

The distinction between paternally and maternally contribution to the trippronuclei in human zygotes

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INTRODUCTION: The aim of this study is to determine the origin of trippronuclei by detecting the number of sperm tail in human triploid (3PN) zygote with FISH.

METHODS: Zygotes with 3PN classified under the inverted microscope on day 1 after sperm insemination were collected. A few hours after morphological evaluation, these 3PN zygotes were successively exposed to mouse anti-tubulin antibody and FITC-labeled goat antibodies against mouse IgG for visualization of sperm tail, Hoechst dye 33342 for visualization of ploid. Fixed spermatozoa from semen sample were processed in parallel controls.

RESULTS: For 18 zygotes confirmed as 3PN by FISH, the total number of ploid detected was 54, while the total number of sperm tails was 35. Thus the observed sperm tail / ploid ratio was 0.65. No statistically significant differences (X^2 test, $P>0.05$) were detected when compared our data and the theoretical values expected in the hypothesis, which the fertilization by two spermatozoa (sperm tail / ploid ratio was 0.66). Moreover, statistical differences appeared when comparing data with theoretical ones corresponding to another hypothesis, which triploid result in digyny, parthenogenesis (sperm tail / ploid ratio was 0.33).

CONCLUSIONS: According to our study, the additional haploid chromosome set of those triploid zygotes is paternal in origin. The application of FISH technique to detect the number of sperm tail provided an indirect evidence to speculate about the origin of 3PN after sperm insemination as the result of two spermatozoa penetrating into a single oocyte.