

uncertainty. Absorption, forward scattering of surface-reflected radiation, and scattering by large particles have been neglected, as in previous work. This fact should be kept in mind when the utility of photometric and polarimetric data for atmospheric pressure determinations is considered. A great deal of analytical and experimental work will be required before these complex problems in real atmospheres are understood.

J. A. GREENSPAN

*Astro Sciences Center,
IIT Research Institute,
Chicago, Illinois 60616*

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a remarkable degree of cultural autonomy and diversity, as evidenced most strikingly by the approximately 500 languages recognized in the Territory and in West Irian.

The villages tested in the Markham Valley region were chosen in order to take maximum advantage of the cultural and ecological variation manifested even in this restricted area. The two major linguistic stocks in the Territory, Melanesian (MN) and non-Austronesian (NAN), are roughly equally represented. Although MN-speaking groups are generally found in coastal areas, mountain and valley villages of both linguistic stocks have been included. Three villages (Nos. 19, 20, and 21 in Tables 1 and 2) belong to the NAN Gadsup-Auyana-Awa-Taiora linguistic family of the East New Guinea Highlands Stock (4), whereas three other NAN-speaking mountain villages, Waigwanom, Tapakanantu, and Gwasiram, are part of the ill-defined cultural complex called Kukukuku (No. 22). Two NAN-speaking villages on the edge of the Saruwaged Range, Mamamban and Narumonke (Nos. 17 and 18), are separated from the other NAN samples by the MN-speaking villages of the Markham Valley. The majority of the remaining villages speak the MN language Atsera including its dialects. In some cases neighboring and highly intermarried villages have been combined for analysis; for example, the three Nasioi-speaking (NAN) villages Rumba Bakatung, and Sirambana which comprise the Bougainville sample (No. 23).

The official name of the village or villages, approximate altitude, location by coordinates, and major linguistic affiliation are presented in Table 1 for the analysis, village-by-village, of the frequencies of the Gm and Inv phenotypes. The results of the tests on the samples from MN speakers are listed in section A of Table 1 and those from NAN speakers are listed in section B. In each group the villages have been arranged as far as possible in order of their geographic relation to one another.

Gene frequencies, calculated for Gm by means devised for the ABO blood group system (5), are shown in Table 2. The individuals comprising the samples were, for purposes of the calculations of gene frequencies, treated as unrelated, though this was patently not the case since as far as possible whole

Gamma-Globulin Factors (Gm and Inv) in New Guinea: Anthropological Significance

Abstract. *Analysis of the hereditary Gm and Inv γ -globulin factors of 1669 New Guineans from the Morobe and Eastern Highlands districts and Bougainville Island demonstrates that the frequencies of the three Gm alleles present (Gm^a, Gm^{ab}, and Gm^{ax}) are similar in general to those in Mongoloids and in particular to those in Southeast Asians and Micronesians. The New Guinea frequencies are distinct from those in other populations, including Australian aborigines. Highly significant differences in frequencies of Gm and Inv alleles occur between Melanesian- and non-Austronesian-speaking New Guineans.*

Several alleles at each of two loci (Gm and Inv) produce a series of antigens on the IgG immunoglobulin molecules of man. The frequencies of the antigens differ among populations (as do those of the red-cell blood group systems) and are inherited by means of different alleles in different populations. Both characteristics make these antigens of great interest to anthropologists, particularly because the population differences coincide remarkably well with traditional major racial groupings. Only in Caucasians, for example, does Gm(a) vary from 100 percent, while Negroids alone lack Gm(x) and show Gm(c). The allele Gm^{ab} is present in Mongoloids and Negroids but is absent among Caucasians (1). Since the number of studies on non-cosmopolitan peoples is severely limited, the analyses, given in this report, of the Gm and Inv determinations on 1669 serum samples from individuals in the Australian Trust Territory of New Guinea provide initial data for an anthropologically important area.

During 1962-63 blood samples and anthropometric, dermatoglyphic, and genealogical data were collected from

3100 New Guineans residing in an area of the Morobe and Eastern Highlands districts. The area measures about 100 by 125 km and extends northwest from Lae at the mouth of the Markham River. Data were also collected from 183 New Guineans from villages near Kieta, Bougainville Island. The blood samples were refrigerated and flown to Sydney, where the serum was separated and sent to Melbourne. At the end of the fieldwork 1669 serum samples were transferred to Cleveland and were typed for Gm and Inv factors by established methods (1-3).

The indigenous unit of orientation, the village, was used as the initial unit of analysis. The New Guinea villages sampled range in population from under 100 to several hundreds and in altitude from sea level to approximately 1500 m. Village life retains its indigenous character, including dependence on a horticultural technology, to a very large degree; however, villages near Lae, an administrative center, and on the two roads to the town, as well as those on Bougainville, are participating increasingly in a market economy. Villages are characterized by

villages were examined. The effect of consanguinity on estimates of gene frequencies based on samples from small primitive populations is a distinct problem; but, on the basis of the investigation of related data from New Guinea and of studies by others (6), we believe that consanguinity does not alter significantly our estimates of the gene frequencies or adversely affect general conclusions. The χ^2 "goodness-of-fit" test was applied to determine possible deviation from the assumed Hardy-Weinberg equilibrium for the Gm gene frequencies. Three village units (Nos. 9, 19, and 21 in Tables 1 and 2) and three combinations of villages (Nos. 14, 15 and 24) showed deviations from the expected frequencies at a level of significance of .05 or less, as shown in Table 2.

However (Table 2, footnote), the deviations among the MN speakers may be due to the entrance, at some time in the past, of at least one NAN speaker into each of two villages (Nos. 5 and 9) and hence be spurious. If this is correct, the MN speakers lack the Gm(x) factor (Table 1) completely; if not correct, they have it in very low frequency. Factor Gm(a) in the absence of Gm(b) is also rare in these people, the overall frequency of the Gm^a allele being about 10 percent and of the Gm(a) phenotype, 1 percent (No. 16 in Tables 1 and 2). The MN speakers also show a consistently low frequency of Inv(1).

The data for the NAN-speaking people show more heterogeneity. Two (Nos. 19 and 21) of the three Eastern Highlands villages (Nos. 19–21) show disagreement with the Hardy-Weinberg equilibrium (Table 2). The two NAN-speaking villages from the northeastern side of the Markham Valley (Nos. 17 and 18) show Gm and Inv patterns similar to MN speakers but have a very small percentage of Gm^{aw} . Bougainville (No. 23), geographically well separated from the other groups, shows Gm^a and Gm^{ab} frequencies similar to those of the MN-speaking samples, but its Gm^{aw} frequency is typical of NAN speakers. Bougainville also has an unusually high frequency of Inv(1).

In general, the Gm pattern of NAN speakers is distinguished from that of the MN speakers by a higher frequency of the Gm^{aw} allele (7 as opposed to 0 or at most 0.1 percent), a higher frequency of the Gm^a allele (37 as opposed to 10 percent), and a lower

Table 1. Village data, sample size, and Gm and Inv phenotype frequencies. Longitude is 146°E plus the indicated number of minutes and latitude is 6°S plus the number of minutes, except for Bougainville which is 155°E longitude. All samples were tested for Gm(a), Gm(b), Gm(x), and Gm(c). Only the positive reactions are recorded.

No. and village	Alti- tude (m)	Longi- tude (min)	Lati- tude (min)	Sample size	Phenotype frequencies						
					Gm				Inv		
					a	ab	ax	abx	1	1—	
<i>Section A. MN speakers</i>											
1	Labubutu	3	57	45	104	0	1.000	0	0	.067	.933
2	Kwasang	1500	44	57	44	.045	.955	0	0	.023	.977
3	Gurakor	525	38	50	27	.074	.926	0	0	.037	.963
4	Chivasing	75	35	35	125	0	1.000	0	0	.248	.752
5	Tsile Tsile	225	22	51	89	0	.989	0	.011	0	1.000
6	Gnarowein*†	125	14	33	106	.009	.991	0	0	.245	.755
7	Guruf*†	125	18	28	47	0	1.000	0	0	.170	.830
8	Bampa- Antir-Siats*†	625	12	27	85	0	1.000	0	0	.176	.824
9	Onga- Naruboin*†	250	11	23	125	.008	.984	.008	0	.088	.912
10	Wompul*	1050	9	22	10	.200	.800	0	0	0	1.000
11	Sukurum- Dumlinan*	800	29	16	85	.012	.988	0	0	.188	.812
12	Kaiapit*	300	16	16	56	.018	.982	0	0	.161	.839
13	Wankum*	375	5	9	45	0	1.000	0	0	.067	.933
14	Onga Census Division				363	.0055	.9917	.0028	0	.1653	.8347
15	Atsera speakers				559	.0107	.9875	.0018	0	.1574	.8426
16	All MN speakers				948	.0105	.9873	.0011	.0011	.1350	.8650
<i>Section B. NAN speakers</i>											
17	Mamamban	1225	28	8	92	.033	.957	0	.011	.033	.967
18	Narumonke	125	42	30	87	0	.989	0	.011	.092	.908
19	Binumarien‡	1375	5	17	43	.302	.349	.093	.256	.233	.767
20	Kusing‡	1375	5	37	7	.429	.143	.429	0	0	1.000
21	Tumbuna‡	1375	4	37	57	.193	.263	.175	.368	.228	.772
22	Kukukuku	1200	11	46	287	.237	.655	.066	.042	.087	.913
23	Bougainville	250	38	18	148	.020	.865	0	.115	.655	.345
24	Eastern Highlands				107	.2523	.2897	.1589	.2991	.2150	.7850
25	NAN speakers (except Bougainville)				573	.1710	.6859	.0628	.0803	.1030	.8970
26	All NAN speakers				721	.1401	.7226	.0499	.0874	.2164	.7836

* Atsera-speaking villages; † Onga Census Division villages; ‡ Eastern Highlands villages.

frequency of the Gm^{ab} allele (56 as opposed to 89 percent).

Data on Gm have been reported for Australian aborigines, Micronesians, American Indians, and Thais and for Chinese, Indians, and Malays from Malaysia (2, 7). Micronesians are similar to the New Guinea MN speakers (8). Australian aborigines tested from the Western Desert had no Gm(b) at all, while samples from northwestern coastal Australia had a Gm^{ab} frequency of only .167. The New Guinea Gm^{ab} frequencies of .894 for MN speakers and .561 for NAN speakers are in striking contrast to those in Australia. On the other hand, Southeast Asian populations are characterized by Gm gene frequencies closely similar to those of New Guinea. Thais, Malays, and Malaysian Chinese all have Gm^{ab} frequencies of .7, approximately. In con-

trast, Indians from Malaysia, as well as Pakistanis and Ceylonese, demonstrate the typical Caucasian alleles, Gm^a , Gm^b , and Gm^{aw} . The Gm^a , Gm^{ab} , and Gm^{aw} alleles found in Mongoloid populations (including American Indians)—rather than those typifying Australian aborigines, Caucasians, or Africans—are the alleles reported here for New Guinea.

Any anthropological inferences must necessarily be tentative, but certain implications of the New Guinea serum factors should be considered. The most pervasive cultural dichotomy recognized in New Guinea has been the MN-NAN linguistic one, but physical anthropological data, especially erythrocyte blood groups, have suggested no concomitant biological difference (9). The Gm and Inv data have been reported for village units in part be-

Table 2. Gm and Inv gene frequencies. Only as marked do Gm gene frequencies deviate from Hardy-Weinberg expectations at a level of significance of .05 or less.

No.	Gm ^a	Gm ^{ab}	Gm ^{ax}	Inv ^t	Inv ^b
Section A. MN speakers					
1	0	1.000	0	.034	.966
2	.213	.787	0	.011	.989
3	.27	.73	0	.02	.98
4	0	1.000	0	.133	.867
5*	0	.994	.006	0	1.000
6	.097	.903	0	.131	.869
7	0	1.000	0	.089	.911
8	0	1.000	0	.093	.907
9*†	.108	.888	.004	.045	.955
10	.45	.55	0	0	1.00
11	.108	.892	0	.099	.901
12	.134	.866	0	.084	.916
13	0	1.000	0	.034	.966
14‡	.083	.916	.001	.086	.914
15‡	.108	.891	.001	.082	.918
16	.105	.894	.001	.070	.930
Section B. NAN speakers					
17	.177	.817	.005	.016	.984
18	0	.994	.006	.047	.953
19†	.465	.350	.182	.124	.876
20	.68	.08	.25	0	1.00
21‡	.333	.362	.299	.121	.879
22	.493	.451	.056	.045	.955
23	.109	.832	.057	.413	.587
24‡	.412	.336	.247	.114	.886
25	.411	.515	.074	.053	.947
26	.368	.561	.071	.115	.885

* In these two samples Gm(ax) and Gm(abx) are represented by one individual each. The responsible genes are likely intrusive, and the gene frequencies of Nos. 5, 9, 14, 15, and 16, respectively, should probably be considered as Gm^a: 0, .090, .074, .104, .103; Gm^{ab}: 1.000, .910, .926, .896, .897; Gm^{ax}: 0, 0, 0, 0, 0. If so regarded, all samples of MN speakers are consistent with the Hardy-Weinberg expectations. † P < .005. ‡ P < .001.

cause these seem the basic biological population entities (10), in part to document the diversity of the tested people, and in part to permit alternative interpretations of the material. But if linguistically based combinations of the samples are made—as we have done—a very significant biological difference is apparent in the Gm allele frequencies between MN and NAN speakers. Furthermore, the allele Gm^{ax} is almost absent from MN speakers. Only two MN-speaking individuals out of 948 tested positively for Gm(x) (compared with 99 out of 721 for NAN speakers) and both came from villages contiguous with NAN-speaking areas (11).

It is suggestive that the Gm gene frequencies of the MN-speaking New Guineans are closer to those found in Southeast Asia than are those of the NAN speakers, particularly the Eastern Highlands (NAN) villages. A widely held anthropological interpretation of the populating of New Guinea posits the spread of an Austronesian-

speaking people out of Southeast Asia perhaps some 5000 years ago (12). Prior to this a technologically less advanced people, speaking NAN languages possibly related in an Indo-Pacific phylum (13), had thinly populated much of the Western Pacific. The first archeological C¹⁴ dates from New Guinea, putting man's known occupation back 10,000 years (approximately 2000 years after the earliest dated Australian artifacts), and the meager archeological evidence, which can be interpreted as showing a cultural innovation in the appearance of ground-edge stone axe-adzes dated about 5000 years ago, do not contradict this hypothesis (14).

A recent alternative explanation of the linguistic evidence (15) suggests that Austronesian languages developed in Melanesia and were carried east and west in several migrations. The Gm genetic data are not easily reconciled with this interpretation. The Gm frequencies imply the existence of two populations with origins separate in

time or space. One of these populations, the MN speakers, appears closely related to modern Southeast Asians and not an autochthonous Melanesian differentiation.

EUGENE GILES

Department of Anthropology,
University of Illinois, Urbana

EUGENE OGAN

Department of Anthropology, Harvard
University, Cambridge, Massachusetts

ARTHUR G. STEINBERG

Department of Biology, Western
Reserve University, Cleveland, Ohio

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