LETTERS TO THE EDITOR

FMR1 fully expanded mutation with minimal methylation in a high functioning fragile X male

I refer to the paper by Wang et al entitled "FMR1 fully expanded mutation with minimal methylation in a high functioning fragile X male" published in *J Med Genet* 1996;33:376-8, in which the authors state that the case described "represents one of fewer than 10 documented which show this mutation pattern." I would like to draw your and the authors' attention to the fact that in 1993 (Am J Hum Genet 1993;53:1064-73) we presented a similar case which were not referred to in the above paper. If these had been added to the list, and the possibility of general under-representation of such males in the total sample of fragile X males ascertained through affected probands were considered, this might have somewhat changed the view expressed in the paper that the discrepancy between the size of CGG repeat and methylation in fragile X is "an extremely rare molecular genetic pattern".

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This letter was shown to Dr Taylor and colleagues, who reply as follows.

We thank Dr Loesch for her comments on our paper by Wang et al and apologise for our oversight in omitting reference to her article. The incidence of unmethylated full mutations among fragile X males is not known, but this molecular finding may be somewhat less rare than initially supposed. At the time of submitting their paper by Wang et al, there were few cases published. Since then there have been several additional reports (for example, by Kambouris et al, *Am J Med Genet* 1996;64:404-7 and by Lachiewicz et al, *J Med Genet* 1997;34:832-3 presented at the 1996 fragile X Conference in Portland Oregon in August). It is of particular interest that all cases have been males with mild manifestations of fragile X syndrome and IQs in the normal range. It is likely that with increasing awareness of the existence of high functioning, non-retarded fragile X males, and of the importance of considering fragile X testing in borderline retarded or learning disabled males, more cases will be identified with minimally methylated or unmethylated fully expanded mutations.

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Raising the sensitivity of fetal RhD typing and sex determination from maternal blood

The fact that all currently available methods for tissue sampling carry procedure related risks has been a motivation for many years to develop less invasive techniques for prenatal diagnosis, ideally by studying fetal cells in the maternal circulation. Methods directly detecting the fetal DNA by using PCR from maternal blood have been developed in a few cases. \(^1\) These methods are based on amplification specific for the fetal Y chromosome (important in the case of X chromosomal recessive diseases) or for fetal RhD status (to manage rhesus sensitisation) without previous enrichment of fetal DNA from maternal blood have successfully been established. \(^1\) However, these methods have so far not reached the precision required for routine application, since rates of false results, about 2.0%, are too high. \(^1\) On testing PCR based sex determination and RhD typing in over 100 samples of amniotic cells, chorionic villi, cord blood, or peripheral blood, we obtained no false results. \(^1\) Y chromosome identification by PCR was performed by a dual amplification procedure using the primers Y1.5 and Y1.6 in a first round PCR. One microtitre of the first round product was reamplified by nested PCR with negative rate by increasing the sensitivity of the sequence detection experiment. We separated the PCR products on an agarose gel and transferred them to nylon membranes by Southern blotting. \(^*\) After UV fixation these blots were hybridised with a relevant, radioactively labelled sense primers, washed, and exposed to x ray films at -70°C using intensifying screens. \(^*\) Artificial dilutions of fetal DNA in adult DNA were used to increase the sensitivity of detection from one fetal cell in a negative background of 100 000 cells to 1 in 10 000 000 cells. Accordingly, using this approach to analyse maternal blood samples the rate of false negative results decreased from about 20% to lower than 3% for RhD as well as for Y chromosome sequences. Our data indicate that false negative PCR results from maternal blood can be more likely based on detection limits rather than on more physiological reasons and our methods increase the potency of PCR to perform less invasive prenatal diagnosis.

However, a major drawback for PCR based prenatal diagnosis from whole maternal blood is the fact that a PCR setting which is highly sensitive, such as one described here, is also very likely to give false positive results. Such false positive results on fetal sex and RhD status determination from maternal blood have also been obtained by other groups. \(^1\) \(^4\) \(^6\) Thus, we believe PCR based sex determination, general concerns about discrepancies between serological typing and PCR derived RhD type have been raised. \(^1\) Recently, a large scale evaluation of the accuracy of PCR based sex determination and RhD typing using DNA derived from adult blood samples was performed. Two out of 632 RhD positive subjects were characterised as RhD negative and seven of the 133 RhD negative subjects were characterised as RhD positive. \(^1\) \(^6\) Although we do not support this interpretation of the findings, we agree with the authors that the need of fetal cells in the maternal circulation from previous pregnancies or a previous maternal blood transfusion. \(^1\) \(^6\) In the cases presented here we could not explain the observed high rate of false positive results this way.

In summary, the data presented here describe a successful approach to increasing the sensitivity of fetal PCR diagnosis from maternal blood by reducing the rate of false negative results. However, as long as the PCR setting is not optimised to diminish the observed positive results, one might wonder whether this diagnostic approach can routinely be used without previous enrichment of fetal cells.

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