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Gut genomics

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Jonathan B Weitzman

Email: jonathanweitzman@hotmail.com

The human intestine is home to numerous populations of microorganisms, but we know little about how the gut **microflora** influence our physiology. As described in the February 2 **Science**, Hooper *et al.* took a **genomics approach** to investigate the affect of resident bacteria on host gene expression in the gut (*Science* 2001, **291**:881-884). The authors infected germ-free mice with the common gut bacterium *Bacteroides thetaiotaomicron* and measured host transcriptional responses using microarray analysis. They performed additional experiments using laser-capture microdissection and quantitative PCR to define the cells responsible for the specific responses. RNA from the ileum of colonized mice was compared with germ-free controls by analyzing about 25,000 mouse genes. Colonization affected the expression of host genes which play roles in several intestinal functions, including absorption, strengthening the mucosal barrier, angiogenesis and drug metabolism. Hooper *et al.* also observed species-specific responses, highlighting the complexity of host-microbial relationships.

References

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