



## ADDAGMA: A database for domestic animal gut microbiome atlas

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### ABSTRACT

Animal gut microbiomes play important roles in the health, diseases, and production of animal hosts. The volume of animal gut metagenomic data, including both 16S amplicon and metagenomic sequencing data, has been increasing exponentially in recent years, making it increasingly difficult for researchers to query, retrieve, and reanalyze experimental data and explore new hypotheses. We designed a database called the domestic animal gut microbiome atlas (ADDAGMA) to house all publicly available, high-throughput sequencing data for the gut microbiome in domestic animals. ADDAGMA enhances the availability and accessibility of the rapidly growing body of metagenomic data. We annotated microbial and metadata from four domestic animals (cattle, horse, pig, and chicken) from 356 published papers to construct a comprehensive database that is equipped with browse and search functions, enabling users to make customized, complicated, biologically relevant queries. Users can quickly and accurately obtain experimental information on sample types, conditions, and sequencing platforms, and experimental results including microbial relative abundances, microbial taxon-associated host phenotype, and P-values for gut microbes of interest. The current version of ADDAGMA includes 290,422 quantification events (changes in abundance) for 3215 microbial taxa associated with 48 phenotypes. ADDAGMA presently covers gut microbiota sequencing data from pig, cattle, horse, and chicken, but will be expanded to include other domestic animals. ADDAGMA is freely available at (<http://addagma.omicsbio.info/>).

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## 1. Introduction

A great number and variety of microorganisms colonize the mammalian intestine. The gastrointestinal microbiome is a consortium of multiple bacteria, archaea, fungi, and protozoa [1]. Increasing evidence has recently demonstrated that the gut microbiota is crucial to many processes in vertebrate hosts, including development [2,3], disease [4–9], immunization [10–13], and metabolism [14–17]. For example, Fuyong Li et al. [18] found significantly different populations of *Firmicutes* and *Chloroflexi* between high- and low-RFI (residual feed intake) animals. Chong Liu et al. [19] reported that the taxonomic composition of gut bacteria changes with age and is correlated with age-related changes in methane

emission. Within the context of constraining factors such as age and diet, the composition of microbial species early in life stages plays a crucial role in the dynamics of late-succession taxa [20]. A broad range of factors is responsible for differences in the intestinal microflora among hosts, including breed, diet, age, health status, environment, genetic background, and antibiotics [21–27].

Metagenomic sequencing technology, with its advantages of high throughput, low cost, and high speed, makes it possible to study gastrointestinal microbiomes solely by extracting DNA from a gut sample, without having to rely on the cultivation of microorganisms from the sample. The development of high-throughput sequencing and the rapid accumulation of genomic and 16S data from human and animal gut microbiota have given rise to various interrelated databases such as the European Nucleotide Archive (ENA) [28], National Center for Biotechnology Information (NCBI), Sequence Read Archive (SRA) [29], and DNA Data Bank of Japan (DDBJ) [30]. These databases store public sequencing results as

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