



STR data for 13 loci from Jewish populations

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Abstract

A total of 124 Jewish individuals, categorized into four groups, have been analyzed for 13 STR loci. No significant differences between the groups were found, except for the FGA system. A high level of genetic variability was found in the overall population.

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1. Introduction

Different methodologies have been used in studies on genetic variability in human populations to assess their genetic composition, their relationships and the evolutionary factors to which they are subject, as well as for forensic purposes. Among these, STRs are a well-known group of highly polymorphic markers. Since their description in the late 1980s [1], they have been increasingly used as populational, forensic and clinical markers, especially those based on a 4-bp motif because of their high level of informativeness. The technique of multiplexing is well established and some multiplex systems are now commercially available, which provide a fast tool for forensic DNA testing. Jewish populations have been studied by geneticists since the turn of the 20th century in an attempt to unravel what must be a complex system of interrelations among Jewish communities and their non-Jewish neighbours, with whom they lived. Several works have attempted to study the evolutionary factors that have come into play during the Diaspora and controversial results can be found [2]. Most of the studies used “classical” genetic markers, but also DNA markers have been used (mtDNA RFLPs, chromosome Y,

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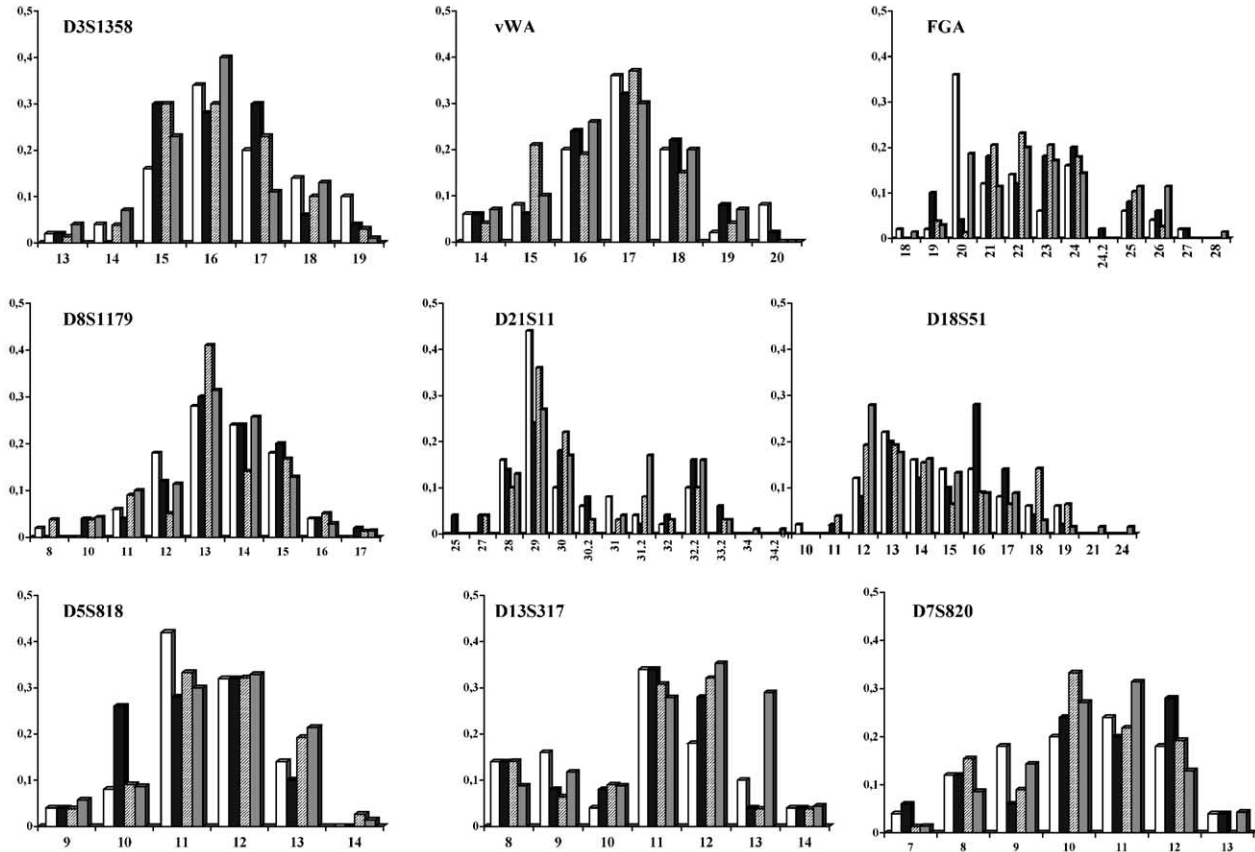


Fig. 1. Allele frequencies for thirteen STR loci from four Jewish populations. Ashkenazi □, Oriental ■, North African ▨, Sephardic ▩

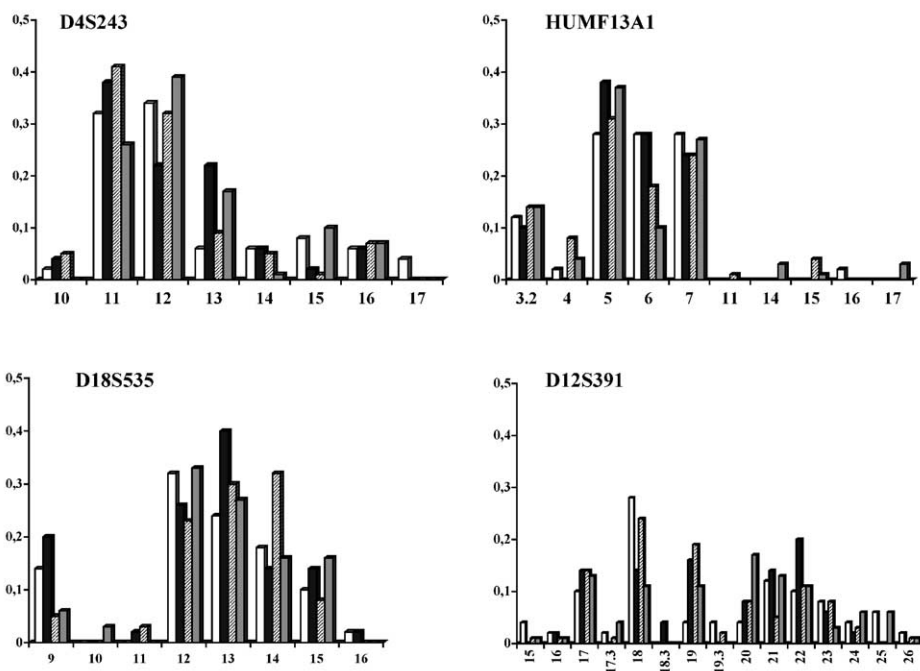


Fig. 1 (continued).

and other nuclear markers). But a few data on short tandem repeats have been published to date in Jewish populations [3].

The purpose of this work was to study the genetic variability of 13 STR loci in Jewish populations.

2. Material and methods

We analyzed 124 Jewish individuals from different populations. Following the classical criteria, they were categorized into four groups: Ashkenazi (25 individuals), Sephardic (35 individuals from Turkey), North African (13 Moroccan, 13 Tunisian and 13 Libyan individuals) and Oriental (12 Iranian and 13 Iraqi individuals). All these samples belong to the collection of The National Laboratory for the Genetics of Israeli Populations at Tel-Aviv University.

The “AmpFISTR Profiler Plus PCR Amplification Kit (PE Applied Biosystem)” co-amplifies nine tetranucleotide STR loci: D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317 and D7S820 and a segment of the gene amelogenin. This set of markers has been approved in the combined DNA Index System (CODIS) database in the USA. Additionally, the STRs D4S243, HUMF13A1, D18S535 and D12S391 have been studied. PCR amplification of these four STR systems was achieved in singleplex under standard conditions. Amplified DNA was analysed on an ABI Prism 310. Allele

Table 1

Statistical parameters of the 13 STRs studied in the Jewish population (pooled). H: heterozygosity; PD: power of discrimination; CE: chance of exclusion; CE2: chance of exclusion if only one parent and child are typed

System	Number of alleles	H obs./exp.	Deficiency of Heterozygotes	P exact test	PD	CE	CE2
D4S243	8	0.715/0.755	0.331	0.825	0.901	0.539	0.362
HUMF13A1	10	0.782/0.767	0.436	0.270	0.907	0.546	0.367
D18S535	8	0.758/0.772	0.005	0.250	0.910	0.553	0.375
D12S391	15	0.839/0.888	0.190	0.354	0.976	0.767	0.620
D3S1358	7	0.766/0.773	0.229	0.820	0.912	0.558	0.380
vWA	7	0.790/0.782	0.475	0.456	0.919	0.576	0.397
FGA	12	0.855/0.861	0.170	0.435	0.963	0.712	0.549
D8S1179	9	0.766/0.797	0.026	0.525	0.931	0.607	0.429
D21S11	13	0.855/0.822	0.918	0.131	0.947	0.655	0.481
D18S51	12	0.829/0.865	0.224	0.151	0.965	0.721	0.561
D5S818	6	0.734/0.744	0.078	0.483	0.890	0.508	0.332
D13S317	7	0.724/0.783	0.005	0.100	0.921	0.581	0.402
D7S820	7	0.766/0.804	0.154	0.148	0.931	0.607	0.429
Average	9.3	0.783/0.801	—	0.246		0.999996	0.999522

resolution of the D4S243 and D18S535 systems was undertaken by nondenaturing conditions, using 6% PAGE on a 0.75-mm-thick gel [4].

3. Results and discussion

Jewish populations were in Hardy–Weinberg equilibrium with respect to the 13 markers. The frequencies obtained in each population are indicated in Fig. 1. No significant differences were found between the four Jewish groups, except in the FGA system. A high level of genetic variability was found in all populations. The observed heterozygosity average was 0.783 in the overall population, with a range from 0.744 to 0.888. The number of alleles observed ranged from 6 to 15. The usefulness of the 13 systems studied can be judged by their combined PD, which corresponded to 1 in 2.392 E + 15 individuals, and their combined CE = 0.999996 (Table 1).

No significant pairwise correlation was observed between the 13 markers, with the exception of the D18S51–D7S820 pair. Therefore, the a priori statistical power of this set of STRs in Jewish populations indicated that they are very informative for the application of these results in paternity and forensic casework.

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