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Distributions of Genetic Markers in United States Populations: III. Serum Group Systems and Hemoglobin Variants

REFERENCE: Gaensslen, R. E., Bell, S. C., and Lee, H. C., **"Distributions of Genetic Markers in United States Populations: III. Serum Group Systems and Hemoglobin Variants,"** *Journal of Forensic Sciences*, JFSCA, Vol. 32, No. 6, Nov. 1987, pp. 1754–1774.

ABSTRACT: All published and unpublished population frequency data that could be located for U.S. populations are tabulated and presented for the serum group systems haptoglobin (α-chain), group specific component, and transferrin and for the common β-chain variants of hemoglobin. Results obtained by combining data for comparable racial/ethnic groups are also presented. Some evidence is presented to indicate that the results obtained from the combined data may give better information on frequencies for the U.S. population at large than is obtainable from studies conducted in restricted geographic areas.

KEYWORDS: forensic sciences, genetic typing, demography, population genetics, United States populations, genetic markers, genotypic frequencies, phenotypic frequencies, isoenzyme systems, human serum protein polymorphism, haptoglobin system, group specific component system, vitamin D binding protein, transferrin system, hemoglobin β-chain variants

The growth and development in forensic serology in the past 25 years has revealed a substantial number of genetic marker systems from which routine parentage testing protocols may be constructed [*1–3*] and for the partial individualization of blood and physiological fluid stains [*4–10*]. Interpretation of the significance of typing results in criminalistics applications and calculations of the probability of paternity in nonexclusion parentage cases both require knowledge of genotypic and phenotypic frequencies in applicable populations.

Thousands of frequency studies on various genetic marker systems have been carried out on many populations throughout the world, the most complete compilation of them being the extraordinary work by Mourant et al. [*11*]. World population data on the haptoglobin (HP) and group specific component (GC) systems were compiled and summarized in 1969 [*12*]. The most complete compilation of population studies on hemoglobin variants was published by Livingstone in 1967 [*13*]. Genetic marker frequency data from the many different

Various aspects of this work were presented in part at the 8th Annual Meeting of the Northeastern Association of Forensic Scientists, Albany, NY, 1982; the 35th Annual Meeting of the American Academy of Forensic Sciences, Cincinnati, OH, 15–19 Feb. 1983; and the International Symposium on Forensic Applications of Electrophoresis, FBI Academy, Quantico, VA, 1984. Received for publication 5 Jan. 1987; accepted for publication 11 Feb. 1987.

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studies of U.S. populations, however, have not to our knowledge been thoroughly compiled. In this paper, we summarize all the published and some unpublished population frequency data that could be located for U.S. populations for the three serum group systems haptoglobin (HP), group specific component (vitamin D binding protein; GC), and transferrin (TF), and for the common β-chain variants of hemoglobin (HBB), along with some results obtained by combining data from different studies. This paper along with two previous companion ones [*14,15*] provides a summary and analysis of U.S. population data for 22 genetic marker systems.

Methods

The conventions used in presenting the tabular data as well as the methods used in combining comparable data from different population studies were fully described previously [*14,15*]. Briefly, within the separate tables, each representing a different system, data are tabulated separately for Caucasian, Negro, Hispanic, Asian, or other populations. Each population studied is identified by location (two-letter abbreviations are used for states) and by a description of the blood donors if provided. A reference is given for each study. References to population studies are given a "T" (for "Table") prefix in the tables and are separately compiled at the end of the paper. Data for each phenotype within each system are reported using an *NNN*(%.%) format, where *NNN* represents the number of individuals who possessed the phenotype and %.% represents the percentage rounded to one decimal place. The total number of people studied is also given, and is not always the sum of the major phenotypes because rare phenotypes were observed. The notes in each table provide data for subtypes, rarer types, unusual or descriptive features of a population, or explanations about the calculations. Data from GC*1 and TF*C subtype studies were used to compute "electrophoretic" GC and TF phenotype frequencies in cases where this was not done in the original paper.

Two calculations were used to combine all the data for a particular racial/ethnic class within a genetic marker system, where a sufficient number of different studies were available for comparatively similar groups within that class.

The first sums the numbers of individuals for all data sets showing numbers, and a percentage value for each phenotype is computed from the resulting totals, yielding what is referred to as the "numerical total." The second weights the percentage distributions (proportions) for each phenotype according to the number of individuals typed and yields what is referred to as the "weighted mean of proportions," or "WMP." A weighted standard deviation of proportions (WSDP) was also calculated for each WMP. Details were given in the previous papers [*14,15*]. Data reported in numbers of individuals were used to calculate proportions. No attempt was made to calculate numbers of individuals from data reported in percentage distributions. Hence, all data are used in computing WMP, whereas only data reported in numbers of individuals are included in the numerical total.

All available data were included in the tables for completeness, but a data set was not used in the calculations in cases where data were incomplete or authors provided only a gene frequency result.

Gene frequencies were calculated by gene counting for data sets in which there was sufficient information to enable the calculation. In HP system data, 2−1, 2−1M, and 0 types are shown separately for those studies in which they were so reported. The 2−1 and 2−1M types were combined and the HP 0 excluded from consideration, however, for calculation of gene frequencies. No separate *HPA*2M* frequency was calculated in these studies. The HP 0 phenotype individuals were excluded from gene frequency calculations because the genetic basis of HP 0 is not very clear. Individuals who are HP 0 are often *HPA*2M/HPA*2M*, *HPA*2M/HPA*1*, or *HPA*2M/HPA*2*, but can possess *HPA*2/HPA*1* or *HPA*2/HPA*2* genotypes as well [*16,17*]. In TF system data, variant TF*B and TF*D types ob-

served are given in the notes. TF*B and TF*D types were combined for gene frequency calculations, however.

A chi-square value was calculated for every data set for which gene frequencies could be meaningfully calculated and for the corresponding numerical totals. In Tables 1 and 2, data sets having χ^2 values corresponding to $0.01 < P < 0.05$ or $P < 0.01$ are indicated. Interpretation of chi-square values calculated for TF and HB data are complicated by the small numbers and correspondingly low gene frequencies of variants. In a number of cases, the number of phenotypic classes is the same as the number of genes whose frequencies are being estimated. In a significant number of cases, it was clear that the χ^2 values obtained were not providing meaningful indications of goodness of fit. Accordingly, gene frequencies for *TF* and *HBB* genes are reported as calculated. In the hemoglobin system, rarer phenotypes involving genes being estimated, such as HBB SC, were counted in computing gene frequencies.

The gene, genotypic, and phenotypic nomenclature rules suggested by Shows et al. [*18*] have been followed for all the systems. Using these rules, hemoglobin variant genes are designated according to the chain in which the substitution occurs, the position number in that chain, and the variant amino acid using one letter abbreviations. The HB sickle gene, for example, is designated *HBB*6V,* indicating that this gene gives rise to a valine substitution at Position 6 in the β chain. Similarly, the HB *C* and HB *D* genes are designated *HBB*6K* and *HBB*121Q,* respectively. The nomenclature of variant GC genes and phenotypes follows Constans and Cleve [*19*].

Most computations were carried out on a Data General MV 8000 mainframe computer with programs written in FORTRAN.

Results and Discussion

Table 1 gives phenotypic and genotypic frequencies for the HP system. HP 2−1M and HP 0 types are seen in significant frequencies only in the Negro populations. The majority of the data sets including the numerical totals show good fit to Hardy Weinberg expectations on the basis of chi-square computations.

Table 2 gives the data for the GC system. As with the HP data, most of the studies exhibit goodness of fit to expectation. Table 3 gives data for the TF system. TF BC occurs more commonly in Caucasians than in Negroes, while TF CD is seen in some 5% of Negroes but is uncommon in Caucasians. A variant of *TF*D, TF*D-CHI,* appears at about the same frequency in Chinese as does TF*D in Negroes. Isoelectric focusing is becoming the method of choice for GC and TF typing, so as to be able to discriminate GC*1 and TF*C subtypes. The results of a few subtyping studies are given in Tables 2 and 3, respectively. Additional data on these subtypes in U.S. populations would be highly desirable, and will doubtless be forthcoming from future surveys.

Table 4 gives the phenotypic proportions for relatively common hemoglobin β-chain variants, and Table 5 provides gene frequencies for those data for which meaningful calculations could be carried out. Although common hemoglobin variants have been employed as genetic markers in some laboratories using electrophoresis for many years [*20–24*], sometimes in conjunction with another established system [*25*], the application of isoelectric focusing procedures to their separation and identification is growing and may offer advantages in resolution [*26–28*].

It may be useful in certain circumstances to have frequency estimates for larger and presumably better randomized samples of the population at large than would result from local population studies, as we have discussed elsewhere [*29,30*]. Computation of WMP for systems in which a number of different studies have been done and in which fairly large numbers of people have been typed provides a possible approach to obtaining such an estimate. Populations are defined by the size of the effective interbreeding gene pool rather than by

TABLE 1—*Genotypic and phenotypic frequencies of haptoglobin α-chain (HPA) types in U.S. populations.*

Population	Total	Frequency—Number (Percent)					Gene Frequency, *HPA*1*	Note[a]	Reference
		1	2−1	2−1M	2	0			
				CAUCASIAN					
Ann Arbor, MI	68	9(13.2)	40(58.8)	...	19(27.9)	...	0.4265	...	*T1*
Michigan and Illinois	161	23(14.3)	77(47.8)	...	61(37.9)	...	0.3820	...	*T2*
Seattle, WA	409	54(13.2)	206(50.4)	...	149(36.4)	...	0.3839	1	*T3*
Southeastern GA	145	27(18.6)	64(44.1)	...	52(35.9)	2(1.4)	0.4126	...	*T4*
Maryland	192	24(12.5)	85(44.3)	...	83(43.2)	...	0.3464	...	*T5*
Chicago, IL	101	18(17.8)	51(50.5)	...	32(31.7)	...	0.4307	...	*T6*
Tecumseh, MI	7 655	1307(17.1)	3734(48.8)	11(0.1)	2575(33.6)	22(0.3)	0.4165	2	*T7*
Orange County, CA	185	(16.0)	(48.0)	...	(36.0)	...	...	3,4	*T8*
Bexar County, TX	200	(17.0)	(50.0)	...	(30.0)	...	...	3	*T9*
Pittsburgh and Allegheny County, PA	1 263	185(14.6)	555(43.9)	26(2.1)	495(39.2)	2(0.2)	0.3771	...	*T10*
California	274	(14.6)	(49.3)	...	(36.1)	...	...	3	*T11*
Philadelphia, PA, including part of NJ	212	33(15.6)	104(49.1)	...	75(35.4)	...	0.4009	5	*T12*
Detroit, MI	502	69(13.7)	213(42.4)	...	220(43.8)	...	0.3496	6	*T13*
Miami/Dade County, FL	366	58(15.8)	161(44.0)	...	141(38.5)	6(1.6)	0.3847	6	*T15*
Los Angeles, CA	311	62(19.9)	149(47.9)	...	100(32.2)	...	0.4389	6	*T16*
CA, TX, HI, and Mexico City	860	154(17.9)	418(48.6)	...	288(33.5)	...	0.4221	...	*T17*
U.S. national sample	5 735	(16.2)	(46.8)	...	(32.8)	...	...	3,7	*T18*
Los Angeles County, CA	393	63(16.0)	196(49.9)	...	134(34.1)	...	0.4097	...	*T19*
North Carolina	395	64(16.2)	199(50.4)	...	132(33.4)	...	0.4139	...	*T20*
				TOTAL CAUCASIAN					
Numerical total	13 033	2150(16.5)	6252(48.0)	37(0.3)	4556(35.0)	32(0.2)	0.4072	...	...
WMP	...	16.4	47.7	0.2	34.3	0.2	...	...	...
WSDP	...	1.194	1.953	0.497	2.580	0.268	...	...	...
				NEGRO					
Seattle, WA	406	(26.4)	(38.2)	(9.8)	(21.4)	(4.2)	...	3	*T21*
Ann Arbor, MI	48	17(35.4)	17(35.4)	...	9(18.7)	5(10.4)	0.5930	...	*T1*
Seattle, WA, and Cleveland, OH	178	45(25.3)	70(39.3)	27(15.2)	31(17.4)	5(2.8)	0.5405	...	*T22*

TABLE 1—*(Continued).*

Population	Total	Frequency—Number (Percent) 1	2−1	2−1M	2	0	Gene Frequency, *HPA*1*	Note[a]	Reference
New York, NY	100	(40.0)	(39.0)	...	(21.1)	...	....	3	*T23*
Seattle, WA	1 657	472(28.5)	641(38.7)	181(10.9)	307(18.5)	56(3.4)	0.5515	8	*T3*
Southeastern GA	167	48(28.7)	61(36.5)	13(7.8)	42(25.1)	3(1.8)	0.5183	...	*T4*
Chicago, IL	101	30(29.7)	47(46.5)	...	24(23.8)	...	0.5297	...	*T6*
Bexar County, TX	200	(35.0)	(49.0)	...	(17.0)	...	...	3	*T9*
Pittsburgh and Allegheny County, PA	721	206(28.6)	293(40.6)	66(9.2)	148(20.5)	8(1.1)	0.5407	...	*T10*
California	124	(33.9)	(41.9)	...	(21.0)	...	...	3,9	*T11*
Philadelphia, PA, including part of NJ	164	56(34.1)	73(44.5)	...	32(19.5)	3(1.8)	0.5745	5	*T12*
Detroit, MI	504	142(28.2)	204(40.5)	59(11.7)	84(16.7)	11(2.2)	0.5548	6,10[b]	*T13*
Miami/Dade County, FL	346	120(34.7)	164(47.4)	...	40(11.6)	22(6.4)	0.6235	6	*T15*
Los Angeles, CA	130	47(36.2)	58(44.6)	...	25(19.2)	...	0.5846	6	*T16*
CA, TX, HI, and Mexico City	463	134(29.2)	236(51.0)	...	89(19.2)	...	0.5464	11	*T17*
U.S. national sample	999	(32.2)	(39.4)	...	(13.3)	...	...	3,12	*T18*
Los Angeles County, CA	153	51(33.3)	77(50.3)	...	25(16.3)	...	0.5850	...	*T19*
North Carolina	317	91(28.7)	142(44.8)	16(5.0)	68(21.5)	...	0.5363	...	*T20*
TOTAL NEGRO									
Numerical total	4 949	1460(29.5)	2083(42.1)	362(7.3)	924(18.7)	113(2.3)	0.5547	...	...
WMP	...	30.1	41.6	5.9	18.1	1.9	...	...	...
WSDP	...	2.910	4.134	5.255	3.138	1.963	...	...	...
HISPANIC									
Bexar County, TX	200	(25.0)	(51.0)	...	(24.0)	...	...	3	*T9*
California	161	(21.7)	(55.9)	...	(22.4)	...	...	3,13	*T11*
Miami/Dade County, FL	360	75(20.8)	179(49.7)	...	97(26.9)	9(2.5)	0.4687	6	*T15*
Los Angeles, CA	145	43(29.7)	67(46.2)	...	35(24.1)	...	0.5276	6	*T16*
CA, TX, HI, and Mexico City	775	218(28.1)	393(50.7)	...	163(21.0)	...	0.5348	14,15	*T17*
Los Angeles County, CA	226	64(28.3)	103(45.6)	...	59(26.1)	...	0.5111	...	*T19*

				TOTAL HISPANIC					
Numerical total	1 506	400(26.6)	742(49.3)	...	354(23.5)	9(0.6)	0.5150	...	...
WMP	...	26.0	50.0	...	23.5	0.5	...	...	...
WSDP	...	3.228	2.612	...	2.408	0.986	...	...	...
				ORIENTAL AND ASIAN					
U.S. Japanese	23	2(8.7)	10(43.5)	...	11(47.8)	...	...	...	*T23*
New York, NY, Chinese	118	(14.7)	(38.3)	...	(47.0)	(0.03)	...	3	*T24*
Seattle, WA, Oriental	494	34(6.9)	190(38.5)	...	270(54.7)	...	0.2611	16	*T3*
New York, NY, Chinese	113	16(14.2)	45(39.8)	...	52(46.0)	...	0.3407	17	*T25*
California and Hawaii Asian	376	(7.7)	(37.8)	...	(53.5)	...	...	3,18	*T11*
CA, TX, HI, and Mexico City Asian	1 105	148(13.4)	444(40.2)	...	512(46.3)	...	0.3348	19	*T17*
Los Angeles County, CA, Asian	12	2(16.7)	1(8.3)	...	9(75.0)	...	...	...	*T19*

[a]NOTES:

1. HPA*1 subtypes determined for 66 Type 1 and 2−1; there were 4(6.1) 1S−1, 5(7.6) 1S−1F, 36(54.5) 2−1S, and 21(31.8) 2−1F.
2. Four were HP Ca and two were HP Johnson.
3. Distributions given in percentages; data not used in calculating numerical totals.
4. Approximately 15% of the population was Hispanic on the basis of surname.
5. Identical twin study; data for one member of each twin pair tabulated and used in calculations.
6. And see Shaler (Ref *T14*).
7. 1.9% were "other."
8. HPA*1 subtypes determined for 222 type 1 and 2−1; there were 26(11.7) 1S−1S, 20(9.0) 1F−1F, 49(22.1) 1S−1F, 61(27.5) 2−1S, 55(24.8) 2−1F, 6(2.7) 2M−1S, and 5(2.3) 2M−1F.
9. 3.2% were "rare."
10. Four were "rare."
11. Three were "rare."
12. 12.1% were "other."
13. "Chicano/Amerindian."
14. One was "rare."
15. Primarily "Mexican."
16. HPA*1 subtypes determined for 80 type 1 and 2−1; there were 14(17.5) 1S−1S, 1(1.3) 1S−1F, 64(80.0) 2−1S, and 1(1.3) 2−1F.
17. HPA*1 subtypes determined; all 16 type 1 were 1S−1S and all 45 type 2−1 were 2−1S.
18. 1.1% were "rare."
19. One was "rare."

[b]$\chi^2 > 3.841$; $0.01 < P < 0.05$.

[c]$\chi^2 > 6.635$; $P < 0.01$.

TABLE 2—*Genotypic and phenotypic frequencies of group specific component (GC; vitamin D binding protein) types in U.S. populations.*

Population	Total	Frequency—Number (Percent) 1	2−1	2	Gene Frequency *GC*1*	Note[a]	Reference
			CAUCASIAN				
New York, NY	122	...	...	...	0.7172	1	*T26*
New York, NY	86	48(55.8)	32(37.2)	6(7.0)	0.7442	...	*T27*
Southeastern GA	292	147(50.3)	114(39.0)	31(10.6)	0.6986	...	*T28*
Boston, MA	407	234(57.5)	146(35.9)	27(6.6)	0.7543	...	*T29*
Tecumseh, MI	7 658	3910(51.1)	3139(41.0)	609(8.0)	0.7155	...	*T7*
California	4 488	(50.2)	(41.0)	(8.5)	...	2,3	*T11*
Philadelphia, PA, including part of NJ	201	96(47.8)	93(46.3)	12(6.0)	0.7090	4	*T12*
Detroit, MI	503	242(48.1)	213(42.3)	48(9.5)	0.6928	5	*T13*
Miami/Dade County, FL	365	168(46.0)	160(43.8)	37(10.1)	0.6795	5	*T15*
Los Angeles, CA	109	59(54.1)	47(43.1)	3(2.8)	0.7569	5	*T16*
Southeastern PA	110	59(53.6)	40(36.4)	11(10.0)	0.7182	6	*T30*
CA, TX, HI, and Mexico City	1 050	537(51.1)	429(40.9)	74(7.0)	0.7157	7	*T17*
U.S. national sample	5 735	(51.9)	(38.5)	(7.4)	...	2	*T18*
Los Angeles County, CA	183	99(54.1)	78(42.6)	6(3.3)	0.7541	[b]	*T19*
Minnesota	7 247	3742(51.6)	2963(40.9)	542(7.5)	0.7208	8	*T31*
Southeastern MO	372	(55.1)	(39.3)	(5.7)	...	2	*T32*
			TOTAL CAUCASIAN				
Numerical total	18 211	9341(51.3)	7454(40.9)	1406(7.7)	0.7176	...	...
WMP	...	51.3	40.4	7.8	...	...	...
WSDP	...	1.350	1.365	0.841	...	...	...
			NEGRO				
New York, NY	144	...	...	...	0.8924	1	*T26*
New York, NY	120	98(81.7)	19(15.8)	3(2.5)	0.8958	...	*T27*
Southeastern GA	231	192(83.1)	38(16.5)	1(0.4)	0.9134	...	*T28*
California	832	(74.5)	(21.0)	(2.0)	...	2,9	*T11*
Philadelphia, PA, including part of NJ	159	122(76.7)	33(20.8)	4(2.5)	0.8711	4	*T12*

Detroit, MI	504	366(72.6)	112(22.2)	4(0.8)	0.8562	5,10[c]	*T13*
Miami/Dade County, FL	339	263(77.6)	64(18.9)	6(1.8)	0.8702	5,11	*T15*
Los Angeles, CA	43	34(79.1)	7(16.3)	2(4.7)	0.8721	5	*T16*
Southeastern GA	219	185(84.5)	26(11.9)	4(1.8)	0.9041	12[b]	*T30*
Philadelphia, PA	273	198(72.5)	61(22.3)	3(1.1)	0.8370	13	*T30*
CA, TX, HI, and Mexico City	867	638(73.6)	183(21.1)	18(2.1)	0.8414	14	*T17*
U.S. national sample	999	(75.5)	(18.6)	(3.0)	...	2	*T18*
Los Angeles County, CA	75	59(78.7)	15(20.0)	1(1.3)	0.8867	...	*T19*
Minnesota	540	403(74.6)	104(19.3)	3(0.6)	0.8426	15	*T31*
Southeastern MO	69	(75.4)	(24.6)	(0.0)	...	2	*T32*
			TOTAL NEGRO				
Numerical total	3 370	2558(75.9)	662(19.6)	49(1.5)	0.8573	...	...
WMP	...	75.6	19.7	1.8	...	...	...
WSDP	...	3.066	2.377	0.891	...	...	...
			HISPANIC				
California	1 417	(59.1)	(35.3)	(5.2)	...	2,16	*T11*
Miami/Dade County, FL	360	207(57.5)	126(35.0)	24(6.7)	0.7500	5,17	*T15*
Los Angeles, CA	102	83(81.4)	17(16.7)	2(2.0)	0.8971	...	*T16*
CA, TX, HI, and Mexico City	1 908	1160(60.8)	655(34.3)	80(4.2)	0.7796	18	*T17*
Los Angeles County, CA	136	87(64.0)	38(27.9)	11(8.1)	0.7794	[b]	*T19*
			TOTAL HISPANIC				
Numerical total	2 506	1537(61.3)	836(33.4)	117(4.7)	0.7801	...	...
WMP	...	60.5	34.1	4.9	...	...	...
WSDP	...	3.650	3.136	1.067	...	...	...
			ASIAN AND ORIENTAL				
New York, NY, Chinese	117	...	...	...	0.7693	1	*T26*
California and Hawaii Asians	3 043	(50.4)	(39.2)	(6.4)	...	2	*T11*
CA, TX, HI, and Mexico City Chinese and Japanese	1 566	780(49.8)	590(37.7)	118(7.5)	0.706	19[c]	*T17*

[a]NOTES:

1. Only gene frequencies and total number of people typed reported.
2. Distributions given in percentages; data not used in calculating numerical totals.

(*footnotes continued*)

3. 0.4% were "rare."
4. Identical twin study; data for one member of each twin pair tabulated and used in calculations.
5. And see Schaler (Ref *T14*).
6. GC*1 subtypes determined; subtypes and rare types: 3(2.7) 1F, 19(17.3) 1F−1S, 37(33.6) 1S, 8(7.3) 2−1F, 32(29.0) 2−1S, and 11(10.0) 2.
7. Ten were "rare."
8. GC*1 subtypes determined: 175(2.4) 1F, 1,266(17.5) 1F−1S, 2,301(31.8) 1S, 633(8.7) 2−1F, 2,330(32.2) 2−1S, and 542(7.5) 2.
9. 2.4% were "rare."
10. 18(3.6) were 1−1A1, 3(0.6) were 2−1A1, and 1 was "rare."
11. 6(1.8) were 1−1A1.
12. GC*1 subtypes determined; subtypes and rarer types: 141(64.4) 1F, 40(18.3) 1F−1S, 4(1.8) 1S, 21(9.6) 2−1F, 5(2.3) 2−1S, 4(1.8) 2, 3(1.4) 1F−1A1, and 1(0.5) 2−1A1.
13. GC*1 subtypes determined; subtypes and rarer types: 130(47.6) 1F, 58(21.2) 1F−1S, 10(3.7) 1S, 51(18.7) 2−1F, 10(3.7) 2−1S, 3(1.1) 2, 6(2.2) 1F−1A1, 3(1.1) 1S−1A1, and 2(0.7) 2−1A1.
14. 28 were "rare."
15. GC*1 subtypes determined; subtypes and rarer types: 244(45.2) 1F, 139(25.7) 1F−1S, 20(3.7) 1S, 89(16.5) 2−1F, 15(2.8) 2−1S, 3(0.6) 2, 7(1.3) 1F−1A1, 4(0.7) 1S−1A1, 2(0.4) 2−1A1, 9(1.7) 1F−1C10, 3(0.6) 1S−1C10, 3(0.6) 2−1C10, 1(0.2) 1A1, and 1(0.2) 1A1−1C10.
16. "Chicano/Amerindian"; 0.5% were "rare."
17. Two were 1−1A1 and 1 was 2−1A1.
18. Primarily "Mexican"; 13 were "rare."
19. Seventy eight were "rare."

[b] $\chi^2 > 3.841$; $0.01 < P < 0.05$.

[c] Original author gene frequency value.

TABLE 3—*Genotypic and phenotypic frequencies of transferrin (TF) types in U.S. populations.*

Population	Total	Frequency—Number (%) C	BC	CD	Gene Frequency *TF*C*	Note[a]	Reference
		CAUCASIAN					
Southeastern GA	107	103(96.3)	1(0.9)	2(1.9)	0.9766	1	*T4*
Southeastern U.S.	2 221	2194(98.8)	17(0.8)	10(0.5)	0.9939	2	*T33*
Chicago, IL	101	101(100.0)	...	...	1.0000	...	*T6*
Tecumseh, MI	7 654	7560(98.8)	83(1.1)	11(0.5)	0.9939	...	*T7*
Philadelphia, PA, including part of NJ	196	193(98.5)	2(1.0)	1(0.5)	0.9924	3	*T12*
CA, TX, HI, and Mexico City	801	786(98.1)	...	...	...	4	*T17*
U.S. national sample	5 735	(96.1)	(1.3)	(0.5)	...	5	*T18*
Philadelphia, PA	149	146(98.0)	2(1.3)	1(0.7)	0.9899	6	*T34*
Minnesota	392	392(100.0)	...	...	1.0000	7	*T35*
Minnesota	947	...	...	...	...	8	*T36, T37*
Baltimore, MD	209	205(89.1)	4(1.9)	...	0.9904	9	*T38*
		TOTAL CAUCASIAN					
Numerical total	4 176	4120(98.7)	26(0.6)	14(0.3)	0.9914	...	...
WMP	...	97.9	1.0	0.3	...	...	...
WSDP	...	1.275	0.349	0.226	...	...	...
		NEGRO					
New York, NY	99	89(89.9)	...	9(9.1)	0.9444	10	*T24*
Southeastern GA	133	120(90.2)	...	13(9.8)	0.9511	...	*T4*
Southeastern U.S.	418	399(95.5)	...	19(4.5)	0.9773	...	*T33*
Chicago, IL	101	93(92.1)	...	8(7.9)	0.9604	...	*T6*
Philadelphia, PA, including part of NJ	164	151(92.1)	...	13(7.9)	0.9604	3	*T12*
CA, TX, HI, and Mexico City	502	467(93.0)	...	...	...	11	*T17*
U.S. national sample	999	(90.8)	(0.2)	(5.8)	...	5	*T18*
Philadelphia, PA	166	151(91.0)	...	15(9.0)	0.9548	12	*T34*
Minnesota	194	182(93.8)	...	12(6.2)	0.9691	13	*T35*
Minnesota	194	...	...	...	...	14	*T36, T37*
Baltimore, MD	183	170(92.9)	1(0.6)	12(6.6)	0.9645	15	*T38*

TABLE 3—*(Continued).*

Population	Total	Frequency—Number (%) C	BC	CD	Gene Frequency *TF*C*	Note[a]	Reference
		TOTAL NEGRO					
Numerical total	1 960	1822(93.0)	1(0.1)	101(5.2)	0.9556	...	...
WMP	...	92.2	0.1	5.4	...	...	...
WSDP	...	1.707	0.147	2.803	...	...	...
		OTHER					
New York, NY—Chinese	116	109(94.0)	...	7(6.0)	0.9698	16	*T24*
CA, TX, HI, and Mexico City—Hispanic	765	742(97.0)	...	...	...	17	*T17*
CA, TX, HI, and Mexico City—Asian	1 295	1259(97.2)	...	...	...	18	*T17*

[a]NOTES:

1. One was B1−2B2; the BC was B2C.
2. Two of the BC were B1C, and 15 were B2C.
3. Identical twin study; data for one member of each twin pair tabulated and used in calculations.
4. Fifteen were "rare."
5. Distributions given in percentages; data not used in calculating numerical totals.
6. TF*C subtypes determined: 99(66.4) C1, 40(26.8) C2C1, 7(4.7) C2, 1(0.7) B2C1, 1(0.7) B2C2, and 1(0.7) C2D2.
7. TF*C subtypes determined: 239(61.0) C1, 107(27.3) C2C1, 9(2.3) C2, 32(8.2) C3C1, 4(1.0) C3C2, and 1(0.3) C3.
8. Only gene frequencies and total number of people typed reported: TF*C1 = 0.775, TF*C2 = 0.163, TF*C3 = 0.056, TF*C6 = 0.001, TF*B2 = 0.004, and TF*B1−2 = 0.001.
9. TF*C subtypes determined: 124(59.3) C1, 59(28.2) C2C1, 8(3.8) C2, 13(6.2) C3C1, 1(0.5) C3C2, 2(1.0) C1B2, 1(0.5) C1B1−2, and 1(0.5) C6B1−2.
10. One D1D1.
11. Thirty five were "rare."
12. TF*C subtypes determined: 115(69.0) C1, 35(21.0) C2C1, 1(0.6) C2, 15(9.0) C1D1.
13. TF*C subtypes determined: 137(70.6) C1, 38(19.6) C2C1, 4(2.1) C2, 3(1.6) C3C1, 11(5.7) C1D1, and 1(0.5) C2D1.
14. Only gene frequencies and total number of people typed reported; TF*C1 = 0.842, TF*C2 = 0.119, TF*C3 = 0.008, TF*C8 = 0.003, TF*D1 = 0.028.
15. TF*C subtypes determined: 134(73.2) C1, 29(15.9) C2C1, 3(1.6) C2, 4(2.2) C3C1, 1(0.5) C1B2, 10(5.5) C1D, 1(0.5) C1D2, and 1(0.5) C2D1.
16. The 7 CD were CD−CHI.
17. Primarily "Mexican"; 23 were "rare."
18. Thirty six were "rare."

TABLE 4—*Phenotypic frequencies of common hemoglobin β-chain (HBB) variant phenotypes in U.S. populations.*

Population	Total	Frequency—Number (Percent)						Note[a]	Reference
		A	AS	S	AD	AC	C		
CAUCASIAN									
Baltimore, MD	500	500(100.0)	...	...	...	...	...	...	*T39*
Ann Arbor, MI	72	72(100.0)	...	...	...	...	...	...	*T40*
Houston, TX	350	350(100.0)	...	...	...	...	...	...	*T41*
Durham, NC	734	732(99.7)	1(0.1)	...	1(0.1)	...	...	...	*T42*
Southern LA Children	140	139(99.3)	1(0.7)	...	...	...	...	...	*T43*
Memphis, TN, Autopsy material	1 250	1 250(100.0)	...	...	...	...	...	...	*T44*
St. Louis, MO, Infants	90	90(100.0)	...	...	...	...	...	...	*T45*
Baltimore, MD, Infants	180	180(100.0)	...	...	...	...	...	...	*T46*
Mississippi	1 045	1 044(99.9)	...	1(0.1)	...	...	...	...	*T47*
California	6 004	(99.8)	(0.2)	...	...	...	...	1	*T11*
Detroit, MI	503	503(100.0)	...	...	...	...	...	2	*T13*
CA, TX, HI, and Mexico City	1 040	1 040(100.0)	...	...	...	...	...	...	*T17*
North Carolina	365	365(100.0)	...	...	...	...	...	...	*T20*
TOTAL CAUCASIAN									
Numerical total	6 197	6 193(99.9)	2(0.03)	1(0.02)	1(0.02)	...	...	...	...
WMP	...	99.9	0.1	0.0	0.0	...	...	...	...
WSDP	...	0.125	0.116	0.027	0.032	...	...	...	...
NEGRO									
Baltimore, MD	500	449(89.8)	36(7.2)	5(1.0)	...	9(1.8)	...	3	*T39*
Ann Arbor, MI	209	(98.6)	...	...	...	(1.4)	...	1	*T40*
St. Louis, MO	1 020	896(87.8)	94(9.2)	...	4(0.4)	26(2.5)	...	...	*T48*
Galveston, TX Patients	1 550	1 369(88.3)	141(9.1)	4(0.3)	...	35(2.3)	1(0.1)	...	*T49*
Houston, TX	400	351(87.7)	36(9.0)	5(1.3)	...	6(1.5)	1(0.3)	3	*T41*
Durham, NC	390	338(86.7)	33(8.5)	1(0.3)	1(0.3)	13(3.3)	...	4	*T42*

TABLE 4—*(Continued).*

Population	Total	Frequency—Number (Percent)						Note[a]	Reference
		A	AS	S	AD	AC	C		
Southern LA									
Children	564	479(84.9)	47(8.3)	18(3.2)	...	10(1.8)	...	5	*T43*
Puerto Rico	602	561(93.2)	29(4.8)	2(0.3)	...	7(1.2)	1(0.2)	6	*T50*
Philadelphia, PA									
Patients	1 000	897(89.7)	74(7.4)	3(0.3)	1(0.1)	23(2.3)	...	6	*T51*
Baltimore, MD	400	...	...	...	4(1.0)	...	...	7	*T52*
Memphis, TN									
Autopsy material	2 800	2 459(87.8)	254(9.1)	19(0.7)	1(0.04)	60(2.1)	...	8	*T44*
Washington, DC									
Tuberculosis patients	310	282(91.0)	28(9.0)	...	...	...	...	...	*T53*
St. Louis, MO									
Infants	449	359(80.0)	47(10.5)	...	2(0.4)	9(2.0)	...	9	*T45*
Washington, DC									
Pregnant women study group	524	490(93.5)	25(4.8)	1(0.2)	...	8(1.5)	...	...	*T54*
Control group	304	283(93.1)	11(3.6)	...	...	10(3.3)	...	...	*T54*
Baltimore, MD									
Infants	900	784(87.1)	67(7.4)	...	...	26(2.9)	...	10	*T46*
Maryland	681	625(91.8)	44(6.5)	...	...	12(1.8)	...	...	*T55*
Southeastern GA	237	214(90.3)	19(8.0)	...	...	4(1.7)	...	...	*T4*
Gainesville, FL									
Pregnant women	944	869(92.1)	65(6.9)	1(0.1)	...	9(1.0)	...	...	*T56*
Mississippi	1 310	1 100(84.0)	114(8.7)	37(2.8)	14(1.1)	38(2.9)	7(0.5)	...	*T47*
Southern LA									
Tuberculosis patients	220	211(95.9)	...	...	...	9(4.1)	...	...	*T57*
Alabama	249 089	220 405(88.5)	21 423(8.6)	574(0.2)	...	6 074(2.4)	102(0.04)	11	*T58*
California	1 025	(89.3)	(8.6)	...	...	(1.8)	...	1,12	*T11*
Philadelphia, PA, including part of NJ	130	118(90.8)	11(8.5)	...	...	1(0.8)	...	13	*T12*
Detroit, MI	504	452(89.7)	37(7.3)	...	...	14(2.8)	...	2,14	*T13*
CA, TX, HI, and Mexico City	792	716(90.4)	54(6.8)	...	...	18(2.3)	...	15	*T17*
				TOTAL NEGRO					
Numerical total	265 220	234 707(88.5)	22 689(8.6)	670(0.3)	23(0.01)	6 421(2.4)	112(0.04)	...	...

WMP	...	88.5	8.5	0.3	0.0	2.4	0.0	...	...
WSDP	...	0.791	0.516	0.240	0.081	0.190	0.037	...	...
				HISPANIC					
Puerto Rico ("white")	1 487	1 486(99.9)	1(0.1)	...	...	...	...	...	*T50*
California	1 596	(99.6)	(0.1)	...	...	(0.2)	...	16	*T11*
CA, TX, HI, and Mexico City	1 569	1 561(99.5)	3(0.2)	...	...	3(0.2)	...	17	*T17*
				TOTAL HISPANIC					
Numerical total	3 056	3 047(99.7)	4(0.1)	...	...	3(0.1)	...	...	...
WMP	...	99.7	0.1	...	...	0.1	...	...	...
WSDP	...	0.177	0.052	...	...	0.091	...	...	...
				ASIAN					
California	3 053	(99.9)	...	...	...	...	...	1,18	*T11*
CA, TX, HI, and Mexico City	1 451	1 448(99.8)	1(0.1)	...	...	...	...	17	*T17*

[a]NOTES:

1. Distributions given in percentages; data not used in calculating numerical totals.
2. And see Shaler, 1978 (Ref *T14*).
3. One was HBB SC.
4. Four were "other."
5. Ten were HBB SC.
6. Two were HBB SC.
7. An unspecified number of HBB AS were further tested to distinguish HBB AD; data not used in calculations.
8. Four were HBB SC; 3 were "other."
9. Thirty two were "other."
10. Twenty three were "other."
11. Of the HBB S, 149 were HBB*S/HBB*TH and 73 were HBB*S/HBB*High F; 329 were HBB SC, 11 were HBB S/Other, 7 were HBB C/Other, and 164 were rarer variants.
12. 0.4% were "rare."
13. Identical twin study; data for one member of each twin pair tabulated and used in calculations.
14. One was "rare."
15. Four were "rare."
16. Chicano/Amerindian; 0.1% were "rare."
17. Two were "rare."
18. 0.1% were "rare."

TABLE 5—*Gene frequencies for common hemoglobin β-chain (HBB) variant genes in U.S. populations.*

Population	Total Number Typed	Gene Frequencies				Reference to Population Study
		*HBB*A*	*HBB*6V*	*HBB*6K*	*HBB*121Q*	
		CAUCASIAN				
Baltimore, MD	500	1.0000	...	...	...	*T39*
Houston, TX	350	1.0000	...	...	...	*T41*
Durham, NC	734	0.9986	0.0007	...	0.0007	*T42*
Southern LA						
Children	140	0.9964	0.0036	...	...	*T43*
Memphis, TN						
Autopsy material	1 250	1.0000	...	...	...	*T44*
St. Louis, MO						
Infants	90	1.0000	...	...	...	*T45*
Baltimore, MD						
Infants	180	1.0000	...	...	...	*T46*
Mississippi	1 045	0.9995	0.0005	...	...	*T47*
Detroit, MI	503	1.0000	...	...	...	*T13*
CA, TX, HI, and Mexico City	1 040	1.0000	...	...	...	*T17*
North Carolina	365	1.0000	...	...	...	*T20*
Total Caucasian	6 197	0.9996	0.0003	...	0.0001	...
		NEGRO				
Baltimore, MD	500	0.9430	0.0460	0.0090	...	*T39*
St. Louis, MO	1 020	0.9392	0.0461	0.0128	0.0020	*T48*
Galveston, TX						
Patients	1 550	0.9450	0.0481	0.0119	...	*T49*
Houston, TX	400	0.9300	0.0575	0.0100	...	*T41*
Durham, NC	390	0.9269	0.0449	0.0167	0.0013	*T42*
Southern LA						
Children	564	0.8998	0.0825	0.0177	...	*T43*
Puerto Rico	602	0.9618	0.0291	0.0091	...	*T50*
Philadelphia, PA						
Patients	1 000	0.9455	0.0400	0.0110	0.0005	*T51*
Memphis, TN						
Autopsy material	2 800	0.9345	0.0529	0.0114	0.0002	*T44*
Washington, DC						
Tuberculosis patients	310	0.9548	0.0452	...	...	*T53*
St. Louis, MO						
Infants	449	0.8641	0.0523	0.0100	0.0022	*T45*
Washington, DC						
Pregnant women study group	524	0.9666	0.0258	0.0076	...	*T54*
Control group	304	0.9655	0.0181	0.0165	...	*T54*
Baltimore, MD						
Infants	900	0.9228	0.0372	0.0144	...	*T46*
Maryland	681	0.9589	0.0323	0.0088	...	*T55*
Southeastern GA	237	0.9515	0.0401	0.0084	...	*T4*
Gainesville, FL						
Pregnant women	944	0.9598	0.0355	0.0048	...	*T56*
Mississippi	1 310	0.9031	0.0718	0.0199	0.0053	*T47*
Southern LA						
Tuberculosis patients	220	0.9796	...	0.0205	...	*T57*
Alabama	249 089	0.9400	0.0457	0.0133	...	*T58*
Philadelphia, PA						
including part of NJ	130	0.9539	0.0423	0.0039	...	*T12*
Detroit, MI	504	0.9474	0.0367	0.0139	...	*T13*
CA, TX, HI, and Mexico City	792	0.9495	0.0341	0.0114	...	*T17*
Total Negro	265 220	0.9399	0.0453	0.0125	0.00004	...

TABLE 5—*(Continued).*

Population	Total Number Typed	Gene Frequencies				Reference to Population Study
		*HBB*A*	*HBB*6V*	*HBB*6K*	*HBB*121Q*	
		HISPANIC				
Puerto Rico ("white")	1 487	0.9997	0.0003	...	...	*T50*
CA, TX, HI, and Mexico City	1 569	0.9968	0.0010	0.0010	...	*T17*
		ASIAN				
CA, TX, HI, and Mexico City	1 451	0.9983	0.0003	...	...	*T17*

geographical boundaries, especially in a country like the United States where mobility is very high. In a previous paper [*14*], we compared the phenotypic proportions for the ABO, Rh, and Secretor systems obtained in a recent study of a relatively large, completely ascertained, randomly selected countrywide population of Caucasian and Negro teenagers [*T18*] with the corresponding WMP values from our calculations. The results suggested that the WMP values compared favorably with the values obtained in the U.S. study. Table 6 gives a similar comparison of WMP values (with the data from the U.S. study omitted from the computation) with the U.S. data for the HP, GC, and TF systems. If the U.S. data are regarded as "expected" and the WMP data as "observed" in a chi-square goodness of fit test, the corresponding P exceeds 0.05 in every case. The greatest χ^2 value was obtained for Negro populations in the HP system. A major reason for this result is that the U.S. study did not report HP 2−1M and HP 0 proportions separately. A significant fraction of the 12.1% "other" types in this population would be expected to be HP 2−1M or HP 0. The comparison given in

TABLE 6—*Comparison of WMP and U.S. phenotypic frequency values[a] for the HP, GC, and TF systems.*

System	Phenotype	Proportion, %			
		Caucasian		Negro	
		U.S.	WMP	U.S.	WMP
HP	1	16.2	16.5	32.2	29.7
	2−1	46.8	48.3	39.4	48.8
	2	32.8	34.9	13.3	18.9
	0	[b]	0.2	[b]	2.3
		$\chi^2 = 0.1880$		$\chi^2 = 4.7946$	
GC	1	51.9	51.1	75.5	75.6
	2−1	38.5	40.9	18.6	20.0
	2	7.4	7.8	3.0	1.5
		$\chi^2 = 0.1836$		$\chi^2 = 0.8555$	
TF	C	96.1	98.7	90.8	93.0
	CB	1.3	0.9	0.2	0.1
	CD	0.5	0.2	5.8	5.2
		$\chi^2 = 0.3734$		$\chi^2 = 0.1654$	

[a]Ref *T18*.
[b]1.9% Caucasian and 12.1% Negro reported as "other."

Table 6 and the previous similar one involving the blood groups [*14*] suggest that the WMP value may provide a reasonably good estimate of the phenotypic proportions based upon the population data which have been gathered.

Acknowledgments

We thank the following for kindly sharing the results of their unpublished population studies for inclusion in the data presented: W. C. Stuver of the Miami/Dade County Metro Police Department Crime Laboratory, Gary Siglar of the Los Angeles Police Department Crime Laboratory, Barry A. J. Fischer of the Los Angeles County Sheriff's Department Criminalistics Laboratory, and Dr. R. C. Briner of the Southeast Missouri Regional Crime Laboratory. In addition, we thank Holly Hammond, now of the Houston Police Department Crime Laboratory, and Matthew Abbott, now of the Maryland State Police Laboratory, for their assistance in modifying programs and management of the extensive data files.

Special Acknowledgments

We take particular pleasure in thanking Dr. Peter Shenkin, Department of Mathematics, John Jay College of Criminal Justice of the City University of New York, and Dr. James Uebelacker, Department of Mathematics, University of New Haven, for their many helpful discussions and suggestions.

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