Yersinia enterocolitica is the main cause of yersiniosis in Europe, one of the five main bacterial gastrointestinal diseases of humans. Beside pigs, companion animals, especially dogs and cats, were repeatedly discussed in the past as a possible source of pathogenic Y. enterocolitica. To investigate the presence and types of Y. enterocolitica in companion animals, a total of 4,325 diagnostic fecal samples from dogs and 2,624 samples from cats were tested. The isolates obtained were differentiating by using matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) and Fourier transform infrared spectroscopy (FT-IR). Isolated Y. enterocolitica strains were bioserotyped. The detection of the ail gene by PCR and confirmation by FT-IR were used as a pathogenicity marker. Y. enterocolitica strains were isolated from 198 (4.6%) of the dog and 8 (0.3%) of the cat fecal samples investigated. One hundred seventy-nine isolates from dogs were analyzed in detail. The virulence factor Ail was detected in 91.6% of isolates. Isolates of biotype 4 (54.7%) and, to a lesser extent, biotypes 2 (23.5%), 3 (11.2%), and 5 (2.2%) were detected. The remaining 8.4% of strains belonged to the ail-negative biotype 1A. All 7 isolates from cats that were investigated in detail were ail positive. These results indicate that companion animals could be a relevant reservoir for a broad range of presumptively human-pathogenic Y. enterocolitica types. MALDI-TOF MS and FT-IR proved to be valuable methods for the rapid identification of Y. enterocolitica, especially in regard to the large number of samples that were investigated in a short time frame.

Yersinia is a genus of bacteria in the family Enterobacteriaceae and includes three well-known human and animal pathogens, Y. enterocolitica, Y. pestis, and Y. pseudotuberculosis. Pathogenic strains of Y. enterocolitica and Y. pseudotuberculosis cause yersiniosis, an acute enteric disease, in humans and animals. In Germany and in the European Union, yersiniosis was the third most frequently reported zoonotic infection in humans in 2008 (1, 2).

The species Y. enterocolitica is traditionally grouped by serological tests into different serotypes and phenotypically by biochemical tests into five biotypes (biotypes 1 to 5) (3, 4). Different bio-serotype combinations are thought to be connected with pathogenic potential, whereas biotype 1A is deemed to be non-pathogenic or less pathogenic for humans; however, some cases were attributed to this biotype as well (5–8). The bio-serotypes usually associated with human disease are 1B/O:8, 2/O:5,27, 2/O:9, 3/O:3, and 4/O:3, the latter being the most common in industrialized countries, including Europe (2, 9).

Pathogenic Y. enterocolitica strains are identified by detection of several gene loci, whereof the ail gene, chromosomally coding for an attachment and invasion factor, is one of the main pathogenic markers (10, 11). The presence of the corresponding Ail factor can be shown with a phenotypic technique by a special Fourier transform infrared spectroscopy (FT-IR) method (12).

The epidemiology of Y. enterocolitica infections is complex and remains poorly understood (13). It is assumed that Y. enterocolitica infections are attributed mainly to the eating of contaminated food, in particular contaminated pork (2, 14). Nevertheless, pathogenic isolates have rarely been recovered from food samples implicated in human illness. In Europe, pigs have been considered to be the primary reservoir for the main human-pathogenic Y. enterocolitica bio-serotype, 4/O:3, or, less commonly, bio-serotype 2/O:9 (2). In 2008, 1.8% of all investigated samples of pork and 1.8% of all pigs were reported to be Y. enterocolitica positive in Europe (2). Objective evidence for food-borne outbreaks of Y. enterocolitica is indeed rare, and most infections are sporadic (9, 13).

In the past, the relevance of companion animals for zoonosis in humans was estimated to be rather low. The European Food Safety Authority stated in 2010 that, “on rare occasions, transmission of Y. enterocolitica may occur by direct contact with infected animals” (2). This claim was substantiated by investigations where presumptively pathogenic Y. enterocolitica isolates in dog samples were found in Europe and Japan at rates of up to 30% (14–22). Although progress in the taxonomy of Yersinia makes the interpretation of data prior to 1988 difficult (4), these older findings shine light on the diversity of results and the difficulty for generalized interpretation of older data.

Fredriksson-Ahomaa et al. expressed some doubts regarding whether the direct route pig-raw meat-human was the only relevant one or whether dogs carrying Yersinia are more significant vectors for humans (23). Recent Chinese studies placed greater...
relevance on companion animals, especially dogs, as primary sources of infection in humans, although dogs consumed as food were an additional source of infection, which is not a factor that needs to be considered in Europe (24, 25). It was shown that some pathogenic Y. enterocolitica strains isolated from ill humans and dogs had the same subtype as well as the same pattern by pulsed-field gel electrophoresis (25). In previous case-control studies, contact with companion animals was shown to be a confirmed risk factor for human yersiniosis (24, 26).

In previous studies, Y. enterocolitica strains isolated from dogs or cats were most frequently attributed to bioserotype 4/O:3, bioserotype 2/O:5,27, or biotype 1A (16–21, 25, 27–29). Although most animals carry Y. enterocolitica without observable symptoms (4, 21, 28, 30), some sporadic cases of enteritis, mainly in younger dogs (27, 31), or isolated cases of hepatic or myocardial yersiniosis have been reported (32, 33).

It is therefore of special interest to investigate the extent to which companion animals might serve as sources of Y. enterocolitica, with special regard to ail gene-positive strains, as a zoonotic pathogen. In this study, the occurrence of potentially pathogenic Y. enterocolitica in feces from dogs and cats was examined for 6,949 diagnostic samples received from Germany and its neighboring states within a 10-week time frame. The strains obtained were differentiated by using matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) for initial strain detection to the genus and species levels and by PCR for the detection of the ail gene. Additionally, a recently developed FT-IR method was used for the detection and confirmation of Ail factor-positive Yersinia, mirroring the phenotype (12). Bioserotyping of the strains was performed so that a comparison with older data could be made.

**MATERIALS AND METHODS**

**Fecal samples.** A total of 4,325 samples of dog feces, sent to Vet Med Labor GmbH (Ludwigsburg, Germany) for bacterial diagnostics, were examined. Although the case history was not available in many cases, the main reason for submission was gastrointestinal symptoms (diarrhea of varying quality and duration, colitis, and dysbacteriosis), as indicated by the veterinarian on the submission form. The samples originated mainly from Germany (77%) as well as from 13 other European countries (Austria, Czech Republic, Denmark, France, Finland, Italy, Luxembourg, Malta, Netherlands, Norway, Poland, Portugal, and Sweden) and were collected on 68 consecutive days between November 2011 and January 2012.

In addition, 2,624 diagnostic samples of cat feces were examined in the same laboratory. The case history of the cats listed the same diseases or symptoms as those given for the dog fecal samples. These samples were collected during the same period as that mentioned above and were sent from Germany (81%) and 10 other European countries (Austria, Denmark, France, Finland, Italy, Luxembourg, Netherlands, Norway, Poland, and Sweden).

**Isolation of bacteria.** Fecal samples were cultured according to standard procedures for the detection of enteropathogenic bacteria. Samples were plated onto tryptic soy agar containing 5% sheep blood (Becton, Dickinson, Heidelberg, Germany), MacConkey agar (Becton, Dickinson), Campylobacter selective agar (Heipha, Eppelheim, Germany), and Salmonella selective agar (Heipha) and incubated according to standard procedures. For the detection of Salmonella, selenite lactose broth (Oxoid, Wesel, Germany) was used for enrichment.

Samples were plated onto yersinia selective agar (CIN-agar; Becton, Dickinson) and incubated for 18 to 24 h at 30°C in order to isolate Yersinia. Additionally, the samples were inoculated into a phosphate-buffered saline solution (Merck, Darmstadt, Germany) and incubated for 4 to 5 days at 4°C. After cold enrichment, these samples were also plated onto yersinia selective agar and incubated as described above. Initial identification of suspicious colonies was performed by using MALDI-TOF MS (see below). Pure cultures of isolates identified as Y. enterocolitica were differentiated further by FT-IR, biochemical tests, and PCR.

**MALDI-TOF MS identification.** Suspicous isolates were selected from the culture plates either from the primary culture or after cold enrichment and then subjected to MALDI-TOF MS according to the manufacturer’s instructions (Vitek MS; bioMérieux, Nürtemingen, Germany). Isolates were prepared by using the direct smear method and analyzed by using Myla, version 2.4.0. The database (V 1.1) comprises the following Yersinia species: Y. enterocolitica, Y. kristensenii, Y. aldovae, Y. frederiksenii, Y. intermedia, Y. pseudotuberculosis, Y. ruckeri, and Y. pestis. According to the manufacturer, each database entry is based on spectra from at least 15 to 20 different isolates. As well as for the calibration control of the instrument, Y. enterocolitica ATCC 9610 was included as an external control strain when the selected isolates were examined.

**Phenotypic and biochemical characterization.** After primary growth on sheep blood agar (Oxoid) for 24 h at 37°C, the strains were characterized by esculin hydrolysis, indole production, and the ability to ferment D-xylene and D-trehalose, according to methods described previously (3, 34). Reaction tubes were incubated at 25°C under aerobic conditions, and reactions were evaluated after 2 days. Temperature-dependent motility of Yersinia was tested on SIT-agar (SIM-agar [Becton, Dickinson] colored with triphenyltetrazolium chloride) incubated at 25°C and 37°C for 2 days (35). Serotyping was performed with a slide agglutination test using Y. enterocolitica O:3, O:5, O:8, O:9, and O:27 commercial antisera (Sifin, Berlin, Germany) with isolates grown at 25°C. Initial agglutination was tested with a drop of 0.9% saline. Isolates without agglutination were subsequently tested using all five sera.

**Molecular detection of the ail gene and sequencing of the gene for 16S rRNA.** Molecular detection of the ail gene by real-time PCR was performed according to a protocol described previously by Mäde et al. (36) on aRotor Gene 6000 real-time PCR machine (Corbett Research, Australia), using Brilliant QPCR Master Mix with Sure Start Taq DNA polymerase (Stratagene, Heidelberg, Germany). The temperature profile included 10 min of predenaturation at 95°C followed by 45 cycles of 10 s at 95°C and 30 s at 60°C (data acquisition at the end of the 60°C step) and subsequent cooling to 40°C. Y. enterocolitica strain S1Z5008/01 was used as a positive control (36). For confirmation of four isolates, the 16S rRNA gene was partially amplified according to a modified protocol described previously and employing primers 27F and 1522Rn (37, 38). The resulting 16S rRNA gene fragments were sequenced stepwise (Microsynth AG, Balgach, Switzerland).

**Identification of Yersinia isolates by FT-IR.** Bacterial isolates were cultivated independently in three replicates at 37°C for 24 h on sheep blood agar plates (Oxoid). Harvesting of cells, sample preparation, and the examination of the dried bacterial films by FT-IR spectroscopy were performed as described previously for Yersinia differentiation (12, 39). The infrared spectra were recorded for each sample in a transmission mode in the wave number range of 500 to 4,000 cm⁻¹ with a FT-IR spectrometer (IFS 28/B; BrukerOptics, Ettlingen, Germany). Acquisition and analysis of data were carried out by using OPUS software (version 4.2; BrukerOptics) and an artificial neural network built by NeuroDeveloper software (Synthon, Heidelberg, Germany) (40). Differentiation was performed with an updated version of a method described previously (12, 39). This method allows for species differentiation of Y. enterocolitica independently of the presence or absence of the ail gene.

**Cluster analysis.** Infrared spectra of all Y. enterocolitica strains were compared by cluster analysis (cf. references 38 and 41). For cluster analysis, the vector-normalized spectra in the wave number ranges of 500 to 1,400 cm⁻¹ and 2,800 to 3,000 cm⁻¹ in the second derivation were used for calculation with Ward’s algorithm (OPUS 4.2) (42). The dendrogram obtained depicts the arrangement of isolates in groups according to their spectral differences (Fig. 1).
RESULTS

Bacterial isolates. *Y. enterocolitica* was isolated from 4.6% of 4,325 dog fecal samples. In 63.6% of these cases, *Y. enterocolitica* was isolated as the only enteropathogenic bacterium. In 36.4% of the cases, other enteropathogenic bacteria were detected in parallel (mainly *Salmonella* sp. and/or *Campylobacter* sp. [data not shown]). Due to various reasons (e.g., loss of culture and overgrowth by contaminants), it was possible to further characterize 179 isolates of *Y. enterocolitica*.

*Y. enterocolitica* was detected in 8 (0.3%) of 2,624 cat fecal samples examined for comparison. Of these, three samples also contained other enteropathogenic bacteria. Seven of the eight isolates were available for further characterization.

Identification by MALDI-TOF MS and FT-IR and determination of bioserotype. Suspicious isolates of *Y. enterocolitica* originating from dog fecal samples were identified to the species level by using Vitek MS (Myla software, version 2.4.0, database V 1.1) with a 99.9% level of confidence for 176 of the 179 isolates; the remaining three isolates yielded confidence levels of 99.7 to 99.8%. The seven isolates from cat fecal samples were all identified with a 99.9% confidence level. All 186 isolates from dogs and cats were assigned to the genus *Yersinia* and...
The isolates were bioserotyped and analyzed for the presence of the Ail factor by FT-IR and the ail gene by PCR to obtain information about their pathogenic potential (12). Of the dog isolates, 91.6% (n = 164) were analyzed to be ail positive by PCR and Ail positive by FT-IR (Table 1). The ail gene was also detected in all 7 isolates available from cat feces.

All 15 ail-negative strains isolated from dog feces belonged to biotype 1A. Three isolates showed bioserotype 1A/O:8, and one was of bioserotype 1A/O:5. The remaining 11 isolates did not agglutinate with any of the five sera used. The other 164 isolates were positive for the ail gene and were typed as biotype 2, 3, 4, or 5 (Table 1). Biotype 4 predominated, with 54.7% (n = 98) of all isolates from dog samples, all but one combined with serotype O:3. One strain did not agglutinate with any serum used. One other bioserotype 4/O:3 strain showed no motility at 25°C. Both of these strains were confirmed to be Y. enterocolitica by comparison with the partially sequenced 16S rRNA gene. Biotype 2 comprised 42 (23.5%) of the isolates. Of this group, 27 strains belonged to bioserotype 2/O:9, and 15 belonged to bioserotype 2/O:5,27. Twenty strains were of biotype 3 (11.1%), combined with the same serotype (O:3) as all of the biotype 4 isolates. Four isolates (2.2%) failed to ferment trehalose; therefore, they were typed as biotype 5. All of these strains were of serotype O:3. Two of the four biotype 5 isolates were confirmed as Y. enterocolitica by partial sequencing of their 16S rRNA genes.

The seven available Y. enterocolitica isolates from cat fecal samples were also bioserotyped. Four isolates were of biotype 4 combined with serotype O:3, one was of bioserotype 3/O:3, and the two remaining isolates were of bioserotype 2/O:9.

The infrared spectra of all canine isolates were compared by cluster analysis (Fig. 1). A clear grouping for the spectra of biotypes 1A and 2, and a group with biotypes 3, 4, and 5, was shown by the formation of two separate main branches. In the first main branch, distinct subbranches were found for biotypes 1A and 2. Only two exceptions were found: the spectrum of an isolate that was of biotype 4 but which showed no agglutination with the sera used was similar to those of biotype 2. Close to this individual strain, the spectrum of a special biotype 3/O:3 isolate was found. The second main branch was separated into a distinct biotype 4 and a close subbranch, comprising the remaining biotype 3 and 5 isolates. The four spectra for the isolates of biotype 5 were found in a distinct branch, close to the majority of biotype 3 spectra. Except for two biotype 3/O:3 isolates found in the biotype 4 branch, the remaining 17 biotype 3 isolates clustered together.

The age of the dog was known for 99.4% (n = 178) of the fecal samples. Most (144 strains) of the 163 strains positive for the ail gene were isolated from dogs younger than 1 year of age (88.3%). In contrast, 53.3% (8/15) of isolates lacking the ail gene were obtained from dogs which were less than 1 year old (Table 1). The cat isolates, all being positive for the ail gene, came from cats younger than 1 year of age for 80% (n = 4) of the five animals whose age was known.

### DISCUSSION

Y. enterocolitica is regarded as a significant food-borne pathogen (1, 2). Besides food from animal sources, especially pork (13, 26), companion animals have been implicated as a potential source for human Yersinia infections (4, 7, 14, 16, 23, 25, 43). Strains isolated from dogs in particular share common genotypes with pathogenic strains isolated from humans (7, 13). The contact between many dogs and cats and their owners has noticeably changed in postindustrial countries during the last decades (44, 45). Because of far-closer human and companion animal contact, the transmission of microorganisms between them is facilitated (46). It is assumed

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**TABLE 1** Bioserotype and ail gene of Y. enterocolitica isolates from companion animal feces

| ail gene detection and bioserotype or biotype<sup>a</sup> | No. (%) of isolates from dogs |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| | Total (n = 179 [100%]) | Aged ≤1 yr (n = 152 [84.9%]) | Aged >1 yr (n = 26 [14.5%]) | Unknown age (n = 1 [0.6%]) | Total no. (%) of isolates from cats (n = 7 [100%]) |
| ail negative | | | | | |
| 1A/O:5 | 1 | | | 1 | |
| 1A/O:8 | 3 | 2 | | 1 | |
| 1A/nag | 11 | 6 | | 5 | |
| Total 1A | 15 (8.4) | | | | |
| ail positive | | | | | |
| 2/O:9 | 27 | 20 | 7 | 2 | |
| 2/O:5,27 | 15 | 14 | 0 | 1 | |
| Total 2 | 42 (23.5) | | | | |
| 3/O:3 | 20 | 18 | 2 | 1 | |
| Total 3 | 20 (11.2) | | | | |
| 4/O:3 | 97 | 87 | 10 | 4 | |
| 4/nag | 1 | 1 | 0 | | |
| Total 4 | 98 (54.7) | | | 45 (57.1) | |
| 5/O:3 | 4 | 4 | 0 | | |
| Total 5 | 4 (2.2) | | | | |
| Total ail negative | 15 (8.4) | 8 | 7 | | |
| Total ail positive | 164 (91.6) | 144 | 19 | 1 | 7 (100) |

<sup>a</sup> Boldface type indicates biotype. nag, no agglutination with sera specific for serotype O:3, O:5, O:8, O:9, or O:27.
that raw pork is a potential source of infection in dogs and cats (18, 23). Dogs can readily become infected by pathogenic \textit{Y. enterocolitica} through feeding or through social interactions with other dogs and can carry and excrete the organism for more than 3 weeks at high cell counts (28, 31, 43).

The symptoms of dogs harboring \textit{Yersinia} range from diseases of various severities to obviously healthy (23, 27, 31–33). Asymptomatic carriage seems to be predominant in dogs and cats (20). Thus, \textit{Y. enterocolitica} was considered a commensal in the intestine of these animals (4). As the asymptomatic carrier status of animals for \textit{Y. enterocolitica} cannot readily be recognized, carriers can easily transmit the infection to other animals, humans, or the environment (15, 20, 21, 31, 43).

Since 1980, European investigations showed prevalences of \(\leq 5\)% and up to 30.1\% for \textit{Y. enterocolitica} in dog feces; none of those studies included more than 250 samples (14–16, 18, 21, 29). On the other hand, the prevalence of \textit{Y. enterocolitica} in cat feces was generally lower (14, 17).

In this study, fecal samples were obtained from dogs and cats suspected of having gastrointestinal symptoms; these symptoms may include diarrhea of various degrees and durations, colitis, as well as dysbacteriosis. Additionally, it can be assumed that an unknown number of samples were obtained from apparently healthy animals as part of a wellness test or therapeutic monitoring. Dogs and cats presenting with gastrointestinal symptoms may have other enteric pathogens that might contribute to the clinical signs. These samples were not examined for viral pathogens and only infrequently tested for endoparasites.

\textit{Y. enterocolitica} was detected in 198 of the 4,325 canine fecal samples. In 63.6\% of these cases, \textit{Y. enterocolitica} was the only bacterial pathogen isolated, while in the remaining samples, other enteropathogenic bacteria were detected along with \textit{Y. enterocolitica}. It is not clear whether seasonality plays a role in the prevalence of \textit{Y. enterocolitica}; however, previous studies have shown no increase in the rate of isolation of this organism from dogs during winter months (19, 22, 28).

The overall prevalence of 4.6\% for \textit{Y. enterocolitica} is an indication of the possible virulence of this organism for dogs, particularly because most isolates (91.6\%) were of \textit{ail}-positive biotypes, a rate which is remarkably high for this kind of sample. A clear preponderance was shown for biotype 4 isolates (54.7\%), followed by biotype 2 (23.5\%), biotype 3 (11.2\%), and, in low numbers, biotype 5 strains (2.2\%) (Table 1). The reported rates of pathogenic bioserotypes isolated from dog samples varied in a broad range, from <0.5\% (15, 29) up to more than 75\%, in which bioserotype 4/O:3 also predominated (19, 30).

Apart from the \textit{ail}-positive bioserotype combinations most frequently isolated from human cases and pigs, such as bioserotypes 4/O:3, 2/O:9, and 2/O:5,27 (9, 13), only a few other bioserotype combinations were observed. In 98 out of 179 samples of dog feces (54.7\%), a biotype 4 profile was found, and only one of these isolates did not possess the classical bioserotype 4/O:3 combination and was not serotypeable with the sera used. The frequent appearance of bioserotype 4/O:3 could be a direct or indirect consequence of contaminated feed (especially raw pork [23]) or a result of a higher susceptibility to this bioserotype, which is assumed for younger dogs and humans (5, 28).

Biotype 2 was the second most frequently detected biotype in this set of strains. In previous reports, biotype 2 isolates ranked second in frequency, and occasionally first, in dog studies (7, 19, 28, 30). This mirrors the presence of these bioserotypes in human cases as well as in pigs or pork (1, 2, 9, 47). All 20 biotype 3 isolates were combined with serotype O:3. This bioserotype combination was occasionally reported in previous Japanese dog studies but not for Europe (28). Biotype 5 isolates have so far been recovered only from infections in animals (4, 9). Bioserotype 5/O:2,3 is recognized as an animal pathogen commonly associated with diseased sheep and goats or hares (4, 7, 48). In our study, four strains isolated from dog feces showed biotype 5, and all were combined with serotype O:3. The relevance of this obviously rare bioserotype for dog remains unclear.

The rate of \textit{ail}-negative biotype 1A isolates in samples from dog feces was 8.4\% and was therefore relatively low compared to the data reported previously by Murphy et al., who found 100\% of the \textit{Y. enterocolitica} isolates from canine samples to be of biotype 1A (29). This could reflect our focus on samples from diseased animals, as can be assumed for the majority of the samples in this study. Hence, a generalized conclusion in regard to the pathogenicity of biotype 1A for dogs is not possible based on this biased data set.

For humans, biotype 1A \textit{Y. enterocolitica} strains were originally considered to be nonpathogenic. This biotype was recently discussed as a possible opportunistic pathogen (5, 8, 49).

In this study, the majority of \textit{Y. enterocolitica} strains isolated from dogs younger than 1 year of age were positive for the \textit{ail} gene (94.7\%) and typed as suspected pathogenic biotype 2, 3, 4, or 5. The few isolates lacking the \textit{ail} gene were more often found in samples from older dogs (46.7\%). This probably reflects the higher susceptibility of young animals to various enteropathogenic microorganisms, with \textit{Yersinia} being either a main or a contributing etiologic factor for clinical symptoms.

In 2,624 cat fecal samples, a significantly low prevalence of \textit{Y. enterocolitica} of 0.3\% was found, compared to the prevalence in dog samples. The seven isolates investigated were of the known pathogenic bioserotypes 4/O:3, 2/O:9, and 3/O:3, which were also found most frequently in samples from dogs (Table 1). Previous studies in cats showed low prevalences (\(\leq 5\)) of pathogenic bioserotypes of \textit{Y. enterocolitica} as well (17, 30).

The identification methods used (MALDI-TOF MS and/or FT-IR) proved to be effective tools for the detection of \textit{Y. enterocolitica} in routine samples (12, 50). The combination of these methods presented a valid base for rapid and detailed diagnostic information. FT-IR not only was used for species determination but also was successfully applied for the detection of the \textit{ail} factor in this study. The obtained IR cluster shows a clear hierarchical grouping of \textit{Y. enterocolitica} according to biotype in general, with marginal exceptions (Fig. 1). In FT-IR cluster analysis, biotype 2 strains represent a compact branch, close to the branch of the biotype 1A isolates. Biotypes 3 and 5 were related to biotype 4 in observed bioserotype combinations and in the main branches of IR cluster analysis. Some spectra of isolates from different dogs were nearly indistinguishable (Fig. 1). An epidemiological approach by comparison of IR spectra, as shown previously for \textit{Bacillus cereus}, \textit{Corynebacterium ulcerans}, or \textit{Staphylococcus aureus}, seems to be attainable (38, 51, 52).

The relevance of \textit{Y. enterocolitica} in companion animals is not yet known. The unexpected high ratio of \textit{ail}-positive, and therefore presumptively human-pathogenic, \textit{Y. enterocolitica} isolates in dog feces, with a broad variety of bioserotypes, should expand the focus on the possibility of transmission of this organism from pigs to companion animals. Interestingly, while the rate of occurrence...
seems to be relatively high in dogs, as shown by the prevalence of 4.6% for Y. enterocolitica in dog feces, the samples from cats revealed a much lower prevalence (0.3%). Further studies need to be conducted to assess the potential risk of transmission of this zoonotic pathogen to animal owners.

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