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FOR THE RECORD

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Supplemented Data on Mutation Rates in 33 Autosomal Short Tandem Repeat Polymorphisms

POPULATION: 106–8598 meioses studied in German Caucasians.

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Mutations have practical consequences for paternity testing and mass disaster investigations (1,2).

Estimation of mutations at DNA polymorphisms can be achieved by comparison of genotypes from offsprings to those of their parents (1). The majority of short tandem repeat (STR) mutations involve the gain or loss of a single repeat unit (3). Paternal mutations often occur more frequently than maternal ones (4), although it can be difficult to ascertain from which parent the mutant allele was inherited. This difficulty can often be solved by appropriate SNP analysis (5).

Herewith, we report on maternal and paternal mutation rates, which were observed in parentage case work throughout the last years. The study is supplementing an earlier report from 1999 (4).

For parentage testing, we used (along with DNA minisatellite polymorphisms) various commercially available kits for multiplex PCR amplification of STR markers:

- AmpF/STR- SGM Plus (Applied Biosystems, Weiterstadt, Germany) (1),
- PowerPlex 16 (Promega, Mannheim, Germany) (1,6),
- FFFL (Promega) (1),
- AmpF/STR Profiler Plus ID (Applied Biosystems) (1),
- Power Plex ES (Promega) (1),
- genres MPX-3SE (Serac, Bad Hamburg, Germany), and
- Humantype Chimera (Biotype, Dresden, Germany).

Loci ACTBP2 (SE 33) (7) and D5S2360 were analyzed in SE 33/FGA and D5S2360/FGA (in house) duplex assays (8).

The observed maternal/paternal mutation rates are compiled in Table 1. As the number of observed two-step mutations was negligibly low, we refrained from listing them separately.

Mutations at primer-binding sites causing null alleles (5) were not covered by this study, either. Decisions to interpret a deviation from the genetic pathway as a mutation were based on corrected

TABLE 1—*Maternal and paternal mutation rates observed at 33 autosomal STR polymorphisms in German parentage case work.*

System	Maternal (M) meioses Paternal (P) meioses	Number of correct meioses	Number of deviations	Total number of meioses	Deviations (%)
F13B	M	247	0	247	0.00
F13B	P	209	0	209	0.00
D2S1338	M	7334	0	7334	0.00
D2S1338	P	5871	9	5880	0.15
D2S1360	M	114	0	114	0.00
D2S1360	P	107	0	107	0.00
TPOX	M	3808	0	3808	0.00
TPOX	P	3012	0	3012	0.00
D3S1358	M	8539	0	8539	0.00
D3S1358	P	6846	18	6864	0.26
D3S1744	M	115	0	115	0.00
D3S1744	P	107	0	107	0.00
D4S2366	M	114	0	114	0.00
D4S2366	P	105	1	106	0.94
FGA	M	8589	9	8598	0.10
FGA	P	6887	28	6915	0.40
CSF1PO	M	3546	2	3548	0.06
CSF1PO	P	2828	10	2838	0.35
D5S2360	M	273	0	273	0.00
D5S2360	P	212	0	212	0.00
D5S2500	M	114	0	114	0.00
D5S2500	P	106	1	107	0.93
D5S818	M	4046	1	4047	0.02
D5S818	P	3211	7	3218	0.22
D6S474	M	114	0	114	0.00
D6S474	P	106	0	106	0.00
F13A01	M	337	0	337	0.00
F13A01	P	274	0	274	0.00
SE33	M	1271	1	1272	0.08
SE33	P	899	15	914	1.64
D7S820	M	3837	1	3838	0.03
D7S820	P	3080	8	3088	0.26
D7S1517	M	116	0	116	0.00
D7S1517	P	108	0	108	0.00
LPL	M	244	2	246	0.81
LPL	P	208	0	208	0.00
D8S1132	M	115	0	115	0.00

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TABLE 1—*Continued.*

System	Maternal (M) meioses Paternal (P) meioses	Number of correct meioses	Number of deviations	Total number of meioses	Deviations (%)
D8S1132	P	106	1	107	0.93
D8S1179	M	7959	2	7961	0.03
D8S1179	P	6396	11	6407	0.17
D10S2325	M	116	0	116	0.00
D10S2325	P	108	0	108	0.00
TH01	M	8481	0	8481	0.00
TH01	P	6818	1	6819	0.01
D12S391	M	115	0	115	0.00
D12S391	P	105	1	106	0.94
vWA	M	8544	4	8548	0.05
vWA	P	6838	35	6873	0.51
D13S317	M	3852	3	3855	0.08
D13S317	P	3107	3	3110	0.10
Penta E	M	2350	3	2353	0.13
Penta E	P	1993	1	1994	0.05
FES/FPS	M	247	0	247	0.00
FES/FPS	P	209	0	209	0.00
D16S539	M	7524	1	7525	0.01
D16S539	P	6052	15	6067	0.25
D18S51	M	8062	6	8068	0.07
D18S51	P	6476	15	6491	0.23
D19S433	M	7337	5	7342	0.07
D19S433	P	5883	5	5888	0.08
D21S11	M	8055	10	8065	0.12
D21S11	P	6477	12	6489	0.18
D21S2055	M	114	0	114	0.00
D21S2055	P	106	0	106	0.00
Penta D	M	2290	1	2291	0.04
Penta D	P	1930	0	1930	0.00

STR, single tandem repeat.

(9) *a posteriori* probabilities of at least 99.999%. Obligatorily, no less than 20 DNA polymorphisms were analyzed.

The complete data set is available to any interested researcher upon request.

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