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Genetic analysis of amniotic fluid shows promise for monitoring fetal development

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Researchers have demonstrated the feasibility of focused fetal gene expression analysis of target genes found in amniotic fluid using Standardized NanoArray PCR (SNAP) technology. This analysis could be used to monitor fetal development, enabling clinicians to determine very early in pregnancy whether fetal organ systems are developing normally. The study appears in the September issue of The *Journal of Molecular Diagnostics*.

Using a previously developed SNAP gene panel as proof of concept, investigators from the Floating Hospital for Children at Tufts Medical Center, Mount Sinai School of Medicine, and Prevail Dx determined that 7 of the 21 genes assayed were expressed differently depending on fetal sex or gestational age. Results were obtained from amniotic fluid supernatant samples from fetuses between 15 to 20 weeks of gestation, when standard amniotic fluid testing is performed.

"In the future, fetal gene expression panels could prove useful in prenatal care to evaluate function in cases of at-risk pregnancies and fetal pathologies," commented lead investigator Lauren J. Massingham, MD, Division of Genetics, Department of Pediatrics, Floating Hospital for Children at Tufts Medical Center, Boston, Massachusetts. According to the investigators, further studies using this gene panel approach could elucidate the complex immune pathways involved in the maternal-fetal relationship.

Dr. Massingham added, "Some genes in the current panel may prove to

be useful components of a fetal gene expression panel. Future studies are warranted to identify additional genes to be incorporated, including inflammatory, developmental, and gastrointestinal genes. This technique could be optimized to examine specific genes instrumental in fetal organ system function, which could be a useful addition to prenatal care."

SNAP technology allows for the simultaneous quantitative assessment of tens to hundreds of genes from reduced and degraded nucleic acid samples, overcoming the quality concerns of processing primary human samples. Gene expression that varies by up to five orders of magnitude can be quantified using a single assay.

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