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Gut microbes: What's your type?

By Eryn Brown, Los Angeles Times

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When European researchers set out to use gene sequencing to catalog the hundreds of species of microbes in the human gut, they expected to find variation between individuals and perhaps even between geographic groups -- but they assumed that there would be a large number of different possible combinations of bacteria.

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Instead, said bioinformatics expert Peer Bork of the European Molecular Biology Laboratory in Heidelberg, Germany, gut bacteria seem to cluster into just three distinct and stable combinations that show up across populations from a variety of backgrounds -- a discovery that could have implications for medicine in the future.

The results were published Wednesday in the journal *Nature*.

Bork, the senior author of the paper, said that finding the three enterotypes (as the team called them) was "a big surprise...we expected more variation."

To find out what microbes were present in the samples, the team took stool samples from 22 European individuals, extracted the DNA, and then attempted to determine the composition of the DNA. That's more complicated than it sounds. Unlike describing the DNA of a single individual, they were looking at gene fragments from hundreds of organisms (mostly bacteria) per sample. They used powerful computers to sort the fragments and match them to the DNA of known organisms. They also compared what they found with published results from Japanese and American subjects.

The three distinct microbe combinations appeared throughout the samples.

"This was a mammoth study," said Russell Doolittle, a molecular biologist and bioinformatics pioneer at UC San Diego. "I can't exaggerate the complexity of keeping [these data] all straight."

Aside from being a technical feat, the discovery of the enterotypes might be useful for diagnosing and treating disease, if Bork and the European team can correlate the three microbe types to "host properties" -- if, for example, it is someday found that people with one disease or characteristic all share enterotype A and people with another all share enterotype B, and so on.

For now, Bork said, the team did not find such global correlations. "We have no clue what is driving the three types," he said. But he added that they did find genes within the enterotypes that matched up with host properties such as age -- hinting at the potential for using gut flora to identify disease sometime in the

future.

Bacteria serve an important function in the human digestive system. They help the body process food and acquire nutrients and vitamins. Researchers have begun to find links between gut microbes and diseases including obesity, cancer and perhaps most notably, peptic ulcers, which are caused by a bacterium called *Helicobacter pylori*.

"We hope there's an application" for this finding, Bork said. If physicians knew a diseased patient's original gut microbe profile, for example -- much as they now take note of a person's blood type -- they might be able to shift his gut microbes back to their original state to treat the illness, he suggested. Or, since it's known that different microbes help the body process drugs differently, doctors might be able to prescribe the medications that work best for a patient's enterotype.

Companies peddling probiotics are keen on the research, too, he added. "Yogurt companies are extremely interested," he said.

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