Prevalence of *Yersinia enterocolitica* in Pigs Slaughtered in Chinese Abattoirs

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The distribution of *Yersinia enterocolitica* in slaughtered pigs in China was studied. A total of 8,773 samples were collected and examined from different pig abattoirs in eleven provinces from 2009 to 2011. Of these, 4,495 were oral-pharyngeal swab (tonsils) samples from pigs, 1,239 were from intestinal

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contents and 3,039 were feces samples from abattoirs or local pigpens. The data showed 1,132 strains were obtained, where the isolation rate for *Yersinia enterocolitica* was 19.53% (878/4,495) from the tonsil samples, 7.51% (93/1,239) from intestinal contents, and 5.30% (161/3,039) from feces. Of the 850 pathogenic *Yersinia* strains, except for three 2/O:9 and three 4/O:3, the others 844/850 were all bioserotype 3/O:3. Interestingly, pathogenic *Y. enterocolitica* accounted for the majority of the isolated strains from most provinces (85.17% - 100%), whereas from Heilongjiang, 96.52% (111/115) were classified as nonpathogenic biotype 1A with various serotypes and only 3.48% of the strains (4/115) were pathogenic 3/O:3. All of the pathogenic strains were analyzed using pulsed-field gel electrophoresis (PFGE), and 49 patterns were obtained for the O:3 pathogenic strains, most of them were K6GN11C30021 (53.13%: 450/847) and K6GN11C30012 (21.37%: 181/847). Several strains from diarrhea patient's samples revealed PFGE patterns identical to that from samples of local pigs, suggesting a possible link between porcine isolates and human infection. The results above suggested that *Yersinia enterocolitica* in slaughtered pigs from Chinese abattoirs was characterized by region-specific PFGE patterns and confirmed that strains isolated from pigs are closely related to those from human infections.

*Yersinia enterocolitica* is a zoonotic pathogen widely distributed in nature that can cause acute gastroenteritis and mesenteric lymphadenitis mimicking appendicitis (4).
Y. enterocolitica are divided into six biotypes (1A, 1B, 2, 3, 4 and 5) and 60 serotypes. Most Y. enterocolitica associated with human yersiniosis belong to bioserotypes 1B/O:8, 2/O:9, 3/O:3, 4/O:3 and 2/O:5,27 (7, 26). Y. enterocolitica are recovered from diverse animal sources, from farm animals and domestic pets to free-living and captive wild animals (5, 11). Pigs are considered to be the primary reservoir of human pathogenic Y. enterocolitica strains in the world, slaughtered pigs are one of the potentially important sources for the infection (9, 17, 21, 24, 27). A previous study showed serotypes O:3 and O:9 were the only pathogenic strains isolated from China (30), it is worth mentioning that the common bioserotype 2/O:9 which followed 3/O:3 in the 1990s has almost disappeared now (12). In China, the predominant pulsed-field gel electrophoresis (PFGE) patterns for pathogenic \textit{Yersinia} O:3 are K6GN11C30021 and K6GN11C30012; and high similarity between strains from slaughtered pigs and patients has been demonstrated by PFGE, indicating that the pigs are the main source of human infection (6, 8). The consumption of pork and products is large in China, with wide-spread farms breeding domestic pigs and abattoirs processing them. Some abattoirs suffer from bad sanitation conditions and low levels of automatization, where if one swine is infected with \textit{Yersinia enterocolitica}, there is a high risk of transmission of pathogenic \textit{Yersinia} in these enclosed areas. During the slaughter process the bacteria can be transmitted easily to the carcass and offal and then further to consumers (1, 3, 21). At present, little information is available concerning the distribution and transmission of \textit{Yersinia enterocolitica} among the slaughtered pigs and patients in China. Thus, we examined several abattoirs located in different regions...
of China to detect the prevalence of pathogenic *Y. enterocolitica*, and studied the geographic distribution, bioserotypes, virulence genes and the prevalent PFGE patterns of pathogenic *Y. enterocolitica* strains.

**MATERIALS AND METHODS**

**Sources of samples.** Abattoirs, pig pens and farms from eleven different provinces of China (Middle-Henan; Southwest-Sichuan, Yunnan; North-Beijing, the Inner Mongolia Autonomous Region, Tianjin; Northeast-Heilongjiang; Northwest-the Ningxia Hui Autonomous Region, Qinghai and East-Jiangsu, Jiangxi) were selected for collection of 8,773 samples during Mar 2009 to Nov 2011. Previous published data showed the isolation rate from tonsil samples was the highest (10). We therefore focused on collecting tonsil samples at the abattoirs (4,495 samples), and intestinal contents at several abattoirs (1,239 samples), and compared them with pig feces samples from pig farms and domestic pigpens (3,039 samples). The largest portion of the tonsil samples was collected in Sichuan and Henan because these areas have the largest population and highest density of pig farms.

**Culture and PCR.** Enrichment was performed using phosphate-buffered saline with sorbitol and bile salts (PSB) at 4°C for 21 days. Nucleic acids from all tonsil samples were extracted using a DNA nucleic acid extraction Kit (TIANGEN, China). The *Y. enterocolitica* conserved gene *foxA*; pathogenic gene *ail*; and the *inv* gene of *Yersinia pseudotuberculosis* were amplified(15, 29). The primers and annealing temperatures are shown in Table 1. The tonsil samples positive for either or both *foxA* and *ail* genes were then inoculated onto *Yersinia* selective agar
(cefsulodin-irgasan-novobiocin [CIN] agar; Difco); and all of the intestinal content
and fecal samples were also inoculated. The presumptive *Y. enterocolitica* strains with
colonies having a typical bulls-eye appearance (deep red centers surrounded by a
outer transparent zone) on CIN agar were inoculated onto BHI agar plates (Braii Heart
Infusion agar) incubated at 25°C for 24 h to obtain pure cultures (30, 32).

**Bioserotype identification and biochemical tests.** The bioserotype identification
and biochemical tests of all the strains were performed using the methods reviewed by
Wang (31).

**Identification of pathogenic *Yersinia enterocolitica* strains.** DNA preparation of
the strains isolated from the samples and PCR were performed as described
previously (31). The relative virulence genes (*ail, ystA, ystB, virF, and yadA*) from the
chromosome and plasmids were amplified. Pathogenic strains were positive for all
(*ail*, *ystA*, *virF*, and *yadA*); however some pathogenic strains lost the plasmid
virulence genes (*ail*, *ystA*, *virF*, and *yadA*) (29-30). The primers sequences and
annealing temperatures are shown in Table 1.

**TABLE 1. Primers used in this study**

**PFGE assay.** The pulsed-field gel electrophoresis (PFGE) method was used to
analyze all of the 850 pathogenic strains isolated in this study, along with 13 samples
from diarrhea patients, using the procedures described by Wang et al.(31-32). The
plugs digested with 25 U *NotI* were electrophoresed with a pulse time from 2 s to 20 s,
plugs were electrophoresed for 18-19 h at 20 V. For data analysis, *.tiff* images of the
gels were imported into the database of the PFGE patterns of *Y. enterocolitica* strains
of China. We performed a cluster analysis for serotypes O:3 and O:9. The patterns of
the strains from clinic patients with diarrhea of Jiangsu, Sichuan, Tianjin and Henan
provinces were compared with those pathogenic strains isolated from pigs slaughtered
in the same regions. Clustering of the band patterns was performed with BioNumerics
software (version 5.1) and using the unweighted-pair group method with average
linkages (UPGMA) and Dice coefficient with a 1.5% tolerance. All patterns were
visually inspected after computer analysis. The patterns identified as indistinguishable
by computer and visual inspections were assigned a pattern designation (31).

RESULTS

Strain isolation. Of the 8,773 samples, 1,132 (12.90%) tested positive for *Y.
*enterocolitica*, 878 from pig oral-pharyngeal swab (tonsil) samples, 93 from intestinal
contents and 161 from fresh pig feces samples (Fig 1). The detection rate of *Y.
*enterocolitica* from tonsil samples by PCR was much higher than cultivation 36.31% (1,632/4,495) vs. 19.53% (878/4,495). In addition, 4 strains of *Yersinia*
*pseudotuberculosis*, 101 strains of *Yersinia frederiksenii* /intermedia, 16 strains of
*Yersinia kristensenii* were isolated in our study (Table 2). Prevalence of *Y.
*enterocolitica* was shown to be significantly higher from the oral-pharyngeal swabs
(19.53%) than from intestinal contents (7.51%), and lowest in pig feces samples
(5.30%) (Table 3,4,5). The prevalence of *Y. enterocolitica* in slaughtered pigs was
higher in the north of China than in the southern areas (15.49 vs 6.43%) (P <0.01).

TABLE 2. *Yersinia* spp. strains isolated and samples collected from eleven provinces

TABLE 3. Detection of pig tonsil samples from eleven provinces by both PCR and *Y.
Bioserotype distribution. Among the 850 pathogenic isolates, only three strains of 2/O:9 (3/850) were isolated; O:3 was the primary serotype isolated at 99.65% (847/850), in which except for three strains of biotype 4 and the rest were all biotype 3. All of the 282 non-pathogenic strains were biotype 1A, (since the serotype identification for non-pathogenic \textit{Y. enterocolitica} was incomplete, we can only determined 93 of the strains, of these, 71 isolates were serotype O:5, and 22 were O:8). The distributions of the above 1,132 \textit{Y. enterocolitica} strains were disproportionately in different areas. Pathogenic \textit{Yersinia} were primarily isolated from Beijing (100%), Jiangxi (100%), Jiangsu (100%), the Ningxia Hui Autonomous Region (100%), Tianjin (100%), the Inner Mongolia Autonomous Region (93.18%), Sichuan (89.47%); however, from Heilongjiang, located in the northeast of China, was just on the contrary, only 3.48% (4/115) of pathogenic 3/O:3 strains were isolated, and the rest, 96.52% (111/115), were non-pathogenic biotype 1A (Table 3). We collected 350 pig tonsil and 350 intestinal content samples from the same abattoir (Beijing), the \textit{Y. enterocolitica} isolation rates were 54.57% and 23.14%, respectively, and the proportion of the pathogenic strains in the tonsil samples was 100%, compared to
79.01% (64/81) from the intestinal contents (one strain was detected to be O:9) (Table 151, 3, 5).

**PFGE.** From 847 pathogenic O:3 *Y. enterocolitica* strains, 49 different PFGE patterns were obtained using enzymes *N*ot*I*, which has been shown to be the most suitable enzyme for characterization of *Y. enterocolitica* in previous studies. The predominant *N*ot*I* pattern: K6GN11C30021 represents 53.13% (450/847) of the strains in pig infections. Patterns K6GN11C30021 and K6GN11C30012 were found in various samples from different provinces, indicating that these patterns are widely distributed in China. More than two types of PFGE patterns were obtained from every abattoir, showing diversities of the strains from Chinese abattoirs. Comparing the patterns before 2009 in our PFGE database, it was found that K6GN11C30012 has existed over the longest period of time, from 1986 to 2011, suggesting that strains with same PFGE pattern could sustain for many years in the same places and *Y. enterocolitica* has some genetic stability. Each region has a primary pattern, e.g. K6GN11C30012 in Beijing, Tianjin and Yunnan; while K6GN11C30021 in Henan, Jiangsu, Jiangxi, Ningxia Hui Autonomous, the Inner Mongolia Autonomous Region, Qinghai and Sichuan. Several regions possess their own specific pattern, such as K6GN11C30044 in Beijing, K6GN11C30042 in Henan, K6GN11C30082 in Inner Mongolia Autonomous Region, K6GN11C30058 in Qinghai and K6GN11C30063 in Sichuan (Fig 2). Two patterns of the serotype O:9 strains were K6GN11C90003 and one was K6GN11C90004.
FIG 2. The distribution of *Y. enterocolitica* and *NotI* patterns of 847 serotype O:3 strains recovered from eleven provinces.

The patterns of the strains from patients (three from Jiangsu province, two from Sichuan province and seven diarrhea patients in our database before 2009) were indistinguishable from the strains isolated from pigs from the same areas (Fig 3). K6GN11C30021 was the predominate pattern isolated from pigs, and was also found in most infected patients (Fig 3 dotted line area).

FIG 3. Distribution map of pulsed-field gel electrophoresis (PFGE) patterns for pathogenic O:3 serotype isolates from patients and pigs from Jiangsu, Sichuan, Henan and Tianjin Provinces*

*The same color suggests the patterns of pigs and patients from the same province.

The dotted line area shows the predominate pattern K6GN11C30021 isolated from pigs and infected patients.

**DISCUSSION**

It is well-known that *Yersinia enterocolitica* are addicted to the lymphoid tissue, so it can be easily parasitic on pig throat tonsils where are rich in lymphoid tissue (14). Pigs (mainly their tonsils) are assumed to be the main reservoirs for pathogenic *Y. enterocolitica* because the pig is so far the only animal species from which pathogenic strains have frequently been isolated (16, 19). In this study, *Yersinia enterocolitica* was isolated from 19.53% (878/4,495) of the tonsil samples, 7.51% (93/1,239) from intestinal contents, and 5.30% (161/3,039) from feces. The isolation rate from pig
tonsil samples was the highest, as observed in European countries (9), indicating tonsils are a more significant source for carcass and offal contamination than feces in slaughterhouses, therefore tonsil samples were chosen instead of fecal and intestinal content samples in our study to show the distribution of *Y. enterocolitica* in pigs. The detection rate in pig tonsil samples was shown to be even higher using PCR, suggesting plating onto selective medium may under-estimate the prevalence of this pathogen in pig (2). Possible causes are as follows: if fewer strains in the samples or the *Y. enterocolitica* in samples are already dead as the adding of the antibiotic in the feeding, all of these will bring about the negative result after cultivation. However the PCR-based methodology is more sensitive than cultivation, so when detected with PCR it may show positive in *Y. enterocolitica*. In Europe, human yersiniosis is the third most common enteric disease after campylobacteriosis and salmonellosis, however the positive PCR rate and isolation rate from pigs are no higher than in China (13), yet in China the yersiniosis is sporadic and uncommon. The low number of reported yersiniosis cases in Chinese diarrhea patients could possibly be due to the lifestyle and better cooking methods or there was simply not looked for yersiniosis in such patients. Besides, under-reporting in clinic occurs, because our research team detected about 20% infection rate from infants feces using the PCR method (unpublished data).

The prevalence of *Y. enterocolitica* was significantly different in every province, which shows geographic difference characteristics. Overall, *Y. enterocolitica* incidence in the cold North of China (15.49%: 971/6,269) was much higher than that
in the warm South areas (6.43%: 161/2,504) (Table 2). Some reports also indicate *Y. enterocolitica* were found more in the cold North region (30-31). Here we show the highest isolation rate from tonsil samples (54.9%) was obtained from Jiangxi province with all of the strains belonging to 3/O:3 (Table 3). This is also the case in the southeastern coast province of Fujian (30), adjacent to Jiangxi province, with a high incidence. The distribution of pathogenic *Y. enterocolitica* may not only be related to local climate, but we presumed that it is related to other environmental factors as well. This is the first report concerning the prevalence of *Y. pseudotuberculosis* in pigs of China, with an isolation rate 0.046% (4/8,773) that was much lower than other countries (10, 22). Additionally, among the 8,773 samples, we detected 117 *Yersinia frederiksenii* /intermedia and *kristensenii*, most of which were obtained from pig tonsils (Fig 1).

Previous studies showed the bioserotypes of pathogenic *Y. enterocolitica* in China differ from other countries, being predominantly in 3/O:3 and 2/O:9, with fewer 4/O:3, and no pathogenic 1B/O:8 strains (30, 32). We got the similar results in this study. However in the Ningxia Hui Autonomous Region, 2/O:9 was once the predominant bioserotype in the 1990s (12, 30); but these strains have gradually decreased in recent years (12). In the United States, 1B/O:8 has also been replaced by O:3 strains which are now dominant (18, 25). Whether this occurs due to increasing use of antibiotics in feed or due to immunization needs to be further determined.

The isolation rate shown here from each abattoir varied and the proportion of pathogenic strains was different. Whereas in Heilongjiang, located in northeast China,
despite a high isolation rate 50.88% (115/226), only 3.48% (4/115) were pathogenic
3/O:3, and 96.52% (111/115) were classified as nonpathogenic biotype 1A (Table 3,
Fig 2). We speculate different bioserotypes compete and suffer mutual interference in
the throats of pigs. The pigs in Heilongjiang were collected from farmers of their own
manual feeding is in small-scale, whereas the pigs from Beijing, Tianjin and other
cities were nurtured primarily in big abattoirs, where \textit{Y. enterocolitica} can be
transmitted between each other through the fecal-oral route easily. If the different
isolation rate is caused by poor feeding models needs to be further studied (20, 22).
The PFGE patterns using \textit{Not} I enzyme were similar within a given farm, suggesting
specific strains circulate in each herd (Fig 2). One possible reason is sows in the same
areas transmit pathogenic \textit{Yersinia} directly to weaning pigs or indirectly to other pigs
when contact with each other via a contaminated environment. The common pattern,
K6GN11C30021, found in most human infections and also widely exists in
slaughtered pigs (Fig 3). A previous study revealed this pattern had existed among
animals and diarrhea patients for a long time (31). The PFGE cluster suggested the
patterns of the strains from the patients in Jiangsu, Sichuan, Tianjin and Henan
provinces were indistinguishable from the strains isolated from pigs from the same
areas (Fig 3). We speculated that the pigs in slaughterhouses may be a source of
infection for humans in this region. A possible explanation may be that the \textit{Y.}
\textit{enterocolitica} were directly transmitted from pigs to man through fecal-oral route or
indirectly transmitted from pigs to man via contaminated pork, especially pig offal,
and via contaminated environment and pets (31). During a case-control study, a
correlation was demonstrated between the consumption of raw or undercooked pork and the prevalence of yersiniosis (23, 28). This shows that the swine is not only the carrier of \textit{Y. enterocolitica}, but also the vector to cause yersiniosis epidemic and outbreaks. Contamination of pig carcasses during the slaughter process with pathogenic \textit{Yersinia} from tonsils, intestinal contents and feces may occur. These factors increase the possibility of \textit{Y. enterocolitica} accessing the food chain and multiplying in food products due to its ability to grow at low temperature (30-31). Meat removed from refrigerators tested positive for \textit{Y. enterocolitica}, where the rate was the highest from pig tongues. If we undercooked or cut raw meat together with the edible food, it may cause human infection.

Domestic dogs belonging to farmers are also a host of \textit{Y. enterocolitica} except the swine in China, yet the pathogenic \textit{Y. enterocolitica} is seldom isolated from other animals (31). Previously, many rodents in the Ningxia Hui Autonomous Region of China were detected carrying \textit{Y. enterocolitica}. Most were around the farmers’ household, so they were in frequent contact with domestic pigs which may raise the risk of transmission of pathogenic \textit{Y. enterocolitica} to them (30). Recently, most areas of China have implemented de-ratting programs, reducing the number of rats significantly, and therefore the inter-infection with pet animals (such as swine and dog) rarely happens. Thus the isolation rate from rodents has declined, especially during the period from 2009 to 2011, the mouse in steppe which far away from the farmer’s houses were negative for \textit{Y. enterocolitica} with culture technology (unpublished data). Therefore, we concluded that swine are the host of \textit{Y. enterocolitica} and the source of
infection for humans.

The epidemiological link between pigs and contact with patients is still unclear and has not been documented. This is the first report of the prevalence and dissemination of the pathogenic *Y. enterocolitica* in pigs of China. The high prevalence and rapid dissemination of *Y. enterocolitica* in pigs is a challenge for food safety and public health. Further epidemiological investigations are necessary to further determine the reservoir of *Y. enterocolitica* in China and its route of transmission.

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FIG 1. Distribution of Yersinia spp. strains isolated from different sources

FIG 2. The distribution of Y enterocolitica and NotI patterns of 847 serotype O:3 strains recovered from eleven provinces

FIG 3. Distribution map of pulsed-field gel electrophoresis (PFGE) patterns for pathogenic O:3 serotype isolates from patients and pigs from Jiangsu, Sichuan, Henan and Tianjin Provinces*
*The same color suggests the patterns of pigs and patients from the same province.

The dotted line area shows the predominate pattern K6GN11C30021 isolated from pigs and infected patients.
TABLE 1. Primers used in this study

<table>
<thead>
<tr>
<th>Target gene and prime direction</th>
<th>Primer Sequence (5′→3′)</th>
<th>Amplicon length</th>
<th>Annealing temp</th>
</tr>
</thead>
</table>
| **foxA**                        | GGT TCC TTG AGC GTA TTG ATG  
GAT CAT CGG TTT CAG CAG TTT  | 1094 bp | 58°C         |
| Forward  
Reverse |  |  |  |
| **ail**                          | TAA TGT GTA CGC TGC GAG  
GAC GTG TTA CTG TCA CTG  | 351 bp | 57°C         |
| Forward  
Reverse |  |  |  |
| **ystA**                        | ATC GAC ACC AAT AAC CGC TGA G  
CCA ATC ACT ACT GA CTT CGG CT  | 79 bp | 61°C         |
| Forward  
Reverse |  |  |  |
| **ystB**                        | GTA CAT TAG GCC AAG AGA CG  
GCA ACA TAC CTC ACA ACA CC  | 146 bp | 61°C         |
| Forward  
Reverse |  |  |  |
| **yadA**                        | CTT CAG ATA CTG GTG TCG CTG T  
ATG CCT GAC TAG AGC GAT ATC C  | 849 bp | 60°C         |
| Forward  
Reverse |  |  |  |
| **virF**                         | GGC AGA ACA GCA GTC AGA CAT A  
GAT GAG CAT AGA GAA TAC GTC G  | 561 bp | 63°C         |

*: Amplicon length in pathogenic *Y. enterocolitica* serotypes O:8.
TABLE 2. *Yersinia* spp. strains isolated and samples collected from eleven provinces$^a$

<table>
<thead>
<tr>
<th>Province</th>
<th>Samples</th>
<th><em>Yersinia enterocolitica</em></th>
<th><em>Yersinia frederiksenii</em> /intermedia</th>
<th><em>Yersinia kristensenii</em></th>
<th><em>Yersinia pseudotuberculosis</em></th>
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<td>700</td>
<td>272</td>
<td>5</td>
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<td>1,072</td>
<td>67</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
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<td>226</td>
<td>115</td>
<td>7</td>
<td>5</td>
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<td>0</td>
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<td>0</td>
<td>0</td>
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<tr>
<td>Inner Mongolia</td>
<td>759</td>
<td>49</td>
<td>1</td>
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<td><strong>Total</strong></td>
<td>8,773</td>
<td>1,132</td>
<td>101</td>
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$^a$ "0" indicates that no strains was isolated
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<tr>
<th>Province</th>
<th>Samples</th>
<th>PCR-positive (%)</th>
<th>Isolation rate</th>
<th>Strains</th>
<th>Pathogenic</th>
<th>Non-pathogenic</th>
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<tr>
<td>Henan</td>
<td>1,358</td>
<td>31.02</td>
<td>25.33(344/1358)</td>
<td>Isolation rate %</td>
<td>Pathogenic %</td>
<td>Non-pathogenic %</td>
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<td>827</td>
<td>21.90</td>
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<td>14.83(51/344)</td>
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<tr>
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<td>667</td>
<td>26.54</td>
<td>3.60(24/667)</td>
<td>89.47(17/19)</td>
<td>10.53(2/19)</td>
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<tr>
<td>Beijing</td>
<td>350</td>
<td>65.14</td>
<td>54.57(191/350)</td>
<td>100(191/191)</td>
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<tr>
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<td>228</td>
<td>36.40</td>
<td>19.30(44/228)</td>
<td>93.18(41/44)</td>
<td>6.82(3/44)</td>
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<td>200</td>
<td>38.00</td>
<td>15.00(30/200)</td>
<td>100(30/30)</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Qinghai</td>
<td>200</td>
<td>23.50</td>
<td>11.00(22/200)</td>
<td>86.36(19/22)</td>
<td>13.64(3/22)</td>
<td></td>
</tr>
<tr>
<td>Ningxia</td>
<td>192</td>
<td>34.90</td>
<td>13.02(25/192)</td>
<td>100(25/25)</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Tianjin</td>
<td>145</td>
<td>24.14</td>
<td>5.52(8/145)</td>
<td>100(8/8)</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Jiangxi</td>
<td>102</td>
<td>58.82</td>
<td>54.90(56/102)</td>
<td>100(56/56)</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>4,495</td>
<td>36.31</td>
<td>19.53(878/4,495)</td>
<td>79.04(694/878)</td>
<td>20.96(184/878)</td>
<td></td>
</tr>
</tbody>
</table>

\(a\) The values are the number positive for either or both \textit{foxA} and \textit{ail} / number of samples

\(b\) The values in parentheses indicate the number of strains isolated from the samples / number of samples tested

\(c\) The values in parentheses indicate the number of pathogenic strains / number of strains isolated from the samples

\(d\) The values in parentheses indicate the number of nonpathogenic strains / number of strains isolated from the samples
TABLE 4. Distribution of *Y. enterocolitica* strains in pig feces samples

<table>
<thead>
<tr>
<th>Province</th>
<th>Samples</th>
<th>Pathogenic %</th>
<th>Non-pathogenic %</th>
<th>Isolation rate (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tianjin</td>
<td>927</td>
<td>100(59/59)</td>
<td>0</td>
<td>6.36(59/927)</td>
</tr>
<tr>
<td>Henan</td>
<td>224</td>
<td>0</td>
<td>100(26/26)</td>
<td>11.61(26/224)</td>
</tr>
<tr>
<td>Ningxia</td>
<td>449</td>
<td>14.29(5/35)</td>
<td>85.71(30/35)</td>
<td>7.80(35/449)</td>
</tr>
<tr>
<td>Yunnan</td>
<td>548</td>
<td>83.33(5/6)</td>
<td>16.67(1/6)</td>
<td>1.10(6/548)</td>
</tr>
<tr>
<td>Qinghai</td>
<td>200</td>
<td>50.00(2/4)</td>
<td>50.00(2/4)</td>
<td>2.00(4/200)</td>
</tr>
<tr>
<td>Jiangsu</td>
<td>160</td>
<td>53.85(14/26)</td>
<td>46.15(12/26)</td>
<td>16.25(26/160)</td>
</tr>
<tr>
<td>Inner Mongolia</td>
<td>531</td>
<td>20.00(1/5)</td>
<td>80.00(4/5)</td>
<td>0.94(5/531)</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>3,039</td>
<td>53.42(86/161)</td>
<td>46.58(75/161)</td>
<td>5.30(161/3,039)</td>
</tr>
</tbody>
</table>
TABLE 5. Distribution of *Y. enterocolitica* strains in pig intestinal content samples

<table>
<thead>
<tr>
<th>Province</th>
<th>Samples</th>
<th>Strains</th>
<th>Isolation rate (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Pathogenic %</td>
<td>Non-pathogenic %</td>
</tr>
<tr>
<td>Beijing</td>
<td>350</td>
<td>79.01(64/81)</td>
<td>20.99(17/81)</td>
</tr>
<tr>
<td>Ningxia</td>
<td>889</td>
<td>50.00(6/12)</td>
<td>50.00(6/12)</td>
</tr>
<tr>
<td>Total</td>
<td>1,239</td>
<td>75.27(70/93)</td>
<td>24.73(23/93)</td>
</tr>
</tbody>
</table>