Tables and Nomogram for Calculating Chances of Excluding Paternity[1]

WILLIAM C. BOYD

School of Medicine, Boston University

THE CHANCES of disproving by blood grouping tests a charge of paternity brought against an innocent man were calculated several years ago by a number of authors (Hooker and Boyd, 1928; Wiener *et al.*, 1930; Koller, 1931; Zarnik, 1930). Since that time, the number of blood group systems which may be employed in such tests has greatly increased, and it is often desired to calculate the combined chances of exclusion of paternity, if certain ones of these systems are tested, and the tests in each system are made with varying degrees of completeness. A table of the results of such calculations by Fisher, for the English population, is given by Race and Sanger (1950).

If it is desired to construct such a table for a different population, with its different gene frequencies, or for the same population with a different combination of tests, or with some tests carried out with a greater or less degree of completeness, this can be done by going back to the basic relations between the probability of excluding paternity in the case of a falsely accused man, and the gene frequencies in the population.

The simplest system is that of a pair of allelic genes, one dominant. Such a system is exemplified by the "secretor" phenomenon in man, or any of the blood group systems such as MN, Kell, Duffy, or Kidd (Race and Sanger, 1950; Ruffié, 1953), when only one antiserum is available. In this case, we can only exclude paternity when the mother and alleged father belong to phenotype D− (genotype dd) and the child is of phenotype D+, where D represents the gene which causes the production of the antigen for which we can test, d is the alternative gene, and D+ represents the phenotype which is made up of genotypes DD and Dd. Then the probability P of excluding a man chosen at random from the population has been shown to be (Wiener *et al.*, 1930; Race and Sanger, 1950)

$$P_{D,d} = Dd^4 \tag{1}$$

where D stands for the frequency of the gene D and d for the frequency of the gene d.

A table of the chances of exclusion for various values of D is given in table 1. It will be noted that the probability is a maximum at $D = 0.2$, $d = 0.8$.

Received August 23, 1954.

[1] The research report in this paper was made possible in part by the use of equipment purchased By Boston University under Contract No. Nonr-492(01) with the Office of Naval Research.

TABLE 1. PROBABILITIES (P) OF PATERNITY EXCLUSION WITH A GENE PAIR D, d, GENE D DOMINANT

D	P	*D*	P	*D*	P	*D*	P	*D*	P	*D*	P
.01	.010	.16	.080	.31	.070	.46	.039	.61	.014	.76	.003
.02	.018	.17	.081	.32	.068	.47	.037	.62	.013	.77	.002
.03	.027	.18	.081	.33	.067	.48	.035	.63	.012	.78	.002
.04	.034	.19	.082	.34	.065	.49	.033	.64	.011	.79	.002
.05	.041	.20	.082	.35	.063	.50	.031	.65	.010	.80	.001
.06	.047	.21	.082	.36	.060	.51	.029	.66	.009	.81	.001
.07	.052	.22	.081	.37	.058	.52	.028	.67	.008	.82	.001
.08	.057	.23	.081	.38	.056	.53	.026	.68	.007	.83	.001
.09	.062	.24	.080	.39	.054	.54	.024	.69	.006	.84	.001
.10	.066	.25	.079	.40	.052	.55	.023	.70	.006	.85	.000
.11	.069	.26	.078	.41	.050	.56	.021	.71	.005	.86	.000
.12	.072	.27	.077	.42	.048	.57	.020	.72	.004	.87	.000
.13	.075	.28	.075	.43	.045	.58	.018	.73	.004	.88	.000
.14	.077	.29	.074	.44	.043	.59	.017	.74	.003	.89	.000
.15	.078	.30	.072	.45	.041	.60	.015	.75	.003	.90	.000

D = frequency of gene D

The gene frequencies may be estimated as $d = \sqrt{\text{D}-}$, $D = 1 - d$.

If two antisera are available, and the products of both genes can be detected, as in the case of the MN blood groups, the probability of exclusion is (Wiener, 1952)

$$P_{\text{M,N}} = mn(1 - mn) \tag{2}$$

A table[2] of the probabilities for various values of the less frequent of the two genes in such a system (called here arbitrarily N) is given in table 2. The maximum probability is reached at $m = n = 0.5$.

The frequency n is best obtained as $n = N + MN/2$, where N represents the frequency of the type positive only with anti-N and MN the type positive with both anti-N and anti-M.

In blood group systems with three allelic genes, as the ABO system, the probability depends upon the frequencies of all three genes. If we let p, q, and r represent the frequencies of the genes A, B, and O, as usual, the chances of exclusion are (Wiener *et al.*, 1930)

$$P_{\text{A,B}} = p(q + r)^4 + q(p + r)^4 + pqr^2(p + q + 2) \tag{3}$$

Since $p + q + r = 1$, there are really only two independent variables in this equation, and we can calculate the chances of exclusion in terms of r and p/q (or q/p). The results of this calculation are shown in table 3. From this table probabilities for any combination of r and p/q which is likely to be encountered can be found by double interpolation. For populations where q is greater than p we enter the table with q/p instead of p/q.

[2] A graph showing the relationship between the probabilities of exclusion and the gene frequencies for the D,d and the M,N cases is given by Cotterman (Cotterman, C. W. A note on the detection of interchanged children. Am. J. Human Genetics *3*, 363–375, 1951).

TABLE 2. PROBABILITIES (P) OF PATERNITY EXCLUSION WITH A GENE PAIR M, N, NO DOMINANCE

n	P	n	P	n	P	n	P	n	P
.01	.010	.11	.088	.21	.138	.31	.168	.41	.183
.02	.019	.12	.094	.22	.142	.32	.170	.42	.184
.03	.028	.13	.100	.23	.146	.33	.172	.43	.185
.04	.037	.14	.106	.24	.149	.34	.174	.44	.186
.05	.045	.15	.111	.25	.152	.35	.176	.45	.186
.06	.053	.16	.116	.26	.155	.36	.177	.46	.187
.07	.061	.17	.121	.27	.158	.37	.179	.47	.187
.08	.068	.18	.126	.28	.161	.38	.180	.48	.187
.09	.075	.19	.130	.29	.164	.39	.181	.49	.187
.10	.082	.20	.134	.30	.166	.40	.182	.50	.188

n = frequency of gene N (less frequent of pair)

It will be noted that for each value of the ratio p/q the probability has a maximum value. For $p/q = 1$ this maximum is 0.1999, and at this point r has the value 0.5574 (Wiener *et al.*, 1930). For other values of p/q there is also a relative maximum at some value of r, which is progressively displaced to the right as p/q increases.

The gene frequencies can be estimated with sufficient accuracy for the present purpose by the usual Bernstein formulas

$$r = \sqrt{(O)}$$
$$p = 1 - \sqrt{(O + B)}$$
$$q = 1 - \sqrt{(O + A)}$$

although if the sum $p + q + r$ deviates greatly from 1 it might be desirable to adjust the crude frequencies so obtained by the Bernstein adjustments

$$r' = (r + D/2)(1 + D/2)$$
$$p' = p(1 + D/2)$$
$$q' = q(1 + D/2)$$

where $D = 1 - (p + q + r)$.

TABLE 3. PROBABILITIES OF PATERNITY EXCLUSION WITH ABO BLOOD GROUPS

p/q (or q/p)	r							
	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
1	0.122	0.155	0.182	0.197	0.198	0.182	0.145	0.086
2	0.118	0.145	0.167	0.181	0.183	0.170	0.138	0.083
3	0.111	0.130	0.148	0.160	0.164	0.155	0.130	0.081
4	0.102	0.117	0.131	0.142	0.148	0.143	0.123	0.078
5	0.094	0.105	0.118	0.129	0.136	0.134	0.117	0.077
6	0.086	0.096	0.107	0.118	0.126	0.127	0.113	0.075
7	0.079	0.088	0.098	0.109	0.118	0.121	0.110	0.074

p = frequency of A gene, q = frequency of B, r = frequency of O

As an example of the use of the table, suppose we calculate the probability of exclusion for the blood group frequencies used in the calculations of Hooker and Boyd (1928), where $p = 0.262$, $q = 0.071$, and $r = 0.671$. In this case $p/q = 3.7$. For p/q we interpolate between the values of P for $r = 0.6$ and $r = 0.7$ to obtain $P = 0.158$, and for $p/q = 4$ we get $P = 0.144$. Interpolating between these values to obtain the probability corresponding to $p/q = 3.7$, we find $P = 0.148$. Hooker and Boyd calculated 1/7 approximately. The correct value is 0.1528. (Wiener *et al.* (1930) reported for these data the erroneous value $P = 0.1434$). It is evident that the table gives results satisfactory for all practical purposes.

Determination of the subgroups of A and AB would slightly increase the chances of exclusion of paternity by the ABO groups, but there is still some uncertainty as to the laws of inheritance of these subgroups (Wiener, 1943; Race and Sanger, 1950), and in any case Wiener has calculated that the chances are only increased in this way by about 3 per cent. Therefore the application of these subgroups is not considered here.

The probabilities of exclusion are more difficult to calculate in the case of blood group systems which depend on more than three allelic genes, such as the MNS and Rh systems. However, such calculations have been made by Fisher (Race and Sanger, 1950) for representative English blood group frequencies, which are close enough to those in the USA for our present purposes. If we make use of these, we may calculate a table like that given by Race and Sanger (1950) showing the combined chances of exclusion.

We can do this by the formula

$$P_{1,2 \ldots n} = 1 - (1 - P_1)(1 - P_2) \cdots (1 - P_n) \qquad (4)$$

where $P_{1,2 \ldots n}$ stands for the combined chances of exclusion and P_1, P_2 etc. for the chances for the individual systems. For instance, if we have $P_{A,B} = 0.147$, and $P_{M,N} = 0.187$, we can write

$$P_{A,B,M,N} = 1 - (0.853)(0.813) = 1 - 0.694 = 0.306$$

The calculation can be performed by the nomogram (fig. 1). The indicator is set to $P_{A,B}$ on one scale and to $P_{M,N}$ on the other. The combined probability, $P_{A,B,M,N}$ is read off from the middle scale. By repeated use of the nomogram any number of independent probabilities can be thus combined.

For the Rh and MNS systems Fisher finds $P_{Rh} = 0.252$ and $P_{MNS} = 0.274$. We may calculate our own value of $P_{A,B}$. There is a wide choice of data for the ABO blood group frequencies for the USA, any set of which would probably be sufficiently representative. If we take the data of Boyd (1939) for Boston, we find $p = 0.236$, $q = 0.089$, $r = 0.675$, and $p/q = 2.6$. From table 3 we find $P_{A,B} = 0.165$.

For the Kell system we may take the frequency of K as 0.052, and for the

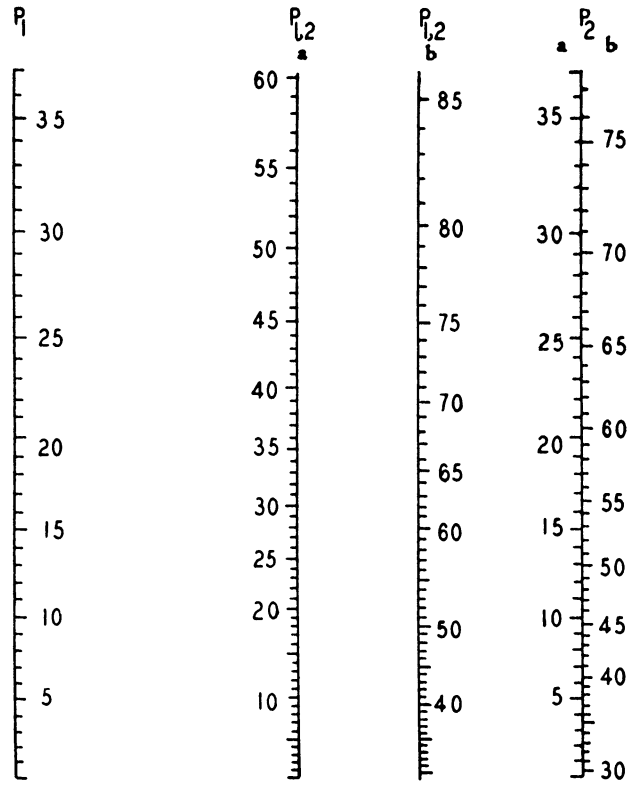

FIG. 1. Nomogram for computing combined probabilities of exclusion of paternity when two independent systems, with probabilities P_1 and P_2, are used. Use stretched thread or transparent ruler with black line. Set at value of P_1 on extreme left-hand scale, and at P_2 on extreme right-hand scale, using scale a or b depending on value of P_2. Read value of combined probability on scales $P_{1,2}$, depending on whether scale P_2 (a) or P_2 (b) was used. For example, if P_1 = 15 per cent, and P_2 = 50 per cent, we find on scale $P_{1,2}$ (b) that the combined probability = 57.5 per cent.

Duffy system Fy^a = 0.410, for the Lutheran system Lu^a = 0.039, for the secretion system S = 0.576 (Race and Sanger, 1950). For the Kidd system we may take Jk^a = 0.520 (Ruffié, 1953).

We may now proceed to construct a table showing the combined chances of exclusion, but it will make a considerable difference how complete we assume the testing for each blood group system to be. From table 1 we find that if anti-D alone is used in the Rh system, as is still common in some clinical laboratories, the chances of exclusion are only 0.018 instead of 0.252. Similarly, the chances in the Kidd system are only 0.028 if only anti-Jk^a is used, but if anti-Jk^b is also available they are increased to 0.187. It therefore seems desirable to arrange the results of the calculations into two columns, one showing the results for the simpler level of testing and the second the probabilities based on the more complete level of testing (table 4).

TABLE 4. PROBABILITIES OF AN ACCUSED MAN'S BEING EXONERATED OF A FALSE CHARGE OF PATERNITY BY BLOOD GROUP TESTS IN U.S.A.

Blood Group System	Exclusion by Each System (first level)	Combined Exclusion (first level)	Exclusion by Each System (second level)	Combined Exclusion (second level)
1. ABO	0.165	0.165	0.165	0.165
2. MNS	0.187	0.321	0.274	0.394
3. Rh	0.018	0.333	0.256	0.549
4. Kell	0.042	0.361	0.047	0.570
5. Lutheran	0.033	0.382	0.033	0.584
6. Secretion	0.019	0.394	0.019	0.592
7. Duffy	0.050	0.424	0.183	0.667
8. Kidd	0.028	0.441	0.187	0.729

Using the tables given here and the nomogram, it is a simple matter to construct similar tables showing the combined chances of exclusion based on any combination of blood grouping tests, for any population.

It will be noted that although we can calculate by equation 1 or table 1 the chances of exclusion by tests with one Rh serum (anti-D or anti-E), or any pair of Rh sera (anti-C, and anti-c or anti-E and anti-e), by equation 2 or table 2, we cannot combine these probabilities by equation 4 or the nomogram (figure 1) because these systems are not independent. However, if we do make such a combination we obtain results which are not greatly in error, which exaggerate somewhat the chances of excluding paternity. For instance, the approximate gene frequencies used by Fisher for calculating the probability in the Rh system give $C = 0.42$, $D = 0.58$, $E = 0.17$. If we assume, as did Fisher, that the usual four anti-sera, anti-C, anti-D, anti-E and anti-c, were used, we obtain $P_{C,c} = 0.184$, $P_D = 0.018$, $P_E = 0.081$. Combining by the nomogram, we obtain $P_{Rh} = 0.265$. The correct result, calculated by Fisher, is $P_{Rh} = 0.252$. Similarly Wiener (1952) shows that the result of making the similar incorrect assumption of independence in the case of the MN and Ss systems gives $P_{MNS} = 0.327$ instead of the correct 0.315 (assuming four sera, anti-M, anti-N, anti-S and anti-s, are used). This means that we can, if we wish, calculate the combined chances of exclusion for a population merely from the tables and nomogram given here, if we keep in mind that our results for MNS and Rh will be a little too high. The values obtained will be sufficiently accurate to serve as a guide.

For instance, suppose we wish to obtain the probability of exclusion of paternity in Lahore, Pakistan, where Boyd and Boyd (1954) determined the ABO, MNS, Rh, Kell, Duffy, and Kidd blood groups. They found $p = 0.184$, $q = 0.260$, $r = 0.556$. Therefore, $q/p = 1.4$, and from table 3, we find $P_{A,B} = 0.191$.

The gene frequencies of M and N can be obtained by the usual formulas

(see p. 427), and the frequency of S can be estimated as $S = 1 - \sqrt{(S-)}$. We find for Lahore $n = 0.427$, $S = 0.299$. The combined probabilities, making the incorrect assumption of independence, give $P_{MNS} = 0.244$, which is doubtless somewhat too high.

The chances of exclusion by the Rh system can be obtained similarly by combining the chances from the C,c; D,d; and E,e pairs. If four sera, anti-C, anti-D, anti-E and anti-c, are used, the C,c pair gives three distinguishable phenotypes, like MN, and we find the chances of exclusion in table 2. The frequency of C can be obtained as CC + Cc/2. The D,d and E,e pairs behave like a simple pair with dominance, and the chances of exclusion can be found in table 1. The frequency of D is calculated as $1 - \sqrt{(D-)}$, and $E = 1 - \sqrt{(E-)}$.

We find $C = 0.619$, $c = 0.381$, $D = 0.753$, $E = 0.110$, and from tables 1 and 2, we find $P_{C,c} = 0.180$, $P_D = 0.003$, $P_E = 0.069$. Combining, we find $P_{Rh} = 0.238$, which again is doubtless somewhat too high.

From the results of the Kell, Kidd and Duffy tests we find $K = 0.084$, $Jk^a = 0.481$, $Fy^a = 0.524$. Since only one serum was used for each system, we find from table 1 the chances of exclusion by these systems to be $P_K = 0.059$, $P_J = 0.035$, $P_F = 0.029$.

Combining all these probabilities, we find the combined chances of exclusion in Lahore, using the sera employed by Boyd and Boyd, are $p_{ABMNSRhKJF} = 0.588$, which is high by perhaps a few per cent, but suffices to give the approximate chances of exclusion in this population, using merely these six blood group systems at the level of testing employed by Boyd and Boyd.

If anti-k, anti-Jk^b and anti-Fy^b sera had also been available, the combined chances would be computed as 0.714.

SUMMARY

Tables are presented for calculating the chances of excluding paternity of a wrongly accused man by blood group tests, and a nomogram is given for combining such chances. Typical calculations are given.

REFERENCES

1. BOYD, W. C. 1939, Blood Groups. *Tabulae Biologicae* 17: 113.
2. BOYD, W. C. AND L. G. BOYD 1954, The blood groups in Pakistan. *Am. J. Phys. Anthrop.* (in press).
3. HOOKER, S. B. AND W. C. BOYD 1928, The probable usefulness of blood-grouping tests in establishing non-paternity. *Science* 68: 620.
4. KOLLER, S. 1931, Statistische untersuchungen zur Theorie der Blutgruppen und zu ihrer Anwendung vor Gericht. *Z. Rassenphysiol.* 3: 1.
5. RACE, R. R. AND R. SANGER 1950, *Blood Groups in Man.* Blackwell Sci. Pub. Oxford.

6. RUFFIÉ, J. 1953, *Les Groupes Sanguins Chez l'Homme*, Masson et Cie, Paris.
7. WIENER, A. S. 1943, *Blood Groups and Transfusion*. C. C Thomas, Springfield.
8. WIENER, A. S. 1952, Heredity of the M-N-S blood types. Theoretico-statistical considerations. *Am. J. Hum. Gen.* 4: 37.
9. WIENER, A. S., M. LEDERER AND S. H. POLAYES 1930, Studies in Isohemagglutination: IV On the chances of proving non-paternity; with special reference to blood groups. *J. Immunol.* 19: 259
10. ZARNIK, B. 1930, Vjerojatnost pozitivnog nalaza kod ispivanja krvnin grupa u svrhu iskljuci vanja ocinstva. *Medicinski Pregled.* 5: 1.