makes it unlikely that partial (12%, Carrel and Willard[3]) escape of the *HSD17B10* gene from X-inactivation in the first female patient would be detectable. Moreover, although monoallelic expression in one of the cell lines indicates that this gene is subject to inactivation, lack of data from other tissue samples makes the inference of widespread monoallelic expression of the *HSD17B10* gene in the second female patient less than convincing. The statement that 'as the girl was severely affected, a similar unfavorable X-inactivation in other tissues could be expected'[1] does not suffice for correcting the defect in data. The conclusion that 'the *HSD17B10* gene does not escape X-inactivation as has been reported previously' is not adequately supported by the data included in this publication.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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Reply to He *et al*

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We appreciate the comments of He *et al*.[1] Our response is outlined below.

In fact, it had been reported that *HSD17B10* is a part of a multigene domain in Xp11.21–p11.22 that escapes X-inactivation.[2] Later results by Carrel *et al*[3] showed that this gene is probably subjected to X-inactivation as only one of nine hybrids escapes from it. This observation can not be inferred from Figure 2 of Yang *et al*,[4] while the results are more clarifying in the adapted figure of the letter of He *et al*.[1]

To elucidate whether *HSD17B10* cDNA doses differed between both sexes, we performed relative quantification (RQ) of wild-type *HSD17B10* cDNA alleles in four female and four male controls. The results did not show any significant difference between the doses in both sexes. Therefore, these results are in favour of an X-linked disease that does not escape X-inactivation and are in agreement with the observations of Carrel *et al*.[3]

Fibroblasts were obtained from a single biopsy, as it would not have been ethical to perform additional biopsies with the only purpose of performing these studies. In fibroblasts we not only performed genetic studies but also determined enzymatic activities with good correlation between both, which gives more strength to the results.

Relatively large deviations are often observed in real-time PCR quantification, owing to the low specificity of the probes and variability of the endogenous controls. However, despite these difficulties, the same expression levels in the first female patient and her brother were observed, which is in agreement with the sequencing results, the low enzymatic activity, the severe clinical presentation and the skewed X-inactivation pattern. The second female showed expression of both mutant and wild-type alleles, which is also in agreement with sequencing results, normal enzymatic activity, slight clinical presentation and random X-inactivation pattern.

In conclusion, our results are adequately supported by the studies in controls and are confirmed by the studies in patients.

We thank He *et al* for giving us the opportunity to clarify some issues, although we think that they do not change the conclusions of our study.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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