河南师范大学
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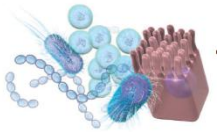
水产动物肠道菌群研究进展

2017. 4. 28

厚德博学·止于至善

主要内容

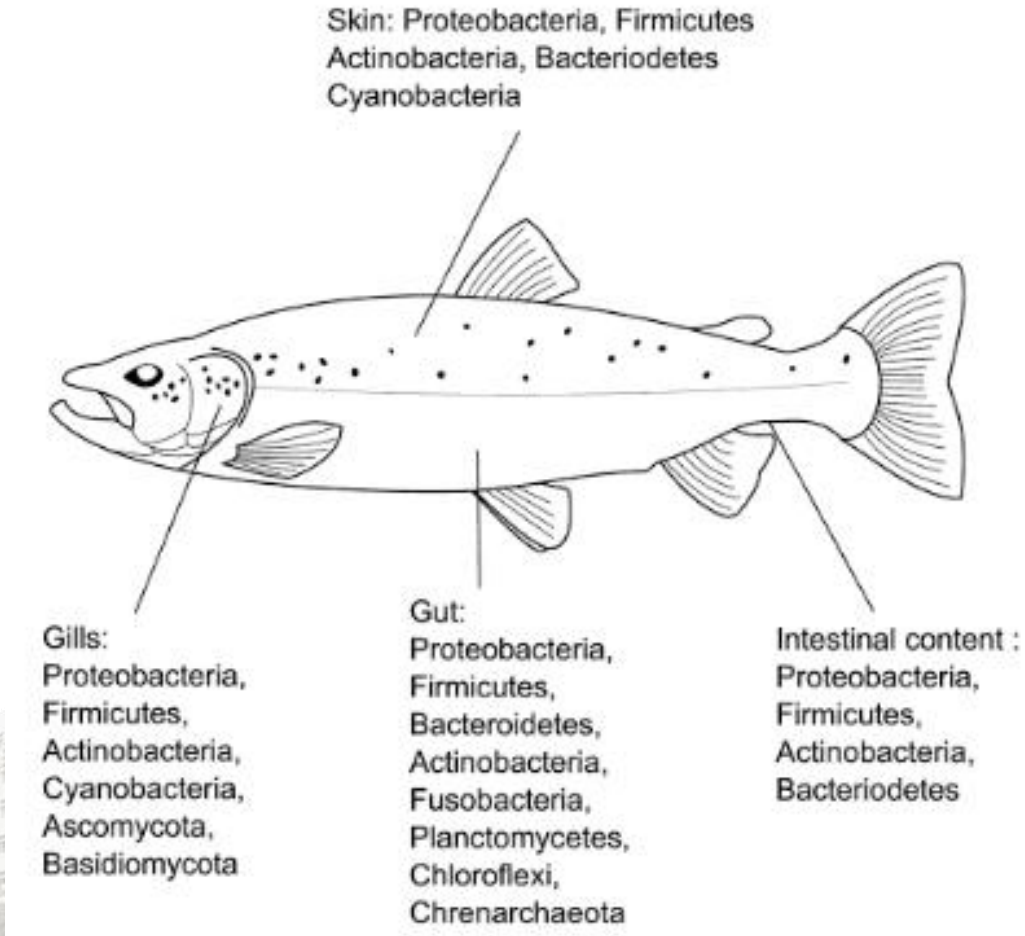


Part Ⅰ 鱼类肠道微生物的结构

Part Ⅱ 鱼类肠道微生物功能研究

Part Ⅲ 评价微生物群落的方法

Part Ⅰ 鱼类肠道微生物的结构



鱼类肠道微生物组成

Proteobacteria
Bacteroidetes
Actinobacteria
Firmicutes
Fusobacterium

Part Ⅰ 鱼类肠道微生物的结构

Enviroment and diet

marine

freshwater

Part Ⅰ 鱼类肠道微生物的结构

Diet

Carnivorous
Omnivorous
Herbivorous

Part Ⅰ 鱼类肠道微生物的结构

Marine fish

兼性厌氧菌

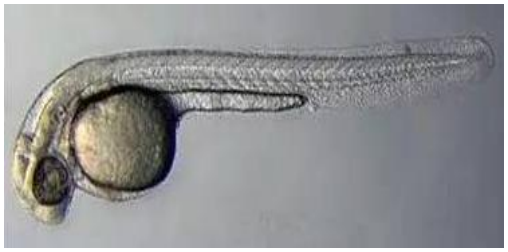
Vibrio,(弧菌属）
Pseudomonas,（假单胞菌属）
Acinetobacter,（不动杆菌属）
Corynebacterium（棒状杆菌属）
Alteromonas （单胞菌属）
Flavobacterium （黄杆菌属）
Micrococcus （微球菌属）

Freshwater fish

Aeromonas, (其单胞菌属）
Pseudomonas,（假单胞菌属）
Bacteroides, （拟杆菌属）
Plesiomonas,（邻单胞菌属）
Enterobacteriaceae （肠杆菌属）
Micrococcus （微球菌属）
Acinetobacter （不动杆菌属）
Clostridium （梭菌属）
Fusarium （镰刀菌属）

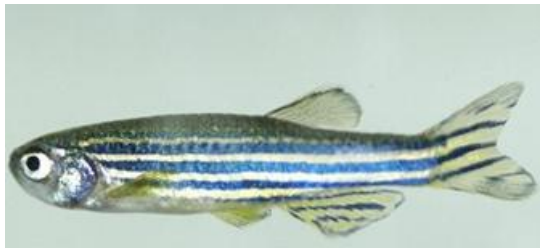
Part Ⅰ 鱼类肠道微生物的结构

Establishment of GI microbiota



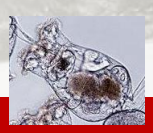
Proteobacteria
Actinobacteria

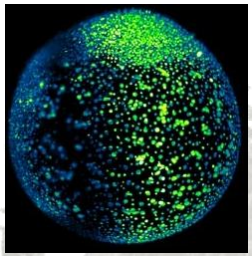
Proteobacteria
Actinobacteria
Firmicutes
Bacteroidetes



2-5 years old
Similar to adult

1. Eggs
2. Larval rearing water
3. Live feed





Cytophaga,
Flavobacterium
pseudomonas

Part Ⅰ 鱼类肠道微生物的结构

Factors affecting GI microbiota of fish

Host factors

Environmental factors

Microbial Factors

Individual Factors

Water and Diet

Genetics,
Gender → Largemouth bronze gudgeon
Weight
Age
Immunity
Intestinal motility

Part Ⅰ 鱼类肠道微生物的结构

The influence of water

Temperature

Diversity and seasonal changes in lactic acid bacteria in the intestinal tract of cultured freshwater fish

Tatsuro Hagi, Daichi Tanaka, Yasutada Iwamura, Takayuki Hoshino*

Institute of Applied Biochemistry, University of Tsukuba, 1-1-1 Ten-nodai Tsukuba, Ibaraki, 305-8572, Japan

Received 8 December 2003; received in revised form 15 January 2004; accepted 15 January 2004

Seasonal Variation

ORIGINAL ARTICLE

Pyrosequencing-based characterization of gastrointestinal bacteria of Atlantic salmon (*Salmo salar* L.) within a commercial mariculture system

K.Z. Zarkasi[1,2], G.C.J. Abell[3], R.S. Taylor[3], C. Neuman[4], E. Hatje[4], M.L. Tamplin[1], M. Katouli[4] and J.P. Bowman[1]

The effect of diet and environmental temperature on the faecal microbiota of farmed Tasmanian Atlantic Salmon (*Salmo salar* L.)

Christina Neuman[1], Eva Hatje[1], Kamarul Z Zarkasi[2], Richard Smullen[3], John P Bowman[2] & Mohammad Katouli[1]

Part Ⅰ 鱼类肠道微生物的结构

Salinity

Response of gut microbiota to salinity change in two euryhaline aquatic animals with reverse salinity preference

Meiling Zhang[a], Yuhong Sun[a], Yukun Liu[a], Fang Qiao[a], Liqiao Chen[a], Wen-Tso Liu[b], Zhenyu Du[a], , , Erchao Li[a], ,

decreased when the host facing hyposaline or hypersaline stress. The alteration of intestinal microbiota was likely attributed to the environmental selection for microbes that could grow better under high or low salinity, the host response to the salinity stress and subsequent stress exerting on the gut microbiota, or both.

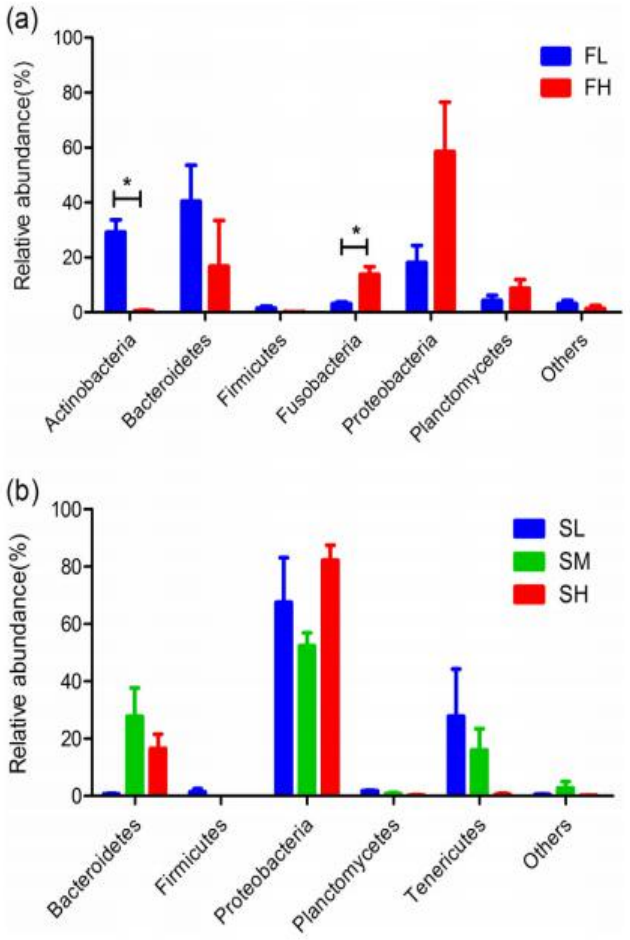


Fig. 2. Relative abundance of the intestinal flora at phylum level in Nile tilapia and Pacific white shrimp reared at different salinities. The most dominant phyla (>1% of the total sequences) were shown. Asterisk (*) represents the difference between groups is significant based on student t-test, $p < 0.05$.

Part Ⅰ 鱼类肠道微生物的结构

The influence of diet and feeding habit

Contents lists available at ScienceDirect

Aquaculture

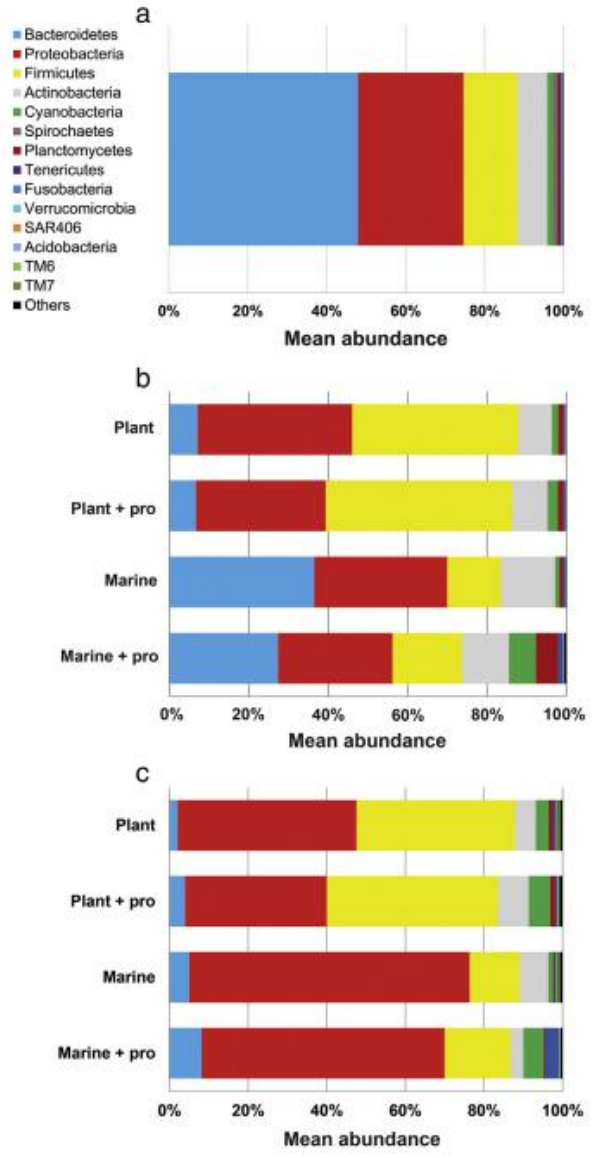
journal homepage: www.elsevier.com/locate/aqua-online

The development of the gut microbiota in rainbow trout (*Oncorhynchus mykiss*) is affected by first feeding and diet type

H.-C. Ingerslev [a,*], L. von Gersdorff Jørgensen [b], M. Lenz Strube [a], N. Larsen [c], I. Dalsgaard [a], M. Boye [a], L. Madsen [a]

f.f: 1 day before first feeding
26 days after f.f
49 days after f.f

Firmicutes dominate the plant source oil
Proteobacteria dominte the fish oil



Part Ⅰ 鱼类肠道微生物的结构

The regional difference of GI microbiota

Density

第9卷第4期 南方水产科学 Vol. 9, No. 4
2013年8月 South China Fisheries Science Aug., 2013

doi：10.3969/j.issn.2095－0780.2013.04.002

鲩鱼消化道细菌群落结构及多样性初步研究

陶 诗，王健鑫，刘雪珠，何芳芳，俞凯成
（浙江海洋学院，海洋生物资源与分子工程实验室，浙江 舟山 316000）

摘要：采用常规分离纯化与构建16S rDNA克隆文库相结合的方法对鲩鱼（*Miichthys miiuy*）消化道细菌多样性进行了初步研究。结果表明，鲩鱼消化道各部位可培养细菌的菌落数量从大到小依次为前肠＞幽门胃＞中肠＞后肠＞前胃＞后胃＞口咽腔，其中肠道部位菌落数量最多。分离细菌菌株主要为杆状细菌和革兰氏阴性菌，对其中的50株典型菌株进行分子鉴定，发现它们主要属于变形菌门的γ-变形菌纲（占52.7%）和β-变形菌纲（占36.8%），以及厚壁菌门的芽孢杆菌纲（占10.5%）；不可培养细菌16S rDNA文库克隆子主要属于γ-变形菌纲、α-变形菌纲和脱铁杆菌纲，部分序列与已报道的物种相似性较低，说明消化道中可能存在新的有待开发的肠道菌株。

Part Ⅰ 鱼类肠道微生物的结构

Composition varied among different GI tract regions

Bacterial microflora in the gastrointestinal tract of Nile tilapia, *Oreochromis niloticus*, cultured in a semi-intensive system

Lígia Maria Molinari[1], Denise de Oliveira Scoaris[2], Raíssa Bocchi Pedroso[3], Nilza de Lucas Rodrigues Bittencourt[4], Celso Vataru Nakamura[4],Tânia Ueda-Nakamura[4], Benício Alves de Abreu Filho[4] and Benedito Prado Dias Filho[4]*

Table 1. Predominant bacteria isolated from gastrointestinal tract of the tilapia *Oreochromis niloticus*.

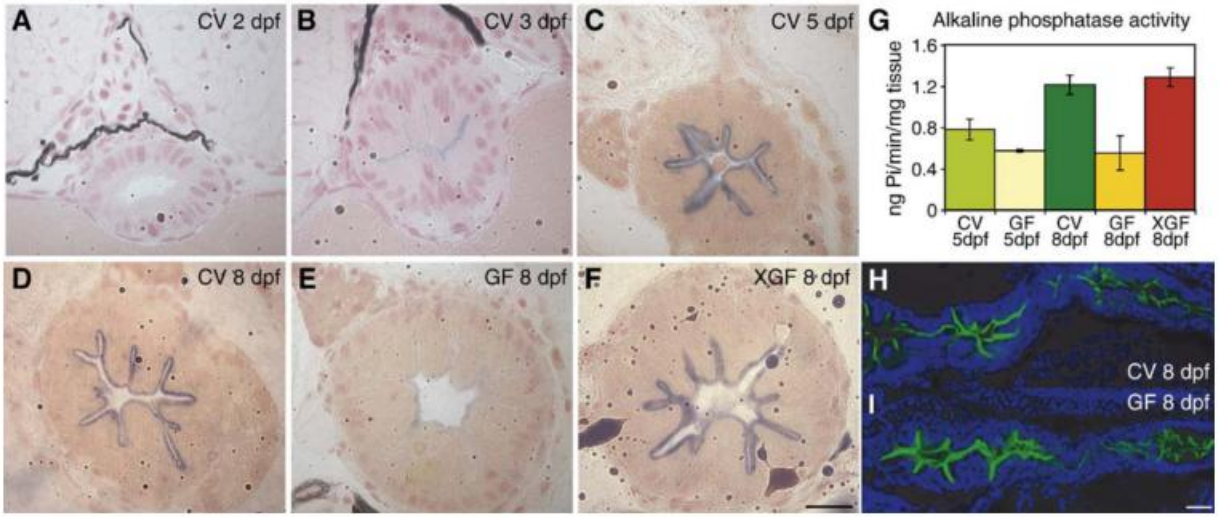
Microorganism	Stomach	Anterior gut	Posterior gut
Aeromonas hydrophila	0.6	0	0
Aeromonas veronii	0	0.2	0.3
Burkholderia cepacia	0	0	3.7
Chromobacterium violaceum	90.0	55.5	0
Citrobacter freundii	0	0	13.0
Escherichia coli	7.4	0	0
Flavimonas oryzihabitans	1.1	0	0
Plesiomonas shigelloides	0.6	4.8	76.0
Unidentified sp	0	39.3	6.6

Values are mean percentages from four independent experiments

Part II 鱼类肠道微生物功能研究

Gnotobiotic zebrafish gut microbiota transplants models

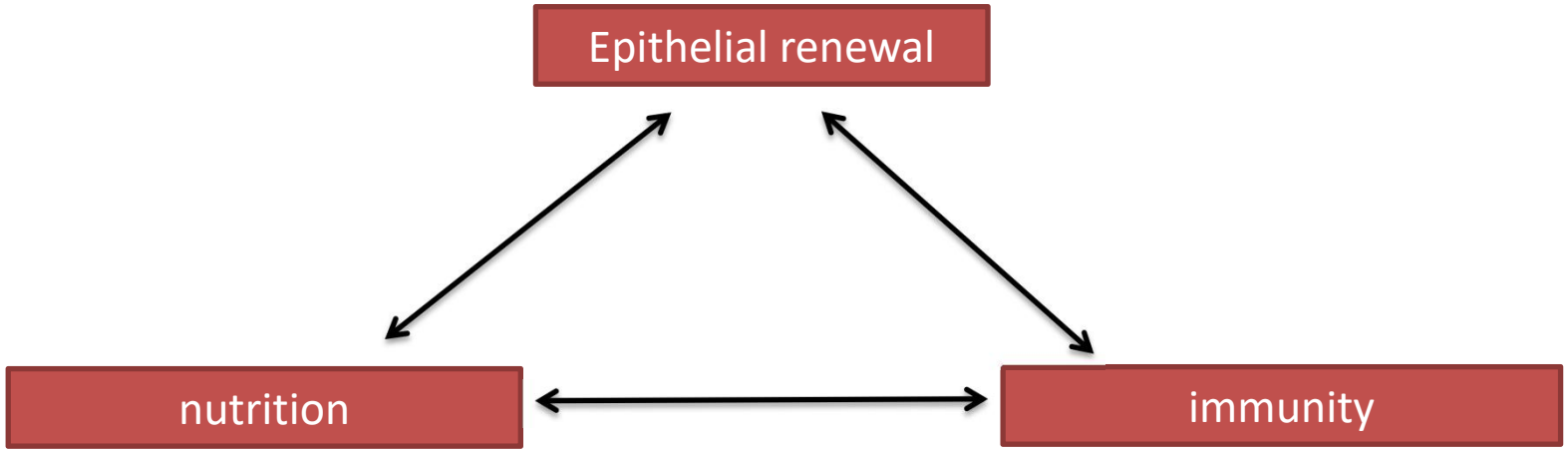
Gnotobio
response
John F. Rawls, Buck
Department of Molecular
Contributed by Jeffrey I. G
Distinct sig
Jennifer M. E



Hatch from 3 days post fertilization (dpf), microbes colonized from 3-4dpf. At 5 dpf, begins food ingestion.

Part II 鱼类肠道微生物功能研究

Role of GI microbiota in fish : gnotobiotic approaches



Part II 鱼类肠道微生物功能研究

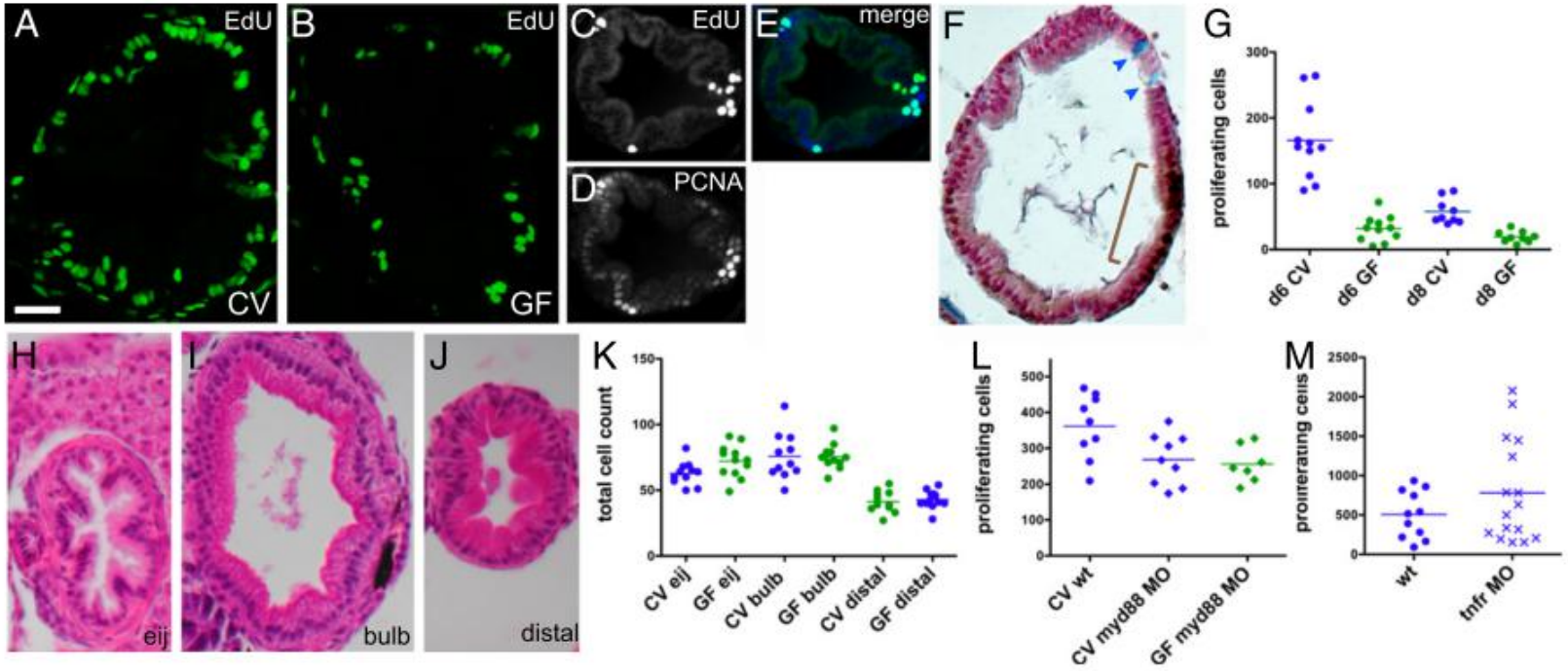


Fig. 1. Microbes induce epithelial cell proliferation in the zebrafish larval intestine via Myd88 and not inflammation. Transverse sections of the intestinal bulb of 6-dpf larvae reared CV (*A*) or GF (*B*) labeled with EdU to reveal S-phase cells are shown. A transverse section of the distal intestine shows colocalization of EdU-labeled (*C*) and PCNA-labeled (*D*) cells (*E*, merge). (*F*) Distinct cell populations are stained with Alcian blue, marking differentiated goblet cells (arrowheads), and anti-PCNA, marking mitotic cells (brown bracket). (*G*) Total numbers of S-phase cells over 30 serial sections in the intestinal bulb of individual 6-dpf larvae are represented for the treatment groups and genotypes indicated. Here and in subsequent figures, the genotype and microbial exposure of each larva are indicated by the shape and color of the data point, respectively. Significantly fewer BrdU-labeled cells were found in 6- and 8-dpf larvae reared GF vs. CV ($P < 0.001$). H&E sections of 8-dpf GF intestines at three locations within the intestinal tract are shown: the esophageal intestinal junction (*H*, eij), defined as position 0; the bulb, 30 sections caudal to the junction (*I*); and the distal intestine, 60 sections caudal to the junction (*J*). (*K*) There was no significant difference between total intestinal epithelial cell counts at the three positions described above in 8-dpf CV vs. GF larvae. (*L*) Significantly fewer EdU-labeled cells were found in CV or GF *myd88* MO vs. CV WT (wt) ($P < 0.05$). *(M)* There was no significant difference in the numbers of EdU-labeled cells between CV vs. GF *myd88* MO or between wt vs. *tnfr* MO. (Scale bars: *A* and *B*, 15 μM; *C–F* and *H–J*, 25 μM.)

Part II 鱼类肠道微生物功能研究

REVIEW ARTICLE

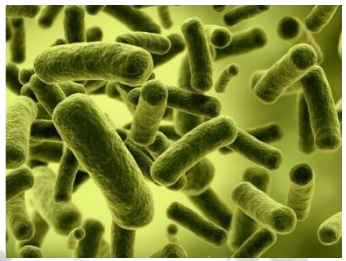
Enzyme-producing bacteria isolated from fish gut: a review

A.K. RAY[1], K. GHOSH[2] & E. RINGØ[3,4]

[1] *Fisheries Laboratory, Department of Zoology, Visva-Bharati University, Santiniketan, West Bengal, India;* [2] *Aquaculture Laboratory, Department of Zoology, University of Burdwan, Burdwan, West Bengal, India;* [3] *Norwegian College of Fishery Science, Faculty of Biosciences, Fisheries and Economics, University of Tromsø, Tromsø, Norway;* [4] *Aquaculture Protein Centre (a CoE), Department of Aquatic Medicine and Nutrition, Norwegian School of Veterinary Medicine, Oslo, Norway*

Amylase, Cellulase, Lipase, Proteases, Chitinase, Phytase

Significant roles in digestion



Protein macromolecules

Fat storage

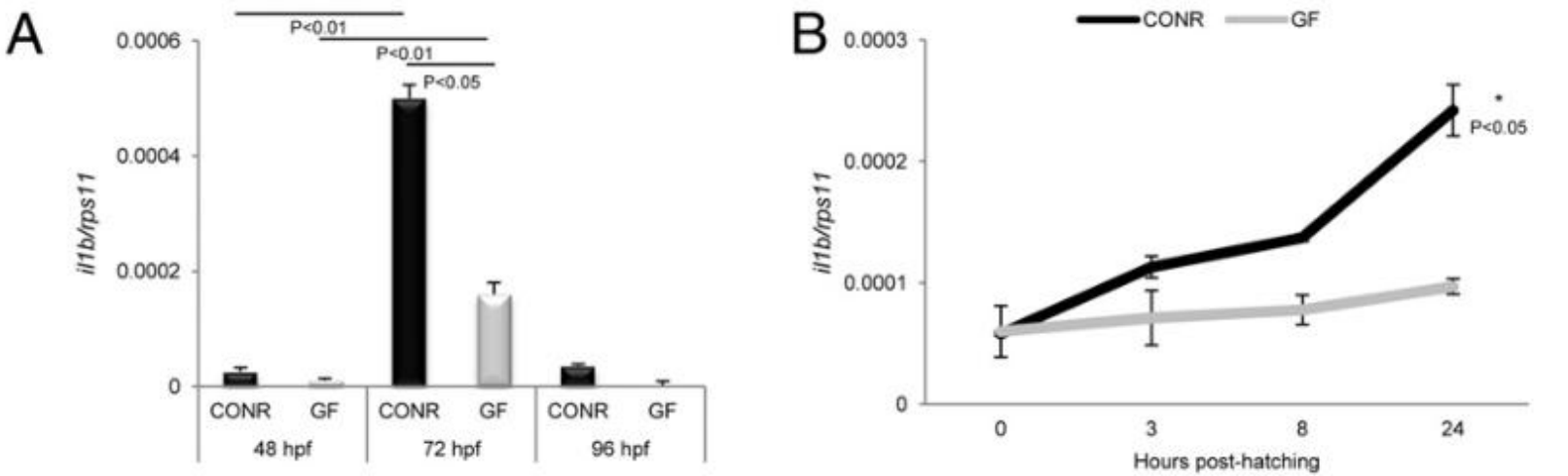
Part II 鱼类肠道微生物功能研究

PNAS

Regulation of immunity and disease resistance by commensal microbes and chromatin modifications during zebrafish development

Jorge Galindo-Villegas[a,b,1], Diana García-Moreno[a,b,1], Sofia de Oliveira[a,c], José Meseguer[a,b], and Victoriano Mulero[a,b,2]

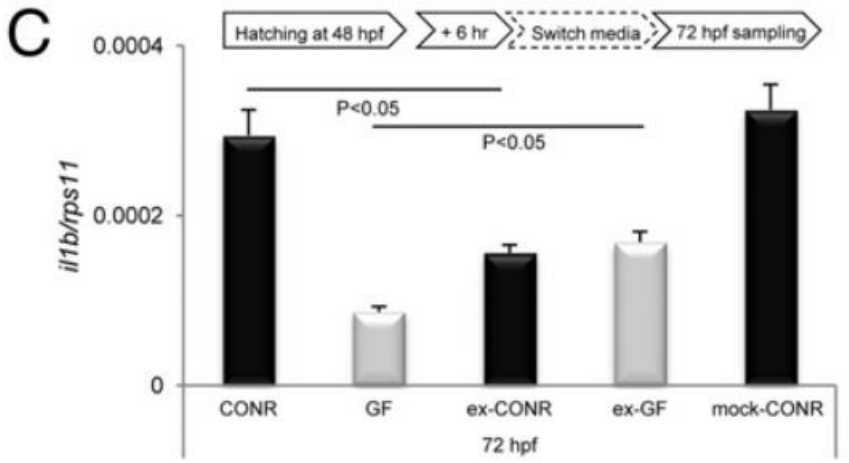
[a]Departamento de Biología Celular e Histología, Universidad de Murcia, 30100 Murcia, Spain; [b]Instituto Murciano de Investigación Biosanitaria, 30120 Mur Spain; and [c]Unidade de Biologia Microvascular e Inflamação, Instituto de Bioquímica-Instituto de Medicina Molecular, Faculdade de Medicina, Universida de Lisboa, 1649-028 Lisbon, Portugal

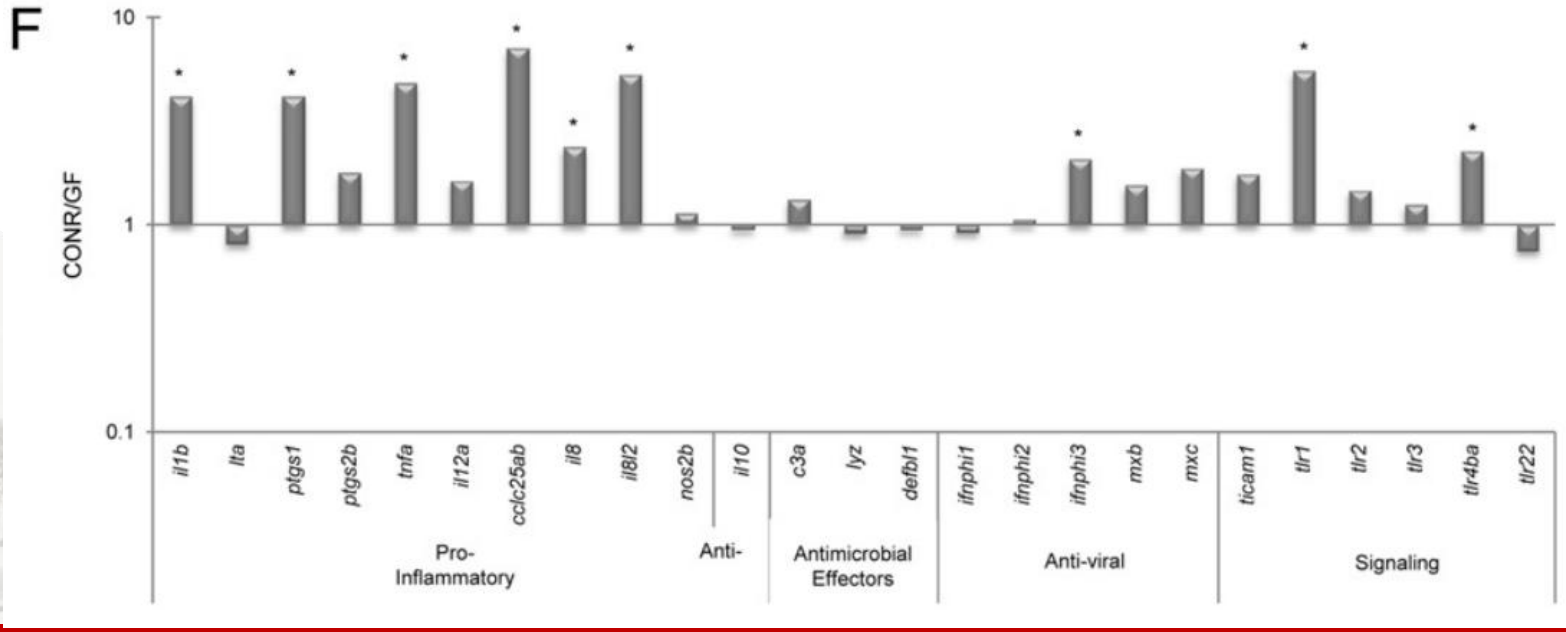


Postfertilization

Post hatching

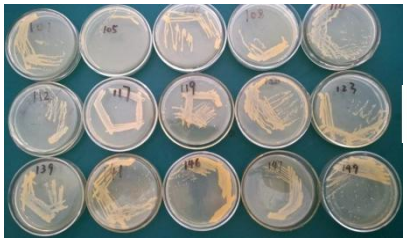
Part II 鱼类肠道微生物功能研究



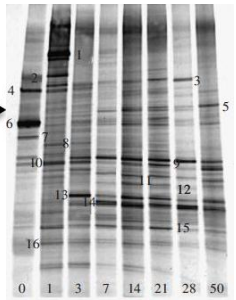


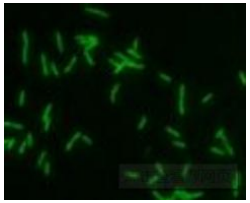
Part III 评价微生物群落的方法

Methods used to assess the bacterial communities



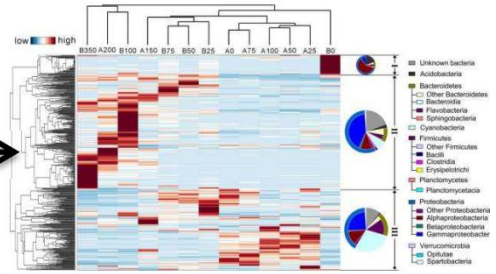
<0.1% of total species of fish





2006-2016

1. Clone library
2. Finger printing
3. qPCR or FISH
4. FISH and immunohistochemistry



NGS

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