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Mitochondrial DNA with a Large-Scale Deletion Causes Two Distinct Mitochondrial Disease Phenotypes in Mice

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ABSTRACT Studies in patients have suggested that the clinical phenotypes of some mitochondrial diseases might transit from one disease to another (e.g., Pearson syndrome [PS] to Kearns-Sayre syndrome) in single individuals carrying mitochondrial (mt) DNA with a common deletion (ΔmtDNA), but there is no direct experimental evidence for this. To determine whether ΔmtDNA has the pathologic potential to induce multiple mitochondrial disease phenotypes, we used trans-mitochondrial mice with a heteroplasmic state of wild-type mtDNA and ΔmtDNA (mito-miceΔ). Late-stage embryos carrying ≥50% ΔmtDNA showed abnormal hematopoiesis and iron metabolism in livers that were partly similar to PS (PS-like phenotypes), although they did not express sideroblastic anemia that is a typical symptom of PS. More than half of the neonates with PS-like phenotypes died by 1 month after birth, whereas the rest showed a decrease of ΔmtDNA load in the affected tissues, peripheral blood and liver, and they recovered from PS-like phenotypes. The proportion of ΔmtDNA in various tissues of the surviving mito-miceΔ increased with time, and Kearns-Sayre syndrome—like phenotypes were expressed when the proportion of ΔmtDNA in various tissues reached >70–80%. Our model mouse study clearly showed that a single ΔmtDNA was responsible for at least two distinct disease phenotypes at different ages and suggested that the level and dynamics of ΔmtDNA load in affected tissues would be important for the onset and transition of mitochondrial disease phenotypes in mice.

Pathogenic mtDNAs having a large-scale deletion (ΔmtDNA), called the “common deletion,” or a point mutation, induce defects of mitochondrial oxidative phosphorylation (mitochondrial respiration defects) and manifest as a wide variety of mitochondrial diseases (Larsson and Clayton 1995; Wallace 1999). It has been well documented that ΔmtDNA is responsible for three clinical phenotypes of mitochondrial diseases: Kearns–Sayre syndrome (KSS), progressive external ophthalmoplegia, and Pearson syndrome (PS) (DiMauro and Garone 2011). KSS is usually sporadic and is characterized by early onset (<20 years of age), lactic acidosis, chronic progressive external ophthalmoplegia, pigmented retinopathy, heart block, diabetes, deafness, cerebellar abnormalities, and renal failure. Progressive external ophthalmoplegia is mainly a skeletal muscle disorder and is characterized by late-onset progressive external ophthalmoplegia, lactic acidosis, myopathy, and exercise intolerance. PS is a rare disorder of early infancy that is characterized mainly by sideroblastic anemia. At present, the precise mechanism by which ΔmtDNA can cause different disease phenotypes is unclear, although it has been considered that different loads of ΔmtDNA in tissues are important to establish the multiple disease phenotypes.

Some studies in patients have reported the possibility that infants with PS who survive into childhood develop the clinical features of KSS (Larsson et al. 1990; McShane et al. 1991; Rotig et al. 1995). Furthermore, Larsson et al. (1990) suggest that the transition of disease phenotypes is governed by the fractional concentration of ΔmtDNA in various tissues; however, there is currently no experimental
evidence for this. Because mitochondrial function is regulated both by nuclear DNA and mtDNA (Larsson and Clayton 1995), it is possible that nuclear genomic background is involved in the pathogenesis of different disease phenotypes. Supporting this hypothesis is the finding that the homoplasmic state of a pathogenic mutant mtDNA does not always induce serious clinical phenotypes in a mother and her children (McFarland et al. 2002).

Here, to experimentally resolve the question of whether mitochondrial disease phenotypes can change in single individuals as a result of the dynamics of the proportion of ΔmtDNA in various tissues, we have used a mouse model carrying pathogenic ΔmtDNA. Previously, we succeeded in generating a trans-mitochondrial mouse model (mito-miceΔ) with a heteroplasmic state for wild-type mtDNA and ΔmtDNA with a 4696-bp deletion from nucleotide position 7759 of the mice ND5 gene to position 12,454 of the ND5 gene (see Figure 1A) (Inoue et al. 2000). The ΔmtDNA introduced in mito-miceΔ is similar to the pathogenic mutant mtDNA with the “common deletion” that is found in patients with KSS or PS (Holt et al. 1988; Larsson et al. 1990; McShane et al. 1991; Rotig et al. 1995). Because the mito-miceΔ all share the same nuclear genomic background (C57BL/6, also called B6), their genetic variation is restricted to the load of ΔmtDNA in various tissues. The mito-miceΔ, therefore, would provide the direct evidence whether a single ΔmtDNA could cause the onset and transition of different mitochondrial disease phenotypes.

By using these mito-miceΔ, we investigated that ΔmtDNA possessed a pathogenic potential for the onset of two distinct phenotypes of mitochondrial diseases, PS-like and KSS-like phenotypes, early in life (days 1–34 after birth) and in midlife (6 months of age), respectively. We also observed that the mice that escaped from the early death probably because PS-like phenotypes developed KSS-like phenotypes in middle age, showing the transition of distinct mitochondrial disease phenotypes in single mito-miceΔ.

**MATERIALS AND METHODS**

**Mice**

Mito-miceΔ were generated by introducing ΔmtDNA from cultivated cells into the zygotes of B6 strain mice by using cell fusion techniques, as described previously (Inoue et al. 2000). Thirty-three female mito-miceΔ carrying 1–63% ΔmtDNA at 2–6 months of age were used as mothers. Embryos on E18.5 and progeny were used for the study. Age-matched wild-type B6 mice were used as normal controls. All animal experiments were performed in compliance with the institutional guidelines of the University of Tsukuba for the care and use of laboratory animals.

**Estimation of ΔmtDNA proportion in tissues**

Proportions of wild-type mtDNA and ΔmtDNA were determined by using real-time polymerase chain reaction, as described previously (Sato et al. 2005). Tail samples were used to deduce the ΔmtDNA load in mito-miceΔ. The proportion of ΔmtDNA was also examined in various tissue samples (peripheral blood, liver, kidney, and eye).

![Gene map of ΔmtDNA introduced in mito-miceΔ and observations of mito-miceΔ on the early life. (A) A wild-type mtDNA (left) is a circular DNA (16.3 kbp) and encodes 37 genes, including 13 mRNAs, 22 tRNAs, and 2 rRNAs. A mtDNA with a common deletion (ΔmtDNA; right) introduced in mito-miceΔ is 11.3 kbp in size, because 13 genes, including 7 mRNAs and 6 tRNAs (arc) are lost by a deletion. Single capitals in maps indicate tRNA genes. (B) Frequency of neonatal death in mito-miceΔ carrying 1–70% ΔmtDNA in their tails. Neonates of mito-miceΔ were classified into four groups carrying 1–34% (n = 23), 35–49% (n = 30), 50–59% (n = 42), and 60–70% (n = 31) ΔmtDNA, respectively, in their tails. Neonates of wild-type B6 mice were used as normal controls (n = 30). (C–E) Life span of mito-miceΔ carrying 1–70% ΔmtDNA in their tails was assessed for days 1 to 34. Based on the observed frequency of neonatal death in mito-miceΔ (see panel B), neonates of mito-miceΔ were classified into two groups carrying 1–49% (n = 53)
Measurement of blood lactate concentration
For the measurement of blood lactate concentration, blood was collected from the tail vein of nonfasted mice. Lactate concentration was measured by using an automatic blood lactate test meter (Lactate Pro, ARKRAY, Kyoto, Japan).

Cytologic and histologic analysis
Blood samples were smeared on glass slides, and inclusions in reticulocytes were visualized by staining with new methylene blue. Cells with granular network inclusions that are a typical structure of reticulocytes were counted (see open arrowheads in Figure 3D) and proportion of these reticulocytes to 1000 red blood cells was estimated. The proportion of reticulocytes in blood samples of mito-mice Δ and age-matched controls was measured. To detect the accumulation of ferric iron, paraffin-embedded sections (5-μm thick) of liver samples were stained with Prussian blue and then Safranin O was used as a counter-staining. Eye samples were fixed in Bouin’s solution, and paraffin-embedded sections (8-μm thick) of the samples were stained with hematoxylin and eosin.

Electron microscopic observation of cytochrome c oxidase (COX) activity
An electron microscopic analysis of COX activity was performed as described previously (Nakada et al. 2001; Seligman et al. 1968) with slight modifications. To summarize, 25-μm cryosections of liver samples were fixed in 2% w/v glutaraldehyde in phosphate-buffered saline for 5 min at 0°C. Ultrathin sections, which were not stained with uranyl acetate or lead nitrate solutions, were viewed directly on a transmission electron microscope (model H-7650, Hitachi High-Technologies Corporation, Tokyo, Japan). In this analysis, enzymatic activity of COX was visualized as a black color (high electron density).

Statistics
The Student’s t-test was used to compare groups of data. All values are presented as means ± SD. The log-rank test was used to compare survival curves. P < 0.05 was considered to indicate statistical significance.

RESULTS
Frequency of early death in mito-mice Δ
We first examined the early life spans (1–34 days after birth) of mito-mice Δ carrying 1–70% ΔmtDNA in their tails (n = 126). The proportion of ΔmtDNA in individual mito-mice Δ was deduced from that in their tails just after birth (day 0). In this assay, we also used wild-type B6 mice as a normal control (n = 30). Approximately 20% of wild-type B6 neonates died on day 1 after birth (Figure 1B), but none died from days 2 to 34 (Figure 1C). The early life spans of mito-mice Δ carrying <50% ΔmtDNA in their tails were similar to those of wild-type B6 mice (Figure 1, C and D). In contrast, when the ΔmtDNA load in the neonates’ tails was ≥50%, the frequency of death on day 1 after birth was definitely increased compared with that of wild-type B6 mice (Figure 1B). The mito-mice Δ carrying 50–70% ΔmtDNA in their tails continued to die after day 1, and only 34% of these neonates survived until day 34 after birth (Figure 1E).

Although the aforementioned results indicated that most mito-mice Δ carrying ≥50% ΔmtDNA died early (≤34 days after birth), a substantial proportion of the progeny of mothers carrying >33% ΔmtDNA died very early (day 1 after birth; Figure 2A). Thus, it was unclear that early death was associated with the proportion of ΔmtDNA either in neonates or mothers. If the latter were the case, then the frequency of early death of pups would be expected to increase with the age of the mother, because ΔmtDNA accumulates in various somatic tissues but disappears in eggs with time (Sato et al. 2007). Therefore, we next examined the frequency of early death in the first and second litters of three female mito-mice Δ carrying 28% (Mouse 28), 52% (Mouse 52), and 61% (Mouse 61) ΔmtDNA, respectively, in their tails just after birth. As expected, the proportion of ΔmtDNA was much greater in the first litter than the second litter (Figure 2B). The rate of early death of pups was greatly and significantly greater in the first litter than in the second delivery (Figure 2, B and C). P < 0.05. The proportion of surviving pups from the second litter (Figure 2C) was comparable with that of pups with wild-type B6 mothers (Figure 1B), despite the ΔmtDNA load of the mothers’ tails increasing with time. Average loads of ΔmtDNA in tail samples were 32.4 ± 21.9% (mean ± SD) and 57.4 ± 16.8% in live and dead mito-mice Δ pups, respectively. On the basis of these results, we concluded that early death of mito-mice Δ was caused by ΔmtDNA load in neonates but not in mothers.

Phenotypic observations of late-stage embryos of mito-mice Δ
To clarify the reason for the frequent early death in progeny carrying ≥50% ΔmtDNA in their tails, we examined clinical phenotypes in embryos at embryonic day 18.5 (E18.5), which is just 1 day before birth. We obtained 55 E18.5 embryos carrying 35–70% ΔmtDNA in (Mouse 52), and 61% (Mouse 61) ΔmtDNA in their tails just after birth (day 0) were used in this assay. Open circles and red crosses indicate pups that were alive and dead, respectively, at 34 days after birth. Blue symbols indicate the proportions of ΔmtDNA in mother’s tails. (C) Comparison between the first and second deliveries in terms of survival rates of pups from Mouse 28, Mouse 52, and Mouse 61 at day 34 after birth. Data are presented as mean ± SD. Asterisk indicates significant differences (P < 0.05).
Figure 3 Phenotypic observations of late-stage embryos of mito-miceΔ. All embryos were obtained at embryonic day 18.5. (A) Morphological observation of late-stage embryos carrying 0–66% ΔmtDNA in their tails, as indicated. The embryo carrying no ΔmtDNA (left side) was a wild-type B6 control. The six embryos carrying ΔmtDNA were obtained from a single mother. The weight of each embryo is shown below the panel. (B) Comparison of littermate number. Average numbers of littermates from mothers carrying 0% (white), 34–47% (gray), or 52–66% (black) ΔmtDNA. Data are presented as mean ± SD. NS, not significant. (C) Relationship between weight and ΔmtDNA load in late-stage embryos carrying 0% (white), 34–47% (gray), or 52–66% (black) ΔmtDNA. Data are presented as mean ± SD. Asterisks indicate significant differences (P < 0.05). (D) Cytological observation of peripheral blood samples from late-stage embryos. Peripheral blood samples carrying 0%, 36%, and 59% ΔmtDNA, respectively, were stained with new methylene blue. In this method, reticulocytes, a type of immature red blood cells (RBC), are visualized as cells with blue inclusions (open arrowheads). Scale bar, 10 μm. (E) Average proportion of reticulocytes in total RBCs in peripheral blood samples from E18.5 embryos carrying 0%, 36%, and 59% ΔmtDNA. Data are presented as mean ± SD. Asterisks indicate significant differences (P < 0.05). (F) Histologic observation of peripheral blood samples from E18.5 embryos carrying 0–66% ΔmtDNA. Data are presented as mean ± SD. Asterisks indicate significant differences (P < 0.05). (G) Histologic observation of liver samples from late-stage embryos. Liver samples carrying 0%, 36%, and 59% ΔmtDNA, respectively, were stained with Prussian blue. In this method, abnormal iron metabolism is visualized as blue deposits. Scale bar, 10 μm. (H) Electron microscopic observation of COX activity in liver samples from late-stage embryos. Mitochondria in hepatocytes and blood cells are shown as (G) and (H), respectively. Arrows indicate mitochondria that appeared normal in shape and COX activity, open arrowheads indicate COX-deficient mitochondria, and the closed arrowheads indicate swollen mitochondria with COX activity. N, nucleus. Scale bar, 1 μm.
in liver is observed in cases of sideroblastic anemia and PS (Camaschella, 2008; Gurgey et al. 1996), we examined pathologic changes in liver samples from E18.5 embryos carrying ΔmtDNA. Deposits of ferric iron indicating abnormal iron metabolism were preferentially observed in liver samples from E18.5 embryos with an increased number of reticulocytes (Figure 3F). On the basis of these observations, we concluded that ΔmtDNA loads could cause PS-like phenotypes in late-stage mouse embryos, although it was not a typical PS.

In our previous studies using mito-miceΔ, accumulation of approximately 70–80% ΔmtDNA loads in various tissues was necessary...
to induce mitochondrial respiration defects, such as deficiencies of complex IV (COX) in mitochondrial respiratory chains, and the resultant onset of various clinical phenotypes. In contrast, E18.5 embryos showed clinical phenotypes, even when they carried $\geq 50\%$ ΔmtDNA. These results were expected that threshold for tolerance to accumulation of ΔmtDNA in embryonic liver and blood cells would be lower than that in other tissues. Because electron microscopic observations of COX activity (COX-EM) can visualize COX activity in individual mitochondria of single cells (Nakada et al. 2001; Seligman et al. 1968), we next performed COX-EM with liver samples from E18.5 embryos carrying various loads of ΔmtDNA. In liver samples carrying $\geq 50\%$ ΔmtDNA, we observed three types of mitochondria in a single cytoplasm of hepatocytes, mitochondrion that appeared normal in COX activity (arrows in Figure 3G), a swollen mitochondrion with COX activity (closed arrowhead in Figure 3G), and a COX-deficient swollen mitochondrion (open arrowhead in Figure 3G). In blood cells of liver samples carrying $\geq 50\%$ ΔmtDNA, heterogeneity of COX activity within individual mitochondria was clearly visible (Figure 3H), although swollen mitochondria were not observed. These observations indicated that $\geq 50\%$ ΔmtDNA loads could induce mitochondrial respiration defects in hepatocytes and blood cells of late-stage embryos. In addition, there were no autophagic ultra-structures around abnormal mitochondria in hepatocytes or blood cells (Figure 3, G and H), indicating that the COX-deficient mitochondria were not eliminated by the mitophagy, even when a single cytoplasm contained mitochondria with different mitochondrial respiratory functions.

**Changes of ΔmtDNA load and clinical phenotypes in mito-miceΔ during early life**

The results of the early life span assay described previously (see Figure 1E) clearly showed that there were two populations of neonates carrying $\geq 50\%$ ΔmtDNA in their tail; the first population showed death phenotypes in the first month after birth, probably due to PS-like phenotypes; and the second population was able to escape early death. In mito-miceΔ, genetic variation is restricted to the load of ΔmtDNA in various tissues, so that phenotypes are strictly induced by the load of ΔmtDNA in affected tissues. Considering the point, there was a possibility that the ΔmtDNA load decreased preferentially in the peripheral blood and liver of surviving neonates by around 1-month after birth. To test this possibility, we examined ΔmtDNA load in affected and nonaffected tissues of surviving neonates at various time points up to and including day 34 after birth (Figure 4A). In this assay, we could not trace the proportion of ΔmtDNA load in tissues from single neonates, because we had to kill neonates to obtain tissue samples. Thus, we estimated the proportion of ΔmtDNA in each sample relative to that in the tail sample taken on day 0 after birth from the same subject. The animals were analyzed as two subgroups defined by the ΔmtDNA load in the tail (i.e., $< 50\%$ and $\geq 50\%$ ΔmtDNA). In kidney samples as a nonaffected tissue, the relative ratios increased with time in both subgroups, suggesting that the proportion of ΔmtDNA in the nonaffected tissues increased independently of the ΔmtDNA load (Figure 4A, $P < 0.05$). In peripheral blood, there were two distinct patterns dependent on ΔmtDNA load. In neonates carrying $< 50\%$ ΔmtDNA in their tails at day 0, the relative ratios increased with time and the pattern was similar to that of kidney samples ($P < 0.05$). In neonates carrying $\geq 50\%$ ΔmtDNA in their tails at day 0, the relative ratios in peripheral blood samples did not increase with time. The relative ratios in liver samples from both subgroups did not increase with time. In the case of liver samples from E18.5 embryos carrying $\geq 50\%$ ΔmtDNA, however, a significant decrease of relative ratios was observed ($P < 0.05$).

To confirm changes in ΔmtDNA load in peripheral blood within same individuals, we collected peripheral blood samples from single neonates carrying $7–64\%$ ΔmtDNA, respectively, in their tails at day 0. We calculated the proportion of ΔmtDNA in peripheral blood on day 34 after birth relative to that on day 14 after birth (Figure 4B). The relative ratios in surviving neonates carrying $< 50\%$ ΔmtDNA in their tails were $> 1$ and particularly high in neonates carrying $< 20\%$ ΔmtDNA in their tails. In contrast, neonates carrying $\geq 50\%$ ΔmtDNA in their tails showed relative ratios $< 1$. There was a significant difference between neonates carrying $< 50\%$ and $\geq 50\%$ ΔmtDNA in their tails ($P < 0.05$). These data indicate that the proportion of ΔmtDNA in peripheral blood decreased at an early age (i.e., from days 14 to 34) when the proportion of ΔmtDNA in peripheral blood was $\geq 50\%$.

Consistent with these results, abnormalities observed in peripheral blood and liver samples of late-stage embryos (Figure 3, D–G) were not detected on day 34 after birth (Figure 4, C–F). There was no significant difference in reticulocyte number between wild-type mice and mito-miceΔ (Figure 4, C and D). Iron deposits that were seen in livers from late-stage embryos carrying $\geq 50\%$ ΔmtDNA were not observed in the livers carrying $47\%$ ΔmtDNA, which was the maximum proportion of ΔmtDNA observed on day 34 after birth (Figure 4E) because of the decreased ΔmtDNA loads in liver. In COX-EM, abnormalities were not observed in liver samples (Figure 4F). These findings indicate that the decrease of ΔmtDNA loading proportion in peripheral blood and liver of neonates carrying $\geq 50\%$ ΔmtDNA would be one reason for recovering from PS-like phenotypes and for the resultant survival.

**Disease phenotypes of surviving neonates when they reach middle life**

At 6 months of age or later, all the surviving mito-miceΔ showed lactic acidosis, heart block, renal failure, male infertility, deafness, and...
abnormalities in long-term memory as reported previously, when the proportion of ΔmtDNA in affected tissues reached approximately 70–80% (Inoue et al. 2000; Nakada et al. 2001, 2004, 2006; Ogasawara et al. 2010; Tanaka et al. 2008). In some of surviving mito-miceΔ carrying >80% ΔmtDNA, retinal abnormalities were observed (Figure 5). These results indicated that neonates that remitted from PS-like phenotypes in early life expressed KSS-like phenotypes in their middle life.

**DISCUSSION**

Taking the current results together with our previous ones, we summarized the development of mitochondrial diseases in mito-miceΔ (Figure 6). On the basis of the difference in ΔmtDNA loads and the resultant mitochondrial disease phenotypes, mito-miceΔ population is classified into four subgroups. The first subgroup was mito-miceΔ carrying ≤10% ΔmtDNA at the birth. They showed normal phenotypes because ΔmtDNA loads did not reach >70–80% in various tissues through the life (Normal subgroup in Figure 6). The second subgroup was mito-miceΔ carrying 11–49% ΔmtDNA just after birth, and the mice appeared healthy until middle age (6 months) or later, but when the ΔmtDNA load reached >70–80% in various tissues, they expressed KSS-like phenotypes (late-onset subgroup in Figure 6). The main clinical features in this subgroup, such as low body weight, lactic acidosis, heart block, renal failure, deafness, male infertility, and abnormal long-term memory, has been reported previously (Inoue et al. 2000; Nakada et al. 2001, 2004, 2006; Ogasawara et al. 2010; Tanaka et al. 2008). The third and fourth subgroups were mito-miceΔ carrying ≥50% ΔmtDNA just after birth. When the ΔmtDNA load in late-stage embryos reached ≥50%, abnormalities of hematopoiesis and iron metabolisms in liver were induced, thus leading to PS-like phenotypes (i.e., abnormalities in hematopoiesis and iron metabolism; Figure 3, D–F), although >70–80% ΔmtDNA loads were necessary for the onset of KSS-like phenotypes in adult mito-miceΔ. Half of those expressing PS-like phenotypes died in early life (≤34 days after birth). The third subgroup, therefore, was the case of onset of PS-like phenotypes and the resultant early death (early-onset and death subgroup in Figure 6). The rest escaped from the early death, because PS-like phenotypes in them disappeared consistent with a decrease of ΔmtDNA load in affected tissues (see Figure 4, D and E for the cases of peripheral blood and liver samples, respectively). However, they expressed KSS-like phenotypes, when ΔmtDNA load reached >70–80% in affected tissues (Figure 5). Thus, the fourth subgroup was the case of transient onsets of PS-like and KSS-like phenotypes in early and middle age, respectively, in a single mito-miceΔ (Early-and late-onsets subgroup in Figure 6).

Heterogeneous distribution of mitochondria with and without COX activity in single cells would be important for elucidating the reason why the pathogenic threshold load of ΔmtDNA in embryonic blood and liver was lower than that in other tissues. We have previously reported that a uniform distribution of mitochondria either with or without COX activity occurs in somatic cells of adult mito-miceΔ, irrespective of whether the tissues contain low or high loads of ΔmtDNA (Nakada et al. 2001). This finding indicates the occurrence of mitochondrial genetic complementation in which individual mitochondria exchange gene products derived from mtDNA through their fusion and fission. Because mitochondria carrying ΔmtDNA can be supplied by mitochondria carrying wild-type mtDNA, tissues carrying ΔmtDNA did not show mitochondrial respiration defects until ΔmtDNA accumulated to a level of >70–80%. In contrast, here we observed that blood cells and hepatocytes in late-stage embryos showing PS-like phenotypes contained mitochondria with heterogeneous ultrastructures and COX activity levels (Figure 3, G and H). This finding suggested the existence of deficiencies of mitochondrial fusion or fission or both, and a lack of mitochondrial genetic complementation in these late-stage embryonic cells. Such deficiencies could be one reason that a load of ≥50% ΔmtDNA could cause pathogenicity in blood cells and hepatocytes of late-stage embryos, whereas a higher load is required in adult mice. Moreover, it has been reported that mitochondrial dynamics, a continuous mitochondrial fusion and fission, is necessary to maintain normal mitochondrial respiratory function in mammals (Chen et al. 2010; Ishihara et al. 2009). Therefore, it is possible that deficiencies of mitochondrial dynamics and genetic complementation in embryonic blood cells and hepatocytes enhance the pathogenicity of ΔmtDNA in the case of a ≥50% ΔmtDNA load.

PS-like phenotypes induced by the abnormalities of hematopoiesis and iron metabolisms in livers of late-stage embryos carrying ≥50% ΔmtDNA were the main clinical features, but it is unclear why a half of the neonates carrying ≥50% ΔmtDNA died early. There are several possible explanations for this phenomenon. The first is that the pups might have suffered acute oxidative stress because newborns and infants are particularly prone to oxidative stress (Saugstad 2005). Newborns and infants have reduced antioxidant defense mechanisms as well as high levels of free iron, which are required for the Fenton reaction (Saugstad 2005); approximately 20% neonates died on day 1 after birth even in wild-type B6 mice (Figure 1, B and C). Because neonates
carrying ≥50% ΔmtDNA in their tails possessed iron deposits in liver (Figure 3F), the high level of iron could promote the Fenton reaction, resulting in additional oxidative stress when the neonates are exposed to a high oxygen concentration after delivery (Singer and Muhlfeld 2007). Another possibility was that abnormalities in metabolic adaptation to the aerobic condition just after birth might cause frequent early death in mito-miceΔ. Anaerobic glycolysis is the major source of cellular ATP in fetal tissues. In cells with mitochondrial respiration defects as the result of pathogenic mutant mtDNAs, glycolysis is enhanced as a compensatory mechanism to maintain ATP levels. Therefore, ΔmtDNA might not demonstrate its pathogenicity in various cells during embryogenesis. Supporting this notion, we observed only rare incidents of embryonic lethality in mito-miceΔ. After birth, neonates carrying ΔmtDNA have to change from anaerobic to aerobic energy metabolism in various cells as soon as possible, but they would find this process difficult due to their systemic and chronic mitochondrial respiration defects.

In summary, our model mouse study showed that a single ΔmtDNA molecule has a pathogenic potential to cause PS-like and KSS-like phenotypes at early and middle life, respectively, and also suggested that difference in threshold for tolerance to accumulation of ΔmtDNA in affected tissues between young infants and adults was a possible reason for the onset of disease phenotypes in mito-miceΔ. In addition, dynamics of ΔmtDNA load in affected tissues well correlated with the transition of disease phenotypes in mito-miceΔ. At this stage, we considered that decreased proportion of ΔmtDNA in peripheral blood and liver from young infants carrying >50% ΔmtDNA was important to recover from PS-like phenotypes. However, we could not rule out a possibility that the decreased proportion of ΔmtDNA in affected tissues was a result by which young infants carrying >50% ΔmtDNA recovered from PS-like phenotypes. Therefore, biological and clinical significance of ΔmtDNA dynamics associating with changes of disease phenotypes remains to be answered.

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