Blood groups, serum proteins and red cell isoenzymes - a population genetic study on South Africa/Mocambique.

A. Rodewald[1], G. Schaekel[1], H. Cleve[2], E. Schwender[2], S. Weidinger[2], and C. Glavce[3]

1) Institute of Human Biology of University, D-2000 Hamburg 13
2) Institute of Anthropology and Human Genetics of University, D-8000 Muenchen 2
3) Blood Bank Pemba/Mocambique and Laboratory of Anthropology, Bucharest/Romania

This study is a part of a general survey aimed at investigating the genetic variability of serological and anthropological characters and to measure the genetic relationship between indigenous groups in South Africa. The blood samples were obtained from individuals living in the districts Cabo Delgado around the village Pemba (eastern pacific coast). Inspite of sporadic marriage contacts with the neighbouring groups, the people of Pemba (all Macua of Bantu origin) practice endogamy (contracting marriages only within their own group); this region has not yet been affected by social changes in the family structure and marriage system. These people share a common dialect and a common ecological zone. Thus, they can be regarded as an homogenous group with respect to linguistical, social, economic and cultural factors (fig. 1).

MATERIAL AND METHODS

109 blood samples were taken from unrelated donors of tribe Macua living around Pemba, and stored at 4°C, until their arrival in West Germany. For ABO and Rh (D factor only) 929 blood data from Blood Bank-Pemba were used. 85 samples (serum and cloths) were stored at -22°C.

We have typed: ABO, CcDEe, MNSs, Fy, Jk, Kk, Lu and P1 (blood groups); Gc Tf, Pi (IEF) (serum proteins); AcP, Ak, ADA, 6-PGD, PGM1 and PGM2 (erythrocyte enzymes); (electrophoresis on celulose acetate foils gel = CAFG). X^2-Test was used to examine the heterogenity and the genetic distance analysis (Edwards and Cavalli-Sforza, 1972) was carried out to compare the data with those of other studies of South African populations.

RESULTS AND DISCUSSION

Table 1 and 2 show the distribution of blood groups, serum proteins, red cell enzymes and their gene frequencies, respectively. The distribution of observed and expected phenotype frequencies are, with exception of the Rhesus (D and E locus) and MNSs systems, in good agreement with the expected Hardy-Weinberg proportion. The frequency of the Rhesus phenotypes CcDee (22.9%), ccddee (14.7%) found in our sample were also relatively high and differ significantly from the ours observed in other South African

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populations. Further frequencies of other phenotypes like A1B (8.3%), NNss (21.1%), Jka+b+ (39.54%) and Lua+b+ (23.8%) found in our sample, differ also from the other populations. No definite conclusion could be reached from this observation in this small population.

The serum protein phenotypes 1F (Gc, 64.6%), M1 (Pi, 81.2%) and C1 (Tf, 69.5%) were the most common alleles in this group. Rare phenotypes were 2-1S,1F-2A3,and 2-2A3 in Gc,M3,M1M2,and M2M3 in Pi.One rare Gc variant 2A3 was found in 2 individuals;however,the Gc variant 1A1 and Tf- C3 in our sample were not observed. The gene frequencies observed in our sample for the red cell enzymes were within the range expected for South African populations studied until now. The phenotypes Ak 2-1/2, ADA 2-1/2, PGM2 2-2, AcP AC/C/RA and 6-PGD B were absent in our sample.

A comparison of our results with the previously published in the literature show that the genetic distance between the two Macua populations (ours and from Da Cunha et al. 1970) is greater than the one observed between the Central Bantu and the Shona/Thonga coast populations. The cluster analysis (fig. 2 and 3) shows, that our Macua group is closer related to the Sena and Shona/ Thonga coast populations, than to the other Macua and Bantu populations. Somewhat, greater heterogenity is observed between our Macua group and other Bantu groups with respect to allelic frequencies for Rh and MNSs. The presence of some rare allele of serum proteins in Macua Negroids gives new anthropological and ecological perspectives of great interest. Further investigations on the polymorphism of the serum proteins and enzymes are needed to give a wider horizon to the biological anthropology of South Africa. Microevolutionary forces like genetic drift combined with founder effect and endogamy are the probable causes for the observed variation of allelic frequencies in the populations studied. Considering the great ethnic heterogenity of the mentioned groups and the diversity of their habitat, the south african populations of Mocambique are largely heterogenous.

REFERENCES

Da Cunha AX, Cunha FA, Fout X (1970) Rev.Cienc biol Lourenco Marques 3: 97-107
Edwards AW, Cavalli-Sforza LL (1972) in: Wiener JS, Huzinga J (edt) Clarendon Press, Oxford
Mourant AE, Copec AC, Domaniewska-Sobczak K (1976) 2nd ed Oxford Univ Press
Reys L, Manso C, Stamatoyannopoulos G, Giblett E (1972) Hum Genet 16:227-233
Giblett ER (1969)Genetic markers in human blood.Blackwell Scien Publications,Oxford and Edinburgh
Spielmann W,Teixidor D,Renninger W,Matznetter T(1970)Hum Genet 10:304-317

Table 1. Distribution of ABO, MNSs, Rhesus, Fy, Jk, Lu, P, Kell phenotype and gene frequencies of the Macua

System		%	X^2	p	Gene frequen.
ABO	A	22.9	X^2=0.140	n.s.	p=0.1925
♂ N=609	B	16.8			q=0.1148
	AB	4.9			r=0.6959
	0	48.4			
♀ N=320	A	35.3	X^2=0.165	n.s.	p=0.2356
	B	17.5			q=0.1269
	AB	6.3			r=0.6379
	0	40.4			
Rhesus	+	98.4		n.s.	Do=0.83
♂ N=609	-	1.6			do=0.17
♀ N=302	+	98.5		n.s.	Do=0.83
	-	1.5			do=0.17
N=109	CCDee	1.8	X^2(Rh/rh)=5.68	p= .05	cde=0.3831
	CcDEE	0.9			cdE=0.0120
	CcDEe	2.8			Cde=0.0239
Rh^-	CcDee	21.1			cDe=0.4296
	ccDEE	1.8			CDe=0.1163
	ccDEe	2.8			cDE=0.1622
	ccDee	51.4			C=0.1514
	ccddee	14.7	X^2=0.1389	n.s.	c=0.8486
Rh^+	Ccddee	1.8			E=0.0596
	ccddEe	0.9	X^2=19.14	p<0.001	e=0.9404
MNSs	MMSS	6.4	X^2=11.52	p<0.001	MS=0.2166
N=109	MMSs	14.7			Ms=0.3430
	MMss	14.7			NS=0.0292
	MNSS	6.4			Ns=0.4112
	MNSs	12.8			M=0.5596
	MNss	21.1			N=0.4404
	NNSS	2.8			S=0.2936
	NNss	21.1			s=0.7064
P_1	P_1+	96.3		n.s.	P_1=0.81
N=109	P_1-	3.7			
Kell	K^-	100.0		-	-
N=109					
Fy	a-b^+	2.8	X^2=0.0203	n.s.	Fy^o=0.9869
N=109	a-b-	97.2			Fy^a=0.0138
Lu	a+b+	23.8	X^2=0.3873	n.s.	Lu^a=0.1190
N=109	a-b+	76.2			Lu^b=0.8810

Table 2. Red cell enzymes (N=85 for every marker) and serum proteins

System		%	X^2	p	Gene frequen.
AcP	A	3.5	X^2=1.5620	n.s.	A=0.2118
	B	60.0			B=0.7823
	AB	35.5			C=0.0059
	BC	1.2			
PGM_1	1-1	76.5	X^2=0.8970	n.s.	PGM_1^1=0.8706
	2-1	21.2			PGM_1^2=0.1294
	2	2.3			
PGM_2	1-1	94.1	X^2=0.6750	n.s.	PGM_2^1=0.9706
	2-1	5.9			PGM_2^2=0.0294
AK	1	100.0	-	-	AK^1=1.000
	2-1	0.0			
ADA	1	100.0	-	-	ADA^1=1.000
	2-1	0.0			
6-PGD	A	81.2	X^2=1.657	n.s.	6-PGD A=0.9058
	AB	18.8			B=0.0942
	B	0.0			
Gc	1F	64.6			
	1F-1S	9.8	X^2=6.7856	n.s.	1F =0.7866
N=82	1S	2.4	df=3		1S =0.0793
	2-1F	17.1			2 =0.1219
	2-1S	1.2			2A3=0.0122
	2	2.4			
	1F-2A3	1.2			
	2 -2A3	1.2			
Tf	C1	69.5			
	C1-C2	11.0	X^2= 1.7868	n.s.	C1=0.8232
N=82	C2	4.9	df=3		C2=0.1036
	C1-D1	14.6			D1=0.0732
Pi	M_1	81.2	X^2=1.975	n.s.	M_1=0.8913
	M_1M_2	2.9	df=3		M_2^1=0.0217
	$M_1M_3^2$	13.0			M_3^2=0.0870
	M_2M_3	1.5			
	M_3^2	1.5			

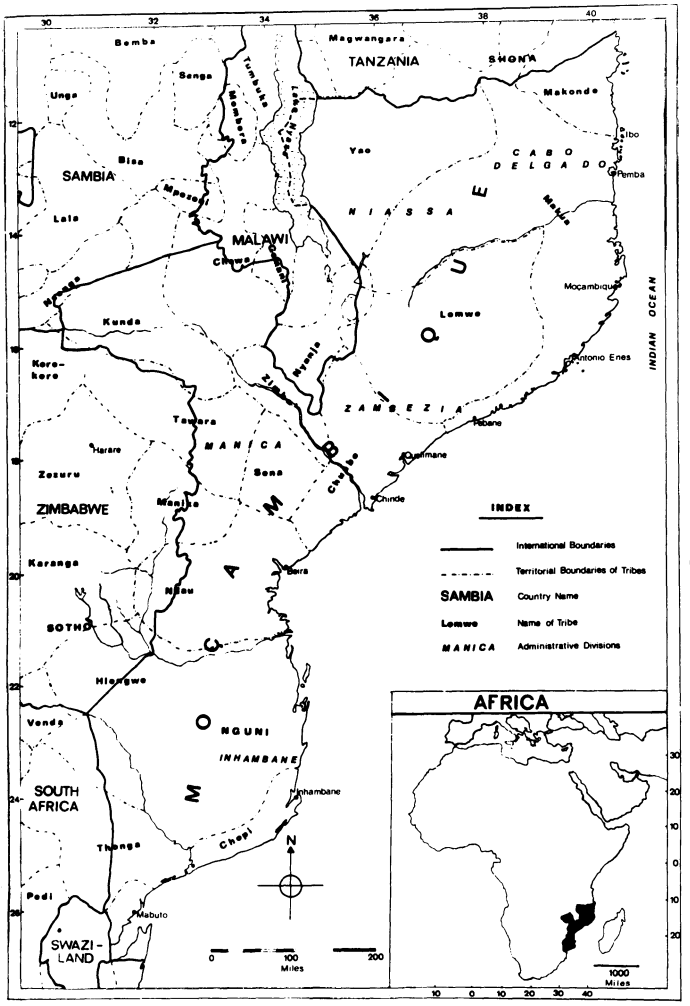

Fig. 1. Map of Mocambique

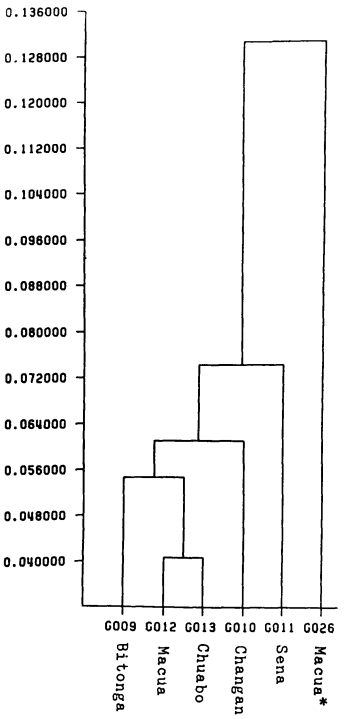

Fig. 2. Cluster based on gene distance coefficients between 6 southafrican populations: ABO, Rh, MNSs, P, Fy, Jk

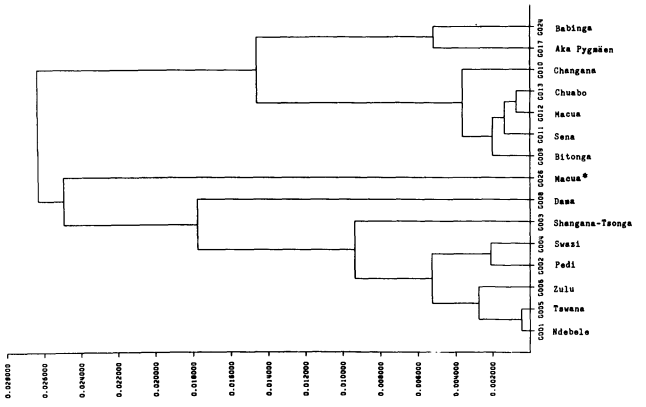

Fig. 3. Cluster based on gene distance coefficients between 15 southafrican populations involving the systems: ABO, Rh, Fy