

# Gut Microbial Diversity Associated With Plant Food Metabolites

February 16, 2015

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While the phrase 'you are what you eat' has long been popular, researchers are getting ever more adept at explaining why certain diets may affect human health. One major area of recent research involves the 'microbiome', measuring the makeup of microorganisms living on or in the human body. Previous research indicates that these microbiota can have distinct impacts on human health, either positive or negative, through metabolic or other processes. In a recent report in *Cancer Epidemiology, Biomarkers, and Prevention*, Drs. Meredith Hullar and Johanna Lampe in the Public Health Sciences Division found that urinary excretion of plant metabolites was associated with both the diversity and the composition of the gut microbial community, potentially impacting downstream health effects.

Lignans are compounds found in the woody portions of plants, seed coats, and the bran layer of grains. Epidemiologic evidence suggests that increased consumption of lignans is associated with lower risk of breast and colon cancer. These lignans are metabolized by the gut microbiota into the enterolignans enterodiol and enterolactone, bioactive chemicals that are thought to possess a variety of activities related to human health. Importantly, several biochemical steps are needed to transform plant lignans into enterolignans, and these steps require an assorted group of gut bacteria for the entire process to occur. This suggests that the complexity and diversity of the gut microbial community is essential for maximizing this conversion.

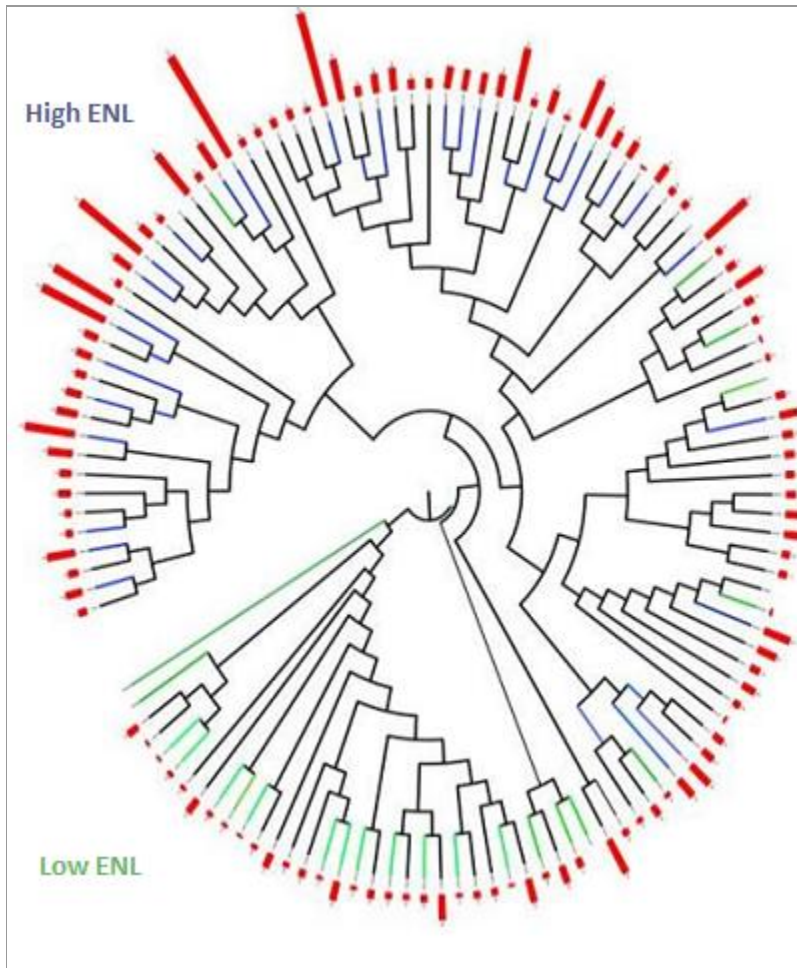
To evaluate and characterize this relationship, the authors measured enterolignan levels and microbial diversity in a group of 115 women. Enterolignan levels were measured from urine samples, and the gut microbial community was measured from stool samples. To determine the makeup of the microbial community in each sample, the authors sequenced the 16s rRNA gene and then aligned the sequences into operational taxonomic units. This taxonomic classification allowed the authors to determine the diversity of the microbial community, both within (alpha diversity) and between (beta diversity) individuals. In order to account for differences in diet, the women also recorded everything they ate or drank for three days.

Overall, the authors found that the global microbial community differed by tertile of enterolactone, but not enterodiol, and that this diversity increased with higher enterolactone excretion. They also found that four bacterial genera were associated with the high enterolactone excretors: *Moryella*, *Streptobacillus*, *Fastidiosipilla*, and *Acetanaerobacterium*. This diversity difference was also positively associated with fiber intake, which aligns with prior evidence that diet can influence the human gut microbiome. This association between dietary patterns high in fiber and increased microbial diversity may also suggest additional health benefits, in terms of resilience to infection, environmental factors, or obesity.

While this cross-sectional study will require additional follow-up, it suggests that the environmental exposures from dietary intake (such as lignans from plant food consumption) can be altered by the metabolic capacity of the gut microbiome (which may be represented by its diversity), which may have downstream health effects (such as alterations in cancer risk). This may be particularly important for the catabolism of dietary fibers, which carry wide biochemical and structural forms. Without these helpful microorganisms, humans might otherwise not be able to process these fibers into their bioactive forms, missing out on all their associated health benefits. The authors hope that future studies will further our understanding of this complicated relationship.

Other PHS researchers contributing to this project were Mr. Samuel Lancaster, Mr. Wade Copeland, and Dr. Timothy Randolph.

[Hullar MA, Lancaster SM, Li F, Tseng E, Beer K, Atkinson C, Wahala K, Copeland WK, Randolph TW, Newton KM, Lampe JW](#). 2014. Enterolignan producing phenotypes are associated with increased gut microbial diversity and altered composition in premenopausal women in the United States. *Cancer Epidemiol Biomarkers Prev*. pii: cebp.0262.2014.



*Image provided by Dr. Meredith Hullar*

The composition of the gut microbial community is significantly different between high and low enterolactone (ENL) excretors (MRPP;  $P < 0.0005$ ). Bars are the amount of urinary ENL (ng/ mg creatinine), color-coded by tertile. (Low = green, Medium = black, and High = blue).