

Human Microbiome Genes Correlate with Sulforaphane Bioavailability in Controlled Clinical Study

BALTIMORE, CA, UNITED STATES, March 23, 2026 /EINPresswire.com/ -- A newly published human clinical study reports correlations between specific gut microbial genes and an individual's ability to convert glucoraphanin — the dietary precursor to [sulforaphane](#) — into its bioactive form.

“For decades, we have understood the biological potency of sulforaphane,” said Jed W. Fahey, ScD, a co-author of the study and a leading authority in glucosinolate research. “What has remained less clear is how consistently individuals can generate it from dietary precursors. This work advances our understanding of the factors contributing to variability in sulforaphane formation.”

The study, published in *Scientific Reports*, a peer-reviewed journal within the Nature Portfolio, represents the first controlled human clinical investigation to correlate previously characterized glucoraphanin-converting bacterial genes with measured in vivo sulforaphane formation.

Sulforaphane, a widely studied plant bioactive known for activating Nrf2-regulated antioxidant and detoxification pathways, is formed from glucoraphanin via enzymatic conversion. While plant-derived myrosinase can catalyze this reaction, the human gut microbiome can also contribute, with conversion capacity varying substantially between individuals.

Researchers observed significant correlations between sulforaphane production and the relative abundance of previously characterized glucoraphanin-metabolizing genes. Participants with higher gene abundance demonstrated greater conversion efficiency. Higher conversion was also observed among participants with greater *Bifidobacterium* abundance, further supporting a role for microbiome composition in the formation of sulforaphane.

The findings also suggest that prior exposure to glucoraphanin may influence subsequent microbial capacity for conversion, consistent with microbiome adaptation.





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Sue Ishaq, PhD

By linking microbial gene presence with measured sulforaphane formation, the study provides new insight into variability in individual conversion capacity and contributes to growing research examining how the gut microbiome influences dietary phytochemical metabolism.

“These findings strengthen the evidence that microbiome composition plays a substantive role in sulforaphane

formation in the gut,” said Sue Ishaq, PhD, microbiome researcher and a co-author of the study. “Differences in microbiome composition may help explain why individuals vary in how effectively they convert glucoraphanin.”

The research was conducted as a collaboration with investigators from North Carolina State University, the University of Maine, Appalachian State University, and Brassica Protection Products.

The study appears in Scientific Reports:

<https://www.nature.com/articles/s41598-026-39389-4>

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