On the power of excluding relatives of the true father from paternity

Yue-Qing Hu[a,*], Wing K. Fung[b], C.T. Yang[b]

[a] *Department of Mathematics, Southeast University, Si Pai Lou 2#, Nanjing 210096, China*
[b] *Department of Statistics and Actuarial Science, The University of Hong Kong, Pokfulam Road, Hong Kong, China*

Abstract. The power of excluding a random man from paternity in a structured population for genetic tests for each of the with-mother and no-mother cases is considered. The situation in which a paternal relative of the child is to be excluded from paternity in such a population is also addressed. A simple relationship is found to hold between the power of excluding a random man from paternity and that of excluding a paternal relative of the child. Population allele frequency data for 12 STR loci in the Hong Kong Chinese are used to show numerically the effect of population structure on the exclusion probabilities. © 2003 Elsevier B.V. All rights reserved.

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1. Introduction

The necessity of taking account of genetic differences between subpopulations for forensic DNA investigation was addressed by various researchers [1–4]. For persons originating from the same subpopulation, Balding and Nichols [2] derived a formula for assigning probabilities to a set of alleles, incorporating the coancestry coefficient θ into the calculation, where the parameter θ is essentially the same as Wright's F_{ST} [5].

A genetic marker can be characterized by its ability to exclude a random man or a relative of the child from paternity in a standard trio (with-mother) or no-mother case. Formulae for the power of excluding (PE) a random man from paternity were provided by Ohno et al. [6]. However in many situations, particularly immigration cases, the false father is more likely to be a relative, e.g. brother, of the true father than an unrelated man. In view of this, Fung et al. [7] considered the probability of excluding a relative of the true father from paternity and provided formulae for estimating such probability under different circumstances. All the above work, however, is premised on the Hardy–Weinberg law which essentially assumes a structureless population. In subdivided populations, the expressions of the power of excluding a random man from paternity in the with-mother

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* Corresponding author. Tel.: +86-25-3792315; fax: +86-25-7712719.
E-mail address: huyq@seu.edu.cn (Y.-Q. Hu).

and no-mother cases were derived in this study. A linear relationship between the power of excluding a random man and that of excluding a paternal relative of the child was exhibited. The Hong Kong Chinese population database of 12 STR loci was used to show numerically the effect of population structure on the probabilities of exclusion.

2. Results

Recently, Ayres [8] and Hu et al. [9] independently derived equivalent expressions of $Q_1(\theta)$ and $Q_2(\theta)$, though look differently, the power of excluding an unrelated man from paternity in a structured population for the with-mother and no-mother cases, respectively. The details of derivation of $Q_1(\theta)$ and $Q_2(\theta)$ can be referred to in Hu et al. [9], and the formulae can be found in Ayres [8] and Hu et al. [9].

It is not uncommon in immigration cases that the false father is more likely to be a paternal relative, e.g. a brother of the true father (TF) than an unrelated man. Thus in the following, we like to evaluate the probability of excluding a paternal relative from paternity, $Q_3(\theta)$ for the with-mother case and $Q_4(\theta)$ for the no-mother case, in a structured population. Here, we use symbol R to stand for a paternal relative of the true father of the child (C). The mother (M) is assumed to be independent on both TF and R.

Let $(k_0, 2k_1, k_2)$ be the kinship coefficients of individuals TF and R, Fung et al. [7] has derived P [none of the alleles of C and R is identical by descent (ibd)]= $k_0 + k_1$. Since R is excluded from the parentage of C, R and C cannot share ibd alleles. Given R and C share no ibd alleles, R can be treated as a random man, i.e. R is unrelated to both M and C, in the process of calculating joint genotype probabilities. Thus, it leads immediately to $Q_3(\theta)=(k_0+k_1)Q_1(\theta)$, and $Q_4(\theta)=(k_0+k_1)Q_2(\theta)$.

The powers of exclusion $Q_1(\theta)$, $Q_2(\theta)$, $Q_3(\theta)$, and $Q_4(\theta)$ for each locus yields immediately the overall powers for several loci. The powers of exclusion allowing for one or two mismatches can also be yielded at once [7].

3. Example and discussion

For the allele frequency data at 12 STR loci for the Hong Kong Chinese [10] and $\theta=0$ and 0.03, the overall powers of exclusion for 0, 1, and 2 mismatches are presented in Table 1. $Q_3(\theta)$ and $Q_4(\theta)$ in Table 1 give the powers of excluding an uncle of the child from paternity. From Table 1, it is observed that the power of exclusion decreases as θ increases.

Table 1
Powers of exclusion for 0, 1 and 2 mismatches, $Q_1(\theta)$, $Q_2(\theta)$, $Q_3(\theta)$, and $Q_4(\theta)$ for Hong Kong Chinese with coancestry coefficient θ

PE	θ	Overall	At most 1 mismatch	At most 2 mismatches
$Q_1(\theta)$	0	0.99998	0.99957	0.99622
	0.03	0.99994	0.99953	0.99590
$Q_2(\theta)$	0	0.99849	0.98636	0.93537
	0.03	0.99682	0.97484	0.89644
$Q_3(\theta)$	0	0.98357	0.90213	0.71846
	0.03	0.97814	0.89991	0.71396
$Q_4(\theta)$	0	0.93659	0.74707	0.46705
	0.03	0.91746	0.69622	0.40435

This is expected as a bigger θ virtually means a higher level of relatedness among members of the population, so it is more difficult to exclude a false father from paternity.

$Q_1(\theta)$ in Table 1 shows that the panel of the 12 STR systems has a high ability to exclude an unrelated man from paternity of the child. In the motherless case, as expected, the power of exclusion $Q_2(\theta)$ in each entry becomes smaller compared to $Q_1(\theta)$.

It is noted that some of the overall powers of exclusion $Q_3(\theta)$ and $Q_4(\theta)$ are rather small, particularly in the case that makes allowances for two mismatches. When θ changes from 0 to 0.03, the overall power of exclusion $Q_4(\theta)$ drops, for 0, 1, and 2 mismatches, by respectively, 2.0%, 6.8%, and 13%. From the results of $Q_3(\theta)$ and $Q_4(\theta)$, it is obvious that the panel of the 12 STR systems may not be very informative for distinguishing close relatives from paternity in a structured population. For doubtful cases, it seems that more loci need to be used.

Acknowledgements

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