Duck Gut Metagenome Reveals the Microbiome Signatures Linked to Intestinal Regional, Temporal Development, and Rearing Condition

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China is the world's largest producer and consumer of waterfowl farming

- The total value of waterfowl production has exceeded 100 billion
- Duck farming accounting for 74.3% of world production

China leads world duck meat production

- Globally, poultry meat accounts for 43.2% of the total meat production
- Duck meat production ranks third after pork and chicken, making it the third largest meat industry in China

Which Country Produces the Most Duck Meat?

Duck Meat Production (Tonnes), 2022 or latest

[Chart showing the production of duck meat by country]

2023 TOTAL BREEDING DUCKS

(Eastern Survey Area)

[Graph showing the population of breeding ducks from 1995 to 2025]
Duck gut microbiota

- The duck gastrointestinal tract (GIT) harbors an abundance of microorganisms that play an important role in duck health and production.
- The duck microbiota plays a crucial role in functions such as nutrients digestion, immune system development, and feed efficiency improvement.
A total of 375 gastrointestinal samples were collected:

- Including: Heilongjiang, Zhejiang, Jiangxi, Henan, Shanghai, Guizhou, Shandong, Jiangsu, Anhui, Fujian, Hebei in China
Experimental design and sample collection

- **Including:**
  1. **Four breeds** (Mallard, Partridge, Peking, and Muscovy)
  2. **Five intestinal segments** (the duodenum, jejunum, and ileum of the small intestine; and the cecum, and colon of the large intestine)
  3. **Five different growth ages** (3, 7, 14, 42, and 70 days)
  4. **Two rearing system** (with water and without water)
Duck microbial gene catalog construction and metagenome-assembling

- Shotgun metagenomic sequencing of genomic DNA extracted from 375 samples

4 regions, 5 intestinal segments and 5 different ages
375 gastrointestinal samples
• Obtained a nonredundant GIT microbial gene catalog (RGMGC) with 24,602,722 genes
• Reconstructed a total of 4,437 bacterial and archaeal genomes and metagenome-assembled genomes (MAGs)
Distinctive taxonomic characteristics of intestinal regional organization and functional potentials

- A different trend in gut microbiome diversity along the digestive tract, as alpha diversity was highest in the small intestine but nearly identical in the cecum and colon;
- Specific microbial taxa show significant enrichment patterns in specific intestinal segment regions

① The dominance of lactic acid-producing bacteria such as *Lactobacillus* in the small intestine;
② the predominance of mucin-degrading taxa such as *Bacteroides* and *Alistipes* in the large intestine
Distinctive taxonomic characteristics of intestinal regional organization and functional potentials

• The small intestine microbiome appeared to be primarily involved in cofactor, vitamin, and amino acid metabolism;
• The large intestine microbiome exhibited a stronger association with lipid metabolism and functions related to protein folding, sorting, and degradation.

The comparison of functional modules, such as KOs, across the intestinal regions provided further insights into the substantial regional functional heterogeneity of the gut microbiome.
The regional signatures of CAZymes in the duck GIT microbiome

- Similar CAZymes are encoded by different bacterial species in different intestinal segments

- The phyla Firmicutes and Bacteroidota, Proteobacteria and Actinobacteriota, exhibited the largest and most diverse repertoire of CAZymes
Developmental trajectory and maturation of the duck microbiome

• The microbial diversities were increased during duck development, peaking at day 14 for genes and genus profiles, and then remaining stable or decreasing slightly thereafter
• PCoA plots displayed clear clustering of samples according to stage groups
• Dominant phyla were Firmicutes, Proteobacteria, Bacteroidetes, Fusobacteria, and Actinobacteria

Significant variability was revealed in the gut microbiome of new ducks (day 3)
• On day 3, the identified major genera included *Klebsiella*, *Lactobacillus*, *Escherichia*, and *Enterobacter*, reflecting the short-term exposure to the environment and the initiation of gut microbial communities;
• The key butyrate-producing bacteria, such as *Blautia* and *Butyricicoccus*, known for their probiotic characteristics, were consistently observed during middle growing stages, suggesting a transition of gut environment towards a healthier stage, which may contribute to improved growth performance and disease resistance in ducks.
Developmental trajectory and maturation of the duck microbiome

- Day 3 — the prominence of sulfur metabolism, along with glutathione and glutamine metabolism
- Day 7 — nutrient uptake and energy metabolism
- Day 14 — carbohydrate metabolism
- Day 42, 70 — amino acid and fatty acid metabolism
Duck cecal microbiome changes under different rearing systems

- Akkermansia muciniphila were more abundant in the WOW duck microbiota

- The WOW condition exhibited significant enrichment in pathways related to carbohydrate, amino acid, lipid, energy, and xenobiotic metabolism
- The WW condition influenced pathways associated with cofactor and vitamin metabolism, glycan metabolism, terpenoids and polyketides metabolism, as well as nucleotide metabolism
Duck cecal microbiome changes under different rearing systems

- In the WW duck microbiomes, we observed a reduction in the sucrose phosphotransferase gene (scrA), while the sucrase gene (sacA) and glucose-6 phosphate isomerase (GPI) showed increased abundance.
- The WW duck microbiome, with increased abundance of lpxA, lpxB, lpxC, and lpxD.
Antimicrobial resistance in ducks with different rearing conditions

- The gut microbiome of WW ducks had significant beta-diversity and a slight increase Shannon diversity of ARGs
- Procrustes analysis revealed a significant correlation between bacterial communities and ARGs composition
- Major phyla Actinobacteria, Bacteroidota, Firmicutes, and Proteobacteria were mainly responsible for the CARD encoding
- MAGs enriched in the WW ducks were mostly belonged to the phyla Bacterioidota and Proteobacteria, which largely encoding Fluoropyrimidine, macrolide, glycopeptide, and tetracycline antibiotics
The microbiota within different duck intestinal segments exhibits both similarities and distinctive taxonomic and functional differences.

Significant shifts in microbiota composition have been observed in newly hatched ducks at 3 days of age, followed by increased diversity and enhanced stability across growth stages (14, 42, and 70 days).

Ducks with free access to water have shown an increased bacterial capacity for lipopolysaccharide biosynthesis, leading to the accumulation of pathogenic bacteria and antibiotic-resistance genes.

“iMeta”由威立、肠菌分会和华人科学家出版的开放获取期刊，主编由中科院微生物所刘双江和荷兰格罗宁根大学傅静远教授共同担任。目的是发表原创研究、方法和综述以促进宏基因组学、微生物组和生物信息学发展。目标是发表前10% (IF>20) 的高影响力论文。期刊特色包括视频投稿、可重复分析、图片打磨、青年编委、中英双语、50万用户的社交媒体宣传等。2022年2月发行，相继被ESCI、Google Scholar、DOAJ、Scopus等数据库收录，发文161篇，被引2316次(Dimension, 2024/2/19)！

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