Dear Sir,

We have read Dr Jakab’s comments on our work (Devillard et al., 2002), where our conclusion is discussed about the possible origin for the polyploid content of large-headed sperm. We believe that in these three patients, as well as in other patients whom were studied later (unpublished results), where most or all sperm are large-headed and multiflagellated, it is indeed an incomplete partition of homologous chromosomes/chromatids during both meiosis I and meiosis II associated with the failure of nuclear cleavage, that is responsible for the observed polyploidy. This conclusion was drawn directly from the observation that (i) all sperm from these patients contained both X and Y chromosomes, with the numbers of FISH signals for the sex chromosomes being X/Y, XX/Y, X/YY, XX/YY; (ii) one to four FISH signals were observed for the studied autosomes (chromosomes 1 and 18) and (iii) no sperm were observed lacking either a sex chromosome or an autosome. In agreement with Dr Jakab, we think that this situation is completely different from that observed in patients with moderately elevated frequencies of
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polyplod sperm associated with other types of sperm defects, where indeed most polyplod sperm are diploid, resulting either from an abnormal meiosis I or a defective meiosis II. In other patients, excluding the above mentioned cases of patients with large-headed multiflagellated sperm, we have also observed important inter-individual variations in sperm diploidy rates. We have read with interest the data described by Dr. Jakab, where in sperm with higher than average diploidy rates, the dominance of either the M1 diploids or M2 diploids was observed. However, this observation is not relevant to the patients with large-headed multiflagellated sperm as described in our paper. We thank Dr. Jakab for his interest in our paper and for giving us the opportunity to clarify this point.

References


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