Mutations in *MKKS* cause Bardet-Biedl syndrome

A.M. Slavotinek *et al*.

Nature Genet. **26**, 15–16 (2001).

Two recent reports[1,2] describing mutations in the gene for McKusick-Kaufman syndrome (*MKKS*) in patients with the Bardet-Biedl syndrome (BBS) require clarification of the overlap in authors and subjects in those studies. Specimens from three Newfoundland BBS families were studied by both research groups, which independently identified pathogenic *MKKS* mutations. Consequently, the three families from Newfoundland are reported in both papers. The original and corrected designations[3] for the overlapping families and the mutations in these two reports are shown here. Different reference points in the same reference sequence (AF221993) were selected in the reports to number the mutations. Slavotinek *et al*. chose the 5′ end of this sequence as '1' and Katsanis *et al*. chose the A of the putative ATG.

Table 1 • Mutation analysis of families with BBS

Slavotinek *et al*.[2]		Katsanis *et al*.[1]	
Family number	Mutation designation	Family number	Mutation designation
2	1316delC;1324–1326delGTA	NF-B13	429delCT;433delAG
3	1167delT	NF-B3	280delT
4	1167delT	NF-B4	280delT

The discrepancy in the naming of the first mutation may be attributed to ambiguity in the nomenclature system and the absence of biological data that can resolve that ambiguity. Slavotinek *et al*. chose to name it as if the mutation was as far 3′ as possible (following rule 5; ref. 3) within the short repeats in this region of the sequence, whereas Katsanis *et al*. described symmetry of the complex mutation and its potential relevance to the mutational mechanism.

Table 2 • Alternative interpretations of the compound mutation

Slavotinek	Family 2	**GGA TTTAGTA CTC**	1316delC;1324–1326delGTA
Katsanis	Family NF-B13	**GGA TT TAGTACTC**	429delCT;433delAG
Normal sequence		GGACTTTAGTAGTACTC	

Moreover, according to the nomenclature convention, 1167delT and 280delT should actually be 1168delT and 281delT, respectively, according to the rule cited above, as the normal sequence has thymidines at positions 1167 and 1168 (280 and 281).
This should clarify that the two papers together, describe 8 distinct BBS families instead of 11, including five Newfoundland pedigrees in which three different disease alleles are present.

1. Katsanis, N. *et al. Nature Genet.* **26**, 67–70 (2000).
2. Slavotinek, A. *et al. Nature Genet.* **26**, 15–16 (2000).
3. Antonarakis, S.E. *Hum. Mutat.* **11**, 1–3 (1998).