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PGM_1 Subtype Polymorphism in 14 Endogamous Dravidian-Speaking Populations of South India

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ABSTRACT Red cell hemolysates from 1,004 persons belonging to 14 population groups drawn from four South Indian states, Andhra Pradesh, Tamil Nadu, Karnataka, and Kerala, were tested for PGM_1 subtypes. The groups are characterized by a high frequency of phenotype 1+1+ (range 36.98–71.64%) and the allele 1+ (range 60–79%). The groups exhibit marked heterogeneity for PGM_1 locus. The results show a clear demarcation between tribes and Brahmin groups.

The enzyme phosphoglucomutase (E.C. 2.7.5.1) occurs in all human tissues and is controlled by three unlinked autosomal loci designated PGM_1, PGM_2, and PGM_3. A polymorphism within the PGM locus 1 of human red cells, with two common alleles, PGM_1^1 and PGM_1^2, was first demonstrated by Spencer et al. (1964). Bark et al. (1976) and Kuhnl et al. (1978), using isoelectric focusing in acrylamide, demonstrated ten common phenotypes and reported the existence of four common alleles instead of two on the PGM_1 locus. The subsequent works of Sutton and Burgess (1978), Welch et al. (1978), and Kuhnl and Spielmann (1977) confirmed the four allele hypothesis.

Rather limited data are available to date on PGM locus 1 subtyping among the Indian populations; altogether 17 populations, three from Himachal Pradesh (Papiha et al., 1981), three from Orissa (Reddy et al., 1982; Papiha, 1983), one from Bihar (Das et al., 1983), eight from West Bengal (Mukherjee et al., 1982), and two from Maharashtra (Reddy, unpublished data) have been studied so far. It is noteworthy that data on South Indian populations are conspicuous by their absence.

The purpose of this paper therefore is to report, for the first time, the distribution of the four common alleles of PGM_1 among the 14 population groups of four South Indian states, namely, Andhra Pradesh, Karnataka, Kerala, and Tamil Nadu.

MATERIALS AND METHODS

As part of the ongoing joint Indo-Soviet collaborative anthropogenetic project, during January through March, 1983, blood samples were collected from 1,004 individuals belonging to 14 endogamous populations spread over the four Dravidian-speaking South Indian states, namely, Andhra Pradesh, Karnataka, Kerala, and Tamil Nadu. The names of the populations investigated together with sample sizes are given in Table 1 and their approximate geographical locations are shown in Figure 1.

The caste system is a unique social institution in India, which, in origin, was based mainly on specialized social and occupational functions. Today, each caste and subcaste behaves as an endogamous community. The scheduled castes referred to here are the endogamous Hindu communities who do not belong to the traditional caste hierarchy and have been declared as "scheduled caste" for administrative purpose by the Government of India.

The three populations investigated from Andhra Pradesh include the Vaidic Brahmin, a priestly caste; the Vysya, a trader caste; and the Kamma, an agriculturist caste. These three groups belong to the Tenali Taluk of Guntur district. In Tamil Nadu, the castes studied were the Chettiar, a trader group from Thirupattur taluk of Ramnad district, and the two scheduled castes, Pariah and Kallan, who were from Trimangalam and Usliampattam Talukas of Madurai and Ramnathpuram districts, respectively. From Karnataka, four populations were studied,

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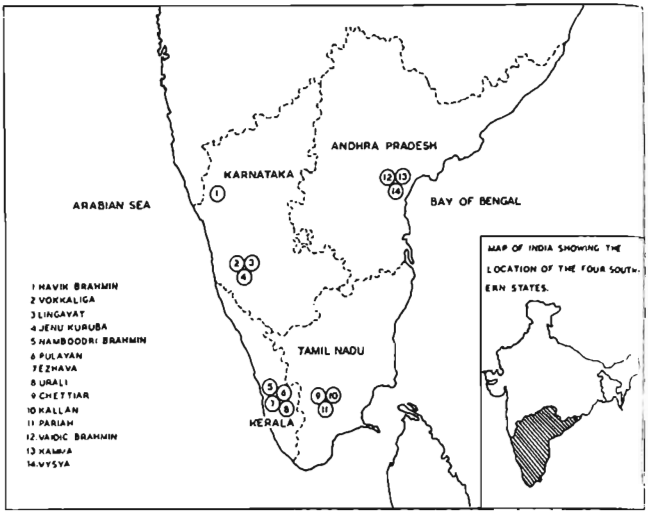

Fig. 1. Locations of the populations studied.

namely, a horticulturist caste of Sirsi taluk of the North Kanara district called the Havik Brahmin; a Saivite religious population, the Lingayat; an agricultural population, the Vokkaliga; and a tribe, the Jenu Kuruba. The latter three populations were sampled from Mysore and Hunsur districts. The four populations investigated from Kerala were a priestly group, the Namboodri Brahmin; an agricultural caste, the Ezhavas; a scheduled caste, the Pulayan from Kottayam district; and the Urali tribe from Idukki district. The ethnographic evidence shows that all the Brahmin and non-Brahmin castes are recent immigrants in this region with variable antiquity (Hutton, 1951), whereas the tribes are the autochthones of the area (Sarkar, 1954).

The practice of consanguineous marriages is prevalent in South India among most of these communities, and it ranges between 12.7% and 63.7% (Roychoudhury, 1979). The castes and tribes under study do practice consanguineous marriages, mostly either maternal uncle-niece or maternal cross-cousin types.

Blood samples were airlifted to Calcutta, and the PGM_1 subtyping was performed in the Anthropometry and Human Genetics Unit of the Indian Statistical Institute, according to the modified IEF method of Reddy et al. (1982), using LKG 2117 Multiphore apparatus as follows. A thin-layer (1 mm) polyacrylamide gel plate was prepared using 7 ml stock solution of 19.4% acrylamide and 0.6% bisacrylamide and adding to it 0.4 ml of pH 4–6 and 1.5 ml of pH 5–7 pharmalytes (Pharmacia Fine Chemicals, Uppsalla, Sweden), 17 ml distilled water, 0.08 ml TEMED, and 0.7 ml ammoniumpersulphate solution (1.2%). The anodal and cathodal electrode solutions were 1 M H_3PO_4 and 1 M NaOH, respectively. The gels were prefocussed at 480 V for 45 min, and the hemolysate samples were soaked in 5 × 6-mm filter paper strips and applied on the gel at a distance of 2 cm from the anode. For the first 30 min, a current at 800 V was passed through the gel, and then the sample strips were removed and the focusing was again continued with increased power at 1,000 V for 50 min; the current was never beyond 24 MA. Visualization of bands was achieved following the method of Spencer et al. (1964).

RESULTS

Table 1 shows the PGM_1 phenotype frequency results obtained in the 14 endogamous populations of South India. Only eight

TABLE 1. Frequency distribution of PGM_1 Subtypes in 14 South Indian populations

Population	Map. ref. No.	No. test (N)	PGM_1 Subtypes															
			1+		1+1−		1−		1+2+		1+2−		2+		2+2−		2−	
			n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Havik Brahmin	1	78	47	60.26	11	14.10	2	2.56	12	15.38	0	0.00	4	5.13	2	2.56	0	0.00
Vokkaliga	2	67	48	71.64	3	4.48	0	0.00	8	11.94	0	0.00	5	7.46	3	4.88	0	0.00
Lingayat	3	37	19	51.35	3	8.11	0	0.00	12	32.43	0	0.00	2	5.41	1	2.70	0	0.00
Jenu Kuruba	4	106	51	48.11	4	3.77	1	0.95	39	36.79	0	0.00	5	4.72	4	3.77	2	1.89
Pulayan	5	73	27	36.98	3	4.11	4	5.48	31	42.47	0	0.00	5	6.85	3	4.11	0	0.00
Namboodri Brahmin	6	77	44	57.14	4	5.19	0	0.00	26	33.77	0	0.00	3	3.90	0	0.00	0	0.00
Ezahava	7	48	26	54.16	3	6.25	0	0.00	14	29.17	0	0.00	2	4.17	3	6.25	0	0.00
Urali	8	53	23	43.40	9	16.98	0	0.00	10	18.87	2	3.77	6	11.32	2	3.77	1	1.88
Chettiar	9	58	30	51.72	4	6.89	0	0.00	11	18.96	0	0.00	7	12.06	5	8.62	1	1.72
Kallan	10	62	28	45.16	6	9.68	4	4.65	17	27.42	0	0.00	5	8.06	2	3.22	0	0.00
Pariah	11	96	57	59.32	2	2.08	0	0.00	26	27.08	0	0.00	9	9.38	2	2.08	0	0.00
Vaidic Brahmin	12	100	50	50.00	8	8.00	1	1.00	34	34.00	3	3.00	4	4.00	0	0.00	0	0.00
Kamma	13	67	39	58.21	2	2.99	0	0.00	26	38.80	0	0.00	0	0.00	0	0.00	0	0.00
Vysya	14	82	46	56.10	10	12.20	2	2.44	18	21.95	0	0.00	4	4.88	2	2.44	0	0.00
Totals		1,004	535		72		14		284		5		62		29		4	

common phenotypes were observed in the present series. Not all occurred in every population examined. The types 1−2+ and 1−2− are not found in any of the present populations. The results show that the observed and expected phenotype frequencies are in reasonable agreement for each population. The type 1+1+ predominated in all the groups, ranging between 36.98% and 71.64% in the Pulayan and Vokkaliga, respectively. The next most prevalent types are 2+2+ and 1−1−. Only three groups showed the 2−2− type. Among the heterozygous types, 1+2+ shows the highest frequency in all the population groups, and rare variants of PGM_1 subtype are not found here.

The estimated gene frequencies of the four common alleles are given in Table 2. The allele 1+ is the most common allele in all the groups, ranging between 60% and 79%. The lowest frequency is registered by allele 2−. Among the Namboodri Brahmins of Kerala and Kammas of Andhra Pradesh, it is totally absent. In this context, it is worth mentioning that the frequency of the 1+ allele among the two Brahmin groups is significantly higher than the tribes (Namboodri Brahmin × Urali, $\chi^2_3 = 11.85$; Havik Brahmin × Jenua Kuruba, $\chi^2_3 = 15.26$). The χ^2 homogeneity test based on gene frequencies was performed among the 14 South Indian populations. The total χ^2 value obtained (94.603, d.f. 39) is highly significant, demonstrating the existence of genetic differentiation between the populations for PGM_1 locus.

DISCUSSION

Including the present study, 31 population groups from India, with a total of 2,455 individuals, have been screened for the PGM_1 subtypes. The mean PGM_1 gene frequencies among the Brahmin and non-Brahmin castes and the tribes are presented in Table 3. With respect to 1+ allele, the frequency is highest among the Brahmins and lowest among the tribes; the non-Brahmin groups occupy an intermediate position. The 2− allele frequency is higher among the tribes than the caste groups.

To examine whether the PGM_1 locus reveals a geographical pattern, the available data on the Indian populations have been pooled under four geographical zones, i.e., South, North, East, and West. The populations of North India tend to show somewhat lower frequencies of the alleles 1+ and 2+ and higher frequencies of 1− and 2− than other regions in India (Table 4).

Table 5 gives the distribution of PGM_1 allele frequencies in various world populations including India. About 62% 1+ gene is observed among the Europeans (Welch et al.,

TABLE 3. Mean PGM_1 subtype gene frequencies in some Indian population groups

Populations	No. tested (N)	Allele freqencies			
		1+	2+	1−	2−
Tribes	1,167	.6705	.2242	.0560	.0493
Non-Brahmins	1,019	.7215	.1935	.0623	.0229
Brahmins	289	.7678	.1656	.0571	.0093

TABLE 2. PGM_1 subtype gene frequencies in 14 South Indian populations

Population	No. tested (N)	Allele frequencies			
		1+	2+	1−	2−
Havik Brahmin	78	.7500	.1410	.0960	.0130
Vokkaliga	67	.7985	.1567	.0224	.0224
Lingyat	37	.7162	.2298	.0405	.0135
Jenkuruba	106	.6840	.2500	.0280	.0380
Pulayan	73	.5030	.3010	.0750	.0210
Namboodri Brahmin	77	.7662	.2078	.0260	.0000
Ezhava	48	.7190	.2190	.0310	.0310
Urali	53	.6321	.2264	.0849	.0566
Chettiar	58	.6466	.2586	.0345	.0603
Kallan	62	.6371	.2339	.1129	.0161
Pariah	96	.7397	.2395	.0104	.0104
Vaidic Brahmin	100	.7250	.2100	.0500	.0150
Kamma	67	.7919	.1940	.0149	.0000
Vysya	82	.7317	.1707	.0854	.0122

TABLE 4. Mean PGM_1 subtype gene frequencies in four regions of India

Region	No. tested (N)	Allele frequencies			
		1+	2+	1−	2−
East	1,047	.7058	.1929	.0526	.0487
South	1,004	.7126	.2166	.0497	.0209
North	254	.6200	.1650	.1540	.0610
West	228	.6995	.2171	.0679	.0153

TABLE 5. Frequencies of four common PGM_1 alleles in various world populations

Population	No. tested (N)	1+	1−	2+	2−	References
England	1,888	.624	.134	.180	.062	Welch et al. (1978)
Germany	291	.619	.143	.172	.067	Kuhnl and Spielmann (1977)
Sweden	2,000	.610	.160	.160	.070	Svensson and Watterling (1979)
Switzerland	501	.628	.130	.194	.049	Scherz et al. (1981)
Japan	218	.656	.117	.167	.051	Nishigaki et al. (1982)
Gambia, West Africa	637	.795	.053	.133	.019	Welch et al. (1978)
Black and West Indian (domiciled in England)	246	.681	.132	.159	.028	Welch et al. (1978)
Newfoundland	300	.547	.150	.232	.071	Welch et al. (1978)
African Black (southern)						
Pedi	98	.633	.184	.158	.026	Tipler et al. (1982)
Zulu	102	.730	.142	.098	.029	Tipler et al. (1982)
Kavango	64	.703	.117	.148	.032	Tipler et al. (1982)
Herero	72	.715	.056	.139	.090	Tipler et al. (1982)
Kgalagadi	81	.586	.204	.179	.025	Tipler et al. (1982)
Ecaprivi	141	.660	.163	.135	.043	Tipler et al. (1982)
Khosian Kung	84	.732	.250	.012	.000	Tipler et al. (1982)
Nama	78	.680	.134	.109	.051	
India						
Himachal Pradesh						
Gaddi Rajput, Cangra (tribe)	141	.621	.165	.152	.062	Papiha et al. (1981)
Gaddi Rajput, Chamba (tribe)	70	.664	.135	.157	.043	Papiha et al. (1981)
Gaddi Brahmin, Chamba (caste)	39	.537	.141	.231	.091	Papiha et al. (1981)
Orissa						
Langia Saora (tribe)	107	.668	.066	.126	.140	Papiha (1983)
Munda (tribe)	72	.646	.076	.237	.041	Mukherjee et al. (1982)
Kissan (tribe)	118	.665	.060	.223	.042	Mukherjee et al. (1982)
West Bengal						
Munda (tribe)	101	.660	.040	.250	.050	Mukherjee et al. (1982)
Bagdi (tribe)	100	.860	.070	.045	.025	Mukherjee et al. (1982)
Lodha (tribe)	113	.672	.018	.217	.093	Mukherjee et al. (1982)
Jalia Kaibarta (caste)	89	.803	.056	.140	.000	Mukherjee et al. (1982)
Rarhi Brahmin (caste)	53	.830	.056	.104	.009	Mukherjee et al. (1982)
Vaidya	25	.770	.019	.211	.000	Mukherjee et al. (1982)
Mech (tribe)	93	.630	.048	.284	.038	Mukherjee et al. (1982)
Garo (tribe)	100	.645	.055	.245	.055	Mukherjee et al. (1982)

N.B., Kgalagadi, Kung, and Nama show .006, .006, and .026 PGM_1 allele respectively, also.

1978, 1979; Kuhnl et al., 1978; Suensson and Watterling, 1979; Scherz et al., 1981); the corresponding allele frequency in the African populations is about 69% (Welch et al., 1978; Tipler et al., 1982), which appears to be little higher; the Indians in general show nearly 68% (Papiha et al., 1981; Papiha, 1983; Mukherjee et al., 1982), which is closer to the Africans; whereas about 65% of the Japanese exhibit the same allele (Nishigaki et al., 1982), which stands between the Europeans and Africans. It has been shown previously, using starch gel electrophoresis, that the frequency of the PGM_1^2 allele is, in general, lower in blacks than in whites, and it is also known to be unusually high in the Asiatic Indians (Giblett, 1969). The present study indicates that the high PGM_1^2 among Indians is due largely to the high 2+ gene frequency. The 2+ allele frequency is not much different among the Indians and whites. It is lower among the African blacks.

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