

1 **Supplementary Tables**

2 **Table S1.** Dietary indices for 35 prey families in male and female *Fejervarya cancrivora*.

Taxon		Male				Female			
Order	Family	N%	F%	V%	IRI	N%	F%	V%	IRI
Hemiptera	Reduriidae	0.65	0.93	0.02	0.62	0.35	0.52	0.29	0.33
Blattaria	Blattidae	0.65	0.93	0.58	1.14	0.35	0.52	0.19	0.28
Ephemeroptera	Ephemeridae	—	—	—	—	0.35	0.52	0.09	0.23
Lepidoptera	Geometridae	0.65	0.93	0.35	0.93	—	—	—	—
	Arctiidae	—	—	—	—	0.35	0.52	0.97	0.69
	Pyralidae	1.95	2.80	0.31	6.33	3.89	5.76	0.90	27.59
	Noctuidae	11.04	10.28	2.05	134.57	3.53	3.66	0.55	14.93

Taxon		Male				Female			
Order	Family	N%	F%	V%	IRI	N%	F%	V%	IRI
	Pieridae	—	—	—	—	0.35	0.52	0.02	0.19
Hymenoptera	Formicidae	1.30	1.87	0.24	2.88	2.83	2.62	0.30	8.20
Coleoptera	Carabidae	1.30	1.87	0.68	3.70	1.41	2.09	0.23	3.43
	Scarabaeidae	1.30	1.87	2.24	6.62	1.41	2.09	0.91	4.85
	Elateridae	—	—	—	—	0.35	0.52	0.06	0.21
	Coccinellidae	3.25	2.80	0.08	9.32	1.06	1.57	0.21	1.99
	Passalidae	—	—	—	—	0.71	1.05	0.53	1.30
Diptera	Anthomyiidae	—	—	—	—	0.35	0.52	0.02	0.19
	Calliphoridae	0.65	0.93	0.06	0.66	0.71	1.05	0.03	0.78

Taxon		Male				Female			
Order	Family	N%	F%	V%	IRI	N%	F%	V%	IRI
Homoptera	Muscidae	—	—	—	—	0.71	0.52	0.01	0.37
	Culicidae	—	—	—	—	0.35	0.52	0.01	0.19
	Cecidomyiidae	0.65	0.93	0.09	0.69	—	—	—	—
	Cicadellidae	0.65	0.93	6.12	6.30	—	—	—	—
Orthoptera	Acrididae	—	—	—	—	0.35	0.52	0.44	0.41
Mesogastropoda	Gryllidae	1.95	0.93	0.52	2.30	—	—	—	—
	Littorinidae	1.95	2.80	0.63	7.22	1.06	1.57	0.18	1.95
	Potamididae	0.65	0.93	0.07	0.67	1.06	1.57	0.09	1.81
	Viviparidae	1.95	2.80	0.18	5.96	3.18	2.62	0.15	8.72

Taxon		Male				Female			
Order	Family	N%	F%	V%	IRI	N%	F%	V%	IRI
	Turritellidae	11.69	9.35	1.52	123.51	5.30	6.28	0.33	35.36
Siphonophorida	Siphonophoridae	—	—	—	—	0.35	0.52	0.04	0.20
Araneida	Salticidae	1.30	1.87	0.16	2.73	3.18	4.71	0.20	15.92
	Araneidae	0.65	0.93	0.14	0.73	2.47	3.14	0.32	8.76
Amphipoda	Talitridae	0.65	0.93	0.06	0.66	—	—	—	—
Decapoda	Grapsidae	12.34	15.89	54.67	1064.79	16.25	20.94	79.23	1999.35
	Ocypodidae	19.48	18.69	27.05	869.65	16.61	16.75	12.67	490.44
	Alpheidae	0.65	0.93	0.34	0.92	0.71	1.05	0.20	0.96
	Palaemonidae	19.48	12.15	1.44	254.18	28.98	13.61	0.73	404.35

Taxon		Male				Female			
Order	Family	N%	F%	V%	IRI	N%	F%	V%	IRI
Perciformes	Periophthalmidae	3.25	4.67	0.43	17.19	1.41	2.09	0.10	3.16

- 3 **Note:** N%, numerical percentage; F%, frequency of occurrence; V%, volumetric percentage; IRI, index of relative importance. “—” indicates zero
- 4 or not recorded.

5 **Table S2.** Summed family-level IRI

Order	Male				Female			
	N%	F%	V%	ΣIRI	N%	F%	V%	ΣIRI
Hemiptera	0.65	0.93	0.02	0.62	0.35	0.52	0.29	0.33
Blattaria	0.65	0.93	0.58	1.14	0.35	0.52	0.19	0.28
Ephemeroptera	—	—	—	—	0.35	0.52	0.09	0.23
Lepidoptera	13.64	14.01	2.71	141.83	8.12	10.46	2.44	43.40
Hymenoptera	1.30	1.87	0.24	2.88	2.83	2.62	0.30	8.20
Coleoptera	5.85	6.54	3.00	19.64	4.94	7.32	1.94	11.78
Diptera	1.30	1.86	0.15	1.35	2.12	2.61	0.07	1.53
Homoptera	0.65	0.93	6.12	6.30	—	—	—	—
Orthoptera	1.95	0.93	0.52	2.30	0.35	0.52	0.44	0.41
Mesogastropoda	16.24	15.88	2.40	137.36	10.60	12.04	0.75	47.84
Siphonophorida	—	—	—	—	0.35	0.52	0.04	0.20
Araneida	1.95	2.80	0.30	3.46	5.65	7.85	0.52	24.68
Amphipoda	0.65	0.93	0.06	0.66	—	—	—	—
Decapoda	51.95	47.66	83.50	2189.54	62.55	52.35	92.83	2895.10
Perciformes	3.25	4.67	0.43	17.19	1.41	2.09	0.10	3.16

6 **Note:** N%, F%, and V% at the order level were obtained by summing the corresponding
7 family-level percentages; ΣIRI represents the sum of IRI values for all families within
8 each order.

9 **Table S3.** Relative abundances of genera with reported chitin-degrading members in

10 *Fejervarya cancrivora*.

Genus	Mean relative abundance (%)	Fig. 4B display
<i>Bacteroides</i>	7.6259	Individual
<i>Clostridium</i>	3.5720	Individual
<i>Aeromonas</i>	1.4809	Individual
<i>Plesiomonas</i>	1.2496	Individual
<i>Acinetobacter</i>	0.7727	Individual
<i>Vibrio</i>	0.6082	Individual
<i>Pseudomonas</i>	0.4394	Individual
<i>Photobacterium</i>	0.3103	Individual
<i>Paenibacillus</i>	0.1821	Individual
<i>Escherichia</i>	0.1758	Individual
<i>Streptomyces</i>	0.1590	Individual
<i>Bacillus</i>	0.1275	Individual
<i>Klebsiella</i>	0.1215	Individual
<i>Streptococcus</i>	0.0948	Others
<i>Enterococcus</i>	0.0855	Others
<i>Enterobacter</i>	0.0845	Others
<i>Staphylococcus</i>	0.0753	Others

Genus	Mean relative abundance (%)	Fig. 4B display
<i>Serratia</i>	0.0335	Others
<i>Hafnia</i>	0.0188	Others
<i>Pantoea</i>	0.0176	Others
<i>Citrobacter</i>	0.0108	Others
<i>Arthrobacter</i>	0.0056	Others
<i>Carnobacterium</i>	0.0056	Others
<i>Pseudoalteromonas</i>	0.0052	Others
<i>Stenotrophomonas</i>	0.0039	Others
<i>Roseateles</i>	0.0037	Others
<i>Enterovibrio</i>	0.0037	Others
<i>Cellulomonas</i>	0.0015	Others
<i>Cellulosimicrobium</i>	0.0003	Others
<i>Kocuria</i>	0.0002	Others
<i>Isoptricola</i>	0.0001	Others

11 **Note:** Candidate genera were compiled from the literature cited in the manuscript.
12 Mean relative abundances were calculated from NR-annotated gene TPM values after
13 normalization within each sample, with the six samples weighted equally. Genera with
14 a mean relative abundance <0.1% were grouped as Others in Fig. 4B. The 31 genera
15 collectively accounted for 17.2754% of the community, and the 18 genera grouped as
16 Others accounted for 0.4507%.

Table S4. Candidate functional genes related to chitin utilization in the gut metagenome of *Fejervarya cancrivora*.

Functional stage	CAZy family	Target gene/system	KO	Functional annotation
Chitin polymer cleavage	GH18	chitinase	K01183	Chitinase
	GH18	endo-chitodextrinase	K21606	Endo-chitodextrinase
	GH19/GH19_1	putative chitinase	K03791	Putative chitinase
Chitooligosaccharide processing	GH3	<i>nagZ</i>	K01207	β -N-acetylhexosaminidase
Chitobiose utilization	GH94	<i>chbP</i>	K18675	N, N'-diacetylchitobiose phosphorylase
GlcNAc transport	—	<i>nagE</i> / PTS	K02804	N-acetylglucosamine PTS system
	—	<i>ngcE-ngcF-ngcG</i>	K10200/K10201/K10202	ABC-type N-acetylglucosamine transport system

<i>Intracellular metabolism</i>	—	<i>nagK</i>	K28207	N-acetylglucosamine kinase
	—	<i>nagA</i>	K01443	N-acetylglucosamine-6-phosphate deacetylase
	—	<i>nagB</i>	K02564	Glucosamine-6-phosphate deaminase

Note: Genes involved in polymer cleavage, chitooligosaccharide processing, and chitobiose utilization were retained when the corresponding CAZy family and KEGG KO annotations occurred on the same GeneID. Transport and intracellular metabolism genes were identified using exact KEGG KO annotations. An em dash (—) indicates that no CAZy-family criterion was applied.