

MARIE DESGEORGES, PAULE KJELLBERG,
JACQUES DEMAILE, AND MIREILLE CLAUSTRÉS
Laboratoire de Biochimie Génétique
Institut de Biologie
Montpellier

Acknowledgment

This work was supported by a grant from the French Association against Cystic Fibrosis (Association Française contre la Mucoviscidose; AFLM). The manuscript was typed by M. Nicolas.

References

- Kerem B-S, Rommens JM, Buchanan JA, Markiewicz D, Cox TK, Chakravarti A, Buchwald M, et al (1989) Identification of the cystic fibrosis gene: genetic analysis. *Science* 245:1073-1080
- Tsui L-C (1992) Mutations and sequence variations detected in the cystic fibrosis transmembrane conductance regulator (CFTR) gene: a report from the Cystic Fibrosis Genetic Analysis Consortium. *Hum Mut* 1:197-203
- Kobayashi K, Knowles MR, Boucher RC, O'Brien WE, Beaudet AL (1990) Benign missense variations in the cystic fibrosis gene. *Am J Hum Genet* 47:611-615
- Macek M Jr, Ladanyi L, Bürger J, Reis A (1992) Missense variations in the cystic fibrosis gene: heteroduplex formation in the F508C mutation. *Am J Hum Genet* 51:1173-1174
- Meschede D, Eigel A, Horst J, Nieschlag E (1993) Compound heterozygosity for the Δ F508 and F508C cystic fibrosis transmembrane conductance regulator (CFTR) mutations in a patient with congenital bilateral aplasia of the vas deferens. *Am J Hum Genet* 53:292-293

© 1994 by The American Society of Human Genetics. All rights reserved.
0002-9297/94/5402-0021\$02.00

Am. J. Hum. Genet. 54:385, 1994

mtDNA: Pathogenic or Nonpathogenic Sequence Changes

To the Editor:

Tatuch et al. (1992) have reviewed the literature on the 8993 mtDNA mutation in a recent case report in this *Journal*. Their evidence that this point mutation causes Leigh disease is strong, even though it has not yet been possible to document the predicted biochemical de-

```
TACCACCTACCTCCCTCACCAA  ATPase 8
*****
TACCACCTACCTCCCTGACAAGC  Patient
*****
TCATCGCTACCTCCCTGACAAGC  ND5
```

Figure 1 Exact homology between bp 8468-8477 (*top strand*) and bp 13580-13589 (*bottom strand*). Asterisks (*) indicate the homologous region.

fect. Their case does not need the spurious support they infer from our data (Poulton et al. 1988). We reported a patient with Kearns-Sayre syndrome (KSS; see Petty et al. [1986]), which we described as group I mitochondrial myopathy, in whom we found two restriction-site losses in the region of the 8993 mutation. Unlike the family they described, our patient was homoplasmic for the point mutation, as were his asymptomatic maternal relatives. Sequence analysis now confirms that there is a G-to-A transition at bp 8994 that does not cause an amino acid substitution. We conclude that this mutation is not pathogenic. Furthermore, this boy has an mtDNA deletion (fig. 1) that is sufficient to explain his clinical syndrome.

JOANNA POULTON* AND L. A. BINDOFF†

**Department of Paediatrics, University of Oxford, John Radcliffe Hospital, Oxford; and* †*Department of Clinical Neurosciences, The Medical School, University of Newcastle upon Tyne, Newcastle upon Tyne*

References

- Petty RKH, Harding AE, Morgan-Hughes JA (1986) The clinical features of mitochondrial myopathy. *Brain* 109:915-938
- Poulton J, Turnbull DM, Mehta AB, Wilson J, Gardiner RM (1988) Restriction enzyme analysis of the mitochondrial genome in mitochondrial myopathy. *J Med Genet* 25:600-605
- Tatuch Y, Christodoulou J, Feigenbaum A, Clarke JTR, Wherret J, Smith C, Rudd N, et al (1992) Heteroplasmic mtDNA mutation (T→G) at 8993 can cause Leigh disease when the percentage of abnormal mtDNA is high. *Am J Hum Genet* 50:852-858

© 1994 by The American Society of Human Genetics. All rights reserved.
0002-9297/94/5402-0022\$02.00