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SHORT REPORT

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A comparison of sample collection methods for quantifying cell-free fetal neurodevelopment transcripts in amniotic fluid

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Abstract

Background: Cell-free RNA (cfRNA) transcripts known to be expressed by the fetal brain are detectable by quantitative reverse transcription PCR (RT-qPCR) in amniotic fluid and represent potential biomarkers of neurodevelopment. The aim of this study was to compare the cfRNA yields from amniotic fluid (AF) collected in a commercial RNA stabilization product with the traditional method of freezing alone.

Findings: Thirteen women undergoing elective Cesarean birth at term without labor had whole AF collected at the time of uterine incision, prior to membrane rupture. Patient samples were split between Streck RNA blood collection tubes (BCT) and plain sterile polypropylene centrifuge tubes. Cell-free RNA from the AF supernatant was extracted according to a previously published protocol. RT qPCR was performed for the reference gene *GAPDH*, and three genes associated with neurodevelopment (*NRXN3, NTRK3*, and *ZBTB18*). The yield from samples collected in Streck RNA BCT and plain centrifuge tubes were compared with the paired t test. *GAPDH, NRXN3* and *ZBTB18* amplified successfully in all samples, but *NTRK3* did not. The RNA yield was significantly lower in samples collected in the Streck RNA BCT compared with the traditional storage method of freezing alone for all three successfully amplified genes ($p < 0.0001$).

Conclusions: Selected cfRNA neurodevelopment transcripts are consistently detectable in third trimester AF. There appears to be no benefit in collecting AF in Streck RNA BCT for quantitative studies of AF cell-free RNA.

Keywords: Amniotic fluid, Cell-free RNA, Fetal development, qPCR, Gene expression

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