

What cures you may also ail you: Antibiotics, your gut and you

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We are always being told by marketers of healthy yogurts that the human gut contains a bustling community of different bacteria, both good and bad, and that this balance is vital to keeping you healthy. But if you target the disease-causing bacteria with medicine, what might be the collateral damage to their health-associated cousins that call the human body home?

A new study by Les Dethlefsen et al, to be published this week in the online open-access journal *PLoS Biology*, looks into the changes that happen in the human gut when it is exposed to the widely used antibiotic, ciprofloxacin. Ciprofloxacin is prescribed for a number of conditions, including common afflictions such as urinary tract infections. It was previously believed to cause only modest harm to the abundant beneficial bacteria of the human body.

To investigate ciprofloxacin's effect on health-associated bacteria a team of researchers, led by Dr. David Relman of Stanford University, catalogued types of bacteria present in the faeces of volunteers who were undergoing a course of treatment of ciprofloxacin. The DNA-analysis technique, massively-parallel pyrosequencing, was central to their approach, which is outlined in a companion paper scheduled for publication in *PLoS Genetics* on Friday the 21st of November. With this technique, the researchers examined the diversity and abundance of bacteria present in human faeces, identifying over 5,600 different bacterial species and strains. The dramatically increased detection power of this approach allowed the team to track carefully the changes in the

gut's bacterial community both during and after the course of treatment.

The study found that while the patients were undergoing treatment the overall abundance of approximately 30% of the species and strains was significantly affected. The effects varied greatly between individuals, with two of the subjects showing a strong reduction in diversity. The effects didn't stop there. Once the course of treatment had been halted, it took up to four weeks for most strains of gut bacteria to return to their pre-treatment levels. Even six months later, some types of bacteria had not managed to return to pre-treatment abundance levels. During this time of population upheaval none of the patients in the study reported signs of gut-related problems.

The bacteria present in the human gut are responsible for various aspects of host nutrition, metabolism and immune responses. This study reveals aspects of resiliency in the indigenous microbiota when subjected to perturbation, but underlines the concern that antibiotic treatment, especially when prolonged or repeated, may have long-lasting effects on overall wellbeing that could go un-noticed.

Citation: Dethlefsen L, Huse S, Sogin ML, Relman DA (2008) The pervasive effects of an antibiotic on the human gut microbiota, as revealed by deep 16S rRNA sequencing. PLoS Biol 6(11): e280.

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