

Study looks at a new method for filtering results from genetic studies

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In a study to be presented Thursday, Jan. 26, in the oral concurrent session, at the Society for Maternal-Fetal Medicine's annual meeting, The Pregnancy Meeting, researchers verified genetic results from one large study of women with spontaneous preterm birth, and highlighted 13 key genes in both mothers and babies which may be involved in preterm birth while also identifying 123 genes as top candidates for further study.

Tracy Manuck, M.D., associate professor of Maternal Fetal Medicine and medical director of the University of North Carolina Prematurity Prevention Clinic at the University of North Carolina-Chapel Hill, is the lead researcher and presenter of the study titled Use of evolutionary triangulation to refine [genetic](#) association studies of spontaneous [preterm birth](#) (SPTB). Manuck has been working to understand which [genes](#) influence why some women deliver preterm but others do not.

Nearly half a million babies are born too soon each year in the U.S. Preterm birth (before 37 weeks of pregnancy), is the leading cause of newborn death and babies who survive an early birth often face the risk of lifetime health challenges such as breathing problems, cerebral palsy, intellectual disabilities and others. Even babies born just a few weeks early have higher rates of hospitalization and illness than full-term infants. It is a serious health problem that costs the U.S. more than \$26 billion annually.

"Although many [genetic studies](#) of preterm birth have been conducted,

results have been inconsistent across populations," said Manuck. She hopes to use a new method for filtering results from genetic studies, based on inheritance patterns across women of different ancestry, in order to fine-tune results from other genetic studies of preterm birth. This technique, termed "evolutionary triangulation," relies on the fact that the rates of preterm birth vary significantly by race. In the United States, black women are almost twice as likely to deliver preterm as white women.

In addition to highlighting 13 key genes in mothers and babies which may be involved in preterm birth, Dr. Manuck and colleagues also examined 640 genes from an online preterm birth genetic database and, using the evolutionary triangulation technique, highlighted 123 additional genes as top candidates for further study. "These results have great potential implications for future studies to identify women at highest risk for spontaneous preterm birth," Manuck stated.

"Evolutionary triangulation is an exciting new way of thinking about genetic data, and one day may be applied to other disorders of pregnancy disproportionately affecting different populations of [women](#)."

More information: Abstract #11: Use of evolutionary triangulation to refine genetic association studies of spontaneous preterm birth (SPTB), The Pregnancy Meeting, 2017.

Provided by Society for Maternal-Fetal Medicine

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