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Data Article

# Microbiome dataset of the cardiopulmonary nematode *Angiostrongylus vasorum*

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ABSTRACT

*Angiostrongylus vasorum* is an emerging parasitic nematode of dogs, red foxes, and other wild canids. The severity of infection in dogs ranges from subclinical to fatal cardiopulmonary and bleeding disorders collectively known as canine angiostrongylosis. A symbiotic relationship between microorganisms such as bacteria and their eukaryotic hosts is commonly observed in nature. The mutualistic role of bacteria has been documented in plant-parasitic nematodes, gastrointestinal nematodes, and filarial nematodes. The importance of the bacteria for the survival of these parasites has been demonstrated with antibiotic treatments. To characterize associated bacteria of adult *A. vasorum* parasites, 36 individual worm samples were used. The worms were extracted from foxes hunted either in the city or in the rural regions within the Canton of Zurich, Switzerland. DNA was isolated and the V3/V4 hypervariable region of the bacterial 16S rRNA gene was amplified. Sequenced Illumina MiSeq reads were analysed using QIIME2. The data were used to profile the abundance and diversity of microbial communities in worms originating from either rural or urban foxes.



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## Specifications Table

| | |
|---|---|
| Subject | Microbiology: microbiome |
| Specific subject area | Profiling of *Angiostrongylus vasorum* bacterial composition using targeted 16S rRNA sequencing |
| Type of data | Table<br>Chart<br>Graph<br>Figure<br>MiSeq Sequencing Datasets (16S rRNA gene) |
| How data were acquired | Targeted sequencing of the V3/V4 hypervariable region of the bacterial 16S rRNA of extracted DNA from 36 individual worms.<br>Instruments: Illumina MiSeq Platform (300 × 2 pair-end)<br>Software: QIIME 2 |
| Data format | Raw (FASTQ)<br>Analysed |
| Parameters for data collection | A total of 36 adult *A. vasorum* specimens were collected post-mortem from 12 foxes (*Vulpes vulpes*) hunted in the rural and urban areas of the Zurich Canton, Switzerland. |
| Description of data collection | DNA was extracted from individual worms and sequenced using the Illumina MiSeq platform. Sequences were analysed using the QIIME 2 microbiome analysing platform |
| Data source location | Institution: Institute of Parasitology, University of Zurich<br>City/Town/Region: Zurich<br>Country: Switzerland<br>Samples were collected from Zurich Canton |
| Data accessibility | Repository name: NCBI SRA<br>Data identification number: BioProject: PRJNA761297<br>Direct URL to data:<br>SRA: https://www.ncbi.nlm.nih.gov/sra/PRJNA761297<br>BioProject: https://www.ncbi.nlm.nih.gov/bioproject/761297<br>Supplementary files Repository name: Mendeley Data<br>Data identification number: doi: 10.17632/z3954hx8vj.1 |
| Related research article | Tayyrov A., Schnetzler M., Gillis-Germitsch N., Schnyder M.: Genetic diversity of the cardiopulmonary canid nematode *Angiostrongylus vasorum* within and between rural and urban fox populations. Infect Genet Evol. 2021; 87:104618. https://doi.org/10.1016/j.meegid.2020.104618. [1] |

## Value of the Data

- These data represent the microbiome composition of the parasitic nematode *A. vasorum.*
- *vasorum* microbiome data generated may be useful for Microbiome and helminth researchers.
- The microbiome dataset of *A. vasorum* can be used to identify essential bacteria of the parasite with the potential to be used as an alternative control measure.

## 1. Data Description

Table 1 shows sampling parameters for 36 individual worms. Half of the worms (18) were isolated from foxes that were shot in rural regions of the Zurich Canton while the other half were from foxes shot in the city. Similarly, half of the worms were extracted from adult foxes (>12 months of age) while the other half were isolated from young (<12 months of age) foxes. One-fourth of the worms was isolated from female foxes. The number of sequenced reads before and after processing is shown in Supplementary file 1. The relative abundance of bacteria was depicted at the phylum (Fig. 1) and class (Fig. 2) levels. The corresponding operational taxonomical unit (OTU) values for all taxonomical levels from kingdom to species are provided in Supplementary Table 2. Figs. 3 and 4 show the analysis of the Shannon diversity index among individual foxes (Fig. 3) and between the rural and urban nematode populations, respectively (Fig. 4).

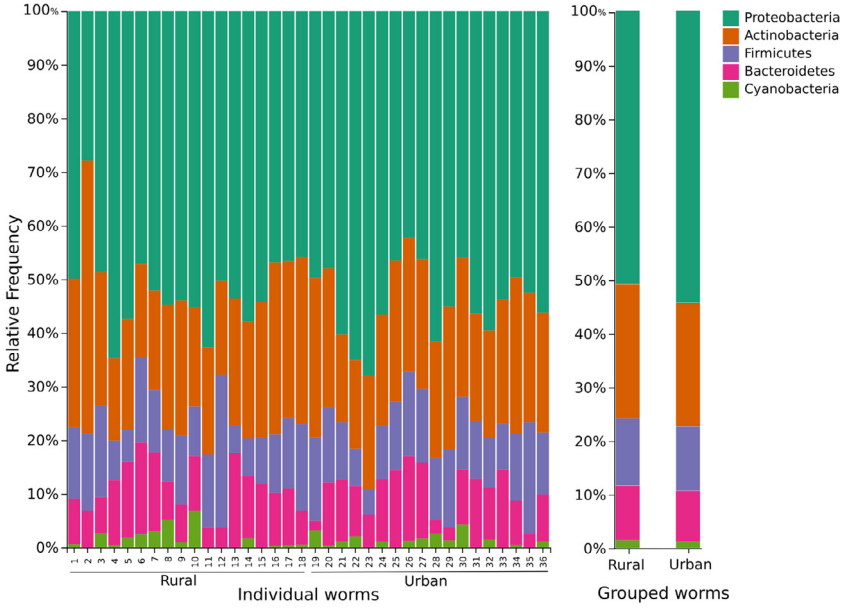


**Fig. 1.** The relative abundance of the bacterial composition of *A. vasorum* at phylum level for each of the 36 worms extracted from urban or rural foxes. The two columns on the right show combined relative abundance of the bacterial composition between rural and urban foxes.

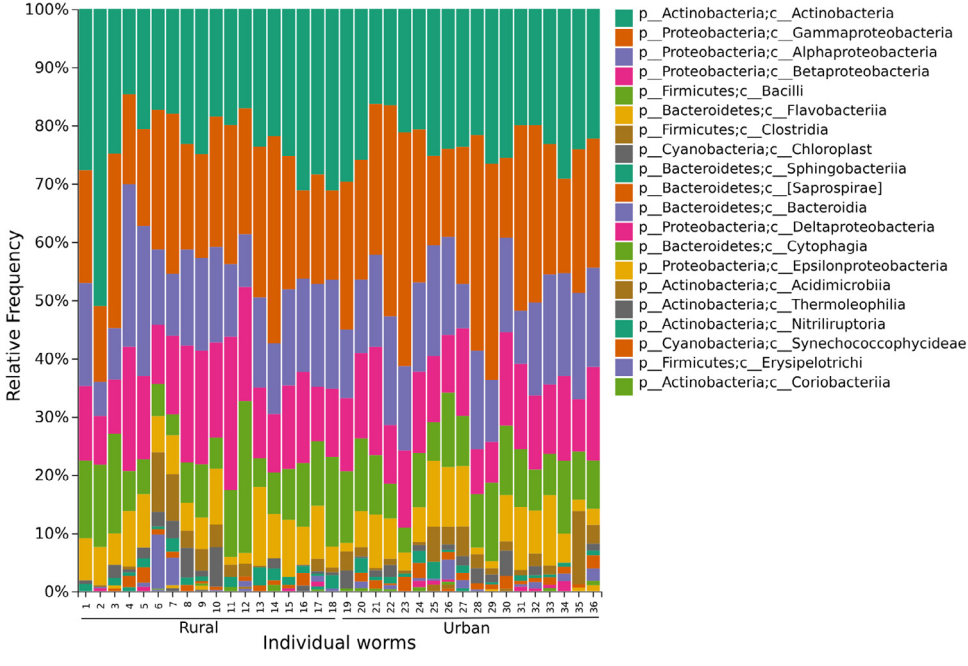


**Fig. 2.** Distribution of class level bacterial taxa of *A. vasorum* for each of the 36 worms originating from either urban or rural foxes.

**Table 1**
Sampling of 36 worms from 12 foxes living in rural or urban areas of Zurich Canton. Young: <12 months of age, Adult: >12 months of age.

| Number | Fox origin | Fox age | Fox gender | Worm per fox |
|---|---|---|---|---|
| 1 | Rural | Adult | Female | 3 |
| 2 | Rural | Adult | Female | 3 |
| 3 | Rural | Adult | Female | 3 |
| 4 | Rural | Young | Male | 3 |
| 5 | Rural | Young | Male | 3 |
| 6 | Rural | Young | Male | 3 |
| 7 | Urban | Adult | Male | 3 |
| 8 | Urban | Adult | Male | 3 |
| 9 | Urban | Adult | Male | 3 |
| 10 | Urban | Young | Male | 3 |
| 11 | Urban | Young | Male | 3 |
| 12 | Urban | Young | Male | 3 |

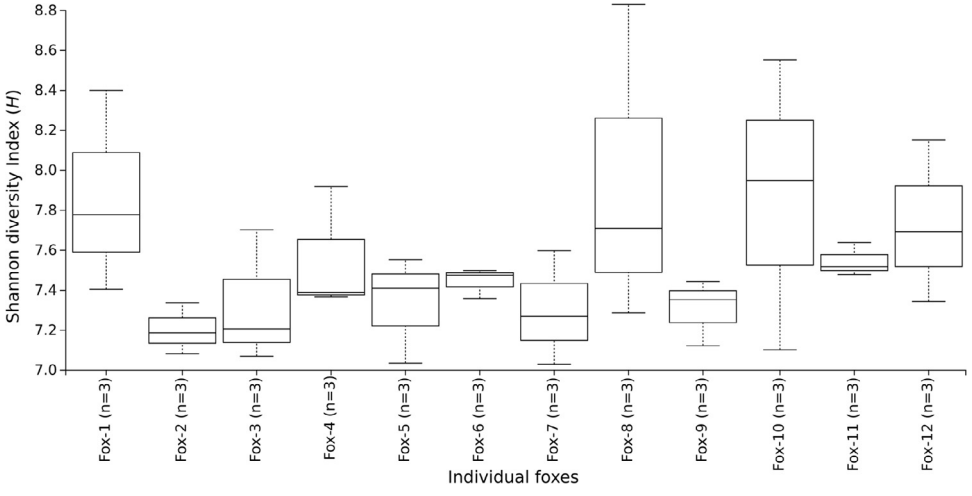


**Fig. 3.** Box plot representation of Shannon diversity index (evenness) of worms isolated from individual foxes. The line inside the box represents the median. The 1.5 interquartile range (IQR) is represented by the whiskers.

The raw FASTQ files generated in this study were deposited at the NCBI SRA database under BioProject PRJNA761297.

## 2. Experimental Design, Materials and Methods

### *2.1. Sample collection*

A total of 36 worms were extracted from 12 foxes that were hunted in the canton of Zurich (area: 1729 $km^2$), Switzerland [1]. To remove external contaminants, the worms were washed with sterile phosphate-buffered saline (PBS), pH 7.4, three times. The individual worms were used for DNA extraction using the E.Z.N.A.® Mollusc DNA extraction kit (Norcross, OMEGA, USA) according to the manufacturer's protocol as before [2]. The DNA was stored at −20 °C.

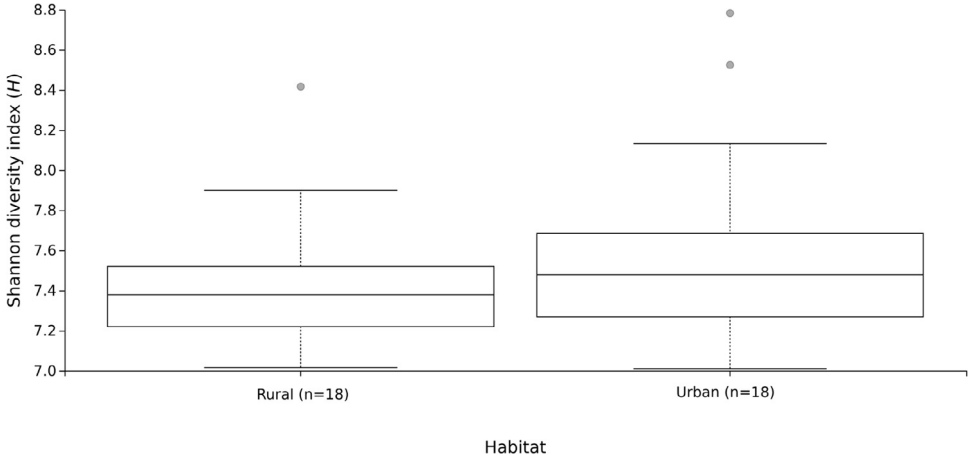


**Fig. 4.** Box plot representation of Shannon diversity index of worms based on the habitat of the host species. The dots present outliers while the line inside the box represents the median. The 1.5 interquartile range is represented by the whiskers.

### *2.2. 16S rRNA gene sequencing*

The V3/V4 hypervariable region (~500 bp) of the 16S rRNA gene was amplified on a PCR. The PCR was performed in a 50 µl volume that contained 25 µl 2 × HotStarTaq Plus Master Mix (Qiagen), 2.5 µl of 10 µM of each forward primer 341F (5′- CCT ACG GGN GGC WGC AG-3′) and reverse primer 805R (5′- GAC TAC HVG GGT ATC TAA TCC-3′) [3], 5 µl DNA and 15 µl ddH2O. The PCR steps comprised of an initial enzyme activation at 95°C for 15 min and 35 cycles of 94°C for 30 sec, 57°C for 1.5 min, and 72°C for 1 min, proceeded by a final extension step at 72°C for 15 min. The expected band length was confirmed by running a 10 µl PCR product on gel electrophoresis and analysing it on Alpha Innotech Gel Image Analysis System. Amplicon libraries were prepared according to Illumina's 16S Metagenomic Sequencing Library Preparation guidelines and sequenced as pair-end (2 × 300 bp) reads on the Illumina MiSeq platform.

### *2.3. Data analysis*

The reads were analysed using the Quantitative Insights Into Microbial Ecology 2 program (QIIME2, version 2018.8.0.) [4]. The de-multiplexed pair-end reads along with manifest file were imported into QIIME2 which creates a compressed *paired-end-demux.qza* file. The reads were pre-processed and filtered using Divisive Amplicon Denoising Algorithm 2 (DADA2) plugin of QIIME2 [5]. Truncation parameters (*–p-trunc-len-f 296, –p-trunc-len-r 226*) for DADA2 was estimated using FIGARO program [6]. De-noised amplicon sequence variants (ASVs) were assigned to their taxonomies using QIIME2 feature-classifier plugin [7] against the pre-trained *Silva 138 99% OTUs full-length sequences* dataset (MD5: b8609f23e9b17bd4a1321a8971303310) [8]. Using diversity alpha-group-significance (*–p-sampling-depth 80387*) plugin of QIIME2, Shannon diversity index – a measure of species evenness, was calculated.

## Ethics Statement

Ethical approval is not required as foxes are being hunted by gamekeepers every year to control the very abundant fox population.

## CRediT Author Statement

**Annageldi Tayyrov:** Methodology, Data curation, Data analysis, Writing-Original draft preparation; **Manuela Schnyder:** Supervision, Writing- Reviewing and Editing.

## Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships which have or could be perceived to have influenced the work reported in this article.

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## Supplementary Materials

Supplementary material associated with this article can be found in the online version at doi:10.1016/j.dib.2021.107648.

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