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Empirical Validation of the Essen-Möller Probability of Paternity

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SUMMARY

The validity of the Essen-Möller formulation probability of paternity is supported by demonstrating its correctness in a model genetic system—the ABO system. An analysis was made of 1,393 paternity cases typed uniformly for HLA-A and -B, ABO, Rh, and MNSs, in which the mother named one man only as the child's father and in which both mother and putative father identified themselves as Caucasian. For purposes of analysis, putative fathers not excluded from paternity by the four systems tested were regarded as actual fathers. The joint distribution of observed triplets of ABO phenotypes is shown to be statistically consistent with expected values, and the fractions of "true" fathers for a given triplet closely approximated the probability of paternity calculated using a realistic prior probability. Recent allegations of fallaciousness of the method by Li and Chakravarty and Aickin are discussed in terms of the results presented.

INTRODUCTION

Recent articles by Li and Chakravarti [1] and by Aickin [2] asserted that the Essen-Möller formulation of probability of paternity is fallacious. If these assertions have merit, the results obtained using the Essen-Möller approach [3] should yield empirically demonstrable false results. It is possible to check this proposition of falsity by considering calculations for the ABO system as a model by considering paternity established if paternity is not excluded by the HLA, ABO, Rh, or MNS systems. The four systems result in about 97% exclusion of unrelated nonfathers in Caucasian populations and result in about 1% misclassification of "fathers" in cases in which the mother names one man only as the child's father and in which the named man is not related to the

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mother—the one-man case. This rate of misclassification is trivial relative to the probabilities of paternity computed for the ABO system only, so that the ABO system provides a convenient test case.

We considered 1,393 successive one-man cases tested at the Paternity Evaluation Section of the UCLA Tissue Typing Laboratory in which both the woman and the man identified themselves as Caucasian. The mother resided in the Los Angeles area in approximately 40% of the cases. The mother resided elsewhere in California in approximately 25% of the cases, and in other states, in approximately 35% of the cases.

The Essen-Möller formula for the one-man case is

$$P = \frac{pP_1(M,F,C)}{pP_1(M,F,C) + (1 - p)P_2(M,F,C)},$$

in which p is the a priori probability that the alleged father is the actual father; M,F,C is a notational representation of an ordered triplet of phenotypes; $P_1(M,F,C)$ is the population relative frequency of the phenotype triplet among mother-father-child persons; and $P_2(M,F,C)$ is the population relative frequency of the phenotype triplet among mother-nonfather-child triplets. The words *mother, father, nonfather,* and *child* denote biological relationships.

In the context of our empirical check, the meaning of the probability of paternity is that it represents the expected fraction of "fathers" among cases in which the parties have the specified triplet of phenotypes. If we sort out the cases in which mother, putative father, and child are each of type O, for example, the result of the formula should approximate the observed fraction of fathers (by our definition). We can make the comparison for all 64 possible triplets (each phenotype can be O, A,B, or AB). If the Essen-Möller formulation is as fallacious as purported [1, 2], we should expect to find gross distortions.

RESULTS

The distributions of phenotype frequencies for mothers, alleged fathers, and children are essentially the same (table 1). The 2 × 4 table considering mothers and putative fathers yields chi-square = 2.83, 3 d.f., $P = .42$, and the goodness of fit for the combined mother and putative father data is chi-square = 0.54, 1 d.f., $P = .46$. Our gene frequency estimates (table 1) are quite similar to those of Selvin [5] and to those of Mourant et al. [6]: .657, .664, and .667 for the O gene for ours, Selvin, and Mourant et al., respectively; .273, .262, .252 for A and .070, .074, .073 for B, respectively. The statistical comparisons of phenotype frequencies were chi-square = 3.14, $P = .37$ for comparison with Selvin's phenotype data (no. = 914) and chi-square = 11.66, $P = .008$ for comparison with Mourant's data (no. = 8,962). Each chi-square has 3 d.f.

It is also of interest to separate the putative fathers into the 1,046 nonexcluded and 347 excluded men. The distribution of ABO types is very similar for both groups (data not shown): chi-square = 0.28, 3 d.f., $P = .96$. Corresponding results for mothers were: chi-square = 5.11, 3 d.f., $P = .12$. The

TABLE 1

ABO PHENOTYPE FREQUENCIES FOR MOTHERS. PUTATIVE FATHERS, AND CHILDREN TOGETHER WITH EXPECTED FREQUENCIES BASED ON ESTIMATED GENE FREQUENCIES

Type	Mother	Putative father	Child	Expected	Gene frequency
O	597	609	611	600.6	.6566
A	617	586	605	604.0	.2733
B	121	143	129	135.1	.0701
AB	58	55	48	53.4	. . .
Total	1,393	1,393	1,393	1,393.1	1.0000
Chi-square	1.16	2.17	1.00		

NOTE: Gene frequencies were estimated from mother and putative father data by method of maximum likelihood [4].

fraction of O's and A's were nearly the same in the two subsets of mothers, but there were disproportionally more AB's in the group with named fathers excluded.

There was no association between mothers' and fathers' ABO types. For all cases combined, the result was chi-square = 6.87, 9 d.f., $P = .65$. The lack of association held in both subgroups: nonexcluded men, chi-square = 11.84, 9 d.f., $P = .22$; excluded men, chi-square = 12.03, 9 d.f., $P = .21$.

Mother and child phenotypes are associated, but the observed values agree well with expected values (table 2): chi-square = 15.93, d.f. = 11, $P = .15$. Expected values were calculated from estimated gene frequencies listed in table 1. We used the gene frequency estimates from mother and putative father data rather than mother and child, so that the chi-square may be slightly inflated. The fit is very good except in the cases of B mother and A child (too few) and A mother and B child (too many). It is of passing interest to note that the table is symmetric for expected values.

Data for B and AB phenotypes were combined in considering the possible association of putative fathers' type with mother-child pairs for the excluded

TABLE 2

OBSERVED AND EXPECTED MOTHER-CHILD ABO PHENOTYPES

CHILD TYPE	MOTHER'S PHENOTYPE			
	O	A	B	AB
O	407* (394.4)†	157 (164.1)	47 (42.1)	0 (0)
A	154 (164.1)	412 (397.6)	10 (17.6)	29 (24.8)
B	36 (42.1)	27 (17.6)	49 (56.0)	17 (19.4)
AB	0 (0)	21 (24.8)	15 (19.4)	12 (9.2)

NOTE: Expected frequencies were computed using gene frequency estimates (maximum likelihood) from mother and putative father data. Chi-square = 15.93, 11 d.f., $P = .15$.

* Observed value.

† Expected value.

men. The chi-square computed for the resulting 3 × 9 table (chi-square = 12.08, 16 d.f., $P = .74$) was consistent with no association.

The general appropriateness of the Essen-Möller formula is illustrated in tables 3–5. Consider, for example, the case of type O for each of child, mother, and putative father. There were 239 such cases. The Essen-Möller formula purports to indicate the fraction of these for which the putative father is the father. The probability of paternity for this triplet (using the estimated gene frequencies and taking $p = .75$) is 82.0%, corresponding to an expected 196 fathers among the 239 putative fathers. The number of nonexcluded men was 198, in excellent agreement. If one allows that 1% of men not excluded by HLA, Rh, or MNS are not the fathers as alleged, the number of fathers would be reduced to 196. Observed and expected numbers for mother-father-child triplets are given in table 3 for the "true" fathers (i.e., not excluded by HLA, ABO, Rh, or MNS) and in table 4 for nonfathers. Results from the two tables are combined in table 5 to provide a comparison between "observed" and calculated probability of paternity. The "observed" is the percent of "true" fathers among cases for a given triplet, and the calculated is the percent based on the expected number of cases. Calculated values in the preceding illustration with mother-father-child all of type O differ slightly from those of tables 3 and 4 because the illustration used the observed number of triplets (239) rather

TABLE 3

OBSERVED AND EXPECTED NOS. MOTHER-CHILD-FATHER ABO PHENOTYPES FOR CASES IN WHICH THE "FATHER" IS CONSIDERED THE ACTUAL FATHER

		ACTUAL FATHER							
		O		A		B		AB	
MOTHER	CHILD	Obs.*	Exp.†	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
O	O	198	194.4	74	80.9	27	20.8	0	0.0
	A	0	0.0	109	114.6	0	0.0	15	8.6
	B	0	0.0	0	0.0	19	23.0	6	8.6
	AB	0	0.0	0	0.0	0	0.0	0	0.0
A	O	74	80.9	39	33.7	3	8.6	0	0.0
	A	121	114.6	165	163.0	12	12.2	9	8.7
	B	0	0.0	0	0.0	17	9.6	5	3.6
	AB	0	0.0	0	0.0	15	13.5	2	5.1
B	O	29	20.8	7	8.6	2	2.2	0	0.0
	A	0	0.0	6	12.2	0	0.0	0	0.9
	B	21	23.0	9	9.6	11	7.6	0	1.9
	AB	0	0.0	13	13.5	0	0.0	0	1.0
AB	O	0	0.0	0	0.0	0	0.0	0	0.0
	A	7	8.6	9	8.7	1	0.9	0	0.4
	B	6	8.6	6	3.6	1	1.9	0	0.4
	AB	0	0.0	4	5.1	1	1.0	3	0.8

NOTE: Chi-square = 45.95, 36 d.f. (Degrees of freedom based on 40 cells with nonzero expected cell size, two gene frequency estimated, estimated fraction nonfathers.)

* Observed.

† Expected, calculated from estimated gene frequencies and fraction of nonfathers.

TABLE 4

OBSERVED AND EXPECTED NOS. MOTHER-CHILD-FATHER ABO PHENOTYPES FOR CASES IN WHICH THE "FATHER" IS NOT THE CHILD'S FATHER (EXCLUDED BY HLA, Rh, MNSs, OR ABO TESTING)

		NONFATHER							
		O		A		B		AB	
MOTHER	CHILD	Obs.*	Exp.†	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
O	O	41	42.4	53	42.6	11	9.5	3	3.8
	A	11	17.6	15	17.7	3	4.0	1	1.6
	B	4	4.5	3	4.6	3	1.0	1	0.4
	AB	0	0.0	0	0.0	0	0.0	0	0.0
A	O	19	17.6	17	17.7	5	4.0	0	1.6
	A	52	42.7	38	42.9	8	9.6	7	3.8
	B	2	1.9	2	1.9	1	0.4	0	0.2
	AB	4	2.7	0	2.7	0	0.6	0	0.2
B	O	4	4.5	4	4.6	0	1.0	1	0.4
	A	2	1.9	0	1.9	1	0.4	1	0.2
	B	4	6.0	2	6.0	1	1.4	1	0.5
	AB	1	2.1	1	2.1	0	0.5	0	0.2
AB	O	0	0.0	0	0.0	0	0.0	0	0.0
	A	5	2.7	6	2.7	1	0.6	0	0.2
	B	2	2.1	2	2.1	0	0.5	0	0.2
	AB	2	1.0	2	1.0	0	0.2	0	0.1

NOTE: Chi-square = 49.3, 52 d.f. (Degrees of freedom calculated from 56 cells with nonzero expected cell size, two gene frequency estimates, one fraction nonfathers.)

* Observed.

† Expected, calculated from estimated gene frequencies and fraction of nonfathers.

than the expected number (236.8) and also because the illustration used the rounded prior probability .75 instead of the empirical value .7509 [= 1046/(1046 + 347)].

The agreement between observed and expected values in tables 3–5 is excellent. There are small numbers of cases in several cells, however, so the tables were collapsed by regarding types A and B as indistinguishable. The effect is to consider a single genetic system with one dominant and one recessive allele. The results, table 6, yield a goodness-of-fit chi-square = 8.50, 11 d.f., $P = .67$. The agreement between observed fraction of fathers with probability of paternity (i.e., expected) is excellent (table 7) and well within the anticipated statistical variation indicated by the standard errors of the observed percents.

DISCUSSION

The excellent agreement between the predictions using the Essen-Möller formulation and the observed numbers of excluded men challenges the assertions that the Essen-Möller probability of paternity is fallacious, and we are entitled to examine the assertions of Li and Chakravarti [1] and Aickin [2].

The Essen-Möller formulation rests on four principle assumptions: (1) the calculation of $P_1(M,F,C)$ is valid; (2) the calculation of $P_2(M,F,C)$ is valid; (3) Bayes' formula is valid; and (4) the value of the prior probability is appropriate.

TABLE 5

OBSERVED FRACTION OF "TRUE" FATHERS AND CALCULATED (EXPECTED) PROBABILITY OF PATERNITY FOR POSSIBLE MOTHER-CHILD-FATHER TRIPLETS OF ABO PHENOTYPES

		PUTATIVE FATHER							
		O		A		B		AB	
MOTHER	CHILD	Obs.*	Exp.†	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
O	O	82.8	82.1	58.3	65.5	71.0	68.5	0.0‡	0.0
	A	0.0	0.0	87.9	86.6	0.0‡	0.0	93.7	84.7
	B	0.0‡	0.0	0.0‡	0.0	86.4	95.8	85.7	95.6
	AB ...	—§	—	—	—	—	—	—	—
A	O	79.6	82.1	69.6	65.5	37.5	68.5	0.0‡	0.0
	A	69.9	72.9	81.3	79.2	60.0	56.0	56.2	69.6
	B	0.0‡	0.0	0.0‡	0.0	94.4	95.8	100.0‡	95.6
	AB ...	0.0‡	0.0	0.0‡	0.0	100.0	95.8	100.0‡	95.6
B	O	87.9	82.1	63.6	65.5	100.0‡	68.5	0.0‡	0.0
	A	0.0‡	0.0	100.0	86.6	0.0‡	0.0	0.0‡	84.7
	B	84.0	79.2	81.8	61.2	91.7	84.9	0.0‡	78.4
	AB ...	0.0‡	0.0	92.9	86.6	0.0‡	0.0	0.0‡	84.7
AB	O	—	—	—	—	—	—	—	—
	A	58.3	76.4	60.0	76.4	50.0‡	60.6	0.0‡	61.8
	B	75.0	80.6	75.0	83.2	100.0‡	80.6	0.0‡	67.5
	AB ...	0.0‡	0.0	66.7	83.7	100.0‡	82.2	100.0‡	89.8

* Observed.
† Expected, calculated from estimated gene frequencies and fraction of nonfathers.
‡ Based on five or fewer cases.
§ Mother-child incompatible.

Had Li and Chakravarti [1] attacked items (1) and (2), we should have been obliged to take them seriously, for these are the special provenence of population genetics. They might have presented evidence that the customary calculations are inherently biased and to such an extent that the results are seriously misleading. Not only did they *not* challenge items (1) and (2), they advocated a formula that requires the same sort of calculation. The empirical results presented here support the validity of the calculations for items (1) and (2). Tables 3 and 4 indicate very good correspondence between observed and expected values. Several of the cells in the table have small positive expected numbers, however, and the tables were recalculated with type AB pooled with type B. The smallest (nonzero) expected cell size was 1.4, so that the resulting chi-squares (23.1, 19 d.f.; 22.7, 24 d.f.) can be compared validly with percentage points of the chi-square distribution. The corresponding P values, .24 and .54, respectively, indicate very good fits. The additional collapsing to a single antigen system, table 6, has larger expected cell sizes and would be expected to be more sensitive to lack of validity. Again, the statistical assessment by chi-square indicates a good correspondence.

It might be objected that the expected numbers are distorted since in constructing the tables we have assumed that all of the nonexcluded men were actual fathers as alleged. Findings from our case material are that about 96.6%

TABLE 6

OBSERVED AND EXPECTED NOS. MOTHER-CHILD-FATHER TRIPLETS AMONG "ACTUAL" FATHER TRIPLETS AND NONFATHER TRIPLETS FOR SYNTHETIC SINGLE ANTIGEN GENETIC SYSTEM OBTAINED BY REGARDING A AND B AS A SINGLE ANTIGEN

		"TRUE" FATHER				NONFATHER			
		O		Not O		O		Not O	
MOTHER	CHILD	Obs.*	Exp.†	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
O	O	198	194.4	101	101.7	41	42.4	67	55.9
	Not O	0	0.0	149	154.9	15	22.1	26	29.2
Not O	O	103	101.7	51	53.2	23	22.1	27	29.2
	Not O	155	154.9	289	285.3	74	63.0	74	83.1

NOTE: "True" father, chi-square = 0.45, 5 d.f.; nonfather, chi-square = 8.05, 6 d.f.
* Observed.
† Expected.

of Caucasian triplet nonfathers are excluded [7]. The 347 excluded males then represent 96.6% of the nonfathers. We would then expect that 347/0.966 = 359.2 men were nonfathers, so that it is expected that 12 of the 1,046 non-excluded men were not the fathers as alleged. In considering all nonexcluded men as actual fathers, the misclassification rate is 12/1,046, or approximately 1%. The sample sizes are not large enough to detect this level of distortion. The main divergence that we have noted is that somewhat fewer than expected men were excluded by ABO. Based on the gene frequency estimation from table 1, 14.26% of nonfathers are expected to be excluded by ABO. The expected number (0.1426)(359.2) = 51.2, is statistically larger than the observed 37 (chi-square = 4.59, P = .03). This apparent divergence is not meaningful in the context of the number of comparisons that were made. Our conclusion is that the presented data strongly support the validity of assumptions (1) and (2)

TABLE 7

FRACTION OF "ACTUAL" FATHERS FROM OBSERVED AND EXPECTED NOS. TRIPLETS FOR A SINGLE ANTIGEN SYSTEM

		PUTATIVE FATHER			
		O		Not O	
MOTHER	CHILD	Obs.*	Exp.†	Obs.	Exp.
O	O	82.8 ± 2.5‡	82.1	60.1 ± 3.8	64.5
	Not O	0.0 ± 0.0	0.0	85.1 ± 2.7	84.1
Not O	O	81.8 ± 3.4	82.1	65.4 ± 5.3	64.5
	Not O	67.7 ± 3.1	71.1	79.6 ± 2.2	77.5

NOTE: Fraction based on expected nos. is the probability of paternity.
* Observed.
† Expected.
‡ Standard error of observed.

underlying the Essen-Möller formulation. We suggest that the burden is on challengers of items (1) and (2) to show empirically any lack of validity.

Li and Chakravarti did not challenge the validity of Bayes' theorem, item (3). Again, not only did they *not* challenge the theorem, but advocated its use in the Wiener formulation [8] of probability of paternity. The same is the case for the prior probability, item (4).

Li and Chakravarti did not challenge the Essen-Möller formulation in any relevant way. Their charge of fallaciousness is entirely unsupported. Strictly speaking, Li and Chakravarti asserted only that the formulation of the paternity index is fallacious. Since the Essen-Möller probability is a monotone increasing function of the paternity index, for given prior probability, it follows that they made the same charge against the probability of paternity. Whatever the merits of their arguments on other grounds, they do not challenge the validity of the Essen-Möller formulation.

Aickin [2] listed what he considered three fallacies. This first "fallacy" does not challenge any of the four elements of the Essen-Möller formulation and is irrelevant. His assertion was that since one cannot distinguish on the basis of phenotypes two men who have the same phenotype, one cannot distinguish the probability that the alleged father is the true father from the probability that the alleged father has the same phenotype as the true father. Our illustration using only the ABO system shows that the Essen-Möller formula does compute probability of paternity and not the probability that the putative father has the same phenotype as the true father. In the case of type O child, mother, and putative father, the probability of paternity was calculated as 82.1%. The probability that the father is of type O given that mother and child are both type O is .657, and, from these results, it follows that the probability that the putative father has the same ABO type as the true father for this case is (.821)(1) + (.179)(.657) = .939; the observed percent of "fathers" was 82.8%. There is no difficulty distinguishing between the propositions that the named man is the child's father and that the named man has the same phenotype as the child's father. It is clear that the Essen-Möller formula applies to the first.

The second of Aickin's "fallacies" appears to challenge items (1) and (2), those relating to computing population frequencies. He rejects the validity of estimates of genetic frequencies obtained other than from a survey designed by an appropriate statistician. Table 2 provides empirical grounds for evaluating the seriousness of Aicken's contention. We would assess the agreement between estimates of gene frequencies based on our case material with those from the studies cited as very satisfactory. Statistical uncertainty in the estimated gene frequencies gives rise to statistical uncertainty in calculated probabilities of paternity, but this is hardly a fallacy.

Aickin's third "fallacy" is to the effect that if the observed data were genotypes instead of phenotypes, one would obtain different values for the probabilities of paternity in most cases. Since the observed data are phenotypes, Aickin's point is irrelevant. A rejection of conditional probabilities as valid would account for many of his conclusions. If one considers probability calculations based on conditional probabilities to be invalid, one would also consider calculations for items (1) and (2) of the Essen-Möller formulation to be invalid.

The value of the prior probability usually associated with the Essen-Möller probability of paternity is .5. In order to support the interpretation of probability of paternity as the fraction of true fathers in cases having the same probability of paternity, a "realistic" value is required. Our case material leads to an estimate of approximately 75%. Chakravarti and Li [9] calculated example estimates of 72% and 79% on the basis of approximate estimates of exclusion rates. Hummel et al. [10] reported estimates of 89% (Denmark), 78% (Freiburg), 74% (Sweden), 73% (Munich), 73% (Switzerland), 65% (East Berlin), and 58% (Austria), average 72.9%. It is of interest that estimates based on quite different material are so similar. Although the numerical value for the probability of paternity for a given phenotype triplet depends on the value assigned to the prior probability, the variation is more a matter of interpretation than of fallaciousness. If the value of the probability of paternity is given for a prior of 50%, call it $P_{.50}$, the value for any other prior, p, is

$$P_p = \frac{1}{1 + \frac{1 - p}{p} \frac{1 - P_{.50}}{P_{.50}}} .$$

For example, if $P_{.50} = 90\%$, the probability of paternity is 95.5% for a 70% prior and 96.4% for a 75% prior.

Another way of using the Essen-Möller probability of paternity is to ask: For what value of the prior probability is the probability of paternity equal to 50%? The answer is: prior $= 1 - P_{.50}$. For example, if the probability of paternity is 95%, using a 50% prior, then the probability of paternity will be greater than 50% (preponderance of evidence) for any prior greater than $(100 - 95) = 5\%$. This is to ask whether the evidence against paternity, on nongenetic grounds, outweighs the evidence on genetic grounds. The prior probability of 50% is the appropriate probability for this comparison.

In our view, the validity of the Essen-Möller formula rests upon the accuracy of its prediction of the fraction of true fathers among cases with the same probability of paternity computed using a "realistic prior." This is a question that can, in principle, be empirically assessed. We have presented data here that demonstrate that the predictions given by the formula have very good accuracy in the case of the ABO system. While this case is not of particular interest in itself, it is significant in showing that the assertions of fallacy are unsupported empirically. This is not surprising since the arguments presented by Li and Chakravarti and by Aickin are mostly irrelevant.

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