

CHARACTERIZATION OF BACTERIA ADHERENT TO COLONIC EPITHELIA OF PIGS WITH DYSENTERY

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Knowledge of microbes that inhabit the large bowel of swine has, for the most part, been limited to studies of fecal populations. Since nothing was known of bacteria attached to colonic epithelia, the present study was conducted to characterize populations at this site in healthy pigs and to compare these with populations from pigs with dysentery induced following oral inoculation with *Treponema hyodysenteriae*.

Colonic tissue from pigs (9-12 weeks old) were rinsed with PBS. Tissues from infected pigs were obtained 2-3 days after the onset of diarrhea. Five discs (12-mm diameter, cut with a cork borer) were placed in 100 ml of anaerobic mineral solution (AMS) and were washed by shaking. Discs were transferred to a second 100 ml volume of AMS and blended for 2 min in a Waring blender that was being flushed with CO₂. Hungate anaerobic roll tube methods were used for preparation of dilutions in AMS and for culturing in a 40% rumen fluid-based medium (medium CCA).

Two hundred ninety isolates from the 7 pigs in this study were grouped using classification criteria described in the VPI Anaerobe Laboratory Manual or other published data (Tables 1 and 2). Many of the isolates have as yet only been identified to the genus level.

Isolates characterized as *Streptococcus* accounted for 55% of the isolates from normal pigs, but were only isolated from 1 of the 4 pigs with dysentery. Most of the streptococci were ureolytic strains. They were anaerobic to aerotolerant with morphological and physiological properties typical for streptococci. Alpha hemolysis was observed and lactic acid was the major fermentation product. Extracted antigens reacted with Lancefield's group G antisera, but a species designation for these has not been made.

The predominant organism associated with colonic epithelia tissue from pigs with dysentery (Table 2) was not detected as part of the population from normal pigs and is a new species that we have designated as *Acetivibrio ethanolgignens*. *Acetivibrio ethanolgignens* are obligately anaerobic, gram-negative, motile, curved rods and produce ethanol and acetate as main fermentation products from carbohydrates. The role of this organism (if any) in the pathogenesis of swine dysentery is not known.

It is evident that the predominantly gram-positive population attached to colonic epithelial tissue of normal pigs is replaced by a predominantly gram-negative population following infection by *T. hyodysenteriae*. The factors which cause these changes and significance of the changes are not as yet understood.

Selected references: Robinson, I.M., Allison, M.J., and Bucklin, J.A.: Appl. Environ. Microbiol. 1981, 41:950; Robinson, I.M. and Ritchie, A.E.: Intern. J. Syst. Bact. 1981, 31:333; Allison, M.J., Robinson, I.M., Bucklin, J.A., and Booth, G.D.: Appl. Environ. Microbiol. 1979, 37:1142; Russell, E.G.: Appl. Environ. Microbiol. 1979, 37:187; Salanitro, J.P., Blake, I.G., and Muirhead, P.A.: Appl. Environ. Microbiol. 1977, 33:79; McAllister, J.S., Kurtz, H.J., and Short, E.C., Jr.: J. Anim. Sci. 1979, 49:868.

TABLE 1
Distribution of Bacteria Adherent to Colonic Epithelia of Normal Pigs

Bacterial Group	No. of Isolates From Pig No.:			% of Flora 3 Pigs
	1	2	3	
	<i>Streptococcus</i> (ureolytic)	31	5	
<i>Bacteroides</i>	9	5	8	16.8
<i>Lactobacillus</i>	0	14	1	11.5
<i>Streptococcus</i>	5	1	2	6.1
<i>Selenomonas ruminantium</i>	1	3	2	4.5
<i>Bifidobacterium</i>	0	1	1	1.5
<i>Fusobacterium prausnitzii</i>	0	1	1	1.5
<i>Anaerovibrio lipolytica</i>	0	0	1	0.8
<i>Gemminger formicilis</i>	0	0	1	0.8
<i>Coprococcus</i>	0	1	0	0.8
<i>Eubacterium</i>	0	1	0	0.8
<i>Eubacterium aerofaciens</i>	1	0	0	0.8
<i>Peptostreptococcus productus</i>	1	0	0	0.8
<i>Peptococcus asaccharolyticus</i>	1	0	0	0.8
<i>Bacteroides amylophilus</i>	1	0	0	0.8
Unclassified	0	3	1	2.3
TOTAL ISOLATES 131				

TABLE 2
Distribution of Bacteria Adherent to Colonic Epithelia of Pigs With Dysentery

Bacterial Group	No. of Isolates From Pig No.:				% of Flora 4 Pigs
	1	2	3	4	
	<i>Acetivibrio ethanolgignens</i>	11	19	10	
<i>Selenomonas ruminantium</i>	5	6	12	2	15.7
<i>Escherichia coli</i>	18	3	3	0	15.1
<i>Fusobacterium plauti</i>	1	0	10	8	11.9
<i>Fusobacterium</i>	0	0	5	8	8.2
<i>Bacteroides</i>	1	5	0	4	6.3
<i>Streptococcus</i> (ureolytic)	0	10	0	0	6.3
<i>Clostridium</i>	5	0	0	0	3.1
<i>Anaerovibrio lipolytica</i>	0	0	0	3	1.9
<i>Bacteroides multiacidus</i>	0	0	0	1	0.6
<i>Desulfomonas pigra</i>	0	0	0	1	0.6
<i>Peptostreptococcus productus</i>	0	1	0	0	0.6
Unclassified	0	1	0	4	2.5
TOTAL ISOLATES 159					