frontiers | Frontiers in Marine Science

TYPE Editorial
PUBLISHED 25 August 2022
DOI 10.3389/fmars.2022.985012

Check for updates

OPEN ACCESS

EDITED AND REVIEWED BY
Yngvar Olsen,
Norwegian University of Science and Technology, Norway

*CORRESPONDENCE
Yun-Zhang Sun
jmusunyunzhang@163.com
Einar Ringø
einar.ringo@uit.no

SPECIALTY SECTION
This article was submitted to Marine Fisheries, Aquaculture and Living Resources, a section of the journal Frontiers in Marine Science

RECEIVED 03 July 2022
ACCEPTED 10 August 2022
PUBLISHED 25 August 2022

CITATION
Sun Y-Z, Zhang Y and Ringø E (2022) Editorial: Composition, functions and modulation of gut microbiota in maricultural animals.
Front. Mar. Sci. 9:985012.
doi: 10.3389/fmars.2022.985012

COPYRIGHT
© 2022 Sun, Zhang and Ringø. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.

Editorial: Composition, functions and modulation of gut microbiota in maricultural animals

Yun-Zhang Sun[1]*, Yanjiao Zhang[2] and Einar Ringø[3]*

[1]Fisheries College, Jimei University, Xiamen, China, [2]Key Laboratory of Aquaculture Nutrition and Feed (Ministry of Agriculture) & Key Laboratory of Mariculture (Ministry of Education), Ocean University of China, Qingdao, China, [3]Norwegian College of Fishery Science, Faculty of Bioscience, Fisheries and Economics, UiT The Arctic University of Norway, Tromsø, Norway

KEYWORDS

gut microbiota, composition, functions, modulation, maricultural animals

Editorial on the Research Topic
Composition, functions and modulation of gut microbiota in maricultural animals

Despite that evaluation of the gut microbiota can be dates to the late 1920`s and early 1930`s (Reed and Spence, 1929; Stewart, 1932; Gibbons, 1933), controversy still existed in the 70s about the existence and role of indigenous microbiota in fish gastrointestinal (GI) tract (Ringø et al., 2016). However, today it is generally accepted that fish gut microbiome, which include e.g., bacteria, fungi and yeast are modulated by dietary components, age, gender, health status and environmental factors (Ringø et al., 2016; Egerton et al., 2018; Bates et al., 2022). The microbiome plays a crucial role in GI development, digestive function, maintaining mucosal tolerance, barrier functions and in the maintenance of its homeostasis, enhance the immune response, provide protection against exogenous microorganisms and diseases (e.g., Rawls et al., 2004; Rawls et al., 2006; Wang et al., 2018; Li et al., 2019), development of metabolic syndrome (Clément, 2011), vitamin synthesis (Rowland et al., 2018), the gut-brain axis (Cryan and O`Mahony, 2011; Butt and Volkoff, 2019), as well as effect on flesh color (Nguyen et al., 2020). Furthermore, several reports highlighted the ability of the gut microbiota to interact with the host's tissue, controlling its energy metabolism, contributing to variations in body weight, fat distribution, insulin sensitivity, and lipid metabolism (e.g., Zhang and Zhang, 2013; Falcinelli et al., 2015; Kim et al., 2018).

Gatesoupe (1994) published a pioneer study on the effect of lactic acid bacteria supplementation on the improved resistance of turbot (*Scophthalmus maximus*) larvae against *Vibrio*. Five years later, published Ringø and Birkbeck (1999) an overview of bacterial species isolated from the GI tract of early developed freshwater and marine species. Since then, numerous studies on larvae and gut bacteria have been published. However, to obtain a sustainable aquaculture it is of high importance to clarify one important bottleneck, proper rearing of the early teleost larvae, their gut microbiota, and the connection between commensal and opportunistic bacteria in larval gut (e.g., Ringø and Birkbeck, 1999; Vadstein et al., 2013; Vadstein et al., 2018; Pan et al., 2022; Vestrum et al., 2022). Furthermore, to achieve successful larval rearing more information is needed on the interactions between gut-, skin- and gill microbiota, along with microbial evaluations of tank biofilms and water.

Modern technology by recirculating aquaculture systems (RASs) was introduced in mid 1990s, and since then numerical studies have been published (e.g., Kroeckel et al., 2012; Xiao et al., 2019), and how RASs affect the gut microbiota (e.g., Dehler et al., 2017; Minich et al., 2020), but as less information is available on larvae (Deng et al., 2021) this topic merits further investigations.

To understand the microbiota participation, zebrafish (*Danio rerio*) has rapidly become the well-recognised animal model to study microbe-host interactions (Nadal et al., 2020; Zhong et al., 2022), and today evaluation of gnotobiotic protocols for aquaculture fish are available. The GI tract bacteria in fish is generally divided into; the allochthonous, the GI lumen bacteria, and the autochthonous, those who adhere and colonise the mucosal surface. This is visualised in the review of Ringø et al. (2003). However, the molecular mechanisms of the interactions between commensal microbes and host are still poorly understood in fish (Yang et al., 2019). Future studies should use gnotobiotic zebrafish technology, combined with multi-omics analysis, RNA interference and other techniques to further explore these problems.

It is well known that fish possess not all essential enzymes to handle with the dietary challenges of aquaculture production. However, the GI microbiota with probiotic potential secrete various digestive and degradation enzymes to degrade a variety of nutritional substrates, thus, use of probiotics in diet can provide a chance of possibility to use different sources of carbohydrates as animal energy source. Further studies are needed to illustrate which and how commensal microbes regulate carbohydrate metabolism, the common characteristics of specific bacteria in regulating carbohydrate metabolism and the possible mechanisms in fish.

To conclude, studies included in the Research Topic *Composition, Functions and Modulation of Gut Microbiota in Maricultural Animals* highlighted the importance of the gut microbiota. Future studies should focus on modulation of gut microbiota and how these changes affect fish physiology, nutrition, homeostasis, and disease resistance. Even though our knowledge on the importance of the fish gut microbiota has increased significantly during the last two decades, there still a long way to go, and the topic is probably *a never-ending story*.

Author contributions

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

Funding

This work was supported by the National natural science foundation of China (32072990), Science and Technology Major/Special Project of Fujian Province (2021NZ029022), Xiamen Marine and Fisheries Development Fund (19CZP018HJ04)

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

References

Bates, K. A., Higgins, C., Neiman, M., and King, K. C. (2022). Turning the tide on sex and the microbiota in aquatic animals. *Hydrobiologia*. doi: 10.1007/s10750-022-04862-4

Butt, R. L., and Volkoff, H. (2019). Gut microbiota and energy homeostasis in fish. *Front. Endocrinol.* 10, 9. doi: 10.3389/fendo.2019.0009

Clément, K. (2011). Bariatric surgery, adipose tissue and gut microbiota. *Int. J. Obes.* 35, S7–S15. doi: 10.1038/ijo.2011.141

Cryan, J. F., and O`Mahony, S. M. (2011). The microbiome-gut-brain axis: from bowel to behavior. *Neurogastroenterol. Motil.* 23 (3), 187–192. doi: 10.1111/j.1365-2982.2010.01664x

Dehler, C. E., Secombes, C. J., and Martin, S. A. M. (2017). Environmental and physiological factors shape the gut microbiota of Atlantic salmon parr (*Salmo salar* l.). *Aquaculture* 467, 149–157. doi: 10.1016/j.aquaculture.2016.07.017

Deng, Y., Kokou, F., Eding, E. H., and Verdegem, M. C. J. (2021). Impact of early-life rearing history on gut microbiome succession and performance of Nile tilapia. *Anim. Microb.* 3, 81. doi: 10.1186/s42523-021-00145-w

Egerton, S., Culloty, S., Whooley, J., Stanton, C., and Ross, R. P. (2018). The gut microbiota of marine fish. *Front. Microbiol.* 9, 873. doi: 10.3389/fmicb.2018.00873

Falcinelli, S., Picchietti, S., Rodiles, A., Cossignani, L., Merrifield, D. L., Taddei, A. R., et al. (2015). *Lactobacillus rhamnosus* lowers zebrafish lipid content by changing gut microbiota and host transcription of genes involved in lipid metabolism. *Sci. Rep.* 5, 9336. doi: 10.1038/srep09336

Gatesoupe, F.-J. (1994). Lactic acid bacteria increase the resistance of turbot larvae (*Scophthalmus maximus*), against vibrio. *Aquat. Living Resour.* 7, 277–282. doi: 10.1051/alr:1994030

Gibbons, N. E. (1933). The slime and intestinal flora of some marine fishes. *Contrib. Can. Biol. Fish.* 8, 275–290. doi: 10.1139/f33-022

Kim, Y. A., Keogh, J. B., and Clifton, P. M. (2018). Probiotics, prebiotics, synbiotics and insulin sensitivity. *Nutr. Res. Rev.* 31, 35–51. doi: 10.1017/8095442241700018x

Kroeckel, S., Harjes, A.-G. E., Roth, I., Katz, H., Wuertz, S., Susenbeth, A., et al. (2012). When a turbot catches a fly: Evaluation of a pre-pupae meal of the black soldier fly (*Hermetia illucens*) as fish meal substitute – growth performance and chitin degradation in juvenile turbot (*Psetta maxima*). *Aquaculture* 364-365, 345–352. doi: 10.1016/j.aquaculture.2012.08.041

Li, X., Ringø, E., Hoseinifar, S. H., Lauzon, H., Birkbeck, H., and Yang, D. (2019). Adherence and colonisation of microorganisms in the fish gastrointestinal tract. *Rev. Aquacult.* 11, 603–618. doi: 10.1111/raq.12248

Minich, J. J. M., Poore, G. D., Jantawongsri, K., Johnston, C., Bowie, K., Bowman, J., et al. (2020). Microbial ecology of Atlantic salmon (*Salmo salar*) hatcheries: Impacts of the built environment on fish mucosal microbiota. *Appl. Environ. Microbiol.* 86, e00411-20. doi: 10.1128/AEM00411-20

Nadal, A. L., Ikeda-Ohtsubo, W., Sipkema, D., Peggs, D., McGurk, C., Forlenza, M., et al. (2020). Feed, microbiota, and gut immunity: Using the zebrafish model to understand fish health. *Front. Immunol.* 11, 114. doi: 10.3389/fimmu.2020.00114

Nguyen, C. D. H., Amoroso, G., Ventura, T., and Elizur, A. (2020). Assessing the pyloric caeca and distal microbiota correlation with flesh color in Atlantic salmon (*Salmo salar* L 1758). *Microorganisms* 8, 1244. doi: 10.3390/microorganisms8081244

Pan, V.-J., Dahms, H.-U., Hwang, J.-S., and Souissi, S. (2022). Recent trends in live feeds for marine larviculture: A mini review. *Front. Mar. Sci.* 9, 864165. doi: 10.3389/fmars.2022.864165

Rawls, J. F., Mahowald, M. A., Ley, R. E., and Gordon, J. I. (2006). Reciprocal gut microbiota transplants from zebrafish and mice to germ-free recipients reveal host habitat selection. *Cell* 127, 423–433. doi: 10.1016/j.cell.2006.08.043

Rawls, J. F., Samuel, B. S., and Gordon, J. I. (2004). Gnotobiotic zebrafish reveal evolutionarily conserved responses to the gut microbiota. *Proc. Nat. Acad. Sci. United States America* 101, 4596–4601. doi: 10.1073/PNAS.0400706101

Reed, G. B., and Spence, C. M. (1929). The intestinal and slime flora of the haddock: a preliminary report. *Contrib. Can. Biol. Fish.* 4, 257–264. doi: 10.1139/f29-019

Ringø, E., and Birkbeck, T.-H. (1999). Intestinal microflora of fish larvae and fry. *Aquacult. Res.* 30, 73–93. doi: 10.1046/j.1365-2109.1999.00302.x

Ringø, E., Olsen, R. E., Mayhew, T. M., and Myklebust, R. (2003). Electron microscopy of the intestinal microflora of fish. *Aquaculture* 227, 395–415. doi: 10.1016/j.aquaculture.2003.05.001

Ringø, E., Zhou, Z., Gonzalez Vecino, J. L., Wadsworth, S., Romero, J., Krogdahl, Å., et al. (2016). Effects of dietary components on the gut microbiota of aquatic animals: a never-ending story? *Aquacult. Nutr.* 22, 219–282. doi: 10.1111/anu12346

Rowland, I., Gibson, G., Heinken, A., Scott, K., Swann, J., Thiele, I., et al. (2018). Gut microbiota functions: metabolism of nutrient and other food components. *Eur. J. Nutr.* 57, 1–24. doi: 10.1007/s00394-017-1445-8

Stewart, M. M. (1932). The bacterial flora of the slime and intestinal contents of the haddock (*Gadus aeglefinus*). *J. Mar. Biol. Ass. UK* 18, 35–50. doi: 10.1017/S0025315400051286

Vadstein, O., Attramadal, K. J. K., Bakke, I., Forberg, T., Olsen, Y., Verdegem, M., et al. (2018). Managing the microbial community of marine fish larvae: A holistic perspective for larviculture. *Front. Microbiol.* 9, 1820. doi: 10.3389/fmicb.2018.01820

Vadstein, O., Bergh, Ø., Gatesoupe, F.-J., Galindo-Villegas, J., Mulero, V., Picchietti, S., et al. (2013). Microbiology and immunology of fish larvae. *Rev. Aquacult.* 5Suppl 1), S1–S25. doi: 10.1111/j.1753-5131.2012.01082x

Vestrum, R. I., Forberg, T., Luef, B., Bakke, I., Winge, P., and Olsen, Y. (2022). Commensal and opportunistic bacteria present in the microbiota in Atlantic cod (*Gadus morhua*) larvae differentially altered the hosts` innate immune responses. *Microorganisms* 10, 24. doi: 10.3390/microorganisms10010024

Wang, A. R., Ran, C., Ringø, E., and Zhou, Z. G. (2018). Progress in fish gastrointestinal microbiota research. *Rev. Aquacult.* 10 (3), 626–640. doi: 10.1111/raq.12191

Xiao, R., Wei, Y., An, D., Li, D., Ta, X., Wu, Y., et al. (2019). A review on the research status and development trend of equipment in water treatment processes of recirculating aquaculture systems. *Rev. Aquacult.* 11, 863–895. doi: 10.1111/raq.12270

Yang, H.L., Sun, Y.Z., Hu, X., Ye, J.D., Lu, K.L., Hu, L.H., and Zhang, J.J.. (2019). Bacillus pumilus SE5 originated PG and LTA tuned the intestinal TLRs/MyD88 signaling and microbiota in grouper (Epinephelus coioides). *Fish shellfish Immunol.* 88:266-271. doi: 10.1016/j.fsi.2019.03.005

Zhang, Y., and Zhang, H. (2013). The effect of probiotics on lipid metabolism. *INTECH*. 443–460. doi: 10.5772/51938

Zhong, X., Li, J., Lu, F., Zhang, J., and Guo, L. (2022). Application of zebrafish in the study of the gut microbiome. *Anim. Models Exp. Med*. doi: 10.1002/ame2.12227