

Journal Club

Bahtiyar YILMAZ

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1st Paper

Gut Microbial Metabolites Fuel Host Antibody Responses

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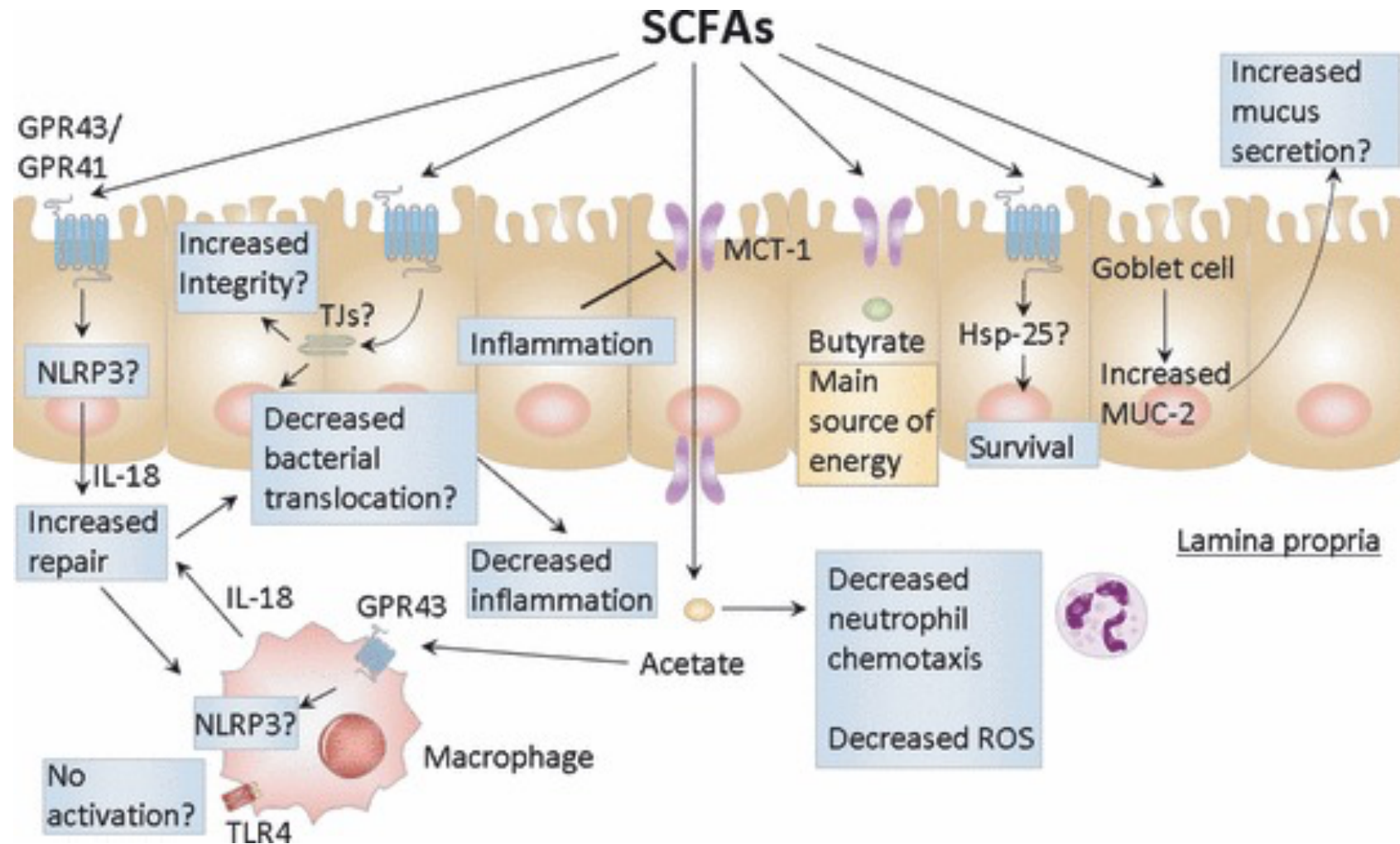
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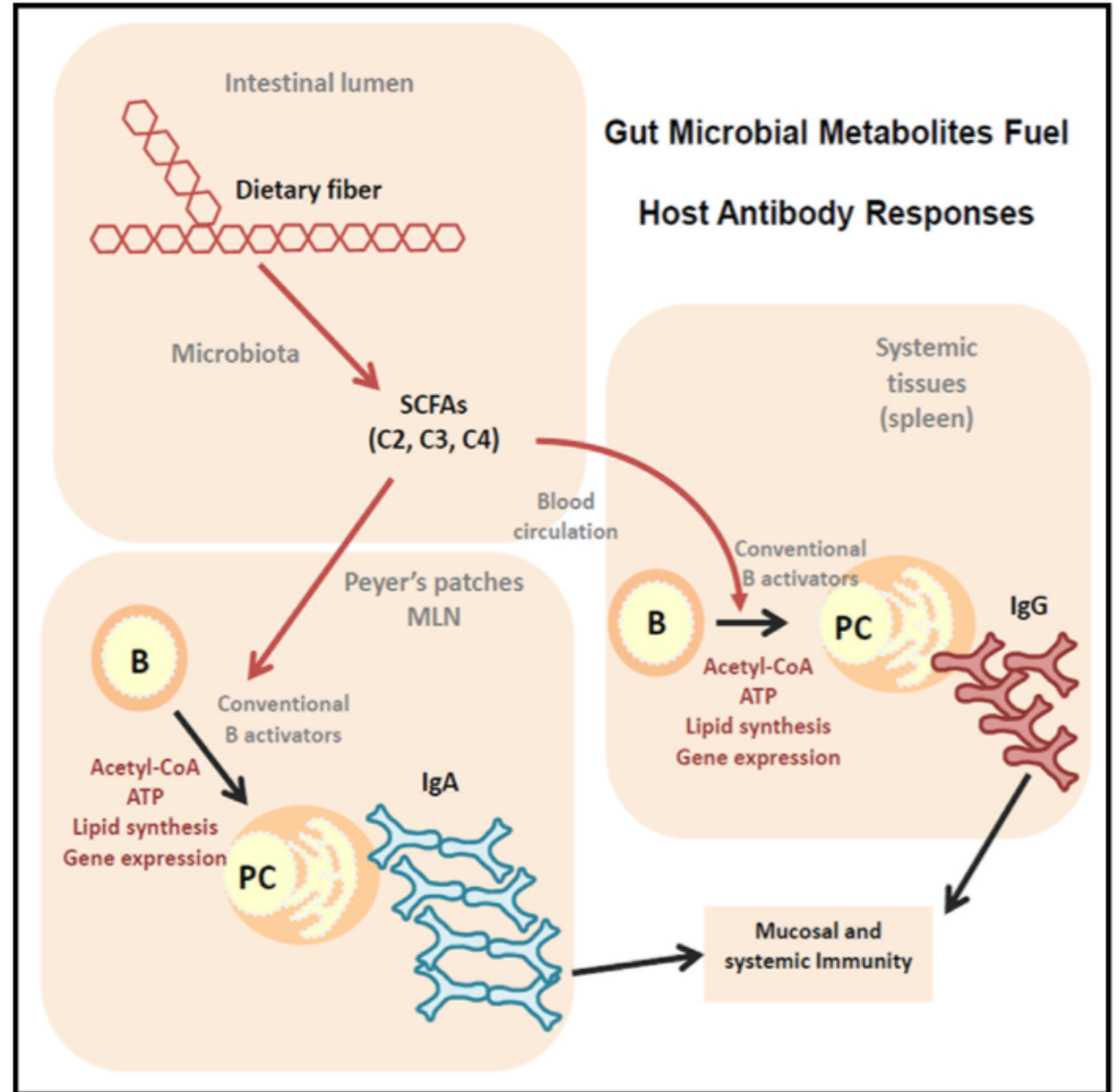
Potential effects of SCFAs on gut epithelial biology and immune cells.



Highlights

- SCFAs
 - Support host antibody production.
 - Increase acetyl-CoA and enhance metabolic sensors for energy and antibody production.
 - Control gene expression for plasma B differentiation.
 - When it is reduced in mice can result with pathogen susceptibility.
 - Can restore immune deficiency.

Major Findings



References

- **Systemic antibody production by gut microbiota:** Zeng, M.Y., Cisalpino, D., Varadarajan, S., Hellman, J., Warren, H.S., Cascalho, M., Inohara, N., and Nunez, G. (2016). Gut microbiota-induced immunoglobulin G controls systemic infection by symbiotic bacteria and pathogens. *Immunity* 44, 647–658.
- **A positive correlation between dietary fiber intake and intestinal IgA levels:** Lim, B.O., Yamada, K., Nonaka, M., Kuramoto, Y., Hung, P., and Sugano, M. (1997). Dietary fibers modulate indices of intestinal immune function in rats. *J. Nutr.* 127, 663–667.
- **SCFAs are the main microbial metabolites of dietary fiber:** Macfarlane, S., and Macfarlane, G.T. (2003). Regulation of short-chain fatty acid production. *Proc. Nutr. Soc.* 62, 67–72.

2nd Paper

Colonic transit time is related to bacterial metabolism and mucosal turnover in the gut

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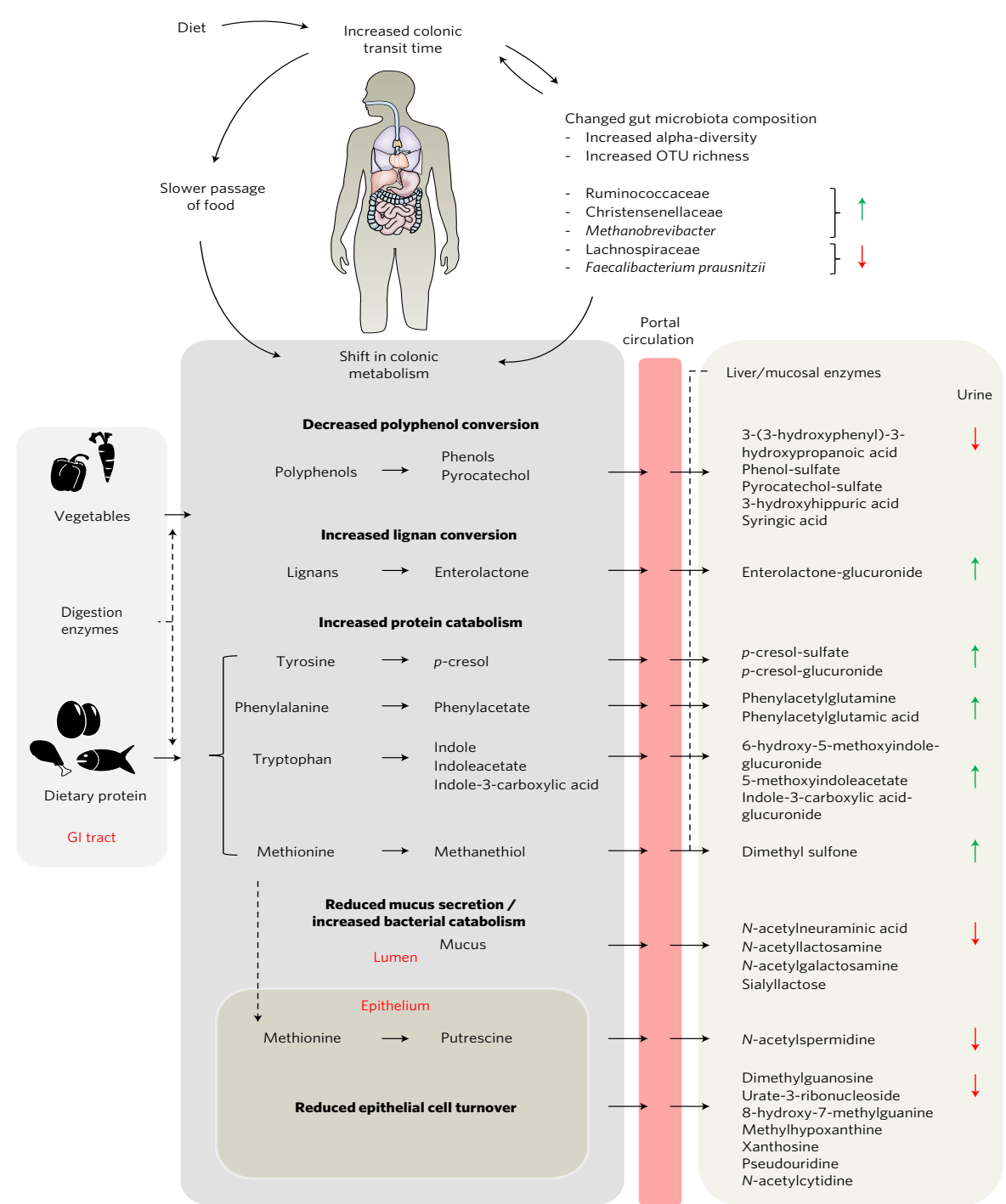
What we know and what we don't...

- A lack of knowledge on modulation of gut microbial metabolism by colonic transit time.
- A firm stool consistency correlates with a high gut microbial richness and favours several bacterial groups involved in colonic fermentation.
- In the colon, the transit of luminal material is considerably slower than in the small intestine.
- If carbohydrate depletion occurs, fermentation in the colon shifts to protein degradation, which results in a range of products including ammonium, hydrogen sulfide, SCFAs and branched-chain fatty acids.
- The bacterial protein degradation products are largely absorbed in the colon and metabolized in the mucosa and liver before being excreted into the urine
- Protein degradation products affect colonic epithelial cells and are associated with diseases such as colorectal cancer, chronic kidney disease and autism , although the mechanisms remain largely unknown.

Highlights

- Colonic transit time is associated with overall gut microbial composition, diversity and metabolism.
- A long colonic transit time associates with high microbial richness and is accompanied by a shift in colonic metabolism.
- A shorter colonic transit time correlates with metabolites possibly reflecting increased renewal of the colonic mucosa.
- Urinary metabolites are less associated with microbial richness than with colonic transit time.
- A healthy gut microbial ecosystem is also associated with colonic transit time.

Major Findings



References

- **Stool consistency as a major confounding factor affecting microbiota composition:** Vandeputte, D. et al. Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. *Gut* 65, 57–62 (2015).
- **The effect of gut microbiota on host metabolism by improving energy yield from food and modulating dietary or the host-derived compounds:** Tremaroli, V. & Bäckhed, F. Functional interactions between the gut microbiota and host metabolism. *Nature* 489, 242–249 (2012).
- **Butyrate and transit time:** Lewis, S. J. & Heaton, K. W. Increasing butyrate concentration in the distal colon by accelerating intestinal transit. *Gut* 41, 245–251 (1997).
- **Importance of diets on colonic function and metabolism:** Cummings, J. H., Hill, M. J., Bone, E. S., Branch, W. J. & Jenkins, D. J. The effect of meat protein and dietary fiber on colonic function and metabolism. II: Bacterial metabolites in feces and urine. *Am. J. Clin. Nutr.* 32, 2094–2101 (1979).