

Numerical Expression of Paternity Test Results Using Predetermined Indexes

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Lee, Chang Ling: Numerical expression of paternity test results using predetermined indexes. *Am J Clin Pathol* 73: 522-536, 1980. Relative chance of paternity (RCP) is a numerical expression used to indicate either paternity (near 100%) or non-paternity (0% or close to 0%). RCP is derived by converting the paternity index (PI) to a percentage, $RCP = PI/(PI + 1)$. PI represents the chance that the alleged father is or is not the father, and is expressed as a number for a given phenotype combination of the mother-child-alleged-father trio. These PI values have been determined and are listed in several tables. Thus, one can find in these tables the individual PI value for each genetic marker system for a given trio, multiply the numbers, and convert the combined PI value into RCP. In this way, a qualitative and quantitative report of a paternity testing can be readily derived. (Key words: Paternity testing; Paternity index; Relative chance of paternity; Paternity testing reports.)

IN 1975, the United States Congress passed a law (Public Law 93-647) requiring each state to develop an appropriate plan, in accordance with HEW standards, for the ascertainment of paternity and for enforcement of child support. This new ruling was aimed both at protecting the rights of the child to have a father and at relieving the public burden of supporting illegitimate children. As a consequence of more sophisticated technology, blood tests provide the best available scientific evidence of paternity. The number of paternity testings has increased markedly, thus, an improvement in the quality and efficiency of paternity determinations would be expected. This report mainly concerns our approach to an effective and meaningful reporting of paternity testing.

It is well known that blood tests can only provide an exclusion of paternity and cannot establish paternity. This was especially true when only a small number of genetic markers were available for paternity testing; to a great extent, it is true even now. However, in view of recent advances in human genetics, some comments on this assumption are appropriate.

The discovery of many genetic variants renders some exclusions, which were unquestionable before, less certain now. Minus-minus phenotypes have been demonstrated to occur in many blood group systems,

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and no one can be sure that similar variants will not be found in the remaining systems. Although many of these variants are relatively rare, one can no longer state that an exclusion is absolute, or 100%. In fact, exceptions have been found in practically all biological systems. One has to accept a confidence of 99.9% or 99.0%, or sometimes even 95%. In a court of law, occasionally a 51% against a 49% confidence may be the basis for a decision.

In cases of an alleged father having a DCcEe phenotype and a child having a dce phenotype, nonexclusion is usually concluded and reported. However, the chance that he is the actual father is about 1/2% if he is a white, and practically zero if he is a black. Should we believe that this report of nonexclusion serves justice?

On the other hand, if the alleged father and the child share a very rare genetic marker, or share several uncommon genetic markers (their chance of occurring being less than one in a million), and if the alleged father's brother, who may have the same genetic marker(s), is not involved, would you doubt that the alleged father may indeed be the father of the child? In practice, such occurrences are rare; also, the number of men who could have been involved with the woman during her conception period is usually very small; should we therefore accept the lower odds? In statistics, odds of 19:1, or 95%, may be considered significant. To be objective, one can present the odds for the court to evaluate in conjunction with other evidence. The final judgement, that based on evidence beyond a reasonable doubt, can thus be more accurately determined.

For many years, and even now in some laboratories, only genetic markers in the ABO, Rh, and MN systems were used for paternity testing. These three systems, varying with the number of individual markers used, can provide a 30% to 60% chance of exclusion if the alleged father is being falsely accused. The availability of many more genetic markers for paternity testing extends the exclusion chance to nearly 99%⁹. If such extensive testing is done and the alleged father is not excluded, then one is inclined to believe that he is the

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GENETIC MARKER SYSTEM	PHENOTYPE			PATERNITY INDEX
	CHILD	MOTHER	ALLEGED FATHER	
NAME	SMITH ALICIA KAY	SMITH MARY ANN	JONES RALPH LEE	
ABO	O	B	O	1.52
MNSs	MS	MS	MNSs	1.66
Rh	DcEe	DcEe	DcEe	0.84
Kell	k-k+	k-k+	k-k+	1.05
Duffy	a+b-	a+b+	a+b-	2.59
Kidd	a+b-	a+b-	a+b+	0.93
F1	F1+	F1-	F1+	1.14
Xs	a+	a-	a+	1.49
AcF	A	AB	AB	1.27
PGM1	1	1	1	1.33
GLO	1-2	1-2	1-2	1.00
GPT	1-2	1-2	1-2	1.00
EsD	1	1-2	1	1.11
ADA	1	1	1	1.05
AK	1	1	1	1.03
PGD	A	A	A	1.03
Hf	1-2	2	1	2.40
Gc	1	1-2	1	1.40
Tf	C	C	C	1.01
Gm	azxfbs	azxbfs	fb	1.44
Km	1+3+	1-3+	1+3-	9.43
COMBINED PATERNITY INDEX				876.34
RELATIVE CHANCE OF PATERNITY				99.89 %
RELATIVE CHANCE OF NON-PATERNITY				0.11 %

FIG. 1. Sample computer printout of an RCP determination.

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father of the child. In practice, such an elaborate approach has certain drawbacks: it is impractical in terms of cost and time, and at best, its result represents only an average value, being higher in certain mother-child combinations than in others.

Estimation of the chance of paternity has been used in some European laboratories for years, and clearly should be used in the United States to comply with the law requiring "ascertainment of paternity." The use of relative chance of paternity (RCP) for reporting paternity testing would offer the following advantages.

The meaning of the term is readily comprehensible by all parties in a paternity dispute. It indicates paternity as well as nonpaternity. The genetic patterns of the

mother and the child, which greatly influence the determination of paternity, are taken into consideration. Only a few basic genetic rules are involved in the derivation of the paternity index, and complex theorems or mathematical formulas are not required. Although the use of a large number of genetic markers usually gives a more meaningful RCP, high RCP values may occasionally be obtained using only a few genetic markers. Of course, only one 0% paternity index (PI) value is necessary to give a 0% RCP. Values for different PI can be predetermined and listed in tables. These values can be used to derive the RCP by simple multiplication and division. Knowledge of genetics is not essential.

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Methods

Table	Race	System	Genetic Markers		
			Erythrocytic Antigens	Erythrocytic Enzymes	Serum Proteins
1	Both	ABO	X		
2	White	MNSs	X		
3	Black	MNSs	X		
4	White	Rh	X		
5	Black	Rh	X		
6	Black	Duffy	X		
7	Both	1 Marker alone	X	X	X
8	Both	2 Dominant markers	X	X	X
9	Both	3 Dominant markers		X	X
10	Both	Gm			X

Four Steps Used to Derive the Relative Chance of Paternity (RCP) Values

Tabulate the phenotypes. Prepare a reporting sheet consisting of five columns, in addition to other appropriate information. Enter the systems of genetic markers used and the phenotypes of the child, mother, and alleged father in the first four columns. See Figure 1.

Assign paternity indexes. From the appropriate table for the child-mother-alleged-father trio, find the paternity index for each system of genetic markers tested, and enter these values into the fifth column. The list of tables at the top of the page may facilitate the search of paternity indexes. Phenotypes which exclude the mother are not included in the tables.

Calculate the combined paternity index. Obtain the products of PI for all systems tested, for example, 876.34 in Figure 1.

Derive the relative chance of paternity. Obtain the RCP by dividing PI by (PI + 1), for example, $876.34 / (876.34 + 1) = 99.89\%$ in Figure 1. The relative chance of nonpaternity = $1 - .9989 = .0011$, or 0.11%.

Computer Printout

The availability of the paternity index for each child-mother-alleged-father trio allows the use of a computer to reduce human errors in printing and computation. A coding system has been designed to simplify the operation (Table 11). A letter has been assigned to represent each genetic marker system, such as O for ABO, N for

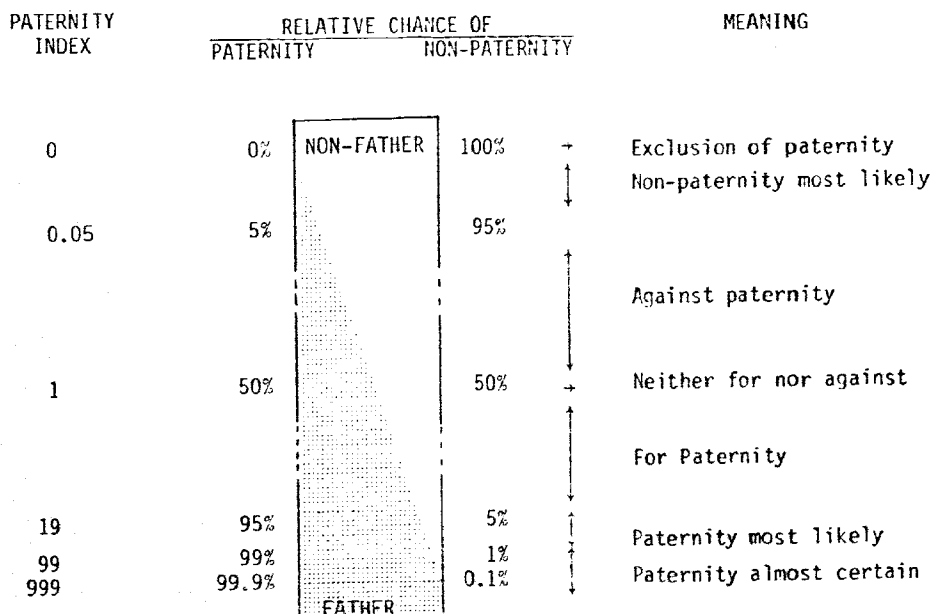


FIG. 2. Relationship between paternity index (PI) and relative chance of paternity (RCP) values.

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Table 1. Paternity Indexes of Different ABO Phenotypes*

Serum Protein	Phenotype		Child's Gene from		PI of the Alleged Father of a Given Phenotype†					
	Child	Mother	Mother	Father	O	A ₁	A ₂	B	A ₁ B	A ₂ B
	O	O, A ₁ A ₂ , B	O	O	1.52 (1.43)	.60 (.61)	.72 (.69)	.72 (.66)		
	A ₁ A ₁ B	O, A ₂ , B B, A ₂ B	O	A ₁		2.75 (4.60)			2.45 (4.31)	
	A ₁	A ₁	A ₁ or A ₂ or O	A ₁ or A ₂ or O A ₁ A ₁	.91 (1.02)	1.32 (1.50)	.91 (1.02)	.44 (.47)	.82 (.96)	.46 (.51)
X X X X	A ₁	A ₁ B	A ₁	A ₁ or A ₂ or O	1.07 (1.14)	1.07 (1.14)	1.07 (1.14)	.51 (.53)	.54 (.57)	.54 (.57)
	A ₂ A ₂ B	O, B A ₁ B, B	O B	A ₂ A ₂		.60 (.62)	7.49 (8.89)			7.13 (8.55)
	A ₂	A ₁	A ₂ or O	A ₂ or O A ₂	.74 (.70)	.60 (.61)	4.21 (4.88)	.35 (.33)		3.67 (4.37)
Obtain the example	A ₂	A ₂	A ₂ or O	A ₂ or O A ₂	1.26 (1.23)	.61 (.61)	1.85 (1.82)	.60 (.57)		1.19 (1.18)
Obtain the example, the relative chance, or 0.11%	A ₂	A ₂ B	A ₂	A ₂ or O	1.37 (1.32)	.60 (.61)	1.37 (1.32)	.65 (.59)		.68 (.66)
	B A ₁ B A ₂ B	O, A ₁ , A ₂ A ₁ A ₁ , A ₂	O A ₁ A ₂	B B B				7.96 (4.34)	7.60 (4.01)	7.60 (4.01)
	B	B	B O	B or O B	1.29 (1.07)	.52 (.46)	.61 (.52)	1.88 (1.57)	1.21 (.99)	1.21 (.99)
each child compute mutation. At the opera- represent BO, N for	B	A ₁ B, A ₂ B	B	B or O	1.38 (1.21)	.55 (.52)	.65 (.58)	1.38 (1.21)	.69 (.61)	.69 (.61)
	A ₁ B	A ₁ B	A ₁ B	B A ₁		2.08 (2.22)		1.94 (2.25)	3.71 (4.15)	1.85 (2.07)
	A ₂ B	A ₂ B	A ₂ B	B A ₂		.32 (.20)	3.86 (2.84)	3.85 (2.95)	3.68 (2.73)	7.35 (5.45)

* Whites, n = 8,965, Michigan; blacks, 3,146, San Francisco; reference 12, p. 230. Blank indicates nonpaternity.

† Numbers in parentheses are values for the black population; numbers without parentheses are for the white population.

MNSs, R for Rh, and so forth. A number or a letter is assigned to represent each phenotype within a system, such as 1, 2, and 3 for A₁, A₂, and B in the ABO system, or for MS, Ms, and MSs in the MNSs system, or for DCcEe, DCce, and DC^wce in the Rh system. The phenotype combination of a trio can then be represented by code, for example:

Code	Phenotype		
	Child	Mother	Alleged Father
O111 =	A ₁	A ₁	A ₁
N111 =	MS	MS	MS
R111 =	DCcEe	DCcEe	DCcEe
O125 =	A ₁	A ₂	A ₁ B
N125 =	MS	Ms	Ns
R125 =	DCcEe	DCce	DCe

To use a computer for RCP determinations, a program and two data files are required: one data file for all the genetic marker systems, and the other for the paternity index for each system, including all possible trios without an exclusion. To obtain a report, initiate the program and enter the relevant genetic marker system-phenotype codes and other routine information. The computer will search the paternity indexes, do the calculations, and print out the appropriate phenotypes, paternity indexes, and relative chance of paternity and nonpaternity, as shown in Figure 1.

Both paternity indexes and relative chance of paternity percentages can be used to express the results of paternity testing (Fig. 2). RCP is preferable because it not only indicates the chance of paternity but also clearly indicates the chance of nonpaternity, which must be taken into consideration. For example, to say that the RCP is 90% automatically implies that there is

ship between
and relative
RCP) values.

Table 2. Paternity Indexes of Different MNSs Phenotypes in a White Population*

Child	Phenotype Mother	Haplotype from Father	PI of the Alleged Father of a Given Phenotype									
			MS	Ms	MSs	NS	Ns	NSs	MNS	MNs	MNSs	
MS MSs MNS MNSs	MS, MSs, MNS, MNSs Ms, MSs NS, NSs Ms	MS	4.04		2.02					2.02		1.66
NS NSs MNS MNSs	NS, NSs, MNS, MNSs Ns, MSs MS, MSs Ms	NS				14.47			7.24	7.24		1.31
Ms MSs MNs MNSs	Ms, MSs, MNs, MNSs MS, MNS Ns, NSs NS	Ms		3.26	1.63						1.63	.29
Ns NSs MNs MNSs	Ns, NSs, MNs, MNSs NS, MNS Ms, MSs MS	Ns						2.65	1.33		1.33	1.09
MNS MNSs	MNS MNs	MS or NS	3.16		1.58	3.16			1.58	3.16		1.58
MNs MNSs	MNs MNS	Ms or Ns		1.46	.73			1.46	.73		1.46	.73
MSs MNSs	MSs NSs	MS or Ms	1.81	1.81	1.81					.91	.91	.91
NSs MNSs	NSs MSs	NS or Ns				2.24	2.24	2.24		1.12	1.12	1.12
MNS	MNSs	MS or NS	1.78		.89	8.10			4.05	4.94		1.46
MNs	MNSs	Ms or Ns		2.57	1.29			.56	.28		1.57	.46
MSs	MNSs	MS or Ms	.61	2.77	1.69					.30	1.39	.50
NSs	MNSs	NS or Ns				6.58	1.44	4.01	3.29		.72	1.18
MNSs	MNSs	MS or Ms or NS or Ns	1.41	.31	.86	.31	1.41	.86	.86	.86	.86	1.22

* San Francisco, n = 8,962; reference 12, p. 307. Blank indicates nonpaternity.

still a 10% chance against paternity; when the same result is expressed as a PI of 10, the negative aspect is no longer obvious, owing to its implication of an overwhelming likelihood of paternity. In statistics, a 95% certainty is usually considered significant; the judge, however, has the option of selecting the level of certainty to suit the needs of a particular case.

Those who are not interested in the derivation of paternity indexes may proceed to the discussion and tables.

Logic Behind the Estimation of the Paternity Index

Each inherited characteristic (genetic marker) is controlled by two allelic genes (or haplotypes) on a pair of chromosomes; one gene is from the mother, and the other is from the father. These genes could be identical, *aa* or *bb*, known as homozygous, or could be different, *ab*, known as heterozygous.

Since 100% of the children of a homozygous parent (*aa* or *bb*) must inherit *a* or *b*, respectively, the

Table 3. Paternity Indexes of Different MNSs Phenotypes in a Black Population*

MNs	MNSs	Phenotype		Haplotype from Father	PI of the Alleged Father of a Given Phenotype																						
		Child	Mother		MS	Ms	MSs	NS	Ns	NSs	MNS	MNs	MNSs	MN	M	N											
					1	2	3	4	5	6	7	8	9	10	11	12											
1.66		1	2,8,10,11	MS	7.34	4.86				3.99		3.21															
		3;7;9	2,8;5,12;5																								
		2	1,7,10,11	Ms		2.54	1.43				1.27	.49															
		3;8;9	1,7;4,12;4																								
1.31		4	5,8,10,12	NS			11.55		9.04	4.78		3.07															
		6;7;9	5,8;2,11;2																								
		5	4,7,10,12	Ns				2.34	1.36		1.15	.90															
		6;8;9	4,7;1,11;1																								
1.63	.29	7	8	MS or NS	5.28	3.50	3.24		2.53	4.25		3.17															
		7	10												NS	4.77	3.16	4.05	3.16	4.30		3.16					
		9	8																				4.70	3.11	4.16	3.25	4.28
.33	1.08	8	7	Ms or Ns		1.83	1.03		.65	.38		1.24	.60														
		8	10												Ns	1.24	.70		1.20	.70		1.21	.70				
		9	7																					.96	.54	1.45	.84
		3;9	3;6	MS or Ms	1.67	1.97	2.21			.92	.98	1.10															
		3	9												Ms	.97	2.21	1.88			.53	1.10	.84				
		6;9	6;3																					NS or Ns			1.51
1.58		6	9	Ns			2.61	1.81	3.09	1.08	.89	1.39															
		9	9												MS or Ms or NS or Ns	1.11	.68	1.12	.49	1.27	1.12	.81	.96	1.23			
		91	.91																						1	1	MS or MS ^u
1;7	3;9;6	6.53	.72	3.27	3.27	.36	2.16	3.27	6.53																		
1	7	6.63	.63	3.46	3.36	.32	2.28	2.87	5.74																		
.12	1.12	7	4	MS or MS ^u	6.75	.52	3.70			3.48	.26	2.44	2.37	7.41													
		2	2,8												Ms or MS ^u	.69	3.12	1.58		.24	1.56	.54	1.40	2.81			
2	3,9	MS ^u	.61	2.54	1.25		.21	1.25	.43	1.25	2.50																
8	5,6											.54	2.50	1.27											.19	1.25	.43
57	.46	4	4	NS or NS ^u			8.51	.88	4.89	4.06	.47	1.66	3.13	6.26													
		4	7												NS ^u			8.07	1.00	4.30	3.96	.54	1.46	3.57	7.14		
		4;7	6,9;3																							7.76	1.09
39	.50	7	1	NS or NS ^u			8.24	.96	4.52	4.00	.51	1.54	3.41	6.82													
		5;8	6,9;2,3												Ns or NS ^u	.82	2.27	1.13	.53	1.13	.75	1.13	2.27				
5	5,8	NS ^u	.72	2.27	1.16	.47	1.14	.77	1.00	1.99																	
7	7										MS or MS ^u	2.49	.24	1.30										2.16	.19	1.30	2.37
7	9	NS or NS ^u	6.30	.50	2.28	2.35	.33	1.17	3.45	.43					1.90	3.45	4.56	2.35									
8	8																		Ms or MS ^u	.26	1.20	.61	.37				
8	9	Ns or NS ^u	.20	.86	.40	.56	1.54	.77	.43	1.17	.65	.40	.80	1.54													
10	7														MS ^u or NS ^u	1.02	.46							3.87	1.50		4.40
10	8	NS ^u	1.62	.73		3.27	1.28		2.73	1.05		7.85	6.59	9.11													
10	10																		1.98	.89	2.91	1.13	2.59				
ity Index		10;11	4,5;1,2,7	MS ^u	4.87	1.89				1.69	1.09		9.94	19.88													
		11	8,10,11																								
ker) is cor-) on a pair er, and the e identical. could be ous parent tively, the		10;12	1,2;4,5,7	NS ^u			4.91	1.91		3.20	1.02		6.81	13.62													
		12	8,10,12																								

* Blacks in Philadelphia, reference 12, p. 313.

chance of paternity (CP) for any homozygote is 1. Only 50% of the children from a heterozygous parent (ab) are expected to have either a or b; the CP for any heterozygote to pass a or b is 1/2. For convenience,

CP for the alleged father is designated X, and that for a random man, Y. The value of Y is represented by the gene frequency of a or b (commonly assigned as p or q). Should the mother and the child both be heterozy-

Table 4. Paternity Indexes for Different Rh Phenotypes in a White Population*

Phenotype		Haplotype that Must Come from Father	PI of Alleged Father of a Given Population									
Child	Mother		DCcEe 1	DCce 2	DC ^w ce 3	DcEe 4	DCe 5	DcE 6	Dce 7	dce 8	dcEe 9	dCce 10
3	1,2,4,7-10	R ^{1w}			50							
1	3,7,8	R ^z	2.94									
2;5	8,9;10	R ¹	1.04	1.05			2.11					
1	9	R ¹ ,R ^z	1.05	1.95			2.10					
5;1	1,2,5;6	R ¹ ,r ¹	1.04	1.05			2.11				1.02	
2	3,4,7		1.04	1.08			2.11				.09	
10	3,4,7,8,9	r ¹	.91	.07			1.96					33.78
7	8,9,10	R ^o	.02	1.41	1.41	1.41			17.58			
2	10	R ^o ,R ¹	.99	1.10	.09	.09	1.98		1.07			
4	9	R ^o ,R ^z	2.73	.26	.26	3.36	5.54		3.17			
4;6	8,10;9	R ^z	3.33			3.67		6.77				
1	10	R ^z ,R ^z	3.33			3.62		6.68				
6	4	R ^z ,r ¹	3.34			3.38		6.75			3.35	
4	2,3		3.33			3.64		6.76			.31	
4	7		3.25			3.49		6.73			1.83	
6	1,6		3.32			3.37		6.70			3.07	
1	5		3.32			3.36		6.70			3.26	
1	2	R ^z ,r ¹ ,R ^z ,r ¹	3.31			3.31		6.62			3.31	
9	2,3,7,8,10	r ¹	3.17			.35		6.07			34.48	
8;10	1-4,7-10;5	r	.01	1.37	1.37	1.37			1.42	2.99	1.49	1.49
2	5	r,R ^o	.01	1.37	1.37	1.37			2.78	2.74	1.37	1.37
4	6		.01	1.37	1.37	1.37			2.86	2.72	1.36	1.36
7	7		.01	1.37	1.37	1.37			3.78	2.55	1.28	1.28
7	1		.01	1.39	1.39	1.39			8.64	1.65	.83	.83
7	2,3,4		.01	1.39	1.39	1.39			9.72	1.45	.73	.73
3	3	r,R ^o ,R ^{1w}	.01	1.34	2.67	1.34			2.67	2.67	1.34	1.34
10	1	r,r ¹	.02	1.36	1.36	1.36	.03		1.43	2.96	1.48	1.92
10	10		.05	1.31	1.31	1.31	.08		1.37	2.87	1.43	2.8
10	2		.87	.12	.06	.06	1.87		.06	.13	.07	32.26
2	1	r,r ¹ ,R ^o ,R ¹	.02	1.37	1.36	1.36	.02		2.75	2.71	1.35	1.35
2	2		.59	1.21	.60	.60	1.18		1.21	1.21	.60	.60
1	4	R ¹ ,r ¹ ,R ^z ,r ¹	1.05	1.05			2.10					1.04
4	1	R ^o ,r,R ^z ,r ¹	.02	1.37	1.37	1.37		.003	2.86	2.71	1.37	1.36
4	4		.92	.93	.93	1.93		1.85	2.00	1.99	2.00	1.00
9	1	r,r ¹	.02	1.36	1.36	1.36		.02	1.42	2.98	1.62	1.49
9	9		.14	1.31	1.31	1.31		.25	1.37	2.86	2.86	1.43
9	4		2.56	.26	.26	.54		4.89	.27	.56	28.09	.28
1	1	All but R ^{1w}	1.58	1.81	.01	.81	2.03	1.69	.02	.02	.79	.73

* New York City, N = 500; reference 12, p. 485.

gous for a given marker, the mother could pass either *a* or *b* to the child. The chance for either allele would be 50%, or 1/2. The Y-value would be 1/2p + 1/2q

= 1/2(p + q). In two allele systems, where p + q = 1, Y would equal 1/2; X would also be 1/2, regardless of the genotype of the alleged father, as shown in the following:

Gene of Child Expected from		CP of Random Man (Y)	CP of Alleged Father (X) of Genotype		
Mother	Father		<i>aa</i>	<i>ab</i>	<i>bb</i>
<i>a</i> (1/2)	<i>b</i> (1/2 × 1 = 1/2)	1/2q	1/2 × 0 = 0	1/2 × 1/2 = 1/4	1/2 × 1 = 1/2
<i>b</i> (1/2)	<i>a</i> (1/2 × 1 = 1/2)	1/2p	1/2 × 1 = 1/2	1/2 × 1/2 = 1/4	1/2 × 0 = 0
		1/2(p + q)	1/2	1/2	1/2
		= 1/2 when p + q = 1			

Table 5. Paternity Indexes of Different Rh Phenotypes in a Black Population*

cEe 9	dCce 10	Phenotype		Haplotype that Must Come from Father	Paternity Index of the Alleged Father of a Given Phenotype															
		Child	Mother		DCcEe	DCce	DC ^w ce	DcEe	DCe	DcE	Dce	dce	D ^w ce	dCce						
					1	2	3	4	5	6	7	8	9	10						
		3	2-4,7-10	R ^{1w}			500													
		1	2,5,10	R ²	4.35			4.35			8.7									
		4	2,3,7-10		4.35			4.35			8.7									
		6	1,4,6		4.35			4.35			8.7									
		7	8,9,10	R ⁰		.72	.68	.68				1.58								
	1.02	2	10	R ⁰ ,R ¹	.74	1.34	.53	.53	1.50			1.23								
	.69																			
	33.78	2	8,9	R ¹	3.38	3.53			6.83											
		10	3,4,7-9	r ¹	3.20	2.14			5.88											26.74
		1	4,6	R ¹ ,r ¹	3.36	3.36			6.72											3.36
		5	1,5		3.36	3.37			6.72											3.00
		2	3,4		3.36	3.41			6.75											2.31
		5	2	R ¹ ,r ¹	3.37	3.38			6.74											3.12
		2	7	R ¹ ,r ¹	3.36	3.40			6.74											2.54
.35																				
.31																				
.83		8	2-4,7-10	r		.63	.68	.68			.99	3.81	1.83						1.90	
.07		10	1,5			.63	.68	.68			.99	3.81	1.83						1.90	
.26		9	2-4,7,8	r, D ^w ce		.53	.65	.65			.84	1.59	28.31						.80	
.31		9	9			.62	.68	.68			.98	3.53	5.22						1.76	
.48		7	3,4	r, D ^w ce, R ⁰		2.38	2.34	2.34			4.89	3.52	3.48						1.71	
.49	1.49	2;4;7	1,5;6,1;2			.64	.60	.60			1.29	1.17	.56						.59	
.37	1.37	7	7			.69	.68	.68			1.40	1.40	.53						.55	
.36	1.36	3	3	r, D ^w ce, R ⁰ , R ^{1w}		.99	1.97	.99			1.97	1.97	.95						.99	
.28	1.28																			
.83	.83	10	2	r, r ¹	.71	.96	.53	.53	1.30		.77	2.96	1.42						7.40	
.73	.73	10	10		.21	.73	.64	.64	.39		.92	3.55	1.71						3.55	
.34	1.34	4	4	r, D ^w ce, R ⁰ , R ²	.59	.59	.59	1.18		1.18	1.18	1.18	1.18						.59	
.48	1.92	2	2	r, D ^w ce, R ⁰ , R ¹ , r ¹	1.08	2.06	.94	.94	2.17		2.00	1.08	1.10						.93	
.43	2.8	1	1	r ¹ , R ¹ , R ²	3.79	1.90		1.90	3.79	3.79									1.90	

* New York City, n = 500; reference 12, p 491.

Table 6. Paternity Indexes of Different Duffy Phenotypes in a Black Population*

Phenotype - Fy()		Gene of the Child from		Paternity Index of the Alleged Father			
Child	Mother	Mother (%)	Father	Fy(a+b-)	Fy(a-b+)	Fy(a-b-)	Fy(a+b+)
				a+b-	a-b+, a-b-	4(100)	a
a+b+	a-b+	b(100)	a	6.49			6.18
a-b+	a+b-, a-b-	4(100)	b		3.49		3.20
a+b+	a+b-	a(100)	b		3.49		3.20
a-b-	a+b-, a-b+	4(100)†	4	.62	.60	1.31	
a-b-	a-b-			.62	.60	1.31	
a+b+	a+b+	a(50) or b(50)	b a	2.21	2.30		4.22
a+b-	a+b-	a(52.5) or 4(47.5)	a,4 a	1.61	.50	1.09	1.04
a+b-	a+b+	a(100)	a,4	1.19	.54	1.19	.59
a-b+	a-b+	b(54.5) or 4(45.5)	b,4 b	.45	1.39	.95	.87
a-b+	a+b+	b(100)	b,4	.52	1.09	1.09	.54

* New York City, n = 179; reference 12, p 593.

† Other alleles are possible but not significant.

+ q = 1.
ess of the
n in the

type

bb

× 1 = 1/2
× 0 = 0

1/4

Table 7. Paternity Indexes of Genetic Markers Often Used Alone or Without a Demonstrable Allele

Genetic Marker	Phenotype of		Gene of Child from		Paternity Index of the Alleged Father						Reference
					Whites			Blacks			
					Child	Mother	Mother	Father	Gene Frequency	+	
K	+	-	k	K	.045	11.37	0	.0038	131.83	0	12
	-	-,+	k	k	.955	.51	1.05	.9962	.5	1	p 532
	+	+	K,K	K,k		1.45	.96		1.49	1	
J _s ^a	+	-	b	a	0			.1031	5.11	0	12
	-	-,+	b	b	0			.8969	.53	1.12	p 537
	+	+	a,b	a,b					1.39	.92	
F _y ^a	+	-	non-a	a	.3858	1.61	0	.0809	6.44	0	12
	-	-,+	non-a	non-a	.6142	.62	1.63	.9191	.52	1.09	p 593
	+	+	a,non-a	a,non-a		1.23	.81		1.41	.93	
J _k ^a	+	-	b	a	.5360	1.27	0	.7426	1.07	0	12
	-	-,+	b	b	.4640	.68	2.16	.2574	.80	3.89	p 601
	+	+	a,b	a,b		1.19	.80		1.14	.84	
P ₁	+	-	non-P ₁	P ₁	.65	1.14	0	.29	2.02	0	11
	-	-,+	non-P ₁	non-P ₁	.35	.74	2.86	.71	.59	1.41	p 120
	+	+	P ₁ ,non-P ₁	P ₁ ,non-P ₁		1.16	.81		1.27	.83	
Lu ^a	+	-	b	a	.0335	15.18	0	.0243	20.83	0	12
	-	-,+	b	b	.9665	.51	1.03	.9757	.51	1.03	p 515
	+	+	a,b	a,b		1.46	.97		1.47	.98	
X _g ^{a*}	+	-	non-a	a	.6709	1.49	0	.5496	1.82	0	12
	-	-,+	non-a	non-a	.3291	0	3.04	.4504	0	2.22	p 631
	+	+	a,non-a	a,non-a		1.09	.82		1.16	.80	
Se	+	-	se	Se	.4957	1.34	0	.4715	1.39	0	12
	-	-,+	se	se	.5043	.67	1.98	.5285	.65	1.89	p 553
	+	+	Se,se	Se,se		1.20	.80		1.21	.80	p 554
G ₁ m ^a	+	-	non-a	a	.2440	2.51	0	.8696	1.02	0	14
	-	-,+	non-a	non-a	.7760	.56	1.29	.1304	.89	7.67	
	+	+	a,non-a	a,non-a		1.31	.85		1.09	.90	
K _m ^l	+	-	non-l	l	.1060	4.98	0	.3000	1.96	0	14
	-	-,+	non-l	non-l	.8940	.53	1.12	.7000	.59	1.43	
	+	+	l,non-l	l,non-l		1.39	.91		1.27	.83	

* For female children only.

This example shows that in a two-allele system, when both the mother and the child are heterozygous, every man has the same chance of being the father.

In the presence of a silent allele or alleles that are not demonstrable in the laboratory, such as *O* with

*A*₁, *A*₂ or *B*; or *A*₂ with *A*₁, the chance of a phenotype such as *A*₁, *A*₂ or *B* passing *A*₁, *A*₂, or *B*, respectively, can be estimated from their expected genotypes. Let group *B* be an example [frequency for *B* is .0658 (=q) and for *O* is .6602 (=r)]. Frequency for

$$BO = 2pq = 2 \times .0658 \times .6602 = .0869, \text{ or } .0869/.0912 = 95.2\%$$

$$BB = q^2 = .0658 \times .0658 = .0043 \quad .0043/.0912 = 4.8\%$$

.0912

100%

Thus, the chance of a group *B* person (mother or father) passing an *O* would be 50% of 95.2% = 47.6%*; a *B* would be 1 - 47.6% = 52.4%

* This approach can be extended to other systems with silent markers. If *q* = gene frequency of the dominant allele, or *r* = gene frequency of the silent marker, then the chance of passing the silent marker = $(\frac{1}{2} \times 2qr)/(q^2 + 2qr) = r/(q + 2r)$; the chance of passing the dominant marker = $1 - (r/(q + 2r)) = (q + r)/(q + 2r)$.

In paternity cases, the mother is always assumed to be the mother. Therefore, a group *A*₁*B* mother is assumed to pass *B*, but not *A*₁, to a group *B* child. If the child is known to have *B* already, the father may provide either *B* or *O*, and the chance of the father's passing either would be in accord with his genotype or estimated genotypes, as demonstrated above.

When the child and the mother are both group *B*, the

mother can pass either *O* or *B* with a chance of .476 or .524, respectively. When the mother passes an *O* gene, the father must pass a *B* gene: the chance of a random man being the father would be $.476 \times .0658 = .0313$ (1); the chance of a group B man being the father would be $.476 \times .524 = .249$ (2). When the mother passes a *B* gene, the father can pass either *O* or *B*: the chance of a random man being the father would be $.524 \times (.0658 + .6602) = .3804$ (3); the chance of a group B man being the father would be $.524 \times 1 = .524$ (4). Thus, the total chance of a random man being the father would be $(1) + (3) = .4117$ (5); the total chance of a

group B man being the father would be $(2) + (4) = .773$ (6). The paternity index for a group B man and a group B child from a group B mother would be $(6)/(5) = .773/.4117 = 1.88$.

Five Steps Used to Derive the Paternity Indexes

Step 1. Establish the gene (or haplotype) of the child that must come from the mother, and the chance of the mother's passing it. If there is only one possibility, the chance would be 1 or 100%. In the case of a group B child with a group A mother, the chance for the mother

Table 8. Paternity Indexes of Two Dominant Allele Systems with Known Genotypes*

Genetic Marker Systems	Genotype		Gene Required From Father	PI of the Alleged Father of Genotype								Reference
	Child	Mother		Whites				Blacks				
				GF	aa	ab	bb	GF	aa	ab	bb	
Erythrocytic antigens												
Kell	<i>KK;Kk</i>	<i>KK,Kk;kk</i>	<i>K(=a)</i>	.045	22.22	11.11		.0038	263	132		12
	<i>kk;Kk</i>	<i>kk,Kk;KK</i>	<i>k(=b)</i>	.955		.52	1.05	.9962		.50	1.0	p 532
Fy	<i>aa;ab</i>	<i>aa,ab;bb</i>	<i>a</i>	.3858	2.59	1.30			See Table 6			12
	<i>bb;ab</i>	<i>bb,ab;aa</i>	<i>b</i>	.6142		.81	1.63					p 591
Jk	<i>aa;ab</i>	<i>aa,ab;bb</i>	<i>a</i>	.5360	1.87	.93		.7426	1.35	.67		12
	<i>bb;ab</i>	<i>bb,ab;aa</i>	<i>b</i>	.4640		1.08	2.16	.2574		1.94	3.89	p 601
Plasma proteins												
Gc	<i>1;1-2</i>	<i>1,1-2;2</i>	<i>1(=a)</i>	.7155	1.40	.70		.8924	1.12	.56		12
	<i>2;1-2</i>	<i>2,1-2;1</i>	<i>2(=b)</i>	.2845		1.76	3.52	.1076		4.65	9.30	p 692
Hp	<i>1;1-2</i>	<i>1,1-2;2</i>	<i>1(=a)</i>	.4169	2.40	1.20		.5500	1.82	.91		12
	<i>2;1-2</i>	<i>2,1-2;1</i>	<i>2(=b)</i>	.5831		.86	1.72	.4500		1.11	2.22	p 654 p 657
Tf	<i>CC;CD</i>	<i>CC,CD;DD</i>	<i>C(=a)</i>		See Table 9			.9973	1.00	.50		12
	<i>DD;CD</i>	<i>DD,CD;CC</i>	<i>D(=b)</i>					.0007		714	1429	p 677
G1m	<i>zz;zf</i>	<i>zz;zf;ff</i>	<i>z(=a)</i>	.2240	4.46	2.23		.8710	1.15	.57		14
	<i>ff;zf</i>	<i>ff,zf;zz</i>	<i>f(=b)</i>	.776		.64	1.29	.1290		3.88	7.75	
Km	<i>1;1-3</i>	<i>1,1-3;3</i>	<i>1(=a)</i>	.1060	9.43	4.72		.3000	3.33	1.67		14
	<i>3;1-3</i>	<i>3,1-3;1</i>	<i>3(=b)</i>	.8940		.56	1.12	.7000		.71	1.43	
Erythrocytic enzymes												
PGM ₁	<i>1;1-2</i>	<i>1,1-2;2</i>	<i>1(=a)</i>	.7520	1.33	.66		.8089	1.24	.62		12
	<i>2;1-2</i>	<i>2,1-2;1</i>	<i>2(=b)</i>	.2480		2.02	4.03	.1911		2.62	5.23	p 765
PGD	<i>AA;AB</i>	<i>AA,AB;AA</i>	<i>A(=a)</i>	.9760	1.03	.51		.9645	1.04	.52		12
	<i>BB;AB</i>	<i>BB,AB;BB</i>	<i>B(=b)</i>	.0240		20.84	41.67	.0355		14.08	28.16	p 756
GPT	<i>1;1-2</i>	<i>1,1-2;2</i>	<i>1(=a)</i>	.4960	2.02	1.01		.8140	1.23	.61		1
	<i>2;1-2</i>	<i>2,1-2;1</i>	<i>2(=b)</i>	.504		.99	1.98	.1960		2.55	5.10	
EsD	<i>1;1-2</i>	<i>1,1-2;2</i>	<i>1(=a)</i>	.9020	1.11	.55		.9020	1.11	.56		3
	<i>2;1-2</i>	<i>2,1-2;1</i>	<i>2(=b)</i>	.0980		5.10	10.20	.0980		5.10	10.20	
GLO	<i>1;1-2</i>	<i>1,1-2;2</i>	<i>1(=a)</i>	.4270	2.34	1.17			Not available			6
	<i>2;1-2</i>	<i>2,1-2;1</i>	<i>2(=b)</i>	.5730		.87	1.75					
ADA	<i>1;1-2</i>	<i>1,1-2;2</i>	<i>1(=a)</i>	.9524	1.05	.53			See Table 9			12
	<i>2;1-2</i>	<i>2,1-2;1</i>	<i>2(=b)</i>	.0476		10.50	21.01					p 784
AK	<i>1;1-2</i>	<i>1,1-2;2</i>	<i>1(=a)</i>	.9724	1.03	.51			See Table 9			12
	<i>2;1-2</i>	<i>2,1-2;1</i>	<i>2(=b)</i>	.0276		18.12	36.23					p 771

* Rare alleles are not included. When the mother and the child are both heterozygotes, the paternity index for every phenotype is 1, and is not included. GF = gene frequency.

Table 9. Paternity Indexes of Three Dominant Allele Systems with Known Genotypes

Genetic Marker System*	Genotype		Gene Required from Father		PI of the Alleged Father of Genotype						Race			
	Child	Mother	Gene	Frequency†	aa	bb	cc	ab	ac	bc				
Erythrocytic enzymes AcP (p 723-4)	aa	aa,ab,ac	a	.3938	2.54	4		1.27	1.27		White			
	ab			.2500								2	2	Black
	ac													
	bb	bb,ab,bc	b	.5466	1.8		.91		.91	White				
	ab			.7200							1.39	.69	.69	Black
	bc													
	cc	cc,ac,bc	c	.0596		16.78	8.39	8.39	White					
	ac			.0140						71.43	35.71	35.71	Black	
	bc													
	ab	ab	a,b	.4702	1.06	1.06	1.06	.53	.53					White
				.4850	1.03	1.03	1.03	.51	.51	Black				
		ac	ac	a,c	.2267	2.21		2.21	1.10	2.21	1.10	White		
				.1320	3.79		3.79	1.90	3.79	1.90	Black			
	bc	bc	b,c	.3031		1.65	1.65	.83	.83	1.65	White			
				.3670		1.37	1.37	.69	.69	1.37	Black			
ADA (p 784)	S		1(=a)	.9785	1.02			.51	.51		Black			
	S		2(=b)	.0161		62.11		31.06		31.06	Black			
	S		3(=c)	.0054			185		92.6	92.6				
	1-2	1-2	1,2	.4973	1.01	1.01		1.01	.50	.50				
	1-3	1-3	1,3	.4920	1.02		1.02	.51	1.02	.51				
	2-3	2-3	2,3	.0175		46.3	46.3	23.15	23.15	46.3				
	AK (p 771)	S		1(=a)	.9934	1.01			.50	.50		Black		
S			2(=b)	.0061		164		82		82	Black			
S			3(=c)	.0005			2000		1000	1000				
1-2		1-2	1,2	.4998	1	1		1	.5	.5				
1-3		1-3	1,3	.4970	1.01		1.01	.5	1.01	.5				
2-3		2-3	2,3	.0033		151.5	151.5	75.8	75.8	151.5				
Serum protein Tf (p 677)		S		B(=a)	.0054	185			92.6	92.6		White		
	S		C(=b)	.9939		1.01		.5		.5	White			
	S		D(=c)	.0007			1428		714	714				
	BC	BC	B,C	.4997	1	1		1	.5	.5				
	BD	BD	B,D	.0031	161.3		161.3	81	161.3	81				
	CD	CD	C,D	.4973		1.01	1.01	.5	.5	1.01				

† Average of two frequencies when there are two possible genes. S = similar to AcP.

* Numbers in parentheses are page number in reference #12.

to pass O is 1. If there are two or more possibilities, establish the chance for each possibility, with the total being 1. In the case of a group AB child of a group AB mother, the chance of passing A or B is 50%, or 1/2.

Step 2. Establish gene or possible genes expected from the father.

Step 3. Establish the chance that a random man (Y-value) could provide the gene required to be the father of the child. If there is only one gene possible, the gene frequency represents the Y-value. The Y-values for A and B are .2740 and .0658, respectively. If there are two or more possibilities, multiply the gene frequency by the appropriate percentage established in step 2, and take the sum of the individual products as

the Y-value. For example, 1/2 x .2740 + 1/2 x .0658 = .1699 is the Y-value for a random man capable of providing A or B to the child.

Step 4. Establish the chance that a man of a known phenotype (alleged father) could provide the expected gene (X-value, or chance of paternity). If there is only one gene possible, the chance is 1 for a homozygote, 1/2 for a heterozygote, or other values when silent markers are involved. If there are two or more possibilities, multiply 1 or 1/2 or the other value by the percentage established for that gene, and take the sum of each product as the X-value.

The following examples illustrate the above four steps.

Vo
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X
E
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de
fu
sa
ap

a c
wl
co

Example	Phenotype		Child's Gene from			CP of Alleged Father (X) of Group	
	Child	Mother	Mother	Father	CP of Random Man (Y)	AB	B
1	B	A	O (1)	B	$1 \times .0658 = .0658$	$1 \times \frac{1}{2} = .5$	$1 \times .524 = .524$
2	AB	AB	A (½)	B	$\frac{1}{2} \times .0658 = .0329$	$\frac{1}{2} \times \frac{1}{2} = .25$	$\frac{1}{2} \times .524 = .262$
			B (½)	A	$\frac{1}{2} \times .2740 = .1370$	$\frac{1}{2} \times \frac{1}{2} = .25$	$\frac{1}{2} \times 0 = .000$
			.1699			.50	
3	B	B	O (.476)	B	$.476 \times .0658 = .0313$	$.476 \times \frac{1}{2} = .238$	$.476 \times .524 = .249$
			B (.524)	B, O	$.524 \times .7269 = .3804$	$.524 \times \frac{1}{2} = .262$	$.524 \times 1 = .524$
			.4117			.773	
Step number			1	2	3	4	

Step 5. Obtain the paternity index by dividing the X-value by the respective Y-value.

Paternity Indexes

Example	Group AB Man	Group B Man
1	$.5/.0658 = 7.60$	$.524/.0658 = 7.96$
2	$.5/.1699 = 2.94$	$.262/.1699 = 1.54$
3	$.5/.4117 = 1.22$	$.773/.4117 = 1.88$

Several genetic marker systems, such as ABO, Rh, and Gm in whites and blacks, and MNSs and Duffy in blacks, contain multiple and silent alleles. The construction of PI tables for such systems can be facilitated by listing: (1) different gene or haplotype frequencies, (2) frequency and percentage of each genotype within a given phenotype, and (3) the chance that each phenotype has to pass a specific marker. An example of such a list is given in Table 12.

Discussion

There are a number of pioneers who have worked on the chance of paternity, notably, Henningsen² in Denmark, Hummel and associates⁴ in Germany, Salmon¹³ in France, Jancik and Speiser⁵ and Mayr¹⁰ in Austria, and Lee^{7,8} in the United States. Each of them deals with this issue slightly differently, but the fundamental principles involved are essentially the same. The results obtained with our relatively simple approach are similar to theirs.

With the predetermined paternity indexes available, a considerable amount of time can be saved, especially when a large number of cases are handled. The use of a computer further reduces the time and minimizes the

calculation error. PI tables also serve as a double-check on the interpretation for an exclusion. In cases of maternal exclusion, the child-mother phenotype combination will not be found. In a paternal exclusion, no value is assigned under a given phenotype for the alleged father.

Since only basic genetics are involved in the derivation of RCP, examples have been given so that one may be able to derive RCP for genetic markers not listed in the tables, or for populations other than the ones listed in this report.

All calculations are based on available gene or haplotype frequencies. For some genetic markers, such frequencies are not found in the literature, especially for nonwhite populations. For others, the survey may involve only a small population and may miss some of the low-frequency markers. Attempts have been made to select the best available sources for these calculations. Obviously, there is an urgent need to establish reliable genetic-marker frequencies for use in paternity testing, so that the precision of this type of estimation can be improved.

With few exceptions, gene frequencies of various white populations are relatively close, whereas significant differences exist in different racial groups; thus, it is essential to know the racial background of the parties involved, especially that of the alleged father, in order to obtain accurate paternity indexes. The possibilities of genetic variants, phenotypes missing from a survey of a small population, and mixed racial heritage should also be taken into consideration. The person who reviews the test results and signs the report must be familiar with all the variations,⁹ and each zero PI must be evaluated individually. The paternity indexes presented in this report are intended to simplify the average routine reports, but are not intended to replace the interpretations of test results completely.

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Table 10. Paternity Indexes of Different GM Phenotypes*

Child	Phenotype -Gm() Mother	Haplo- type from Father	PI of the Alleged Father of a Given Phenotype -GM()†									
			f;b (1)	az;b (2)	az:g (3)	azf;b (4)	afz;bg (5)	azxf;bg (6)	az;bg (7)	azx;bg (8)	azx:g (9)	
1	1,4,5,6											
4	2,7,8	f;b	1.44			.72	.72	.72				
5	3,7,9		(7.35)			(3.68)	(3.69)	(3.68)				
6	8,9											
2	2,4,7,8											
4	1,5,6	az;b		62.5		31.25			31.25	31.25		
7	3,5,9		(1.26)		(.63)			(.63)	(.63)			
8	6,9											
3	3,5,7,9											
5	1,4,6	az:g			5.44			2.72		2.72		2.12
7	2,4,8		(25)		(12.5)		(12.5)	(12.5)			(9.75)	
9	6,8											
9	3,5,6,7,8											
6	1,4,5	azx;g						4.95		4.95	6.04	
8	2,4,7		(23.81)					(23.81)	(23.81)	(29.05)		
4	4	f;b or az;b	1.41 (1.07)	1.41 (1.07)		1.41 (1.07)	1.41 (1.07)	1.41 (1.07)	1.41 (1.07)	1.41 (1.07)		
5	5	f;b or az:g	1.14 (5.68)		1.14 (5.68)	1.14 (5.68)	1.14 (5.68)	1.14 (5.68)	1.14 (5.68)			.89 (4.43)
6	6	f;b or azx;g	1.25 (6.33)			1.25 (6.33)	1.25 (6.33)	1.25 (6.33)			1.25 (6.33)	1.53 (7.72)
7	7	az;b or az:g		5 (1.19)	5 (1.19)	5 (1.19)	5 (1.19)		5 1.19	5 1.19	3.90 .93	
8	8	az;b or azx;g			8.47 (1.22)	8.47 (1.22)		8.47 (1.22)	8.47 (1.22)	8.47 (1.22)	10.34 (1.49)	
9	9	azx;g or az:g			2.93 (13.45)		1.47 (6.72)	2.49 (10.52)	1.47 (6.72)	2.29 (10.52)	6.38 (29.94)	

* Haplotype frequencies were kindly supplied by Dr. Moses Schanfield of the American Red Cross National Blood Service, Washington, D. C.

† Values in parentheses are for black population; values with no parentheses are for white population.

Glossary

Alleged father: The alleged father is a man who is accused of being the father of a child or children. He may or may not be the father of the child. A falsely accused alleged father is essentially the same as a random man. The difference between the two is that the former has been accused and tested, whereas the latter has not.

Random man: A random man is a man who is of the same racial group as the alleged father, and is essentially the same as a falsely accused man. He may or may not be involved with the mother.

Genetic marker: Genetic markers include allotypes of erythrocytic antigens, lymphocytic (HLA) antigens, erythrocytic enzymes, and serum proteins, as well as their controlling genes or gene complexes (haplotypes). Genetic markers occur in pairs; one of a pair is inherited from the mother, and the other from the father. A homozygote has a pair of identical markers, whereas a heterozygote has a pair of different markers. Homozygous and heterozygous are expressions of genotypes that may or may not be demonstrable by laboratory tests. Demonstrable genetic markers

are designated phenotypes. A group of allelic markers is known as a system.

Chance of paternity (CP): CP represents the chance that a man is able to provide a sperm carrying all of the genetic markers that are required for him to be the father of the child from a known mother. For a random man, CP is the same as the gene (or haplotype) frequency (GF). For the alleged father, CP is determined by his genotype.

Paternity index (PI): PI represents the ratio between the CP of the alleged father and that of a random man. $PI = CP/GF$ where the GF is adjusted to 1. PI indicates essentially how many times the alleged father is more likely than not to be the father of the child.

Relative chance of paternity (RCP): RCP has the same meaning as the PI except that RCP is expressed in percentage. $RCP = PI/(PI + 1)$. Therefore, RCP differs distinctively from CP, because RCP uses the CP of a random man as a reference for the CP of the alleged father. In other words, the odds that the alleged father is actually the father is RCP, whereas the odds that he is not the father is $1 - RCP$. When RCP is equal to or close to 0%, nonpaternity (exclusion) is indicated; when RCP is close to 100%, paternity is most likely.

Table 11. Coding of Various Phenotypes Demonstrable in Paternity Testing for Computer Analysis

Genetic Marker		Number or Letter Assigned to Each Phenotype											
System	Assigned	0	1	2	3	4	5	6	7	8	9	A	B
Rh	R	dCce	DCcEe	DCce	DC ^w ce	DcEe	DCE	DcE	Dce	dce	dcEe*		
MNSs	N	MN ⁺	MS	Ms	MSs	NS	Ns	NSs	MNS	MNs	MNSs	M ⁺	N ⁺
Gm (1)	G		f; b	az; b	az; g	azf; b	azf; bg	azxf; bg	az; bg	azx; bg	azx; g		
ABO	O	O	A ₁	A ₂	B		A ₁ B	A ₂ B					
AcP	A		A	B	C	AB	AC	BC					
ADA	D		1	2	3	1-2	1-3	2-3					
AK	V		1	2	3	1-2	1-3	2-3					
Tf	W		B	C	D	BC	BD	CD					
Duffy	F	a-b-	a+b-	a-b+		a+b+			a+	a-			
Kell	K		K+k-	K-k+		K+k+			Js(a+)	Js(a-)			
Kidd	J		a+b-	a-b+		a+b+			a+	a-			
Km(Inv)	I		1+3-	1-3+		1+3+			1+	1-			
Hp	H		1	2		1-2							
Gc	C		1	2		1-2							
PGM ₁	M		1	2		1-2							
GPT	T		1	2		1-2							
EsD	E		1	2		1-2							
GLO	L		1	2		1-2							
PGD	Q		A	B		AB							
Lutheran	U								a+	a-			
Secretor	S								Se+	Se-			
Xg	X								a+	a-			
P ₁	P								P ₁ +	P ₁ -			

* R9 = dcEe in whites, = D^wce in blacks.

† S-s-

Table 12. Useful Information for Deriving Paternity Indexes of Different ABO Phenotypes*

Genes	O	A ₁	A ₂	B
Gene frequencies†	.6602(r) (.7006)	.2039(p ₁) (.1161)	.0701(p ₂) (.0585)	.0658(q) (.1248)

Pheno- types	Genotypes			Chance of Passing the Gene			
	Type	Frequency	Percentages	O	A ₁	A ₂	B
A ₁	A ₁ A ₁	.0416 (.0135)	12.3 (7.1)	.3965 (.4285)	.5615 (.5345)	.0420 (.0360)	0 (0)
	A ₁ A ₂	.0286 (.0136)	8.4 (7.2)				
	A ₁ O	.2692 (.1627)	79.3 (85.7)				
A ₂	A ₂ A ₂	.0049 (.0034)	5.0 (4.0)	.4749 (.4800)	0 (0)	.5251 (.5200)	0 (0)
	A ₂ O	.0926 (.0820)	95.0 (96.0)				
B	BB	.0043 (.0156)	4.8 (8.2)	.4760 (.4590)			.5240 (.5410)
	BO	.0926 (.1749)	95.2 (91.8)				
A ₁ B	A ₁ B	.0268 (.0230)	100.0 (100.0)	0 (0)	.5 (.5)	0 (0)	.5 (.5)
A ₂ B	A ₂ B	.0092 (.0146)	100.0 (100.0)	0 (0)	0 (0)	.5 (.5)	.5 (.5)
O	OO	.4359 (.4908)	100.0 (100.0)	1 (1)	0 (0)	0 (0)	0 (0)

* Whites, n = 8,965, Michigan; blacks, n = 3,146, San Francisco; reference 12, p 230.

† Values in parentheses are for black population; values without parentheses are for white population.

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