



Cystic Fibrosis Research News

Title:

RNA sequencing data from neutrophils of patients with cystic fibrosis reveals potential for developing biomarkers for pulmonary exacerbations

Authors:

Kaiyu Jiang¹, Kerry E. Poppenberg², Laiping Wong¹, Yanmin Chen¹, Drucy Borowitz³, Danielle Goetz³, Daniel Sheehan³, Carla Frederick⁴, Vincent M. Tutino², Hui Meng², and James N Jarvis¹

Affiliations:

¹Department of Pediatrics, Pediatric Rheumatology Research, University at Buffalo Jacobs School of Medicine and Biomedical Sciences, Clinical and Translational Research Center, 875 Ellicott St, Buffalo, NY 14203, USA

²Department of Biomedical Engineering, University at Buffalo Jacobs School of Medicine and Biomedical Sciences, Clinical and Translational Research Center, 875 Ellicott St, Buffalo, NY 14203, USA

³Department of Pediatrics, Pulmonology Section, University at Buffalo, Women and Children's Hospital of Buffalo, 239 Bryant St, Buffalo, NY 14203

⁴Department of Medicine, Section on Pulmonary, Critical Care, and Sleep Medicine, Buffalo General Medical Center Heart and Lung Center
219 Bryant St./100 High St. B-8, Buffalo, NY 14222

What was your research question?

We wanted to know whether we could use patterns of gene expression (i.e., what genes get turned on or off) in blood cells called neutrophils to identify patients with CF who are about to experience worsening of their lung disease. Neutrophils are very sensitive indicators of potential bacterial infection.

Why is this important?

Periods of worsening lung disease (so called "CF pulmonary exacerbations" - CFPE) are one of the factors contributing to irreversible lung damage in people with CF. We are hoping that, by detecting CFPE earlier, before symptoms arise, we can reduce the amount of lung damage done by CFPE.

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cfresearchnews@gmail.com



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What did you do?

We looked at the patterns of gene expression in neutrophils in patients with CF who were admitted to the hospital for CFPE. Then, we repeated those studies after the patients were treated and were getting better. Our thinking was that those genes that changed over that time period would be good ones to monitor in the future. The other thing we did was look at the entire pattern of gene expression before and after treatment using a mathematic technique called "machine learning."

What did you find?

We found lots of potential "candidates" for things we might monitor to try to detect CFPE earlier. However, there was a lot of variation between patients, making it hard to develop so-called "biomarkers" that would work for everybody. However, when we analyzed the data using machine learning, it was a lot easier to identify active CFPE compared to patients who were recovering. We then showed we could do this on a small blood sample.

What does this mean and reasons for caution?

The machine learning approach outperformed what other groups have been able to do along these lines, but it requires special skill that a typical hospital laboratory wouldn't have. Also, we found that 2 weeks wasn't a sufficiently long time between the collection of specimens, so we still don't know what the best "biomarkers" are or will be.

What's next?

We need to repeat this study in a much larger group of patients and wait longer before collecting the second sample.

Original manuscript citation in PubMed

<https://www.sciencedirect.com/science/article/pii/S1569199318306192>