Composition of intestinal *Enterobacteriaceae* populations of healthy domestic pigs

Peter Schierack,¹ Nicole Walk,¹ Katja Reiter,² Karl D. Weyrauch² and Lothar H. Wieler¹

¹Institut für Mikrobiologie und Tierseuchen, Freie Universität Berlin, Philippstr. 13, 10115 Berlin, Germany
²Institut für Veterinär-Anatomie, Freie Universität Berlin, Koserstr. 20, 14195 Berlin, Germany

In this study, the *Enterobacteriaceae* microbiota, including their diversity as well as the distribution of haemolytic and virulence gene-harbouring *Escherichia coli* of 56-day-old healthy piglets, was characterized. Both the composition and the diversity of *Enterobacteriaceae* populations varied considerably between individual pigs and intestinal sections. *E. coli*, *Enterobacter cloacae*, *Citrobacter freundii* and *Klebsiella pneumoniae* dominated the *Enterobacteriaceae* microbiota. However, mucosa-associated *Enterobacteriaceae* were scarce or in some cases undetectable. The majority of *E. coli* clones from the jejunum were also found in the colon, with up to 10 different *E. coli* clones in one intestinal section. Other *Enterobacteriaceae* species were represented by only one clone localized to one intestinal section. While several piglets did not harbour virulence gene-positive or haemolytic *E. coli*, such strains dominated intestinal sections of other animals. This study reveals that the diversity of intestinal *Enterobacteriaceae* is clearly individual. In general, *Enterobacteriaceae* do not appear to be a consistent fraction of the microbiota of the jejunum. High numbers of adherent bacteria do not appear to be essential for successful intestinal colonization, and *E. coli* clones do not necessarily colonize distinct intestinal sections based on the particular phylogenetic affiliation. Furthermore, dominance of haemolytic or virulence gene-positive *E. coli* does not correlate with disease. Finally, probiotic *Enterococcus faecium* feed supplementation does not affect the *Enterobacteriaceae* microbiota.

**INTRODUCTION**

The family *Enterobacteriaceae* consists of many genera and strains that colonize the small and large intestine, and includes members of the non-pathogenic autochthonous (commensal) microbiota as well as pathogens. Several pathogenic *Enterobacteriaceae*, especially *Escherichia coli* strains, cause diarrhoea, urinary tract infections, mastitis, arthritis and meningitis in both humans and animals (Alexander, 1994; Ewers et al., 2007; Fairbrother et al., 2005; Hermansson et al., 1978; Kaper et al., 2004; Nagy & Fekete, 2005).

A number of studies of pathogenic *E. coli* have been performed, partly because *E. coli* is economically one of the most important pathogenic bacteria in pig production (Barth et al., 2007; Fairbrother et al., 2005; Nagy & Fekete, 2005; Wieler et al., 2001). However, few data are available on the composition of the commensal *E. coli* microbiota in pigs. The *E. coli* microbiota in pigs appears to be individual, dynamic and age-dependent (Katouli et al., 1995, 1999), and determinations of the *Enterobacteriaceae* microbiota are generally only snapshots of a highly dynamic intestinal steady state. It has also been reported that the *E. coli* microbiota in pigs is highly structured, and that different compartments of the gut are preferentially colonized by distinct phylogenetic *E. coli* clones (Dixit et al., 2004).

Compared to *E. coli*, there are very little data about other non-pathogenic or facultatively pathogenic *Enterobacteriaceae* species. The few studies deal almost exclusively with those associated with sporadic infections, virulence determinants, antibiotic resistance or metabolism. To our knowledge, data about their distribution in the intestine, ratios to other *Enterobacteriaceae* species and diversity under physiological conditions have not been reported.

The aim of this study was to evaluate the *Enterobacteriaceae* populations in healthy domestic pigs, with consideration of their intestinal distribution, relative ratios and diversity. *E. coli* isolates were further evaluated for the presence of virulence genes, haemolysis and phylogenetic affiliation. In
addition, the effects of probiotic Enterococcus faecium feed supplementation on the Enterobacteriaceae microbiota were examined.

**METHODS**

**Animal housing.** Piglets (hybrids of Deutsche Landrasse and Duroc) were stalled in groups and fed according to the National Research Council (NRC) recommendations (National Research Council, 1998). Piglets had ad libitum access to feed, with (probiotic piglets) or without (control piglets) probiotic supplementation. The principal components of the liquid diet were wheat and soybean. The administration of antibiotics was prohibited for both sows and piglets for at least 3 months prior to the trial. In addition, the health status of piglets was monitored for signs of clinical illness. The study was approved by the local animal welfare committee of the Federal Ministry of Agriculture, Food and Consumer Protection, Germany (no. G0037/02).

The probiotic strain Ent. faecium SF68 (NCIMB 10415; Benyacoub et al., 2003; Wunderlich et al., 1989) was obtained from a commercial batch of the feed additive Cylactin (Cerbios-Pharma). The mean concentration of the Ent. faecium in the feed was 2.0 ± 0.4 × 10^7 viable cells per gram food, as determined by colony hybridization (Macha et al., 2004). Supplementation resulted in approximately 10^8 c.f.u. (g wet weight)^−1 of Ent. faecium SF68 in faeces of probiotic piglets. The absence of the probiotic strain in control piglets was confirmed in random faecal samples.

**Cultivation of Enterobacteriaceae.** Enterobacteriaceae were isolated from either the distal jejunum (50 cm proximal to the Plica ileoceleacalis) or the proximal colon (apex of the ascending colon) of piglets from different litters. The distal jejunum was chosen as representative of the small intestine, since the more proximal jejunum generally contained no intestinal contents, and bacteria of different sections of the small intestine are thought to be similar (Dixit et al., 2004). The proximal colon was chosen as part of the large intestine, as other authors have found a uniformity of bacterial adhesion at a number of sites of the large intestine, indicating that small biopsy samples are likely to be representative of wide areas of the gut epithelium (Hartley et al., 1979; Swidsinski et al., 2002). Piglets aged 56 days post-partum were euthanized by injection with sodium Pentobarbital, and clamped intestinal sections were removed for bacterial isolation from intestinal contents. Enterobacteriaceae were isolated from intestinal contents and mucosa and plated by serial dilutions on Gassner agar plates. Bacteria from the mucosa included bacteria associated with mucus and epithelial cells.

Mucus and epithelial cells were derived from an ~2 × 5 cm section of intestinal tissue, as described elsewhere (Solano-Aguilar et al., 2000). Briefly, sections of intestinal tissues were washed twice in PBS to remove visible faecal material. Tissues were transferred to an Erlenmeyer flask containing 25 ml PBS and incubated for 5 min (220 r.p.m., 37 °C). It was expected that these short washing steps would not affect mucosa-attached bacteria, as other authors have reported high numbers of mucosa-attached or epithelial cell-attached E. coli even after four to six changes of physiological saline washes (Hartley et al., 1979; Swidsinski et al., 2002). The resulting suspension was removed and plated to Gassner agar plates. For mucus extraction, tissues were incubated in 25 ml Hanks' balanced salt solution/DTT [HBSS-DTT; HBSS without Ca^2+ and Mg^2+ (Cambrex), 2 mM DTT, 0.01 mM HEPES] for 10 min (220 r.p.m., 37 °C). The suspension was passed through sterile 210 μm nylon mesh (Sefar) and plated to Gassner agar plates. For epithelial cell isolation, washed tissues were incubated with 25 ml HBSS-EDTA (HBSS without Ca^2+ and Mg^2+, 1 mM EDTA, 1 mM HEPES) for 45 min (220 r.p.m., 37 °C). The suspension was passed through sterile 210 μm nylon mesh and plated to Gassner agar plates. Three additional controls were performed to determine the reliability of the procedure with respect to isolation of Enterobacteriaceae associated with epithelial cells: (1) solutions were sporadically tested for the presence of epithelial cells by light microscopy; (2) tissue sections were directly laid on Gassner agar plates after the last wash step to transfer attached bacteria; and (3) approximately 1 g mucosal tissue was homogenized in PBS after the second wash with a Dounce homogenizer, and homogenates were plated to Gassner agar plates.

Enterobacteriaceae-like colonies on Gassner agar plates were randomly picked and replica-plated to CHROMagar Orientation plates (Merlin et al., 1996). The differences in the numbers of tested isolates between pigs and intestinal sections were due to the substantial variation in the absolute numbers of mucosa-attached bacteria from each pig. Blue/green/yellow Enterobacteriaceae-like colonies on Gassner agar plates that appeared violet on CHROMagar Orientation plates were initially defined as E. coli. The haemolytic activity of these colonies (n=3471) was tested on sheep blood agar plates. After macrorestriction analysis of 643 E. coli isolates, each clone determined was finally verified as E. coli using LIM agar, Kligler agar, urea agar, citrate agar and malonate liquid culture. Blue/green/yellow Enterobacteriaceae-like colonies on Gassner agar plates which were blue or white on CHROMagar Orientation plates were initially defined as bacteria other than E. coli. After macrorestriction analysis, non-E. coli clones were finally tested using API 20E (bioMérieux) tests for further species identification. Four E. coli isolates initially isolated from the jejunum of piglet A were not recovered after storage and were therefore not included in the data shown.

**Scanning electron microscopy and periodic acid–Schiff (PAS) staining.** Intestinal segments were cut open lengthwise at the antimesenterial side, washed twice in PBS to remove visible faecal material, and fixed in 0.1 M cacodylate buffer, 2% paraformaldehyde, 2.5% glutaraldehyde (pH 7.2). Samples were post-fixed in 1% osmium tetroxide. After dehydration in a graded series of ethanol and hexamethyldisilazane (HMDS; Roth), they were mounted on aluminium stubs, sputter-coated with gold and finally examined using a scanning electron microscope (Nanolab 2000, Bausch & Lomb). For the PAS reaction after washing, segments were fixed in 4% paraformaldehyde and embedded in paraffin. Mucopolysaccharides were demonstrated using PAS reagents (Merck).

**Virulence gene and ECOR (E. coli Reference Collection) group determinations using PCR.** The presence of virulence genes associated with porcine pathogenic E. coli, fseG, fanA, fasA, fedA, fimF41a (F4, F5, F6, F18, F41 fimbriae), stx2e (shiga-toxin 2e), est-Ia, est-II (heat-stable toxins 1 and 2) and estB-lp (heat-labile toxin), was determined by PCR for all E. coli clones isolated, as previously described (Moon et al., 1999; Schierack et al., 2006). The E. coli phylogenetic groups of all detected clones were determined by PCR, as described by Clermont et al. (2000).

**Discrimination of Enterobacteriaceae strains by macrorestriction analysis and calculation of diversity.** Enterobacteriaceae colonies were differentiated by macrorestriction analysis (PFGE), as previously described (Moser et al., 2002). Bacterial DNA was digested with XbaI (Promega). If the macrorestriction patterns of isolates did not differ by more than one band, these isolates were considered to belong to a single clone. The diversity of the coliform bacteria was determined using Simpson’s index of diversity (D) as described elsewhere (Hunter & Gaston, 1988; Katouli et al., 1999). This calculation allows comparisons of the diversity of populations to be made, even where different numbers of isolates are included.
RESULTS

Comparison of Enterobacteriaceae populations between probiotic and control piglets

The 15 piglets included in this study showed no clinical symptoms of disease. There were also no obvious differences between animals of the probiotic and the control groups with respect to the numbers, composition, mucosal attachment, intestinal distribution or diversity of intestinal Enterobacteriaceae, or the occurrence of virulence gene-positive and haemolytic E. coli (Table 1, Figs 1 and 2, Supplementary Figs S2 and S3). Further analyses of the Enterobacteriaceae from both groups were therefore based on pooled samples, which were treated as a representative population.

Sporadic absence of Enterobacteriaceae in the distal jejunum; comparative characterization of colonies from the mucosa with those from intestinal contents

In four cases, we were unable to isolate any Enterobacteriaceae from the distal jejunum of the animals. Although high numbers of Enterobacteriaceae from intestinal contents of other animals were detected, generally only low numbers of bacteria associated with the mucus and the epithelial-cell fractions from these same animals were isolated (Table 1). We therefore tested the applicability of the established protocol. Treatment of the mucosa with EDTA-containing solutions resulted in the release of single epithelial cells, and this was confirmed using light microscopy. The numbers of bacterial colonies per mucosal sample (mucus plus epithelial cells) were similar using the physiological buffer and EDTA solutions compared to tissue homogenization with a homogenizer. If no bacteria were detectable with the physiological buffer and EDTA solutions and tissue homogenization with a homogenizer, no bacteria were detected after direct contact-transfer of tissues to Gassner agar plates. Using electron microscopy, it was shown that even the first washing step removed a considerable proportion of the secreted mucins, although remnants remained visible (see Supplementary Fig. S1A, B). Cell-bound mucins were not removed, as confirmed in parallel studies using PAS staining.

High numbers of bacteria associated with the mucosa were only found sporadically, including bacteria associated with the remaining secreted mucins, cell-bound mucins and glycocalyx. As shown in Table 1, the numbers of associated Enterobacteriaceae varied considerably, with large differences from animal to animal that appeared to be species-dependent. Even when strong attachment was observed, \(<10^{-4}\) attached bacteria per epithelial cell was determined. From 11 animals, \(<100\) colonies were isolated from the mucosa of the jejunum, corresponding to \(<10^{-9}\) bacteria per epithelial cell. The low numbers of mucosa-associated Enterobacteriaceae were verified by scanning electron microscopy, which also showed only sporadically associated bacteria (see Supplementary Fig. S1C, D). Comparing the sparse colonies from the mucus with those from the epithelial-cell fractions, the diversity was similar, and often the same bacterial clones were detected in both fractions.

An obvious difference in the occurrence of clones between the intestinal contents and the mucosa was found in one jejunal sample. In all other samples, most clones were

<table>
<thead>
<tr>
<th>Sample</th>
<th>Piglet (control)</th>
<th>Piglet (probiotic)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A</td>
<td>B</td>
</tr>
<tr>
<td>Mucosa, jejunum</td>
<td>1.7×10^4†</td>
<td>1.1×10^3</td>
</tr>
<tr>
<td>Mucosa, colon</td>
<td>6.7×10^5</td>
<td>5×10^3</td>
</tr>
<tr>
<td></td>
<td>0</td>
<td>3.8×10^3</td>
</tr>
</tbody>
</table>

*Total numbers of mucosa-associated bacteria.
†92% C. freundii, 3% E. coli, 5% others, not defined.
‡95% Ent. cloacae, 5% E. coli.
§80% E. coli, 20% others, not defined.
‖92% E. coli, 8% Ent. cloacae.
¶84% K. pneumoniae, 16% E. coli.
found to be associated with both the mucosa and intestinal contents, and the dominant clones of the intestinal contents were the dominant clones of the mucosa. Likewise, the diversity of *E. coli* from both fractions was similar. For these reasons, and due to the low numbers of mucosa-associated bacteria, data for one intestinal section (mucosa and intestinal contents) were pooled for further comparison between the jejunal and the colonic sections.

**Identification and numbers of isolated Enterobacteriaceae**

In four animals, *Enterobacteriaceae*-like isolates were not detected in the jejunum. Whenever *Enterobacteriaceae* were cultivated from the jejunum of the other animals, *E. coli* was always present. In four animals, *Enterobacter cloacae* and/or *Klebsiella pneumoniae* and/or *Leclercia adecarboxylata* or *Citrobacter freundii* were also detected. Isolates of these species in some cases dominated the *Enterobacteriaceae* microbiota. In the colon, *Enterobacteriaceae*-like bacteria, including *E. coli*, were always present. In three animals, *Ent. cloacae* or *K. pneumoniae* were also detected, although these species did not dominate (Fig. 1).

**Diversity of Enterobacteriaceae other than *E. coli* and diversity of *E. coli* strains**

In contrast to *E. coli*, only one clone of each non-*E. coli* species was detected in a single animal (with the exception of one animal). In that animal, one specific *Ent. cloacae* clone was detected in the jejunum and a second *Ent. cloacae* clone in the colon. When *E. coli* was present in one intestinal section, in general more than one clone could be recovered. The diversity of *E. coli* was on average higher in the colon ($D_i=0.61 \pm 0.23$) than in the jejunum ($D_j=0.39 \pm 0.26$). The *E. coli* diversity was only sporadically higher in the jejunum than in the colon. *E. coli* clones from the jejunum were also found in the colon of the same animal. The occurrence of *Enterobacteriaceae* other than *E. coli* did not affect the diversity of *E. coli* (Fig. 2).

**Virulence genes in *E. coli* clones**

Virulence gene-positive *E. coli* were isolated from eight animals. These *E. coli* were always found in the colon, and in three of the eight animals also in the jejunum. Up to four different clones originating from one animal were virulence gene-positive, with virulence gene profiles *stx*2,
-Ia, est-II or est-Ia + est-II. In some cases, virulence gene-positive E. coli were also found to dominate the E. coli population (Fig. 2).

**Haemolytic E. coli**

Haemolytic E. coli were detected in seven animals. Such strains were occasionally also found to dominate the E. coli microbiota (see Supplementary Fig. S2). However, the occurrence of haemolytic E. coli did not affect the diversity of the E. coli population. None of the haemolytic E. coli possessed any of the tested virulence genes.

**ECOR groups of E. coli clones**

Isolates of each of the four ECOR groups were found in the jejunum as well as in the colon. ECOR group A isolates were mostly detected, regardless of which intestinal section was investigated, followed by ECOR groups B2, D and B1. Isolates from ECOR groups A, B2 and D were able to dominate the E. coli microbiota (see Supplementary Fig. S3).

**DISCUSSION**

This study indicates that the intestinal Enterobacteriaceae population of pigs is highly individual. If Enterobacteriaceae were isolated, E. coli was always isolated and dominated most samples. The most common member of the Enterobacteriaceae of the porcine intestine was E. coli, consistent with a previous study of 642 Australian mammals in which E. coli was the most common of the 24 enteric species recovered (Gordon & FitzGibbon, 1999). However, in several samples, E. coli numbers were lower than numbers of Ent. cloacae, K. pneumoniae and C. freundii. The dominant species or single dominating E. coli clone of an intestinal section was not necessarily found in the other intestinal section. Many different clones of E. coli were found to colonize the intestinal tract of pigs, whereas other Enterobacteriaceae species were always found to be represented by a single clone in an intestinal section. Two possible explanations could be advanced for the latter observation: either only one clone of a species other than E. coli colonizes an intestinal section, or only one clone always dominates, such that other clones are not detectable.
However, both possibilities are conceivable, since Enterobacteriaceae species other than E. coli can also be highly diverse in animal populations. In a previous study, the genome diversity of intestinal Enterobacteriaceae from a variety of Australian mammals was estimated, and a high diversity among species was reported, with C. freundii exhibiting the highest diversity (Gordon & Lee, 1999).

E. coli, Ent. cloacae, K. pneumoniae and C. freundii can all be isolated as dominant Enterobacteriaceae in pigs. Information about the distribution in hosts of Enterobacteriaceae other than E. coli generally relates to pathogenicity. Ent. cloacae, K. pneumoniae, C. freundii and L. adecarboxylata are thought to be opportunistic pathogens. Most data about these species relate to human infection (de Baere et al., 2001; Fattal & Deville, 2000; Kumar & Sharma, 1978; Omwandho et al., 2006; Scheld & Tyson, 1979; Temesgen et al., 1997; Tschape et al., 1995). Data from pigs are not available, are very scarce or have not been related to infection or distribution in the intestine (Bertschinger et al., 1977; Ross et al., 1975). In this study it was shown that the porcine intestine is a source of all these different Enterobacteriaceae species. However, while they successfully colonize the intestine, they do not appear to affect the health of their hosts, despite high numbers.

The occasionally poor yield of mucosa-associated Enterobacteriaceae contrasts with previous reports, in which 10^3–10^5 E. coli per gram mucosal tissue was found even after four to six physiological saline washes (Hartley et al., 1979; Swidsinski et al., 2002). In four mucosal samples were more than 10^3 Enterobacteriaceae per gram isolated, despite the high recovery of Enterobacteriaceae in intestinal contents. Although the secreted mucin layer could have been removed by the two short washes, bacteria attached to the remaining secreted mucin layer or to the surface of the epithelial cells were never detected in high numbers. We conclude that Enterobacteriaceae do not necessarily have to adhere to the mucosa in high numbers to successfully colonize the intestine.

Haemolysis by E. coli is thought to correlate with the presence of virulence genes and therefore with pathogenicity (Frydendahl, 2002). In a previous study, the majority of haemolytic E. coli clones isolated in a swine population were found to harbour no virulence genes and were therefore considered to be non-pathogenic (Schirack et al., 2006). In this study, seven animals harboured haemolytic E. coli in the jejunum and/or the colon. Confirming our previous results, these haemolytic clones did not harbour virulence genes. Furthermore, even when present in high numbers in a given intestinal section (up to 78 % of all E. coli isolates), these E. coli did not affect the health status of the piglets, which showed no signs of disease. Haemolysis alone would therefore appear not to be an indicator of virulence, and does not correlate with the presence of other virulence-related markers.

It is generally accepted that bacterial intestinal pathogens have to compete successfully with the autochthonous microbiota of the host, adhere to the intestinal wall and proliferate to cause disease. Most porcine pathogenic E. coli adhere to specific membrane receptors on villous enterocytes of the small intestine, and autochthonous bacteria have been shown to block adhesion of pathogenic bacteria to these receptors (Cox & Houvenaghel, 1993; Fujiwara et al., 1997; Schroeder et al., 2006). Likewise, other bacteria introduced into the intestinal microbiota can also affect the course of infection by intestinal pathogens. For example, it has been shown both in vivo and in vitro that probiotic bacteria can prevent infection and disease caused by Salmonella and pathogenic E. coli (Kleta et al., 2006; Schroeder et al., 2006). The presence of probiotics or the integrity of a ‘protective’ intestinal mucosa-associated microbiota have therefore been considered to be possibilities for the prevention of infection (Kühbacher et al., 2006). However, in this study, no or only very low numbers of Enterobacteriaceae in jejunal sections were detected. Even homogenized intestinal mucosa plated onto blood agar or CHROMagar plates was essentially bacteria-free, suggesting that this phenomenon might also apply to other bacterial species (e.g. lactobacilli or enterococci, which would be detectable on the CHROMagar plates). These observations suggest that the efficacy of the protective effects of specific established species in healthy individuals should be considered critically, as there are clear indications that no bacteria of otherwise abundant species are associated with intestinal sections.

Probiotic Ent. faecium supplementation showed no significant effect on the numbers and diversity of Enterobacteriaceae species, or on the total counts, diversity, haemolysis and distribution of virulence gene-positive E. coli. However, additional probiotic effects have recently been attributed to this strain (Lodemann et al., 2006; Pollmann et al., 2005; Taras et al., 2006), and Ent. faecium has been reported to reduce the incidence of potentially pathogenic E. coli, as defined by serotypes associated with disease (Scharé et al., 2005). Based on the results of this study, however, these probiotic effects are unlikely to be the result of general effects on the commensal Enterobacteriaceae microbiota. Ent. faecium might affect other intestinal bacterial species, as has been shown for other probiotics, e.g. lactobacilli, which increase the richness and diversity of intestinal bacteria (Kühbacher et al., 2006; Lan et al., 2004).

E. coli populations in swine have been reported to be highly structured in their intestinal distribution (Dixit et al., 2004). In this study, we found no association between the occurrence of E. coli clones in intestinal sections and a specific phylogenetic ECOR group. However, a few clones dominant in the jejunum were not detected in the colon when the diversity increased. Nonetheless, these clones might still successfully colonize the jejunum as well as the colon. We suggest that E. coli populations might not be as structured as previously proposed. Such associations between phylogenetically distinct animal/bacterial species and a specific biotope are based on the existence of spatially
determined habitats over long periods. This might not be an appropriate model for E. coli, since developments in animal production and breeding, changing feeding regimes and controlled housing conditions might have altered the intestinal milieu of swine and promoted colonization by more adaptive clones rather than distinct phylogenetic groups. In addition, E. coli can exchange genetic information, which also supports the establishment of E. coli in broadly varying habitats. We therefore consider it unlikely that specific clones are adapted to specific intestinal sections.

In conclusion, the Enterobacteriaceae microbiota of pigs is particular to the individual, and several different species can dominate. Attachment of bacteria to the mucosa in particular to the individual, and several different species and controlled housing conditions might have altered the intestinal milieu of swine and promoted colonization by more adaptive clones rather than distinct phylogenetic groups. In addition, E. coli can exchange genetic information, which also supports the establishment of E. coli in broadly varying habitats. We therefore consider it unlikely that specific clones are adapted to specific intestinal sections.

ACKNOWLEDGEMENTS

This work was supported by grant FOR 438/1-1 from the Deutsche Forschungsgemeinschaft. We thank A. Luebbe-Becker for identification of Enterobacteriaceae and K. Tedin (both Institut für Mikrobiologie und Tierseuchen, Berlin) for carefully reading the manuscript.

REFERENCES


Kumar, A. & Sharma, V. K. (1978). Enterobacteria of emerging pathogenic significance from clinical cases in man and animals and detection of toads and wall lizards as their reservoirs. Antonie Van Leeuwenhoek 44, 219–228.


