



The Gastrointestinal Parasites and Bacteria Community of Sable (*Martes zibellina*) in Northeastern China

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ABSTRACT

The sable was one species of holarctic carnivores and it was mainly in Russia, China, and Japan. There have little information about gastrointestinal parasite and bacterium of the sable, but it was important for its health. Five parasitic species and two hundreds thirty four gut bacteria (genus) of the sable were detected by the saturated NaCl floating and next sequencing methods. The parasites were *Capillaria* sp., *Baylisascaris devosi*, *Echinochasmus* sp., and two Coccidian species. The *Echinochasmus* sp. and two Coccidian species were first time found either in sable or in other martens. The 434 genus of bacteria, belong to 30 phylum, the more popular bacteria were Proteobacteria (33.54%), following by Firmicutes (18.58), Acidobacteria (12.82%), Actinobacteria (9.27%), Bacteroidetes (5.44%), Crenarchaeota (4.58%), Fusobacteria (2.66%), Verrucomicrobia (2.29%), Gemmatimonadetes (2.18%) and Planctomycetes (1.39%), and they were more than 92.75%. The gut bacteria of the sable have more diversity than Siberian tiger, panda, horse, and human, and it may originate from the more divertible diet of the sable.

Article Information

Received 07 November 2016

Revised 30 July 2017

Accepted 27 September 2017

Available online 02 August 2018

Authors' Contribution

DZ wrote the article and did lab work. YL and QS collected the samples and analysis of data. ZP helped in morphological observation of the eggs. YH and ZH designed the study.

Key words

Sable (*Martes zibellina*), Parasite, Bacteria community, Northeastern China.

INTRODUCTION

Sable, *Martes zibellina* (Linnaeus, 1758), one of eight species of *Mustela* (Mustelidae, Carnivora), is a circumboreal ones (Li, 2012; Steven *et al.* 1996). Four species of the *Mustela*, *Martes zibellina* (sable), *Martes americana* (American marten), *Martes martes* (pine marten), and *Martes melampus* (Japanese marten) are forest-dwelling carnivores that occur allopatrically in coniferous and deciduous forests in the Holarctic region (Ishida *et al.*, 2013). The sables were widespread in all taiga zoogeographical zones of Eurasia, primarily in Russia from the Ural Mountains throughout Siberia, in northern Mongolia and northeastern China, and on Hokkaido in Japan (Malyarchuk *et al.*, 2014; Li, 2012; Zhu *et al.*, 2017).

The sable is generally considered to have the most beautiful and richly tinted pelt among martens. Since the nineteenth century, intensive hunting for pelts has resulted in sable population dramatic declined in Russia and China (Li *et al.*, 2011). Habitat changes associated with forestry utilization had contributed to this loss (Steven *et al.*, 1996). In Russia, sables reached a nadir of distribution and abundance early in this century, but recovered

following protection, development of sable farming, and reintroduction (Steven *et al.*, 1996). To protect the sable, the Chinese government has added it to the list of wildlife under special state protection and has completely prohibited hunting and fur trade for this species since 1988, but the population still has not yet recovered in China until now (Li *et al.*, 2011).

Many studies, especially in the phylogeny, genetic variability and diversity, population genetic structure, species molecular distinguished, and ecology, had been done on the sables (Malyarchuk *et al.*, 2014; Ishida *et al.*, 2013; Mustonen *et al.*, 2006; Zhigileva *et al.*, 2014; Sato *et al.*, 2011; Rozhnov *et al.*, 2010, 2013; Nagai *et al.*, 2012; Monakhov, 2014; Maliarchuk *et al.*, 2010; Li *et al.*, 2014; Kinoshita *et al.*, 2015; Dubinin, 2010). There were also some articles on the parasitism of martens (Table I), but as to our knowledge, this was first report on sable parasitic fauna in China, and there was not any information of gut bacteria community about sable excepting this study.

MATERIALS AND METHODS

The fresh fecal samples of two rescued sable individuals originated from Northeastern China were collected when they were discharged into the environment timely. The samples was stored frozen at -20°C for using in later.

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0030-9923/2018/0005-1681 \$ 9.00/0

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Table I.- The parasites community of *Marets* have been documented.

<i>M. americana</i>	<i>M. martes</i>	<i>M. fonia</i>	<i>M. pennati</i>	<i>M. melampus</i>	<i>M. zibellina</i>
<i>Alaria taxideae</i>	\	<i>Angiostrongylus</i> sp.	\	\	\
<i>Baylisascaris devosi</i>	\	<i>Ascaridida</i>	\	\	<i>Ascaris</i>
<i>Crenosoma petrowi</i>	\	<i>Capillaria</i> sp.	\	\	<i>Crenosoma</i> sp.
<i>Dioctophyme renale</i>	\	<i>Dirofilaria</i>	\	\	<i>Capillaria</i> sp.
<i>Eucoleus aerophilus</i>	\	\	\	\	\
<i>Euryhelmsis aquamula</i>	\	\	\	\	\
<i>Filaroides martes</i>	\	\	\	\	<i>Filaroides</i> sp.
<i>Mesocestoides</i> sp.	\	\	\	<i>Hepatozoon</i>	<i>Mesocestoides</i> sp.
<i>Molineus patens</i>	<i>Skrjabinogylus petrowi</i>	<i>Skrjabinogylus petrowi</i>	\	\	<i>Skrjabinogylus petrowi</i>
<i>Pearsonema plica</i>	\	\	\	\	\
<i>Physaloptera</i> sp.	\	\	\	\	\
<i>Soboliphyme baturini</i>	\	\	<i>Sarcocystis</i> spp.	\	<i>Soboliphyme</i> sp.
<i>Taenia marits americanan</i>	\	<i>Taenia marits</i>	<i>Toxoplasma gondii</i>	\	<i>Taenia</i> sp.
<i>Taenia mustelae</i>	\	<i>Taenia</i> sp.	\	\	<i>Thominx</i> sp.
<i>Trichinella spiralis</i>	<i>Trichinella britovi</i>	<i>Molineus patens</i>	\	\	\
Hoberg <i>et al.</i> (1990), Zarnke <i>et al.</i> (2004), Seville and Addison (1995) and Poole <i>et al.</i> (1983)	Heddergott <i>et al.</i> (2015) and Moskwa <i>et al.</i> (2012)	Heddergott <i>et al.</i> (2015), Kornas <i>et al.</i> (2013), Real and Torino (2011) and Miterpakova <i>et al.</i> (2013)	Larkin <i>et al.</i> (2011)	Kubo <i>et al.</i> (2009)	Li (2012) and Heddergott <i>et al.</i> (2015)

There was no any report in published document.

Subsequently, the parasitic fauna was examined by centrifugal flotation in concentrated NaCl solutions to detect parasitic eggs as described by Kocjan *et al.* (2008). The stored examples with dry ice were transformed to Sangon Biotech (Shanghai Co., Ltd.) for detecting the Bacteria fauna. The V3-V4 regions of the bacterial 16S rDNA were amplified and sequenced on the Illumina Miseq platform. The primers were 341F and 805R. 341F: CCCTACACGACGCTCTTCCGATCTG (barcode) CCTACGGGNGGCWGCAG; 805R: GACTGGAGT TCCTTGCGACCCGAGAATTCCAGACTACHVG-GGTATCTAATCC) barcodes, chimeras, and out target numbers or ambiguous bases were removed dataset. The remaining Sequences were then clustered into OTUs at a cutoff of 97% similarity using uclust (v1.1.579). Taxonomic assignments of the OTUs were made down to the genus level (cutoff, 0.8) using the Ribosomal Database Project (RDP) classifier with the Bayesian method.

RESULTS

Five parasitic species, two nematodes, one trematode, and two protozoa (Coccidian), were found in sable feces, and they are *Capillaria* sp., *Baylisascaris devosi*, *Echinochasmus* sp., and two different Coccidian species (each of them maybe *Eimeria* sp. or *Isospora* sp.) (Fig. 1). The *Echinochasmus* sp. and two Coccidian species

were first time found either in sable or in other martens. There were 434 genres of bacteria, belong to 30 phylums homed in the gut of the sable (Fig. 2, Table I). The more popular bacteria were Proteobacteria (33.54%), Firmicutes (18.58), Acidobacteria (12.82%), Actinobacteria (9.27%), Bacteroidetes (5.44%), Crenarchaeota (4.58%), Fusobacteria (2.66%), Verrucomicrobia (2.29%), Gemmatimonadetes (2.18%), and Planctomycetes (1.39%), they were more than 92.75%.

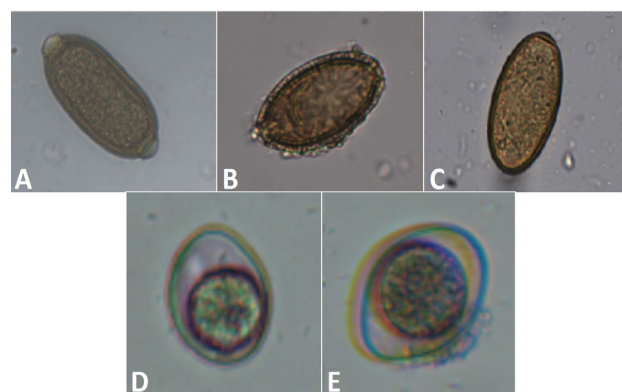


Fig. 1. A, *Capillaria* sp. (63.9×25.9μm); B, *Baylisascaris devosi* (55.6×32.1μm); C, *Echinochasmus* sp. (66.9×37.4μm); D and E, two different Coccidian species (31.9×25.9μm) (42.4×31.7μm).

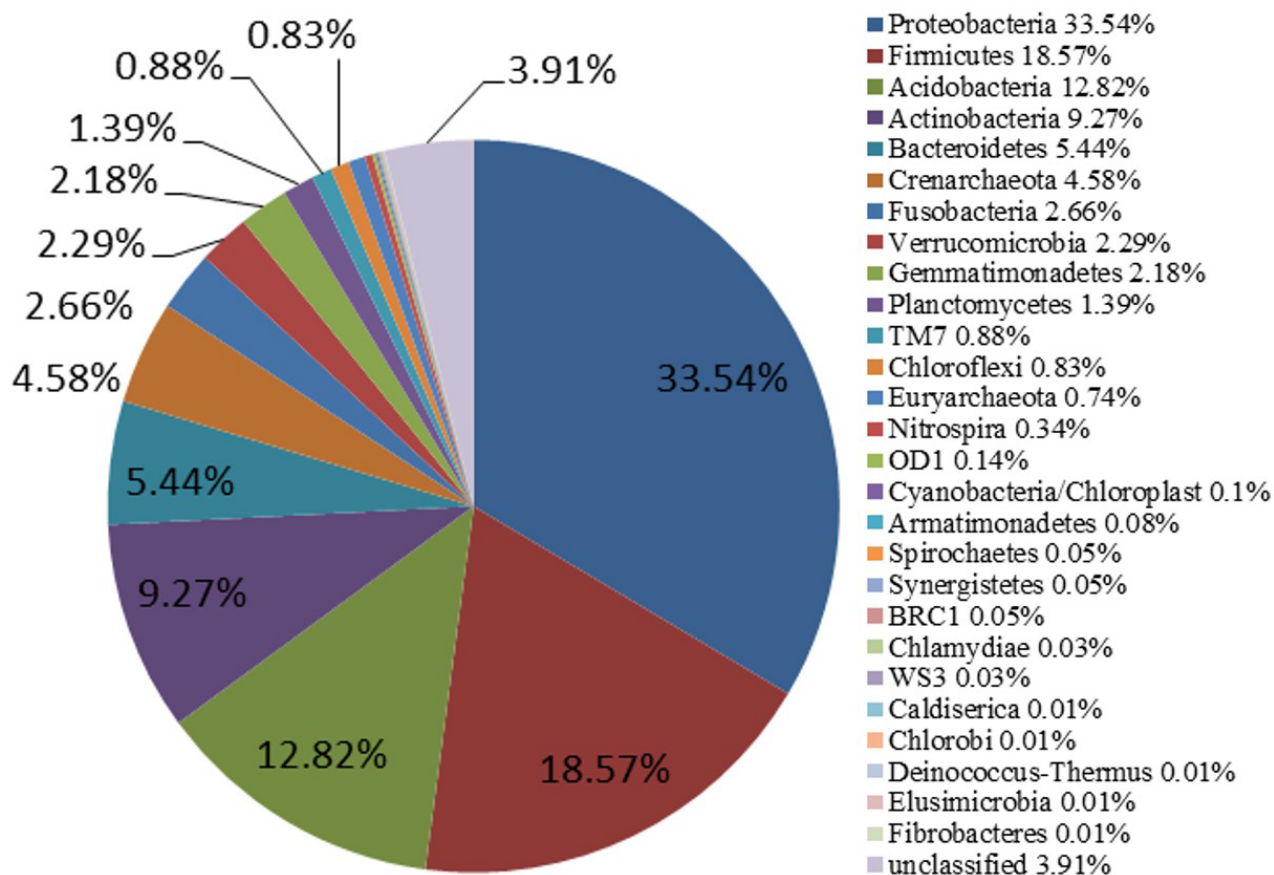


Fig. 2. The bacteria community of the sable gut on phylum.

Table II.- The bacteria communities of the sable, Siberian tiger, panda, horse and human on phylum.

Bacteria groups	Sable	Siberian tiger	Panda	Horse	Human
Proteobacteria	33.54%	6.16	15.77	0.95	2.81
Firmicutes	18.57%	33.56	83.90	69.21	57.20
Acidobacteria	12.82%	0	0	Nearby 0 or 0	Nearby 0 or 0
Actinobacteria	9.27%	2.95	0	0	2.22
Bacteroidetes	5.44%	23.82	0.02	5.71	32.00
Crenarchaeota	4.58%	0	0	Nearby 0 or 0	0
Fusobacteria	2.66%	33.47	0.16	0	2.2
Verrucomicrobia	2.29%	0	0	18.13	Nearby 0
Gemmatimonadetes	2.18%	0	0	Nearby 0 or 0	0
Planctomycetes	1.39%	0	0	Nearby 0 or 0	0

DISCUSSION

Although nine parasitic species had been reported could infect the sable in Russia, only five species were

found in this study. Although this may attribute to the zoogeographical zone difference of the sable between in Russia and China, but the limited samples numbers of this study is another cannot be ignored factor.

The *Echinochasmus* sp. could infect the sable was discovered in this research at first time. As the document, the rodents, fox, cat, dog, or other some carnivores could be as the final host of the *Echinochasmus* sp., the river snail as first intermediate host, and fish or frog as the second intermediate host (Kong, 1997). Obviously the *Echinochasmus* sp. infected the final host when they eaten the frog or fish, which as the second intermediate host. But this situation, it may be not really for sable. Kang *et al.* (2003) and Xu *et al.* (1996) had reported that many plants or plant seeds and animals excepting the fish and frog can be as the diet for the sable in China, so if the *Echinochasmus* sp. was disseminated between sables by fish or frog or by other ways we still unknown was in doubt, and the fact need additional research to do in the future.

Two Coccidian obviously different on the shape (Fig. 1) were detected from the sable feces, but we could not confirmed which specific species they were *Isospora*, *Eimeria*, or other coccidian specie, based only on the shape. And egg incubating or molecular way would be a useful method to the fact in next step.

There was three species, *Echinochasmus* sp., and *Eimeria* sp. or *Isospora* sp., were reported either in sables or in other martens at first time, but any other information more that could be afforded in this study, and the potential health risks of those new found parasites for the sable require more additional research.

The sable gut bacteria belong to 26 phylum, contrast with the Siberian tiger, panda, horse, and human, they were 6, 6, 16, and 20 one, and it could be concluded that the gut bacteria of the sable had more diversity (Table II). The majority gut bacteria of the sable were Proteobacteria, but other animal ones were Firmicutes. More interesting, the Acidobacteria (12.82%) were mainly bacteria of the sable, but they were zero or nearby zero in other animals. Those may attribute to the diet diversity of the sable.

Although the data reported in this paper are limited due to relatively small sample size and can therefore be considered preliminary, this study revealed which bacteria and parasites are present in the digestive tract of the sable members. And addressing questions such as the potential health risks for the sable or its role in disease transmission require more exhaustive sampling and additional research.

CONCLUSION

Five parasitic species and two hundreds thirty four gut bacteria (genus) of the sable were detected. The study concluded that gut bacteria of the sable have more diversity.

ACKNOWLEDGMENT

This research was supported by the National Key Research and Development Program of China (No. 2018YFD0502201); The Fundamental Research Funds for the Central Universities (No. 2572018BE07).

Statement of conflict of interest

There was not any interest conflicts with others person or affiliation, and all authors have seen the manuscript and approved to submit to your journal. This manuscript has neither been submitted nor to be submitted to any other journal.

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