

Mitochondrial DNA inheritance in patients with deleted mtDNA

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EDITOR—Mitochondrial diseases encompass a large group of clinical disorders resulting from numerous genotypes, with variable age of onset and all possible modes of heredity, which have been extensively studied over the past decade.¹⁻³ So far, more than 50 point mutations and a significant number of complex rearrangements, including deletions and duplications, have been identified in mitochondrial DNA (mtDNA) of patients with oxidative phosphorylation diseases (MITOMAP⁴). In most cases, there is a cell to cell variable load of mutant to wild type (wt) mtDNA, a condition called heteroplasmy. The severity of the resulting mitochondrial defects depends not only on the nature of the mutation but also on the proportion of mutant to wild type mtDNA.

The origin and mechanism of the accumulation of mutant mtDNA (up to 99% in some tissues) in patients with mitochondrial diseases are still a matter of debate.⁵ Different hypotheses have been proposed. First, the mutant mtDNA may already be present in the mother's oocytes. Then, by simple genetic drift, mutant mtDNA could finally represent a high proportion of the total mtDNA in a specific organ or tissue. It has already been shown that a small amount of founder mtDNA can populate the organism and that the number of segregating units (*n*) could be as low as a single mitochondrion.^{6,7} This proposal of a genetic bottleneck has been supported by the observation of significant levels of rearranged mtDNA in the oocytes of a patient with Kearns-Sayre syndrome⁸ and by studies of mtDNA heteroplasmy in mice.⁷ Another explanation could be that the mutational event occurs later during embryogenesis. Accordingly, the accumulation of mutant molecules could reflect a proliferative advantage for the mutant mtDNA over the wild type during replication or segregation. This hypothesis comes from studies of mutant mtDNA segregation *in vitro*.⁹⁻¹¹

A new alternative hypothesis is based on the particular pattern of inheritance of mtDNA. This is assumed to be strictly maternally inherited with no apparent paternal contribution to the mtDNA pool of the offspring. It is known that paternal mitochondria entering the egg are rapidly eliminated by active processes during the first stages of mammalian embryogenesis.^{12,13} However, the presence of paternal mtDNA has been detected at the blastocyst stage in some abnormal human embryos.¹⁴

Furthermore, in contrast to the orthodox view of clonal maternal inheritance, several recent articles have shown that recombination events can occur in human mtDNA, casting doubts on the strict maternal inheritance of mtDNA.¹⁵⁻¹⁷ However, while attracting a lot of attention, these results remain contentious.¹⁸⁻²²

Based on these observations, it could be hypothesised that the presence of mutant mtDNA in the zygote could result from a partial degradation of paternal mtDNA after fertilisation. To address this question, we have ascertained the parental origin of the deleted mtDNA (Δ -mtDNA) in a group of patients with Pearson syndrome, villous atrophy, and/or encephalomyopathy.²³⁻²⁷ All patients had a proportion of Δ -mtDNA higher than 80% of the total mtDNA pool in the tissue studied, except for one case where the proportion of Δ -mtDNA was 30%. We first looked for the presence of Δ -mtDNA in the blood cells of the mothers by PCR amplification of the relevant fragments, using primers flanking the deletion. The Δ -mtDNA was absent in all tested samples. In the case of a paternal origin of the Δ -mtDNA, we expected to find a paternal haplotype in the patients. The mitochondrial control region (CR) haplotypes were therefore defined in six families where DNA samples from both parents of the affected child were available. Variation in the CR sequence was determined by direct sequencing of a total of 401 bp (from nucleotide position (np) 16 000 to np 16 400) encompassing the CR hypervariable segment I (HVS-I), as described previously.²⁸ Sequence variants were ascertained by alignment and comparison with the Cambridge Reference Sequence (CRS).

The mtDNA CR haplotypes in the six families analysed are reported in table 1 together with the proportion of Δ - *v* wt-mtDNA. Out of the six families analysed, two (families 2 and 4) turned out to be uninformative since all members shared the same mtDNA lineage. Among the four informative cases (families 1, 3, 5, and 6), all patients showed only the maternal mtDNA lineage. Thus, all mtDNA molecules present in the affected children were transmitted following strict maternal inheritance, ruling out the possibility of a paternal origin of the Δ -mtDNA molecules found in the offspring. Our results also show that mtDNA deletions occur on different mtDNA backgrounds, for example, the common deletion (4977 bp) was

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Table 1 HVS-I haplotypes in the six families analysed. Relevant information on % of deleted mtDNA, extent of the deleted region, and clinical presentation is also given

Family	Clinical presentation	Tissue	Deleted mtDNA	Deletion extent	HVS-I haplotype
P1 M1 F1	Pearson syndrome	Lymphocytes	90%	8484–13460	239G 256 311 239G 256 311 069 097G 104A 126 261
P2 M2 F2	Villous atrophy + encephalomyopathy	Muscle	90%	10665–14856	CRS CRS CRS
P3 M3 F3	Villous atrophy + encephalomyopathy	Lymphocytes	30%	10744–14124	291 291 224 270
P4 M4 F4	Progressive encephalomyopathy	Lymphocytes	90%	(Multiple deletions) 7845–15761, 7931–15761, 7619–15032, 9844–16064, 9966–15801	126 193 278 126 193 278 298 311
P5 M5 F5	Pearson syndrome	Bone marrow	80%	5793–12767	069 126 145 222 261 069 126 145 222 261 069 126 145 222 261
P6 M6 F6	Pearson syndrome	Lymphocytes	85%	8484–13460	224 311 362 224 311 362 192 224 311

found in families 1 and 6 on two different mtDNA genetic backgrounds. Although sample size was rather small and deletion breakpoints heterogeneous, these observations suggest an absence of correlation between a particular mtDNA background and higher occurrence of mtDNA deletion.

Strict maternal transmission could be an advantage for preventing the spread of deleterious mitochondrial genomes from the spermatozoa.²⁹ Nevertheless, assisted reproductive techniques, such as intracytoplasmic sperm injection (ICSI), using immature spermatozoa during fertilisation, could increase the risk of a leakage of paternal mtDNA in the zygote.³⁰ Moreover, in two independent studies, no paternal mtDNA could be detected in the blood of children born after ICSI.^{31 32} In contrast, paternal mtDNA was still detectable in polyploid embryos generated by standard in vitro fertilisation or ICSI.¹⁴ Moreover, both recipient and donor female mtDNA was present in the first babies born after egg cytoplasmic donation.³³

In conclusion, we report the absence of paternally transmitted mtDNA in children with mitochondrial deletions. While we only studied sporadic cases of mitochondrial disease, this should be extended to familial cases with more than one affected child harbouring multiple or single Δ -mtDNA. Characterising the origin of the mutant mtDNA molecules could help in understanding the genetic complexity of mitochondrial diseases and improve genetic counselling and prenatal diagnosis in families with mtDNA heteroplasmy.

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