Intragenic recombination within the PGM_1 locus

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INTRODUCTION

The formal genetics of the PGM_1 system has been questioned due to unexplained maternity exclusions and single paternity exclusions (Wetterling 1986, 1988; Bertrams 1988).

In 1979 Carter et al described a phylogeny theory of the PGM_1 locus, which later was further developed by Takahashi et al (1982). They proposed that two point mutations and one intragenic recombination had produced the four common PGM_1 alleles defined today. From gene frequency studies and PGM_1 typings on higher primates the PGM_1 1A allele was considered to be the ancestral gene. Two point mutations at this locus gave the PGM_1 2A and 1B alleles. In addition a cross-over between the 1B and 2A alleles resulted in the PGM_1 2B allele (Fig. 1).

Thus the PGM_1 locus can be divided into two subloci and it would be more correct to refer to the PGM_1 system as haplotypes rather than alleles. The exclusions reported are examples of cross-overs in indivuduals with the phenotypes 1A2B and 1B2A. These two types are the only genotypes that can give rise to recombinant gametes, and this verifies the theory.

The aim of this report is to describe the consequences of the PGM_1 system as an excluding system in paternity cases.

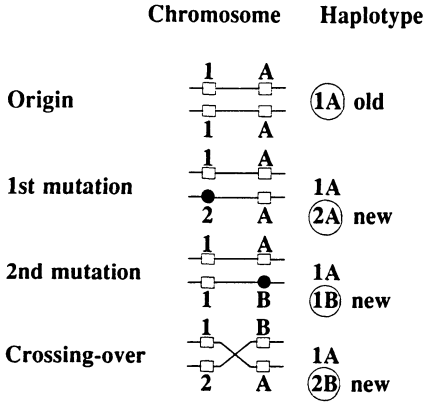

Fig. 1. Phylogeny theory of the PGM_1 locus

Advances in Forensic Haemogenetics 3
Edited by H. F. Polesky and W. R. Mayr

MATERIAL AND METHODS

Blood samples from 16 463 parent-child pairs involved in paternity cases in Sweden during 1980-1988 have been typed for PGM_1 by isoelectric focusing according to an previously published method by Wetterling (1986).

RESULTS AND DISCUSSION

Eight cases of recombination were observed in the material shown in Table 1. Five of these were found because none of the PGM_1 alleles of the heterozygote mother had been inherited by the child. Three cases were observed as a result of single paternity exclusions in the PGM_1 system despite very high probability of paternity. They are not included in the calculation of the recombination fraction.

In all these cases the recombination has occurred during the oogenesis. A cross-over during the spermatogenesis seems to give less viable sperms. However, one such case could be found in Dr Bertrams material (Bertrams 1988).

Table 1. Isolated PGM exclusions during 1980-1988 (16 463 families tested). The recombinant haplotype marked with an asterisk

Mother-child exclusions				
Case	Mother	Child	Father	Probability of maternity
1	1B2A	1A*1A	1A1B	95.3
2	1A2B	1B*2A	1A2A	99.9
3	1B2A	1A*1A	1A1B	85.5
4	1A2B	1B2A*	1A1B	98.4
5	1B2A	1A2B*	1A1B	83.4
Father-child exclusions				
Case	Mother	Child	Father	Probability of paternity
6	1A2B	1A1B*	1A	99.8
7	1A2B	1A1B*	1A	>99.9
8	1A2B	1A1B*	1A2A	99.8

The recombination frequency is calculated as follows (J. Valentin, Stockholm, personal commun.):

Number of mother-child pairs (N)=16 463, number of recombinants (n)=5

PGM_1 1A(p)=0.6136 1B(q)=0.1642 2A(r)=0.1555 2B(s)=0.0656

Phenotypes	1A2B	1B2A	Sum
Mothers	2ps x N=1325.3	2qr x N=840.7	2166.0
Inform. families	2ps x N x (q+r)=423.7	2qr x N x (p+s)=571.0	994.7

Recombination freq.=recomb.children/tot.children=5/994.7=0.005

All cases where there is a risk for a false paternity exclusion due to recombination in the oogenesis are listed in Table 2 and the excluding capacity of each such case is also shown. Thus if PGM_1 is used as a single excluding system in paternity testing, it is advisable not to exclude fathers in these combinations. In this way the exclusion capacity of the PGM_1 system in paternity testing in Sweden will be reduced from 33.6 % to 30.8 %. However, one must have in mind that recombination can also occur during the spermatogenesis, though more unusual.

With the knowledge of the above mentioned limitations, the conclusion must still be that the PGM_1 system is a valuable tool in paternity investigations.

Table 2. Parent-child combinations where a recombination causes false exclusions

Mother	Child	Father	E %
1A2B	1A1B	1A	0.0050
		1A2A	0.0024
		1A2B	0.0011
1A2B	1A2A	1A	0.0047
		1A1B	0.0025
		1A2B	0.0010
1A2B	1B2B	2B	0.0001
		1A2B	0.0011
		2A2B	0.0003
1A2B	2A2B	2B	0.0001
		1A2B	0.0010
		1B2B	0.0003
1B2A	1A1B	1B	0.0008
		1B2A	0.0016
		1B2B	0.0007
1B2A	1A2A	2A	0.0008
		1B2A	0.0016
		2A2B	0.0006
1B2A	1B2B	1B	0.0001
		1A1B	0.0007
		1B2A	0.0002
1B2A	2A2B	2A	0.0001
		1A2A	0.0006
		1B2A	0.0002
		Tot.	0.0276

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