

Enterotoxigenic *E. coli* worldwide are closely related

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The strains of enterotoxigenic *Escherichia coli* (ETEC) that infect adults and children in Asia, Africa, and the Americas, have notably similar toxins and virulence factors, according to research published ahead of print in the *Journal of Bacteriology*. That bodes well for vaccine development, says corresponding author Åsa Sjöling, now of the Karolinska Institutet, Stockholm, Sweden. ETEC infects 400 million people annually, or 5.3 percent of the world's population, killing 400,000.

In the study, Sjöling et al. set out to determine whether the heat labile toxin (LT) had become more toxic over time, and whether the bacterium had evolved to secrete more of it. LT causes the "travelers' diarrhea" that so frequently afflicts Americans abroad, and that plagues residents of many low and [middle income countries](#). But they found that over the 30 year period from which they had isolates, the two most potent toxin types, LT1 and LT2, had changed little but had spread globally.

"When new ETEC [strains](#) acquire either LT1 or LT2 they seem to have a much better chance to persist and spread," says Sjöling. Colonization factors, the compounds the bacterium uses to adhere to the lining of the human gut, also remained conserved over time, and the most common colonization factors identified globally were often associated with LT1 and LT2.

The research results from a collaboration between the University of Gothenburg (where Sjöling did this research), which has the world's

largest collection of ETEC strains, and sequencing experts at the Sanger Institute, Cambridge, UK. "We soon saw that strains with similar toxin variants and colonization factor profiles often remained closely related despite having been isolated on different continents, with time spans between those isolations ranging up to 30 years," says Sjöling.

The paper is published concurrently with a paper in *Nature Genetics* by many of the same authors. In that paper, investigators developed whole-genome sequence data for 362 ETEC strains over 30 years, in 20 countries. "This research strengthens our belief that it is possible to target a broad range of ETEC groups with one [vaccine](#)," says Gordon Dougan of the Sanger Institute, a coauthor of both papers.

"We believe that the vaccine developed at the University of Gothenburg will be protective and useful globally since this vaccine is based on the toxin types and colonization factors we found to be most successful worldwide," says Sjöling.

While ETEC was believed to vary widely from place to place, the *Nature Genetics* investigators traced many of the 21 lineages to an individual bacterium that acquired the genetic information needed to infect humans between 51 and 174 years ago, and then spread. That, in turn, suggests that the [bacterium](#) is stable, and that it is unlikely to become vaccine-resistant, and that the vaccine will be effective worldwide in both children and adults, says Sjöling.

Provided by American Society for Microbiology

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