

## GENETICS, SURNAMES, GRANDPARENTS' NATIONALITIES, AND ETHNIC ADMIXTURE IN SOUTHERN BRAZIL – DO THE PATTERNS OF VARIATION COINCIDE?

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### ABSTRACT

A total of 2,708 individuals from the European-derived population of Rio Grande do Sul, divided into seven mesoregions, and of 226 individuals of similar origin from Santa Catarina were studied. Seventeen protein genetic systems, as well as grandparents' nationalities, individuals' surnames, and interethnic admixture were investigated. The alleles which presented the highest and lowest differences were **GLO1\*2** (16%) and **PGD\*A** (2%), respectively, but in general no significant genetic differences were found among mesoregions. The values observed were generally those expected for individuals of European descent, with the largest difference being a lower prevalence (34-39%) of **P\*1**. Significant heterogeneity among mesoregions was observed for the other variables considered, and was consistent with historical records. The Amerindian contribution to the gene pool of European-derived subjects in Rio Grande do Sul was estimated to be as high as 11%. Based on the four data sets, the most general finding was a tendency for a northeast-southwest separation of the populations studied. Seven significant phenotype associations between systems were observed at the 5% level (three at the 0.1% level). Of the latter, the two most interesting (since they were also observed in other studies) were MNSs/Duffy and Rh/ACP.

### INTRODUCTION

The non-Indian populations of the States of Rio Grande do Sul and Santa Catarina have been fairly well studied in the last three decades (Tondo and Salzano, 1962; Tondo *et al.*, 1963; Salzano, 1963; Schwantes *et al.*, 1967; Salzano *et al.*, 1967, 1968a,b; Lewgoy and Salzano, 1968; Hutz *et al.*, 1977; Weimer *et al.*, 1981, 1987, 1993; Franco *et al.*, 1981, 1982, 1986; Silva *et al.*, 1981; Franco and Salzano, 1985; Rieger *et al.*, 1988; Arai *et al.*, 1989; Bortolini *et al.*, 1992, 1994, 1995, 1997a,b, 1998; Heidrich *et al.*, 1995; Robinson *et al.*, 1998). However, these investigations have not provided a detailed distribution pattern of the polymorphisms investigated, nor a comparison with attributes such as grandparents' nationalities or the individuals' surnames, which could give clues about the history of these groups. Ethnic admixture was evaluated using dihybrid (European/African-derived) models only. In addition, genetic diversity measures were seldom employed, and the relationships between markers in different genetic systems rarely considered. Over the years, we have collected a large amount of information during paternity determinations in these populations. These data include 17 protein genetic systems studied in about 3,000 European-derived subjects living in the States of Rio Grande do Sul and Santa Catarina. Analysis of these results showed that despite a general homogeneity, there was a tendency

towards a northeast-southwest division. Three significant associations between systems were detected, and the Amerindian contribution to the gene pool of people from Rio Grande do Sul phenotypically classified as white was estimated to be as high as 11%.

### SUBJECTS AND METHODS

The data used in this analysis were obtained in 1617 cases of paternity determinations performed in our Department between 1962 and 1996. Only European-derived, unrelated subjects were considered, and some of the subjects investigated in the early part of the study were excluded because the determinations did not include the full set of systems finally established. Non-Caucasian individuals were omitted from the analysis because they were few in number.

The 17 genetic systems investigated and the references for the methods of determination employed are listed in Table I.

For the analysis, the samples from the State of Rio Grande do Sul were grouped according to the seven mesoregions proposed by the Brazilian Institute of Geography and Statistics (IBGE, 1991), namely northwest (NW), northeast (NE), center-west (CW), center-east (CE), metropolitan Porto Alegre (MPOA), southwest (SW), and southeast (SE). They are indicated on the maps in Figures 1-4. Since the number of individuals studied living in Santa Catarina (SC) was much smaller, this sample was not divided into regions.

Frequencies of the phenotypes, alleles, grandparents' nationalities, and individuals' surnames were obtained using the SPSS™ (Anonymous, 1992) and MAXLIK (Reed and Schull, 1968) programs. Heterogeneity among mesoregions was analyzed by chi-square tests using the PEPI program (Gahlinger and Abramson, 1995). D<sub>A</sub> dis-

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**Table I** - Genetic systems and laboratory methods employed in the present study.

Method	Systems	References
Starch gel electrophoresis	Acid phosphatase ( <b>ACP</b> )	Harris and Hopkinson (1976)
	Adenylate kinase ( <b>AK</b> )	Fildes and Harris (1966); Spencer <i>et al.</i> (1968)
	Albumin ( <b>ALB</b> ) <sup>1</sup>	Kueppers and Bearn (1966)
	Ceruloplasmin ( <b>CP</b> )	Bowman and Bearn (1965)
	Esterase D ( <b>ESD</b> )	Harris and Hopkinson (1976)
	Glucose-6-phosphate dehydrogenase ( <b>G6PD</b> )	Fildes and Parr (1963)
	Haptoglobin ( <b>HP</b> )	Poulik (1957)
	Phosphoglucomutase ( <b>PGM1, PGM2</b> ) <sup>2</sup>	Spencer <i>et al.</i> (1964); Blake and Omoto (1975)
	Phosphogluconate dehydrogenase ( <b>PGD</b> )	Fildes and Parr (1963)
	Transferrin ( <b>TF</b> )	Poulik (1957); Bowman and Bearn (1965); Geserick <i>et al.</i> (1968)
Agarose starch electrophoresis	Glyoxalase 1 ( <b>GLO1</b> )	Rieger <i>et al.</i> (1988); Parr <i>et al.</i> (1977)
Immunological	<b>ABO</b> <sup>3</sup>	Dunsford and Bowley (1967)
	Duffy ( <b>FY</b> )	
	<b>MNSs</b>	
	<b>P</b>	
	<b>RH</b>	

<sup>1</sup>To confirm variants: Weitkamp *et al.* (1967); <sup>2</sup>Typing by isoelectric focusing was performed according to Yuasa *et al.* (1986); <sup>3</sup>A subtypes were identified using *Ulex europaeus* extract (Boyd and Shapleigh, 1954).

tances were calculated as indicated in Nei *et al.* (1983) and Nei and Roychoudhury (1993). The corresponding dendrograms were obtained by UPGMA (unweighted pair-group method with arithmetic mean; Sneath and Sokal, 1973), and the reliability of the trees evaluated by the bootstrap test using 2,000 replications (Hedges, 1992). All these calculations were done using the DISPAN program (Ota, 1993). The same distances were used for a principal coordinate analysis using the NTSYS program (Rohlf, 1987).

The congruence between the matrices obtained for the genetic, nationality, surname, and admixture frequencies was evaluated by Mantel's (1967) method, using NTSYS and a DOS program kindly provided by J.C. Long.

Association between phenotypes, considering the different systems, was evaluated by chi-square tests. When more than 20% of the numbers showed less than five values, the method of Roff and Bentzen (1989) was employed. Correction for the large number (52) of comparisons made was obtained by dividing the formal 5% level by this number (Fañanás *et al.*, 1997). The degree of intra- and inter-population variability was evaluated using Nei's (1973, 1986, 1987) statistics and the DISPAN program.

Estimates of interethnic admixture were calculated by the gene identity method (Chakraborty, 1985) using the ADMIX program kindly provided by this author. Parental allele frequencies were estimated by weighted averages of the data compiled by Mourant *et al.* (1976), Tills *et al.* (1983), Roychoudhury and Nei (1988), Bortolini *et al.* (1995), and Salzano *et al.* (1997).

## RESULTS

Table II presents the allele frequencies for the 17 genetic systems studied in the seven mesoregions of Rio

Grande do Sul and in Santa Catarina (phenotype frequencies are too extensive to be shown here, but can be supplied on request). The albumin, ceruloplasmin, phosphoglucomutase 2 and transferrin loci presented very restricted variability, while the remaining 13 loci showed nonsignificant variations among regions. The largest dissimilarity occurred with the **GLO1\*2** allele of the glyoxalase 1 system, which showed a frequency of 47% in the Center-West region of Rio Grande do Sul and 63% in Santa Catarina. The values were generally those expected for an European-derived population, the average deviation from a putative parental group (which included Portuguese, Italians, Germans and Spaniards) being only 4% for all of Rio Grande do Sul, and 3% for Santa Catarina. The largest deviation was observed for **P\*1** of the P blood group, which had an average prevalence of 39% in Rio Grande do Sul and 34% in Santa Catarina; the frequency in the reference population was 53%.

There was little genetic diversity among the mesoregions, with the average heterozygosity varying between 30 and 32%. Total variability ( $H_T$ ) was calculated as 0.309, only 0.6% of which was attributable to differences among mesoregions.

The distribution of the grandparents' nationalities is given in Table III. As expected, grandparents of Brazilian nationality were the most frequent in all regions, but their prevalence varied from 78% in the NE to 94% in the CE. Grandparents of Italian nationality were the second most common in five of the eight mesoregions (with frequencies varying from 2% in the SW to 19% in the NE), with German in two (4% in the CW and the CE), and Portuguese in one (3% in the SE). The heterogeneity among mesoregions proved to be statistically highly significant.

**Table II** - Allele frequencies for the 17 genetic systems studied in seven mesoregions of the State of Rio Grande do Sul (RS) and in Santa Catarina (SC)<sup>1</sup>.

Genetic systems and alleles or haplotypes	Mesoregions <sup>2</sup>									Total
	NW	NE	CW	CE	MPOA	SW	SE	Total RS	SC	
<b>ABO</b>										
<b>A1</b>	0.202	0.167	0.226	0.205	0.192	0.193	0.239	0.199	0.216	0.196
<b>A2</b>	0.071	0.059	0.040	0.074	0.057	0.064	0.052	0.057	0.053	0.061
<b>B</b>	0.072	0.057	0.106	0.082	0.069	0.063	0.103	0.071	0.060	0.070
<b>O</b>	0.655	0.717	0.628	0.639	0.682	0.680	0.606	0.673	0.671	0.673
N.º studied	684	298	50	176	1261	172	67	2708	224	2932
<b>ACP</b>										
<b>A</b>	0.291	0.277	0.308	0.304	0.277	0.299	0.280	0.285	0.330	0.288
<b>B</b>	0.664	0.669	0.671	0.646	0.685	0.660	0.652	0.672	0.606	0.667
<b>C</b>	0.045	0.054	0.021	0.050	0.038	0.041	0.068	0.043	0.064	0.045
N.º studied	682	296	47	171	1211	169	66	2642	226	2868
<b>ALB</b>										
<b>A</b>	0.999	1.000	1.000	0.997	1.000	1.000	1.000	0.999	1.000	0.999
<b>V</b>	0.001	0.000	0.000	0.003	0.000	0.000	0.000	0.001	0.000	0.001
N.º studied	680	288	48	174	1237	170	67	2664	226	2890
<b>AK</b>										
<b>1</b>	0.970	0.970	0.988	0.985	0.979	0.970	0.948	0.974	0.978	0.974
<b>2</b>	0.029	0.029	0.012	0.015	0.021	0.030	0.045	0.025	0.022	0.025
<b>3</b>	0.001	0.001	0.000	0.000	<0.001	0.000	0.007	0.001	0.000	0.001
N.º studied	668	287	41	171	1205	170	66	2608	226	2834
<b>CP</b>										
<b>A</b>	0.001	0.000	0.000	0.000	0.002	0.000	0.000	0.001	0.000	0.001
<b>B</b>	0.999	1.000	1.000	1.000	0.997	1.000	1.000	0.998	1.000	0.999
<b>V</b>	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.001	0.000	<0.001
N.º studied	682	288	48	174	1241	168	67	2668	226	2894
<b>ESD</b>										
<b>1</b>	0.852	0.853	0.878	0.857	0.855	0.837	0.828	0.853	0.858	0.853
<b>2</b>	0.147	0.147	0.122	0.143	0.145	0.163	0.172	0.147	0.142	0.147
<b>3</b>	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
N.º studied	682	279	45	171	1164	166	64	2571	226	2797
<b>DUFFY</b>										
<b>A</b>	0.291	0.316	0.175	0.275	0.272	0.310	0.304	0.283	0.242	0.279
<b>A-</b>	0.709	0.684	0.825	0.725	0.728	0.690	0.696	0.717	0.758	0.721
N.º studied	677	286	50	175	1225	168	64	2645	226	2871
<b>GLO1</b>										
<b>1</b>	0.446	0.401	0.533	0.415	0.416	0.373	0.437	0.422	0.369	0.418
<b>2</b>	0.554	0.599	0.467	0.585	0.584	0.627	0.563	0.578	0.631	0.582
N.º studied	680	279	45	171	1153	165	64	2557	225	2782
<b>G6PD (males)</b>										
<b>A</b>	0.006	0.000	0.000	0.020	0.009	0.000	0.026	0.003	0.009	0.008
<b>A-</b>	0.003	0.007	0.000	0.000	0.003	0.000	0.000	0.008	0.000	0.003
<b>B</b>	0.985	0.980	1.000	0.980	0.984	1.000	0.974	0.985	0.982	0.984
<b>Med</b>	0.006	0.000	0.000	0.000	0.002	0.000	0.000	0.002	0.000	0.002
<b>V</b>	0.000	0.013	0.000	0.000	0.002	0.000	0.000	0.002	0.009	0.003
N.º studied	338	148	25	88	579	79	39	1296	113	1409
<b>G6PD (females)</b>										
<b>A</b>	0.015	0.011	0.045	0.000	0.011	0.018	0.020	0.013	0.013	0.013
<b>A-</b>	0.000	0.004	0.000	0.000	0.006	0.012	0.000	0.004	0.004	0.004
<b>B</b>	0.985	0.985	0.955	1.000	0.980	0.964	0.980	0.981	0.979	0.981
<b>Med</b>	0.000	0.000	0.000	0.000	0.001	0.000	0.000	<0.001	0.000	<0.001
<b>V</b>	0.000	0.000	0.000	0.000	0.002	0.000	0.000	0.001	0.004	0.001
N.º studied	330	135	22	84	570	83	25	1249	113	1362
<b>HP</b>										
<b>1</b>	0.429	0.408	0.398	0.454	0.444	0.447	0.470	0.437	0.409	0.434
<b>2</b>	0.570	0.592	0.602	0.543	0.556	0.550	0.530	0.562	0.591	0.565
<b>V</b>	0.001	0.000	0.000	0.003	0.000	0.003	0.000	0.001	0.000	<0.001
N.º studied	685	294	49	176	1254	170	67	2695	226	2921

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Table II - *Continued*

Genetic systems and alleles or haplotypes	Mesoregions <sup>2</sup>									
	NW	NE	CW	CE	MPOA	SW	SE	Total RS	SC	Total
<b>MNSs</b>										
<b>MS</b>	0.205	0.225	0.168	0.176	0.199	0.210	0.183	0.202	0.205	0.203
<b>Ms</b>	0.401	0.366	0.374	0.351	0.355	0.398	0.357	0.371	0.337	0.367
<b>NS</b>	0.095	0.052	0.092	0.081	0.094	0.098	0.111	0.089	0.076	0.088
<b>Ns</b>	0.299	0.357	0.366	0.392	0.352	0.294	0.349	0.338	0.382	0.342
N.º studied	667	274	48	167	1200	167	63	2586	226	2812
<b>P</b>										
<b>1</b>	0.372	0.418	0.409	0.350	0.384	0.444	0.432	0.387	0.339	0.383
<b>1-</b>	0.628	0.582	0.591	0.650	0.616	0.556	0.568	0.613	0.661	0.617
N.º studied	637	275	43	161	1192	155	62	2525	213	2738
<b>PGD</b>										
<b>A</b>	0.982	0.978	0.989	0.974	0.975	0.975	0.969	0.977	0.978	0.977
<b>C</b>	0.017	0.022	0.011	0.026	0.025	0.025	0.031	0.022	0.022	0.022
<b>R</b>	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	<0.001
N.º studied	672	281	47	172	1163	163	65	2563	226	2789
<b>PGM1</b>										
<b>1</b>	0.771	0.718	0.685	0.692	0.745	0.729	0.823	0.745	0.709	0.744
<b>2</b>	0.229	0.279	0.315	0.308	0.255	0.271	0.177	0.254	0.291	0.256
<b>7</b>	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.001	0.000	<0.001
N.º studied	385	165	27	91	854	98	48	1668	98	1766
<b>PGM1 (isoelectric focusing)</b>										
<b>1A</b>	0.568	0.623	0.525	0.601	0.612	0.643	0.632	0.599	0.657	0.606
<b>1B</b>	0.167	0.130	0.200	0.161	0.131	0.147	0.105	0.147	0.138	0.145
<b>2A</b>	0.187	0.194	0.200	0.202	0.192	0.147	0.184	0.189	0.134	0.183
<b>2B</b>	0.078	0.053	0.075	0.036	0.065	0.063	0.079	0.065	0.071	0.066
N.º studied	301	131	20	84	385	71	19	1011	128	1139
<b>PGM2</b>										
<b>1</b>	0.999	1.000	1.000	1.000	0.999	1.000	1.000	0.999	1.000	0.999
<b>2</b>	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.001	0.000	0.001
N.º studied	362	164	24	83	818	101	48	1600	80	1680
<b>Rh</b>										
<b>DCE</b>	0.013	0.009	0.014	<0.001	0.007	0.000	<0.001	0.008	0.001	0.008
<b>DCe</b>	0.405	0.401	0.399	0.379	0.402	0.483	0.369	0.405	0.419	0.406
<b>DcE</b>	0.113	0.114	0.096	0.129	0.135	0.134	0.097	0.125	0.113	0.124
<b>Dce</b>	0.095	0.046	0.064	0.038	0.093	0.097	0.106	0.083	0.081	0.083
<b>dCE</b>	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	<0.001
<b>dCe</b>	0.020	0.028	0.048	0.025	0.028	<0.001	0.019	0.024	0.012	0.024
<b>dcE</b>	0.012	0.009	0.000	0.007	0.007	0.000	0.000	0.008	0.006	0.008
<b>dce</b>	0.342	0.393	0.379	0.422	0.328	0.286	0.409	0.347	0.362	0.347
N.º studied	685	297	50	176	1260	171	67	2706	226	2932
<b>TF</b>										
<b>B</b>	0.002	0.000	0.000	0.006	0.001	0.000	0.000	0.001	0.000	0.001
<b>C</b>	0.997	1.000	1.000	0.994	0.999	1.000	1.000	0.998	1.000	0.999
<b>D</b>	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	<0.001
N.º studied	684	292	48	174	1240	170	67	2675	226	2901

<sup>1</sup>To simplify the table, rare variants were grouped under the letter V. Their names are as follows: (a) albumin - NW mesoregion: Passo Fundo, CE: Vera Cruz (Franco *et al.*, 1998); (b) ceruloplasmin - Porto Alegre (Franco *et al.*, 1981); (c) G6PD - NE: Seattle and Farroupilha, MPOA: Seattle, SW: São Borja, SC: Seattle and Lages (Weimer *et al.*, 1993, 1998); (d) Haptoglobin - not studied in detail and therefore no definite nomenclature should be applied.

<sup>2</sup>NW: Northwest; NE: Northeast; CW: Center-West; CE: Center-East; MPOA: Metropolitan Porto Alegre; SW: Southwest; SE: Southeast; RS: Rio Grande do Sul; SC: Santa Catarina.

**Table III** - Distribution (%) of the grandparents' nationalities of individuals living in the seven mesoregions of the State of Rio Grande do Sul (RS) and in Santa Catarina (SC).

Grandparents' nationalities	Mesoregions <sup>1</sup>								
	NW	NE	CW	CE	MPOA	SW	SE	RS	SC
Argentinean	0.1	0	0	0	0.1	0.4	0	0.1	0
Brazilian	89.0	77.5	90.4	94.1	89.3	93.4	93.2	88.6	92.8
German	3.2	0.9	4.3	4.3	3.1	0.7	0.8	2.8	2.3
Italian	6.0	18.9	3.2	1.0	3.7	2.4	0.4	5.6	3.9
Polish	0.9	1.0	0	0.6	0.9	0	0.4	0.8	0
Portuguese	0.2	1.0	1.1	0	0.7	0	3.2	0.6	0.4
Uruguayan	<0.1	0	0.5	0	0.7	1.0	1.6	0.4	0
Others	0.6	0.7	0.5	0	1.5	2.1	0.4	1.1	0.6
Total	2668	1164	188	684	4859	676	252	10491	876

<sup>1</sup>Abbreviations as defined in Table II.  $\chi^2 = 686.55$ ; d.f. = 49;  $(P \pm SE) < (0.001 \pm 0.000)$  (Roff and Bentzen's (1989) method).

**Table IV** - Distribution (%) of the surnames of individuals living in the seven mesoregions of the State of Rio Grande do Sul (RS) and in Santa Catarina (SC).

Surnames	Mesoregions <sup>1</sup>								
	NW	NE	CW	CE	MPOA	SW	SE	RS	SC
Arabian	0.3	0	2.0	0	0.2	0.6	0	0.2	1.0
English	0.7	1.0	0	1.1	1.0	0.6	1.5	0.9	0.5
French	2.1	0.7	2.0	0.6	1.0	2.3	1.5	1.3	1.5
German	16.7	5.8	22.5	35.6	16.1	5.8	10.4	15.7	12.0
Greek	0.1	0	0	0	0.1	0	1.5	0.1	1.0
Italian	30.7	50.5	10.2	16.7	13.6	13.4	10.4	22.0	32.0
Latin	0.4	0	0	0.6	0.3	0	0	0.3	5.5
Polish	3.4	1.3	0	0.6	2.0	0.6	0	2.0	4.5
Portuguese	42.5	37.3	57.2	41.3	61.3	68.6	73.2	53.4	38.0
Spanish	2.2	3.4	6.1	2.9	3.7	7.5	1.5	3.5	4.0
Others	0.9	0	0	0.6	0.7	0.6	0	0.6	0
Total	678	295	49	174	1256	172	67	2691	200

<sup>1</sup>Abbreviations as defined in Table II.  $\chi^2 = 340.68$ ; d.f. = 70;  $(P \pm SE) < (0.001 \pm 0.000)$  (Roff and Bentzen's (1989) method).

Individuals with Portuguese surnames were the most frequent (from 38% in the SC to 73% in the SE) in seven of the eight mesoregions (Table IV). In the NE, however, Italian surnames predominated (50%). Italian surnames were also the second most frequent in three other mesoregions (in the SE the frequency of 10% was the same as for German surnames). The latter were the second most common in three other cases. Again, the heterogeneity was highly significant.

There was considerable diversity in the interethnic admixture among regions (Table V). The trihybrid model did not fit the CW data, indicating little contribution from Amerindians. The calculations for this mesoregion were therefore repeated considering only European and African ancestries. This new analysis showed an African admixture of 14%. In Santa Catarina, the African and Amerindian contributions were estimated as being 5%

each, lower than those estimated for Rio Grande do Sul as a whole (7 and 11%, respectively). The largest African influence (12%) was estimated for the SE, while the SW presented the highest Amerindian admixture (13%).

Multivariate approaches were employed to analyze similarities among mesoregions based on the four data sets.  $D_A$  genetic distances provided dissimilarity matrices for the construction of UPGMA dendrograms and three-dimensional principal coordinate diagrams. The results of these two grouping methods were generally concordant and are shown in Figures 1-4 along with corresponding maps.

Figure 1 summarizes the findings for the 17 genetic systems studied. A cluster incorporating five mesoregions (NW, MPOA, SC, NE and CE) is apparent; of the remaining regions, the most deviant is mesoregion CW. A general northeast-southwest division is discernible.

**Table V** - Estimated interethnic admixture in the European-derived populations of seven mesoregions of the State of Rio Grande do Sul (RS) and in Santa Catarina (SC).

Mesoregions <sup>1</sup>	Contributions					
	European		African		Amerindian	
	Mean	SE	Mean	SE	Mean	SE
NW	0.825	0.010	0.066	0.006	0.109	0.008
NE	0.871	0.018	0.032	0.012	0.097	0.014
CW	0.957	0.019	0.069	0.015	-0.027	0.017
CE	0.869	0.003	0.075	0.002	0.056	0.002
MPOA	0.796	0.015	0.081	0.011	0.122	0.013
SW	0.802	0.013	0.070	0.009	0.129	0.011
SE	0.812	0.001	0.123	0.001	0.065	0.001
RS	0.821	0.012	0.072	0.008	0.107	0.010
SC	0.895	0.012	0.051	0.008	0.054	0.010
Results of the dihybrid analysis						
CW	0.856	0.024	0.144	0.024	-	-

<sup>1</sup>Abbreviations as defined in Table II.

Three of the five mesoregions which clustered in the genetic distribution analysis (NW, MPOA, SC) also associated when the grandparents' nationalities were considered (Figure 2). In this case, however, mesoregion CW was included in this cluster and the most deviant mesoregion was now NE.

Two main groups were obtained when surnames were considered (Figure 3). Three of the mesoregions forming the cluster in Figure 1 (NE, NW, SC) were now separated from the other five, leading again to a northeast-southwest partition.

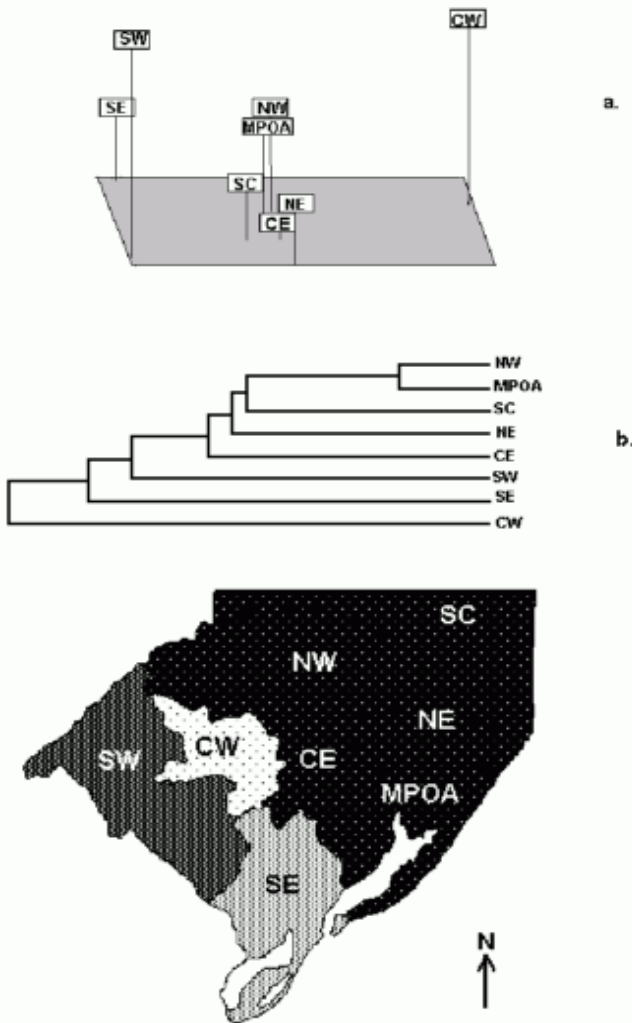
Finally, Figure 4 depicts the interethnic admixture. Two clusters were discernible, with mesoregion CW being completely isolated from both of them. One of the clusters included three of the five mesoregions grouped together in Figure 1 (NW, MPOA, NE), the other connecting SC with CE and, at a lower level, SE.

Mantel's (1967) coefficients were calculated to verify the congruence between these four sets of results (Table VI). As expected, distances based on genetic markers were correlated with those obtained using admixture estimates ( $r: 0.57; P = 0.044$ ), while distances based on grandparents' nationalities correlated with those calculated for the individuals' surnames ( $r: 0.61; P = 0.002$ ). On the other hand, there were no significant correlations between genetics, grandparents' nationalities and individuals' surnames. A multiple Mantel's (1967) correlation coefficient comprising these three matrices was also nonsignificant (multiple  $r: 0.317; P = 0.560$ ).

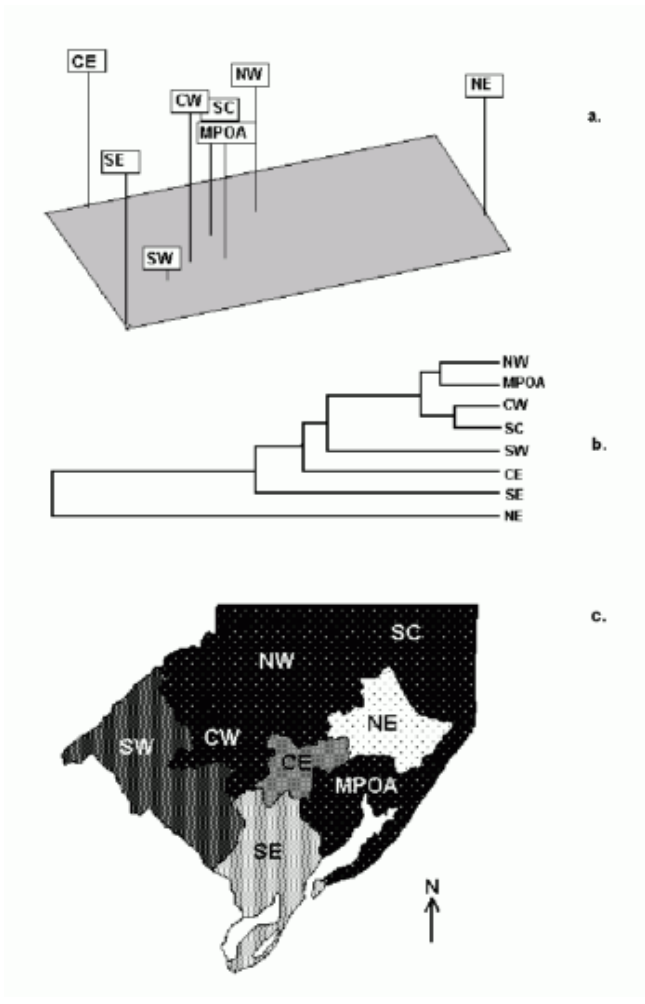
Table VII lists the seven phenotype associations between systems for which significant results were obtained at the 5% level. Based on the number of comparisons made (52), and using a probability value of 0.1%, only three of these associations (ACP/Hp, MNSs/Duffy, and Rh/ACP) remained significant.

**DISCUSSION**

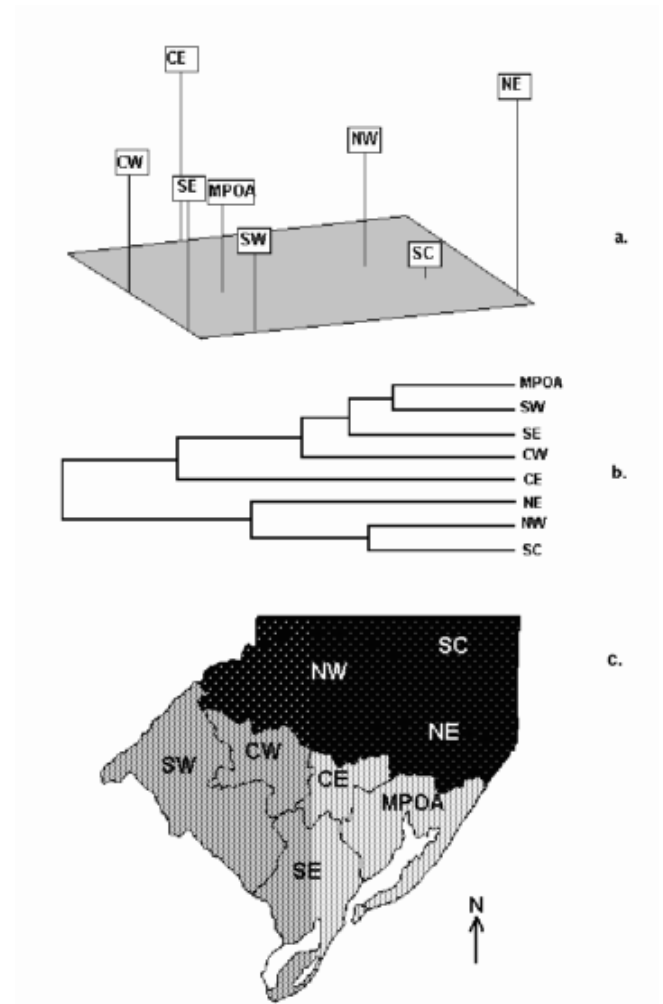
The allele frequencies obtained in the present study did not differ markedly from those found by others (cited in the Introduction and Subject and Method sections) in Rio Grande do Sul and Santa Catarina or in their putative parental groups. As expected, the level of interpopulation variability observed here ( $G_{ST}': 0.006$ ) was lower than that obtained for Europe as a whole ( $0.016 \pm 0.002$ ; Cavalli-Sforza *et al.*, 1994), since the geographical area considered was smaller, and the number of populations and loci examined was much less than those studied by the authors indicated above. The latter also evaluated more diversified populations.



**Figure 1** - Multivariate analyses of the genetic variation: (a) principal coordinates, (b) dendrogram obtained from the  $D_A$  distances, (c) map of both distributions. Shading is arbitrary, but indicates the major associations among mesoregions.



**Figure 2** - Multivariate analyses of the distribution of grandparents' nationalities: (a) principal coordinates, (b) dendrogram obtained from the  $D_A$  distances, (c) map of both distributions. Shading is arbitrary, but indicates the major associations among mesoregions.

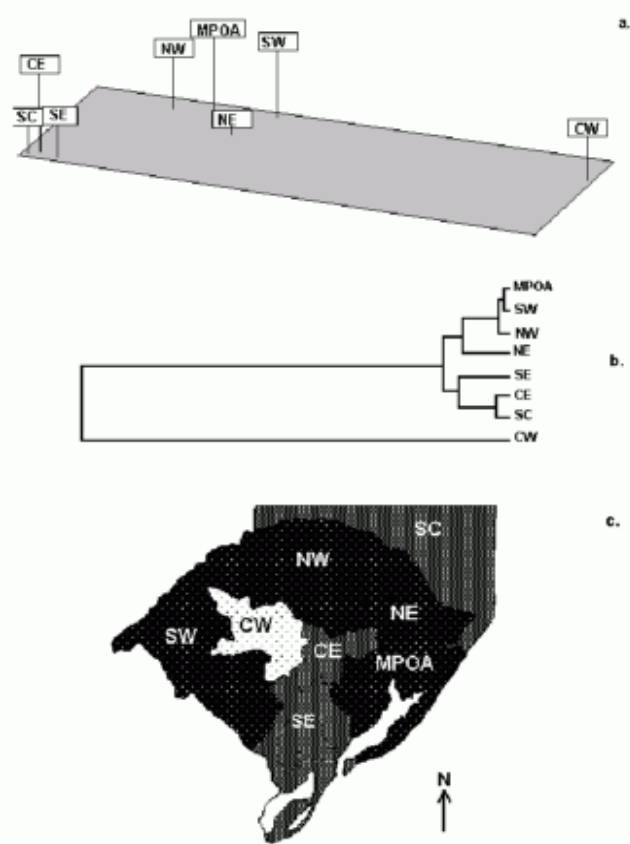


**Figure 3** - Multivariate analyses of the distribution of surnames: (a) principal coordinates, (b) dendrogram obtained from the  $D_A$  distances, (c) map of both distributions. Shading is arbitrary, but indicates the major associations among mesoregions.

The higher percentage of European contribution to the interethnic admixture in Santa Catarina (89%) compared to Rio Grande do Sul (82%) was expected, since the former has received a smaller number of non-Caucasian immigrants. But there are differences within Rio Grande do Sul that would also be expected on historical grounds. Thus, the lowest African admixture (3%) was found in mesoregion NE, an area in which the Italian contribution was most marked, while the highest (12%) was encountered in the SE, a region in which there was a high concentration of slave labor during the colonial period (Cesar, 1972). The average Amerindian contribution for Rio Grande do Sul as a whole (11%) was higher than expected, but the highest estimated Amerindian proportions were located in regions (SW, NW, and coastal portion of MPOA) where historically there were higher Indian concentrations (Freitas, 1987). Salzano (1997) summarized the previous estimates of interethnic admixture found in Southern Bra-

zil. For the European-derived population of Porto Alegre, the African contribution was found to be 8% (Franco *et al.*, 1982), exactly the same value observed here for metropolitan Porto Alegre. However, no trihybrid estimates were done in the above studies, which were restricted to urban populations. As shown by Sans *et al.* (1997) for Uruguay, important urban/rural differences in the prevalence of interethnic crossings may exist.

Four data bases (gene frequencies, grandparents' nationalities, individuals' surnames, and interethnic admixture) were used to analyze heterogeneity in the region studied. Although there was agreement between the two types of multivariate evaluations (dendrograms and principal coordinate analysis) used for all variables, differences were found when the four sets of data were considered. The non-genetic data clearly reflected the different European contributions to the composition of these populations. The clustering of mesoregions was attributable mainly to simi-



**Figure 4** - Multivariate analyses of the interethnic admixture: (a) principal coordinates, (b) dendrogram obtained from the  $D_A$  distances, (c) map of both distributions. Shading is arbitrary, but indicates the major associations among mesoregions.

**Table VI** - Agreement between distance matrices based on four sets of data obtained in Rio Grande do Sul and Santa Catarina. Upper triangle: Mantel's (1967) coefficients; lower triangle: P values.

	Genetic systems	Grandparents' nationalities	Individuals' surnames	Interethnic admixture
Genetic systems		0.253	0.307	0.574
Grandparents' nationalities	0.233		0.612	-0.136
Individuals' surnames	0.130	0.002		0.107
Interethnic admixture	0.044	0.476	0.319	

larities in the frequencies of German and Italian grandparents, on one hand, and similar prevalences of Italian, Polish, and Portuguese surnames on the other. The groups obtained were in agreement with the known first settlements of immigrants to these mesoregions. The Portuguese and Spanish were the first Europeans to arrive in Rio Grande do Sul, and the frequency of grandparents with these nationalities was low, the majority already being classified as Brazilians. The more recent migration of Germans (1824) and Italians (1870) (Cesar, 1972; Flores, 1990) was well represented by the separation of the NE (colonized mainly by Italians) and CE (Germans) mesoregions. The individuals' surnames, on the other hand, indicated that the state's population was becoming more homoge-

**Table VII** - Phenotype associations between systems (results significant at the 5% or lower levels).

Systems and their chromosome location	$\chi^2$	Degrees of freedom	Probability (P)	Corrected significance <sup>1</sup>	Phenotypes with highest associations
(9) <b>ABO/GLO1</b> (6)	18.17	10	0.052	NS	O/1-1 A1/2-1
(2) <b>ACP/Hp</b> (16)	285.41	10	<0.001 <sup>2</sup>	S	A/1-1 B/2-1
(2) <b>ACP/Duffy</b> (1)	11.03	5	0.051	NS	AB/Fya
(22) <b>P/Duffy</b> (1)	7.96	1	0.005	NS	P+/Fya
(4) <b>MNSs/Duffy</b> (1)	32.25	8	<0.001	S	MNSs/Fya Ms/Fya-
(4) <b>MNSs/P</b> (22)	22.26	8	0.004	NS	MSs/P NS/P-
(1) <b>Rh/ACP</b> (2)	105.85	52	0.001 <sup>2</sup>	S	DcEe/BC dce/AB

<sup>1</sup>Significance corrected relative to the number of comparisons made (52). NS: Nonsignificant; S: significant. <sup>2</sup> $\chi^2$  by Roff and Bentzen's (1989) method.



neous, still reflecting, however, the effect of more recent European migrations (Polish, among others).

The history told by social data is not completely matched by the genetic results. This may reflect the fact that the genetic markers used are too similar within Europe to detect the different capabilities of the derived ethnic and social groups to intercross, or to assess the length of time they have coexisted in a region. The only generalization possible is that of a distinction between the northern regions of Rio Grande do Sul and Santa Catarina, and the southern and western of Rio Grande do Sul. It is, however, noteworthy that despite the intense migratory flux that occurs in the whole area, we still have been able to detect this subdivision, which is probably a reflection of past settlements.

For the phenotype associations, nine previous studies (Shreffler *et al.*, 1971; Sinnock and Sing, 1972a,b; Brackenridge *et al.*, 1975; Rasmuson *et al.*, 1979; Mohan Raj *et al.*, 1990; Engrácia *et al.*, 1991; Hatagima and Krieger, 1994; Fañanás *et al.*, 1997) may be compared with the present one. Only three of the seven associations which were significant at the 5% level in our study were also found by the above authors. Two of these, MNSs/Duffy and Rh/ACP, showed a particularly strong association ( $P \leq 0.001$ ) here and were also observed by Rasmuson *et al.* (1979) and Engrácia *et al.* (1991), respectively. The remaining association (P/Duffy;  $P:0.005$ ) was also observed by Shreffler *et al.* (1971), although further analyses in the same population (Sinnock and Sing, 1972a,b) yielded conflicting results.

Since in all cases the systems involved are localized in different chromosomes, we can only speculate about the reasons for these associations. Population heterogeneity cannot explain these findings, since no significant genetic differences were observed among mesoregions. The remaining possibility is selective interaction, but there are as yet no specific physiological or biochemical indications in this direction. This is a subject worth further investigation.

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#### RESUMO

Uma amostra de 2.708 descendentes de europeus que vivem no Rio Grande do Sul, o qual foi subdividido em sete mesorregiões, e de 226 pessoas da mesma procedência provenientes de Santa Catarina foi estudada quanto a 17 sistemas genéticos protéicos, nacionalidades dos avós, sobrenomes dos indivíduos e mistura interétnica. Não foram encontradas

diferenças significantes entre as mesorregiões, os alelos que apresentaram a maior e a menor diferença sendo **GLO1\*2** (16%) e **PGD\*A** (2%), respectivamente. Os valores observados foram os esperados para descendentes de europeus, a maior diferença sendo uma menor prevalência do alelo **P\*1** (34-39%). Por outro lado, foi encontrada heterogeneidade significativa entre mesorregiões em relação às outras variáveis consideradas, a qual foi consistente com dados históricos. A contribuição ameríndia estimada para o conjunto gênico de descendentes de europeus da população do Rio Grande do Sul foi tão alta quanto 11%. O resultado mais geral obtido, considerando os quatro conjuntos de dados, foi o de uma tendência de divisão nordeste-sudoeste para as populações estudadas. Sete associações fenotípicas significativas entre sistemas foram obtidas a nível de 5% (três a nível de 0.1%). Duas destas foram também observadas por outros autores: MNSs/Duffy e Rh/ACP.

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