

# Disease-causing gut bacteria common in children

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A type of bacteria, which can cause diarrhea and inhibit growth in children in developing countries, has been found in 14% of a sample of children in an industrialized country. However, the children had only mild gastrointestinal symptoms or no symptoms at all. Understanding why is the next step for these researchers.

The [bacteria](#), called *Enteroaggregative E. coli*, can produce persistent diarrhea and inhibit the growth of children in developing [countries](#). These bacteria have also been linked to traveler's diarrhea and are behind large outbreaks of [diarrhea](#) in several industrialized countries. One outbreak in Germany in 2011 left 54 people dead, as the bacterial strain produced a particularly potent toxin. However, the bacteria can also reside in the gut of some carriers without producing any symptoms and so researchers are trying to identify which strains of *Enteroaggregative E. coli* and which other factors, such as nutrition and using antibiotics, result in diarrheal disease.

A team of Danish scientists has investigated the prevalence of the bacteria in the guts of children in daycare in Denmark. In research recently published in *Frontiers in Cellular and Infection Microbiology*, the team monitored 179 children from ages 0-6 for a full year. In that time, they monitored the presence of the bacteria in the gut of the children, using stool samples, and their parents noted any gastrointestinal symptoms in a questionnaire.

The team found that *Enteroaggregative E. coli* was highly prevalent, with

14% of the children who tested positive for the bacteria at some point during the yearlong study. Of the children who tested positive, 50% experienced some gastrointestinal symptoms, but these were mostly mild and the bacteria had no effect on the growth of the children. Numerous strains of *Enteroaggregative E. coli* were isolated from the children, and of these 35% were resistant to several types of antibiotics.

So given that the children who tested positive for *Enteroaggregative E. coli* did not present with serious symptoms, do we need to be concerned with these bacteria, drug resistant or not? Under normal circumstances, the microbes in the gut keep each other in balance by competing. However, when outside factors disrupt this balance, diarrheal disease can arise. Professor Karen A. Krogfelt, senior author on the study, tells *Frontiers Blog* that the results are of concern. "In most healthy children the bacteria will not cause harm due to the natural 'colonization resistance' provided by other types of bacteria in the gut. However, a small shift in the balance of the microbes in the gut (due to other treatments or changes in diet), and then the *Enteroaggregative E. coli* could take over and produce severe symptoms."

As 35% of the isolated *Enteroaggregative E. coli* strains were resistant to multiple antibiotics, treating the children with these antibiotics might have limited effects on the resistant bacteria, while killing many other types of bacteria in the gut. This could effectively kill off the competition, allowing the *Enteroaggregative E. coli* to take over.

Other factors that affect the ability of the bacteria to cause disease include strain-specific genetic features and the nutritional health of the [children](#), which may explain why the bacteria appear to cause more diarrheal disease in developing countries. The research team hopes to investigate these factors further. Professor Krogfelt advocates using probiotic agents and foods to provide microbial balance in the gut. This is particularly important following a course of antibiotics. The team

hopes that anti-bacterial drugs in the future will be more specific and be less disruptive to our gut microbes, making it more difficult for potentially dangerous bacteria, such as *Enteroaggregative E. coli*, to cause disease.

**More information:** Betina Hebbelstrup Jensen et al, Enteroaggregative *Escherichia coli* in Daycare—A 1-Year Dynamic Cohort Study, *Frontiers in Cellular and Infection Microbiology* (2016). [DOI: 10.3389/fcimb.2016.00075](https://doi.org/10.3389/fcimb.2016.00075)

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