



Structure of dietary fiber and gut microbiota: what Feng's review shows

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1. ABSTRACT

The review examines why the term fiber encompasses very different plant substances. The central point is that chemical composition, physical form, and the way a fiber retains water can alter its digestive path and contact with gut microorganisms. The authors bring together studies on dietary fiber from the molecular scale to the food scale. They describe how the type of sugars that make up the fiber, chemical bonds, branching, crystallinity, porosity, and particle size can change accessibility to gut bacteria. A more accessible fiber can be fermented more easily; a more compact structure or one trapped within the plant matrix can instead slow down this process. The review also addresses tools used to characterize these properties, such as X-ray diffraction, useful for assessing crystalline order, and gas adsorption techniques, useful for estimating surface area and pores. It also discusses how milling, extrusion, enzymatic treatments, and other processing methods can modify structure, solubility, and fermentability. The biological message is that classifying a fiber as soluble or insoluble is not enough to anticipate its behavior. However, the publication is a narrative review: it integrates results obtained with humans, animals, and laboratory models, without producing a new clinical trial or proving that a given change in the gut microbiota improves health.

VIDEO ARTICLE



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2. WHAT THIS RESEARCH ANALYZED

For the body, dietary fiber is not a single material: some types form dense solutions, others remain more intact, and others are rapidly utilized by microorganisms in the colon. Feng and colleagues (2025) analyzed this variability by linking the structure of fibers to their behavior during digestion and fermentation. The publication distinguishes between molecular characteristics, such as the monosaccharides that make up the fiber and the bonds between them, and physical characteristics, such as crystallinity, porosity, exposed surface area, and particle size. It also examines the food matrix—the architecture of the plant material—which can make a fiber more or less accessible to enzymes and bacteria. Finally, it describes characterization techniques and processing methods capable of altering these properties. This prepares the reader to interpret the results with greater precision.

3. WHAT RESULTS EMERGE FROM THE STUDY

The main finding is that structural properties help explain why two fibers with the same general label can follow different paths. A less accessible structure can slow down degradation; a more exposed or less compact one can facilitate contact with microbial enzymes and, therefore, fermentation in the colon. The authors emphasize that solubility, viscosity, and fermentability are related but not equivalent properties. Viscosity indicates how much a fiber thickens a liquid; fermentability, on the other hand, indicates how well the gut microbiota can utilize it. Crystallinity and chemical cross-linking can limit access to the fiber, while pores, branching, and size reduction can modify it. The practical significance is mechanistic: these elements can influence the metabolites produced by bacteria, but they do not automatically demonstrate a clinical benefit.

4. WHY THIS STUDY IS RELEVANT

This review is relevant because it avoids a common oversimplification: treating all fibers as if they produce the same intestinal response. Instead, it proposes considering composition, physical structure, processing, and the baseline gut microbiota together. This framework also helps in interpreting

experimental results. If the fiber structure changes, the bacteria capable of utilizing it and the short-chain fatty acids—molecules produced during fermentation—may also change. However, a microbial change is not, in itself, a prognostic biomarker (i.e., an indicator of the future course of a disease) nor a predictive biomarker (i.e., an indicator of response to a treatment). Targeted clinical studies are needed to link these steps to health outcomes.

5. STUDY LIMITATIONS AND WHAT IT DOES NOT DEMONSTRATE

Feng and colleagues (2025) did not assign fibers to participants nor measure specific clinical outcomes. The publication is a narrative review and brings together evidence with different designs, doses, foods, animal species, and laboratory conditions. Therefore, it does not estimate an average effect or a single causal relationship. It does not demonstrate that modifying porosity, crystallinity, or branching improves health in all people. It does not establish which fiber is best in absolute terms and does not allow for the direct transfer of data obtained in test tubes, in animals, or with isolated fibers to a whole plant-based food. The initial gut microbiota, the overall diet, and the dose can also change the response. Independent evidence clarifies how much the narrative is supported and how much it depends on the context.

6. INDEPENDENT SUPPORTING EVIDENCE

A randomized clinical trial by Deehan and colleagues compared three type 4 resistant starches, which are starches modified to resist digestion. In healthy adults, small structural differences produced distinct changes in the gut microbiota and a relative prevalence of either propionate or butyrate; the dominant effects increased with the dose up to a plateau at 35 g per day [1]. The confirmed pathway is fiber structure selective utilization by bacteria fermentation profile. The confirmation is direct and relatively strong for those three ingredients, but it does not equate to proof for all fibers or clinical outcomes. In a fermentation model using fecal microbiota from different subjects, Cantu-Jungles and colleagues observed that more complex fibers utilized by fewer bacteria generated responses that were more similar across donors compared to low-specificity fibers [2]. With insoluble beta-glucan, *Anaerostipes* increased on average from

0.3% to 16.5% and *Bacteroides uniformis* from 2.5% to 17.9%; the variations were associated with butyrate and propionate ratios. The confirmation is direct for the principle of selectivity, but the model does not replicate the human organism. Jensen and colleagues fermented 55 fibers for 72 hours with pooled feline fecal inoculum. The monosaccharide composition was associated with final pH, short-chain fatty acids, and microbial community [3]. This supports the chemical composition fermentation pathway, but it is indirect confirmation because it concerns an *in vitro* system and non-human microbiota.

7. CONFLICTING EVIDENCE

Evidence does not indicate that fiber structure alone determines a predictable response. In a crossover study of 76 healthy adults, with 59 participants completing the protocol, Devarakonda and colleagues compared type 2 resistant starch, type 4 resistant starch, and digestible starch for ten days each. The

baseline gut microbiota, habitual dietary fiber intake, and the order of interventions helped predict some responses; furthermore, short-chain fatty acid concentrations increased more with digestible starch [4]. This reduces the generalizability of a linear relationship between structure and metabolites, without denying it. Moncada and colleagues also compared 16 fibers *in vitro* using healthy gut microbiota and four fibers using microbiota associated with ulcerative colitis. In the latter case, for all four selected fibers, fermentation, gas, and short-chain fatty acids were lower [5]. This finding indicates that the initial microbial community can limit the effect expected from the structure. This limitation is significant: the comparison with ulcerative colitis is derived from a single donor. No sufficiently relevant directly conflicting evidence beyond these contextual conditions has been identified; this does not prove the absence of contrary results.

8. QUADRO COMPARATIVO E SINTESI DELLE EVIDENZE

The following publications evaluate how fiber structure, baseline gut microbiota, and experimental model contribute to fermentation.

Quadro comparativo

Publication	Model and sample size	Main result	Relationship to the study
Deehan et al., 2020 [1]	RCT, healthy adults; sample size not available in the verified source	Three structurally different resistant starches directed different microbial and metabolic profiles.	Direct confirmation in humans, limited to specific modified starches.
Cantu-Jungles et al., 2021 [2]	In vitro fermentation with fecal inocula from different donors	More specific fibers induced more consistent microbial changes across donors.	Direct confirmation of the role of complexity, but without <i>in vivo</i> exposure.
Jensen et al., 2024 [3]	In vitro bioreactors; 55 fibers, pooled feline fecal inoculum	Fiber monosaccharides were associated with fermentation, pH, and microbial community.	Indirect confirmation of the relationship between composition and microbial response.
Devarakonda et al., 2024 [4]	Human crossover; 76 enrolled, 59 completed	Response to resistant starches varied with baseline microbiota, diet, and order of interventions.	Contextual evidence: structure is not enough to predict every response.
Moncada et al., 2024 [5]	In vitro fermentation; 16 fibers, comparison with microbiota associated with ulcerative colitis	Dysbiosis and fiber properties reduced fermentation and metabolites in the four fibers tested.	Contextual evidence, limited by the single donor with ulcerative colitis.



9. SINTESI EDITORIALE E CONCLUSIONI

EDITORIAL CONCLUSION

The review by Feng and colleagues shows that dietary fiber should be considered as a family of structures, not as a uniform ingredient. Monosaccharide composition, chemical bonds, branching, porosity, crystallinity, particle size, and the plant matrix can all change how accessible a fiber is to the gut microbiota. Independent studies support this approach: structurally distinct fibers can select for different microbial communities and fermentation profiles. However, the available evidence also indicates a strong dependence on context. The initial microbiota, the dose, the food containing the fiber, and the experimental model can all modify the response. The most robust results concern fermentation mechanisms and microbiological changes, not the prevention or treatment of diseases. For the reader, the message is therefore one of caution: the soluble-insoluble distinction remains useful, but it is not enough to describe what a fiber will do in the gut. Future research will need to link these characteristics to measurable clinical outcomes.

Aggiornato al 25/10/2026. Questo contenuto riflette una sintesi divulgativa delle evidenze scientifiche al momento della pubblicazione e non sostituisce il parere medico.

10. TRANSPARENCY AND SCIENTIFIC RESPONSIBILITY

Artificial Intelligence was used solely as a tool for editorial and documentary support. All content, interpretations, bibliographic citations and conclusions have been verified, reviewed and approved by the author, who assumes full scientific responsibility for them.

The manuscript was also subjected to independent peer review prior to publication.

To ensure the greatest transparency, the complete history of the article, including the dates of submission, revision, acceptance and publication, as well as information on the peer review process, is available on the dedicated Article History page.

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