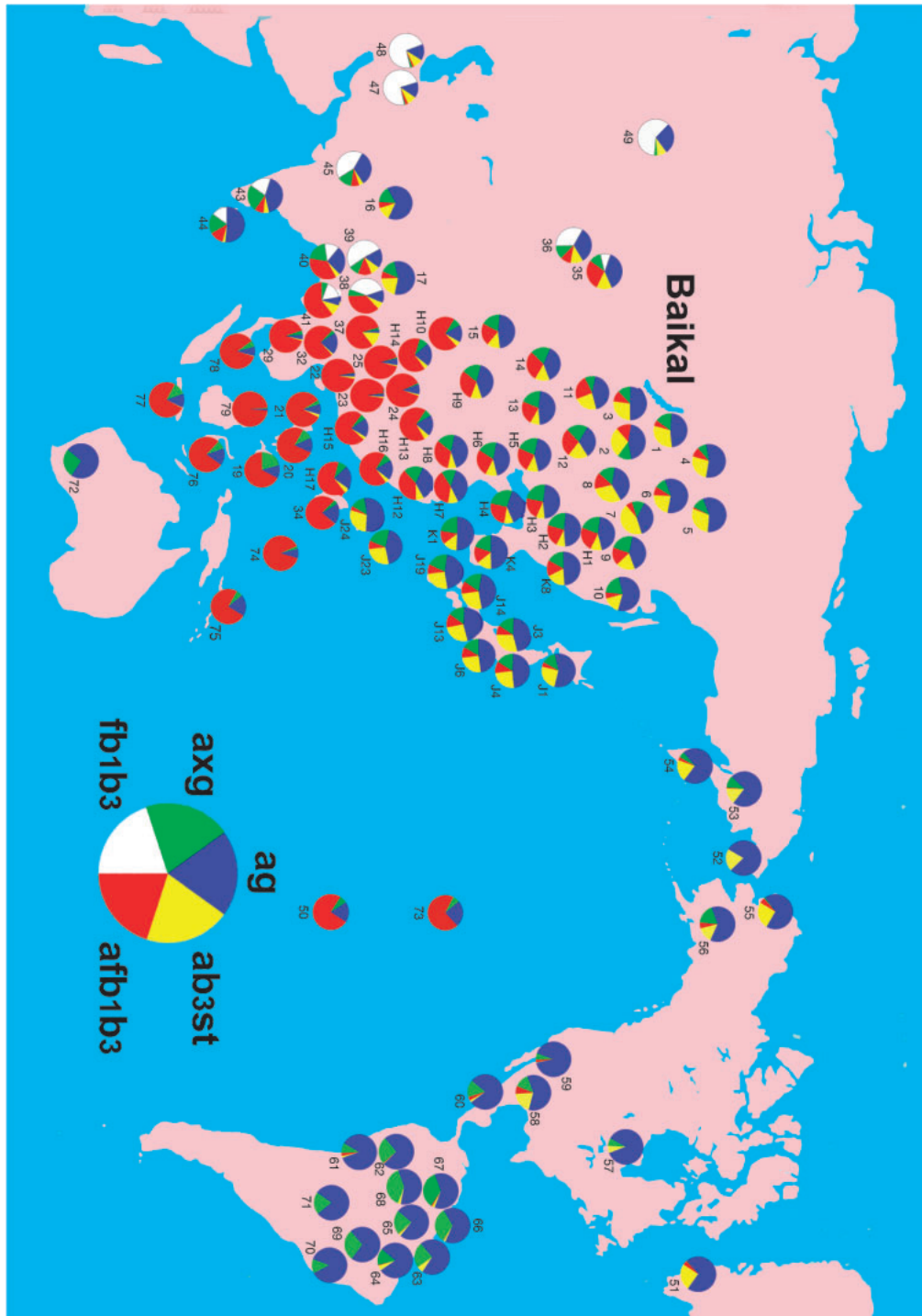
Fig. 2. Distribution of the Gm genes in Asia, North and South America, Oceania, and Pacific islands. Circle graphs on the map indicate the locations of the populations listed in Tables 1–5 and codes by the graphs correspond to those of the first column in each Table. The Gm gene frequencies in each population are reflected in the colored area of a graph. Indigenous South American and Aborigine in Australia migrated there long ago, because these populations have only the 2 old Gm genes, ag (in blue) and axg (in green). The ab3st gene (in yellow), characterizing northern Mongoloid, flowed from the Baikal area in almost all directions to the Japanese Archipelago, Tibet, and North America. The afb1b3 gene (in red), characterizing southern Mongoloid, centering around the south of China, infiltrated all around even to the islands in the Pacific Ocean, Cook Islands and Hawaii.

ab3st, and afblb3. Of particular note are the geno-clines, which are observed for the 2 northern Gm ag and ab3st genes, and the southern Gm afb1b3 gene, in Asia and America. Based on our Gm data, the degree of genetic differentiation between the Mongoloid populations was approximated for our Gm data by using the fixation index (F_{st}) of Wright.[20] The calculations indicated that the degree of genetic differentiation among the Mongoloid populations concerned was very great and almost equivalent to those of the worldwide differentiation for the Rh and Duffy systems reported by Cavalli-Sforza and Bodmer.[21] Furthermore, these results may provide evidence that the differences in Gm gene frequencies, particularly those for Gm ag, ab3st, and afb1b3, are due to factors such as natural selection and gene flow (one gene permeating into another race or nation crossing over the barrier between them from some race or nation) rather than random genetic drift. Thus, it can be inferred from such geographical differences in frequencies of the 3 genes that 2 distinctive Mongoloid populations existed among the paleo-Mongoloid of East Asia in the past.

As shown in Fig. 2, the Mongoloid was divided into northern and southern groups. A clear geno-cline was found for the Gm ab3st gene, which is a marker gene for the northern Mongoloid. Namely, the Gm ab3st gene is found at the highest frequencies in the Baikal area, and then flows regularly to the Mongol, Tibetan, Yakut, Olunchun, Tungus, Korean, Japanese, and Ainu still at high frequencies; although the gene frequency decreased markedly from mainland China to Taiwan and Southeast Asia, and from North to South America. The center of dispersal of this Gm gene is considered to be in the Baikal area. On the basis of these Gm findings, the Japanese belong basically to the northern Mongoloid and originated most likely in the Baikal area.

Discussion

Regarding the roots of the Japanese, Hanihara[1] proposed the "dual structure model", which suggests that the Jomon (12,000-2300 years ago) and Yayoi (2300-1700 years ago) peoples originated from South Asia and North Asia, respectively. This model assumes that people of the South Mongoloid lineage settled Japan first, later followed by a considerable number of immigrants of the North Mongoloid lineage and that the Mongoloid of both lineages mixed with each other to form the present-day Japanese people. Furthermore, the Ainu are assumed to be Jomon people of the South Mongoloid lineage that had evolved with little or no mixture with other races. This model was based on the computer multivariate analysis of the results of osteometry, an outdated, uncertain method. It is known that such physical measurement values easily change with nutrition, environment, and culture in a short time, as is well understood from the physique of the present young generation.

Instead of morphological studies, polymorphic markers harbored in macromolecules such as proteins and glycoconjugates including blood group systems have been widely applied during the last century to studies of genetic variation in human populations because of their simple Mendelian inheritance. Among them, Gm types are unique genetic markers that can define a Mongoloid population in terms of its origin by the combination pattern of the gene types and the ratios of them, even though Gm is a classical marker. In sharp contrast to the "dual structure model", our data on the geographical distribution of Gm gene types throughout the Asian and American Continents, and Pacific islands show that the Japanese population belong basically to the northern Mongoloid group; that the Ainu, as well as the Ryukyu islanders, are genetically closer to the northern Mongoloid group than to the general Japanese population; and that Taiwanese have a Gm gene composition characteristic of the southern Mongoloid group. The extent to which Japanese were admixed with the southern group is estimated at as low as 7–8%, assuming the admixture with southern groups having the highest frequencies of the Gm afb1b3 gene.

The results of a population study by Bannai et al.,[22] who analyzed HLA polymorphisms, suggested that the Ainu might share the same ancestor in eastern Asia with native Americans (Tlingit and Amerindians). Their findings indicate that the indigenous Japanese people, i.e., the Ainu, belong to the northern Mongoloid group, and are in good agreement with our results that the Ainu have the northern Mongoloid Gm genes at higher proportions than the present-day Japanese people. Tokunaga et al.[23] recognized that 20 Mongoloid populations could be divided into 2 major groups

(north and south) by phylogenetic analysis on the basis of HLA systems and indicated that the Japanese belong to the northern group. Phylogenetic analysis by Nei,[24] using gene frequencies of many conventional blood group systems, found that all 3 Japanese populations (Ainu, main-island Japanese, and Okinawans) originated from northern Asia, thus invalidating Hanihara's dual structure model. Nei also described that the Japanese are essentially descendants of northeast Mongoloids rather than southeast Mongoloids.[24] Therefore, one may call this the "out-of-Northeast" theory. This view is similar to my earlier conclusion,[10] although mine is based on the geographical distribution of only the Gm genes in eastern Asia and the Pacific.

Recently, analyses of mitochondrial, Y chromosomal, and autosomal DNA markers have rapidly accumulated, the former two defining maternal and paternal lineages, respectively. Harihara et al.[25] showed from analysis of mitochondrial DNA (mtDNA) polymorphisms that the Ainu are closely related to East Mongoloids, and claimed that the Ainu are descendants of ancient Mongoloids who lived in the Japanese Islands in the Paleolithic and Jomon periods. According to Shinoda and Kanai[26] and Shinoda,[27] many of the human skeletal remains excavated from the Nakazuma Jomon site had the mtDNA M10 gene, which is present in 1.3% (a low frequency) of the Japanese, and had a nucleotide sequence identical to that of the DNA of the Buryat living in the Baikal area. In addition, cluster analysis of mtDNA gene frequencies showed that the gene composition of the mainland Japanese was almost the same as that of northeastern Chinese and Korean populations. On the other hand, the gene composition of a southern Chinese population closely resembled that of indigenous Taiwanese, and obviously differed from that of the Japanese. Okinawans were completely different from indigenous Taiwanese and the southeastern Mongoloid, suggesting that it was from mainland Japan, not from the south including Taiwan that people migrated to the Okinawa Islands. More recently, based on the comparative analyses of a voluminous number of complete and partial mtDNA sequences, Tanaka et al.[28] described a striking coincidence of their results with our northern origin of Japanese.

Similarly, Hammer et al.[29] outlined the peopling of the Japan on the basis of Y chromosomal lineages, inferring that 3 major groups, D, C, and O-47z, began expansions ∼20,000, ∼12,000, and ∼4,000 years ago, respectively. They hypothesized that the primary candidate region of Paleolithic Japanese founding Y chromosomes having C and D groups should be placed in the area between Tibet and the Altai Mountains with varying levels of admixture between these and other Y chromosomes carrying O-47z group from Southeast Asia. Further Japanese samples would remain to be analyzed for drawing conclusions from Y chromosomal data.

Evidence from both mtDNA and Y chromosomes indicates that earlier Japanese came from around northern Asia, not from the South, which is not inconsistent with our Gm results indicating that the Japanese including the Ainu and the Ryuku islanders belong basically to the northern Mongoloid group with a little additional admixture of the southern gene, Gm afb1b3. Genome-wide analyses of autosomal DNA markers at about 640,000 sites among 17 Asian populations demonstrated distinct latitudinal changes in the ratio of their northern and southern ancestries in proportion to the north-to-south localities of the populations, and in addition homogeneity and a higher proportion of the northern ancestry in Japanese.[30]

Grubb,[31] who first disclosed the Gm system, stated that the Gm genes were characteristic enough for discriminating between Mongoloid and Negroid, making it possible to clarify the process of migration of ethnic groups. Further, quoting our distribution map of the genes,[32] he pointed out that Gm ab3st was characteristic of northern Mongoloids and varied gradually in its frequency among them and that many interesting relations between those populations were well shown on the map. He expressed his scientific approval of our data and conclusion that the Japanese population belongs basically to the northern Mongoloid and originated in the Baikal area and furthermore indicated that our study represented excellent probes of the Gm system.

Linguistic studies also have negated the "dual structure model". Although there has been the legend of the theory of the southern origin of the Japanese people, based on the similarity between Japanese and South Eastern words, Yasumoto,[33],[34] a quantitative linguist, considers that closely similar words encountered in Japanese and South Mongoloid language were brought, along with the

rice culture, by a small number of Chinese people from the lower Yangtze River region in the Yayoi era when they emigrated. However, the distribution of languages that use the same "subject-object-verb" word order as Japanese is roughly in agreement with that of races with the genetic patterns of the northern Mongoloid group, as shown in Fig. 1; and Chinese is an entirely different language, as it uses the "subject-verb-object" word order. The important point of Yasumoto's paper is that the distribution of languages classified according to grammatical structure, which is fairly resistant to change, agrees with our Gm results.

As mentioned above, abundant DNA evidence has been reported in recent years. None of these data oppose the Gm data; rather, they support it. Mongoloids generally have northern and southern ancestries in each population with varying ratios depending mainly to their latitudinal locations; northern populations have a unique gene, Gm ab3st (yellow in the Figures). Although data from mtDNA and Y-chromosome polymorphisms differ from the Gm data in the extent to which a southern contribution has been made to the Japanese, the geographical distribution of the 2 northern Gm genes leads us to conclude that the genes flowed from northern Asia even to the most southwestern island (Yonakunijima) of Japan, followed by culturally great but genetically small streams from southern Asia.

In summary, our results demonstrate that the Japanese race belongs basically to the northern Mongoloid group and originated in northeast Asia, most likely in the Baikal area of Siberia. In the case of migrations of human populations, migrants would not have been allowed to escape from changes in a wide range of habitats and climates, and thus would have to have adapted to their new environments. Such adaptation would have been expressed in the very phenotypes of Gm since immunoglobulins play an important role in environmental adaptation. Further accumulation of DNA data on much more samples from both modern and ancient humans and the interdisciplinary scientific approach will provide the evidence needed to test our model to explain the origins and dispersal of the first Japanese.

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Profile

Hideo Matsumoto was born in 1924. After graduating from Osaka Medical College in 1952, he started his career at Department of Legal Medicine in Osaka University School of Medicine and in 1953 commenced studies on blood group systems for personal identification and for paternity testing. He was appointed as an educational assistant of Osaka University School of Medicine, Department of Legal Medicine in 1955 and then he received MD degree from Osaka University School of Medicine in 1958. After that, he was appointed as an associate professor of Osaka Medical College, Department of Legal Medicine. In the meantime, he studied human genetics and immunoglobulin allotypes (Gm) for two years at Case Western Reserve University in Ohio, U.S.A. as a visiting fellow (1962–1964). He was appointed as a professor of Osaka Medical College, Department of Legal Medicine in 1973. Thereafter, in 1977, he received PhD degree from Tokyo Metropolitan University. He was elected as the President for the 28th General Meeting in 1983 of the Japanese Society of Human Genetics. Dr. Matsumoto received the Commendation from the Ministry of Justice in 1977 and the Medal from the Police Agency, Secretary in 1984. He received the Testimonial from the Ministry of Health and Welfare in 1987. He was elected as the President of Osaka Medical College in 1989 and officially retired at the expiration of his term of office in 1995. Since then, he has been an Emeritus Professor. As additional honors, Dr. Matsumoto was elected as the President of International Symposium on DNA polymorphisms (at Hakone) in 1990, and was made an Honorary Citizen of Toulouse, France in 1989, and an Honorary Member of the International Society of Forensic Haemogenetics in 1990. He was conferred the Decoration from the Emperor of Japan in 1999.