Am J Hum Genet 27:528–542, 1975

Gammaglobulin Groups of the Khoisan Peoples of Southern Africa: Evidence for Polymorphism for a $Gm^{1, 5, 13, 14, 21}$ Haplotype among the San

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The Gm allotypes are located on the heavy chains of IgG molecules. They are transmitted as haplotypes (arrays of alleles at closely linked loci), that is, in patterns reminiscent of the HL-A system. As in the HL-A system, each antigen may be determined by more than one haplotype, and each haplotype determines more than one antigen. The distribution of the haplotypes varies markedly among different races and ethnic groups. Since the Gm allotypes are not nearly as complex to determine as those of the tissue antigens and since they include markers of greater apparent ethnic specificity than the blood group systems, they are more useful than any other single system for characterizing human populations and for studying gene exchange among them. Characteristic arrays of haplotypes are known to exist in the major races of mankind [1], and some examples of these are shown in table 1.

Studies on American and West African Negroes [2] established that four haplotypes, $Gm^{1, 5, 6}$, $Gm^{1, 5, 6, 14}$, $Gm^{1, 5, 13, 14}$, and $Gm^{1, 5, 14}$, exist in Negroid peoples. Jenkins and Steinberg [3], studying Gm allotypes 1, 2, 3, 5, 6, 13, and 14, found that a group of Kalahari San (Bushmen) possessed two haplotypes, Gm^{1} and $Gm^{1, 13}$, not previously found in indigenous African peoples. The San had the characteristic Negro haplotypes as well. Subsequent studies (Jenkins and Steinberg, unpublished; [4]) confirmed that the $Gm^{1, 13}$ haplotype was by far the commonest in the San and that it could be used as a marker in the determination of San admixture in peoples as remote as the Sidamo of Ethiopia [1, 5].

The San inhabit much the same geographical area as the Khoikhoi (Hottentots). There is historical evidence that at one time the two peoples were more closely associated with one another than at present, and that early European visitors did

Received August 27, 1974; revised October 31, 1974.

This investigation was supported in part by grant GM 07214 from the National Institute of General Medical Sciences and grant MH 13611 from the National Institute of Mental Health.

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TABLE 1

Gm HAPLOTYPES COMMONLY PRESENT IN SOME MAJOR RACES

Race	Haplotypes*
Caucasoid	(1, 17, 21), (1, 2, 17, 21), (3, 5, 13, 14)
Negroid	(1, 5, 13, 14, 17), (1, 5, 6, 17), (1, 5, 6, 14, 17), (1, 5, 14, 17)
Mongoloid	(1, 17, 21), (1, 2, 17, 21), (1, 13, 17), (1, 3, 5, 13, 14)
Khoisanoid (San)	(1, 17, 21), (1, 5, 17), (1, 13, 17), (1, 5, 13, 14, 17)
Melanesian	(1, 17, 21), (1, 2, 17, 21), (1, 3, 5, 13, 14), (1, 5, 13, 14, 17)
Micronesian	(1, 17, 21), (1, 3, 5, 13, 14)

NOTE.—Data adapted from Steinberg et al. [1].
* When tested for Gm (1, 2, 3, 5, 6, 13, 14, 17, 21).

not always distinguish between them [6]. It has been suggested [7] that together they comprise a separate and distinct race, the Khoisanoid. A calculation of genetic distances among southern African populations based on alleles at 14 loci suggested that the two groups of Khoikhoi studied were genetically as close to Negro populations as to San [8]; but the two peoples do have certain characters not shared by the Negroes. Among these are high frequencies of the Fy^a allele in the Duffy system, low or absent PGD^c in the red cell 6-phosphogluconate dehydrogenase system, virtual absence of glucose-6-phosphate dehydrogenase deficiency, and a high frequency in some samples of the so-called "A_{Bantu}" allele in the ABO system [8]. Consequently, there seems to be enough evidence in the distribution of alleles, either particularly common or particularly uncommon in one or the other group of peoples, to make an association between San and Khoikhoi likely and to distinguish them from the Negroes. The only Gm characterization of any Khoikhoi population which has been reported hitherto is that of Jenkins and Brain [9] on a small sample of Topnaar from the Kuiseb Valley.

The Inv polymorphism is dependent on an inherited antigenic determinant present on the κ light chain of all immunoglobin classes. The three known Inv antigens are determined by three alleles, Inv^1, $Inv^{1,2}$, and Inv^3. Inv (2) has not been observed in the absence of Inv (1), and recent biochemical studies of an Inv (1) Bence Jones protein indicate that it will not be [10, 11].

Most populations have been tested for Inv (1) only, because reagents for Inv (2) and Inv (3) are scarce. The data for all populations indicate polymorphism for the allele(s) determining Inv (1) and for the allele determining Inv (3). Previous studies of the distribution of the Inv groups among the Khoisan consist of those by Jenkins and Steinberg ([3] and unpublished), Jenkins and Brain [9], and Jenkins et al. [4]. The loci for Gm and Inv are not closely linked [12].

The present paper (1) compares the findings in the earlier studies with the results of the Gm and Inv grouping of an additional eight San and two Khoikhoi populations, (2) presents family data on the San, and (3) provides evidence for the existence of a novel haplotype which appears to occur at polymorphic frequencies in certain San populations.

SUBJECTS AND METHODS

The earliest studies were concerned with two mixed populations of San from southwestern and western Botswana, one consisting of members of the !Kõ division of the Southern linguistic group mixed in unspecified proportions with individuals of the /Dukwe division of the Central group [3], and the other consisting of members of all three linguistic groups but with a preponderance of !Kõ (Jenkins and Steinberg, unpublished) and with a small sample of Khoikhoi from the Kuiseb Valley just south of Walvis Bay in South West Africa [9].

Included in the present study are representatives of a further seven geographically distinct populations of speakers of Northern Bushman languages. The largest single group in that linguistic division consists of the !Kung, represented here by samples drawn from Dobe, /du/da, /ai/ai, and the Lake Ngami area in Botswana (fig. 1) as well as by

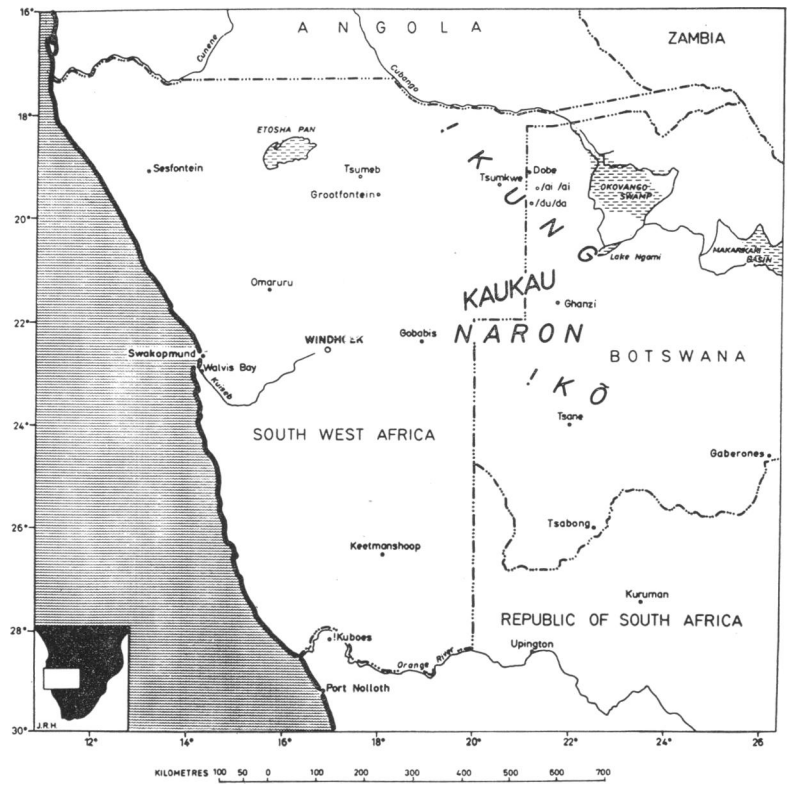

FIG. 1.—Map showing area from which samples are drawn. Because the San populations sampled tend to be seasonally migrant, their names are indicated in large capital letters over the regions in which the migrations take place. The Khoikhoi are sedentary, and their places of provenance are shown as ordinary place names. Kgalagadi may be found anywhere between the Orange River and the Okavango Swamp; in South West Africa they are unlikely to be found north of Gobabis or west of Keetmanshoop.

samples collected in the far northwest of the country (here referred to as Northern) and at Tsumkwe in South West Africa. The Kaukau or //au//en sample, also of a Northern Bushman-speaking population, was collected near Ghanzi, and it was in that vicinity that

samples representing a division of Central Bushman speakers, the Naron, also were drawn (fig. 1). The two new Khoikhoi samples were collected in South West Africa, one at Sesfontein in the north and the other at Keetmanshoop in the south (fig. 1). In addition, it has been possible to collect data on 112 San nuclear families in which the haplotypes of both parents could be unambiguously determined, on 65 families in which the haplotypes of one or of both parents could not be stated with certainty, and on three families in which the phenotypes establish that a novel haplotype is segregating. Blood samples were collected from 132 inhabitants of !Kuboes in the northwestern Cape Province. This "Coloured" population is composed of descendants of an admixture of Caucasoid and Khoisan peoples. The admixture is known to have occurred before the area was accessible to Negroes.

Blood samples were collected at or near the usual places of residence of the subjects. All specimens were kept at 4°–6°C and transported as soon as feasible to Johannesburg. There the serum was isolated and frozen at —20° C, and aliquots of serum were sent to Cleveland where Gm and Inv typing was carried out by methods previously described [13]. All sera were tested for Gm(1), Gm(2), Gm(3), Gm(5), Gm(6), Gm (13), Gm (14), and Gm (21). Tests for Gm (15) were also carried out on members of three of the families to establish the presence of a new haplotype. The sera used are identified in table

TABLE 2

REAGENTS USED TO DETECT Gm AND Inv ANTIGENS

ANTIGEN		ANTIGLOBULIN		ANTI-D	
Alphabetic	Numeric	Antibody	Dilution	Identification	Dilution
Gm					
a	1	Wils.	1/8	251	1/3
x	2	Tay.	1/16	Ham.	1/3
$b^2 = f$	$3 = 4$	Ewe.	1/8	Jac.	1/3
b^1	5	Dra.	1/8	21369	1/32
c^3	6	Deb.	1/4	War.	1/3
		Will.	1/4	War.	1/3
$b^3 = b\alpha$	$13 = 10$	Tho.	1/4	21369	1/32
				3419	1/5
b^4	14	Bur.	1/16	21369	1/32
				3419	1/5
s	15	Van Dijk	1/8	Vai.	1/3
		2167	1/8	Vai.	1/3
g	21	Monkey F	1/32	Ham.	1/3
Inv					
1	1	Mat.	1/4	Roe.	9/10

2. Gene frequencies were determined by the maximum-likelihood solution of equations based on the Hardy-Weinberg equilibrium, using the computer program MAXIM [14].

RESULTS AND DISCUSSION

The results of the investigation of Gm and Inv types of the 10 new Khoisan populations and of the Coloured from !Kuboes are set out in tables 3–7.

TABLE 3

Gm Phenotypes in San Populations

Population	No.		Phenotype: 1, 5, 13, 14	1, 5, 13, 14, 21	1, 13	1, 13, 21	1, 21	1, 5, 6, 13, 14	1, 5, 6, 14	1, 5, 6, 14, 21	1, 5, 6, 13	1, 5, 6, 21	1, 5, 6	1, 5, 13	1, 5, 21	1, 5	1, 5, 6, 13, 14, 21	1, 5, 14	1, 5, 14, 21	χ^2 Value	χ^2 df
!Kung:																					
Northern ..	100	O	26	30	13	12	2	12	0	4	...	...	...	1	0	0	0	...	...	...	...
		E	27.6	27.6	13.3	12.4	2.9	10.2	0.8	2.7	...	...	...	0.6	0.3	0.0	1.7	...	...	3.46	3
Ngami	152	O	52	20	32	23	2	6	1	0	3	0	0	13	0	0	0	...	...	...	...
		E	52.6	19.3	36.3	18.8	2.4	5.5	0.5	0.7	2.1	0.6	0.0	9.4	2.4	0.6	0.6	...	...	7.63	4
Dobe	394	O	155	33	142	40	2	19	0	1	2	0	0	...	...	...	0	...	...	...	...
		E	156.0	32.1	143.1	38.6	2.6	17.5	0.3	1.6	1.7	0.2	0.0	...	...	...	0.4	...	...	1.34	2
/ai/ai	62	O	33	4	16	5	2	2	0	0	...	...	...	...	...	...	...	...	...	...	...
		E	32.4	4.9	15.5	6.5	0.7	1.8	0.0	0.2	...	...	...	...	...	...	...	...	...	1.22	1
/du/da	100	O	38	11	33	11	1	6	0	0	...	...	...	...	...	...	...	...	...	...	...
		E	41.5	7.1	30.8	13.3	1.4	5.1	0.1	0.7	...	...	...	...	...	...	...	...	...	3.87	2
Tsumkwe ..	197	O	77	13	74	17	5	1	0	...	6	0	0	...	...	...	...	0	4	...	...
		E	79.4	10.0	69.4	26.1	2.4	1.6	0.3	...	4.2	0.8	0.1	...	...	...	...	0.5	2.2	11.31	4
Kaukau*	258	O	86	29	62	44	6	21	1	0	0	1	1	7	0	0	0	...	...	...	...
		E	88.2	27.6	64.3	40.0	6.2	17.1	1.1	3.3	1.7	0.5	0.1	5.7	1.8	0.1	0.3	...	...	9.37	5
Naron	138	O	46	14	40	18	1	13	0	2	2	1	0	1	0	0	...	...	...	...	...
		E	49.6	10.0	38.1	19.5	2.5	12.1	0.6	1.8	2.2	0.6	0.1	0.7	0.2	0.0	...	...	...	3.06	3

NOTE.—All samples were tested for Gm (1, 2, 3, 5, 6, 13, 14, 21).
* One Gm (1, 5, 14, 21) sample omitted.

TABLE 4

Gm HAPLOTYPE FREQUENCIES IN SAN POPULATIONS

Population	1, 5, 13, 14	1, 13	1, 21	1, 5, 6, 14	1, 5	1, 5, 13, 14, 21	1, 5, 6	1, 5, 14
!Kung:								
Northern	.272	.364	.170	.080	.008	.106	...	...
	.042	.043	.033	.019	.008	.031	...	...
Ngami	.254	.489	.126	.019	.063	.033	.014	...
	.030	.033	.022	.009	.017	.017	.008	...
Dobe	.268	.603	.081	.024	...	.020	.004	...
	.018	.020	.011	.006	...	.008	.002	...
/ai/ai	.378	.501	.105	.016	...	...	...	...
	.050	.051	.028	.011	...	...	...	...
/du/da	.295	.555	.120	.030	...	...	...	...
	.036	.039	.023	.012	...	...	...	...
Tsumkwe	.227	.593	.112	...	...	...	.018	.050
	.031	.026	.016	...	...	...	.007	.022
Kaukau	.262	.499	.155	.041	.022	.014	.006	...
	.023	.025	.018	.009	.008	.011	.004	...
Naron	.270	.526	.134	.050	.005	...	.015	...
	.030	.033	.021	.014	.005	...	.009	...

NOTE.—±SE appears below each frequency value.

Population Genetics of Gm among the Khoisan

The Gm data for the eight newly sampled San populations are presented in tables 3 and 4. The data for all populations except the Tsumkwe show satisfactory agreement with the Hardy-Weinberg distribution (table 3). Failure of the Tsumkwe data to conform is due largely to the Gm (1, 13, 21) and Gm (1, 21) phenotypes. This suggests the possibility that one or more families with these phenotypes contributed disproportionately to the sample.

It will be noted that the $Gm^{1,\ 5,\ 13,\ 14,\ 21}$ haplotype, previously found in only one San family (Jenkins and Steinberg, unpublished), has been used to explain the data for Northern, Ngami, Dobe, and Kaukau samples (table 4). In each instance, omission of this haplotype led to an unsatisfactory fit to the Hardy-Weinberg distribution (data not reported). Addition of this haplotype to the haplotype array of the Tsumkwe sample does not improve the agreement with the Hardy-Weinberg distribution. The data for the /ai/ai, /du/da, and Naron populations give satisfactory fits to the Hardy-Weinberg distribution without invoking the $Gm^{1,\ 5,\ 13,\ 14,\ 21}$ haplotype. Since the frequency of this haplotype is relatively high only in the Northern population (.106) and much lower in the other three populations in which it seems to be present (.014–.033), it may well be present in the /ai/ai and the /du/da in low frequency and have been missed because of small sample size. The Naron (sample size, 138), who belong to another linguistic group and come from the central region of Botswana, may not have this haplotype, but, once again, it may be present in low frequency.

TABLE 5

Gm PHENOTYPES IN KHOIKHOI POPULATIONS

PHENOTYPE	KEETMANSHOOP		SESFONTEIN	
	Obs.	Exp.	Obs.	Exp.
1, 5, 13, 14	86	91.3	20	19.7
1, 5, 13, 14, 21	19	12.9	...	...
1, 13	18	14.0	4	4.6
1, 13, 21	4	10.1	...	...
1, 21	0	1.8	...	...
1, 5, 6, 13, 14	5	4.3	12	11.4
1, 5, 6, 14	0	1.2	1	1.5
1, 5, 6, 14, 21	1	0.6	...	...
1, 5, 6, 13	1	0.6	1	0.8
1, 5, 6, 21	0	0.2	...	...
1, 5, 6	0	0.0	0	0.0
1, 5, 14	4	3.7	...	...
1, 5, 14, 21	8	5.2	...	...
1, 2, 13, 21	1	0.6	2	1.3
1, 2, 21	1	0.2	0	0.1
1, 2, 5, 13, 14, 21	0	0.8	1	1.7
1, 2, 5, 6, 21	0	0.0	0	0.1
1, 2, 5, 6, 14, 21	0	0.0	1	0.6
1, 2, 5, 14, 21	0	0.3	...	...
1, 3, 5, 13, 14	1	0.8	...	...
1, 3, 5, 13, 14, 21	0	0.1	...	...
1, 3, 5, 6, 13, 14	0	0.0	...	...
1, 2, 3, 5, 13, 14, 21	0	0.0	...	...
3, 5, 13, 14	0	0.0	...	...
Total	149	148.7	42	41.8

NOTE.—All samples were tested for Gm (1, 2, 3, 5, 6, 13, 14, 21). For Keetmanshoop, $\chi^2 = 14.92$, df = 4, $P < .02$; for Sesfontein, $\chi^2 = 0.94$, df = 2, $P > .50$.

Family data in support of the presence of the $Gm^{1,\ 5,\ 13,\ 14,\ 21}$ haplotype in these populations are presented in a later section of this paper.

The data were recalculated omitting Gm (21) to permit comparison with the data for the two San populations previously reported who had not been tested for Gm (21). The data are not presented here, but the fit to the Hardy-Weinberg

TABLE 6

Gm HAPLOTYPE FREQUENCIES IN KHOIKHOI POPULATIONS

Population	1, 5, 13, 14	1, 13	1, 21	1, 5, 6	1, 5, 6, 14	1, 5, 14	1, 2, 21	3, 5, 13, 14
Keetmanshoop	.391	.307	.111	.006	.017	.158	.007	.003
	.044	.035	.018	.007	.009	.032	.005	.003
Sesfontein	.429	.333	...	.027	.163	...	.048	...
	.071	.069	...	.027	.045	...	.023	...

NOTE.—±SE appears below each frequency value.

TABLE 7

Gm PHENOTYPES AND HAPLOTYPE FREQUENCIES OF COLOURED INHABITANTS OF !KUBOES

Phenotype	Observed	Expected	Haplotype	Frequency	$\pm\sigma$
1, 5, 13, 14	34	35.7	$Gm^{1,\ 5,\ 13,\ 14}$	.211	.032
1, 2, 13, 21	18	14.7	$Gm^{1,\ 21}$	.160	.024
1, 5, 13, 14, 21	13	8.9	$Gm^{1,\ 13}$	.284	.031
1, 13, 21	14	12.0	$Gm^{1,\ 2,\ 21}$	.196	.025
1, 2, 21	10	13.4	$Gm^{1,\ 5,\ 14}$	.107	.025
1, 13	9	10.7	$Gm^{3,\ 5,\ 13,\ 14,}$ ...	.042	.012
1, 2, 5, 14, 21	9	5.5			
1, 2, 5, 13, 14, 21	9	10.9			
1, 5, 14, 21	5	4.5			
1, 3, 5, 13, 14	5	6.6			
1, 3, 5, 13, 14, 21	4	1.8			
1, 2, 3, 5, 13, 14, 21	2	2.2			
1, 21	0	3.4			
1, 5, 14	0	1.5			
3, 5, 13, 14	0	0.2			
Total	132	132.0	...	1.000	...

NOTE.—All samples were tested for Gm (1, 2, 3, 5, 6, 13, 14, 21). $\chi^2 = 15.0750$, df $= 8$, $.10 > P > .05$.

equilibrium is satisfactory for all samples except the Kaukau ($\chi^2 = 10.42$, 3 df, $.001 < P < .025$).

The present findings [excluding Gm (21)] confirm those previously published [3, 4, 9]. The $Gm^{1,\ 13}$ haplotype is the most frequent in all San populations tested, regardless of the language group to which they belong. The haplotype varies, often significantly, among geographically diverse groups of the same tribal and linguistic division. For example, the Dobe, /ai/ai, /du/da, and Ngami live not very far from one another along the border between South West Africa and Botswana; these !Kung populations have frequent social contact and intermarry, yet comparisons of the Dobe and /ai/ai show significant differences between them for $Gm^{1,\ 13}$ frequencies ($t = 2.65$, $P < .01$) as well as for the presence of the $Gm^{1,\ 5,\ 13,\ 14,\ 21}$ haplotype (table 4).

The Gm data for the two Khoikhoi populations are presented in tables 5 and 6. The data for the sample from Sesfontein show good agreement with the expected frequencies based on the Hardy-Weinberg equilibrium, while those for the sample from Keetmanshoop do not ($\chi^2 = 14.92$, df $= 4$, $P < .02$). The latter population shows evidence of Caucasoid admixture [the Gm (1, 3, 5, 13, 14) individual, requiring the $Gm^{3,\ 5,\ 13,\ 14}$ haplotype] and of San admixture (the necessity for the $Gm^{1,\ 5,\ 13,\ 14,\ 21}$ haplotype and of the $Gm^{1,\ 21}$ haplotype to explain the data; see later). In this population as in the case of the Kaukau, the poor fit is due largely to the Gm (1, 13, 21) phenotype.

Neither the Sesfontein sample (tables 5 and 6) nor the Kuiseb sample [9] show evidence for the presence of the $Gm^{1,\ 21}$ haplotype. The Keetmanshoop sample does seem to have the $Gm^{1,\ 21}$ haplotype (tables 5 and 6), but this is probably due to admixture. When the tests for Gm (21) are ignored, the data may be explained

without assuming the presence of Gm^1, and neither of the other two Khoikhoi populations have Gm^1. If our interpretation of the Keetmanshoop data is correct, the San and Khoikhoi may be distinguished on the basis of the $Gm^{1,\ 21}$ and the $Gm^{1,\ 2,\ 21}$ haplotypes in that the former is present only in the San (table 4) and the latter is present only in the Khoikhoi (table 6; [9]). The Khoikhoi are the first population to be studied in which $Gm^{1,\ 2,\ 21}$ is more frequent than $Gm^{1,\ 21}$. The San and Khoikhoi may also be differentiated on the basis of the $Gm^{1,\ 5,\ 13,\ 14,\ 21}$ haplotype, which seems to be present only in the former (see later).

The $Gm^{1,\ 5,\ 13,\ 14}$ haplotype, which is the haplotype of highest frequency in Negro populations [4], is consistently that of second highest frequency among the San (table 4), but among the Khoikhoi attains frequencies in excess of those of $Gm^{1,\ 13}$ (table 6): it may consequently be regarded on the African Continent with fair confidence as an "African" marker rather than a specifically "Negro" one.

The haplotypes determining the Gm (6) antigen, $Gm^{1,\ 5,\ 6,\ 14}$ and $Gm^{1,\ 5,\ 6}$, occur in much lower frequencies among the San than among the Negroes. In the Khoikhoi their frequencies vary considerably, and only when considered in conjunction with another "Negro" marker, $Gm^{1,\ 5,\ 14}$, do they present a coherent picture. $Gm^{1,\ 5,\ 14}$ is found in Keetmanshoop in the highest frequency yet reported ($.158 \pm .032$) but not at all in the other two Khoikhoi populations (table 6; [9]); on the other hand, the frequencies of $Gm^{1,\ 5,\ 6}$ and $Gm^{1,\ 5,\ 6,\ 14}$ are comparable between the Kuiseb and Sesfontein samples, with $Gm^{1,\ 5,\ 6,\ 14}$ reaching moderately high frequencies in both, but a frequency of less than .01 among the Keetmanshoop Khoikhoi. This would suggest possible independent Negro contributions to the Kuiseb and Sesfontein populations on the one hand and to the Keetmanshoop population on the other, or drift operating over a number of generations during which there was essentially no interbreeding between the Keetmanshoop population and the Kuiseb or Sesfontein people, or both. Similar explanations can account for the high $Gm^{1,\ 5,\ 14}$ frequency in the Keetmanshoop population and its absence from the other two Khoikhoi populations. It is interesting to note that this haplotype has not been found in any of the South West African Negro populations so far studied [8]; it does, however, occur in the Kgalagadi ($.079 \pm .044$) [3, 8], a desert-dwelling semi-Negro people of Botswana with whom the Keetmanshoop people, living as they do on the edge of the Kalahari, may have had closer contact in the past than now. The Kgalagadi sample, which consists of only 48 individuals, also lacked $Gm^{1,\ 5,\ 6,\ 14}$.

There are a number of objections to these interpretations. The location of the Keetmanshoop population in a town on a trade route provides much opportunity for admixture. Admixture, however, would tend to produce a diluting rather than an enhancing effect on a rare allele. Yet the frequency of $Gm^{1,\ 5,\ 14}$ in the Keetmanshoop population is not merely higher, but very much higher, than its frequency in the Kgalagadi ($t = 3.38$, $P < .01$). Drift, however, could account for the observed frequencies. This question will be discussed in a later section.

The inhabitants of !Kuboes are the decendants of an admixture of Caucasoid

and Khoisan stocks which is known historically to have taken place before the area where they live could have been accessible to Negroes. Their Gm data are presented in table 7. It will be seen that haplotypes determining the Gm (6) antigen have not been found among the members of this population and that the $Gm^{1,\ 5,\ 14}$ haplotype is present. The presence of $Gm^{3,\ 5,\ 13,\ 14}$ in this population is clear evidence of Caucasoid admixture. The presence of $Gm^{1,\ 21}$ also indicates admixture, but the admixture may be with San as well as with Caucasoids.

The source of the $Gm^{1,\ 5,\ 14}$ haplotype requires explanation. This haplotype was first observed in Negroid populations and not in other populations [2] and was assumed to be confined to these people. Since Negro admixture with the !Kuboes community seems unlikely, the possibility that this haplotype occurs among the Khoisan as well seems likely. Thus Negroids and Khoisan share the $Gm^{1,\ 5,\ 13,\ 14}$ and $Gm^{1,\ 5,\ 14}$ haplotypes and possibly the $Gm^{1,\ 5,\ 6}$ and $Gm^{1,\ 5,\ 6,\ 14}$ haplotypes.

The $Gm^{1,\ 2,\ 21}$ haplotype has not been found in any of the 10 San populations studied (table 4; [3, 4]), but it has been found in each of three Khoikhoi populations (table 6; [9]) and in the Coloured of !Kuboes (table 7) who are primarily of Khoikhoi origin. On the other hand, $Gm^{1,\ 21}$ has been found in each of the 10 San populations but not in the two Khoikhoi populations with little evidence of admixture: the Sesfontein (table 6) and the Kuiseb [9]. The Coloured from !Kuboes do have $Gm^{1,\ 21}$, but this may have come from Caucasoid and/or San admixture. The high frequency of $Gm^{1,\ 21}$ (.160) in this sample compared to the low frequency of $Gm^{3,\ 5,\ 13,\ 14}$ cannot be entirely accounted for by San admixture. The only reasonable explanation is drift, due either to a founder effect or to sampling errors because of small population size, or both. At any rate, it seems likely that in Africa $Gm^{1,\ 21}$ is characteristic of the San and $Gm^{1,\ 2,\ 21}$ is characteristic of the Khoikhoi.

We suggest that the haplotype array of the San is composed of $Gm^{1,\ 21}$, $Gm^{1,\ 13}$, $Gm^{1,\ 5,\ 13,\ 14}$, $Gm^{1,\ 5,\ 13,\ 14,\ 21}$, and possibly also $Gm^{1,\ 5,\ 6}$ and $Gm^{1,\ 5,\ 6,\ 14}$, although the latter two may have been acquired through admixture with Negroes. The Khoikhoi haplotype array appears to be $Gm^{1,\ 2,\ 21}$, $Gm^{1,\ 13}$, and $Gm^{1,\ 5,\ 13,\ 14}$. The presence of $Gm^{1,\ 5,\ 6}$ and $Gm^{1,\ 5,\ 6,\ 14}$ may, as in the case of the San, be due to admixture. Therefore, the San and the Khoikhoi differ from each other in that the former has the $Gm^{1,\ 21}$ and $Gm^{1,\ 5,\ 13,\ 14,\ 21}$ haplotypes not present in the latter, and the latter has the $Gm^{1,\ 2,\ 21}$ haplotype not present in the former. These three haplotypes and $Gm^{1,\ 13}$ serve to distinguish the Khoisan people from other African peoples.

The $Gm^{1,\ 5,\ 14}$ haplotype occurs sporadically among the Khoisan peoples we have studied (tables 4 and 6) as it does among various southern African Negroid populations [4]. We find it difficult to account for its distribution.

Family Studies of the Gm System in the San

Details on the offspring of the 112 San couples whose genotypes could be unambiguously determined are set out in table 8. A further 65 families were investi-

TABLE 8

Gm Data on Offspring of San Couples Whose Genotypes Were Unambiguously Determined

Mating Class	No. Families	Offspring Genotype: 1, 5, 13, 14/1, 13	1, 13/ 1, 13	1, 13/ 1, 21	1, 5, 13, 14/1, 13 or 1, 5, 13, 14	1, 5, 13, 14/1, 21	1, 21/ 1, 21	1, 5, 6, 14/1, 13	1, 5, 6, 14/1, 5, 13, 14 or 1, 13	1, 5, 6, 14/1, 21	1, 5, 6/ 1, 13	Total
1, 5, 13, 14/1, 13 × 1, 13/1, 13	27	23	33	...	...	...	...	...	...	...	...	56
1, 13/1, 21 × 1, 13/1, 13	14	...	12	18	...	...	...	...	...	...	...	30
1, 13/1, 13 × 1, 13/1, 13	14	...	27	...	...	...	...	...	...	...	...	27
1, 5, 13, 14/1, 21 × 1, 13/1, 13	5	6	...	6	...	...	...	...	...	...	...	12
1, 5, 13, 14/1, 13* × 1, 5, 13, 14/1, 13	7	2*	6	...	6	...	...	...	...	...	...	14
1, 5, 13, 14/1, 13* × 1, 13/1, 21	9	3	1	5	...	4	...	...	...	...	...	13
1, 5, 13, 14/1, 21 × 1, 13/1, 21	6	7	...	7	...	3	4	...	...	...	...	21
1, 5, 6, 14/1, 13 × 1, 13/1, 13	6	...	14	...	...	...	...	5	...	...	...	19
1, 5, 13, 14/1, 21 × 1, 5, 13, 14/1, 13	6	...	...	3	4	4	...	...	...	...	...	11
1, 5, 13, 14/1, 13 × 1, 5, 6, 14/1, 13	2	...	3	...	...	...	...	...	2	...	...	5
1, 5, 13, 14/1, 5, 6, 14 × 1, 13/1, 21	3	4	...	...	...	2	...	3	...	3	...	12
1, 13/1, 13 × 1, 21/1, 21	2	...	...	2	...	...	...	...	...	...	...	2
1, 5, 6, 14/1, 13 × 1, 13/1, 21	3	...	...	3	...	...	...	...	...	...	...	3
1, 13/1, 21 × 1, 13/1, 21	1	...	1	...	...	...	...	...	...	...	...	1
1, 21/1, 21 × 1, 5, 13, 14/1, 13	1	...	...	1	...	3	...	...	...	...	...	4
1, 5, 13, 14/1, 21 × 1, 5, 13, 14/1, 21	1	...	...	...	...	1	...	...	...	...	...	1
1, 5, 13, 14/1, 21 × 1, 5, 6, 14/1, 21	1	...	...	...	...	...	...	...	...	1	...	1
1, 13/1, 21 × 1, 21/1, 5, 6, 14	1	...	...	...	...	...	...	1	...	...	...	1
1, 5, 6, 14/1, 13* × 1, 5, 6, 14/1, 13*	1	...	...	...	...	...	...	1*	...	...	...	1
1, 5, 6, 14/1, 21 × 1, 21/1, 21	1	...	...	...	...	...	...	...	...	1	...	1
1, 13/1, 5, 6 × 1, 13/1, 13	1	...	1	...	...	...	...	...	...	...	4	5
Total	112	45	98	45	10	17	4	10	2	5	4	240

Note.—All samples were tested for Gm (1, 2, 3, 5, 6, 13, 14, 21).

* Genotypes determined from supplementary family data.

gated, but the haplotypes of one or both parents could not be determined with certainty. Data concerning these 65 families are not reported here but are available to interested persons on request. The genotypes of many of the parents shown in table 8 were determined by their offspring or by supplementary family data. It will be seen that confirmation is provided for the presence in the San of all the haplotypes previously reported as characterizing them (table 4; [3, 4]).

In earlier studies (Jenkins and Steinberg, unpublished; [4]), the possible existence of a *Gm* $^{1, 5, 13, 14, 21}$ haplotype was reported, but definite proof was lacking. The population data shown in tables 3 and 4 indicate that this haplotype is present among the San. The data from the original family (family XVIIa, Jenkins and Steinberg, unpublished) and from two new San families (families 52b-1 and 87) offer further confirmation of the existence of this haplotype (table 9). As a pre-

TABLE 9

Gm PHENOTYPES AND PROBABLE GENOTYPES OF SAN FAMILIES WITH Gm$^{1, 5, 13, 14, 21}$ HAPLOTYPE

Family and Individual	Gm Phenotype	Probable Genotype
Family XVIIa:		
42 (Fa.)	1, 13, 15, 21	1, 21/1, 13, 15
43 (Mo.)	1, 5, 13, 14, 15, 21	1, 5, 13, 14, 21/1, 13, 15
47	1, 5, 13, 14, 15, 21	1, 5, 13, 14, 21/1, 13, 15
49	1, 5, 13, 14, 21	1, 5, 13, 14, 21/1, 21
55	1, 13, 15	1, 13, 15/1, 13, 15
Family 52b-1:		
3168 (Fa.)	1, 5, 13, 14, 15, 21	1, 5, 13, 14, 21/1, 13, 15
3160 (Mo.)	1, 13	1, 13/1, 13
3158	1, 5, 13, 14, 21	1, 5, 13, 14, 21/1, 13
3161	1, 5, 13, 14, 21	1, 5, 13, 14, 21/1, 13
3257	1, 5, 13, 14, 21	1, 5, 13, 14, 21/1, 13
Family 87:		
3042 (Fa.)	1, 5, 13, 14, 15, 21	1, 5, 13, 14, 21/1, 13, 15
3053	1, 13	1, 13/1, 13
3037	1, 5, 13, 14, 21	1, 5, 13, 14, 21/1, 13
3039	1, 13	1, 13/1, 13

NOTE.—All samples were tested for Gm (1, 2, 3, 5, 6, 13, 14, 21). Only those samples with Gm (15) indicated in the phenotype were tested for Gm (15). See text for further details.

caution, all samples from these three families were retyped in 1974 with three different anti-Gm (21) sera; these reagents come from Monkey F (i.e., the antiserum used originally), from a rabbit (R20), and from a human donor (Cli.). The animal sera were diluted with a human Gm (—21) serum which was itself diluted 1/8 in saline before use. The data obtained with all three antisera were concordant for each of the 14 samples listed in table 9 and confirmed the original observations.

In family XVIIa, the child with the Gm (1, 13, 15) phenotype establishes that both parents carry a *Gm*$^{1, 13, 15}$ haplotype. The father's probable genotype is consequently *Gm*$^{1, 13, 15}$/*Gm*$^{1, 21}$, and the mother's must therefore be *Gm*$^{1, 13, 15}$/

$Gm^{1,\ 5,\ 13,\ 14,\ 21}$ or $Gm^{1,\ 13,\ 15}/Gm^{1,\ 5,\ 14,\ 21}$, more probably the former because $Gm^{1,\ 5,\ 13,\ 14}$ is common among these people and $Gm^{1,\ 5,\ 14}$ is not. The genotype of the mother of family 52b-1 is probably $Gm^{1,\ 13}/Gm^{1,\ 13}$. Since in the San the $Gm^{1,\ 13}$ haplotype always determines Gm (15), she would, if fuller typing had been carried out, probably be $Gm^{1,\ 13,\ 15}/Gm^{1,\ 13,\ 15}$. Her husband has the unusual phenotype Gm (1, 5, 13, 14, 15, 21), and the presence of Gm (15) establishes that one of his haplotypes is $Gm^{1,\ 13,\ 15}$. He has transmitted Gm (21) as well as Gm(5) and Gm (14) to all three children. The assumption that the same haplotype is responsible for these three antigens as well as for Gm (1) and Gm (13) seems reasonable; that is, he has the $Gm^{1,\ 5,\ 13,\ 14,\ 21}$ haplotype. A similar situation exists in family 87, except that the Gm (1, 13) phenotype of the second child establishes the $Gm^{1,\ 13}$ haplotype in the father, confirming the evidence provided by the presence of Gm (15) in the father. The father must therefore have transmitted a $Gm^{1,\ 5,\ 13,\ 14,\ 21}$ haplotype to his elder child. It consequently appears certain that a $Gm^{1,\ 5,\ 13,\ 14,\ 21}$ (or $Gm^{1,\ 5,\ 14,\ 21}$) haplotype does occur in the San, and, at least in some San populations, at polymorphic frequencies (table 4).

Inv in the Khoisan

The Inv system is of little anthropological interest in the Khoisan peoples (table 10). Jenkins et al. [4] have shown that the proportion of individuals with Inv (1) in their phenotype among the indigenous southern African populations falls generally within the range 46%–71%; the samples lying below this range

TABLE 10

Inv Phenotype and Allele Frequencies in San and Khoikhoi Populations

Population	No.	Inv (1)		Inv^1	
		No.	%	f	$\pm\sigma$
San:					
Central and Southern*	112	62	55.4	.332	.035
!Ko mainly†	72	37	51.4	.303	.042
!Kung:					
Northern	103	62	60.2	.369	.038
Ngami	156	97	62.2	.385	.031
Dobe	394	253	64.2	.402	.020
/ai/ai	62	35	56.5	.340	.048
/du/da	100	60	60.0	.367	.039
Tsumkwe	198	136	68.7	.440	.029
Kaukau	263	150	57.0	.345	.023
Naron	140	82	58.6	.356	.032
Khoikhoi:					
Kuiseb‡	57	17	29.8	.162	.036
Keetmanshoop	150	90	60.0	.367	.032
Sesfontein	42	25	59.5	.364	.059

Note.—All samples were tested for Inv (1) only.
* From [3].
† From [4].
‡ From [9].

(one of them the Kuiseb Khoikhoi sample [9]) included either a number of family groups or had been subjected to appreciable Caucasoid admixture. The Inv (1) frequency among the new populations included in this study fall within a range of 51%–69%. These data would be of relevance in genetic comparisons between peoples mainly when they are included with a number of other loci; they would tend to contribute to a reduction in the contrasts between Khoisan and Negro peoples, and, like the frequencies of $Gm^{1,\ 5,\ 13,\ 14}$, to suggest the existence in the past of a characteristically "African" genetic profile.

SUMMARY

The Gm and Inv types were determined for eight San (Bushman) populations, two Khoikhoi (Hottentot) populations, one Coloured population, 112 San families in which the genotypes of the parents could be unambiguously determined, and for 65 San families in which the genotype of one or both parents could not be determined with certainty.

The population and family data establish that the haplotype array of the San is composed of $Gm^{1,\ 21}$, $Gm^{1,\ 13}$, $Gm^{1,\ 5,\ 13,\ 14}$, and $Gm^{1,\ 5,\ 13,\ 14,\ 21}$; $Gm^{1,\ 5,\ 6}$ and $Gm^{1,\ 5,\ 6,\ 14}$ are also present but may have been acquired through admixture with Negroes. The $Gm^{1,\ 5,\ 13,\ 14,\ 21}$ haplotype has not been found to be polymorphic in any other population.

The haplotype array of the Khoikhoi is composed of $Gm^{1,\ 2,\ 21}$, $Gm^{1,\ 13}$, and $Gm^{1,\ 5,\ 13,\ 14}$; $Gm^{1,\ 5,\ 6}$ and $Gm^{1,\ 5,\ 6,\ 14}$ are also present but, as in the case of the San, may be due to admixture.

The San and Khoikhoi differ from each other in that the former have the $Gm^{1,\ 21}$ and $Gm^{1,\ 5,\ 13,\ 14,\ 21}$ haplotypes not present in the latter, and the Khoikhoi have the $Gm^{1,\ 2,\ 21}$ haplotype not present in the San. These three haplotypes and $Gm^{1,\ 13}$ serve to distinguish the Khoisan people from other African peoples.

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