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Red Cell Enzyme Variation Among Two Sub Populations of Rellis of Andhra Pradesh, South India

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ABSTRACT A total of 221 blood specimens belonging to two sub populations of Rellis, a Scheduled Caste of Visakhapatnam, South India, were tested for 8 biochemical genetic marker systems: ACP 1, ESD, GLO 1, 6 PGD, LDH, MDH 1, SOD 1, PGM 1 and PGM 2. Inter group comparison by Chi-square analysis revealed significant differences for 6 PGD and PGM 1 systems only. An attempt was made to compare with those available for other populations from Andhra Pradesh.

INTRODUCTION

India offers enormous scope and unique opportunities for genetic investigations. The Indian populations have been stratified into numerous endogamous castes, tribes and religious communities based on language, ethnicity, traditions and several other cultural aspects. The State of Andhra Pradesh, South India, harbours a number of castes and tribes, which are an ideal source for studies of human variation by population geneticists.

The present investigation report the distribution of some biochemical genetic markers of two sub populations of Rellis, a Scheduled Caste residing in different localities of Visakhapatnam of Andhra Pradesh, South India. The Rellis occupy the lowest stratum in the Hindu caste hierarchy. The origin of the Rellis is not clear. They are a migrant group from the neighbouring State of Orissa about one and a half centuries ago. They are presently divided into two traditional endogamous broad divisions namely, the fruit vendors (Relli-I) and scavengers (Relli-II). This reflects the differential state of economy. The fruit vendors are rich and the scavengers are poor. However presently some of their members involved in a number of other pursuits like trade and a variety of Government jobs.

The investigated area, Visakhapatnam district is one of the North-Eastern districts of Andhra Pradesh situated within the geographic coordinates of 17° 15' and 18° 32' of Northern latitude and 18° 6' and 83° 32' of Eastern longitude.

MATERIAL AND METHODS

A total of 221 blood specimens were collected intravenously from unrelated, healthy adult male and female Rellis (Relli-I : 111; Relli-II : 110) residing in different localities of Visakhapatnam city.

Intravenous blood samples were collected in sterile test tubes containing ACD solution as an anticoagulant and brought to the lab the same day by keeping them in a vacuum flask containing ice cubes. The plasma was separated, haemolysates prepared and stored at –20°C until use. The systems analysed were Acid Phosphatase (ACP 1), Esterase-D (ESD), Lactate Dehydrogenase (LDH), Malate Dehydrogenase (MDH 1), 6-phosphogluconate Dehydrogenase (6PGD), Phosphoglucomutase locus 1 and 2 (PGM 1 and 2) and Superoxide Dismutase (SOD 1) by horizontal starch gel electrophoresis using the methods described by Harris and Hopkinson (1976). While Glyoxalase-I were typed on starch-agarose gel electrophoresis following the method of Pflugshaupt et al. (1978). The gene frequencies were estimated by using maximum likelihood methods of Balakrishnan (1988).

RESULTS AND DISCUSSION

Phenotype frequency for the red cell enzymes are shown in table 1 and 2, and gene frequencies are shown in table 3.

The observed phenotypes agree with those expected under Hardy-Weinberg equilibrium among two sub populations for only two systems namely, ESD and 6PGD, but not for the other three systems the ACP 1, GLO 1 and PGM 1.

Table 1: Distribution of red cell enzyme phenotypes in two sub populations of Rellis

System	*Phenotype*	*Rellis-I*		*Rellis-II*		*Rellis*	
		Observed	*Expected*	*Observed*	*Expected*	*Observed*	*Expected*
ACP 1	A	9	2.30	12	3.64	21	5.87
	B	88	81.30	82	73.64	170	154.86
	AB	14	27.40	16	32.72	30	60.27
	Total	111	111.00	110	110.00	221	221.00
	χ_1^2	26.6229 ($p < 0.001$)		28.6935 ($p < 0.001$)		55.6808 ($p < 0.001$)	
ESD	1-1	57	56.94	42	45.83	99	102.49
	2-1	45	45.12	58	50.34	103	96.02
	2-2	9	8.94	10	13.83	19	22.49
	Total	111	111.00	110	110.00	221	221.00
	χ_1^2	0.0008 ($0.98 > p > 0.95$)		2.5464 ($0.20 > p > 0.10$)		1.1678 ($0.30 > p > 0.20$)	
GLO 1	1-1	15	10.41	22	13.12	37	23.46
	2-1	38	47.17	32	49.74	70	97.09
	2-2	58	53.42	56	47.14	114	100.45
	Total	111	111.00	110	110.00	221	221.00
	χ_1^2	4.1992 ($0.05 > p > 0.02$)		14.0025 ($p < 0.001$)		19.9903 ($p < 0.001$)	
6PGD	A	108	108.02	100	100.24	208	208.20
	AC	3	2.96	10	9.53	13	12.61
	C	0	0.02	0	0.23	0	0.19
	Total	111	111.00	110	110.00	221	221.00
	χ_1^2	0.0205 ($0.90 > p > 0.80$)		0.0254 ($0.70 > p > 0.50$)		0.2023 ($0.70 > p > 0.50$)	
PGM 1	1-1	75	66.63	50	43.91	125	109.41
	2-1	22	38.74	39	51.18	61	92.18
	2-2	14	5.63	21	14.91	35	19.41
	Total	111	111.00	110	110.00	221	221.00
	χ_1^2	20.7294 ($p < 0.001$)		6.2307 ($0.02 > p > 0.01$)		25.2899 ($p < 0.001$)	

Table 2: Distribution of monomorphic red cell enzyme systems in two sub populations of Rellis

System	*Phenotype*	*Relli-I*	*Relli-II*	*Rellis*
LDH	Normal	111	110	221
MDH 1	1	111	110	221
PGM 2	1	111	110	221
SOD 1	1	111	110	221

These deviations from genetic equilibrium are probably due to surpluses of homozygous and deficits of heterozygous phenotypes, which in turn may be either due to consanguinity and inbreeding or chance fluctuations. (The rates of consanguinity as reported here are in Relli-I : 40%, Relli-II : 42%).

The Chi-square test for heterogeneity between two sub populations did not show any statistically significant differences in the frequencies with the exceptions of the 6PGD and PGM 1 systems for which a significant heterogeneity was found. The reasons for these significant intergroup differences in these two systems may be primarily due to drift effects and prolonged biological isolation, probably 6 or 7 generations. Both these factors have reduced gene flow between these two populations and thus contributed to some amount of genetic heterogeneity between them. Further considering 5 loci (ACP 1, ESD, GLO 1, 6 PGD and PGM 1) the values of Fi estimates for endogamy for these two populations are recorded as 0.2207 in Relli-I and 0.1810 in Relli-II.

The frequency of *ACP1*A* allele is estimated at about 0.1441 and 0.1818 and Relli-I and II sub populations, respectively. The available data on ACP 1 for the Andhra Caste populations show that the *ACP1*A* frequency in the majority of populations ranges between 0.1070 in Brahmin (Srikumari, 1985) and 0.3200 in Muslim (Roberts et al. 1980) and the value of 0.1629 in Rellis

Table 3: Gene frequencies in two sub populations of Rellis

System (allele)	*Relli-I*	*Relli-II*	*Rellis*	χ^2 *heterogeneity*	*d.f.*
ACP 1					
A	0.1441 ± 0.03	0.1818 ± 0.03	0.1629 ± 0.02	0.7706	2
B	0.8559 ± 0.03	0.8182 ± 0.03	0.8371 ± 0.02	(0.70 > p > 0.50)	
ESD					
1	0.7162 ± 0.04	0.6455 ± 0.04	0.6810 ± 0.03	3.9617	2
2	0.2838 ± 0.04	0.3545 ± 0.04	0.3190 ± 0.03	(0.20 > p > 0.10)	
GLO 1					
1	0.3063 ± 0.04	0.3454 ± 0.04	0.3258 ± 0.03	1.8657	2
2	0.6937 ± 0.04	0.6546 ± 0.04	0.6742 ± 0.03	(0.50 > p > 0.30)	
6PGD					
A	0.9865 ± 0.01	0.9546 ± 0.02	0.9706 ± 0.01	4.0739	1
C	0.0135 ± 0.01	0.0154 ± 0.02	0.0294 ± 0.01	(0.05 > p > 0.02)	
PGM 1					
1	0.7748 ± 0.04	0.6318 ± 0.04	0.7036 ± 0.03	11.1384	2
2	0.2252 ± 0.04	0.3682 ± 0.04	0.2964 ± 0.03	(0.01 > p > 0.001)	

The *LDH*N, MDH 1*1, PGM2*1* and *SOD 1*1* allele frequencies are 1.0000 in two sub populations of Rellis

lies within the above range (Bhasin et al., 1992).

For the ESD system, the frequency of *ESD*2* allele among two sub populations are 0.2838 and 0.3545 respectively. In general the frequency of *ESD*2* allele range is between 0.2160 in Hindu (Roberts et al., 1980) and 0.4050 in Mala (Char and Rao, 1986). The value of *ESD*2* allele in Rellis (0.3190) fall within the range (Bhasin et al., 1992).

The *GLO1*1* allele was estimated at 0.3063 and 0.3454 in Relli-I and II sub groups at the GLO 1 locus. Relatively few populations from Andhra Pradesh have been typed for GLO1 system. Interestingly, the *GLO1*1* allele reveals wide variation in various populations is found to be between 0.1941 in Brahmin (Naidu et al., 1985) and 0.3565 in Mala (Char and Rao, 1986b). Therefore, the present study Rellis are well within the range of Andhra Pradesh populations (Bhasin et al., 1992). No rare variants were reported from Andhra Populations.

The frequency of *6PGD*C* allele varies between 0.0147 in Brahmin (Naidu et al., 1985) and 0.0337 in Andhras (Busi et al., 1979). The Rellis, with a frequency of 0.0294 for *6PGD*C* fall within the range. Five variants have been reported fro the populations of South India. PGD 'Gadaba' in Gadabas (Rao et al., 1995) PGD 'Waltair' in Brahmins (Naidu et al., (1985) and PGD 'Friendship' in Koya (Chahal, 1981) of Andhra Pradesh. PGD 'Kadar' in Kadars of Kerala (Saha et al., 1974) and PGD 'Hackney' in Tamil Nadu (Anantha Krishnan, 1972).

For the PGM 1 system, the frequency of *PGM1*2* allele among two sub groups are 0.2252 and 0.3682 respectively. Very few population groups have been reported from Andhra Pradesh and the *PGM 1*2* allele frequency in them is found to be ranging from 0.1831 in Nagavamsam (Rao et al., 1981) to about 0.3706 in Brahmin (Naidu et al., 1985). Rare variants at PGM 1 locus such as 5-1 (Veerraju et al., 1980 and Roberts et al., 1980) and 3-1 (Lakshmi, 1994) have been reported from Andhra Caste populations.

No variation was found at LDH, MDH 1, SOD 1 and PGM 2 loci in the present study of Rellis. Similar trend is found for most of the Andhra Pradesh populations investigated so far. However, a heterozygous variant SODA 2-1 among Kotia tribe (Naidu et al., 1995) and an extremely rare homozygous phenotype variant SODA 2-2 among Shia Muslims (Khaja et al., 1996) populations of Andhra Pradesh are reported from South India. Sporadic reports of rare variants at PGM2 locus among Andhra Castes, such as PGM2 4, PGM 6IND and PGM2 9 (Santachiara Benerecetti et al., 1972) and tribes PGM2 10-1 (Blake et al., 1981) were reported.

From the above discussion it is evident that the present study of the Relli caste of Andhra Pradesh are in good accordance with the red cell enzyme systems data reported on the other Andhra caste populations. However, further more population studies from several regions of Andhra Pradesh, South India is necessary in

order to understand the variability of these polymorphic systems in this part of India in detail.

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