Distribution of Gm and Km Allotypes Among Ten Populations of Assam, India

HUBERT WALTER, HIDEO MATSUMOTO, TOKIKO MIYAZAKI, BISWA N. MUKHERJEE, KAILASH C. MALHOTRA, BHUBAN M. DAS, KLAUS GILBERT, AND PETER LINDENBERG
Department of Human Biology/Physical Anthropology, University of Bremen, Bremen, Federal Republic of Germany (H.W., K.G., P.L.); Department of Legal Medicine, Osaka Medical School, Takatsuki, Osaka, Japan (H.M., T.M.); Indian Statistical Institute, Calcutta, India (B.N.M., K.C.M.); Department of Anthropology, Gauhati University, Guwahati (Assam), India (B.M.D.)

KEY WORDS Population genetics, Ethnohistory

ABSTRACT Serum samples from ten endogamous populations of Assam, India—Brahmins, Kalitas, Kaibartas, Muslims, Ahoms, Karbis, Kacharis, Sonowals, Chutiyas, and Rajbanshis—were typed for G1m (1, 2, 3, 17), G3m (5, 10, 11, 13, 14, 15, 16, 21, 26), and Km (1). Among Brahmins, Kalitas, Kaibartas, Muslims, Ahoms, Sonowals, Chutiyas, and Rajbanshis, five different Gm haplotypes were found: Gm1,17;21,26; Gm1,17;10,11,13,15,16; Gm1,2,17;21,26; Gm1,3;5,10,11,13,14,26; and Gm3;5,10,11,13,14,26. Kacharis and Karbis show only four of these haplotypes: Gm3;5,10,11,13,14,26 is absent among them. The intergroup variability in the distribution of these haplotypes is considerable, which can be explained by the ethnohistory of these populations. Genetic distance analysis, in which five Chinese population samples were included, revealed the existence of three main clusters: 1) North and Central Chinese; 2) Kalitas, Kaibartas, Chutiyas, Rajbanshis, Muslims, and Brahmins; and 3) Ahoms, Sonowals, Kacharis, South Chinese, and Karbis. The clusters suggest some genetic relation between these four Assamese populations and South Chinese, which is again understandable considering the ethnohistory of the populations of Northeast India. In the Km system, too, a remarkable variability is seen in distribution of phenotype and allele frequency.

Over the last 2 decades, many studies have been conducted on Indian populations for Gm and Km markers showing the considerable value of these two polymorphic systems for evaluation of genetic differentiation processes among the populations of the Indian subcontinent. Such studies have been presented by Bhasin et al. (1986) for Sikkim and by Chakraborty et al. (1987) for West Bengal. Unfortunately, however, most of the hitherto published Gm studies on Indian populations have considered only a few Gm markers; thus, in view of the complexity of the Gm polymorphism, our knowledge of the distribution of Gm allotypes among Indian populations is still rather limited. The results of all these Gm studies have been summarized and critically reviewed by Steinberg (1973), Steinberg and Cook (1981), Walter (1985), and Walter et al. (1980, 1985). Larger sets of Gm allotypes have been examined to date by Daveau et al. (1980), Ray and Field (1981), and Schanfield and Kirk (1981).

This study on ten endogamous population groups of Assam (Northeast India) contributes to our knowledge of the distribution of Gm and Km allotypes among Indian populations. It forms part of an extensive population genetic survey in this hitherto scarcely investigated region of India.

MATERIALS AND METHODS

Serum samples from a total of 716 unrelated individuals belonging to ten different

Received December 8, 1986; revision accepted March 6, 1987.

Assamese populations were collected in early 1984. These samples were air-mailed to the Department of Legal Medicine, Osaka, Japan, where the Gm and Km typings were done. All the samples were typed for G1m (1, 2, 3, 17), G3m (5, 10, 11, 13, 14, 15, 16, 21, 26), and Km (1). The reagents used for that are presented in Table 1. Haplotype frequencies and degree of fit with the Hardy-Weinberg equilibrium were determined (in Osaka) using the computer program MAXIM (Kurczynski and Steinberg, 1967).

TABLE 1. Reagents used for Gm and Km allotype determination

Alphabetic	Numerical	Antiallotype	Anti-Rh_0
G1m			
a	1	3552	2880
x	2	2984	2880
f	3	2871	Ko-Ro
z	17	3272	2880
G3m			
b1	5	7514	3656
b0	11	0058	3656
b3	13	4721	3656
b4	14	0663	3656
b5	10	1340	3656
g	21	1642	3359
s	15	2624	3068
t	16	J198	3068
u	26	1369	Eggen
Km			
1	1	5872	2447

Populations

For this population genetic survey in Assam (Fig. 1), ten population groups were selected, all of which are usually related to two major races: caucasoids and mongoloids. However, in that each of these populations may have other ethnic elements along with admixture from the two major racial groups mentioned above, this classification is somewhat objectionable. Thus, for lack of any better description, the three Assamese Hindu castes, Brahmins, Kalitas, and Kaibartas, and the Assamese Muslims are regarded as caucasoids. They all speak Assamese, which forms part of the Indo-European language family, and are distributed all over the Brahmaputra valley. Our samples come from various parts of Assam. A detailed description of

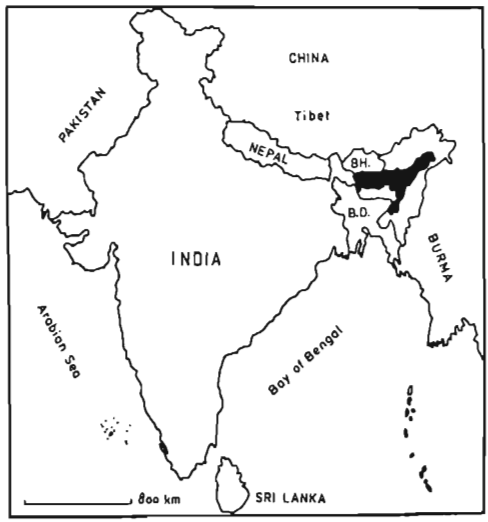

Fig. 1. Location of Assam (darkened area). BH., Bhutan; B.D., Bangladesh.

TABLE 2. Gm phenotype frequencies among ten populations of Assam

Gm phenotype	Brahmins		Kalitas		Kaibartas		Muslims		Ahoms	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
1,17;21,26	4	2.5	2	1.3	1	0.6	4	2.3	0	0.5
1,17;10,11,13,15,16,21,26	0	2.3	1	1.4	0	0.6	0	1.0	1	1.3
1,2,17;21,26	3	3.1	2	1.7	1	0.5	3	3.7	1	1.0
1,3,17;5,10,11,13,14,21,26	17	17.7	15	16.2	9	9.5	14	15.8	11	9.7
1,2,17;10,11,13,15,16,26	1	1.2	1	0.8	0	0.2	1	0.6	0	0.9
1,3,17;5,10,11,13,14,15,16,26	10	8.4	8	9.0	6	4.8	4	3.3	11	12.2
1,17;10,11,13,15,16	1	0.6	1	0.4	0	0.2	0	0.1	2	0.8
1,2,3,17;5,10,11,13,14,21,26	9	8.8	8	8.6	3	3.3	10	9.6	8	7.1
1,3;5,10,11,13,14,26	11	11.2	39	37.9	29	29.1	20	19.8	44	44.5
3;5,10,11,13,14,26	20	20.4	14	13.6	7	7.0	7	6.9	2	2.0
Total	76	76.0	91	91.0	56[1]	56.0	63	63.0	80	80.0
χ^2	3.693		1.506		0.701		1.957		1.295	
d.f.	4		4		1		3		3	
P	0.449		0.825		0.407		0.581		0.730	

[1]Uncommon phenotypes were excluded (see text).

Gm phenotype	Karbis		Kacharis		Sonowals		Chutiyas		Rajbanshis	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
1,17;21,26	0	0.0	1	0.0	0	0.0	0	0.1	2	0.3
1,17;10,11,13,15,16,21,26	0	0.1	1	0.6	1	0.5	0	0.3	0	0.5
1,2,17;21,26	2	4.6	0	0.1	1	1.4	1	0.6	1	1.6
1,3,17;5,10,11,13,14,21,26	1	0.8	1	3.2	2	2.4	3	2.8	3	5.5
1,2,17;10,11,13,15,16,26	4	1.8	0	0.6	2	2.4	0	0.8	0	0.6
1,3,17;5,10,11,13,14,15,16,26	4	5.8	19	19.4	16	15.2	11	8.9	5	3.6
1,17;10,11,13,15,16	0	0.2	2	1.7	1	1.5	0	0.5	0	0.1
1,2,3,17;5,10,11,13,14,21,26	31	28.0	4	3.2	14	12.8	7	6.9	9	7.6
1,3;5,10,11,13,14,26	44	44.7	56	55.0	36	36.7	28	28.9	18	18.1
3;5,10,11,13,14,26	0	0.0	0	0.0	3	3.1	9	9.3	4	4.0
Total	86	86.0	84	84.0	76[1]	76.0	59	59.0	42	42.0
χ^2	5.029		2.133		0.449		0.789		2.277	
d.f.	1		1		3		1		2	
P	0.025		0.146		0.929		0.379		0.321	

TABLE 3. Gm haplotype frequencies among ten populations of Assam

Gm haplotype	Brahmins		Kalitas		Kaibartas		Muslims		Ahoms	
	Freq.	SE	Freq.	SE	Freq.	SE	Freq.	SE	Freq.	SE
1,17;21,26	0.180	0.031	0.119	0.024	0.106	0.029	0.193	0.036	0.080	0.022
1,17;10,11,13,15,16	0.085	0.023	0.066	0.018	0.054	0.021	0.040	0.017	0.100	0.024
1,2,17;21,26	0.089	0.024	0.063	0.018	0.037	0.018	0.117	0.029	0.058	0.019
1,3;5,10,11,13,14,26	0.127	0.035	0.366	0.048	0.449	0.063	0.319	0.058	0.603	0.061
3;5,10,11,13,14,26	0.518	0.046	0.387	0.048	0.354	0.062	0.331	0.058	0.159	0.055

Gm haplotype	Karbis		Kacharis		Sonowals		Chutiyas		Rajbanshis	
	Freq.	SE	Freq.	SE	Freq.	SE	Freq.	SE	Freq.	SE
1,17;21,26	0.006	0.007	0.024	0.012	0.021	0.012	0.029	0.016	0.090	0.032
1,17;10,11,13,15,16	0.046	0.016	0.143	0.027	0.138	0.028	0.093	0.026	0.059	0.026
1,2,17;21,26	0.226	0.032	0.024	0.012	0.117	0.026	0.072	0.024	0.124	0.037
1,3;5,10,11,13,14,26	0.721	0.063	0.809	0.062	0.523	0.061	0.408	0.060	0.416	0.075
3;5,10,11,13,14,26	0.000	0.053	0.000	0.054	0.201	0.056	0.397	0.059	0.310	0.073

these population groups will be given elsewhere (Das et al., in preparation).

Ahoms, Karbis, Kacharis, Sonowals, and Chutiyas are called mongoloids. The Ahoms are originally a Shan or Thai people and linguistically form part of the Siamese-Chinese branch of the Tibeto-Chinese language family, though at present their language is Assamese. Their ancestors migrated in the early part of the 13th century from the upper courses of the Irrawady river in Burma and gradually established a kingdom in Assam. The Ahom dynasty ruled Assam until 1826, when the annexation of Assam by the British took place. At present, the Ahoms live primarily in Upper Assam, from which part our Ahom sample is taken. The Karbis are a mongoloid tribe of Assam and live in the southern parts of Middle Assam. Though their language has some peculiarities, they can be considered as Tibeto-Burman speakers. The Kacharis, another mongoloid tribe of Assam, are distributed all over Assam. Our sample comes from Lower Assam. They speak Boro, which forms part of the Tibeto-Chinese language family. The Sonowals are a division of the Kachari tribe. They live mainly in Upper Assam, from which area our sample stems. The Chutiyas form a very old population of Assam. Their original language was Tibeto-Burman, but long ago they accepted Assamese as their mother tongue. They live mostly in Upper Assam, where our samples were collected. For further details, refer to Das et al. (in preparation).

The last population group of our Assam series are the Rajbanshis, who live in different parts of Assam but are also found outside Assam. Our sample comes from Lower Assam. Originally, the Rajbanshis of Assam were most likely pure mongoloids. Over time, they became part of the Hindu caste folk, and are now recognized as a backward caste by the government. This process was started in the distant past and still continues. Since they are accepted as a Hindu caste, they have been admixed with certain caucasoid groups. Thus the present Rajbanshis are a population of mixed origin. Caucasoid elements have been added from time to time to their original mongoloid stock (Das et al., in preparation).

RESULTS AND DISCUSSION

Table 2 shows the observed and expected Gm phenotype frequencies of the ten Assamese populations under study. The esti-

mated Gm haplotype frequencies are presented in Table 3. Six to ten different Gm phenotypes were observed among these populations, which can be explained by five haplotypes: Gm1,17;21,26; Gm1,17;10,11,13,15,16; Gm1,2,17;21,26; Gm1,3;5,10,11,13,14,26; and Gm3;5,10,11,13,14,26. It is worth mentioning that the latter haplotype does not occur in Karbis and Kacharis. All the populations under study are in Hardy-Weinberg equilibrium.

In addition to the Gm phenotypes presented in Table 2, some uncommon ones could be observed, which were excluded from haplotype frequency estimations. There were two uncommon phenotypes, namely Gm1,2,3,17;5,10,11,13,14,15,16,26, found among the Kaibartas, and Gm1,17;5,10,11,13,14,15,16, found among the Sonowals. The probable haplotype combination of the Kaibartas phenotypes might be Gm1,2,17;15,16|3;5,10,11,13,14,26 and that of the Sonowals Gm1,17;5,10,11,13,14|1,17;15,16. However, because no family data are available, this assumption remains speculative.

The haplotype distributions (Table 3) demonstrate a considerable intergroup variability, which is statistically highly significant: $\chi^2_{36} = 426.418$, $p < 0.001$. However, the Gm haplotypes are not distributed irregularly but show some clear distribution patterns. This refers in particular to the haplotypes Gm1,17;21,26; Gm1,3;5,10,11,13,14,26; and Gm3;5,10,11,13,14,26, which show frequency differences between the caucasoid and mongoloid groups. The haplotype Gm1,17;21,26 is more frequent in Brahmins, Kalitas, Kaibartas, and Muslims (0.106–0.193) than in Ahoms, Karbis, Kacharis, Sonowals, and Chutiyas (0.006–0.080); the Rajbanshis show an intermediate position: 0.090. The caucasoid group is also characterized by high Gm3;5,10,11,13,14,26 frequencies (0.331–0.518), whereas these frequencies are generally much lower (or even zero) in the mongoloids, with the exception of the Chutiyas. Again, the Rajbanshis are closer to the caucasoid group. The Gm1,3;5,10,11,13,14,26 haplotype varies in the caucasoid group from 0.127 in Brahmins to 0.449 in Kaibartas, whereas in the mongoloid group these frequencies are generally much higher: 0.408 in Chutiyas and 0.809 in Kacharis. Thus the Rajbanshis are closer to the caucasoids than to the mongoloids. These different genetic patterns of the Assamese caucasoids and mongoloids, with the somewhat intermediate position of the Rajbanshis, are in line with the distribution of other genetic markers (Das et al., in preparation; Walter et al., 1986). Considering the above-mentioned ethnic peculiarities of the Rajbanshis, their position between caucasoids and mongoloids is not surprising, but a detailed evaluation of

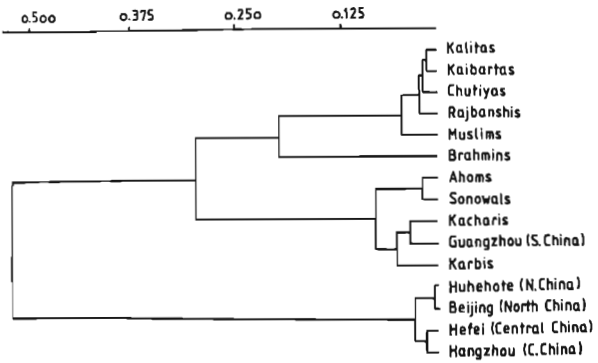

Fig. 2. Genetic distances based on Gm haplotypes.

the genetic structure of the Assamese populations under study can be effected only when the complete set of tested genetic markers becomes available.

Following Steinberg and Cook (1981), the typical caucasoid array of Gm haplotypes is Gm1,17;21,26; Gm1,2,17;21,26; and Gm3;5,10,11,13,14,26; and that of mongoloids is Gm1,17;21,26; Gm1,2,17; 21,26; Gm1,17;5,10,11,13,14,15,16; and Gm1,3;5,10,11,13,14,26. Table 3 reveals that the "caucasoid" haplotype Gm3;5,10,11,13,14,16 occurs not only in the caucasoid populations (Brahmins, Kalitas, Kaibartas, and Muslims) but also in some of the mongoloids, namely, Ahoms, Sonowals, and Chutiyas. The rather high frequency of this haplotype in the Rajbanshis has been mentioned already. On the other hand, the two "mongoloid" haplotypes, Gm1,17;5,10,11,13,14,15,16 and Gm1,3;5,10,11,13,14,26, are also present in the caucasoid populations. This suggests genetic contact between the two major races living in Assam and thus gene flow in both directions. Discussion of further genetic markers will be detailed elsewhere (Chakraborty et al., in preparation).

Finally, the distribution of Gm haplotypes among these Assamese populations is compared with some Chinese data recently published by Matsumoto et al. (1986). The results of genetic distance analysis (Nei,1972) are shown in Figure 2. From this, three distinct clusters emerge: Cluster 1 includes North and Central Chinese populations; Cluster 2 comprises six Assamese populations, namely, Kalitas, Kaibartas, Chutiyas, Rajbanshis, Muslims, and, somewhat separate from these groups, Brahmins, and Cluster 3 includes Ahoms and Sonowals, who form one subcluster, and Kacharis, South Chinese, and Karbis, who form a second subcluster. It seems that this cluster pattern is mostly caused by the distribution of the haplotypes Gm1,3;5,10,11,13,14,26, and Gm3;5,10,11,13,14,26 (see Table 3). One can conclude from Figure 2 that Ahoms, Sonowals, Kacharis, and Karbis preserved their mongoloid Gm pattern to a higher degree than did Chutiyas and Rajbanshis. The possible reasons for this might be seen in different rates of admixture with caucasoid populations, which will be analyzed in further studies.

Note must be made of the rather close genetic proximities between Kacharis, Karbis, and South Chinese. These three populations are characterized by high Gm1,3;5,10,11,13,26 haplotype frequencies (Kacharis, 0.809; Karbis, 0.721; South Chinese, 0.730) and by the absence of the Gm3;5,10,11,13,14,26 hap-

TABLE 4. Km phenotype and allele frequencies among ten populations of Assam

	Brahmins	Kalitas	Kaibartas	Muslims	Ahoms	Karbis	Kacharis	Sonowals	Chutiyas	Rajbanshis
Km phenotype										
1+	8	17	10	9	21	38	29	26	8	9
1−	68	74	48	54	59	48	55	51	51	33
Total	76	91	58	63	80	86	84	77	59	42
Km allele frequency										
Km^1	0.054	0.098	0.090	0.074	0.141	0.253	0.191	0.186	0.070	0.114

lotype. Considering the ethnohistory of Southeast Asia, these close genetic relations are understandable. V. Eickstedt (1934, 1952) has pointed to migration processes, which started in the distant past from South China and resulted in an expansion of mongoloid populations over the whole of Southeast Asia, including Burma and Assam. More recently, Allchin and Allchin (1982) stated in their review of the results of archaeological research in India, "... the eastern border regions, represented by the hills of Assam and Bengal show many profound influences from Burma and South China, and it is not surprising that the Neolithic culture known from surface collections of stone implements and from the few excavations should reflect cultural traits deriving from the same direction."

Table 4 shows the distribution of Km(1) phenotype and allele frequencies. The intergroup variability in the distribution of Km^1 is statistically highly significant: $\chi^2_{(8)} = 54.838$ $p < 0.001$. However, as emerges from Table 1 the caucasoid populations under study Brahmins, Kalitas, Kaibartas, and Muslims show Km^1 frequencies generally lower (0.054–0.098) than the mongoloids (0.070–0.253). The Rajbanshis have a somewhat intermediate position (0.114). As high Km^1 frequencies are characteristic of mongoloids the distribution pattern of this allele among the Assamese caucasoids might be the result of gene flow of different intensity. The Km^1 frequencies found in Assam are in line with observations made of South Asian and other populations, which have been reviewed recently by Walter et al. (1985).

ACKNOWLEDGMENTS

This study was supported in part by a grant from the Deutsche Forschungsgemeinschaft (Wa 122/31-1).

LITERATURE CITED

Allchin, B. and Allchin, R. (1982) The Rise of Civilization in India and Pakistan. Cambridge: Cambridge University Press, p. 351.

Bhasin, MK, Walter, H, Chahal, SMS, Bhardwaj, V, Sudhakar, K, Danker-Hopfe, H, Dannewitz, A, Singh, IP, Bhasin, V, Shil, AP, Sharma, MP, and Wadhavan, D (1986) Biology of the people of Sikkim, India. I. Studies on the variability of genetic markers. Z. Morphol Anthopol 77:49–86

Chakraborty, R, Mukherjee, BN, Das, BM, Walter, H, and Malhotra, KC, Gene differentiation among ten endogamous population groups of Assam, India (in preparation).

Chakraborty, R, Walter, H, Mukherkee, BN, Malhotra, KC, Sauber, P, Banerjee, S, and Roy, M (1987) Immunoglobulin (Gm and Km) allotypes in nine endogamous population groups of West Bengal, India. Ann Hum Biol 4:57–167

Das, BM, Walter, H, Mukherjee, BN, Gilbert, K, Lindenberg, P, Depa, R, Malhotra, KC, and Chakraborty, R, Genetic variation of five blood group polymorphisms in ten populations of Assam, India (in preparation)

Davenu, M, Rivat, L, Lalouel, JM, Langaney, A, Robert, DF, and Simons, MJ (1980) Frequencies of Gm and Km allotypes in the population of Singapore, Sri Lanka, and Punjab in North India. Hum Hered 30:237–244.

v. Eickstedt, E (1934) Rassenkunde und Rassengeschichte der Menschheit. Stuttgart: Enke Verlag

v. Eickstedt, E (1952) Rassentypen und Typendynamik von Asien. Historia Mundi 1:147–166

Kurczynski, TW, and Steinberg, AG (1967) A general program for maximum likelihood estimation of gene frequencies. Am J Hum Genet. 19:178–179

Matsumoto, H, Miyazaki, T, Xu, X, Watanabe, H, Kawai, N, and Suzuki, K (1986) Distribution of Gm and Km allotypes among five populations in China. Am J Phys. Anthropol 70:161–165

Nei, M (1972) Genetic distance between populations. Am Naturalist 106:283–292

Ray, AK, and Field, LL (1981) Immunoglobulin (Gm) allotypes in a sample of upper-caste Hindus from Bengal, India. Hum. Hered. 31:358–362

Schanfield, MS, and Kirk, RL (1981) Further studies on the immunoglobulin allotypes (Gm, Am, and Km) in India. Acta Anthropogenet. 5:1–21

Steinberg, AG (1973) The Gm and Inv immunoglobulin allotypes in Indian populations. A review. In LD Sanghvi (ed), Population Genetics in India (Proc 1st Ann Conf. Indian Soc. Hum Genet., Bombay), pp. 112–126.

Steinberg, AG, and Cook, CE (1981) The Distribution of the Human Immunoglobulin Allotypes. Oxford: Oxford University Press.

Walter, H (1985) On the distribution of some genetic markers in Indian caste and tribal populations. J. Hum. Evol. 14:327–333

Walter, H, Hilling, M, Singh, IP, Bhasin, MK, Goud, JD, and Veerraju, P (1980) Gm and Inv phenotypes and gene frequencies in Indian populations. South Asian Anthropol 1:69–75.

Walter, H, Bhasin, MK, and Danker-Hopfe, H (1985) Investigations on the variability of Km^1 gene frequencies in South Asia. Biol. J. Life Sci. (Patiala) 1:123–137.

Walter, H, Mukherjee, BN, Gilbert, K, Lindenberg, P, Dannewitz, A, Malhotra, KC, Das, BM, and Deka, R (1986) Investigations on the variability of haptoglobin: Transferrin and Gc polymorphisms in Assam, India. Hum. Hered. 36:388–396.