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DRGM: A Comprehensive Reference Catalog of the Dog Gut Microbiome

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The gut microbiome plays a crucial role in host health, and this relationship is equally significant in dogs. However, existing dog gut microbiome reference catalogs are constrained by small sample sizes and limited diversity, which can introduce bias. To address these limitations, we developed the Dog Reference Gut Microbiome (DRGM) catalog. Using whole metagenomic sequencing (WMS) data from 1,752 publicly available fecal samples and 16 newly collected ones across Asia, Africa, and Europe, we reconstructed Metagenome-Assembled Genomes (MAGs) through de novo assembly, yielding 931 genome species of medium quality or higher. Most DRGM species were classified into Bacillota_A, with additional representation from Bacteroidota, Pseudomonadota, and Bacillota. Comparative analysis with human gut microbiomes revealed that 399 DRGM species were shared with humans. Among these, Fusobacteriota showed the highest shared rate, followed by Bacillota_C, Bacillota, and Actinomycetota. Given that dogs differ in their degree of contact with humans, we next compared pet and kennel dogs, and found that the proportion of shared species was significantly higher in pet dogs. We further extended the catalog beyond bacteria by including viral genomes, providing a more comprehensive multi-kingdom resource. The DRGM catalog thus offers a geographically diverse and taxonomically broad reference that enables comparative studies of human and dog gut microbiomes, advancing research on host–microbe interactions within the One Health framework.