

ENVIRONMENTAL MICROBIOLOGY

You are what you eat

“ contact with environmental microorganisms associated with ingested food tailors the metabolic capabilities of our resident gut microbiota ”

The bacteria in the human gut provide their host with energy by degrading dietary polysaccharides. Writing in *Nature*, Hehemann *et al.* now show that bacteria present in the gut of Japanese individuals have acquired a carbohydrate-degrading enzyme from marine bacteria that allows them to degrade a polysaccharide found only in seaweed.

While investigating the carbohydrate-active enzymes present in *Zobellia galactanivorans*, a member of the marine Bacteroidetes, Hehemann *et al.* identified five putative enzymes that distantly resembled glycoside hydrolases of the GH16 family but lacked the residues that provide specificity for carbohydrates such as agarose or κ -carrageenan that are found in marine algae. Two of these enzymes were cloned and purified and then screened against a range of natural polysaccharides extracted from various marine macrophytes. The authors found that the enzymes were active only against extracts from red algae of the genus *Porphyra*, which contain high levels of the polysaccharide porphyran, leading the authors to classify these enzymes as the first β -porphyranases to be identified and to name them PorA and PorB.

The authors then determined the crystal structures of PorA and PorB, identified the key regions of the proteins that were important for binding to porphyran and

used this information to screen sequence databases for other putative β -porphyranases. They found six candidates, five of which were present in marine bacteria. Interestingly, one candidate (Bp1689) originated from *Bacteroides plebius*, a bacterium isolated from the intestinal microbiota of Japanese individuals. To test whether porphyranases are common in Japanese gut bacteria, Hehemann *et al.* analysed the gut metagenome data from 13 Japanese individuals, identifying 7 different β -porphyranases in 4 individuals. By contrast, the gut metagenomes of 18 individuals from North America contained no β -porphyranases. Therefore, bacteria that have acquired porphyran-degrading enzymes, most likely through horizontal gene transfer from a marine bacterium, are common in the gut microbiota of Japanese individuals, whose daily diet includes porphyran-containing seaweeds.

These findings suggest that contact with environmental microorganisms associated with ingested food tailors the metabolic capabilities of our resident gut microbiota, meaning that there is some truth in the old adage, ‘you are what you eat’.

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ORIGINAL RESEARCH PAPER Hehemann, J. H. *et al.* Transfer of carbohydrate-active enzymes from marine bacteria to Japanese gut microbiota. *Nature* **464**, 908–912 (2010)



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