

Convergent Evolution of Metabolic Functions: Evidence from the Gut Microbiomes of Humans and Dogs

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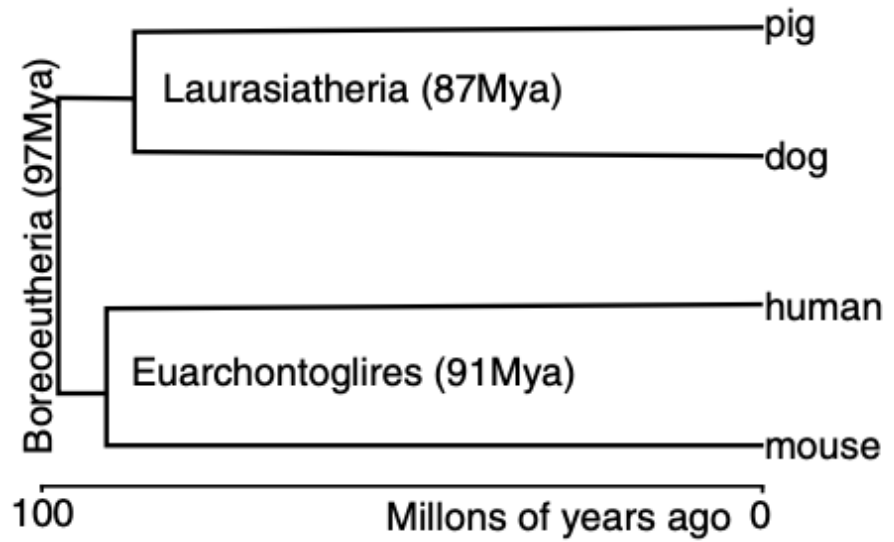
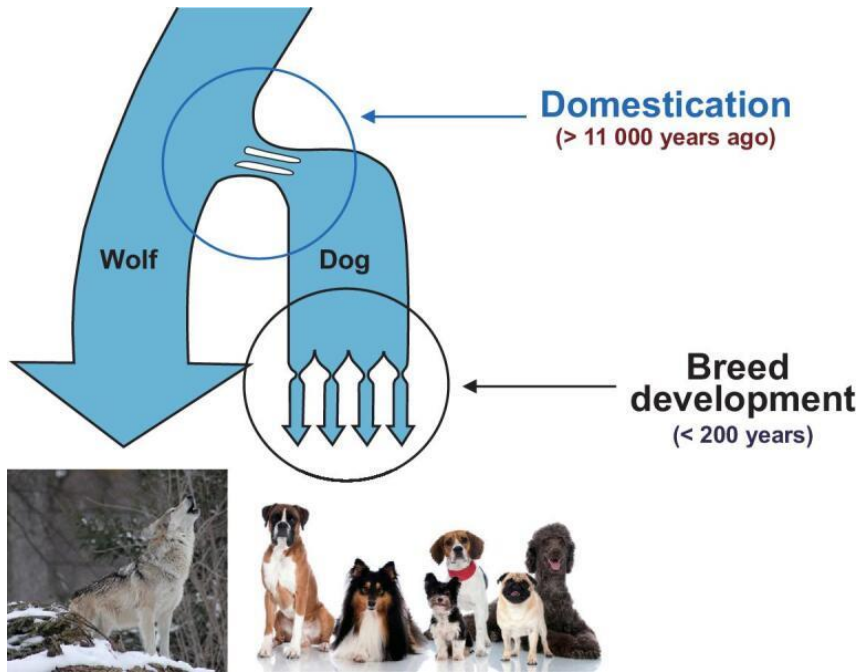
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Introduction



Coelho et al., 2018



Dogs and humans have convergent evolution
in genes related to the starch-based diet



Materials and Methods

Fecal
samples
from six
groups



Macaques

Zoo
wolves



Wild
wolves



Working dogs

nature
biotechnology

RESOURCE

<https://doi.org/10.1038/s41587-020-0603-3>

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A unified catalog of 204,938 reference genomes from the human gut microbiome

Alexandre Almeida^{1,2}✉, Stephen Nayfach^{3,4}, Miguel Boland¹, Francesco Strozzi⁵, Martin Beracochea⁶, Zhou Jason Shi^{6,7}, Katherine S. Pollard^{6,7,8,9,10,11}, Ekaterina Sakharova¹, Donovan H. Parks¹², Philip Hugenholtz¹², Nicola Segata¹³, Nikos C. Kyrpides^{3,4} and Robert D. Finn¹✉

Human metagenomes from public

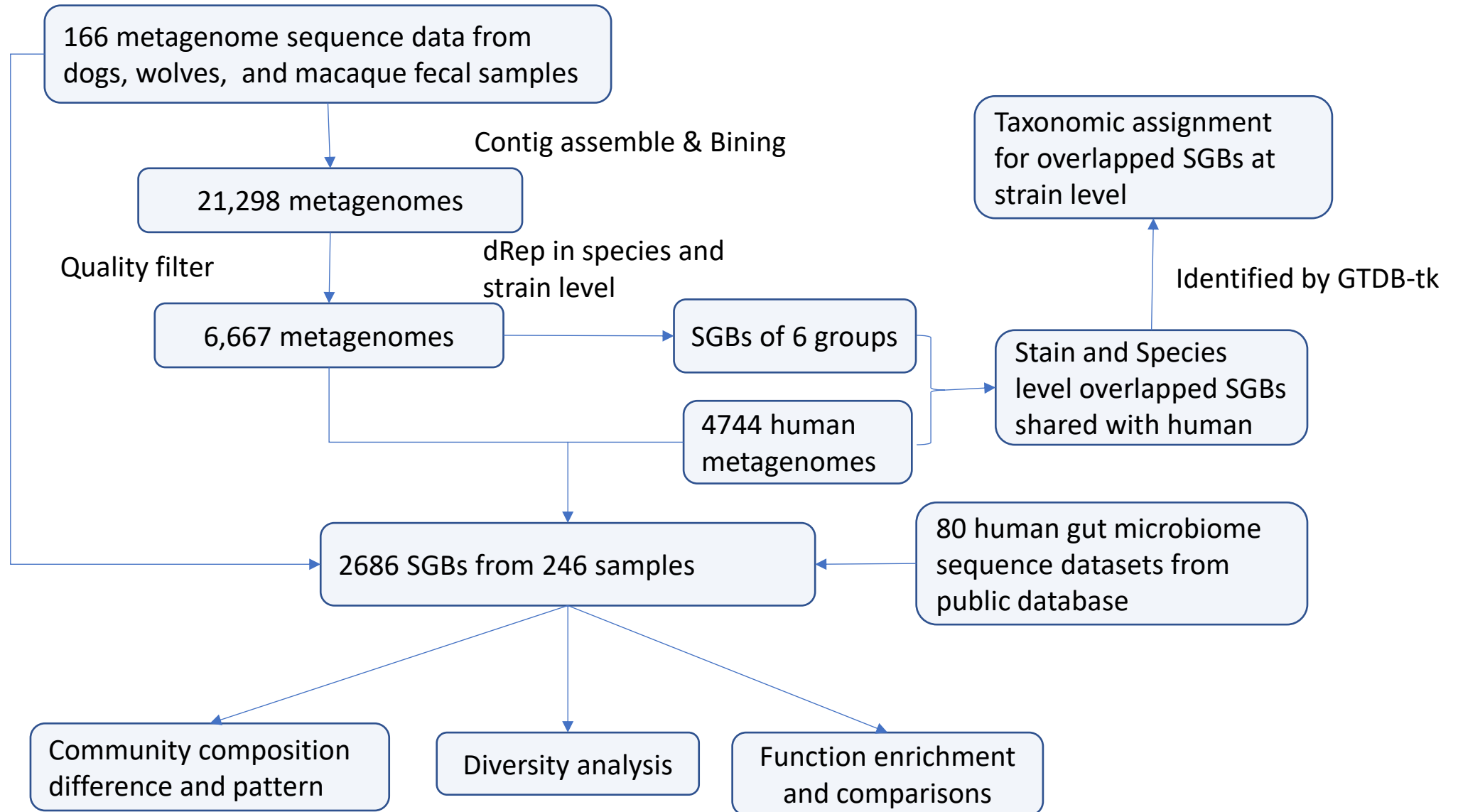


Indigenous dogs



Pet dogs

Materials and Methods



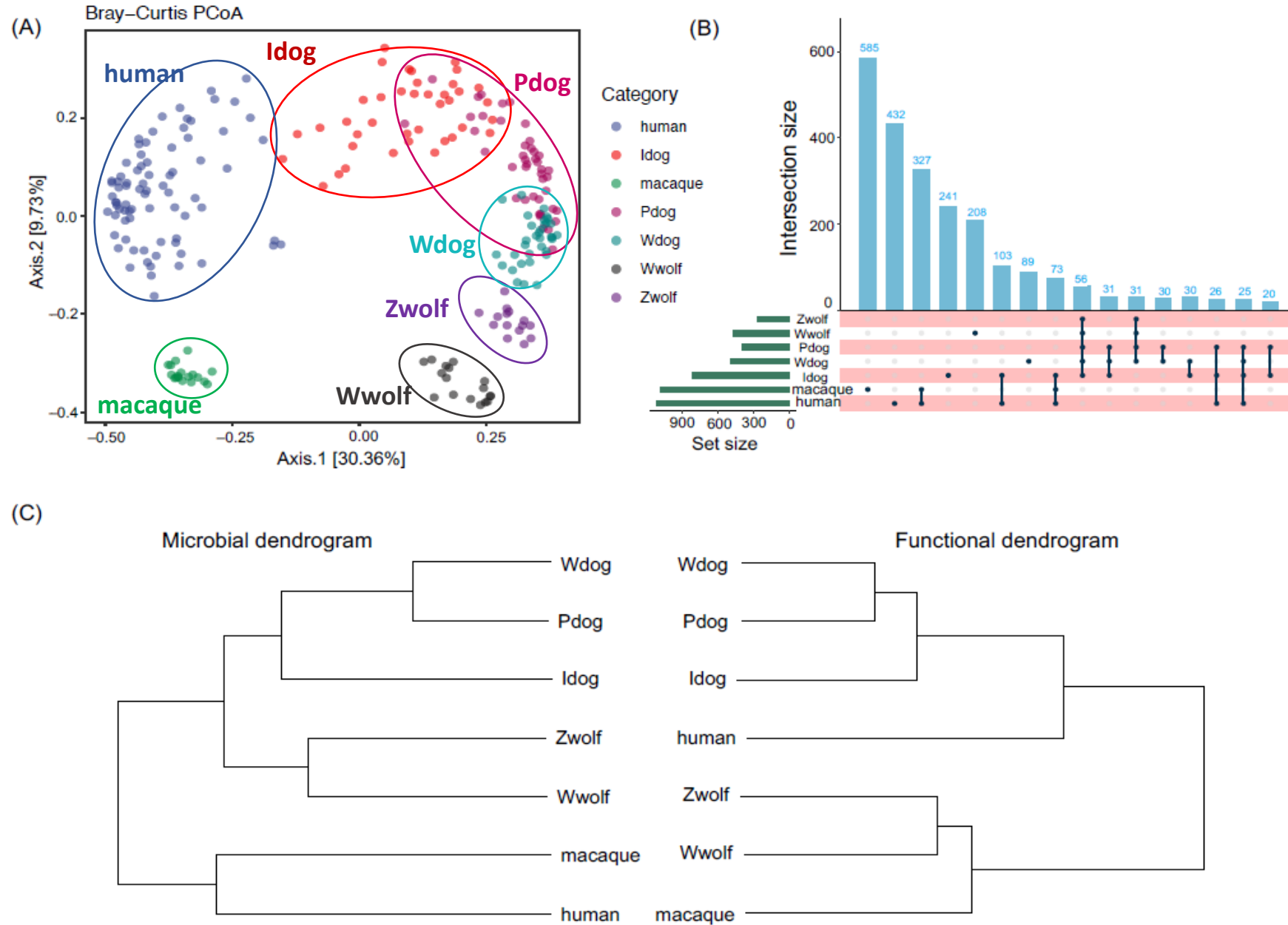
Results

Group	Specimens	MAGs	QS	dRep99	dRep95	Overlapped in stain level	Ratio (%)	Overlapped in species level	Ratio (%)
Zoo wolf	15	1818	384	148	119	8	5.41	45	37.82
Wild wolf	17	3009	982	496	352	6	1.21	48	13.64
Indigenous dog	39	3452	1140	673	426	88	13.08	235	55.16
Pet dog	43	4803	1481	495	240	60	12.12	142	59.17
Working dog	34	5076	1515	441	326	43	9.75	125	38.34
Macaque	18	3131	1165	639	374	34	5.32	225	60.16
Total	166	21,289	6667	2892	1837	239	8.26	820	44.64

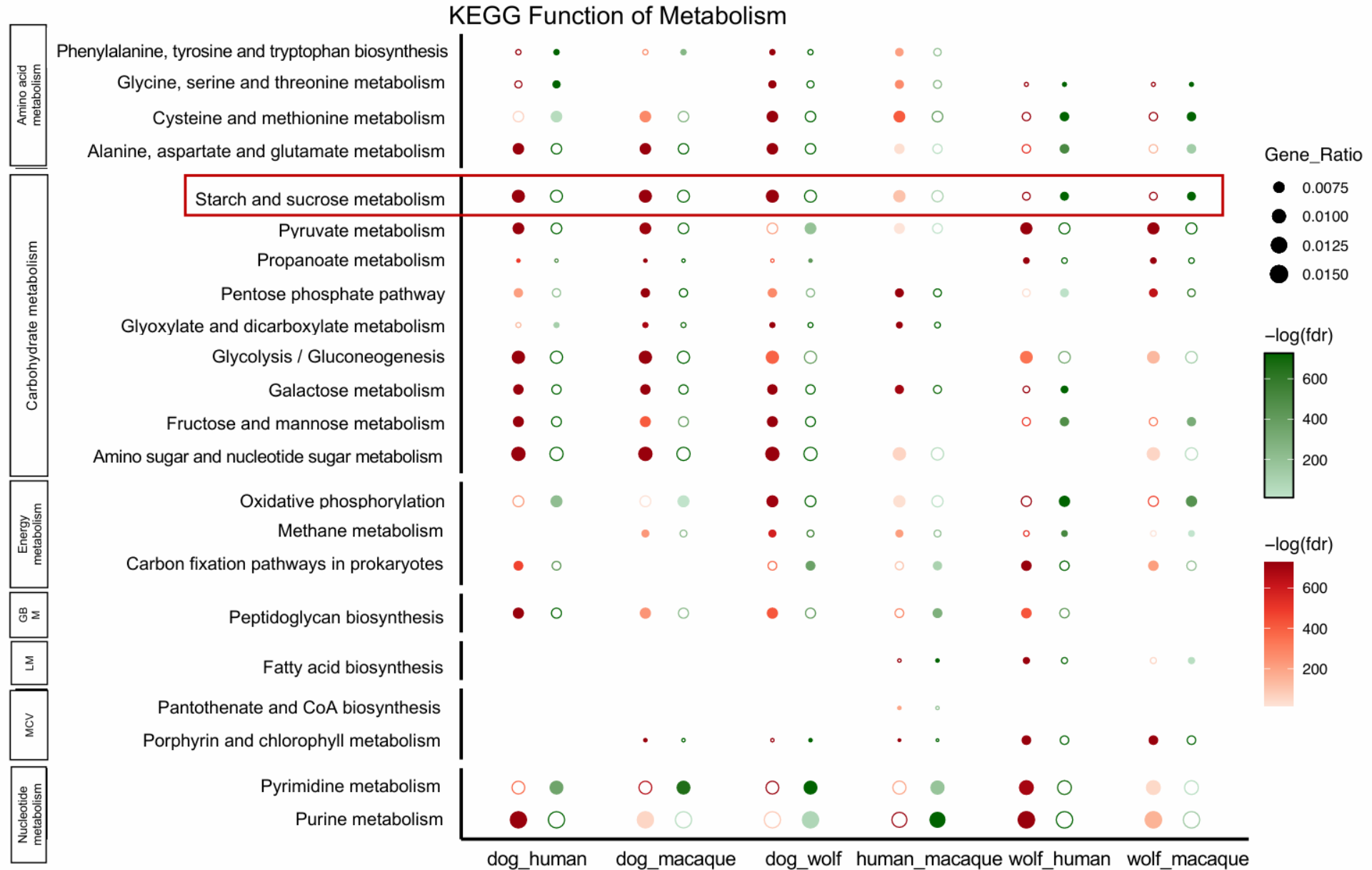


- Low number of gut microbial species was detected in zoo wolf samples.
- At the **species level** (95%), **macaques** shared the most gut microbial species with humans, followed by **dogs (pet dogs)**.
- At the **strain level** (99%), however, **dogs (indigenous dog)** shared the most microbial strains with humans.

Results



Results

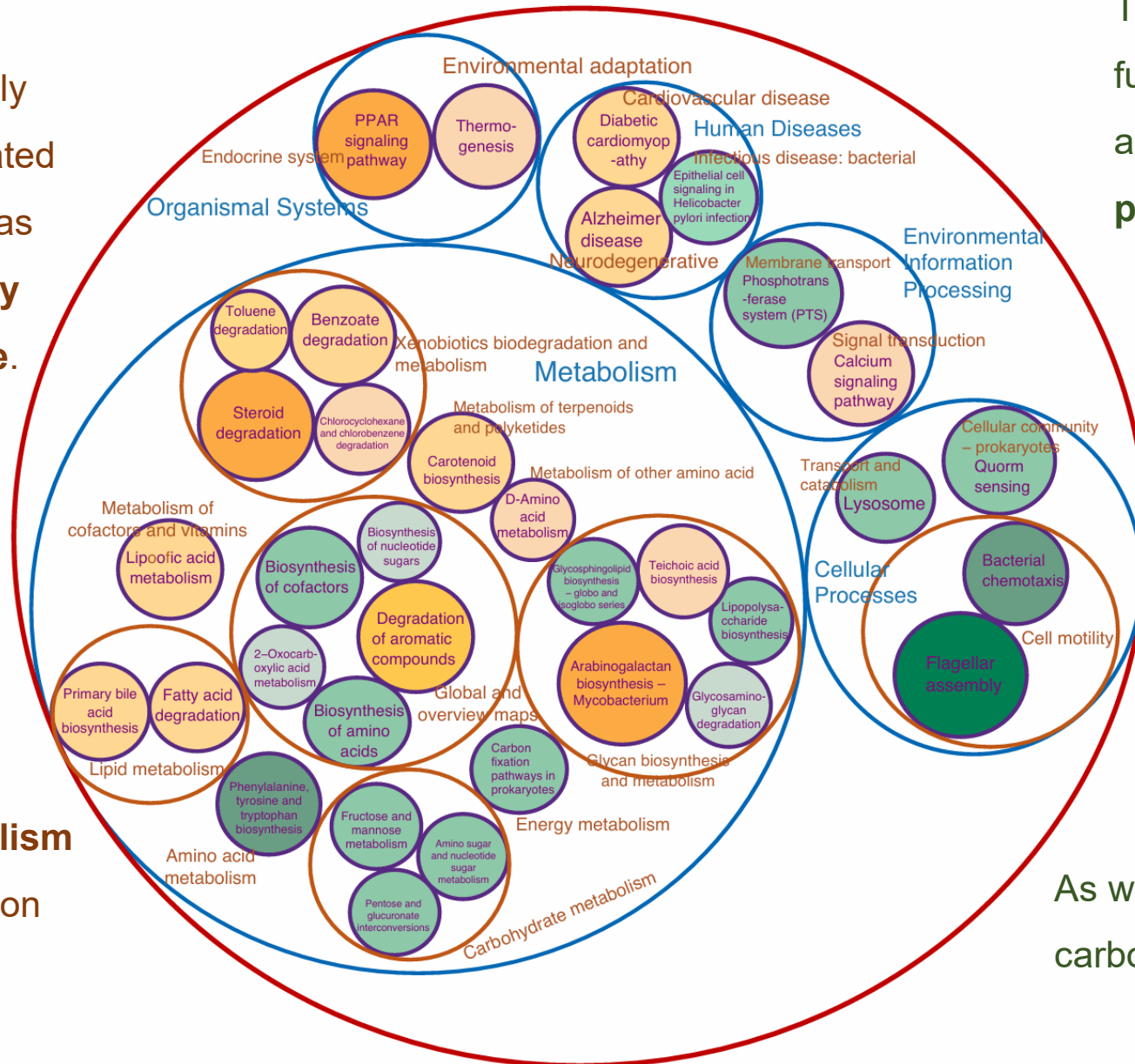


Results

In working dogs, the gut microbiota was functionally enriched in pathways related to human diseases such as **diabetic cardiomyopathy** and **Alzheimer's disease**.



As well as in pathways involved in **lipid metabolism** and xenobiotic degradation et al.



The gut microbiota of pet dogs was functionally enriched in the pathway associated with **human *Helicobacter pylori* infection**.

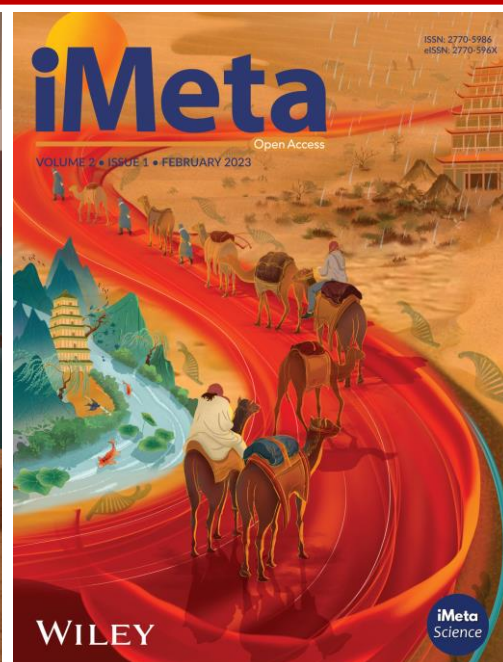
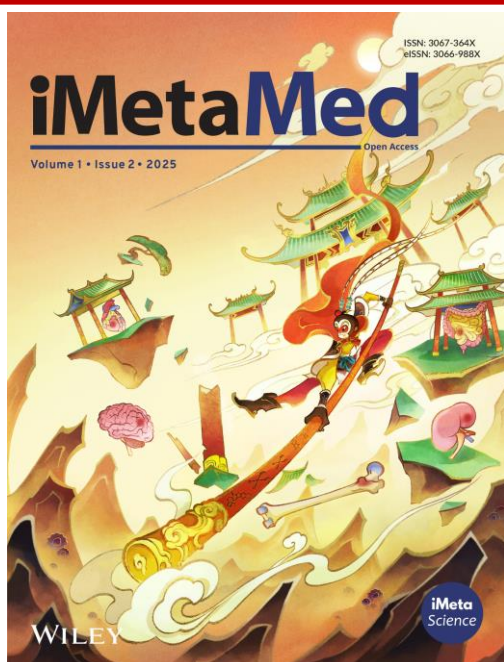
As well as in pathways for amino acid, carbohydrate, and energy metabolism

Summary

- ❑ In this study, we first compared the gut microbiomes of macaques, dogs with three lifestyles, and wolves from two different habitats with the human gut microbiome;
- ❑ Comparative analysis at both the species and strain levels revealed that the gut microbiome of dogs exhibits greater similarity to humans than that of macaques.
- ❑ Microbial community analysis showed that macaques are closer to humans in microbial community structure and composition, which consistent with their phylogenetic relationship. However, functional analysis demonstrated that the gut microbiome of dogs is functionally more similar to humans, particularly in metabolic pathways, providing evidence for convergent evolution of metabolic functions between dogs and humans.
- ❑ Further analysis of functional profiles in working dogs and pet dogs revealed that lifestyle-induced metabolic and disease differences in dogs parallel those observed in human responses to occupational environments.



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