

Diarrheagenic Potential of *Escherichia coli* in Children in a Developed Country

Escherichia coli is an underestimated diarrheal pathogen in developed countries. This organism may cause gastroenteritis by many different mechanisms, and on the basis of this, diarrheagenic *E. coli* has been subdivided into different groups, of which the most important ones are Shiga-toxigenic *E. coli*, enteropathogenic *E. coli* (EPEC), other attaching and effacing *E. coli* (A/EEC), enteroaggregative *E. coli* (EAEC), enterotoxigenic *E. coli*, and enteroinvasive *E. coli*. The latter two are associated with travel to less developed countries. Shiga-toxigenic *E. coli* is a well-established pathogen, whereas the pathogenic role of EPEC, A/EEC, and EAEC is less well established.

We read the paper by Pabst et al. in the June issue of the *Journal of Clinical Microbiology* (1) with great interest. The authors try to shed light on the role of diarrheagenic *E. coli* in Switzerland by using a case-control setup and molecular diagnostic methods for the identification of the different *E. coli* groups. However, the study has a couple of shortcomings that makes us wonder if all of the conclusions presented are correct.

Firstly, the authors do not take into account the potential bias of the travel history of the patients when comparing cases and controls. Travel may be an important confounder because none of the controls reported traveling, whereas travel was quite common among the patients; i.e., if a pathogen is more common in travelers than in patients with domestically acquired cases, it will not be possible to ascertain the relative importance of travel if the patients are compared with a group of controls who have not traveled in a univariate analysis. A way of circumventing the problem would be to exclude the travel-associated cases from the analysis. In the case of EAEC, the number of patients who had traveled was 9 or 47%; the total number of diarrheal patients who had traveled was 31. It is thus possible to compare the occurrence of EAEC in patients and controls with no travel history: The prevalence in patients was 9 of 156, and that in controls was 3 of 137. This difference is not statistically significant ($P = 0.21$; Fisher's two-tailed exact test).

Secondly, the authors did not find any difference in the prevalence of EPEC between cases and controls. This conclusion may be questioned too, because the EPEC definition used is based solely on detection of the intimin gene (*eae*). In the definition of EPEC, the serotype of the strains should also be taken into account (2). We performed a study similar to that of Pabst et al. and found a strong correlation between disease in infants less than 2 years of age and EPEC, defined as *eae*-positive strains belonging to the classical EPEC O groups, whereas other A/EEC showed no correlation to disease (B. Olesen, P. Schiellerup, M. Helms, J. Neimann, F. Scheutz, and P. Gerner-Smidt, Abstr. 12th Eur. Congr. Clin. Microbiol. Infect. Dis., abstr. P607, 2002). Classical EPEC is the most common bacterial cause of diarrhea in children less than 2 years old in Denmark. We wonder if Pabst et al. would have reached the same conclusion had they serotyped their *eae*-positive isolates.

REFERENCES

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Authors' Reply

We thank P. Gerner-Smidt et al. for the interest conferred on our study (3). They are indeed right in stating that travel history is a confounder and that the difference in the prevalence of EAEC among children with and without diarrhea is not statistically significant anymore after the exclusion of patients with a travel history. However, there is still a clear trend that is confirmed by previous studies showing a significantly higher prevalence of EAEC among children who acquired their infections in Western Europe than among controls (1).

The second point raised concerns the definition of EPEC. This has been debated for a long time, with particular serogroups and the presence of the intimin gene (*eae*) or the bundle-forming pilus gene (*bfp*) being among the factors considered to be important. In our study, as described in Materials and Methods, we did not check single colonies and thus were not able to do serotyping. We based our diagnosis of EPEC on the detection of *eae* and the absence of genes coding for verotoxins. When *eae* and genes coding for verotoxins could be detected in a single stool specimen, it was interpreted as containing EHEC. On the basis of this procedure, no significant difference was found between patients and controls. The serologic workup of *eae*-positive bacteria by Gerner-Smidt et al. shows very interesting results that point in the direction that the presence of the *eae* gene in *E. coli* is necessary but not sufficient to be regarded as EPEC. Possibly, we might have found differences in the prevalence of certain EPEC serotypes

in our analysis, too. However, serotyping is no longer absolutely necessary to diagnose EPEC (2), nor is it practical in a diagnostic setting.

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