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Saliva as a Window Into Cystic Fibrosis: Metabolic Biomarkers and Clinical Potential

**Ryan Quigley:**

You're listening to *Clinician's Roundtable* on ReachMD, and this is an *AudioAbstract*. I'm Ryan Quigley, and today, we'll be diving into a recent study that explored salivary metabolites as potential biomarkers in cystic fibrosis.

Now, cystic fibrosis is one disease with many faces. It's driven by a single genetic defect, but the way it shows up can look very different in each patient. And while CFTR-modulating therapies have reshaped treatment, clinicians are still looking for reliable biomarkers.

In a 2025 study published in *Scientific Reports*, researchers turned to a simple and unexpected fluid: saliva. The idea is appealing—saliva is easy to collect, non-invasive, and may carry molecular clues about what's happening throughout the body.

The team studied saliva samples from 70 adults with cystic fibrosis and compared them with 63 healthy controls. Using a powerful technique called liquid chromatography-tandem mass spectrometry, also known as LCMS, they profiled more than a hundred different metabolites, including amino acids, fatty acids, bile acids, biogenic amines, carboxylic acids, hormones, indoles derivatives, alkaloids, amine oxides, cresols, vitamins and cofactors. The key question was whether these tiny molecules in saliva could point to differences linked with common cystic fibrosis complications—things like pancreatic insufficiency, *Pseudomonas* infection, diabetes related to cystic fibrosis, or liver disease.

They identified 60 metabolites that were significantly different between cystic fibrosis patients and controls. Most were increased in cystic fibrosis, but 11 were decreased. And a few patterns really stood out—for example, methionine was reduced in patients with pancreatic insufficiency, while histamine levels were lower in those with *Pseudomonas* colonization.

In patients with cystic fibrosis-related diabetes, the levels of ADMA, N-acetylornithine, and methionine all dropped, pointing to disruptions in arginine and methylation pathways. And for patients with cystic fibrosis-related liver disease, the dopamine precursor, DOPA, was noticeably lower, which hints at shifts in the dopaminergic pathway.

Amino acid metabolism seemed to be up-regulated, while lipid metabolism was down, especially fatty acid pathways.

Importantly, the study didn't stop at group comparisons. The researchers also looked at lung function, measured by forced expiratory volume in 1 second, or FEV1. They found that higher levels of several amino acids, including asparagine, glycine, threonine, and others, as well as amines, including AABA, BABA, and GABA, were linked to better FEV1 scores. In other words, what showed up in saliva also tracked with respiratory health.

So what does all this mean for practice? While the findings need to be confirmed in larger, independent cohorts, the message is clear: saliva could become a powerful, non-invasive window into cystic fibrosis. It may help stratify patients, flag risks like diabetes or liver disease earlier, and even give clinicians an easy way to monitor how well therapies are working.

Ultimately, this research suggests that a single saliva sample could carry a wealth of information. It's an exciting, fresh angle in the search for biomarkers that match the complexity of cystic fibrosis itself.

This has been an *AudioAbstract*, and I'm Ryan Quigley. To access this and other episodes in our series, visit *Clinician's Roundtable* or *AudioAbstracts* on ReachMD.com, where you can Be Part of the Knowledge. Thanks for listening!

**References**

Caterino M, Costanzo M, Castaldo A, et al. Metabolomic profiling of saliva from cystic fibrosis patients. *Sci Rep*. 2025;15(1):479.

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