Veterinary Microbiology 178 (2015) 125–131

Contents lists available at ScienceDirect

Veterinary Microbiology

journal homepage: www.elsevier.com/locate/vetmic

# Ecology and geographic distribution of *Yersinia enterocolitica* among livestock and wildlife in China

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ARTICLE INFO

*Article history:*
Received 10 November 2014
Received in revised form 30 April 2015
Accepted 5 May 2015

*Keywords:*
Ecology distribution of *Yersinia*
Livestock
Multi-host pathogens
Pulsed-field gel electrophoresis
Wildlife
Zoonosis

ABSTRACT

The results in this study show the prevalence of *Yersinia* enterocolitica varies in different animal species and regions of China. The highest prevalence is among pigs (12.91%), followed by dogs (9.80%), *Ochotona curzoniae* (plateau pica) (6.76%), chickens (4.50%), rodents (3.40%), cattle (2.78%) and sheep (0.89%). Pathogenic isolates comprised the majority of the *Y. enterocolitica* recovered from pigs (73.50%) and dogs (59.44%); whereas the nonpathogenic *Y. enterocolitica* made up most of poultry and wildlife recovered strains. A correlation analysis comparing the prevalence and geographic factors showed the isolation rate of *Y. enterocolitica* in pigs and dogs was negatively correlated with elevation ($r = -0.50$, $P < 0.05$) and annual average air temperature ($r = -0.43$, $P < 0.05$), but there was positive correlation with annual precipitation ($r = 0.43$, $P < 0.05$); conversely, the isolation rate from wildlife is positively correlated with elevation ($r = 0.3$, $P < 0.05$) contrary to the result seen in livestock. Twelve novel biotype 2 pathogenic *Y. enterocolitica* carried *ail* and *ystB* virulence genes, and one biotype 1A nonpathogenic strain positive with *ail*, *ystB* and *ystA* genes were isolated from *Microtus fuscus* (Qinghai vole) on plague foci of the Qinghai–Xizang plateau. The PFGE pattern K6GN11C30021 was predominant in pigs (44.25%) and patients (41.18%); K6GN11C30068 was predominant in dogs (40.16%). Animal isolates from the same region shared the same pattern (K6GN11C30021 and K6GN11C30012), indicating they may be from the same clone and arose through cross infection. Moreover, the identical PFGE pattern among local animals and diarrhea patients suggested that the animals may be the source of infections in these areas.



## 1. Introduction

There is a significant rise in the popularity of open farms and petting zoos in China with the increased development of the social economy. People may expose to zoonotic disease, especially multi-host pathogens, through activities such as feeding and

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http://dx.doi.org/10.1016/j.vetmic.2015.05.006
0378-1135/

handling of the animals, which make it difficult to control infections in animals and humans (Jones et al., 2013; Virtanen et al., 2011). Precautions to control the spread of zoonotic disease require an understanding of the ecology and distribution of the pathogens in their hosts and vectors (Keesing et al., 2006). Yersiniosis has three well known human and animal pathogens, *Yersinia pestis*, *Yersinia* enterocolitica, and *Yersinia* pseudotuberculosis. *Y. enterocolitica* and *Y. pseudotuberculosis* are enteropathogens with diverse animal hosts and are more prevalent in recent years due to human transmission via the fecal/oral route and prevalence in farm animals (Galindo et al., 2011). *Y. pestis* causes the plague and is a mammalian vector-borne disease transmitted by fleas that serves as the vector between the rodent hosts (Achtman et al., 1999; Easterday et al., 2012).

*Y. enterocolitica* is a Gram-negative member of the *Enterobacteriaceae* family and observed on many continents (McNally et al., 2004; Wren, 2003). In Europe, human yersiniosis is the third most common enteric disease after campylobacteriosis and salmonellosis (Backhans et al., 2011; Bucher et al., 2008). *Y. enterocolitica* is divided into six biotypes (1A, 1B, 2, 3, 4, and 5) and 60 serotypes (Fredriksson-Ahomaa and Korkeala, 2003a). Most *Y. enterocolitica* types associated with human yersiniosis belong to bioserotypes 1B/O:8, 2/O:9, 3/O:3, 4/O:3 and 2/O:5,27 (Prentice et al., 1991). Two outbreaks causing more than 500 infections were reported in China in the 1980s (Wang et al., 2008). *Y. enterocolitica* is recovered from diverse animal sources including farm animals, domestic pets, and free-living and captive wild animals. Pigs serve as the primary reservoir having a high prevalence of pathogenic *Y. enterocolitica* (Bucher et al., 2008; Fosse et al., 2009; Liang et al., 2012), and dogs are also considered to be the potential source of human infections in China (Wang et al., 2010). In addition, isolates from goats, sheep, cattle, cats, wild rodents and wild boars have also been reported as carriers by other countries (Backhans et al., 2011; Bottone, 1999; Fredriksson-Ahomaa and Korkeala, 2003b; Lanada et al., 2005; Wang et al., 2009). As a zoonotic pathogen, the geographic distribution of pathogenic *Y. enterocolitica* in China significantly differed (Wang et al., 2009), and the prevalence of *Y. enterocolitica* has a close relationship with distribution and activity of local animals. Therefore, there is a need to identify different sources of *Y. enterocolitica* and to understand the prevalence and transmission of *Y. enterocolitica* in China. In this study, we examined the prevalence of *Y. enterocolitica* among livestock and wildlife living in different regions of China and performed a homology study of the strains isolated and discussed the factors that impact the distribution and transmission of *Y. enterocolitica*.

## 2. Materials and methods

### 2.1. Animal collection and field sampling

Samples from livestock (pig, dog, sheep, cattle, chicken, and duck) and wildlife (rodents, *Ochotona curzoniae* (plateau pica) and bats) were collected from 60 different counties in China in different ecology landscapes: the Qinghai–Tibet Plateau (Qinghai, Sichuan–Shiqu County, Gansu); Loess Plateau (the Ningxia Hui Autonomous Region); Inner Mongolian Plateau (the Inner Mongolia Autonomous Region); Yunnan–Guizhou Plateau (Yunnan, Guizhou); Sichuan Basin (Sichuan–Mianyang, Ziyang and Jianyang); the Northeast China Plain (Heilongjiang); North China Plain (Henan, Beijing); Yangtze Plain (Jiangxi, Anhui, Jiangsu,

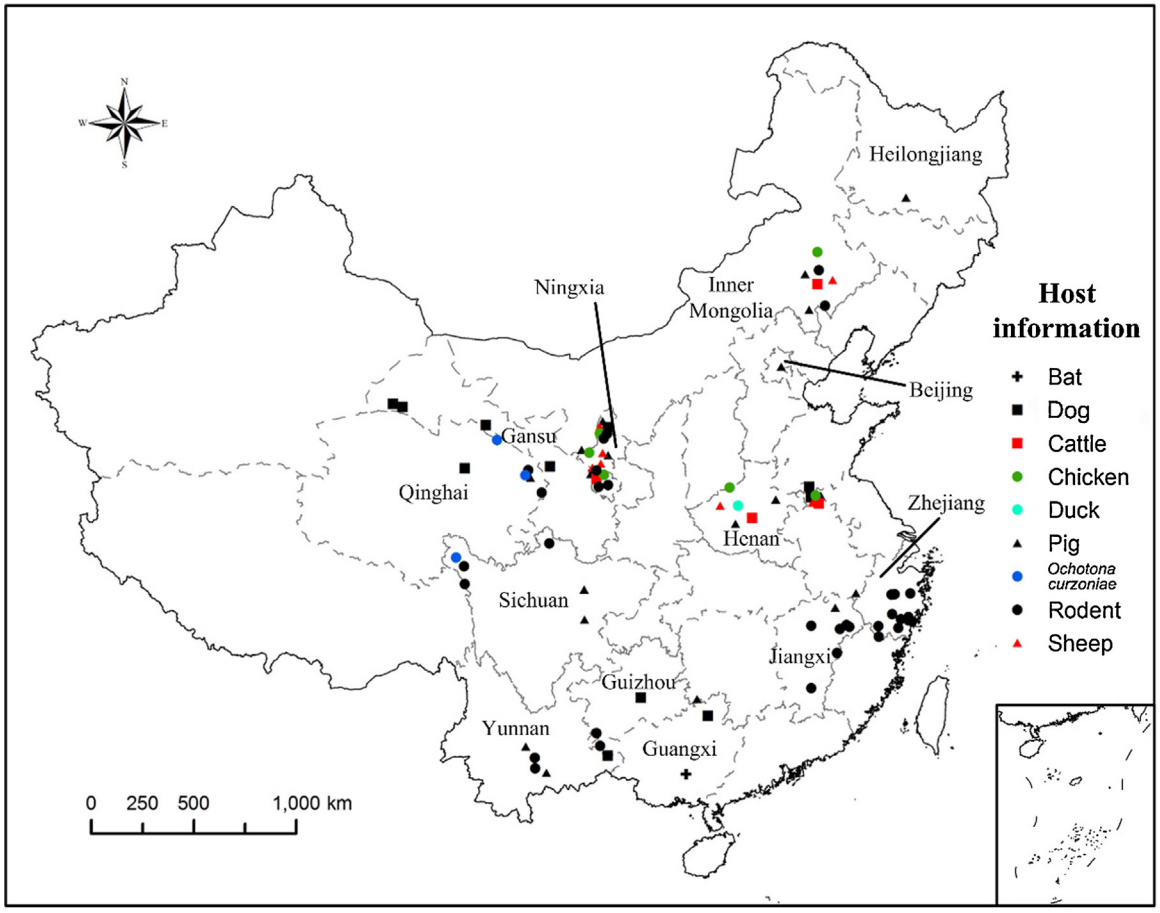


**Fig. 1.** Animal collection type and field sampling districts.