JOURNAL OF
HUMAN ECOLOGY

J. Hum. Ecol., 5(4): 259-270 (1994)

PRINT: ISSN 0970-9274 ONLINE: 2456-6608

DOI: 10.31901/24566608.1994/05.04.02

Forensic Status of 20 Blood Genetic Marker Systems in India

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KEY WORDS Blood Genetic Markers. Forensic Potential. India.

ABSTRACT This report provides a ready reference to the forensic status of a total of 20 blood genetic marker systems investigated in Indian populations. In order to assess the forensic potential of each system, the available phenotypic data from all over India were compiled zone-wise and subjected to statistical treatment for computing phenotype and allele frequencies and measures like individualization potential (PI), discrimination potential (PD) and probability of exclusion of paternity (Pe). A sequence of the use of these systems to obtain maximum information at any stage of analysis had been brought out which makes the analysis cost and time effective.

INTRODUCTION

Blood genetic markers are increasingly being used in resolving varied problems of forensics, especially those relating to disputed parentage and criminal investigation. Weightage given to the genetic evidence by the Indian courts in recent times in such cases (Kushwaha, 1991) encourages forensic serologists in India to further develop and use more and more genetic systems in their laboratories in the interest of justice.

Two decades back as many as 50 serogenetic marker systems were listed for use in cases of disputed parentage (Chakraborty et al., 1974). Rapid strides in the field of forensic serology have increased the number of such systems to nearly 62 (Damodran et al., 1985), albeit it is impracticable for every laboratory to make use of all of them due to lack of technical facilities and prohibitively high cost of tests. In addition, differences in power of their effectiveness (based on the presence and degree of polymorphism in the concerned populations) necessitate selective usage of these markers. For this, it is essential to know the phenotypic and allelic frequencies of various systems in the relevant populations for :

(a) having check over the testing methods.

(b) calculating the likelihood of the respondent or the claimant as being the bilogical father or mother when the tests fail to exclude parentage of the child, and computing the individualization probabilities in the crime and mass catastrophic cases.

(c) assessing the effectiveness of the various systems in terms of individualization potential (PI) - the probability of two individuals selected at random from the population, being identical with respect to the genetic marker in question, discrimination potential (PD) - the probability with which two individuals in the population would differ with respect to the phenotype, and the average probability of paternity exclusion (Pe)– likelihood of a particular genetic marker system that will exclude an inocent person from the paternity.

The present work is an attempt to bring out an abridgement of reference wherein phenotype percentages, allele frequencies and various measures of forensic importance of as many as 20 different genetic marker systems have been given for India as a whole as well

as for its different geographical regions *viz.* North, West, Central, East and South Indian zones. For this, phenotypic data on the distribution of various genetic markers in different population groups inhabiting almost all parts of India generated by the anthropological researches during the last several decades were compiled from Bhasin et al. (1992) and a few studies reported from Haryana by Kushwaha (1988), Kushwaha et al. (1992) and Kushwaha and Chahal (1994) for statistical treatment and finally, based on their forensic status, the systems were marshalled to obtain maximum information at any stage of analysis.

MATERIAL AND METHODS

Phenotypic data available for 20 different blood genetic marker systems including 8 blood groups (A_1A_2BO, Rh(D), MN, Kell, Duffy, Kidd, Lutheran, Diego), 8 red cell enzymes (PGM_1, GLO I, EsD, EAP, AK, ADA, GPT, 6-PGD) and 4 serum proteins (Hp, Bf, C_3, Gc) from all over India were pooled and subjected to statistical treatment for computing phenotypic percentages, allele frequencies and forensic potentials in terms of PI, PD and Pe values. However, for zone-wise (arrangement following Bhasin et al., 1992) analysis data were available for only 18 systems (barring Diego and 6-PGD) in North India, 16 in West (barring Duffy, Kidd, Bf and C_3) and Central (barring Lutheran, Diego, GPT and Bf) India, 18 (barring GPT and Bf) in East India and 17 (barring Duffy, Kidd and Lutheran) in South India. For both Kell and Duffy blood group systems only those data were included where two antisera were used for typing.

The allelic frequency computations were done using formulae given in Mourant et al. (1976) except for the A_1A_2BO system for which the formulae derived by Yasuda (1984) were used.

In order to assess the forensic potential of each system, various values were calculated as described below.

PI and PD Values

PI value for each system was calculated according to Fisher (1951) using equation, $PI = \Sigma X_i^2$ where X_i is the frequency of i^{th} phenotype in the polymorphic system. PD value was obtained as, PD = 1-P1. The cumulative PI (CPI) values were calculated by multiplying the PI value of each system as, $PCI=P_1 \times P_2 \times P_3 \ldots \times Pn$. The values for cumulative discrimination power (CPD) were obtained as, CPD=1–CPI.

Pe Values

For the A_1A_2BO system following formula given by Wiener et al. (1923) was used.

$Pe = p_1(q+r)^4 + q(p_1+r)^4 + p_1qr^2(p_1+q) + 2p_1qr^2 + p_2(q+r)^4 + p_2qr^2 (p_2+q) + 2p_2qr^2.$

Where p_1, p_2, q and r represent the frequencies of A_1, A_2, B and 0 alleles, respectively.

For the Rh(D) system, the equation, $Pe=r^4-r^5$ given by Wiener and Socha (1976) was used, where r is the frequency of D-negative allele.

For the two codominant allele systems, the equation Pe=pq (1-pq) given by Wiener et al. (1930) was used, where p and q are allele frequencies of the two codominant alleles.

For the three codominant allele systems, following formula given by Gahne (1961) was used.

$Pe=pq\ (1-pq)+pr(1-pr)+qr\ (1-qr)\ +3pqr\ (1-pq-pr-qr)$

Where *p, q, r* represent the frequencies of the three codominant alleles.

The cumulative values of paternity exclusion (Pm) were computed using equation

$Pm=1-(1-Pe_1)\ (1-Pe_2)\ (1-Pe_3)\ (1-Pe_m)$

Where m is the number of systems involved.

RESULTS AND DISCUSSION

The results are presented in table 1 for India, and in tables 2-6 for North, West, Central, East and South Indian zones. Number of populations and number of subjects tested, phenotype percentage, allele frequencies alongwith PI, PD and Pe values have been shown separately for each system in these

tables. In addition, cumulative values of PI, PD and Pe have also been given. The arrangement of marker systems in each table is in the ascending order of their PI values.

Among all the twenty systems, A_1A_2BO system emerges as the most effective discriminator in India as well as in its different zones excepting Central India where Duffy system shows marginally higher value of PD.

Among the red cell enzymes, GPT system shows the highest potential for discrimination in India and its North, West and South zones (data from Central and East India were not available). As for serum proteins, the Bf system in North and South Indian zones (data from other zones were not available) shows the highest potential for discrimination.

The values under CPD column reflect that the maximum degree of individualization or discrimination can be achieved at any stage of analysis by observing the sequence of various systems as given in the tables 2 to 6 for respective zones of India and that of table 1 for the country as a whole, when the genetic affiliation of the person(s) to any zone is uncertain. By adopting these sequences, the analysis becomes both time and cost effective. The use of all the 20 genetic systems listed in table 1 increases the probability of discrimination to almost unity providing the high degree of individualization and can exonerate about 92% of falsely accused persons of the Indian origin.

CONCLUSION

The different blood genetic marker systems investigated in the Indian populations,

Table 1 : Phenotype percentages, allele frequencies, individualization potential (PI), cumulative PI (CPI), discrimination potential (PD), cumulative PD (CPD), probability of exclusion of paternity (Pe) and cumulative Pe (Pm) values of various marker systems investigated in the Indian populations.

System	*Number of populations*	*Number tested*	*Phenotype percentage*	*Allele frequency*	*PI*	*CPI*	*PD*	*CPD*	*Pe*	*Pm*
A_1A_2BO	379	84692	A_1=24.2 A_2=3.3 A_1B=7.5 A_2B=1.4 B=30.7 O=32.9	A_1=0.174 A_2=0.028 B=0.223 O=0.575	0.268	—	0.732	—	0.222	—
Duffy	44	3968	Fy^{a+b-}=50.8 Fy^{a+b+}=36.3 Fy^{a-b+}=12.9 Fy^{a-b-}=0.05	Fy^a=0.657 Fy^b=0.294 Fy^O=0.049	0.342	0.091656	0.658	0.908344	0.156	0.344
Kidd	34	2151	Jk^{a+b-}=35.3 Jk^{a+b+}=41.2 JK^{a-b+}=22.9 JK^{a-b-}=0.6	Jk^a=0.562 Jk^b=0.438	0.379	0.034737	0.621	0.965263	0.186	0.466
GPT	12	957	1-1=19.3 2-1=47.1 2-2=33.6	GPT^1=0.429 GPT^2=0.571	0.380	0.013200	0.620	0.986800	0.185	0.565
MN	255	38556	M=41.7 MN=43.5 N=14.8	M=0.634 N=0.366	0.395	0.005214	0.605	0.994786	0.178	0.642
Bf	12	1049	S=41.9 SF=40.1 F=14.4 Variants = 1.6	Bf^S=0.646 Bf^F=0.346 Bf^V=0.008	0.400	0.002085	0.600	0.997915	0.176	0.705

Table 1 : Contd...

System	*Number of polulations*	*Number tested*	*Phenotype percentage*	*Allele frequency*	*PI*	*CPI*	*PD*	*CPD*	*Pe*	*Pm*
PGM_1	189	19408	1-1=50.4 2-1=38.4 2-1=10.1 Variants = 1.1	PGM^1=0.704 PGM^2=0.294 PGM^V=0.002	0.424	0.000884	0.576	0.999116	0.165	0.754
GLO I	75	9296	1-1 = 7.9 2-1=36.7 2-2=55.4	GLO^1=0.263 GLO^2=0.737	0.450	0.000397	0.550	0.999603	0.156	0.792
EsD	196	20465	1-1=55.6 2-1=36.6 2-2=7.8	EsD^1=0.739 EsD^2=0.261	0.452	0.000179	0.548	0.999821	0.156	0.825
EAP	242	26407	A = 7.4 BA=34.3 B=57.6 CA=0.2 CB=0.4 Variants = 0.03	p^a=0.247 p^b=0.750 p^c=0.003 p^v=5x10^{-5}	0.457	0.000082	0.543	0.999918	0.155	0.852
Gc	69	7138	1-1=59.5 2-1=31.3 2-2=9.2	Gc^1=0.752 Gc^2=0.248	0.462	0.000038	0.538	0.999962	0.152	0.875
Hp	318	35496	1-1=3.1 2-1=27.1 2-2=68.3 0-0=1.3	Hp^1=0.167 Hp^2=0.819 Hp^0=0.014	0.556	0.000021	0.444	0.999979	0.121	0.890
ADA	100	9316	1-1=78.0 2-1=19.9 2-2=2.1 Variants = 0.05	ADA^1=0.880 ADA^2=0.120 ADA^V=2x10^{-4}	0.644	0.000013	0.356	0.999987	0.095	0.901
C_3	49	5531	S=84.2 SF=14.5 F=1.1 Variants = 0.2	C_3^S=0.915 C_3^F=0.084 C_3^V=0.001	0.729	0.000010	0.271	0.999990	0.071	0.908
AK	195	20061	1-1=85.7 2-1=13.7 2-2=0.6	AK^1=0.925 AK^2=0.075	0.752	0.000007	0.248	0.999993	0.064	0.913
Rh(D)	309	91876	D+=95.1 D-=4.9	D=0.780 d=0.220	0.908	0.000006	0.092	0.999994	0.002	0.914
6-PGD	121	12913	A=91.5 CA=7.8 C=0.5 Variants=0.2	PGD^A=0.954 PGD^C=0.044 PGD^V=0.002	0.912	0.000006	0.088	0.999994	0.040	0.917
Kell	45	5276	KK=0.05 Kk=2.5 kk=97.4	K=0.014 K=0.986	0.947	0.000006	0.053	0.999994	0.013	0.918
Diego	24	2371	Di^{a+}=2.2 Di^{a-}=97.8	Di^a=0.011 Di^b=0.989	0.958	0.000005	0.042	0.999995	0.010	0.919
Luthera n	15	1349	Lu^{a+b-}=0.3 Lu^{a+b+}=1.1 Lu^{a-b+}=98.6	Lu^a=0.009 Lu^b=0.991	0.967	0.000005	0.033	0.999995	0.008	0.920

Table 2 : Phenotype percentage, allele frequencies, individualization potential (PI), cumulative PI (CPI), discrimination potential (PD), cumulative PD (CPD), probability of exclusion of paternity (Pe) and cumulative Pe (Pm) values of various marker systems investigated in populations of North India

System	*Number of populations*	*Number tested*	*Phenotype percentage*	*Allele frequency*	*PI*	*CPI*	*PD*	*CPD*	*Pe*	*Pm*
A_1A_2BO	116	21998	A_1=22.1 A_2=3.1 A_1B=8.8 A_2B=1.5 B=35.0 0=29.5	A_1=0.169 A_2=0.028 B=0.260 O=0.543	0.267	—	0.733	—	0.217	—
Duffy	25	3048	Fy^{a+b-}=47.5 Fy^{a+b+}=38.5 Fy^{a-b+}=13.9 Fy^{a-b-}=0.03	Fy^a=0.641 Fy^b=0.318 Fy^O=0.041	0.345	0.092115	0.655	0.907885	0.162	0.344
GPT	4	482	1-1=21.8 2-1=48.1 2-2=30.1	GPT^1=0.459 GPT^2=0.541	0.377	0.034727	0.623	0.965273	0.187	0.467
Kidd	14	1226	Jk^{a+b-}=37.6 Jk^{a+b+}=38.2 Jk^{a-b+}=24.2	Jk^a=0.567 Jk^b=0.433	0.380	0.013196	0.620	0.986804	0.185	0.565
MN	94	11352	M=40.1 MN=44.0 N=15.9	M=0.621 N=0.379	0.391	0.005159	0.609	0.994841	0.180	0.644
Bf	11	971	S=44.6 SF=40.3 F=13.4 Variants =1.7	Bf^S=0.654 Bf^F=0.337 Bf^V=0.009	0.404	0.002084	0.596	0.997916	0.171	0.706
PGM_1	62	6128	1-1=50.8 2-1=38.6 2-2=10.2 Variants=0.4	PGM^1=0.703 PGM^2=0.296 PGM^V=0.001	0.424	0.000884	0.576	0.999116	0.165	0.754
EAP	55	5955	A=9.0 BA=36.8 B=53.3 CA=0.3 CB=0.5 Variants=0.05	p^a=0.276 p^b=0.720 p^c=0.004 p^v=$2x10^{-4}$	0.443	0.000391	0.567	0.999609	0.165	0.795
Gc	25	2480	1-1=54.3 2-1=38.1 2-2=7.6	Gc^1=0.733 Gc^2=0.267	0.447	0.000175	0.553	0.999825	0.157	0.827
GLO I	30	3380	1-1=7.3 2-1=37.6 2-2=55.1	GLO^1=0.261 GLO^2=0.739	0.452	0.000079	0.548	0.999921	0.156	0.854
EsD	65	6347	1-1=61.2 2-1=33.1 2-2=5.7	EsD^1=0.778 EsD^2=0.222	0.488	0.000038	0.512	0.999962	0.143	0.875
Hp	83	8222	1-1=4.4 2-1=32.2 2-2=61.6 0-0=1.7 Variants=0.04	Hp^1=0.205 Hp^2=0.777 Hp^O=0.017	0.503	0.000019	0.497	0.999981	0.138	0.892

Table 2 : Contd...

System	Number of popu-lations	Number tested	Phenotype percentage	Allele frequency	PI	CPI	PD	CPD	Pe	Pm
ADA	56	5628	1-1=80.1 2-1=18.1 2-2=1.8 Variants=0.03	ADA^1=0.892 ADA^2=0.108 ADA^V=2x10^{-4}	0.670	0.000013	0.330	0.999987	0.087	0.902
C_3	28	2588	S=79.7 SF=18.7 F=1.3 Variants=0.3	C_3^S=0.891 C_3^F=0.107 C_3^V=0.002	0.673	0.000009	0.327	0.999991	0.086	0.910
AK	75	7177	1-1=82.8 2-1=16.6 2-2=0.6	AK^1=0.911 AK^2=0.089	0.715	0.000006	0.285	0.999994	0.075	0.917
Rh(D)	149	39133	D+=92.9 D-=5.1	D=0.774 d=0.226	0.903	0.000005	0.097	0.999995	0.002	0.917
Kell	32	3633	KK=0.0 Kk=2.9 kk=97.1	K=0.014 k=0.986	0.945	0.000005	0.055	0.999995	0.014	0.918
Lutheran	7	626	Lu^{a+b-}=0.0 Lu^{a+b+}=0.9 Lu^{a-b+}=99.1	Lu^a=0.005 Lu^b=0.995	0.981	0.000005	0.019	0.999995	0.005	0.919

Table 3 : Phenotype percentages, allele frequencies, individualization potential (PI), cumulative PI (CPI), discrimination potential (PD), cumulative PD (CPD), probability of exclusion of paternity (Pe) and cumulative Pe (Pm) values of various marker systems investigated in populations of West India

System	Number of popu-lations	Number tested	Phenotype percentage	Allele frequency	PI	CPI	PD	CPD	Pe	Pm
A_1A_2BO	77	34894	A_1=27.0 A_2=3.9 A_1B=7.0 A_2B=1.4 B=27.2 O=33.3	A_1=0.189 A_2=0.033 B=0.199 O=0.579	0.264	—	0.736	—	0.219	—
MN	46	9497	M=36.7 MN=46.3 N=17.0	M=0.598 N=0.402	0.385	0.101640	0.615	0.898360	0.183	0.360
GPT	2	106	1-1=16.0 2-1=38.7 2-2=45.3	GPT^1=0.354 GPT^2=0.646	0.399	0.040554	0.601	0.959446	0.176	0.474
PGM_1	31	3549	1-1=48.3 2-1=39.6 2-2=11.5 Variants=0.6	PGM^1=0.693 PGM^2=0.305 PGM^V=0.002	0.419	0.016992	0.581	0.983008	0.166	0.562
GLO I	6	1047	1-1=7.4 2-1=40.7 2-2=51.9	GLO^1=0.278 GLO^2=0.722	0.439	0.007459	0.561	0.992541	0.160	0.632
EAP	37	3991	A=8.6 BA=35.4 B=55.4 CA=0.1 CB=0.4 Variants=0.05	p^a=0.263 p^b=0.734 p^c=0.003 p^v=2x10^{-4}	0.444	0.003312	0.556	0.996688	0.160	0.691

Table 3 : Contd...

System	Number of popu-lations	Number tested	Phenotype percentage	Allele frequency	PI	CPI	PD	CPD	Pe	Pm
Gc	5	500	1-1=56.4 2-1=33.6 2-2=10.0	Gc^1=0.732 Gc^2=0.238	0.446	0.001477	0.554	0.998523	0.158	0.740
EsD	22	2242	1-1=63.5 2-1=30.6 2-2=5.9	EsD^1=0.788 EsD^2=0.212	0.499	0.000737	0.501	0.999263	0.139	0.776
Hp	61	7269	1-1=2.8 2-1=27.7 2-2=67.4 0.0=2.1	Hp^1=0.166 Hp^2=0.813 Hp^O=0.021	0.555	0.000409	0.445	0.999591	0.121	0.803
ADA	6	429	1-1=75.1 2-1=23.1 2-2=1.4 Variants=0.4	ADA^1=0.870 ADA^2=0.130 ADA^V=2x10^{-3}	0.624	0.000255	0.376	0.999745	0.100	0.823
AK	15	2043	1-1=84.5 2-1=14.9 2-2=0.6	AK^1=0.919 AK^2=0.081	0.735	0.000187	0.265	0.999813	0.069	0.825
6-PGD	15	2309	A=94.3 CA=5.5 C=0.1 Variants=0.1	PGD^A=0.971 PGD^C=0.028 PGD^V=0.001	0.894	0.000167	0.106	0.999833	0.027	0.839
Rh(D)	37	26904	D+=95.1 D-=4.9	D=0.779 d=0.221	0.907	0.000152	0.093	0.999948	0.002	0.840
Diego	2	364	Di^{a+}=3.6 Di^{a-}=96.4	Di^a=0.018 Di^b=0.982	0.931	0.000141	0.069	0.999959	0.017	0.843
Lutheran	5	352	Lu^{a+b-}=1.1 Lu^{a+b+}=1.1 Lu^{a-b+}=97.7	Lu^a=0.017 Lu^b=0.983	0.935	0.000132	0.065	0.999968	0.016	0.845
Kell	5	578	KK=0.0 Kk=2.4 kk=97.6	K=0.012 k=0.988	0.953	0.000126	0.047	0.999974	0.012	0.847

Table 4 : Phenotype percentages, allele frequencies, individualization potential (PI), cumulative PI (CPI), discrimination potential (PD), cumulative PD (CPD), probability of exclusion of paternity (Pe) and cumulative Pe (Pm) values of various maker systems investigated in populations of Central India

System	Number of popu-lations	Number tested	Phenotype percentage	Allele frequency	PI	CPI	PD	CPD	Pe	Pm
Duffy	1	140	Fy^{a+b-}=36.4 Fy^{a+b+}=40.0 Fy^{a-b+}=22.9 Fy^{a-b-}=0.7	Fy^a=0.515 Fy^b=0.393 Fy^O=0.092	0.258	—	0.742		0.161	—
A_1A_2BO	16	2544	A_1=26.4 A_2=2.5 A_1B=9.8 A_2B=1.3 B=32.8 O=27.2	A_1=0.202 A_2=0.024 B=0.252 O=0.523	0.261	0.067338	0.739	0.932662	0.215	0.342

Table 4 : Contd...

System	*Number of populations*	*Number tested*	*Phenotype percentage*	*Allele frequency*	*PI*	*CPI*	*PD*	*CPD*	*Pe*	*Pm*
Kidd	2	175	Jk^{a+b-}=30.9 Jk^{a+b+}=46.9 Jk^{a-b+}=21.8 Jk^{a-b-}=1.1	Jk^a=0.549 Jk^b=0.451	0.377	0.025386	0.623	0.974614	0.186	0.464
MN	12	1920	M=50.1 MN=36.8 N=13.1	M=0.685 N=0.315	0.416	0.010561	0.584	0.989439	0.169	0.555
PGM_1	3	480	1-1=54.2 2-1=35.2 2-2=14.2 Variants=0.2	PGM^1=0.719 PGM^2=0.280 PGM^V=0.001	0.435	0.004594	0.565	0.995406	0.161	0.627
EAP	4	504	A=7.9 BA=38.9 B=52.8 CA=0.4 CB=0.0	p^a=0.276 p^b=0.722 p^c=0.002	0.437	0.002007	0.563	0.997993	0.162	0.687
Gc	1	75	1-1=53.3 2-1=40.0 2-2=6.7	Gc^1=0.733 Gc^2=0.267	0.447	0.000897	0.553	0.999103	0.157	0.736
EsD	1	143	1-1=58.0 2-1=31.5 2-2=10.5	EsD^1=0.738 EsD^2=0.262	0.451	0.000405	0.549	0.999595	0.156	0.778
GLO I	1	89	1-1=7.8 2-1=27.0 2-2=65.2	GLO^1=0.213 GLO^2=0.787	0.498	0.000201	0.502	0.999799	0.140	0.809
Hp	4	539	1-1=4.1 2-1=27.8 2-2=66.8 0-0=0.9	Hp^1=0.184 Hp^2=0.807 Hp^0=0.009	0.533	0.000107	0.467	0.999893	0.128	0.833
ADA	3	484	1-1=77.9 2-1=20.7 2-2=1.4	ADA^1=0.882 ADA^2=0.118	0.649	0.000069	0.351	0.999931	0.093	0.849
C3	1	91	S=85.7 SF=14.3 F=0.0	C_3^S=0.929 C_3^F=0.071	0.761	0.000053	0.239	0.999947	0.062	0.858
AK	2	229	1-1=91.3 2-1=8.7 2-2=0.0	AK^1=0.956 AK^2=0.044	0.843	0.000044	0.157	0.999956	0.040	0.864
6-PGD	1	145	A=93.1 CA=6.9 C=0.0	PGD^A=0.966 PGD^C=0.034	0.873	0.000039	0.127	0.999961	0.032	0.868
Rh(D)	4	1192	D+=93.3 D-=6.7	D=0.741 d=0.259	0.875	0.000034	0.125	0.999966	0.003	0.869
Kell	2	333	KK=0.0 Kk=1.2 kk=98.8	K=0.006 k=0.994	0.976	0.000033	0.024	0.999967	0.006	0.869

Table 5 : Phenotype percentages, allele frequencies, individualization potential (PI), cumulative PI (CPI), discrimination potential (PD), cumulative PD (CPD), probability of exclusion of paternity (Pe) and cumulative Pe (Pm) values of various marker systems investigated in populations of East India

System	*Number of populations*	*Number tested*	*Phenotype percentage*	*Allele frequency*	*PI*	*CPI*	*PD*	*CPD*	*Pe*	*Pm*
A_1A_2BO	86	12942	A_1=24.2 A_2=1.9 A_1B=8.1 A_2B=1.1 B=32.5 O=32.1	A_1=0.178 A_2=0.017 B=0.237 O=0.568	0.275	—	0.725	—	0.224	—
Kidd	18	750	Jk^{a+b-}=32.5 Jk^{a+b+}=44.8 Jk^{a-b+}=21.2 Jk^{a-b-}=1.5	Jk^a=0.558 Jk^b=0.442	0.378	0.103950	0.622	0.896050	0.186	0.369
MN	46	8506	M=43.9 MN=44.3 N=11.8	M=0.661 N=0.339	0.405	0.042099	0.595	0.957901	0.174	0.480
EsD	54	4810	1-1=51.9 2-1=37.4 2-2=10.7	EsD^1=0.706 EsD^2=0.294	0.428	0.018018	0.572	0.981982	0.164	0.565
PGM_1	49	3829	1-1=53.7 2-1=37.4 2-2=8.5 Variants=0.4	PGM^1=0.726 PGM^2=0.266 PGM^V=0.008	0.443	0.007982	0.557	0.992018	0.159	0.634
Gc	14	1698	1-1=58.8 2-1=33.1 2-2=8.0	Gc^1=0.754 Gc^2=0.246	0.465	0.003712	0.535	0.996288	0.151	0.690
EAP	65	5821	A=6.6 BA=31.4 B=60.7 CA=0.3 CB=0.9 CC=0.1	p^a=0.225 p^b=0.769 p^c=0.006	0.472	0.001752	0.528	0.998248	0.152	0.737
GLO I	16	1573	1-1=7.1 2-1=31.4 2-2=61.5	GLO^1=0.228 GLO^2=0.772	0.482	0.000844	0.518	0.999156	0.145	0.775
Duffy	18	780	Fy^{a+b-}=67.2 Fy^{a+b+}=26.7 Fy^{a-b+}=7.1	Fy^a=0.796 Fy^b=0.204	0.509	0.000430	0.491	0.999570	0.136	0.810
ADA	25	1765	1-1=71.3 2-1=24.8 2-2=3.8 Variants=0.05	ADA^1=0.820 ADA^2=0.180 ADA^V=$3x10^{-4}$	0.540	0.000232	0.460	0.999768	0.126	0.834
Hp	77	7542	1-1=2.5 2-1=27.3 2-2=69.3 0-0=0.9	Hp^1=0.162 Hp^2=0.830 Hp^0=0.008	0.565	0.000131	0.435	0.999869	0.118	0.854
6-PGD	32	2299	A=84.1 CA=13.9 C=2.0	PGD^A=0.911 PGD^C=0.089	0.715	0.000094	0.285	0.999906	0.075	0.865
AK	59	4967	1-1=90.8 2-1=8.7 2-2=0.5	AK^1=0.952 AK^2=0.048	0.829	0.000077	0.171	0.999923	0.044	0.871

Table 5 : Contd...

System	Number of populations	Number tested	Phenotype percentage	Allele frequency	PI	CPI	PD	CPD	Pe	Pm
C_3	2	184	S=92.4 SF=7.6 F=0.0	C_3^S=0.962 C_3^F=0.038	0.862	0.000067	0.138	0.999933	0.035	0.875
Rh(D)	35	11335	D+=96.5 D-=3.5	D=0.813 d=0.187	0.932	0.000062	0.068	0.999938	0.001	0.876
Diego	14	1412	Di^{a+}=2.6 Di^{a-}=97.4	Di^a=0.013 Di^b=0.987	0.949	0.000059	0.051	0.999941	0.013	0.877
Kell	5	708	KK=0.0 Kk=1.7 kk=98.3	K=0.008 k=0.992	0.967	0.000057	0.033	0.999943	0.008	0.878
Lutheran	3	371	Lu^{a+b-}=0.0 Lu^{a+b+}=1.3 Lu^{a-b+}=98.7	Lu^a=0.007 Lu^b=0.993	0.968	0.000055	0.032	0.999945	0.007	0.879

Table 6 : Phenotype percentages, allele frequencies, individualization potential (PI), cumulative PI (CPI), discrimination potential (PD), cumulative PD (CPD), probability of exclusion of paternity (Pe) and cumulative Pe (Pm) values of various marker systems investigated in populations of South India

System	Number of populations	Number tested	Phenotype percentage	Allele frequency	PI	CPI	PD	CPD	Pe	Pm
A_1A_2BO	84	12314	A_1=19.5 A_2=3.4 A_1B=4.9 A_2B=1.6 B=30.4 O=40.2	A_1=0.131 A_2=0.027 B=0.206 O=0.637	0.297	—	0.703	—	0.227	—
Bf	1	78	S=34.6 SF=38.5 F=26.9	Bf^S=0.538 Bf^F=0.462	0.376	0.111672	0.624	0.888328	0.187	0.372
GPT	6	369	1-1=17.1 2-1=48.2 2-2=34.7	GPT^1=0.412 GPT^2=0.588	0.383	0.042770	0.617	0.957230	0.184	0.487
MN	57	7281	M=45.8 MN=40.1 N=14.1	M=0.658 N=0.342	0.404	0.017279	0.596	0.982721	0.174	0.577
PGM_1	48	5430	1-1=48.1 2-2=38.8 2-2=10.4 Variants = 2.6	PGM^1=0.692 PGM^2=0.303 PGM^V=0.005	0.413	0.007136	0.587	0.992864	0.166	0.647
EsD	54	6923	1-1=50.5 2-1=41.3 2-2=8.2	EsD^1=0.711 EsD^2=0.289	0.432	0.003083	0.568	0.996917	0.163	0.705
GLO I	22	3207	1-1=9.2 2-1=37.2 2-2=53.6	GLO^1=0.278 GLO^2=0.722	0.439	0.001353	0.561	0.998647	0.161	0.752
EAP	81	10136	A=6.4 BA=33.8 B=59.5 CA=0.2 CB=0.1	p^a=0.234 p^b=0.764 p^c=0.001	0.473	0.000640	0.527	0.999360	0.149	0.789

Table 6 : Contd...

System	*Number of popu-lations*	*Number tested*	*Phenotype percentage*	*Allele frequency*	*PI*	*CPI*	*PD*	*CPD*	*Pe*	*Pm*
Gc	24	2385	1-1=66.2 2-1=22.3 2-2=11.5	Gc^1=0.774 Gc^2=0.226	0.484	0.000310	0.516	0.999690	0.144	0.819
Hp	93	11924	1-1=2.8 2-1=23.2 2-2=73.0 0-0=1.0	Hp^1=0.144 Hp^2=0.846 Hp^0=0.010	0.596	0.000185	0.404	0.999815	0.109	0.839
Kell	1	24	KK=12.5 Kk=0.0 kk=87.5	K=0.125 k=0.875	0.634	0.000117	0.366	0.999883	0.097	0.855
ADA	10	1010	1-1=79.2 2-1=19.7 2-2=1.1	ADA^1=0.891 ADA^2=0.109	0.667	0.000078	0.333	0.999922	0.088	0.868
AK	44	5645	1-1=85.0 2-1=14.2 2-2=0.8	AK^1=0.921 AK^2=0.079	0.740	0.000058	0.260	0.999942	0.061	0.876
C_3	18	2667	S=88.1 SF=11.0 F=0.9 Variants = 0.03	C_3^S=0.936 C_3^F=-.064 C_3^V=2x10^{-4}	0.782	0.000045	0.218	0.999955	0.056	0.883
Rh(D)	84	13311	D+=95.0 D-=5.0	D=0.776 d=0.224	0.905	0.000041	0.095	0.999959	0.002	0.883
6-PGD	40	4936	A=94.9 CA=4.5 C=0.2 Variants = 0.4	PGD^A=0.972 PGD^C=0.025 PGD^V=0.003	0.907	0.000037	0.093	0.999963	0.024	0.886
Diego	8	595	Di^{a+}=0.2 Di^{a-}=99.8	Di^a=0.001 Di^b=0.999	0.997	0.000036	0.003	0.999964	0.001	0.886

considered here, can effectively be used in forensics, and on adopting the sequential order A_1A_2BO, Duffy, Kidd, GPT, MN, Bf, PGM_1, GLO I, EsD, EAP, Gc, Hp, ADA, C_3, AK, Rh(D), 6-PGD, Kell, Diego, Lutheran, maximum information can be extracted at any stage of analysis.

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