

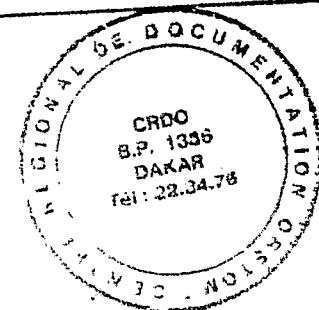
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Table 1: Identification of *Salmonella* and *Shigella* spp. among 3,897 lactose-negative strains from stool specimens using the API Z system.

Results after 2 h (API Z)	Results after 24 h (reference method)
Not <i>Salmonella</i> or <i>Shigella</i> spp. 2,653 (68.1 %)	<i>Salmonella</i> spp. 401 (10.2 %)
<i>Pseudomonas aeruginosa</i> 71 (8.8 %)	<i>Shigella sonnei</i> 4
Probably <i>Salmonella</i> spp. 404 (10.4 %)	<i>Yersinia enterocolitica</i> 1
No identification 769 (19.7 %)	<i>Salmonella</i> spp. 12 (0.3 %)
	<i>Shigella</i> spp. 82 (2.1 %)
	Commensal bacteria 670



dysenteriae strains which produce β -galactosidase. The fifth enzyme is an esterase produced by *Salmonella* spp. In cupule B the oxidase test is performed to identify those *Pseudomonas aeruginosa* strains which also produce esterase.

Each of the five strains to be tested was inoculated in a pair of cupules and incubated at 37 °C for 2 h. The results are summarized in Table 1. After 2 h, 2,724 of the strains (69.9 %) could be excluded, 71 of these were *Pseudomonas aeruginosa* strains. Results indicated that 404 (10.4 %) of the strains were probably *Salmonella* spp.; further tests confirmed the identification in 401 strains. Of the 769 strains (19.7 %) which could not be identified by the API Z system, further tests indicated that four were *Shigella sonnei* strains, twelve were *Salmonella* spp., 82 were *Shigella* spp., one was a *Yersinia enterocolitica* strain and the remaining 670 strains were commensal.

The classical technique for identifying *Salmonella* and *Shigella* spp. among lactose negative strains is the urease test. Although this method is rapid, cheap and easy to perform, it eliminates only the *Proteus* spp. Other members of the intestinal flora such as *Enterobacter*, *Citrobacter*, *Serratia*, and *Klebsiella* spp. and *Pseudomonas aeruginosa* (5) are not eliminated by the urease test. The advantage of the API Z system lies in the fact that a large number of commensal bacteria can be eliminated within 2 h in addition to *Proteus* and *Providencia* spp.

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Campylobacter fetus subspecies *jejuni* in Senegal

Sir,

Campylobacter jejuni has been found to cause diarrhea in the developed countries (1-3) and also to play an important role in the pathogenicity of infectious diarrhea in Africa, e.g. in Rwanda (4), in the Gambia (5), Nigeria (6) and Zaire (7). Our study focused on the isolation frequency of this bacteria in Senegal. The results are part of a longitudinal study on the cause of infantile gastroenteritis in children from Pikine, a semi-urbanized suburb (625,000 inhabitants) located 15 km northeast of Dakar, Senegal.

From November 1981 to December 1982, 605 stools were collected from children aged 8 to 32 months. The culture medium for isolated *Campylobacter* was similar to Skirrow's medium, consisting of sheep blood agar plus vancomycin, polymyxin and trimethoprim (Campylosel Biomérieux). Cultures were grown in anaerobic jars with hydrogen + CO₂ atmosphere without catalysts (Gaspak BBL). Petri dishes with subcultures were incubated at 43 °C for 48 h.

Liquid or semi-liquid stools were considered diarrheic. There was no significant difference in the isolation

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Table 1: Isolation rate of enteric pathogens from diarrheic and non-diarrheic stools of children aged 8 to 22 months.

	<i>Campylobacter jejuni</i>	<i>Salmonella</i> spp.	<i>Shigella</i> spp.
Diarrheic stools n = 302 (49.9 %)	20 (6.6 %)	12 (4.0 %)	15 (5.0 %)
Non-diarrheic stools n = 303 (51.1 %)	(5.9 %)	(3.6 %)	(2.0 %)

frequency of *Campylobacter jejuni* from diarrheic or non-diarrheic stools. These findings agree with the results of Billingham (5) for children less than five years old in the Gambia, but contradict De Mol's observations in Rwanda and Zaire (4, 7). Our results suggest that either *Campylobacter jejuni* is not a universal pathogen or there are healthy carriers of *Campylobacter jejuni*, as is true for *Salmonella*, which were also isolated from the same children. Since the bacteria can be isolated for 2-7 weeks after cure of diarrhea, its presence in a non-diarrheic stool does not exclude the possibility of infection prior to collection of stool specimens. In seven children *Campylobacter jejuni* was reisolated after a few months. Since serotyping was not feasible, we were not able to determine whether healthy carriers are a potential reservoir.

Thus, although *Campylobacter* is frequently isolated from the stools of young children in Senegal, it does not seem to play a more pathogenic role than other bacteria causing infectious diarrhea. Nor is it more implicated than other bacteria as an indirect cause of severe malnutrition, as De Mol et al. (7) showed to be the case in Zaire. However, its precise role in the pathogenicity of infectious diarrhea still remains to be determined.

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A Modified Method for Testing the Antimicrobial Susceptibility of Anaerobic Gram-Positive Cocci

Sir,

Improved laboratory methods have resulted in increased frequency of isolation of anaerobic gram-positive cocci from clinical specimens (1, 5). Knowledge of their antimicrobial susceptibility patterns is very important. However, since a standardized procedure for testing antimicrobial susceptibility has not yet been accepted, the selection of antimicrobials for treatment of infections due to these organisms is still often empiric. Although the National Committee for Clinical Laboratory Standards (NCCLS) has addressed this problem by proposing a standardized protocol for susceptibility testing of anaerobic bacteria (2), the cultivation conditions recommended are not optimal for anaerobic gram-positive cocci. A precise methodology that accounts for changing susceptibility patterns and the emergence of resistant strains (3) should be developed to provide satisfactory treatment of infections in which these organisms are involved. Previous work in our laboratory resulted in a standardized cultivation procedure whereby maximum cell yield can be produced within 12-16 h for selected species of clinically significant anaerobic gram-positive cocci (4). We report here the susceptibilities of 202 clinical isolates (representing five species) of anaerobic gram-positive cocci to five of the most frequently prescribed antimicrobials for treatment of infections in

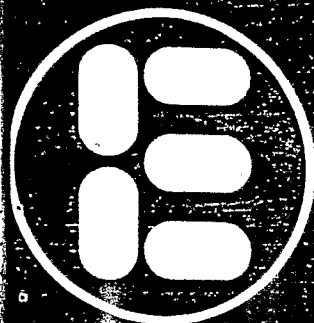
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