Editorial Communication

Journal Policy on the Publication of DNA Population Genetic Data

Effective immediately, the journal will no longer accept manuscripts in any category submitted for the sole purpose of reporting population genetic data, allele or genotype frequencies. Submissions of that kind will be returned to authors without prejudice, but with no further action.

Authors **may** submit population genetic data to the journal in summary form, following a tabular format illustrated below, subject to certain conditions. The tabular data, when typeset, would ideally fit on one printed page, although it is recognized that studies involving multiple loci for several distinct racial/ethnic population groups may run to several pages. Authors must report the name of the population, the racial or ethnic group(s), the number of people typed, and the allele frequencies. Standard typing and statistical analysis methods used should be noted. The detection method used should also be stated briefly, especially for STR loci (i.e., manual silver stain, automated fluorescent, etc.). The results of statistical analyses showing that the population exhibits HWE proportions should also be reported in the tabular format. If classes were combined for purposes of statistical tests, this fact should be noted. In reports covering multiple loci, any deviations from independence between or across loci should be reported in a brief statement.

Examples are provided below. They are intended to convey the spirit of this policy and models to achieve the desired brevity, not necessarily to dictate the format for every data set.

Authors reporting summary data in accordance with this policy are required to: (a) state that the complete data set is available to any interested researcher upon request, and be prepared to fulfill requests for the data set; or (b) provide a world wide web site URL where the complete data set can be found, and accessed by interested parties and researchers. Authors are strongly encouraged to follow option (b). The editor reserves the right to verify that data are at a stated web site in complete form before proceeding. The data set does not have to be downloadable, but it must be viewable.

This policy is designed to insure that the journal fulfills its responsibilities to be a record of data of importance to forensic science laboratories and researchers, but to do so in a more efficient way. It may also help to encourage the formation of one or more web-based population genetic data sites that would prove useful to population genetics researchers and to DNA typing laboratories alike. The need for a web-based repository is fairly widely recognized, and efforts are being made to address it.

These summary reports will be published as "For the Record" communications. They will not be subjected to in-depth peer review, but the editor has full discretion in judging the accuracy, usefulness and appropriateness of a data set.

The journal will publish summary data for loci that are currently widely used in forensic DNA typing, or that are under consideration for the purpose.

The journal will continue to consider manuscripts for review that provide new statistical genetic analyses, and/or useful summaries, of large collections of population data of relevance to forensic identity testing.

R. E. Gaensslen, Ph.D.
Editor

Hypothetical Example 1: HLA-DQA1 and Polymarker Data

For the Record

HLA-DQA1 and Polymarker Locus
Allele Frequencies for Chicago, Illinois, USA

R. E. Johnson, Ph.D.[1] and John Peterson, M.S.[1]

Populations: Caucasian, African-American and Hispanic

Specimens were collected from unrelated volunteer blood donors. DNA was obtained from blood specimens using Qiagen extraction (1). DNA typing by PCR, using 1 ng target DNA, followed manufacturer's instructions (2). Data were analyzed using the DNA TYPE programs written by Chakraborty and Zhong.

The dataset can be accessed at http://www.uacs.edu/pharmacy/data/forensic/popgen/dqapm.html

References

1. Scherzinger CA, Bourke MT, Ladd C, Lee HC. DNA extraction from liquid blood using QIAamp. J Forensic Sci 1997;42(5):893–6.
2. Perkin-Elmer/ABI, AMFISTR User's Manual, Revised ed., April 1998.

[1]Forensic Science Group, College of Public Health, University of Central Illinois, M/S 461, 4313 South Western Avenue, Chicago, IL 60625 USA.

HLA-DQA1 N	Caucasian 345	African- American 275	Hispanic 215
Allele			
1.1	0.154	0.136	0.155
1.2	0.217	0.282	0.143
1.3	0.040	0.044	0.059
2	0.159	0.105	0.126
3	0.162	0.100	0.216
4.1	0.224	0.189	0.227
4.2/4.3	0.856	0.144	0.074
P (Heterozygosity)*	0.65	0.78	0.63
P (Exact Test)**	0.45	0.48	0.37

	N	LDLR		GYPA		HBGG			D7S8		GC		
		A	B	A	B	A	B	C	A	B	A	B	C
Caucasian	200	0.433	0.567	0.535	0.465	0.587	0.406	0.007	0.619	0.381	0.312	0.156	0.532
African-American	230	0.215	0.785	0.476	0.524	0.426	0.257	0.317	0.628	0.371	0.100	0.746	0.154
Hispanic	215	0.485	0.515	0.615	0.385	0.375	0.580	0.045	0.623	0.377	0.202	0.335	0.463
P (Heterozygosity)*		0.65		0.78		0.63			0.85		0.79		
P (Exact Test)**		0.45		0.49		0.37			0.51		0.46		

*χ^2_{1df} based on unbiased estimate with 2000 shufflings.
**Based on 2000 shufflings.
HBGG B and C for Caucasian combined for statistical tests.

Hypothetical Example 2: STR Data

For the Record

CODIS Core Locus Allele Frequencies for Chicago, Illinois, USA

R. E. Johnson, Ph.D.[1] and D. K. Peterson, M.S.[1]

Population: Caucasian, N = 285

Buccal scrapings were collected from unrelated volunteer student donors. DNA was obtained from buccal scrapings by organic extraction (1). DNA typing by PCR, using 1 ng target DNA, followed manufacturer's instructions (2). Data were analyzed using the DNA TYPE program written by Chakraborty and Zhong. The dataset can be accessed at http://www.uacs.edu/ pharmacy/ data/forensic/popgen/dqapm.html; the complete file in Adobe Acrobat format can be downloaded from ftp/uacs.edu/pub/etc/gendata/codischi.pdf

References

1. Sambrook J, Fritsch EF, Maniatis T. Molecular cloning. A laboratory manual. 2nd ed. Cold Spring Harbor NY: Cold Spring Harbor Laboratory Press, 1989.
2. Promega Corp. GenePrint PowerPlex User's Manual, Revised ed., March, 1998.

Data Table next page

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Allele	D3S1358	VWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	THO1	D16S539
5	—	—	—	—	—	—	—	—	—	—	—	0	—
6	—	—	—	—	—	—	—	—	0.024	0	0	0.226	—
7	—	—	—	—	—	—	0	0	0.017	0.003	0.003	0.172	—
8	—	—	—	—	—	—	0	0.099	0.163	0.005	0.544	0.126	0.019
8.3	—	—	—	—	—	—	—	—	—	—	—	0.002	—
<9	—	—	—	0.014	—	—	—	—	—	—	—	—	—
9	—	—	—	0.010	—	—	0.030	0.076	0.138	0.019	0.123	0.165	0.105
9.3	—	—	—	—	—	—	—	—	—	—	—	0.306	—
10	—	—	—	0.101	—	—	0.043	0.051	0.281	0.254	0.037	0.002	0.067
10.1	—	—	—	—	—	—	—	—	0	—	—	—	—
10.3	—	—	—	—	—	—	—	—	—	0.002	—	—	—
<11	—	—	—	—	—	0.012	—	—	—	—	—	—	—
11	—	0	—	0.058	—	0.012	0.41	0.318	0.202	0.305	0.253	—	0.272
11.3	—	—	—	—	—	—	—	—	0	—	—	—	—
<12	0	—	—	—	—	—	—	—	—	—	—	—	—
12	0	—	—	0.145	—	0.125	0.352	0.308	0.140	0.325	0.039	—	0.339
13	0.003	0.005	—	0.329	—	0.121	0.136	0.112	0.029	0.071	0	—	0.163
13.2	—	—	—	—	—	0	—	—	—	—	—	—	—
14	0.140	0.104	—	0.201	—	0.163	0.008	0.036	0.007	0.015	—	—	0.033
14.2	—	—	—	—	—	0	—	—	—	—	—	—	—
15	0.246	0.113	—	0.104	—	0.127	0.025	0	—	0.005	—	—	0.002
15.2	0	—	—	—	—	0	—				—		
22.2	—	—	0.010	—	—	—	—	—	—	—	—	—	—
22.3	—	—	0	—	—	—	—	—	—	—	—	—	—
>22	—	—	—	—	—	0	—	—	—	—	—	—	—
23	—	—	0.157	—	—	—	—	—	—	—	—	—	—
23.2	—	—	0	—	—	—	—	—	—	—	—	—	—
24	—	—	0.132	—	—	—	—	—	—	—	—	—	—
24.2	—	—	0	—	0.051	—	—	—	—	—	—	—	—
24.3	—	—	0	—	0	—	—	—	—	—	—	—	—
25	—	—	0.067	—	—	—	—	—	—	—	—	—	—
26	—	—	0.018	—	0	—	—	—	—	—	—	—	—
27	—	—	0.010	—	0.035	—	—	—	—	—	—	—	—
28	—	—	0	—	0.161	—	—	—	—	—	—	—	—
29	—	—	0	—	0.171	—	—	—	—	—	—	—	—
29.2	—	—	—	—	0	—	—	—	—	—	—	—	—
30	—	—	0	—	0.223	—	—	—	—	—	—	—	—
>30	—	—	0	—	—	—	—	—	—	—	—	—	—
30.2	—	—	—	—	0.037	—	—	—	—	—	—	—	—
30.3	—	—	—	—	0	—	—	—	—	—	—	—	—
31	—	—	—	—	0.061	—	—	—	—	—	—	—	—
31.2	—	—	—	—	0.092	—	—	—	—	—	—	—	—
32	—	—	—	—	0.012	—	—	—	—	—	—	—	—
32.1	—	—	—	—	0	—	—	—	—	—	—	—	—
32.2	—	—	—	—	0.108	—	—	—	—	—	—	—	—
33	—	—	—	—	0	—	—	—	—	—	—	—	—
33.2	—	—	—	—	0.031	—	—	—	—	—	—	—	—
34	—	—	—	—	0	—	—	—	—	—	—	—	—
34.2	—	—	—	—	0	—	—	—	—	—	—	—	—
35	—	—	—	—	0	—	—	—	—	—	—	—	—
35.2	—	—	—	—	0.021	—	—	—	—	—	—	—	—
36	—	—	—	—	0	—	—	—	—	—	—	—	—
>36	—	—	—	—	0	—	—	—	—	—	—	—	—
P1*	0.65	0.78	0.63	0.85	0.79	0.53	0.64	0.71	0.56	0.71	0.38	0.59	0.68
P2**	0.45	0.49	0.37	0.51	0.46	0.48	0.37	0.58	0.32	0.49	0.16	0.31	0.51

*χ^2_{ldf} P based on unbiased estimate of heterozygosity with 2000 shufflings.
**Exact test based on 2000 shufflings.
Interclass correlations yielding $p < 0.05$ for pairwise comparisons: D3S1358/D8S1179, D3S1358/FGA, and D7S820/D16S539.
— means that allele not applicable to that locus.