Int J Legal Med (1998) 111:273–275

SHORT COMMUNICATION

I. Medintz · C. Kingston · L. Levine · P. Fogarty
E. Mar · L. McCurdy · L. Kobilinsky

DIS80 allele frequencies in Hasidic and non-Hasidic New York City Jewish populations

Received: 15 December 1997 / Received in revised form: 25 February 1998

Abstract Allele frequencies were determined for the VNTR locus D1S80 in Hasidic and non-Hasidic Ashkenazi New York City Jewish subpopulations. Samples were amplified via the polymerase chain reaction and underwent genotyping using polyacrylamide gel electrophoresis. In the Hasidic population 14 alleles were observed as opposed to 19 alleles in the non-Hasidic community. Both populations were tested for Hardy-Weinberg equilibrium. The frequency data obtained can be used for comparison to other populations and for allele and genotype frequency estimates in genetic marker profiling of evidentiary specimens.

Key words D1S80 · Ashkenazi Jews

Introduction

In order to provide potentially useful D1S80 frequency data from two historically related subpopulations, we undertook a study of allele and genotype frequencies of the D1S80 locus in a Hasidic and non-Hasidic group of individuals. Both subpopulations are parts of a more general Jewish group known as the Ashkenazi which migrated to the United States from Eastern and Central Europe. The Ashkenazi are distinguished from the group known as the Sephardi which came from Spain [1].

The New York Metropolitan area has a Jewish population of 1.45 million and at least 70% of this population, or one million, are of Ashkenazi Jewish descent. This group constitutes 5.8% of the New York State population and 0.4% of the United States population [2–4].

Members of the Hasidic subpopulation are largely descendants of a religious sect that grew out of the Ashkenazi Jewish population in Eastern Europe during the 18th century. Hasidim are a close-knit group who live in separate communities and practice an ultra-orthodox form of Judaism. They will accept new members into their group, but only those who assimilate completely. New members usually come from the non-Hasidic Ashkenazi community. There are approximately 125,000 Hasidim in the New York area. They constitute 0.7% of the New York State and 0.048% of the United States populations [1–6].

We have previously reported the HLA-DQA1 and Amplitype Polymarker (LDLR, GYPA, HBGG, D7S8, and Gc) allele and genotype frequencies [2] of these two New York City subpopulations. We found that the Hasidic and non-Hasidic populations did not differ from each other at these loci, but the Hasidic population did differ from a reference Caucasian population at 2 loci, HLA-DQA1 and D7S8 [2].

Materials and methods

Samples

Genomic DNA was extracted [2] from peripheral blood samples of volunteers from the Hasidic and non-Hasidic Jewish populations of New York City. All samples were collected with informed consent that they may be used anonymously for other research purposes. Hasidic individuals were defined by the communities from which samples were collected. Ashkenazi non-Hasidic individuals were self-declared. These populations were selected for study since they represent two related subpopulations within a larger metropolis that have differing levels of endogamy and admixture. Samples were amplified and typed according to the AmpliFLP D1S80 PCR Amplification Kit (Perkin-Elmer, Foster City).

Statistical analysis

Testing for Hardy-Weinberg equilibrium (HWE) utilized both χ^2-analysis and a Monte Carlo based Exact Test using the procedures

I. Medintz · L. Kobilinsky
Graduate School and University Center,
City University of New York, NY 10036 USA

C. Kingston · P. Fogarty · E. Mar · L. McCurdy
L. Kobilinsky (✉)
Science Department, John Jay College of Criminal Justice,
City University of New York, New York, NY 10019, USA

L. Levine
Biology Department, City College,
City University of New York, New York, NY 10031, USA

Table 1 Results of tests for Hardy Weinberg equilibrium

	Hasidic $n = 98$	non-Hasidic $n = 256$
Exact Test	$P = 0.5509$	$P = 0.0\phi$
(MC)	SE = 0.3656	SE = 0.0
χ^2	$\chi^2 = 12.5165$ $P = 0.0019$	$\chi^2 = 46.6459$ $P = 0.0000$
Minimum for expected values	1	2
Degrees of freedom	2	7
Cells combined	105 > 19	190 > 29

All Monte Carlo (MC) runs used 17000 trials (20 groups of 850)
ϕThe Monte Carlo Exact Test values for this column were calculated using 500,000 trials (10 groups of 50,000 each). The Exact Test results were: $P = 2.00 \times 10^{-6}$, SE = 6.32×10^{-6}.
Cells combined X > Y means that X cells were combined into Y cells

described in our earlier paper [2, 7–9]. In order to meet Cochran's rule for χ^2 [7], the genotype cells were combined as described in Table 1.

The populations were compared to each other and to a reference Caucasian population of similar sample size for homogeneity by using contingency tables and calculating the χ^2 and G statistic with a Monte Carlo method based on a program code generously supplied by George Carmody (Carleton University, Ottawa) [8–10].

Table 2 Observed D1S80 allele frequencies in the Hasidic and non-Hasidic Ashkenazi Jewish subpopulations

Allele	Hasidic Population $n = 98$		Non-Hasidic Population $n = 256$	
	Obs.	Freq.	Obs.	Freq.
16			1	0.002
17				
18	59	0.301	105	0.205
19	1	0.005	1	0.002
20	1	0.005	7	0.014
21	3	0.015	19	0.037
22	4	0.020	18	0.035
23	1	0.005	4	0.008
24	98	0.500	242	0.473
25	14	0.071	36	0.070
26	1	0.005	7	0.014
27	2	0.010	5	0.010
28	5	0.026	28	0.055
29	3	0.015	7	0.014
30			1	0.002
31	3	0.015	20	0.039
32			7	0.014
33				
34	1	0.005	2	0.004
35			1	0.002
36				
37			1	0.002

Results and discussion

Table 2 presents the observed D1S80 allele frequencies for the Hasidic and non-Hasidic Ashkenazi Jewish subpopulations. The Hasidic population ($n = 98$) was tested for HWE using both χ^2-analysis and the Exact Test. The significance level of χ^2 and the Exact Test are significantly different (see Table 1). The χ^2 result may be due to the inherent insensitivity caused by the folding in of cells (105 to 19) to accomplish this test. The non-Hasidic population ($n = 256$) χ^2 and Exact Test HWE compliance tests were both well below any reasonable significance level (see Table 1).

In the Hasidic population 14 alleles were observed versus 19 in the non-Hasidic population. The Hasidic population demonstrated a 39.8% (39 out of 98) homozygosity for genotyope frequencies versus a 35.5% (91 out of 256) value for the non-Hasidic population. Values of 21.6% homozygosity and 78.4% heterozygosity have been reported for the North American Caucasian population [11]. In χ^2-tests, using the actual numbers of homozygotes and heterozygotes, it was found that the number of homozygotes within both the Hasidic and non-Hasidic groups was significantly greater than within a reference North American Caucasian population ($P < 0.005$) [11]. There was no statistically significant difference between Hasidic and non-Hasidic groups ($0.5 > P > 0.3$).

Table 3 presents a comparison of allele frequencies between the Hasidic, non-Hasidic and a reference Caucasian population [10]. Results indicate that the non-Hasidic population is similar to the Hasidic population. However, both populations differ significantly from the reference Caucasian population.

A comparison of the results obtained in the present study of DlS80 with those obtained in our earlier investigations [2] of the HLA-DQA1, LDLR, GYPA, HBGG, D7S8, and Gc loci reveal some interesting differences. In our previous study of Hasidic and non-Hasidic New York City subpopulations we found that, with the possible exception of HBGG, all loci showed no significant deviation from HWE by both the Monte Carlo Exact and χ^2-tests. It was found that the distribution of HBGG genotypes appeared not to be in conformity with HWE.

In the data for the D1S80 locus reported here, we found that the Hasidic population showed no significant deviation from HWE only when tested with the Monte Carlo Exact test but not the χ^2-test, whereas the non-Hasidic population showed significant deviation from HWE criteria, using both tests. There are conflicting test results between the Exact Monte Carlo and the calculated χ^2-value. Due to the necessity of combining many cells to avoid very small or zero expected values, the calculated χ^2 results for all sample groups is therefore questionable.

The significant differences in D1S80 allele frequencies in both Hasidic and non-Hasidic groups compared to the reference North American Caucasian population parallels to some extent our earlier findings of statistically significant differences in HLA-DQA1 and D7S8 allele frequencies between the Hasidic and the reference population. It may be that the greater polymorphism of the D1S80 locus

Table 3 Comparison of allele frequencies of selected populations

Populations Compared	χ^2			G			Accept HO at $\alpha = 0.05$	
	χ^2	P	SE	G	P	SE	χ^2	G
H:NH	20.8433	0.2706	0.0034	24.8850	0.1992	0.0031	Accept	Accept
H:Cau	31.2955	0.0014	0.0003	34.3898	0.0045	0.0005	Reject	Reject
NH:Cau	39.3406	0.0012	0.0003	40.0246	0.0022	0.0004	Reject	Reject

H Hasidic (*n* = 98)
NH Non-Hasidic Combined (*n* = 256)
Cau A reference North American Caucasian population sampling (*n* = 94) [11]
Null Hypothesis (HO) is that the two populations are similar (homogeneous)
χ^2 is the Monte Carlo exact test
G is the Monte Carlo G-test
P is the right tail probability (P)
SE is the Standard Error of P
Results based on a significance level of 0.05 (Accept if $P >= 0.05$)
Monte Carlo calculation based on Roff and Bentzen [9] using a program (rxc) generously supplied by George Carmody (Carleton University, Ottawa)

compared to the other two loci results in greater opportunities for the chance presence of rare allele groupings in the non-Hasidic group. The fact that these populations meet HWE at certain loci but not at others [2, present study] may reflect founder effects, selection pressure, rare allele groupings or even sampling variance.

Our present findings have continued a study of forensically important loci in two closely related New York City Jewish subpopulations. The results of the present investigation have provided databases at the D1S80 locus for future use.

References

1. Encyclopaudia Judaica (1973) Keter Publishing House, Israel 7: 1383–1431
2. Medintz I, Levine L, McCurdy L, Chiriboga L, Kingston C, Desnick RJ, Eng CM, Kobilinsky L (1997) HLA-DQA1 and Polymarker allele frequencies in two New York City Jewish populations. J Forensic Sci 42:919–922
3. Singer D (ed) (1992) American Jewish Yearbook. American Jewish Committee. Jewish Publication Society, Philadelphia, Pennsylvania
4. Hertzberg A (1989) The Jews in America. Simon and Schuster, New York
5. Livshits G, Sokal RR, Kobyliansky E (1991) Genetic affinities of Jewish populations. Am J Hum Genet 9:131–146
6. Nedler I (1994) Hasidism in America. American Jewish Committee, Jewish Publication Society, Philadelphia
7. Cochran WG (1954) Some methods for strengthening the common χ^2 tests. Biometrics 110:417–451
8. Roff DA, Bentzen P (1989) The statistical analysis of mitochondrial DNA polymorphisms: χ^2 and the problem of small samples. Mol Biol Evol 6:539–545
9. Guo SW, Thompson EA (1992) Performing the exact test of Hardy-Weinberg proportion for multiple alleles. Biometrics 48:361–372
10. Sajantilla A, Budowle B, Strom M, Johnson V, Lukka H, Peltonen L, Enholm C (1992) PCR amplification of alleles at the D1S80 locus: comparison of a Finnish, and a North American Caucasian population sample, and forensic casework evaluation. Am J Hum Genet 40:816–825
11. Budowle B, Baechtel FS, Smerick JB, Presley KW, Giusti AM, Parsons G, Alevy MC, Chakraborty R (1995) D1S80 population data in African Americans, Caucasians, Southeastern Hispanics, Southwestern Hispanics and Orientals. J Forensic Sci 40:38–44