

The Relationship of the HLA Phenotype Frequency of the Alleged Father to the Resulting Paternity Index in Caucasian Non-Exclusion Paternity Cases

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INTRODUCTION

The system paternity index (PI) is derived from the phenotypes of the trio and its value in non-exclusion cases is primarily determined by the gene frequency of the paternal gene (obligatory gene) transmitted to the child. This study was undertaken to determine: 1) The range of HLA phenotype frequencies observed in our laboratory among non-excluded caucasian alleged fathers, 2) the distribution of the resulting paternity index values in these cases and 3) the relationship of these two distributions to each other.

METHODS

Five hundred consecutive trio paternity cases involving caucasians with non-exclusions were reviewed to tabulate the HLA phenotype frequencies of the alleged fathers and the resulting HLA paternity index values. The HLA phenotype frequencies and PI values were derived using the Traver (1989) computer program. Haplotype frequencies in the data base were those published by Mickey et al. (1983) based on 5559 caucasian individuals from paternity cases and the HLA A and B specificities recognized by the 1980 Histocompatibility Workshop. The laboratory was able to define 16 A locus and 28 B locus serological specificities which could yield over 45,000 possible phenotypes.

RESULTS

Observed HLA phenotype frequencies ranged from 0.000002 (1 in 500,000) to 0.0094 (1 in 106) with a median of 0.00038 (1 in 2600) (Fig. 1). Observed HLA PI values ranged from 1 to 1438 with a median of 27 (Fig. 2). Subpopulations of the study group are shown in the table below.

<u>Phenotype Frequencies</u>	<u>n</u>	<u>%</u>	<u>Median PI</u>
>1 in 1,000	135	27	9
1 in 1,000 - 1 in 10,000	236	47	26
1 in 10,000 - 1 in 100,000	112	23	76
<1 in 100,000	<u>17</u>	<u>3</u>	<u>175</u>
	500	100	27

The distribution of the observed HLA phenotype frequencies, paternity index values, and the relationship of these two distributions are displayed in Figures 1,2, and 3, respectively.

DISCUSSION

The biologic father, by definition, must share genetic markers with his child in all genetic systems. When they share an infrequent marker, the likelihood of paternity is greatly increased. In the HLA system, all genetic markers are infrequent, although there is a 4 log range of variance in the Class I gene frequencies. The HLA phenotype frequencies and the resulting PI values were negatively correlated ($r = -0.606$; $p \leq 0.00001$). Alleged fathers phenotype frequencies of <1 in 100,000 have PI values which are usually >100 (median 175) while alleged fathers phenotype frequencies of >1 in 1,000 have PI values <70 (median 9). Deviations from the usual reciprocal relationship occur when the alleged father has a phenotype of relatively moderate frequency in which instance he could transmit either a rare haplotype resulting in a high PI value or a more common haplotype resulting in a low PI. Therefore, the correlation in this mid-range (1 in 1,000 to 1 in 100,000) has little predictive value due to the broad distribution in the data about the least squares line of regression.

REFERENCES

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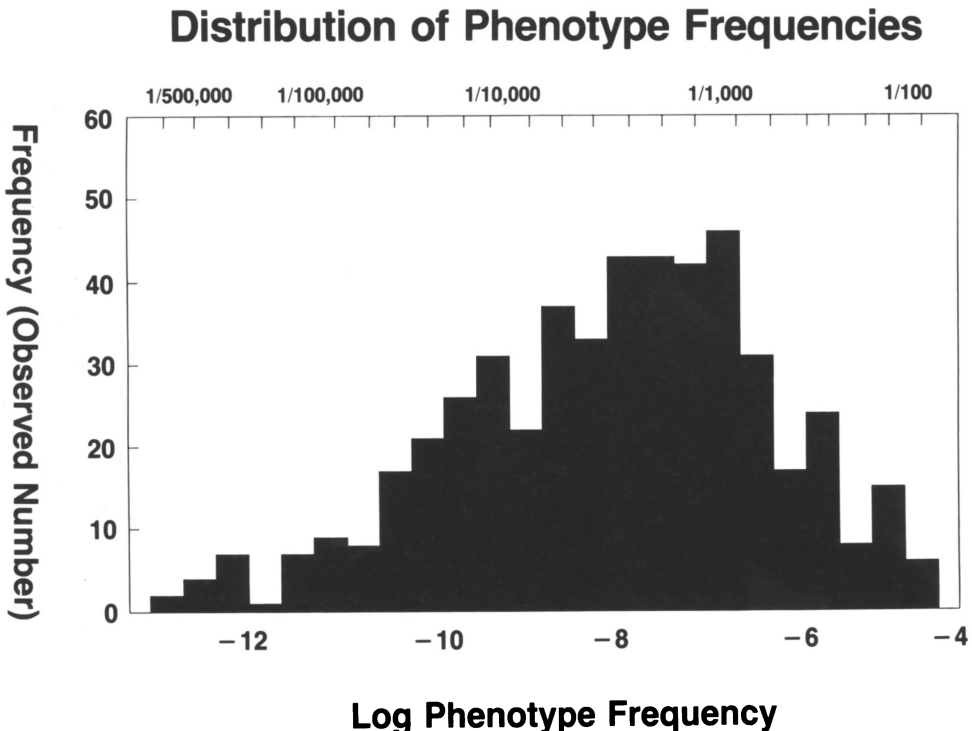


Fig. 1. Distribution of Phenotype Frequencies

Distribution of Paternity Index Values

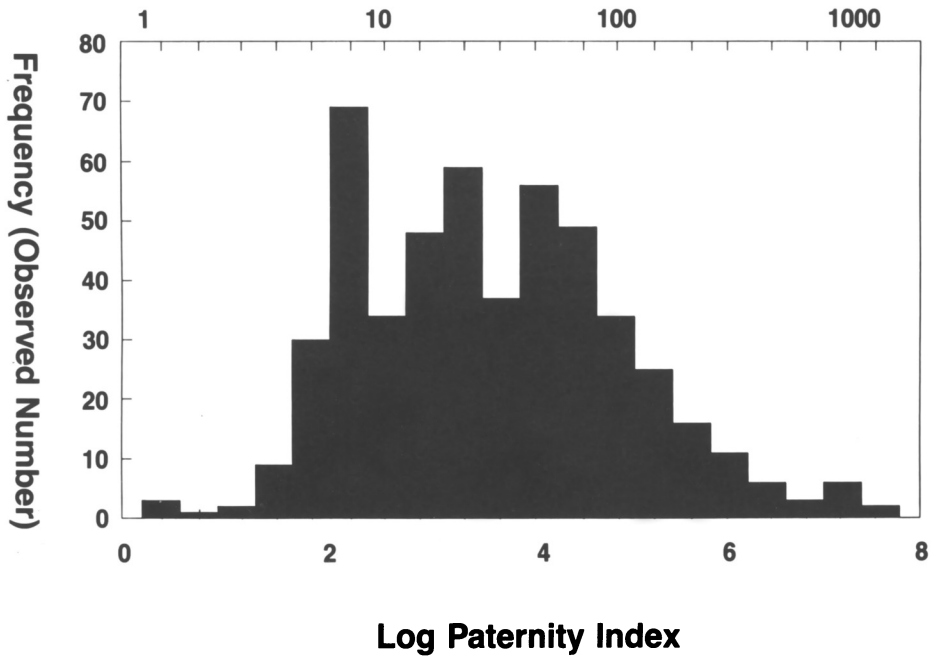


Fig. 2. Distribution of Paternity Index Values

Regression of Log Paternity Index Versus Log Phenotype Frequency

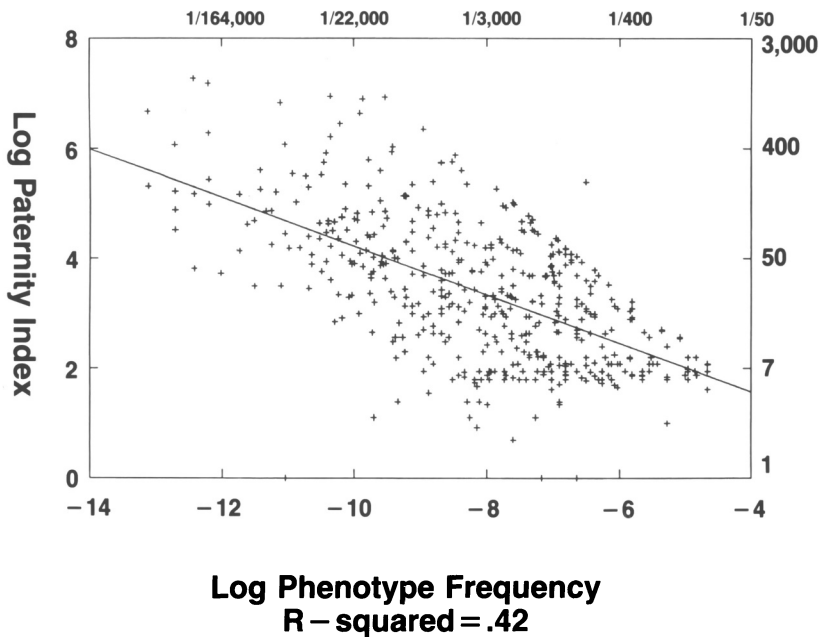


Fig. 3. Phenotype Frequency versus Paternity Index