

## Letter to the Editor

### PROBABILITY OF NONPATERNITY DETERMINED BY MULTIPLE ALLELE CODOMINANT SYSTEMS

*To the Editor:* The average probability of nonpaternity is usually defined as the likelihood a specific genetic system will exclude a falsely accused male in a paternity action. A number of published reports explore the chances of proving nonpaternity employing evidence from genetic analysis. Weiner [1] briefly reviews the history of these calculations for the major blood group systems. The exact formulas for many of these calculations depend on the specific system being considered (e.g., ABO [2], Rh [3], and MNSs [4]).

For codominant systems where all genotypes are detectable, it is possible to express the probability of nonpaternity in a general form. If

$$p_1, p_2, \dots, p_k \left( \sum_{i=1}^k p_i = 1.0 \right)$$

represent the gene frequencies associated with a codominant system with  $k$  alleles, then  $P$  (nonpaternity) =

$$\sum_{i=1}^k \{p_i [1 - p_i]\}^2 + \sum_{i>j} p_i p_j \{[1 - p_i]^3 + [1 - p_j]^3 + [p_i + p_j] [1 - (p_i + p_j)]^2\},$$

where the assumption is made that all individuals involved in the paternity case come from a large random mating population at equilibrium (random with respect to the genetic system employed).

The following justifies the above expression for the average probability of paternity for a  $k$  allele system. Consider two specific alleles symbolized by  $A$  and  $B$  with gene frequencies  $p_i$  and  $p_j$ . Four possible exhaustive and mutually exclusive mother-child pairs arise, namely, (1)  $AX-AA$ , (2)  $AY-AB$ , (3)  $BZ-AB$ , and (4)  $AB-AB$ .  $X$  represents the presence of any one of the  $k$  alleles,  $Y$  represents the presence of any one of the  $k$  alleles not equal to  $B$  (frequency,  $1 - p_j$ ), and  $Z$  represents the presence of any one of the  $k$  alleles not equal to  $A$  (frequency,  $1 - p_i$ ). Therefore, the population frequencies of the four mother-child pairs in a large random mating population at Hardy-Weinberg equilibrium are: (1)  $AX-AA = p_i^2$ , (2)  $AY-AB = p_i p_j (1 - p_j)$ , (3)  $BZ-AB = p_i p_j (1 - p_i)$ , and (4)  $AB-AB = p_i p_j (p_i + p_j)$ . These mother-child pairs each exclude specific paternal genotypes. These genotypes and their associated probability of exclusion are: (1) the  $AX-AA$  pair excludes all men who do not possess an  $A$  allele. The population frequency of these men is  $(1 - p_i)^2$ ; (2)  $AY-AB$  pair excludes all men who do not possess a  $B$  allele. The population frequency of these men is  $(1 - p_j)^2$ ; (3) the  $BZ-AB$  pair excludes all men who do not possess an  $A$  allele. The population frequency

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of these men is  $(1 - p_i)^2$ ; and (4) the  $AB-AB$  pair excludes all men who possess neither an  $A$  nor a  $B$  allele. The population frequency of these men is  $(1 - p_i - p_j)^2$ . The probability that a randomly selected man possess allele  $A$  or  $B$  or both is  $p_i(2 - p_i) + p_j(2 - p_j) - 2p_i p_j$ , giving the complementary probability  $1 - [p_i(2 - p_i) + p_j(2 - p_j) - 2p_i p_j] = (1 - p_i - p_j)^2$  of possessing neither alleles  $A$  nor  $B$ .

Combining the exclusion probability for each mother-child pair with the frequency of the mother-child pairs in the population gives the probability of exclusion for a specific system from evidence supplied by the genes  $A$  and  $B$  as  $p_i^2[(1 - p_i)^2] + p_j^2[(1 - p_j)^2] + p_i p_j(1 - p_j)[(1 - p_j)^2] + p_i p_j(1 - p_i)[(1 - p_i)^2] + p_i p_j(p_i + p_j)[(1 - p_i - p_j)^2]$ . The sum over all  $k$  alleles yields the expression given above for the average probability of paternity.

Special cases of the probability of nonpaternity expression are well known. For example, a codominant system with two alleles ( $k = 2$ ) yields a probability of nonpaternity of  $p_1 p_2(1 - p_1 p_2)$ , which appears in several textbooks [5]. For three alleles ( $k = 3$ ), the general expression given above agrees with the results obtained by Weiner [1], which are somewhat more compact.

The maximum value for the probability of nonpaternity for  $k$  allele codominant systems is achieved when all gene frequencies are equal. That is, the maximum  $P$  (nonpaternity) is  $(k - 1)(k^3 - k^2 - 2k + 3)/k^4$ , which occurs when  $p_1 = p_2 = \dots = p_k = 1/k$ , and can be demonstrated by applying Lagrange's method of maximization [6]. Maximum probability of nonpaternity values are given in table 1 for genetic systems with up to 10 alleles ( $k = 2, 3, \dots, 10$ ). Also noteworthy is that the probability of nonpaternity increases as the number of alleles within a system increases.

The probability of detecting nonpaternity plays a fundamental role in judging the efficacy of various genetic systems for detecting nonpaternity. For example, the erythrocyte acid phosphatase (EAP) system among whites ( $p_1 = .327$ ,  $p_2 = .612$ , and  $p_3 = .061$ ) gives  $P(\text{nonpaternity}) = .234$ , whereas among blacks ( $p_1 = .223$ ,  $p_2 =$

TABLE 1  
MAXIMUM PROBABILITY OF NONPATERNITY FOR CODOMINANT GENETIC SYSTEMS OF  $k$  ALLELES WHEN ALL GENOTYPES ARE DETECTABLE

| $k$ | Maximum*          |
|-----|-------------------|
| 2   | 3/16 = .188       |
| 3   | 30/81 = .370      |
| 4   | 43/256 = .504     |
| 5   | 372/625 = .595    |
| 6   | 855/1296 = .660   |
| 7   | 1698/2401 = .707  |
| 8   | 3045/4096 = .743  |
| 9   | 5064/6561 = .772  |
| 10  | 7447/10000 = .795 |

\* Maximum =  $(k - 1)(k^3 - k^2 - 2k + 3)/k^4$ .

.771, and  $p_3 = .006$ ), the same probability is .151. Both cases show that the EAP system is fairly effective for detecting nonpaternity when compared with the maximum possible value of .370.

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