Determination of Incest in Forensic Casework Using Multi-locus DNA Profiling

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INTRODUCTION

Recently we have described an approach based on computer Monte-Carlo simulations of human multi-locus DNA fingerprints, to estimating genetic relatedness between individuals (Ivanov et al. in press). Briefly, we have developed, through statistical modelling, frequency distributions of similarity between DNA profiles belonging to the known types of relatives. Thus, the probability that the given estimate of similarity is associated with a particular degree of relatedness could be directly assayed. As we have shown, the model yielded reliable estimates for detecting consanguinity and distinguishing biological relationships.

In the present study, we used the principle of this treatment to go on to establish a method for determining incest in forensic casework.

METHODOLOGY

The large number of "phantom" multi-band DNA profiles were independently computer simulated in the spirit of the model previously described (Ivanov et al.; Maljutov et al. in press) in line with the basic genetic formalization underlying the DNA fingerprinting technique (Jeffreys et al.1985,1987). These profiles constitute the parent population for producing offspring phantom profiles. For each randomly chosen pair of profiles which is considered to be the parent pair, the offspring phantom profile was simulated, where the inheritance of bands was modelled according to Evett et al.(1989). Then, for this offspring phantom, the partner profile was randomly chosen to constitute the new parent pair, and the next degree offspring phantom was generated as above. Such a cycle can be repeated as many times as needed for reaching the desired genetic level. On the other hand, instead of random partner one can consider the partner to be relative of prescribed genetic order. Thus, an incest case of any type could be modelled. The whole procedure was prepared independently L=1000 times to produce statistically acceptable data.

Then, frequency distributions of similarity were computer deve-

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loped for pairwise comparisons between DNA profiles of questioned individuals. Statistic relation index, R, was used as an operational measure of similarity (Ivanov and Verbovaya 1990). R is defined as a ratio: the amount of matched bands/total amount of scorable band positions within the pair of profiles A and B: $R = S_{AB}/(n_A + n_B - S_{AB})$, where n_A and n_B are the numbers of component bands in each fingerprint under comparison; S_{AB} is the number of shared bands.

RESULTS AND DISCUSSION

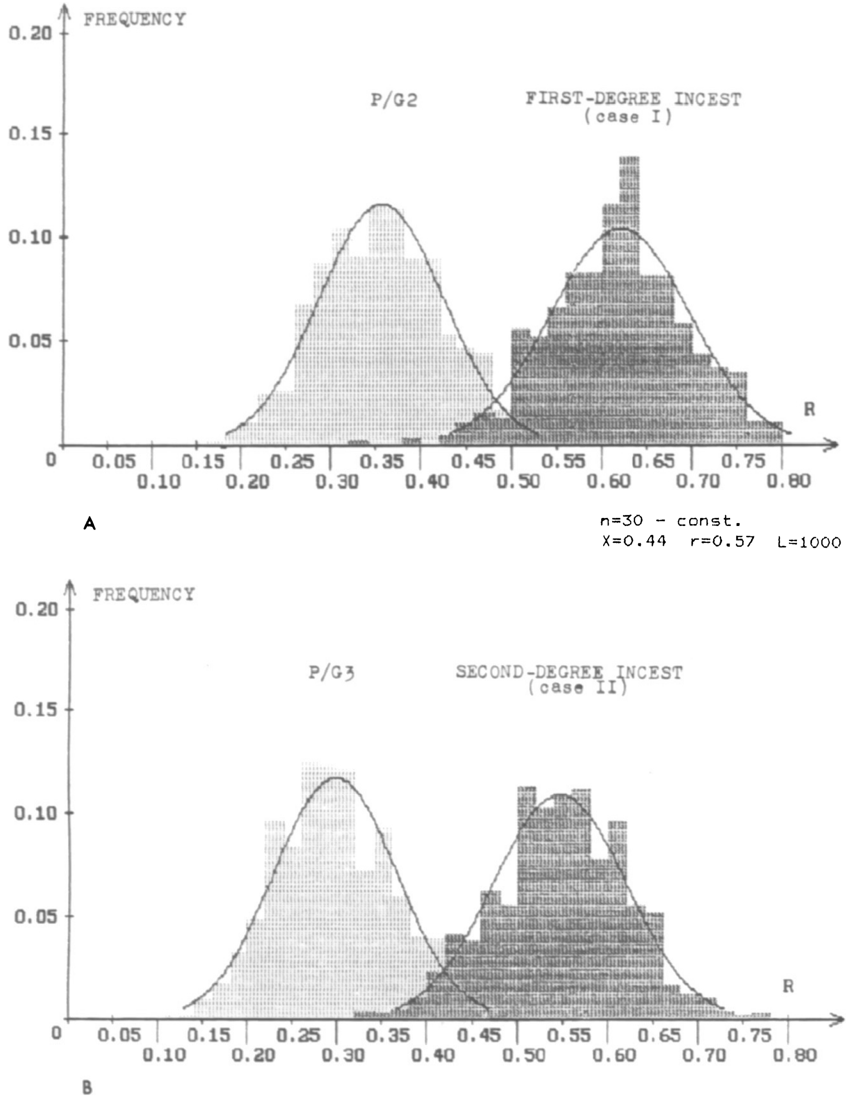
Several types of the extreme parentage cases involving incest were modelled. In Case I, a father and a child is the first-degree relative of the mother (i.g. her father or brother). In Case II, a father of a child is the second-degree relative of the mother (i.g. her uncle or grandfather). The alternative outbred version of each pedigree in dispute was modelled as well. For each class of cases R frequency distributions were simulated between DNA fingerprints of inbred father and the child and,in parallel, between the corresponding outbred relatives: parent and second- or third-degree offspring (for Case I and Case II, respectively). The results are presented in Fig. 1, where graphic hystograms and approximating normal densities as well as corresponding numerical hystograms are shown.

It is apparent, that R is appreciably higher in parentage cases involving incest when compared with alternative relative pairs from outbred pedigrees. One can consider differences between R value averages as being statistically significant in such kind of comparisons. The mean probability of non-distinguishing between alternative degrees of relatedness in situations as modelled was estimated to be approximately 10%, which corresponds to discriminatory capability of 90%.

It should be noted that incest will also increase the similarity of DNA profiles between the child and the mother (data not shown). However, distinguishing between outbred and inbred maternity cannot be readily made because of intrinsic very short genetic distance. Meanwhile, when the focus is being on paternity, the two hypotheses are fairy distinguishable in the mean. Therefore, the approach is sufficiently informative for establishing incest or, alternatively, for identifying falsely accused relative in the majority of practical cases. On the other hand, inclusionary statistics for particular case can be produced using the tail probabilities for predicted relatedness, as it is illustrated in Case report.

CASE REPORT

By means of this approach, the authors succeeded in determining incest in forensic case when the suspect was charged with violation against his grand-daughter involving impregnation of the victim (Fig. 2).



n=30 - const.
X=0.44 r=0.57 L=1000

R	P/G2	INCEST case I
0.025	0	0
0.050	0	0
0.075	0	0
0.100	0	0
0.125	0	0
0.150	0	0
0.175	0	0
0.200	4	0
0.225	21	0
0.250	38	0
0.275	56	0
0.300	97	0
0.325	115	0
0.350	167	0
0.375	145	1
0.400	114	0
0.425	100	1
0.450	64	4
0.475	28	16
0.500	25	18
0.525	19	64
0.550	5	72
0.575	1	105
0.600	1	108
0.625	0	133
0.650	0	160
0.675	0	77
0.700	0	91
0.725	0	56
0.750	0	44
0.775	0	33
0.800	0	8
M	0.353	0.620
SD	0.067	0.075

R	P/G3	INCEST caseII
0.025	0	0
0.050	0	0
0.075	0	0
0.100	0	0
0.125	1	0
0.150	8	0
0.175	30	0
0.200	40	0
0.225	86	0
0.250	72	0
0.275	157	1
0.300	149	0
0.325	121	2
0.350	145	2
0.375	67	5
0.400	66	14
0.425	27	29
0.450	10	51
0.475	13	80
0.500	5	64
0.525	3	138
0.550	0	127
0.575	0	124
0.600	0	95
0.625	0	94
0.650	0	89
0.675	0	28
0.700	0	28
0.725	0	20
0.750	0	5
0.775	0	3
0.800	0	1
M	0.294	0.549
SD	0.068	0.078

Fig. 1. Monte-Carlo simulations of similarity between human multi-band DNA profiles for alternative degrees of relatedness. Graphic hystograms, approximating normal densities and numerical consequences of the treatment are shown.
A: frequency distributions of "MvaI/M13" relation index (R) simulated among parent/second-degree offspring pairs (P/G2), and corresponding critical relatives as modelled for incest Case I.
B: frequency distributions of "MvaI/M13" relation index (R) simulated among parent/third-degree offspring pairs (P/G3), and among corresponding critical relatives as modelled for incest Case II.
Parameters of the basic model (Maljutov et al., in press), corresponding means (M) and standard deviations (SD) are indicated. The data used to detect incest in particular forensic investigation are boxed. For detailes see text

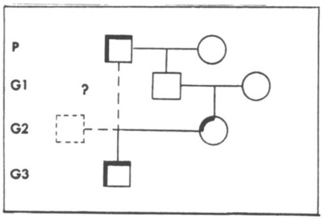


Fig. 2. Scheme for the questioned pedigree

Significantly, that DNA fingerprint test has not revealed any unassigned bands in a disputed trio. In standard paternity dispute, when the parents of the child are nonrelatives, such a result is satisfactory evidence to prove paternity positively. However, family relatedness between the mother and alleged father will obviously increase the possibility that this could have occured by chance. Therefore, as the direct exclusion by parental mismatches cannot be made, the probabilities should be calculated for inclusion estimate.

The critical pair alleged father/son, which should be apriori considered as formal P/G3 (i.e. great-grandfather/great-grandson) yielded R value of 0.65. In the spirit of the approach reported here, this is suggestive of high degree of relatedness and one could argue that the suspect might be rather biological father of the child, than his great-grandfather (Fig.1B). Following the reasoning by Evett and Buckleton (1989), we evaluated the evidence under these two alternative explanations, by calculating the Bayesian likelihood ratio, which in this case exceeded 900.

Such an evidence strongly supports paternity version, and has been accepted by court as satisfactory evidence for establishing incest.

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