Gut microbiome seasonality is associated with dietary plasticity and coexistence in three sympatric Pamir

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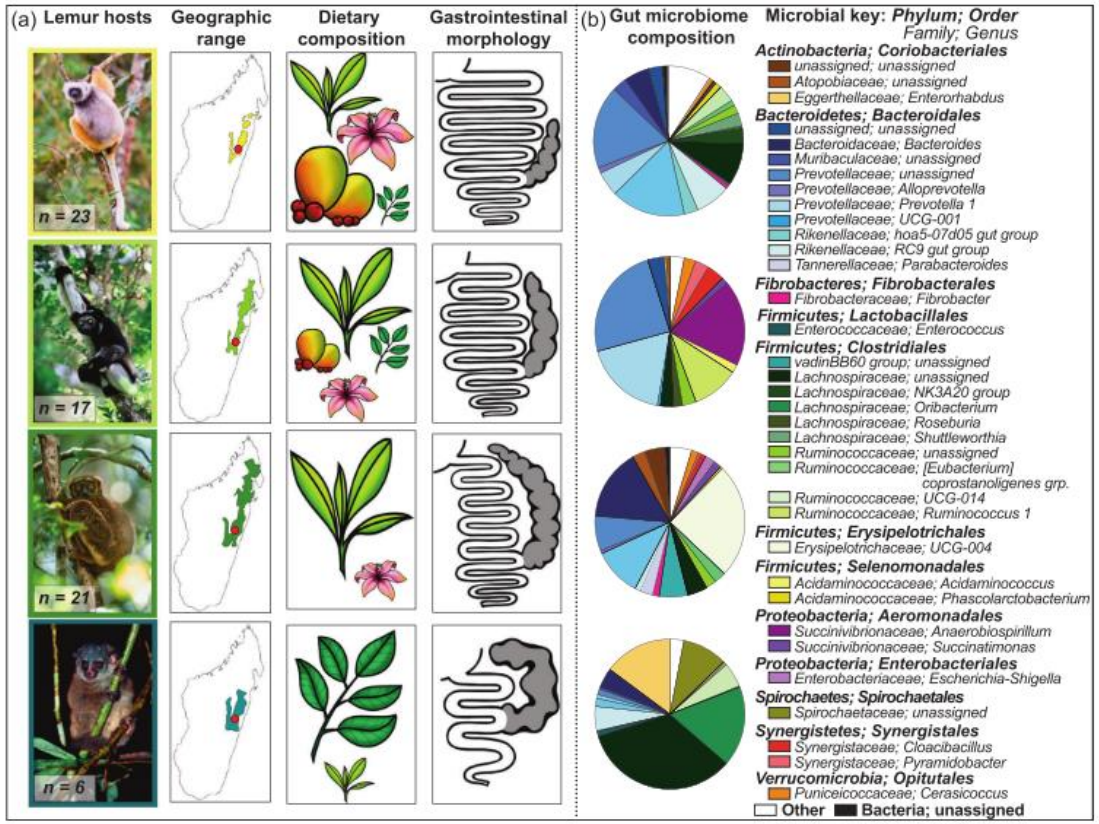
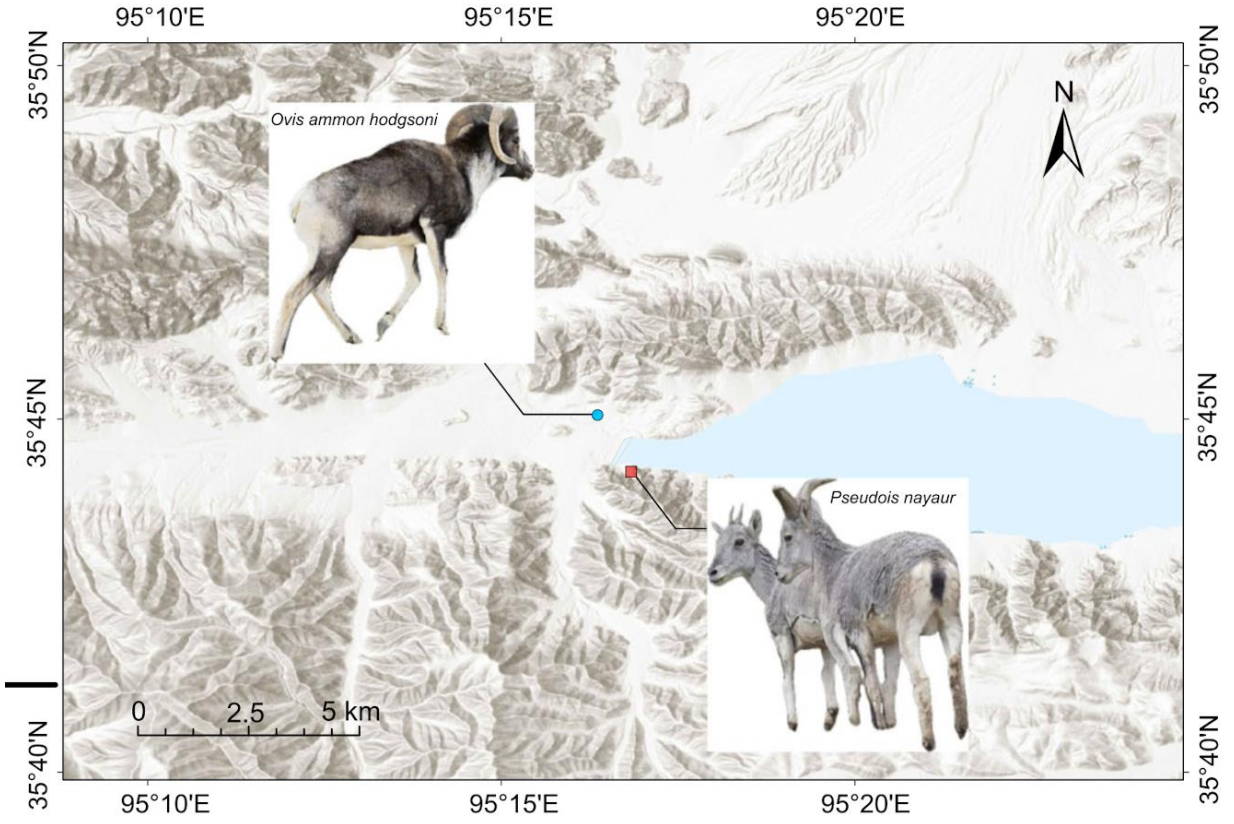
Dilala Tuoliu, Lijiao Zhang, Muyang Wang, Wenxuan Xu, Kathreen Ruckstuhl, António Alves da Silva, Joana Alves, Hongchen Jiang, Weikang Yang. (2026), Gut microbiome seasonality is associated with dietary plasticity and coexistence in three sympatric Pamir ungulates. iMetaOmics e70135. https://doi.org/10.1002/imo2.70135

Introduction



Diet and gut microbiome characteristics of 4 sympatric lemur species

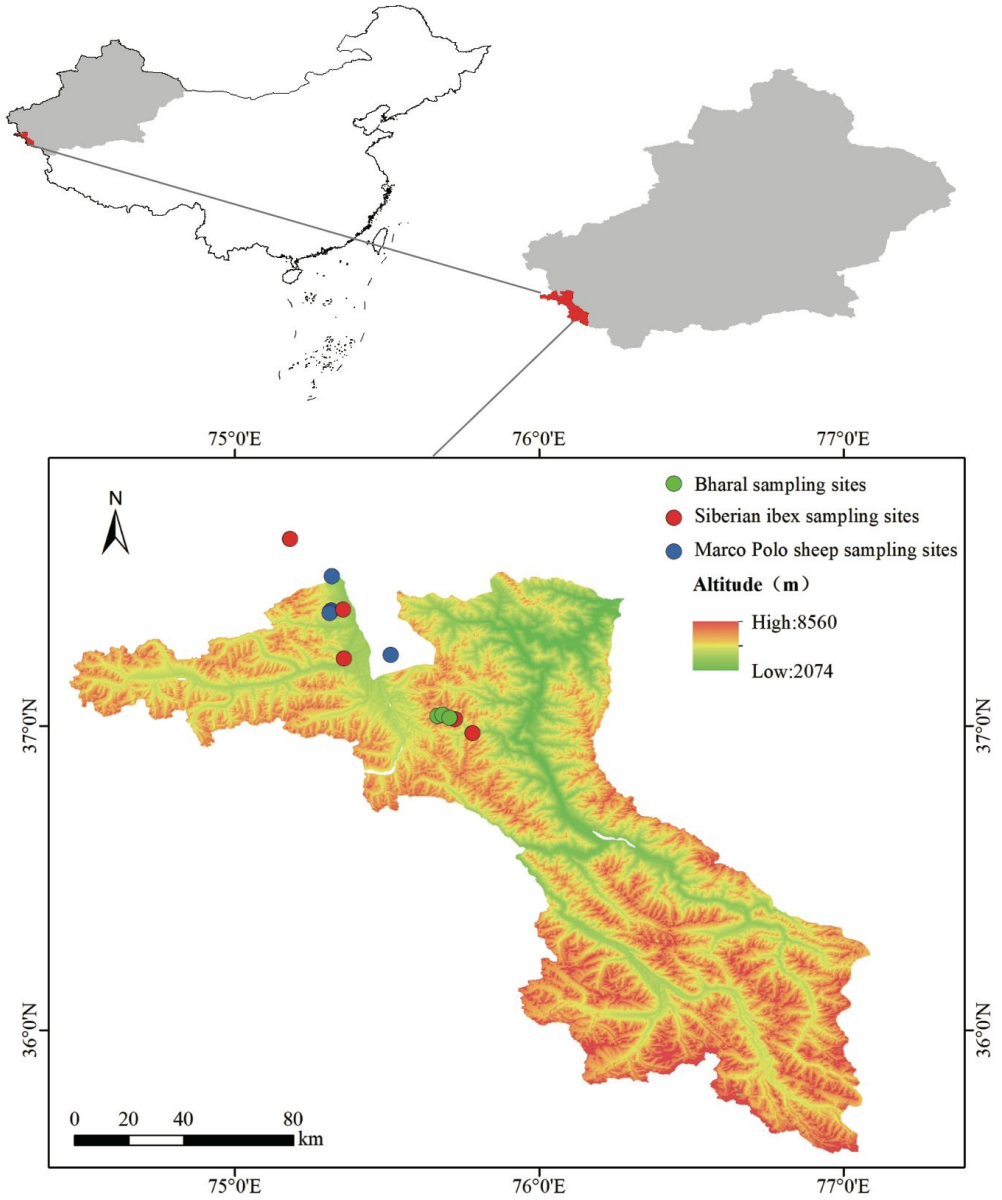


Microbiome-driven niche partitioning between Argali and blue sheep during the growing season

➤ To maintain ecosystem stability, sympatric herbivores mitigate interspecific competition through niche partitioning across dietary, temporal, and spatial dimensions.

➤ Fine-scale microbiome specialization plays a crucial role in maintaining niche partitioning among herbivores.

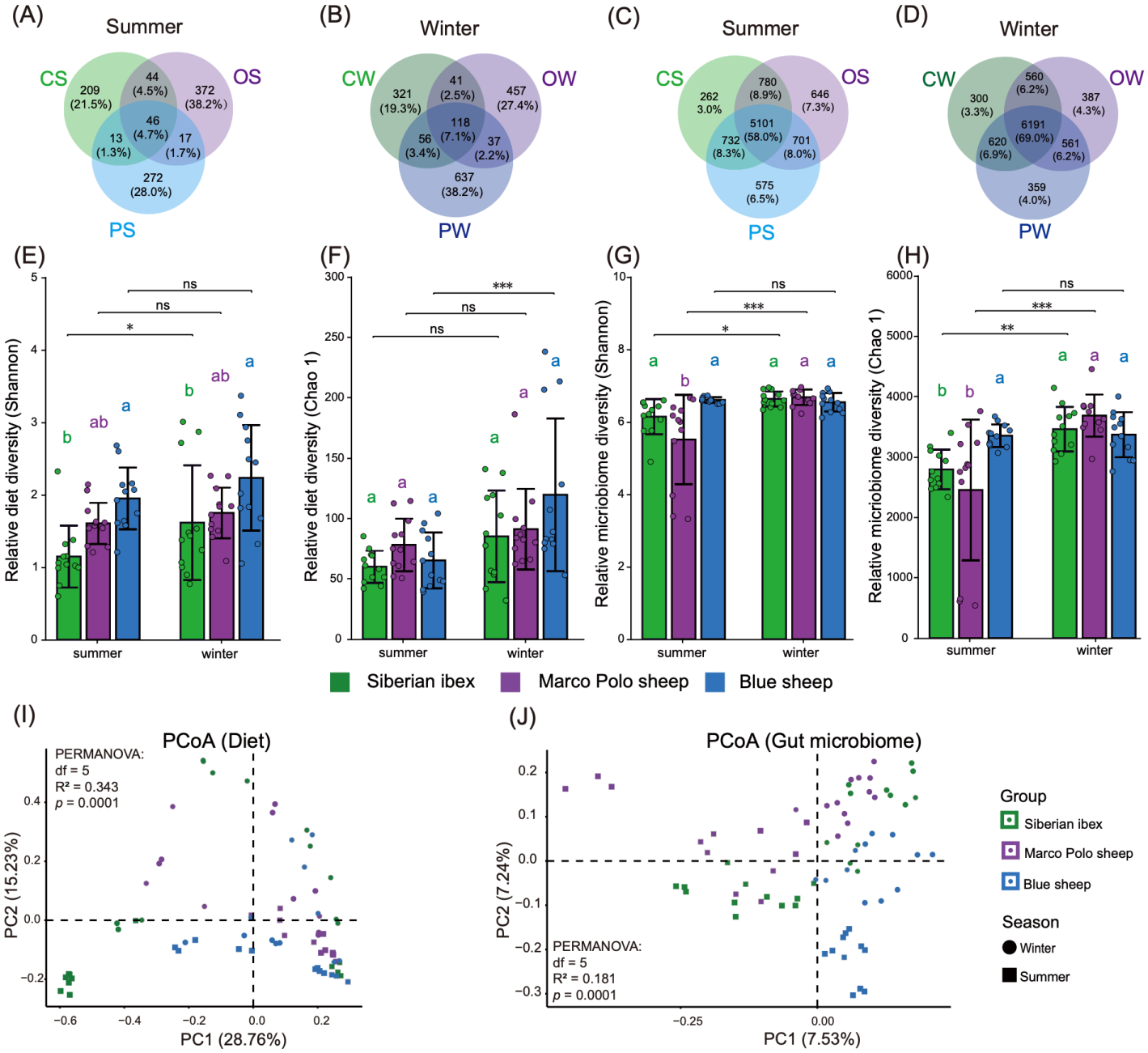
Experimental Design and Multi-omics Methods



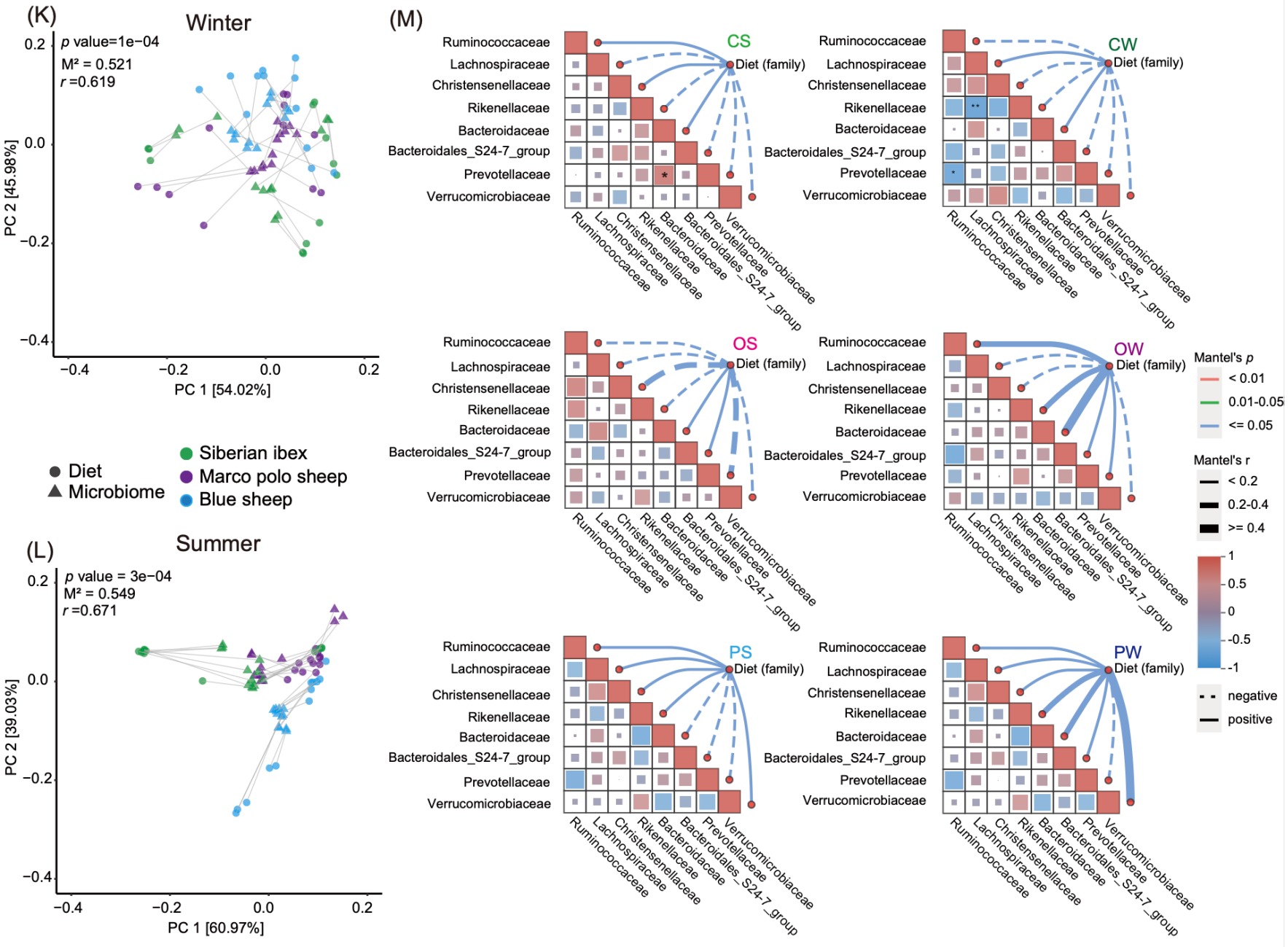
Summer Habitat

Winter Habitat

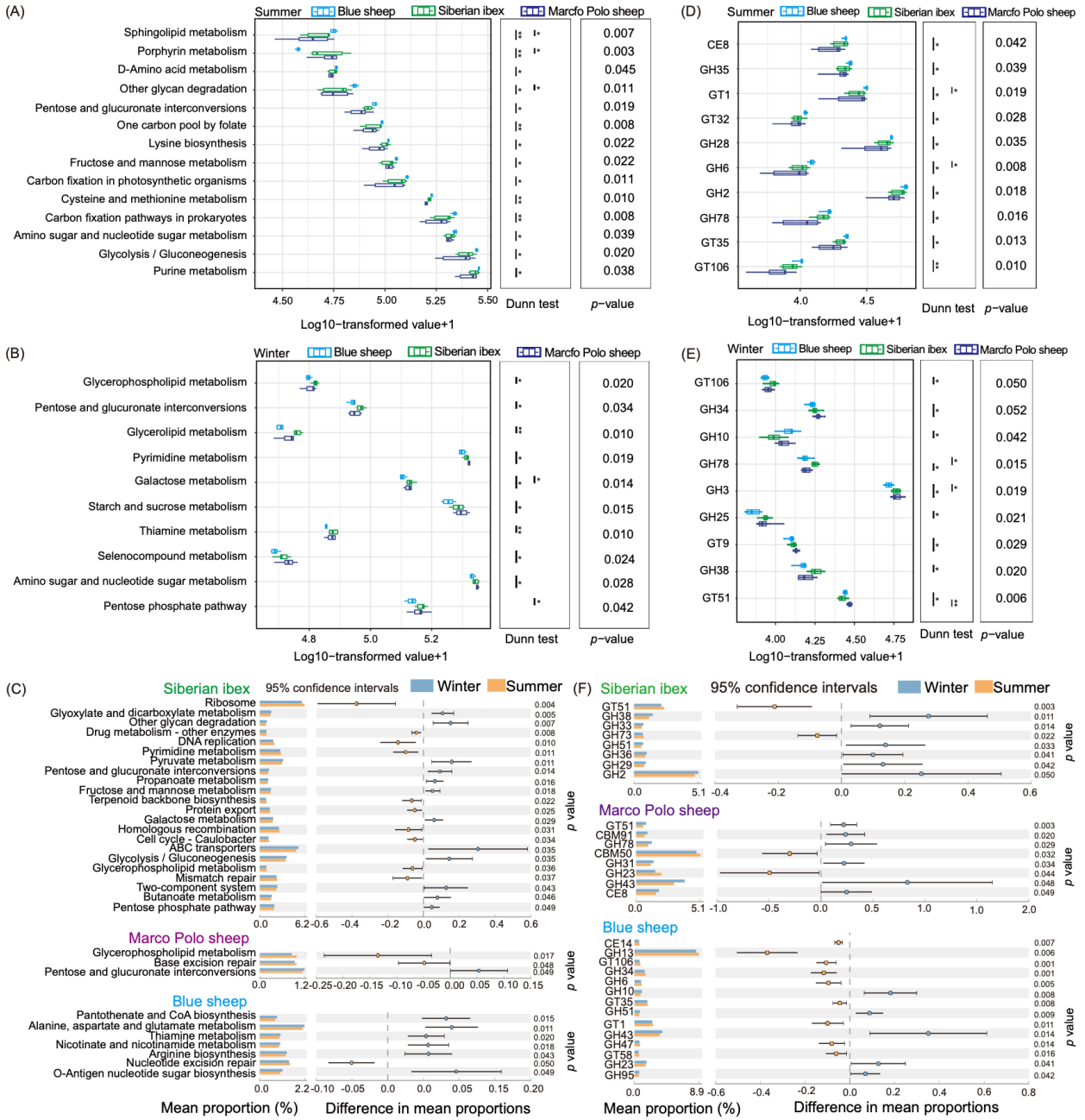
Results


(A)
Summer
CS
OS
PS
209 (21.5%)
44 (4.5%)
372 (38.2%)
46 (4.7%)
13 (1.3%)
17 (1.7%)
272 (28.0%)
(B)
Winter
CW
OW
PW
321 (19.3%)
41 (2.5%)
457 (27.4%)
118 (7.1%)
56 (3.4%)
37 (2.2%)
637 (38.2%)
(C)
Summer
CS
OS
PS
262 3.0%
780 (8.9%)
646 (7.3%)
5101 (58.0%)
732 (8.3%)
701 (8.0%)
575 (6.5%)
(D)
Winter
CW
OW
PW
300 (3.3%)
560 (6.2%)
387 (4.3%)
6191 (69.0%)
620 (6.9%)
561 (6.2%)
359 (4.0%)
(E)
Relative diet diversity (Shannon)
summer
winter
(F)
Relative diet diversity (Chao 1)
summer
winter
(G)
Relative microbiome diversity (Shannon)
summer
winter
(H)
Relative microbiome diversity (Chao 1)
summer
winter
Siberian ibex
Marco Polo sheep
Blue sheep
(I)
PCoA (Diet)
PERMANOVA:
df = 5
R² = 0.343
p = 0.0001
PC2 (15.23%)
PC1 (28.76%)
(J)
PCoA (Gut microbiome)
PERMANOVA:
df = 5
R² = 0.181
p = 0.0001
PC2 (7.24%)
PC1 (7.53%)
Group
Siberian ibex
Marco Polo sheep
Blue sheep
Season
Winter
Summer

Results

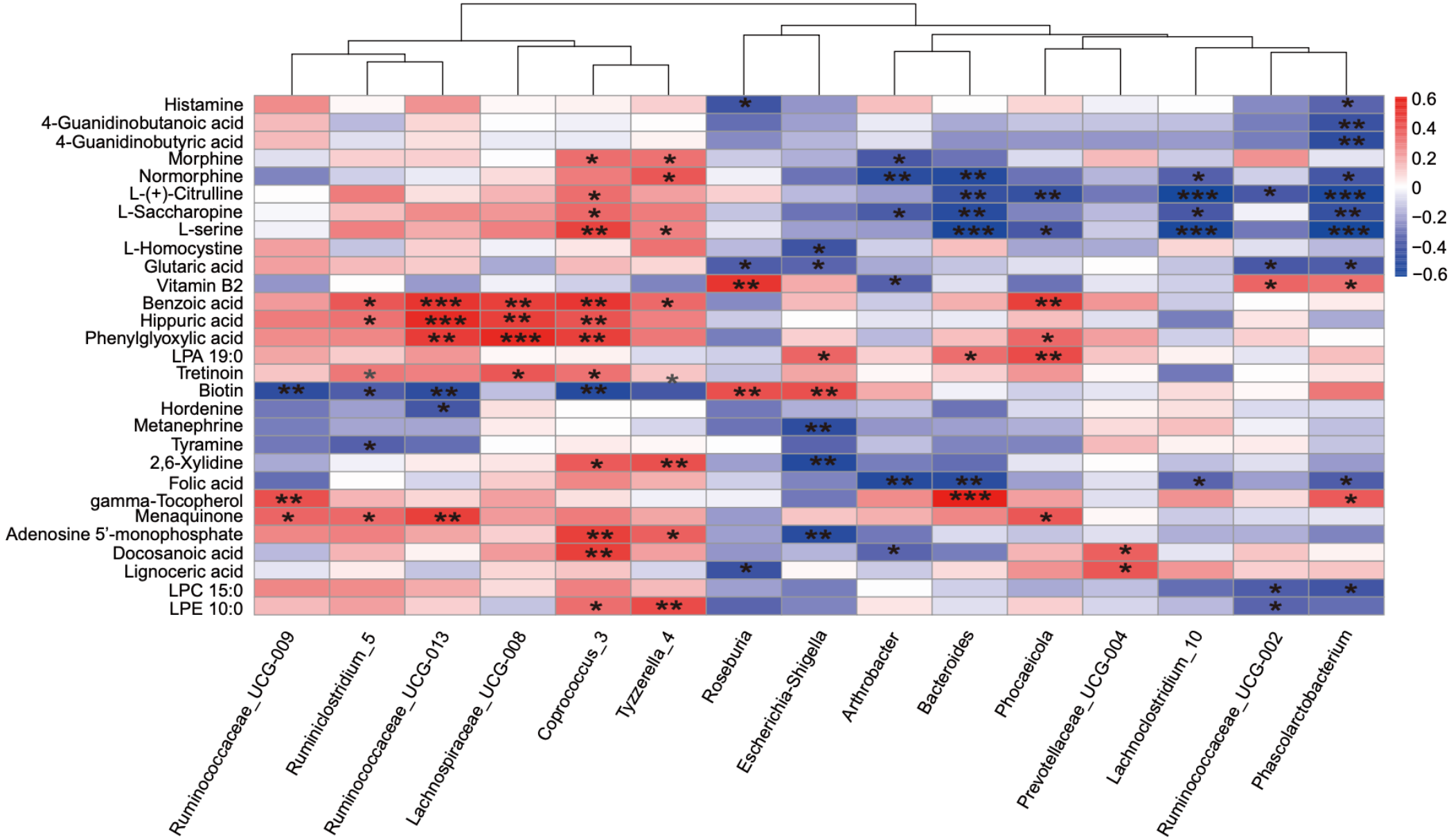

(K)
Winter
p value=1e−04
M² = 0.521
r =0.619
PC 2 [45.98%]
PC 1 [54.02%]
Diet
Microbiome
Siberian ibex
Marco polo sheep
Blue sheep
(L)
Summer
p value = 3e−04
M² = 0.549
r =0.671
PC 2 [39.03%]
PC 1 [60.97%]
(M)
CS
CW
OS
OW
PS
PW
Diet (family)
Ruminococcaceae
Lachnospiraceae
Christensenellaceae
Rikenellaceae
Bacteroidaceae
Bacteroidales_S24-7_group
Prevotellaceae
Verrucomicrobiaceae
Mantel's p
< 0.01
0.01-0.05
<= 0.05
Mantel's r
< 0.2
0.2-0.4
>= 0.4
negative
positive

Results


(A)
Summer
Blue sheep
Siberian ibex
Marcfo Polo sheep
Sphingolipid metabolism
Porphyrin metabolism
D-Amino acid metabolism
Other glycan degradation
Pentose and glucuronate interconversions
One carbon pool by folate
Lysine biosynthesis
Fructose and mannose metabolism
Carbon fixation in photosynthetic organisms
Cysteine and methionine metabolism
Carbon fixation pathways in prokaryotes
Amino sugar and nucleotide sugar metabolism
Glycolysis / Gluconeogenesis
Purine metabolism
0.007
0.003
0.045
0.011
0.019
0.008
0.022
0.022
0.011
0.010
0.008
0.039
0.020
0.038
4.50
4.75
5.00
5.25
5.50
Log10−transformed value+1
Dunn test
p−value
(D)
Summer
Blue sheep
Siberian ibex
Marcfo Polo sheep
CE8
GH35
GT1
GT32
GH28
GH6
GH2
GH78
GT35
GT106
0.042
0.039
0.019
0.028
0.035
0.008
0.018
0.016
0.013
0.010
4.0
4.5
Log10−transformed value+1
Dunn test
p−value
(B)
Winter
Blue sheep
Siberian ibex
Marcfo Polo sheep
Glycerophospholipid metabolism
Pentose and glucuronate interconversions
Glycerolipid metabolism
Pyrimidine metabolism
Galactose metabolism
Starch and sucrose metabolism
Thiamine metabolism
Selenocompound metabolism
Amino sugar and nucleotide sugar metabolism
Pentose phosphate pathway
0.020
0.034
0.010
0.019
0.014
0.015
0.010
0.024
0.028
0.042
4.8
5.0
5.2
Log10−transformed value+1
Dunn test
p−value
(E)
Winter
Blue sheep
Siberian ibex
Marcfo Polo sheep
GT106
GH34
GH10
GH78
GH3
GH25
GT9
GH38
GT51
0.050
0.052
0.042
0.015
0.019
0.021
0.029
0.020
0.006
4.00
4.25
4.50
4.75
Log10−transformed value+1
Dunn test
p−value
(C)
Siberian ibex
95% confidence intervals
Winter
Summer
Ribosome
Glyoxylate and dicarboxylate metabolism
Other glycan degradation
Drug metabolism - other enzymes
DNA replication
Pyrimidine metabolism
Pyruvate metabolism
Pentose and glucuronate interconversions
Propanoate metabolism
Fructose and mannose metabolism
Terpenoid backbone biosynthesis
Protein export
Galactose metabolism
Homologous recombination
Cell cycle - Caulobacter
ABC transporters
Glycolysis / Gluconeogenesis
Glycerophospholipid metabolism
Mismatch repair
Two-component system
Butanoate metabolism
Pentose phosphate pathway
0.004
0.005
0.007
0.008
0.010
0.011
0.011
0.014
0.016
0.018
0.022
0.025
0.029
0.031
0.034
0.035
0.035
0.036
0.037
0.043
0.046
0.049
p value
Marco Polo sheep
Glycerophospholipid metabolism
Base excision repair
Pentose and glucuronate interconversions
0.017
0.048
0.049
p value
Blue sheep
Pantothenate and CoA biosynthesis
Alanine, aspartate and glutamate metabolism
Thiamine metabolism
Nicotinate and nicotinamide metabolism
Arginine biosynthesis
Nucleotide excision repair
O-Antigen nucleotide sugar biosynthesis
0.015
0.011
0.020
0.018
0.043
0.050
0.049
p value
Mean proportion (%)
Difference in mean proportions
(F)
Siberian ibex
95% confidence intervals
Winter
Summer
GT51
GH38
GH33
GH73
GH51
GH36
GH29
GH2
0.003
0.011
0.014
0.022
0.033
0.041
0.042
0.050
p value
Marco Polo sheep
GT51
CBM91
GH78
CBM50
GH31
GH23
GH43
CE8
0.003
0.020
0.029
0.032
0.034
0.044
0.048
0.049
p value
Blue sheep
CE14
GH13
GT106
GH34
GH6
GH10
GT35
GH51
GT1
GH43
GH47
GT58
GH23
GH95
0.007
0.006
0.001
0.001
0.005
0.008
0.008
0.009
0.011
0.014
0.014
0.016
0.041
0.042
p value
Mean proportion (%)
Difference in mean proportions

Results

(G)


Histamine
4-Guanidinobutanoic acid
4-Guanidinobutyric acid
Morphine
Normorphine
L-(+)-Citrulline
L-Saccharopine
L-serine
L-Homocystine
Glutaric acid
Vitamin B2
Benzoic acid
Hippuric acid
Phenylglyoxylic acid
LPA 19:0
Tretinoin
Biotin
Hordenine
Metanephrine
Tyramine
2,6-Xylidine
Folic acid
gamma-Tocopherol
Menaquinone
Adenosine 5'-monophosphate
Docosanoic acid
Lignoceric acid
LPC 15:0
LPE 10:0
Ruminococcaceae_UCG-009
Ruminiclostridium_5
Ruminococcaceae_UCG-013
Lachnospiraceae_UCG-008
Coprococcus_3
Tyzzerella_4
Roseburia
Escherichia-Shigella
Arthrobacter
Bacteroides
Phocaeicola
Prevotellaceae_UCG-004
Lachnoclostridium_10
Ruminococcaceae_UCG-002
Phascolarctobacterium
0.6
0.4
0.2
0
−0.2
−0.4
−0.6

Summary

- Established a multi-omics analytical framework for the gut microbiome of sympatric ungulates in the Pamir Plateau: Integrated dietary DNA metabarcoding, 16S rRNA amplicon sequencing, deep metagenomics, and metabolomics to construct a multidimensional research system.

- Proposed a novel cold-season diet-microbiome synergistic adaptation strategy, challenging the classic "winter diversity suppression" hypothesis: Demonstrated that in winter, hosts effectively mitigate interspecific food competition by broadening dietary breadth and increasing gut microbial diversity.

- Elucidated the high synergy between seasonal gut microbiome restructuring and niche partitioning: Revealed that dietary overlap among hosts significantly decreases in winter, while the functions of the core gut microbiota undergo an adaptive shift towards highly efficient cellulose degradation and short-chain fatty acid (SCFA) synthesis.
- Uncovered a microbiome-mediated "nutritional safety net" compensatory strategy: Discovered the specific enrichment of riboflavin (Vitamin B2) in winter Marco Polo sheep and a significant increase in gut butyrate in Siberian ibex, revealing key pathways for microbe-driven energy and vitamin compensation under extreme nutritional stress.

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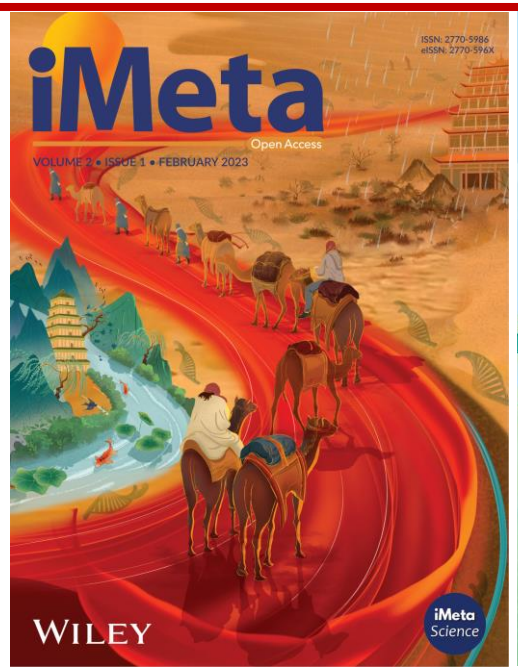

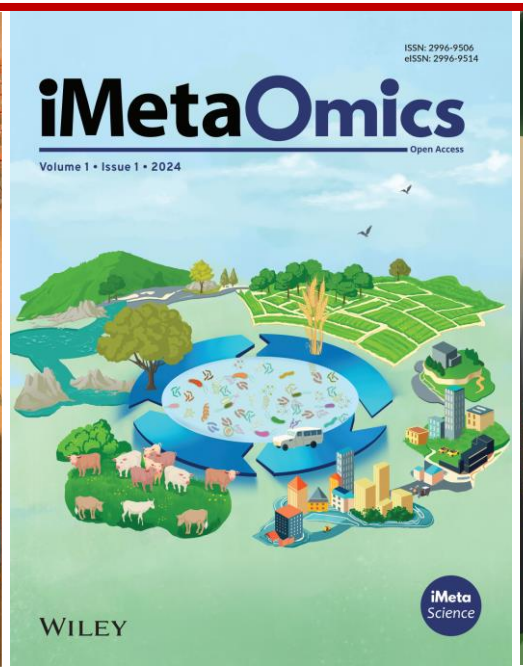

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