Table 2 Analysis using Fisher's method for partitioning Chi-squared under the null hypothesis of 1:1 sex ratio (origin), 1:1 segregation ratio (allele) and their interaction

Source	d.f	χ^2	Probability	Significance after correction
Origin	1	0.149	0.9>*P*>0.1	ns
Allele	1	5.355	0.025>*P*>0.01	ns
Origin × Allele	1	0.595	0.9>*P*>0.1	ns

Analysis of the data of Carey *et al.* Table 1. We exclude the data in which the parent of origin is unknown. The appropriate level for experiment-wise significance at the 5% level is a χ^2 of ~5.9 for 1 d.f. for three tests.

is a heterozygote and when the father is a heterozygote and not just from a 1:1 ratio. We thus treated the data as a contingency table under the assumption that no *a priori* expectations exist for either segregation ratio or the sex ratio of the parental origin of the alleles. Our analysis of both data sets finds no evidence for such a difference (χ^2=0.522, *P*>0.40 for data from Carey *et al.*; χ^2=1.551, *P*>0.20 for data from Gennarelli *et al.*: 1 d.f. in both instances).

(3) Gennarelli *et al.* have claimed that fathers occur more frequently than mothers as a source of the long allele and that sons are more likely to receive the long allele. We have hence analysed both teams' data[1,2] using Fisher's method for partitioning Chi-squared (and again applying a correction for Type I Errors). *A priori* assumptions were made about the sex ratio of the source of alleles, indeed, the null hypothesis tested here was that there was no bias of any kind (all sex ratios and segregation ratios were 1:1). Under this set of assumptions we additionally find in the data of Carey *et al.* no significant deviation of the parental sex ratio from 1:1 and, as above (but employing a slightly different analysis), no evidence that the sex of the parent affects the transmission ratio of the long and the short alleles (Table 2).

Our re-analysis of the Gennarelli *et al.* data (results not shown), reveals two significant results: (i) there is an excess of the long version of the *DM* allele (*P*<0.005) and (ii) there are more heterozygous fathers in the sample than heterozygous mothers (*P*<0.005). The latter result we do not know how to interpret. There are, however, good reasons to expect a strong ascertainment bias in favour of males when certain sampling procedures are employed[4]. There is no evidence of preferential transmission by fathers if the correction for Type I Errors is included, nor is there evidence of preferential transmission by fathers to sons as is claimed.

In sum, we find no evidence to support the conclusion that long versions of the DM allele have male-specific meiotic drive. The data are, however, consistent with selection in favour of bearers of the relatively long allele and/or segregation distortion (non-mendelian inheritance processes such as meiotic drive and biased gene conversion) acting in the same direction in both sexes. As noted above, meiotic drive operating in both sexes has not previously been reported. Any of the above forces can in principle account for the relative abundance of the long versions of DM alleles in sub-clinical individuals.

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IN REPLY — Whilst we accept some of the criticisms of Hurst *et al.*, we feel that their overall conclusion is unnecessarily negative and stand by our original conclusion that segregation distortion occurs for normal DM alleles. Hurst *et al.* are correct in stating that in our paper[1] the results for a one-tailed test were quoted inappropriately. However, if the total number of meioses are re-analysed using a two-tailed test without division into male and female transmissions, preferential transmission of the longer ≥19 repeat allele occurs at a statistically significant level (*P*<0.04). This represents the outcome of one test and is consistent with segregation distortion, which is the effect which we actually claimed was operating — meiotic drive was simply postulated as a possible mechanism for this effect.

Although we accept the general caveats about performing multiple analyses (and for this reason did not include in our original paper a geographical breakdown of the figures), we believe that it would be unusual to apply it in this circumstance, where the data are simply divided into the two sexes. The re-analysis by Hurst *et al.* runs the risk of artificially rendering a statistically significant result insignificant, by the application of a number of inappropriate tests followed by multiple hypotheses corrections.

Our re-analysis of the data still shows significant segregation distortion in favour of the transmission of the larger normal alleles. Larger sample numbers are required to investigate this effect more fully.

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