

STUDIES ON POLYMORPHISM SEGREGATION IN NORTHEASTERN BRAZIL. I. ANALYSIS OF MULTILOCI

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ABSTRACT

The population dynamics of several polymorphic systems were studied in two samples originated from Northeastern Brazil. A high frequency of gametic disequilibrium values between loci pairs was observed, which could be explained by the recent history of racial admixture of the population. However, for multiple loci segregation, no significant differences between the expected and observed numbers of homozygotes could be detected, indicating a lack of biological mechanisms acting on these complex genetic structures.

INTRODUCTION

Due mainly to methodological limitations and to the lack of suitable large samples, studies on genetic dynamics in natural populations are usually carried out on only one, or a maximum of two loci. Estimates of pairwise linkage disequilibrium values tend, in general, to seriously underestimate the intensity of gametic disequilibrium in multigenic models (Franklin and Lewontin, 1970). The concept of heterosis in quantitative genetics, the multiple homozygosity hypothesis (phenodeviants), constructed in order to explain the observed inbreeding effects on deleterious traits (Lerner, 1954) as well as simulation studies (cf. Yang *et al.*, 1990) are examples of theoretical approaches to the understanding of simultaneous behavior of several genes in populations.

In this communication we analyze the simultaneous segregation of several polymorphic loci, to verify the existence of possible disturbances at the multiple gene level.

MATERIAL AND METHODS

Two large samples, which have similar origins, were used in the analyses. Both were obtained at the "Hospedaria de Imigrantes", in the city of São Paulo, collected ten years apart and were composed of migrant families originated mainly from Northeastern Brazil. The first, called **Hosp I**, consisted of 3843 individuals belonging to 705 sibships. The following polymorphic systems were studied: ABO, PTC, Secretor, Gm, MNSs, Hp, Tf, Rh, Inv and Hb. Sampling details and other characteristics of the population sample are described elsewhere (Morton, 1964; Krieger *et al.*, 1965; Morton *et al.*, 1966).

The second sample, called **Hosp II**, consists of 1163 individuals belonging to 201 sibships with six polymorphic systems studied: ABO, Secretor, Hp, EsD and CA II (for details see: Krieger *et al.*, 1965; Barbosa, 1971, 1976; Cabello, 1972, 1976; Penalva da Silva, 1971, 1975; Mestriner, 1976; Mestriner *et al.*, 1977; Moro-Furlani, 1977; Russo, 1972).

The pair system analyses were performed by contingency tables and by comparisons between the observed joint phenotype frequencies and those expected under the assumption of genetic equilibrium for the two loci, on 2136 individuals of the parental generation of Hosp I and 3612 individuals from the same generation from Hosp II.

For the analysis of multiple loci segregation, the expected values for each locus studied were obtained either from the corresponding probabilities of the mating type

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pattern (for codominant systems) or from the conditional probabilities given by incomplete ascertainment (in which case, due to dominance, the genotype of the parents could not be inferred). For each family, probabilities were calculated for the offspring being homozygote for the genes of one, two, ..., n loci, by multiplying the separate probabilities and adding the corresponding terms.

RESULTS AND DISCUSSION

Tables I and II show, below the main diagonal, the values of the χ^2 contingency tables between genetic systems; the upper part shows the χ^2 values obtained from the comparisons between the observed joint phenotype frequencies and those expected under the assumption of genetic equilibrium, for both Hosp I and Hosp II, respectively.

The results show that in both samples there is an excess of genetic system pairs exhibiting significant departures from gametic equilibrium: only 2.25 and 0.75 would

be expected to be significant by chance alone for Hosp I and Hosp II, respectively. Although these figures include some systems showing internal departures from Hardy-Weinberg ratios, even with the removal of pairs including these genetic systems there remains an excess of systems pairs which depart significantly from gametic equilibrium.

The results of multilocus analyses are shown in Tables III and IV. For both samples, no significant departures from the genetic expectancies were detected. In fact, the segregation ratios show a remarkable degree of fit to the observed data, indicating that there is no excess (or lack) of homozygosity *per se*, when several loci are being analyzed simultaneously.

The above results are consistent with the fact that two loci haplotype frequencies are more often in gametic disequilibrium, than would be expected by theoretical consideration (Franklin and Lewontin, 1970), even in the absence of linkage. This fact, if not due to chance, is probably due to the recent history of racial admixture of the rural Northeastern Brazilian population (Krieger *et al.*,

Table I - Contingency (lower diagonal) and gametic proportions (upper diagonal) tables for a population from Northeastern Brazil (Hospedaria I) (chi-squared values).

	Gm	Inv	Hb	Hp	Tf	ABO	PTC	Rh	MNS ^U	Sec
Gm		99.6203* (24)	95.6333* (21)	96.8622* (24)	111.5075* (18)	105.1191* (33)	84.2058* (14)	188.6042* (71)	169.0868* (79)	81.2955* (14)
Inv	23.6732 (18)		17.5936* (6)	8.7858 (6)	11.1803* (4)	12.2895 (8)	8.5091* (3)	55.9597* (21)	55.5987* (23)	5.3931 (3)
Hb	34.1244 (27)	9.9370 (6)		6.9935 (6)	4.0780 (2)	8.0201 (8)	2.8241 (3)	32.3456* (19)	56.4841* (19)	9.0358* (3)
Hp	31.0211* (18)	2.9878 (4)	3.3008 (6)		5.8600 (6)	7.4620 (8)	6.9180 (3)	22.9412 (23)	51.9896* (24)	21.4868* (3)
Tf	18.8402 (27)	4.9095 (6)	1.8870 (9)	3.0965 (6)		5.7415 (7)	4.8102 (3)	40.7986* (14)	140.4813* (17)	1.5349 (3)
ABO	34.5421 (27)	6.2492 (6)	5.5719 (9)	4.7919 (6)	4.6121 (9)		3.7012 (4)	48.5460* (28)	119.7112* (33)	0.4365 (4)
PTC	14.0638 (9)	3.1602 (2)	1.2296 (3)	4.8274 (2)	2.9507 (3)	3.3131 (3)		16.1907 (12)	46.7659* (15)	3.9076* (1)
Rh	122.8153* (90)	43.5022* (20)	21.9201 (30)	15.7080 (20)	11.2416 (30)	36.3077 (30)	9.7757 (10)		218.0121* (62)	15.3395 (11)
MNS ^U	99.9500 (90)	17.5852 (20)	16.1545 (30)	25.7889 (20)	108.2253* (30)	36.4364 (30)	11.3250 (10)	102.4256 (100)		42.7062* (15)
Sec	15.7010 (9)	0.3659 (2)	7.2609 (3)	15.6298* (2)	0.9719 (3)	0.1251 (3)	3.8956* (1)	9.4124 (10)	5.5405 (10)	

* = Significant association at the 5% level.

() = Degrees of freedom.

Table II - Contingency (lower diagonal) and gametic proportions (upper diagonal) tables for a population from Northeastern Brazil (Hospedaria II) (chi-squared values).

	Sec	ABO	Hp	MN	Es D	CA II
Sec		2.1982 (4)	10.7156* (3)	3.5924 (3)	4.1079 (3)	4.8596 (3)
ABO	5.4788 (3)		18.3314* (8)	7.7355 (8)	11.8022 (8)	23.8312* (8)
Hp	0.8871 (2)	6.6274 (6)		17.7618* (6)	15.2631* (6)	14.5843* (6)
MN	2.4833 (2)	5.5792 (6)	6.4358 (4)		7.2035 (6)	10.1179 (6)
Es D	0.5480 (2)	5.3773 (6)	3.4140 (4)	1.6124 (4)		9.2901 (6)
CA II	0.1055 (2)	11.3001 (6)	2.7241 (4)	1.5275 (4)	0.5313 (4)	

* = Significant association at the 5% level. () = Degrees of freedom.

Table III - Simultaneous segregation analysis of 10 loci.

		HOSP I												
		Number of homozygous offspring for												
		0 locus		1 locus		2 loci		3 loci		4 loci		5 loci		
TNF		obs.	exp.	obs.	exp.	obs.	exp.	obs.	exp.	obs.	exp.	obs.	exp.	
705		1	0.3035	18	15.5719	175	161.1401	586	578.8191	831	828.8586	539	572.6300	
d =		1.5981		0.3786		1.1921		0.0891		0.0055		1.9750		
		6 loci		7 loci		8 loci		9 loci		10 loci		N	χ^2	DF
TNF		obs.	exp.	obs.	exp.	obs.	exp.	obs.	exp.	obs.	exp.			
705		212	206.7600	40	38.8800	5	5.4100	2	0.5000	0	0.0300	2409	2150.1240	1966
d =		0.1328		0.0322		0.0317		4.5219		0.0264				

Note: $d = \frac{(obs - exp)^2}{exp}$

TNF = Total number of families.

$\chi^2 = 9.9835$

χ^2

DF

Total	2150.1240	1966
Effect	9.9835	10
Residual	2140.1404	1956

1965; Russo, 1972). Mi and Morton (1966) using part of the same material, reached a somewhat different conclusion. This could be due to rather different approaches (they used binary factors, rather than alleles) and to the significance level utilized.

When several loci were considered simultaneously, the approach used did not reveal the existence of

evolutionary mechanisms acting on structures more complex than single loci or pairs of loci.

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Table IV - Simultaneous segregation analysis of six loci.

TNF	HOSP II												N	χ^2	DF		
	Number of homozygous offspring for																
	0 locus		1 locus		2 loci		3 loci		4 loci		5 loci					6 loci	
obs.	exp.	obs.	exp.	obs.	exp.	obs.	exp.	obs.	exp.	obs.	exp.	obs.	exp.				
201	4	2.8330	38	44.8069	172	175.4277	251	262.4431	207	196.1185	75	66.2131	6	5.1548	753	591.3872	597
d -	0.4808		1.0341		0.0670		0.4989		0.6938		1.1661		0.1386				
$\chi^2 - 3.9892$																	
		χ^2		DF													
Total		591.3872		597													
Effect		3.9892		6													
Residual		587.3979		591													

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RESUMO

A dinâmica de dois ou mais sistemas foi estudada em duas amostras do nordeste brasileiro. Uma alta frequência de desequilíbrio gamético entre pares de locos foi observada, podendo ser explicada pela história recente de mistura racial daquela população. Na análise de segregação de múltiplos locos, não foram observadas diferenças entre os números de homozigotos observados e esperados, indicando a ausência de mecanismos biológicos atuando sobre estruturas genéticas complexas.

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