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# Researchers achieve 26-hour rapid whole-genome sequencing in critically ill infants

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A study published today in *Genome Medicine* describes how researchers at Children's Mercy Kansas City cut in half the time needed for rapid whole-genome sequencing and genetic diagnosis in critically-ill infants, called STAT-Seq. Through a variety of enhancements, the Center for Pediatric Genomic Medicine at Children's Mercy completed the STAT-Seq test in 26 hours compared to 50 hours, improving on a turnaround time that was already the fastest available in the world.

STAT-Seq can identify mutations across the genome associated with approximately 5,300 known genetic diseases, and in some cases even identify previously unknown genetic diseases. In contrast, standard clinical practice calls for an array of genetic tests to be performed, which are time-consuming, costly and can only test for a limited set of disorders. Lead authors of the study were Neil Miller and Emily Farrow, PhD, CGC, of Children's Mercy Kansas City, and Stephen Kingsmore, MB, ChB, BAO, DSc, FRCPath, now with Rady Children's Hospital-San Diego.

"We believe rapid genome sequencing of critically-ill infants with suspected genetic diseases is a breakthrough application for genomic medicine," said Farrow, Director of Laboratory Operations and a genetic research scientist at the Center for Pediatric Genomic Medicine at Children's Mercy. "We have found STAT-Seq can significantly decrease the time to diagnosis for some of our sickest patients."

The symptoms of genetic diseases in infants are often overlapping,

making identification of a specific diagnosis difficult. Further, infants frequently show only a fraction of the full set of symptoms of genetic diseases, further complicating diagnosis and specific treatment. STAT-Seq bypasses these difficulties by casting the widest net possible in order to rapidly define the underlying cause of the disease.

"Establishing fast, scalable methods is a key step toward making genome sequencing a routine part of healthcare, not only for the diagnosis of genetic disease, but for a wide range of precision medicine applications" said Miller, Director of Informatics and Software Development at the Center for Pediatric Genomic Medicine at Children's Mercy. "This is only possible through collaboration among a uniquely interdisciplinary team of clinical, informatics, laboratory, and genetic counseling experts."

In the retrospective study, blinded DNA samples from infants with known genetic diseases were reanalyzed using various parameters and technologies as a proof of concept. Significant time-savings were achieved with Edico Genome's DRAGEN processor, which sped up data analysis from 22.5 hours to 41 minutes. To achieve the 26-hour result, the team at the Center for Pediatric Genomic Medicine also developed ultra-rapid run mode on an Illumina HiSeq 2500 sequencing instrument, saving five hours; replaced manual interpretation and reporting process with in-house VIKING software program, saving three hours; and optimized in-house software, RUNES (Rapid Understanding of Nucleotide variant Effect Software), to more quickly detect mutations in gene sequences, saving two hours.

**More information:** *Genome Medicine* , www.genomemedicine.com/content/7/1/100

Provided by Children's Mercy Hospital