

A wide-angle photograph of a vast, flat landscape under a clear blue sky. In the foreground, a large number of birds, likely geese or ducks, are scattered across a dry, yellowish-brown field. In the middle ground, a calm, blue lake stretches across the horizon. In the background, a range of low, hazy mountains is visible. Two birds are captured in flight, one in the upper right and another in the center, both with wings spread. The overall scene depicts a natural habitat, possibly a wetland or a breeding ground for waterfowl.

中亚重要雁形目物种——斑头雁的肠道微生物多样性分析

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学科组简介

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长期从事青藏高原鸟类学研究, 对该地区鸟类系统学、迁徙与地理分布、种群动态与监测、关键物种的生态与行为等方面有丰厚研究积累。



图例

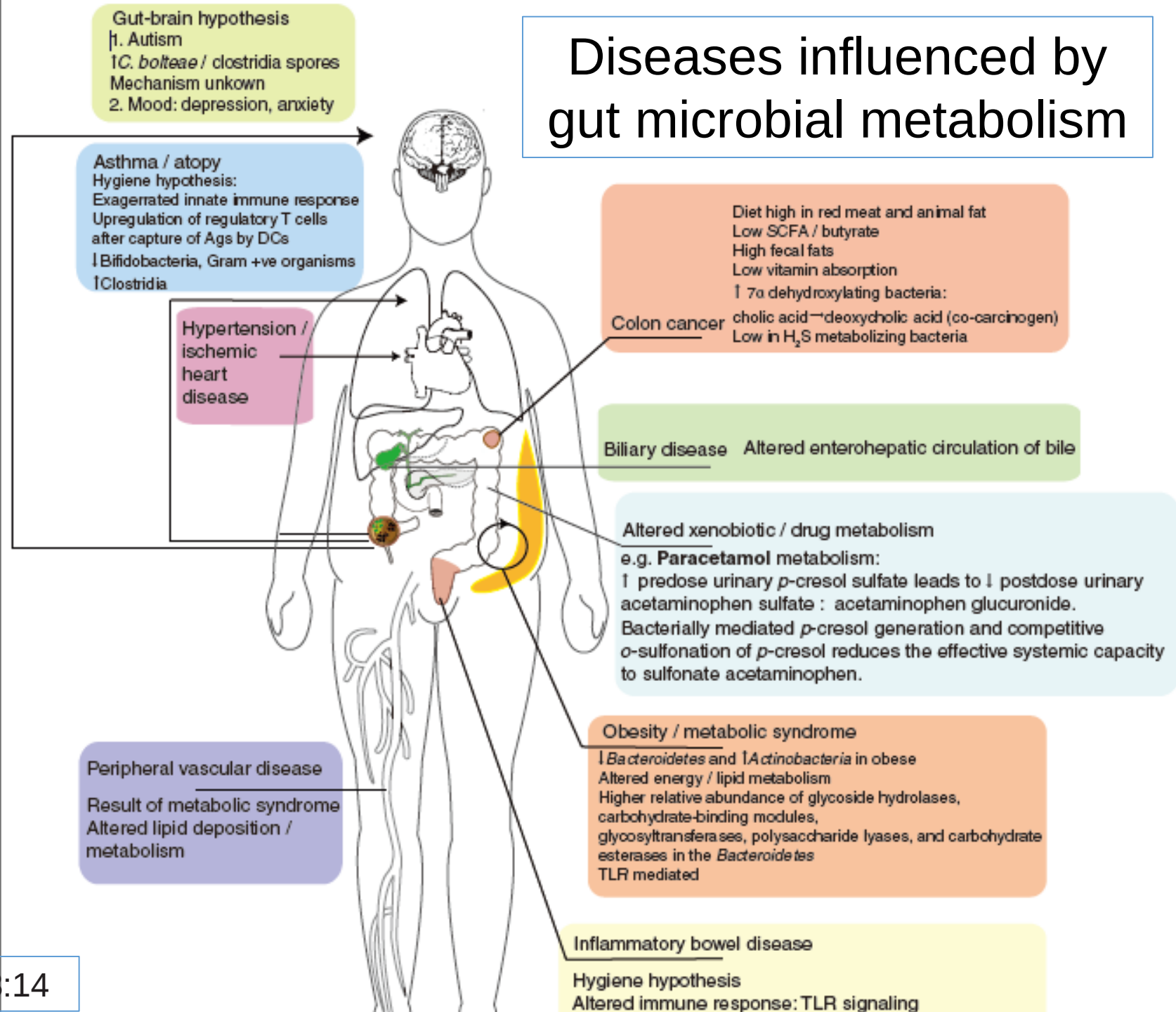
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|-------------------|-----------------------|
| ○ 鸟类种群数量调查点 | ● 鸿雁口咽拭子、泄殖腔拭子采样点 |
| ★ 斑头雁粪便采样点 | ◆ 鸬鹚粪便采样点 |
| ▲ 黑颈鹤粪便采样点 | ● 绿头鸭血清、口咽拭子、泄殖腔拭子采样点 |
| ◆ 家禽口咽拭子、泄殖腔拭子采样点 | ☑ 赤麻鸭粪便采样点 |

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Examples of large human microbiome research initiatives.

Programme	Programme period	Programme focus	Countries involved
National Institutes of Health (NIH) 'Human Microbiome Project' (HMP), phase one ²³	2007-2012	Develop community resources to support the field: computational tools for sequence-based analyses; experimental methodologies; clinical protocols; microbial genome, whole metagenome and 16S metagenome reference databases; reference microbial culture collection; as well as ethical, legal, social implications of microbiome research. Included research on the microbiomes of five major body regions (skin, oral, nares, gastrointestinal (GI) tract, urogenital) and some associated diseases/disorders.	USA
European Commission (EC) 'Metagenomics of the Human Intestinal Tract' (MetaHIT) programme ²⁴	2008-2012	Research on the GI tract microbiome.	China, Denmark, France, Germany, Italy, The Netherlands, Spain, UK
Canadian Microbiome Initiative ²⁵	2008-2012	Research on a variety of body region microbiomes.	Canada
Irish government 'Metagenomics of the Elderly' (ELDERMET) programme ²⁶	2008-2013	Research on the elderly GI tract microbiome.	Ireland
Six additional human microbiome research initiatives ²⁷	2008-2012	Diversity of microbiome studies.	Australia, China, France, Japan, Singapore, South Korea
International Human Microbiome Consortium (IHMC) ²⁸	2007 to present	Establish standards for the field and coordinate international human microbiome research activities.	Australia, Canada, China, France, Gambia, Germany, Kazakhstan, Ireland, Japan, South Korea, Spain, USA
NIH HMP, phase two ²⁹	2013 to present	Develop community resources to support the field: computational tools for omics-based functional data analysis; experimental methodologies; clinical protocols; methods to analyse longitudinal functional data from microbiome and host; also bioinformatics approaches to organization of multiple datatype databases. Research on the nares, GI tract and vaginal microbiomes.	USA

Diseases influenced by gut microbial metabolism



- 肠道是人体微生物含量最多的部位
- 微生物种类多达1000种
- 数量高达 10^{14} 个（100万亿个，是人体细胞总量的10倍）
- 基因总数约是人类基因总数的300倍
- 被称为“人体第二基因组”



“佛即人肠”

鸟类肠道微生物研究的国际国内现状

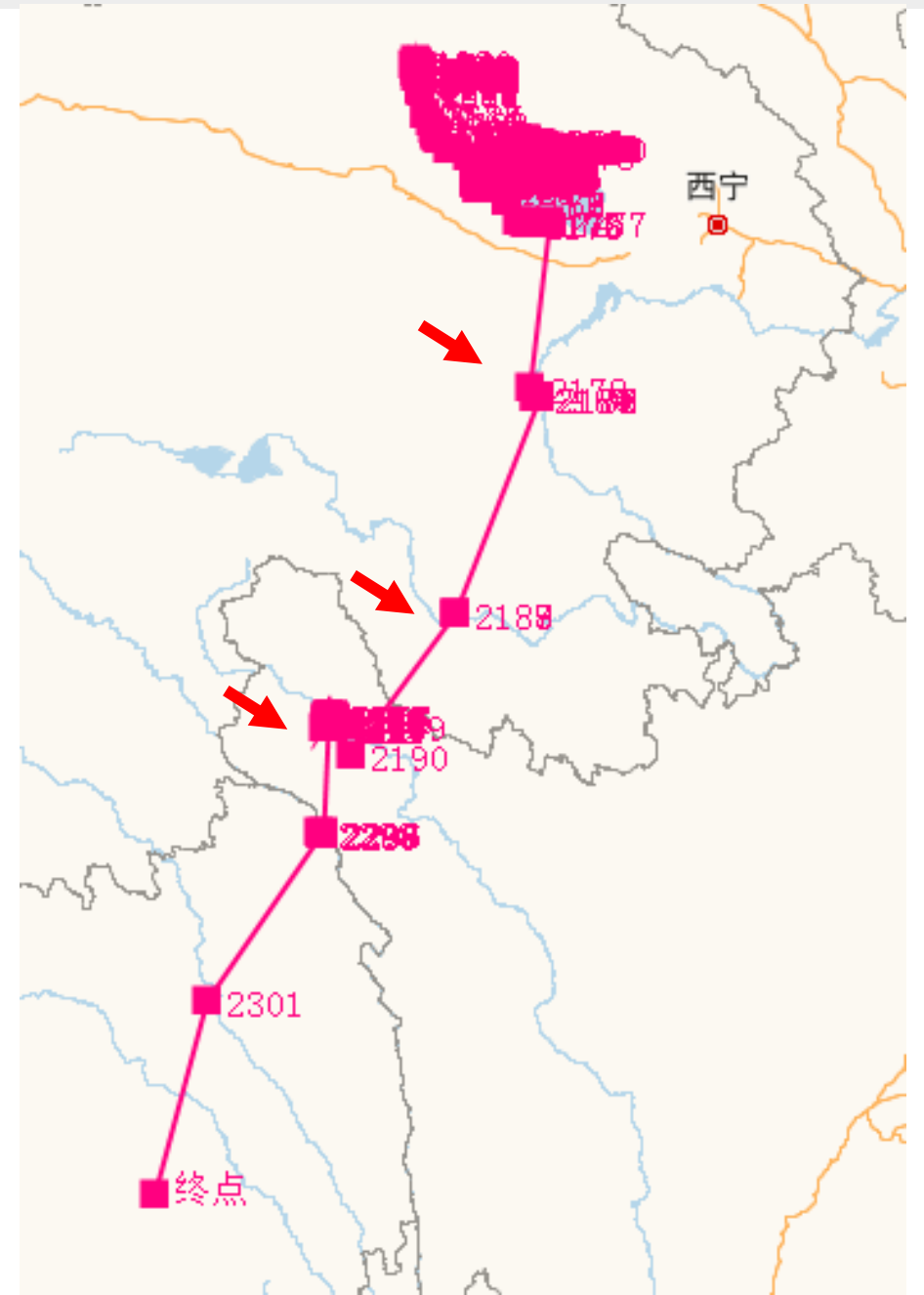
➤ 世界现存鸟类共**10659**种，**20413**个亚种。

➤ 鸟类作为研究肠道微生物的模式物种：

- ①巢寄生（遗传 **VS** 巢环境和食物）
- ②亲鸟喂食（肠道微生物的获取方式）
- ③泄殖腔（交配对肠道微生物的影响）
- ④鸟鼠同穴（肠道微生物的跨物种交换）
- ⑤候鸟迁徙（国际尺度，湖泊）

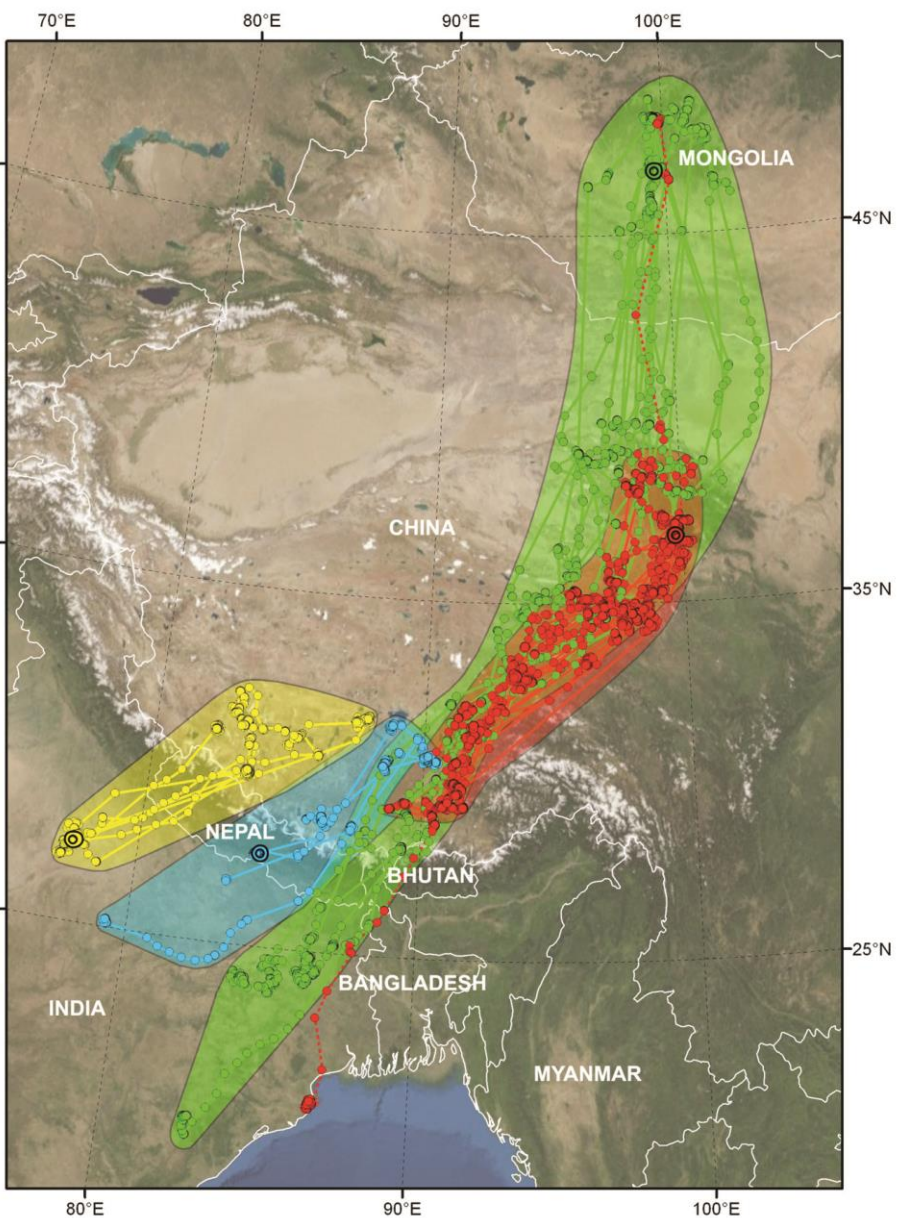
➤ 国外：
共**20**种鸟类的肠道微生物得以揭示。

➤ 国内：
共**7**种鸟类的肠道微生物得以揭示。



斑头雁（Bar-headed goose）的研究、保护及经济利用

➤ 斑头雁高海拔飞行的适应机制



➤ 2012年，被世界自然保护联盟（IUCN）列入濒危物种红色名录，等级定为Least Concern。2016年，湿地国际（Wetlands International）认为全球种群数量为52,000-60,000只。



Who is there?

What are they doing?

Who is doing what?

How are they doing it?

How can this be used to benefit host health?

野生斑头雁的核心肠道微生物

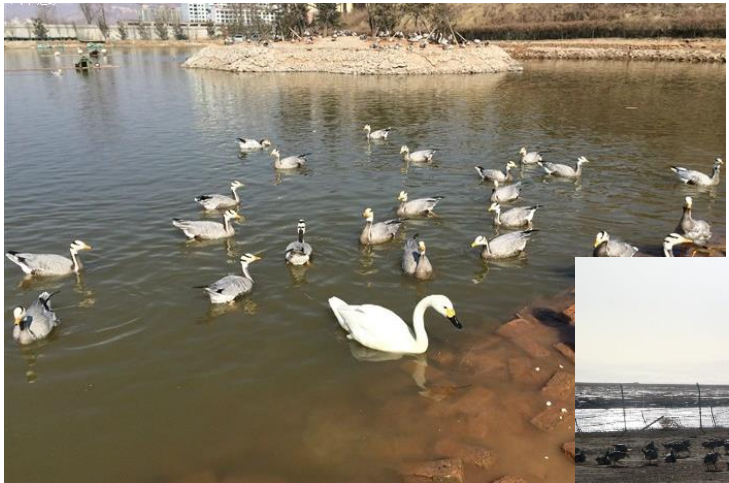


Phylum	Relative abundance
Firmicutes	74.78%
Proteobacteria	7.84%
Actinobacteria	7.49%
Bacteroidetes	6.65%

Table 2. The relative abundance of core genera (100% core threshold) in each sample.

Phylum	Genus	The relative abundance (%)									Average
		F1_1	F1_2	F1_3	F2_1	F2_2	F2_3	F3_1	F3_2	F3_3	
Firmicutes	Lactococcus	56.67	52.93	4.27	3.52	38.74	21.05	50.97	46.43	52.37	36.33
Firmicutes	Bacillus	14.68	15.38	1.05	0.88	11.92	5.53	16.00	13.76	16.21	10.60
Proteobacteria	Pseudomonas	6.27	7.10	0.32	0.26	4.85	1.83	6.73	5.70	6.62	4.41
Firmicutes	Solibacillus	6.37	6.62	0.41	0.33	4.88	2.06	6.42	5.67	6.83	4.40
Actinobacteria	Arthrobacter	4.38	5.58	0.37	0.34	4.30	1.74	5.55	4.68	5.45	3.60
Bacteroidetes	Bacteroides	0.01	0.02	9.62	18.25	0.06	0.02	0.08	0.33	0.00	3.15
Firmicutes	Streptococcus	1.99	2.03	2.05	0.13	1.56	0.83	1.84	1.57	2.30	1.59

斑头雁肠道微生物的变化（野生、半野生半人工养殖、完全人工养殖）

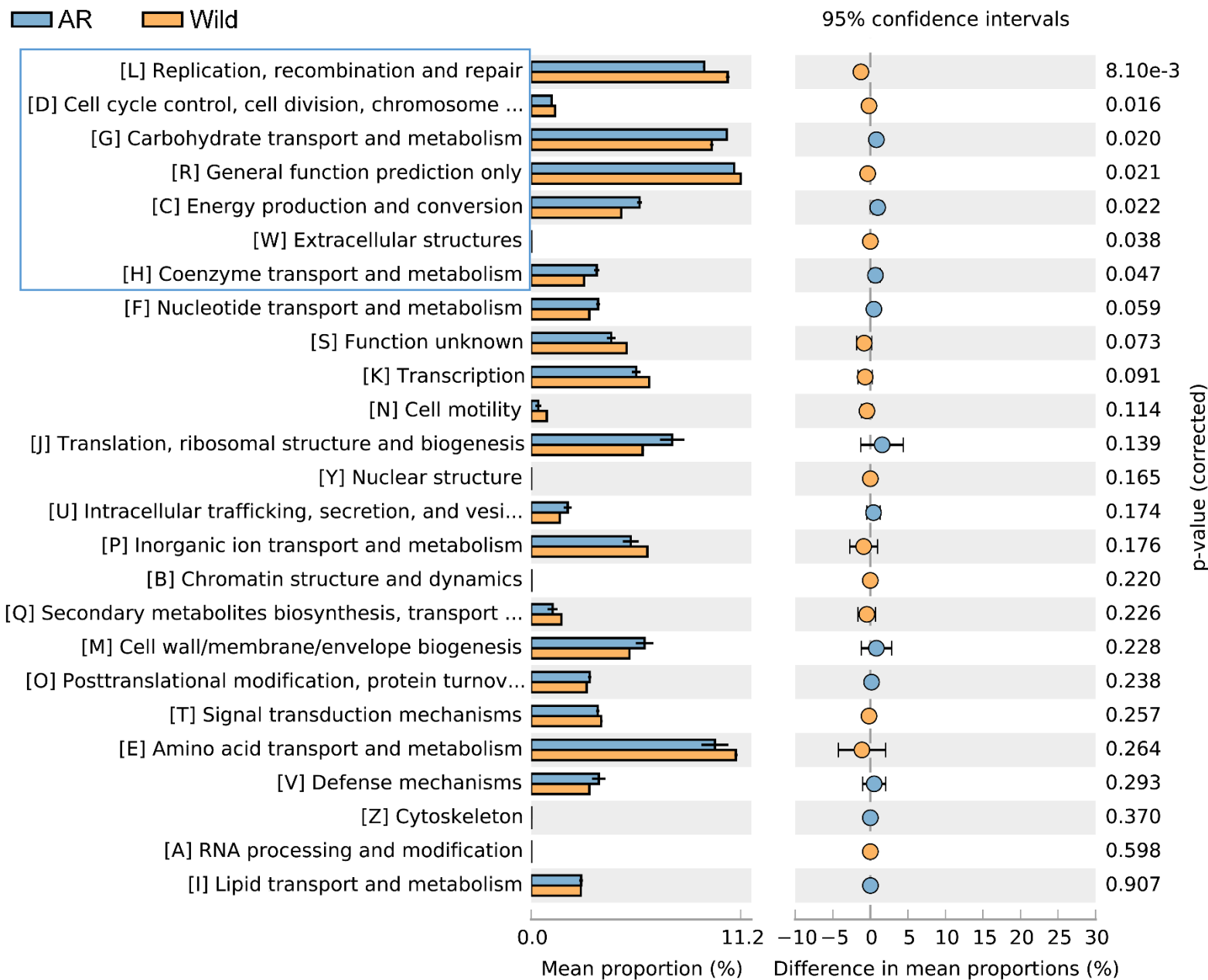


The most abundant genus (% of phylum) of each phylum.

Phylum	SAB	Wild	AB
Firmicutes	<i>Turicibacter</i> (23.33%)	<i>Lactococcus</i> (77.67%)	<i>SMB53</i> (51.00%)
Proteobacteria	<i>Pseudomonas</i> (41.33%)	<i>Pseudomonas</i> (77.00%)	<i>Escherichia</i> (81.00%)
Actinobacteria	<i>Arthrobacter</i> (29.67%)	<i>Arthrobacter</i> (91.00%)	–
Bacteroidetes	<i>Bacteroides</i> (59.00%)	<i>Myroides</i> (44.33%)	–
Fusobacteria	<i>f_Fusobacteriaceae</i> ^a (100%)	–	<i>f_Fusobacteriaceae</i> ^a (33.67%)

^a Family level, cannot be assigned to genus level.

斑头雁肠道宏基因组的变化（野生 VS 半野生半人工养殖）



➤ AR group:

1. carbohydrate transport and metabolism (COG category [G])
2. energy metabolism (COG category [C])
3. coenzyme transport and metabolism (COG category [H]).

➤ Wild group:

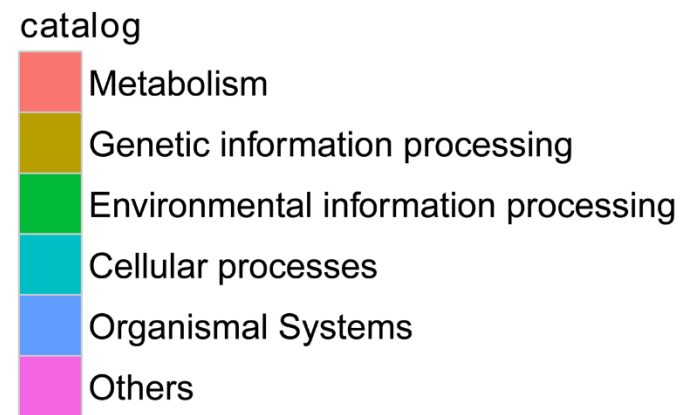
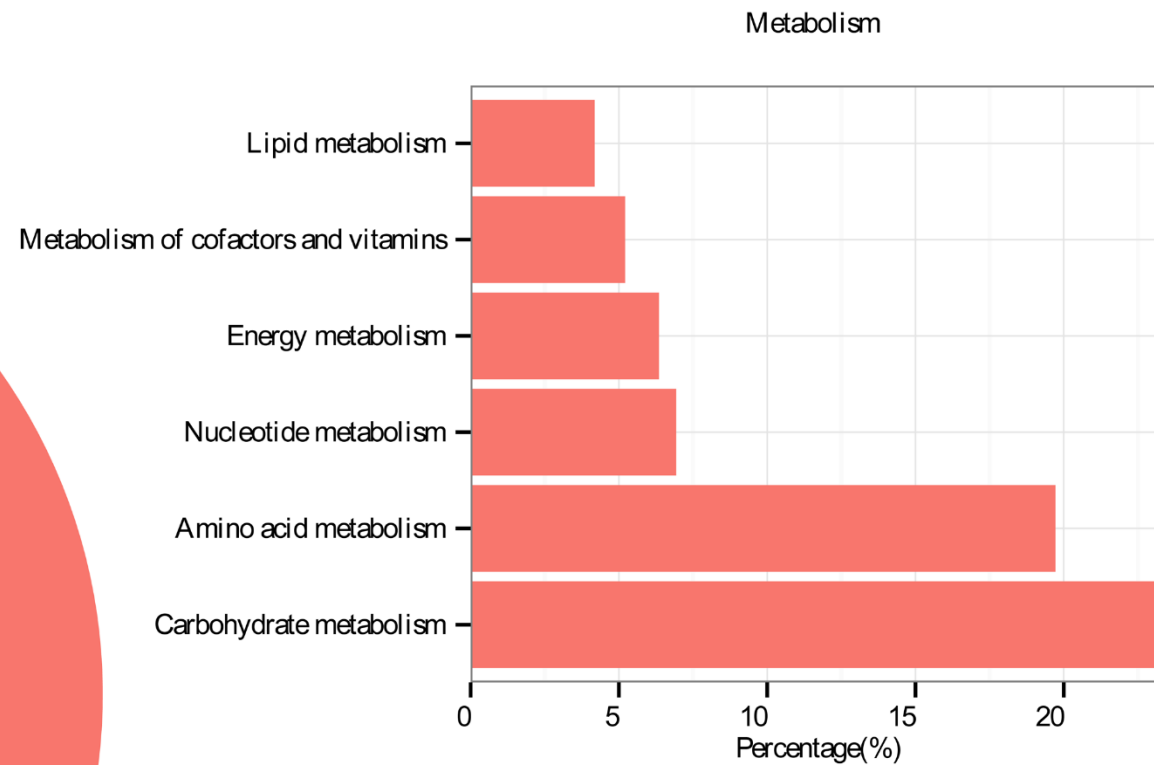
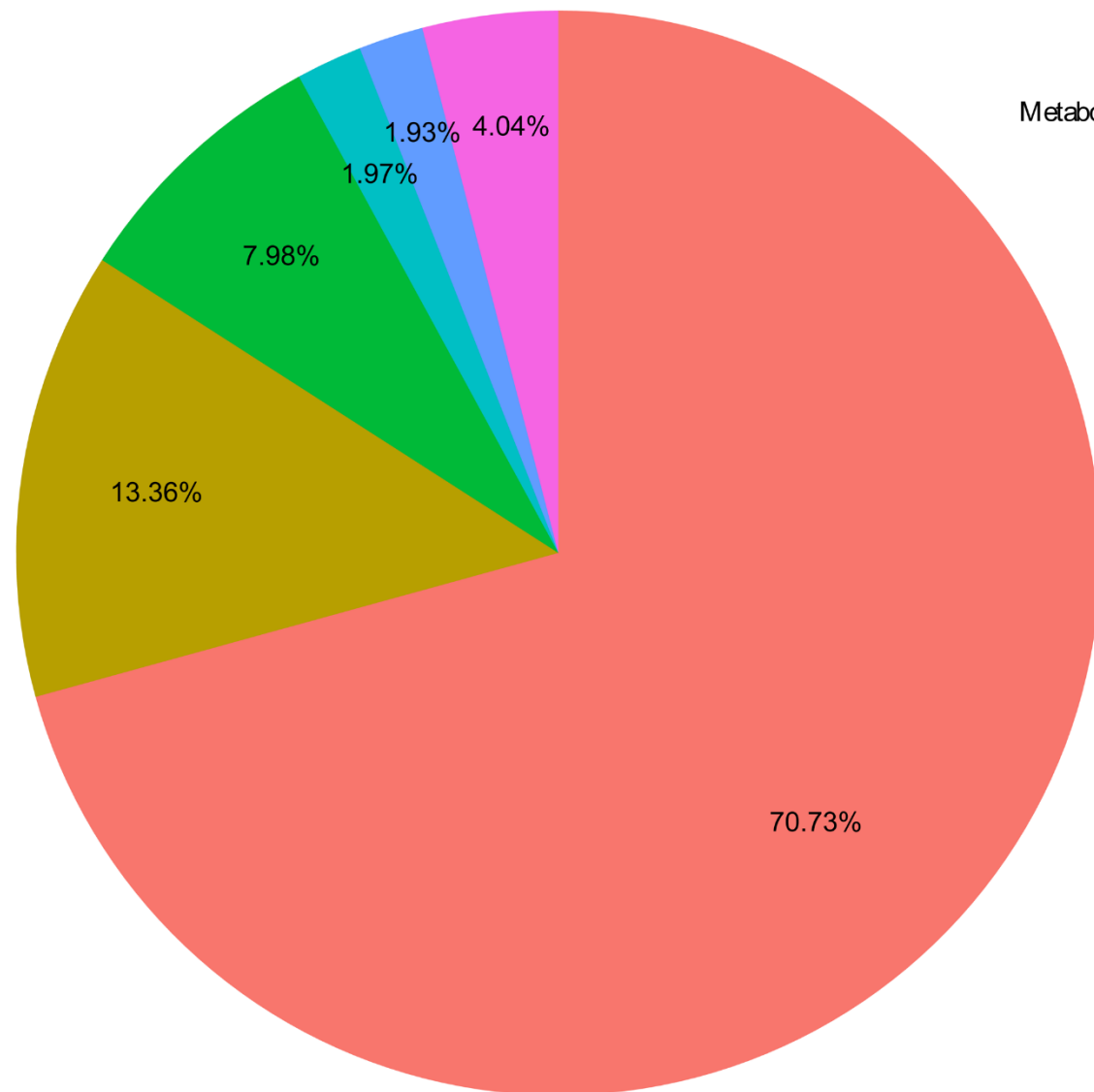
1. chromosome partitioning (COG category [D])
2. replication, recombination and repair (COG category [L])
3. extracellular structures (COG category [W])

斑头雁肠道宏基因组的变化（野生 VS 半野生半人工养殖）

Table 1. The top 3 enriched KEGG pathways and corresponding top BLASTX hit organisms in AR group.

Pathway	Name	KOs significantly abundant in AR group	Top BLASTX hit organism in AR group
ko04974	Protein digestion and absorption	K01278, dipeptidyl-peptidase 4 [EC:3.4.14.5]	Bacteroidetes (98.84%)
ko00604	Glycosphingolipid biosynthesis - ganglio series	K12373, hexosaminidase [EC:3.2.1.52]	Bacteroidetes (92.84%)
ko04142	Lysosome	K01201, glucosylceramidase [EC:3.2.1.45]	Bacteroidetes (75.09%)
		K01205, α , N-acetylglucosaminidase [EC:3.2.1.50]	Bacteroidetes (99.29%)
		K01195, beta-glucuronidase [EC:3.2.1.31]	Bacteroidetes (42.57%)
		K12373, hexosaminidase [EC:3.2.1.52]	Bacteroidetes (92.84%)
		K01192, beta-mannosidase [EC:3.2.1.25]	Bacteroidetes (73.63%)
		K01186, sialidase-1 [EC:3.2.1.18]	Bacteroidetes (85.21%)
		K01134, arylsulfatase A [EC:3.1.6.8]	Bacteroidetes (92.09%)

斑头雁肠道宏基因组的组装及参考基因集的分析





斑头雁肠道微生物组学
(Gut microbiome)

不同养殖方式
(Breeding Patterns)

不同越冬种群
(Wintering Flocks)

核心肠道菌群
(Core gut microbe)

Metagenomic Sequencing



uncultivation methods
(99%)

cultivation methods
(1%)

Classification	Phylum	Genus (most abundant)
Core	Firmicutes	<i>Lactococcus</i>
	Proteobacteria	<i>Pseudomonas</i>
	Actinobacteria	<i>Arthrobacter</i>
	Bacteroidetes	<i>Bacteroides</i>
		<i>Prevotella</i>
		<i>Myroides</i>
		<i>Flavobacterium</i>

谢谢， 请批评指正。