UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

# DAFTAR PUSTAKA

Abraham, T. J., Mallick, P. K., Adikesavalu, H., & Banerjee, S. (2015). Pathology of *Edwardsiella tarda* infection in African catfish, *Clarias gariepinus* (Burchell 1822), fingerlings. Archives of Polish Fisheries, 23, 141–148.

Abriouel, H., Lerma, L. L., Casado Muñoz, M. C., Montoro, B. P., Kabisch, J., Pichner, R., Cho, G. S., Neve, H., Fusco, V., Franz, C. M. A. P., Gálvez, A., & Benomar, N. (2015). The controversial nature of the Weissella genus: Technological and functional aspects versus whole genome analysis-based pathogenic potential for their application in food and health. Frontiers in Microbiology, 6*,* 1197.

Ahmad, A. A., Zhang, J., Liang, Z., Du, M., Yang, Y., Zheng, J., Yan, P., Long, R., Tong, B., Han, J., & Ding, X. (2022). Age-dependent variations in rumen bacterial community of Mongolian cattle from weaning to adulthood. BMC Microbiology, 22(213), 1–15.

Amann, R. I., Ludwig, W., Schleifer, K. H. (1995). Phylogenetic identification and in situ detection of individual microbial cells without cultivation. Microbiol Rev 59, 143–169.

American Veterinary Medical Association (AVMA) (2020). AVMA Guidelines for the Euthanasia of Animals: 2020 Edition.

Anderson, M. J., Crist, T. O., Chase, J. M., Vellend, M., Inouye, B. D., Freestone, A. L., & Swenson, N. G. (2011). Navigating the multiple meanings of β diversity: a roadmap for the practicing ecologist. Ecology letters, 14(1), 19-28.

Anjaly, M. A., Sarasan, M., Kachiprath, B., Sukumaran, V., Bright Singh, I. S., & Puthumana, J. (2025). Engineering the fish gut microbiome: could it serve as future-proof strategy for sustainable aquaculture? Blue Biotechnology, 2, Article 6.

Ardiansyah & Alkemega (2024). Analysis of Catfish Farming Business Development Strategy in Fish Farm Agribusiness Karang Sari Village South Lampung. International Journal of Accounting, Management, Economics and Social Sciences (IJAMESC) 2, 707–717.

Arpaia, N., Campbell, C., Fan, X., Dikiy, S., Van Der Veeken, J., Deroos, P., Liu, H., Cross, J. R., Pfeffer, K., Coffer, P. J. (2013). Metabolites produced by commensal bacteria promote peripheral regulatory T-cell generation. Nature 504, 451–455.

Atarashi, K., Tanoue, T., Shima, T., Imaoka, A., Kuwahara, T., Momose, Y., Cheng, G., Yamasaki, S., Saito, T., Ohba, Y., Taniguchi, T., Takeda, K., Hori, S., Ivanov, I.I., Umesaki, Y., Itoh, K., Honda, K. (2011). Induction of colonic regulatory T cells by indigenous Clostridium species. Science (1979) 331, 337–341.

Auclert, L. Z., Chhanda, M. S., & Derome, N. (2024). Interwoven processes in fish development: microbial community succession and immune maturation. PeerJ, 12, e17051. https://doi.org/10.7717/peerj.17051

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

Austin, B., & Austin, D. A. (2016). Bacterial fish pathogens: Disease of farmed and wild fish (6th ed.). Springer International Publishing.

Austin, B. (2006). The bacterial microflora of fish, revised. Sci World J 6:931–945

Avershina, E., Lundgård, K., Sekelja, M., Dotterud, C., Storrø, O., Øien, T., Johnsen, R., & Rudi, K. (2021). Successional stages in infant gut microbiota maturation. mBio*,* 12(6), e01857-2.

Bakke, I., Coward, E., Andersen, T., Vadstein, O. (2015). Selection in the host structures the microbiota associated with developing cod larvae (*Gadus morhua*). Environ Microbiol 17:3914–3924

Bashiardes, S., Zilberman-Schapira, G., & Elinav, E. (2016). Use of metatranscriptomics in microbiome research. Bioinformatics and Biology Insights, 10, 19-25.

Bates, J. M., Mittge, E., Kuhlman, J., Baden, K. N., Cheesman, S. E., Guillemin K. (2006). Distinct signals from the microbiota promote different aspects of zebrafish gut differentiation. Dev Biol 297:374–386

Benítez-Páez, A., & Sanz, Y. (2017). Multi-locus and long amplicon sequencing approach to study microbial diversity using the MinION™ nanopore sequencer. *GigaScience,* 6(7), 1–12. https://doi.org/10.1093/gigascience/gix043

Bhat, R. A., Dhillon, O., Hoque, F., & Sundaray, J. K. (2023). Insights on fish gut microbiome: A review. Journal of Aquacultivation, 32, 1–33.

Bledsoe, J. W., Waldbieser, G. C., Swanson, K. S., Peterson, B. C., & Small, B. C. (2018). Comparison of Channel Catfish and Blue Catfish Gut Microbiota Assemblages Shows Minimal Effects of Host Genetics on Microbial Structure and Inferred Function. Frontiers in Microbiology, 9, 1073.

Bledsoe, J. W., Peterson, B. C., Swanson, K. S., Small, B. C. (2016). Ontogenetic characterization of the gutal microbiota of channel catfish through 16S rRNA gene sequencing reveals insights on temporal shifts and the influence of environmental microbes. PLoS One 11.

Borges, I., Nóia, M., Camarinho, R., Rodrigues, A. S., Soares, A. O. (2015). Characterization of the alimentary canal of the aphidophagous ladybird, *Adalia bipunctata* (Coleoptera: Coccinellidae): Anatomical and histological approaches. Entomol Sci 18, 66–73. https://doi.org/10.1111/ens.12096

Bottino, G. F., Bonham, K. S., Patel, F., McCann, S., Zieff, M., Naspolini, N., Ho, D., Portlock, T., Joos, R., Midani, F. S., Schüroff, P., Das, A., Shennon, I., Wilson, B. C., O'Sullivan, J. M., Britton, R. A., Murray, D. M., Kiely, M. E., Taddei, C. R., Beltrão-Braga, P. C. B., Campos, A. C., Polanczyk, G. V., Huttenhower, C., Donald, K. A., & Klepac-Ceraj, V. (2025*).* Early life microbial succession in the gut follows common patterns in humans across the globe. Nature Communications, 16, 660.

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

Boyd, C. E., Tucker, C. S., & Somridhivej, B. (2016). Alkalinity and hardness: Critical but elusive concepts in aquacultivation. Journal of the World Aquacultivation *Society, 47*(1), 6–41. https://doi.org/10.1111/jwas.12241

Boyd, C. E., & Tucker, C. S. (2012). Pond aquacultivation water quality management. Springer Science & Business Media.

Burgos, F. A., Ray, C. L., & Arias, C. R. (2018). Bacterial diversity and community structure of the gutal microbiome of channel catfish (*Ictalurus punctatus*) during ontogenesis. Systematic and Applied Microbiology, 41(5), 494-505.

Butt, R. L., & Volkoff, H. (2019). Gut Microbiota and Energy Homeostasis in Fish. Frontiers in Endocrinology, 10, 9. https://doi.org/10.3389/fendo.2019.00009

Cahyadi, A., Riyanto, I. A., Ramadhan, F., Widyastuti, M., & Fatchurohman, H. (2023). Multitemporal water quality analysis of an epikarst spring for agricultural irrigation in the Gunungsewu Karst Area, Indonesia. E3S Web of Conferences.

Cai, K., Chen, J., Zhang, Z., Ye, Y., Sang, S., Luo, X., Wang, Y., Shan, K., Ou, C., Jia, L., & Wang, J. (2025). Recent progress of *Clostridium butyricum* in fish cultivation: Maintenance of gutal homeostasis, improvement of disease resistance, activation of immune signaling pathways, and positive effects on fish. Aquacultivation, 596, 741723.

Caporaso, J. G., Lauber, C. L., Walters, W. A., Berg-Lyons, D., Lozupone, C. A., Turnbaugh, P. J., Fierer, N., & Knight, R. (2011). Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. Proceedings of the National Academy of Sciences, 108(Suppl. 1), 4516–4522.

Chen, L., Xu, Y., Chen, X., Fang, C., Zhao, L., & Chen, F. (2017). The maturing development of gut microbiota in commercial piglets during the weaning transition. Frontiers in Microbiology, 8, 1688.

Chervochkina, A. S., Aksenov, A. S., & Ilmast, N. V. (2025). Yolk-Sac Stage Bacteriome: Gaps of Knowledge and Demand for Fish Science. Current Microbiology, 83(1), 59.

Coyte, K. Z., Schluter, J., & Foster, K. R. (2015). The ecology of the microbiome: Networks, competition, and stability. Science, 350(6261), 663–666.

De Coster, W., & Rademakers, R. (2023). NanoPack2: population-scale evaluation of long-read sequencing data. Bioinformatics, 39(5), btad311.

de Verdal, H., Komen, H., Quillet, E., Chatain, B., Allal, F., Benzie, J. A. H., & Vandeputte, M. (2018). Improving feed efficiency in fish using selective breeding: A review. Reviews in Aquaculture, 10(4), 833–851.

Dehler, C. E., Secombes, C. J., & Martin, S. A. M. (2017). The gut microbiota of Atlantic salmon (*Salmo salar*) is affected by different dietary protein sources and is distinct from the microbiota of the surrounding water. MicrobiologyOpen, 6(3), e00461. https://doi.org/10.1002/mbo3.461

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

Dill-McFarland, K. A., Breaker, J. D., & Suen, G. (2017). Microbial succession in the gastrointestinal tract of dairy cows from 2 weeks to first lactation. Scientific Reports, 7, 40864.

Dong, Z. X., Chen, Y. F., Li, H. Y., Tang, Q. H., & Guo, J. (2021). The succession of the gut microbiota in insects: A dynamic alteration of the gut microbiota during the whole life cycle of honey bees (*Apis cerana*). Frontiers in Microbiology, 12, 513962.

Feng, L., Xu, Q., Feng, J., Wang, Y., Li, S., Zhang, Q., Zhou, L., Xu, J. (2025). Exploring the potential regulation mechanisms of host-microbiome comprehensive interactions on growth traits in *Cyprinus carpio*. Aquacultivation 605.

Finegold, S. M., Vaisanen, M. L., Molitoris, D. R., Tomzynski, T. J., Song, Y., Liu, C. & Lawson, P. A. (2003). *Cetobacterium somerae* sp. nov. from human feces and emended description of the genus Cetobacterium. Systematic and applied microbiology, 26(2), 177-181.

Fjellheim, A. J, Playfoot KJ, Skjermo J, Vadstein O. (2012). Interindividual variation in the dominant gutal microbiota of reared Atlantic cod (*Gadus morhua* L.) larvae. Aquac Res 43:1499–1508

Food and Agricultivation Organization of the United Nations. (2024). The state of world fisheries and aquacultivation 2024: Blue transformation in action. FAO. https://doi.org/10.4060/ccf961en

Foster, K. R., Schluter, J., Coyte, K. Z., & Rakoff-Nahoum, S. (2017). The evolution of the host microbiome as an ecosystem on a leash. Nature, 548(7665), 43–51. https://doi.org/10.1038/nature23292

Foysal, M.J., Momtaz, F., Kawsar, A.Q.M.R., Rahman, Md.M., Gupta, S.K., Tay, C.Y., (2019). Next-generation Sequencing Reveals Significant Variations in Bacterial Compositions Across the Gastrogutal Tracts of the Indian Major Carps, Rohu (*Labeo rohita*), Catla (Catla Catla) and Mrigal (*Cirrhinus cirrhosis*). Lett Appl Microbiol 70, 173–180.

Frank, J. A., C. I. Reich, S. Sharma, J. S. Weisbaum, B. A. Wilson, & G. J. Olsen. (2008). Critical Evaluation of Two Primers Commonly Used for Amplification of Bacterial 16S rRNA Genes. Applied And Environmental Microbiology, 74(8): 2461-2470.

Fraune S, Bosch T. C. G. (2010). Why bacteria matter in animal development and evolution. BioEssays 32:571–580

Fusco, V., Quero, G. M., Cho, G. S., Macaluso, J., Treven, P., Vancanneyt, M., De Vuyst, L., Holzapfel, W. H., & Franz, C. M. A. P. (2015). The genus Weissella: taxonomy, ecology and biotechnological potential (Genus Weissella: taksonomi, ekologi, dan potensi bioteknologinya). Frontiers in Microbiology, 155(6).

Furusawa, Y., Obata, Y., Fukuda, S., Endo, T.A., Nakato, G., Takahashi, D., Nakanishi, Y., Uetake, C., Kato, K., Kato, T. (2013). Commensal microbe-derived butyrate induces the differentiation of colonic regulatory T cells. Nature 504, 446–450.

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

Gerritsen, J., Hornung, B., Ritari, J., Paulin, L., Rijkers, G. T., Schaap, P. J. & Smidt, H. (2019). A comparative and functional genomics analysis of the genus Romboutsia provides insight into adaptation to a gutal lifestyle. BioRxiv, 845511.

Gerritsen, J., Fuentes, S., Grievink, W., van Niftrik, L., Tindall, B. J., Timmerman, H. M., Rijkers, G. T., & Smidt, H. (2014). Characterization of Romboutsia ilealis gen. nov., sp. nov., isolated from the gastro-gutal tract of a rat, and proposal for the reclassification of five closely related members of the genus Clostridium into the genera Romboutsia gen. nov., Gutibacter gen. nov., Terrisporobacter gen. nov. and Asaccharospora gen. nov. International Journal of Systematic and Evolutionary Microbiology, 64(Pt 5), 1600–1616.

Ghanbari, M., Kneifel, W., Domig, K.J. (2015). A new view of the fish gut microbiome: Advances from next-generation sequencing. Aquacultivation.

Giatsis, C., Sipkema, D., Smidt, H., Heilig, H., Benvenuti, G., Verreth, J., & Verdegem, M. (2015). The impact of rearing environment on the development of gut microbiota in tilapia larvae. Scientific reports, *5*(1), 18206.

Giatsis, C., Sipkema, D., Smidt, H., Verreth, J. A. J., & Verdegem, M. C. J. (2014). The Colonization Dynamics of the Gut Microbiota in Tilapia Larvae. PLoS ONE, *9*(7), e103641. https://doi.org/10.1371/journal.pone.0103641

Givens, C. E., Ransom, B., Bano, N., & Hollibaugh, J. T. (2015). Comparison of the gut microbiomes of 12 bony fish and 3 shark species. Marine Ecology Progress Series, 518, 209-223.

Goodwin, S., McPherson, J. D., & McCombie, W. R. (2016). Coming of age: ten years of next-generation sequencing technologies. Nature Reviews Genetics, 17(6), 333-351.

Guo, J., Xu, Y., Chen, Q., & Zhang, H. (2025). Integrative analysis of transcriptomics and gut microbiome in grass carp under alkalinity stress. Comparative Biochemistry and Physiology-Part D: Genomics and Proteomics.

Hao, Y.T., Wu, S.G., Jakovlić, I., Zou, H., Li, W.X., Wang, G.T. (2017). Impacts of diet on hindgut microbiota and short-chain fatty acids in grass carp (*Ctenopharyngodon idellus*). Aquac Res 48, 5595–5605.

Hasan, I., Rimoldi, S., Saroglia, G., Terova, G. (2023). Sustainable Fish Feeds with Insects and Probiotics Positively Affect Freshwater and Marine Fish Gut Microbiota. Animals. https://doi.org/10.3390/ani13101633

Hatamoto, M., Kaneshige, M., Nakamura, A., & Yamaguchi, T. (2014). *Bacteroides luti* sp. nov., an anaerobic, cellulolytic and xylanolytic bacterium isolated from methanogenic sludge. International Journal of Systematic and Evolutionary Microbiology, 64(5), 1770–1774. https://doi.org/10.1099/ijs.0.056630-0

Hays, K.E., Pfaffinger, J.M., Ryznar, R., (2024). The interplay between gut microbiota, short-chain fatty acids, and implications for host health and disease. Gut Microbes. https://doi.org/10.1080/19490976.2024.2393270

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

He, T, Xiao ZZ, Liu QH, Ma DY, Xu SH, Xiao YS, Li J. (2012). Ontogeny of the digestive tract and enzymes in rock bream *Oplegnathus fasciatus* (Temminck et Schlegel 1844) larvae. Fish Physiol Biochem 38:297–308

Heberle H, Meirelles GV, da Silva FR, Telles GP, Minghim R. (2015). InteractiVenn: a web-based tool for the analysis of sets through Venn diagrams. BMC Bioinformatics, 16:169. https://doi.org/10.1186/s12859-015-0611-3

Hendriana, A. (2012). Pembesaran lele di kolam terpal. PT Niaga Swadaya.

Hugenholtz, P. (2003). Chimeric 16S rDNA sequences of diverse origin are accumulating in the public databases. Int. J. Syst. Evol. Microbiol. 53, 289–293.

Hung, J.-H., & Weng, Z. (2016). Designing Polymerase Chain Reaction Primers Using Primer3Plus. Cold Spring Harbor Protocols, 2016(9), pdb.prot093096.

Hunter, K. C., Lawson, P. A., Dowd, S. E., & McLaughlin, R. W. (2021). *Clostridium chrysemydis* sp. nov., isolated from the faecal material of a painted turtle. International Journal of Systematic and Evolutionary Microbiology, 71, 005023.

Illumina (2021). 16S Metagenomic Sequencing Library Preparation. Illumina Protocol Guide.

Ingerslev, H.C., von Gersdorff Jørgensen, L., Strube, M.L., Larsen, N., Dalsgaard, I., Boye, M., Madsen, L. (2014). The development of the gut microbiota in rainbow trout (*Oncorhynchus mykiss*) is affected by first feeding and diet type. Aquacultivation 424, 24–34.

Jandhyala, S.M., Talukdar, R., Subramanyam, C., Vuyyuru, H., Sasikala, M., Reddy, D.N. (2015). Role of the normal gut microbiota. World J Gastroenterol 21, 8836–8847. https://doi.org/10.3748/wjg.v21.i29.8787

Jin, H., Li, L., Lu, W., Zhang, Z., Xing, Y., & Wu, D. (2024). Identification of the regulatory roles of water qualities on the spatio-temporal dynamics of microbiota communities in the water and fish guts in the Heilongjiang River. Frontiers in Microbiology, 15, 1435360. https://doi.org/10.3389/fmicb.2024.1435360

Johnson, J. S., Spakowicz, D. J., Hong, B. Y., Petersen, L. M., Demkowicz, P., Chen, L., Leopold, S. R., Hanson, B. M., Agresta, H. O., Gerstein, M., Sodergren, E., & Weinstock, G. M. (2019). Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. Nature Communications, 10, 5029.

Kanika, N. H., Liaqat, N., Chen, H., Ke, J., Lu, G., Wang, J., & Wang, C. (2025). Fish gut microbiome and its application in aquacultivation and biological conservation. Frontiers in Microbiology, 15, 1521048.

Kebschull, J. M., & Zador, A. M. (2018). Cellular barcoding: lineage tracing, screening and beyond. Nature Methods, 15(11), 871-879.

Kelly, C., & Salinas, I. (2017). Under pressure: Interactions between commensal microbiota and the teleost immune system. Frontiers in Immunology, 8, 559.

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

Kementerian Kelautan dan Perikanan (2025). Laporan Kinerja Direktorat Jenderal Triwulan I 2025. Jakarta.

Khaw, Y. S., Teng, H. T., & Yusoff, F. M. (2025). Chapter Six – Primers in Microalgae: Design, Applications and Future Directions. In Methods in Microbiology (Vol. 57, pp. 137–175). Elsevier. 10.1016/bs.mim.2024.04.002

Kim, B. R., Shin, J., Guevarra, R., Lee, J. H., Kim, D. W., Seol, K. H., Lee, J. H., Kim, H. B., & Isaacson, R. (2017). Deciphering Diversity Indices for a Better Understanding of Microbial Communities. Journal of Microbiology and Biotechnology, 27(12), 2089–2093. https://doi.org/10.4014/jmb.1709.09027

Kita, A., Miura, T., Okamura, Y., & Aki, T. (2015). *Dysgonomonas alginatilytica* sp. nov., an alginate-degrading bacterium isolated from a microbial consortium. International Journal of Systematic and Evolutionary Microbiology, 65(10), 3570–3575.

Klappenbach, J.A., Saxman, P.R., Cole, J.R., Schmidt, T.M. (2001). rrndb: the ribosomal RNA operon copy number database. Nucleic Acids Res. 29, 181–184

Klindworth, A., Pruesse, E., Schweer, T., Peplies, J., Quast, C., Horn, M., & Glöckner, F. O. (2013). Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. Nucleic Acids Research, 41(1), e1. https://doi.org/10.1093/nar/gks808

Knobloch, S., Skirnisdóttir, S., Dubois, M., Mayolle, L., Kolypczuk, L., Leroi, F., Leeper, A., Passerini, D., & Marteinsson, V. Þ. (2024). The gut microbiome of farmed Arctic char (Salvelinus alpinus) is shaped by feeding stage and nutrient presence. FEMS Microbes, 5, xtae011. https://doi.org/10.1093/femsmc/xtae011

Koenig, J. E., Spor, A., Scalfone, N., Fricker, A. D., Stombaugh, J., Knight, R., Angenent, L. T., & Ley, R. E. (2011). Succession of microbial consortia in the developing infant gut microbiome. Proceedings of the National Academy of Sciences of the United States of America, 108(Supplement_1), 4578–4585.

Kokou, F., Sasson, G., Nitzan, T., Doron-Faigenboim, A., Harpaz, S., Cnaani, A., & Mizrahi, I. (2018). Host genetic selection for cold tolerance shapes microbiome composition and modulates its response to temperature. eLife, 7, e36398.

Koll, R., Hauten, E., Theilen, J., Bang, C., Bouchard, M., Thiel, R., Möllmann, C., Woodhouse, J.N., Fabrizius, A. (2024). Spatio-temporal plasticity of gill microbiota in estuarine fish. Science of the Total Environment 957.

Kong, M., Sun, H., Zhao, G., Chen, Z., Qi, J., Liu, J., Zhang, Q. (2024). Diet overwhelms host growth in governing the ecological succession of gut microbiota in golden pompano (*Trachinotus ovatus*). Aquac Rep 36.

Kong, J., Feng, J., & Sun, L. (2023). Evaluating the Reproducibility of Amplicon Sequencing Data. Microbiology Spectrum, 11(3).

Kwong, W. K., Medina, L. A., Koch, H., Sing, K.-W., Soh, E. J. Y., Ascher, J. S., Jaffé, R., & Moran, N. A. (2017). Dynamic microbiome evolution in social bees. Science Advances, 3(3), e1600513. https://doi.org/10.1126/sciadv.1600513

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

Land, M., Held, B., Gronow, S., Abt, B., Lucas, S., Glavina Del Rio, T., Nolan, M., Tice, H., Cheng, J. F., Pitluck, S., Liolios, K., Pagani, I., Ivanova, N., Mavromatis, K., Mikhailova, N., Pati, A., Tapia, R., Han, C., Goodwin, L., Lapidus, A. (2011). Non-contiguous finished genome sequence of Bacteroides coprosuis type strain (PC139T). Standards in Genomic Sciences, 4(2), 233–243.

Lanh, P. T., Duong, B. T. T., Thu, H. T., Hoa, N. T., Yoo, M. S., Cho, Y. S., & Quyen, D. V. (2022). The gut microbiota at different developmental stages of *Apis cerana* reveals potential probiotic bacteria for improving honeybee health. Microorganisms, 10(10), 1938.

Larsen, A. M., Mohammed, H. H., & Arias, C. R. (2014). Characterization of the gut microbiota of three commercially valuable warmwater fish species. Journal of Applied Microbiology, 116(6), 1396–1404.

Lawson, P.A., Citron, D.M., Tyrrell, K.L., Finegold, S.M. (2016). Reclassification of clostridium difficile as clostridioides difficile (Hall and O'Toole 1935) Prévot 1938. Anaerobe 40, 95–99.

Legrand, T. P. R. A., Wynne, J. W., Weyrich, L. S., & Oxley, A. P. A. (2020). A microbial sea of possibilities: Current knowledge and prospects for an improved understanding of the fish microbiome. Reviews in Aquacultivation, 12(2), 1101–1134.

Lozupone, C. A., & Knight, R. (2008). Species divergence and the measurement of microbial diversity**.** FEMS Microbiology Reviews, 32(4), 557–578.

Li, Z., Lv, J., Chen, J., Sun, F., Sheng, R., Qin, Y., Rao, L., Lu, T., Sun, L. (2025). Comparative study of gut content microbiota in freshwater fish with different feeding habits: A case study of an urban lake. J Fish Biol 106, 823–835.

Li, J.J., Ni, J.J., Wang, C., Yu, Y.H., Zhang, T. L. (2020). Different response patterns of fish foregut and hindgut microbiota to host habitats and genotypes. Appl Ecol Environ Res 18, 7369–7378.

Li, T., Long, M., Li, H., Gatesoupe, F. J., Zhang, X., Zhang, Q., & Li, A. (2017). Multi-omics analysis reveals a correlation between the host phylogeny, gut microbiota and metabolite profiles in cyprinid fishes. Frontiers in Microbiology, *8*, 454.

Li, XM, Yu YH, Feng WS, Yan QY, Gong YC. (2012). Host species as a strong determinant of the gutal microbiota of fish larvae. J Microbiol 50:29–37

Li, K., & Brownley, A. (2010). Primer Design for RT-PCR. In N. King (Ed.), RT-PCR Protocols (Methods in Molecular Biology, Vol. 630, pp. 271–299). Humana Press, Totowa, NJ. https://doi.org/10.1007/978-1-60761-629-0_18

Liu, Y., Lu, M., Xu, W., Wang, Y., Zhang, C., & Zhang, W. (2024). Fish gut microbiome and its application in aquacultivation and biological conservation. Frontiers in Microbiology, 15, 1521048. https://doi.org/10.3389/fmicb.2024.1521048

Liu, A., Lu, X., Ji, Z., Dong, L., Jiang, J., Tian, J., Wen, H., Xu, Z., Xu, G., & Jiang, M. (2023). Preliminary study to assess the impact of dietary rutin on growth,

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

antioxidant capacity, and gutal health of yellow catfish, *Pelteobagrus fulvidraco*. Animals, 13(21). https://doi.org/10.3390/ani13213386

Liu, C., Zhao, L. P., & Shen, Y. Q. (2021). A systematic review of advances in gutal microflora of fish. Fish Physiology and Biochemistry, 47(6), 2041–2053.

Lokesh, J., Kiron, V., Sipkema, D., Fernandes, J.M.O., & Moum, T. (2019). Succession of embryonic and the gutal bacterial communities of Atlantic salmon (*Salmo salar*) reveals stage-specific microbial signatures. MicrobiologyOpen, 8, 1–16.

Lomeu, E.A.C., Valle, A. de A., Azevedo, J. de S. (2024). Fishing Grounds and the Invasive Species Impact: A Case Study in a Coastal Brazilian Watershed. Brazilian Archives of Biology and Technology 67. https://doi.org/10.1590/1678-4324-2024230345

Lorgen-Ritchie, M., Uren Webster, T., McMurtrie, J., Bass, D., Tyler, C. R., Rowley, A., & Martin, S. A. M. (2023). Microbiomes in the context of developing sustainable intensified aquacultivation. Frontiers in Microbiology, 14, 1200997.

Louis, P., & Flint, H. J. (2017). Formation of propionate and butyrate by the human colonic microbiota. Environmental Microbiology, 19(1), 29–41.

Lozupone, C.A., Stombaugh, J.I., Gordon, J.I., Jansson, J.K., Knight, R. (2012). Diversity, stability and resilience of the human gut microbiota. Nature 489, 220–230.

Lu, J., & Salzberg, S. L. (2020). Ultrafast and accurate 16S rRNA microbial community analysis using Kraken 2. *Microbiome, 8*, 124. https://doi.org/10.1186/s40168-020-00900-2

Luan, Y., Li, M., Zhou, W., Yao, Y., Yang, Y., Zhang, Z., Ringø, E., Olsen, R. E., Clarke, J. L., Xie, S., Mai, K., Ran, C., & Zhou, Z. (2023). The fish microbiota: Research progress and potential applications. Engineering, 29, 137–146.

Lynch, M. D. J., & Neufeld, J. D. (2015). Ecology and exploration of the rare biosphere. Nature Reviews Microbiology, 13(4), 217–229.

Margareta, A. (2023). Wawasan Bioinformatika Next Generation Sequencing Dalam Sampel Metagenomik Mikobioma Usus: Review. Jurnal Medical Laboratory 2, 41–57.

Matsuo, Y., Komiya, S., Yasumizu, Y., Yasuoka, Y., Mizushima, K., Takagi, T., Kryukov, K., Fukuda, A., Morimoto, Y., Naito, Y., & Okada-Hatakeyama, M. (2021). Full-length 16S rRNA gene amplicon analysis of human gut microbiota using MinION™ nanopore sequencing confers species-level resolution. BMC Microbiology, 21, 35. https://doi.org/10.1186/s12866-021-02094-5

Merrifield, D.L., & A. Rodiles. (2015). The fish microbiome and its interactions with mucosal tissues. Mucosal Health in Aquacultivation, 273-295.

Miller, R.A., & Harbottle, H. (2018). Antimicrobial Drug Resistance in Fish Pathogens. Microbiology Spectrum, 6(1). DOI: 10.1128/microbiolspec.ARBA-0017-2017

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

Miller, M. L., & Koburger, J. A. (1985). *Plesiomonas shigelloides:* An opportunistic food and waterborne pathogen. Journal of Food Protection, 48(5), 449–457.

Mohammed, H. H., ElBanna, N. I., Erdogan, O., Aarattuthodi, S., Tekedar, H. C., Abdelhamed, H., & Díaz-Delgado, J. (2026). *Plesiomonas shigelloides* as an emerging pathogen in catfish aquacultivation: A case from a South Texas commercial farm. Microorganisms*, 14*(1), 144.

Mohindra, V., Tripathi, R.K., Singh, A., Patangia, R., Singh, R.K., Lal, K.K., Jena, J.K. (2016). Hypoxic stress responsive genes in air breathing catfish, *Clarias magur* (Hamilton 1822) and their possible physiological adaptive function. Fish Shellfish Immunol 59, 46–56.

Moran, N. A. (2015). Genomics of the honey bee microbiome. Current Opinion in Insect Science, 10, 22–28. https://doi.org/10.1016/j.cois.2015.04.003

Mougin, J., & Joyce, A. (2023). Fish disease prevention via microbial dysbiosis-associated biomarkers in aquacultivation. Reviews in Aquacultivation, 15(2), 579–594.

Morris, M.T., Hauton, C., Baylay, A.J., Peruzza, L., Targett, T.E., Ciotti, B.J. (2021). Spatial variation in the gastrogutal microbiome, diet, and nutritional condition of a juvenile flatfish among coastal habitats. Mar Environ Res 170.

Navarrete, P., Espejo, R. T., & Romero, J. (2009). Molecular analysis of microbiota along the digestive tract of juvenile Atlantic salmon (*Salmo salar* L.). Microbial ecology, 57(3), 550-561.

Nayak, S. K. (2010). Probiotics and immunity: A fish perspective. Fish & Shellfish Immunology, 29(1), 2–14. DOI: 10.1016/j.fsi.2010.02.017

Nchanji, G. T., Fossi, B. T., Fru-Cho, J., Shey, R. A., Andoh, A. A., Kemajou Tchamba, A. L., Hasan, N. A., & Wanji, S. (2025). Bacterial Diversity in Aquacultivationd African Catfish and Source Pond Water in Buea, Cameroon. International Journal of Microbiology, 2025, 6132661. https://doi.org/10.1155/ijm/6132661

Neiffer, D. L., & Stamper, M. A. (2009). Fish sedation, anesthesia, analgesia, and euthanasia: Considerations, methods, and types of drugs. ILAR Journal, 50(4), 343–360.

Nemergut, D. R., Schmidt, S. K., Fukami, T., O'Neill, S. P., Bilinski, T. M., Stanish, L. F., Knelman, J. E., Darcy, J. L., Lynch, R. C., Wickey, P., & Ferrenberg, S. (2013). Patterns and processes of microbial community assembly. Microbiology and Molecular Biology Reviews, 77(3), 342–356.

Nguyen, H. N. K., Van, T. T. H., Nguyen, H. T., Smooker, P. M., Shimeta, J., & Coloe, P. J. (2014). Molecular characterization of antibiotic resistance in Pseudomonas and Aeromonas isolates from catfish of the Mekong Delta, Vietnam. Veterinary Microbiology, 171(3–4), 397–405.

Nicholson JK, Holmes E, Kinross J, Burcelin R, Gibson G, Jia W, Pettersson S. (2012). Host-gut microbiota metabolic interactions. Science 336:1262–1267

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

Nogal, A., Valdes, A.M., Menni, C. (2021). The role of short-chain fatty acids in the interplay between gut microbiota and diet in cardio-metabolic health. Gut Microbes. https://doi.org/10.1080/19490976.2021.1897212

Nolasco-Soria, H., Yúfera, M., & Nolasco-Alzaga, H. R. (2025). Fish Digestive Capacity: Definition and Methods. Fishes, 10(11), 546.

Ofek, T., Lalzar, M., Laviad-Shitrit, S., Izhaki, I., Halpern, M. (2021). Comparative Study of Gutal Microbiota Composition of Six Edible Fish Species. Front Microbiol 12. https://doi.org/10.3389/fmicb.2021.760266

Older, C. E., Goodman, P. M., Reifers, J. G., & Yamamoto, F. Y. (2025). Differences in the bacterial communities along the gutal tract of juvenile channel (*Ictalurus punctatus*) and hybrid (I. punctatus× I. furcatus) catfish. Physiological Genomics, 57(5), 299-307.

Olsson, C. (2024). Gut anatomy, in: Encyclopedia of Fish Physiology. pp. 339–347. https://doi.org/10.1016/B978-0-323-90801-6.00106-3

Olsson, C. (2011). GUT ANATOMY AND MORPHOLOGY | Gut Anatomy, in: Encyclopedia of Fish Physiology: From Genome to Environment: Volume 1-3. pp. 1268–1275. https://doi.org/10.1016/B978-0-12-374553-8.00071-X

Pakingking, R., Solis, F. D., Palma, P., & de la Peña, L. D. (2025). Bacterial microbiota of African catfish Clarias gariepinus during the hatchery and nursery phases of cultivation in the Philippines. International Aquatic Research, 17(2), 149–164. https://doi.org/10.22034/iar.2025.2009291.1840

Pan, B., Han, X., Yu, K., Sun, H., Mu, R., Lian, C. A. (2023). Geographical distance, host evolutionary history and diet drive gut microbiome diversity of fish across the Yellow River. Mol Ecol 32, 1183–1196.

Parks, D. H., Tyson, G. W., Hugenholtz, P., & Beiko, R. G. (2016). STAMP: statistical analysis of taxonomic and functional profiles. Bioinformatics, 30(21), 3123-3124.

Pérez-Jiménez, G.M., Alvarez-Villagomez, C.S., MartínezPorchas, M., Garibay-Valdez, E., Sepúlveda-Quiroz, C.A., MéndezMarín, O., Martínez-García, R., Jesús-Contreras, R., Alvarez-González, C.A., De la Rosa-García (2024). The Indigenous Probiotic Lactococcus lactis PH3-05 Enhances the Growth, Digestive Physiology, and Gut Microbiota of the Tropical Gar (*Atractosteus tropicus*) Larvae. Animals, 14, 2663.

Piazzon, M.C., Naya-Català, F., Simó-Mirabet, P., Picard-Sánchez, A., Roig, F.J., Calduch-Giner, J.A., Sitjà-Bobadilla, A., Pérez-Sánchez, J. (2019). Sex, age, and bacteria: How the gutal microbiota is modulated in a protandrous hermaphrodite fish. Front Microbiol 10.

Pielou, E. C. (1966). The measurement of diversity in different types of biological collections. Journal of theoretical biology, *13*, 131-144.

Rai, N., Kachore, A., Julka, J. M., Panigrahi, A., Das, S. P., & Nan, F.H. (2025). Symbiotic strategies: deciphering the role of gut microbiota in the nutrition and

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

metabolism of fish and shellfish. Frontiers in Cellular and Infection Microbiology, 15, 1639426. https://doi.org/10.3389/fcimb.2025.1639426

Rajilić-Stojanović, M., & de Vos, W. M. (2014). The first 1000 cultivationd species of the human gastrogutal microbiota. FEMS Microbiology Reviews, 38(5), 996–1047. https://doi.org/10.1111/1574-6976.12075

Ramette, A. (2007). Multivariate analyses in microbial ecology. FEMS microbiology ecology, 62(2), 142-160.

Ramírez, C., & Romero, J. (2017). Fine flounder (*Paralichthys adspersus*) microbiome showed important differences between wild and reared specimens. Frontiers in Microbiology, 8, 271.

Rawls, JF, Mahowald MA, Ley RE, Gordon JI. (2006). Reciprocal gut microbiota transplants from zebrafish and mice to germ-free recipients reveal host habitat selection. Cell 127:423–433

Ray, A.K., Ghosh, K., & Ringø, E. (2012). Enzyme-producing bacteria isolated from fish gut: a review. Aquacultivation Nutrition, 18(5), 465–492.

Ringø, E., Harikrishnan, R., Soltani, M., & Ghosh, K. (2022). The effect of gut microbiota and probiotics on metabolism in fish and shrimp. Animals, 12(21), 3016. https://doi.org/10.3390/ani12213016

Ringø, E., Van Doan, H., Lee, S. H., Soltani, M., Hoseinifar, S. H., Harikrishnan, R., & Song, S. K. (2020). Probiotics, lactic acid bacteria and bacilli: interesting supplementation for aquacultivation. Journal of Applied Microbiology, 129(1), 116–136. https://doi.org/10.1111/jam.14628

Ringø, E., Hoseinifar, S. H., Ghosh, K., Doan, H. V., Beck, B. R., & Song, S. K. (2018). *Lactic acid* bacteria in finfish—An update. Frontiers in microbiology, 9, 1818.

Ringø, E., Zhou, Z., Vecino, J. L. G., Wadsworth, S., Romero, J., Krogdahl, Å., Olsen, R. E., Dimitroglou, A., Foey, A., Davies, S., Owen, M., Lauzon, H. L., Martinsen, L. L., De Schryver, P., Bossier, P., Sperstad, S., & Merrifield, D. L. (2016). Effect of dietary components on the gut microbiota of aquatic animals. A never-ending story?. Aquacultivation Nutrition, 22(2), 219–282.

Risely, A. (2020). Applying the core microbiome to understand host–microbe systems. Journal of Animal Ecology, 89(7), 1549–1558. https://doi.org/10.1111/1365-2656.13229

Roeselers, G., Mittge E. K., Stephens W. Z., Parichy D. M., Cavanaugh C. M., Guillemin K., Rawls J. F. (2011). Evidence for a core gut microbiota in the zebrafish. ISME J 5:1595–1608

Romero, S. M., Cabrera, E., & Corona, M. (2019). The honey bee gut microbiota: strategies for study and characterization. Insect Molecular Biology, 28(4), 455–472. https://doi.org/10.1111/imb.12567

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

Rosado, D., Pérez-Losada, M., Pereira, A., Severino, R., & Xavier, R. (2021). Effects of aging on the skin and gill microbiota of farmed seabass and seabream. Animal Microbiome, 3, 10.

Rosário, A. E. C. do, Barbanti, A. C. C., Matos, H. C., Maia, C. R. M. da S., Trindade, J. M., Nogueira, L. F. F., Pilarski, F., Gallani, S. U., Leal, C. A. G., Figueiredo, H. C. P., & Tavares, G. C. (2024). Antimicrobial resistance in *Lactococcus* spp. isolated from native Brazilian fish species: A growing challenge for aquacultivation. Microorganisms, 12(11), 2327.

Rosenau, S., Oertel, E., Mott, A. C., & Tetens, J. (2021). The Effect of a Total Fishmeal Replacement by *Arthrospira platensis* on the Microbiome of African Catfish *(Clarias gariepinus)*. Life, 11(6), 558. DOI: 10.3390/life11060558

Sarika, A. R., Aishwarya, M. S., Rachanamol, R. S., Lipton, A. P. & Abhirami, C. R. (2023). Isolation and identification of fish gut microbiome, in Diwan, A., Harke, S. N., and Panche, A. (eds.) Microbiome of finfish and shellfish. Singapore: Springer Nature Singapore: 35–46. doi: 10.1007/978-981-99- 0852-3_2

Savard, P., Fernandes, T., Dao, A., McMeans, B., Lazar, C.S. (2023). Seasons Influence the Native Gut Microbiome of Lake Trout Salvelinus namaycush. Appl Microbiol 3, 276–287. https://doi.org/10.3390/applmicrobiol3010019

Segata, N., Izard, J., Waldron, L., Gevers, D., Miropolsky, L., Garrett, W. S., & Huttenhower, C. (2011). Metagenomic biomarker discovery and explanation. Genome Biology*, 12*(6), R60. https://doi.org/10.1186/gb-2011-12-6-r60

Senarat, S., Kettratad, J., Poolprasert, P., Mongkolchaichana, E., Yenchum, W., Angsirijinda, W. (2014). Histological and histochemical Description of Mesentero-Proctodeal regions in the striped blister beetle, *Epicauta waterhousei* (Haag-Rutenberg, 1880) (Coleoptera: Meloidae). Walailak J Sci Technol 11, 851–856.

Shade, A., & Handelsman, J. (2012). Beyond the Venn diagram: the hunt for a core microbiome. Environmental Microbiology, 14(1), 4–12.

Shannon, C. E. (1948). A mathematical theory of communication. The Bell system technical journal, 27(3), 379-423.

Shendure, J., & Ji, H. (2008). Next-generation DNA sequencing. Nature Biotechnology, 26(10), 1135–1145. https://doi.org/10.1038/nbt1486

Shi, Q., Li, Y., Deng, S., Zhang, H., Jiang, H., Shen, L., Pan, T., Hong, P., Wu, H., & Shu, Y. (2023). The succession of gut microbiota in the concave-eared torrent frog (*Odorrana tormota*) throughout developmental history. Ecology and Evolution, 13(5), e10094. https://doi.org/10.1002/ece3.10094

Singh, B., Thakur, K., Kumari, H., Mahajan, D., Sharma, D., Sharma, A. K., Kumar, S., Singh, B., Pankaj, P. P., & Kumar, R. (2025). A review on comparative analysis of marine and freshwater fish gut microbiomes: Insights into environmental impact on gut microbiota. FEMS Microbiology Ecology, 101, fiae169.

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

Simpson, E. H. (1949). Measurement of diversity. Nature, 163(4148), 688-688.

Sivan A, Corrales L, Hubert N, Williams JB, Aquino-Michaels K, Earley ZM, Benyamin FW, Lei YM, Jabri B, Alegre ML, Chang EB, Gajewski T. F. (2015). Commensal Bifidobacterium promotes antitumor immunity and facilitates anti-PD-L1 efficacy. Science 350:1084–1089

Skvortsova, E. G., Filinskaya, O. V., Postrash, I. Y., Bushkareva, A. S., & Mostofina, A. V. (2023). Biodiversity of Gut Microorganisms in Aquacultivationd African Catfish. E3S Web of Conferences, 463, 01039.

Smith, P., Willemsen, D., Popkes, M., Metge, F., Gandiwa, E., Reichard, M., & Valenzano, D. R. (2017). Regulation of life span by the gut microbiota in the short-lived African turquoise killifish. eLife, 6, e27014. https://doi.org/10.7554/eLife.27014

Smith, D. G. E., & Lawson, G. H. K. (2001). *Lawsonia intracellularis:* Getting inside the pathogenesis of proliferative enteropathy. Veterinary Microbiology, 82(4), 331–345. https://doi.org/10.1016/S0378-1135(01)00397-2

Smith, L.S. (1980). Digestion in teleost fishes. Fish feeds technology AO/UNDP Aquacultivation Development and Coordination Programme. Rome 3–18.

Starr, K., Montesanto, F., Perisho, E., Aluthge, N., Pegg, M., & Fernando, S. C. (2024). Gut Microbial Composition of *Cyprinella lutrensis* (Red Shiner) and *Notropis stramineus* (Sand Shiner): Insights from Wild Fish Populations. Microbial Ecology, 87, Article 75. https://doi.org/10.1007/s00248-024-02386-z

Stephens, W.Z., Burns, A.R., Stagaman, K., Wong, S., Rawls, J. F., Guillemin, K., Bohannan, B. J. M. (2016). The composition of the zebrafish gutal microbial community varies across development. ISME J 10, 644–654.

Subramanian, S., Huq, S., Yatsunenko, T., Haque, R., Mahfuz, M., Alam, M. A., & Gordon, J. I. (2014). Persistent gut microbiota immaturity in malnourished Bangladeshi children. Nature, 510(7505), 417–421.

Sullam, K. E., Essinger, S. D., Lozupone, C. A., O'connor, M. P., Rosen, G. L., Knight, R., Kilham, S. S., & Russell, J. A. (2012). Environmental and ecological factors that shape the gut bacterial communities of fish: a meta-analysis. Molecular Ecology, 21(13), 3363-3378.

Sun, H., Chen, F., Hao, H., Wang, K. J. (2022). Multi-dimensional investigation and distribution characteristics analysis of gut microbiota of different marine fish in Fujian Province of China. Front Microbiol 13.

Sun, P., Zhang, H., Jiang, Y., Gao, Q., Tang, B., Ling, J., Yuan, X. (2021). Relationships between the gut microbiota of juvenile black sea bream (*Acanthopagrus schlegelii*) and associated environment compartments in different habitats. Microorganisms 9.

Sun, F., Wang, C., & Yang, H. (2021). Physicochemical factors drive bacterial communities in an aquacultivation environment. Frontiers in Environmental Science, 9*, 709541.* https://doi.org/10.3389/fenvs.2021.709541

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

Sun, Y., O'Riordan, M. X. D. (2013). Regulation of bacterial pathogenesis by gutal short-chain fatty acids, in: Advances in Applied Microbiology. Academic Press Inc., pp. 93–118. https://doi.org/10.1016/B978-0-12-407672-3.00003-4

Susilawati, E., Mulyati, I., Mulyani, Y., Lolan, Y. P., Widyawati, W., Sani, D. N. (2022). Budi daya Ikan Lele untuk Peningkatan Kesehatan Mayarakat di Cibiru Asri 1 Desa Cibiru Wetan, Bandung. Jurnal Abdi Masyarakat Indonesia 2, 857–862.

Talwar, C., Nagar, S., Lal, R., & Negi, R. K. (2018). Fish gut microbiome: current approaches and future perspectives. Indian journal of microbiology, 58(4), 397-414.

Tao, L., Chai, J., Liu, H., Huang, W., Zou, Y., Wu, M., Peng, B., Wang, Q., & Tang, K. (2022). Characterization and Dynamics of the Gut Microbiota in Rice Fishes at Different Developmental Stages in Rice-Fish Cocultivation Systems. Microorganisms, 10(12), 2373.

Tesfahun, A. & Alebachew, S. (2024). Diet composition and feeding habits of the African sharptooth catfish Clarias gariepinus from Ribb Reservoir, South Gondar, Ethiopia. Cogent Food & Agricultivation.

Thomas, F., Hehemann, J. H., Rebuffet, E., Czjzek, M., & Michel, G. (2011). Environmental and gut bacteroidetes: the food connection. Frontiers in microbiology, 2, 93.

Tremblay, J., Singh, K., Fern, A., Kirton, E. S., He, S., Woyke, T., Lee, J., Chen, F., Dangl, J. L., & Tringe, S. G. (2015). Primer and platform effects on 16S rRNA tag sequencing. Frontiers in Microbiology, 6, 771.

Tran, H. Q., Dvořáková Prokešová, M., Fanizza, C., Brambilla, F., Ferrocino, I., Kokou, F., & Stejskal, V. (2025). Feed and gut microbiota of African catfish (*Clarias gariepinus*) fed complementarity of fish and poultry-derived protein meals. Italian Journal of Animal Science, 24(1), 2346–2358.

Tripathi, R.K., Mohindra, V., Singh, A., Kumar, R., Mishra, R.M., Jena, J.K. (2013). Physiological responses to acute experimental hypoxia in the air-breathing Indian catfish, *Clarias batrachus* (Linnaeus, 1758). J Biosci 38, 373–383.

Tsuchiya, C., Sakata, T., & Sugita, H. (2008). Novel ecological niche of *Cetobacterium somerae,* an anaerobic bacterium in the gutal tracts of freshwater fish. Letters in Applied Microbiology, 46(1), 43–48.

Uddin, N., & Al-Harbi, A. H. (2012). Bacterial flora of polycultivationd common carp (*Cyprinus carpio*) and African catfish (*Clarias gariepinus*). International Aquatic Research, 4(1), 10.

Uniacke-Lowe, S., Stanton, C., Hill, C., & Ross, R. P. (2024). The marine fish gut microbiome as a source of novel bacteriocins. Microorganisms, 12*(7),* 1346. https://doi.org/10.3390/microorganisms12071346

Usende, I. L. (2020). Investigation of Some Aspects of the Neuro-Morphometry of the African Catfish (*Clarias gariepinus*). Journal of Veterinary and Biomedical Sciences 2, 19–29.

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

Vagnon, C., Bazin, S., Cattanéo, F., Goulon, C., Guillard, J., & Frossard, V. (2022). The opportunistic trophic behaviour of the European catfish (Silurus glanis) in a recently colonised large peri-alpine lake. Ecology of Freshwater Fish, 31, 650–661. https://doi.org/10.1111/eff.12659

van Dijk, E. L., Auger, H., Jaszczyszyn, Y., & Thermes, C. (2014). Ten years of next-generation sequencing technology. Trends in Genetics, 30(9), 418–426.

Vannucci, F. A. & Gebhart, C. J. (2014). Recent advances in understanding the pathogenesis of *Lawsonia intracellularis* infections. Veterinary Pathology, 51(2), 465–477. https://doi.org/10.1177/0300985813520249

Vetrovsky, T., Baldrian, P. (2013). The variability of the 16S rRNA gene in bacterial genomes and its consequences for bacterial community analyses. PLoS One 8, e57923.

Vetizou M, Pitt JM, Daillere R, Lepage P, Waldschmitt N, Flament C, Rusakiewicz S, Routy B, Roberti MP, Duong CPM, PoirierColame V, Roux A, Becharef S, Formenti S, Golden E, Cording S, Eberl G, Schlitzer A, Ginhoux F, Mani S, Yamazaki T, Jacquelot N, Enot DP, Berard M, Nigou J, Opolon P, Eggermont A, Woerther PL, Chachaty E, Chaput N, Robert C, Mateus C, Kroemer G, Raoult D, Boneca IG, Carbonnel F, Chamaillard M, Zitvogel L. (2015). Anticancer immunotherapy by CTLA-4 blockade relies on the gut microbiota. Science 350:1079–1084

Videnska, P., Sedlar, K., Lukac, M., Faldynova, M., Gerzova, L., Cejkova, D., Sisak, F., & Rychlik, I. (2014). Succession and replacement of bacterial populations in the caecum of egg laying hens over their whole life. *PLOS ONE*, 9(12), e115142.

Videvall, E., Song, S.J., Bensch, H.M., Strandh, M., Engelbrecht, A., Serfontein, N., Hellgren, O., Olivier, A., Cloete, S., Knight, R. (2019). Major shifts in gut microbiota during development and its relationship to growth in ostriches. Mol Ecol 28, 2653–2667.

Wang, B., Cao, X., Ren, W., Zhao, C., Li, Q., Fan, R., Men, X., Zhou, Y., Ren, Y. (2025). A Comparative Study on Gut Microbiota and Metabolomics in Atlantic Salmon Salmo salar at Different Growth Stages. Journal of Ocean University of China 24, 404–416.

Wang, J., Hao, Y., Zhang, L., Gao, X., Xu, Y., Wang, J., Hanafiah, F., Khor, W., Sun, Y., & Wu, C. (2024). Profiling the gut structure and microbiota, and identifying two dominant bacteria belonging to the Weissella genus in mandarin fish *(Siniperca chuatsi)* fed an artificial diet. Frontiers in Microbiology, 15, 1486501.

Wang, M., Z. Fan, Z. Zhang, M. Yi, Z. Liu, X. Ke, F. Gao, J. Cao, & M. Lu. (2022). Effects of diet on the gut microbial communities of nila tilapia (*Oreochromis niloticus*) across their different life stages. Frontiers in Marine Science. 9: 1-11.

Wang, A. R., Ran, C., Ringø, E., & Zhou, Z. G. (2018). Progress in fish gastrogutal microbiota research. Reviews in Aquacultivation, *10*(3), 626-640.

Wang, Y., Song, J., Zhai, Y., Zhang, C., Gerritsen, J., Wang, H., Chen, X., Li, Y., Zhao, B., Zhao, B., & Ruan, Z. (2015). *Romboutsia sedimentorum* sp. nov., isolated

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

from an alkaline-saline lake sediment and emended description of the genus *Romboutsia*. International Journal of Systematic and Evolutionary Microbiology, 65(Pt 4), 1193–1198. https://doi.org/10.1099/ijs.0.000079

Wexler, A. G. & Goodman, A. L. (2017). An insider's perspective: Bacteroides as a window into the microbiome. Nature Microbiology, 2, 17026.

Whitehead, T. R., Cotta, M. A., Collins, M. D., Falsen, E., & Lawson, P. A. (2005). *Bacteroides coprosuis* sp. nov., isolated from swine-manure storage pits. International Journal of Systematic and Evolutionary Microbiology, 55(Pt 6), 2515–2518. https://doi.org/10.1099/ijs.0.63869-0

Wilkinson, L. & Friendly, M. (2009). The history of the cluster heat map. The American Statistician, 63(2), 179–184. https://doi.org/10.1198/tas.2009.0033

Willis, A. (2019). Rarefaction, alpha diversity, and statistics. Frontiers in Microbiology, 10, 2407. https://doi.org/10.3389/fmicb.2019.02407

Whittaker, R. H. (1972). Evolution and measurement of species diversity. Taxon, 21(2–3), 213–251. https://doi.org/10.2307/1218190

Wong, S. & Rawls, J. F. (2012). Gutal microbiota composition in fishes is influenced by host ecology and phylogeny. Immunity, 37(2), 257-267.

Wood, D. E., Lu, J. & Langmead, B. (2019). Improved metagenomic analysis with Kraken 2. Genome Biology, 20, 257. https://doi.org/10.1186/s13059-019-1891-0

Wu, Y., Xu, H., Tu, X., Gao, Z. (2021). The Role of Short-Chain Fatty Acids of Gut Microbiota Origin in Hypertension. Front Microbiol.

Wu, S., Wang, G., Angert, E. R., Wang, W., Li, W., & Zou, H. (2012). Composition, diversity, and origin of the bacterial community in grass carp gute. PloS one, 7(2), e30440.

Wurts, W. A. (2002). Alkalinity and hardness in production ponds. World Aquacultivation, 33(1), 16–17.

Xiao, F., Zhu, W., Yu, Y., Huang, J., Li, J., He, Z., Wang, J., Yin, H., Yu, H., Liu, S., Chen, P., Huang, Z., He, J., Wang, C., Shu, L., & Yan, Q. (2022). Interactions and stability of gut microbiota in zebrafish increase with host development. Microbiology Spectrum, 10(2), e01696-21.

Xiao, F., Zhu, W., Yu, Y., He, Z., Wu, B., Wang, C., Shu, L., Li, X., Yin, H., Wang, J., Juneau, P., Zheng, X., Wu, Y., Li, J., Chen, X., Hou, D., Huang, Z., He, J., Xu, G., Xie, L., Huang, J., Yan, Q. (2021). Host Development Overwhelms Environmental Dispersal in Governing the Ecological Succession of Zebrafish Gut Microbiota. NPJ Biofilms Microbiomes 7. https://doi.org/10.1038/s41522-020-00176-2

Yamada, T. & Sekiguchi, Y. (2009). Cultivation of uncultivationd chloroflexi subphyla: significance and ecophysiology of formerly uncultivationd chloroflexi subphylum

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

with natural and biotechnological relevance. Microbes and Environments, 24(3), 205-216.

Yan, Q., Li, J., Yu, Y., Wang, J., He, Z., Van Nostrand, J. D., Kempher, M. L., Wu, L., Wang, Y., Liao, L., Zhou, J., & Ning, D. (2016). Environmental filtering decreases with fish development for the assembly of gut microbiota. Environmental Microbiology, 18(12), 4739–4754. https://doi.org/10.1111/1462-2920.13365

Yang, R. B, Xie C. X., Fan Q. X., Gao C., Fang L. B. (2010). Ontogeny of the digestive tract in yellow catfish *Pelteobagrus fulvidraco* larvae. Aquacultivation 302:112–123

Zhang, S., Liu, S., Liu, H., Li, H., Luo, J., Zhang, A., Ding, Y., Ren, T., Chen, W. (2024). Stochastic assembly increases the complexity and stability of shrimp gut microbiota during aquacultivation progression. Marine Biotechnology 26, 92–102.

Zhang, Y., Qi, X., Zhang, Z., Jin, Z., Wang, G., & Ling, F. (2023). Effects of dietary *Cetobacterium somerae* on the gutal health, immune parameters and resistance against *Nocardia seriolae* of largemouth bass, *Micropterus salmoides*. Fish & Shellfish Immunology, 135, 108693. https://doi.org/10.1016/j.fsi.2023.108693

Zhang, Z., Fan, Z., Yi, M., Liu, Z., Ke, X., Gao, F., Cao, J., Wang, M., Chen, G., & Lu, M. (2022). Characterization of the core gut microbiota of Nile tilapia (*Oreochromis niloticus*): indication of a putative novel *Cetobacterium* species and analysis of its potential function on nutrition. Archives of Microbiology, 204(12), 690.

Zhang, Z., Li, D., Refaey, M. M., Xu, W., Tang, R., & Li, L. (2018). Host Age Affects the Development of Southern Catfish Gut Bacterial Community Divergent From That in the Food and Rearing Water. Frontiers in Microbiology, 9, 495.

Zhang, Z., Li, D., Refaey, M. M., & Xu, W. (2017). High spatial and temporal variations of microbial community along the southern catfish gastrointestinal tract: Insights into dynamic food digestion. Frontiers in Microbiology, 8, 1531.

Zhao, R., Symonds, J. E., Walker, S. P., Steiner, K., Carter, C. G., Bowman, J. P., & Nowak, B. F. (2023). Relationship between gut microbiota and Chinook salmon (*Oncorhynchus tshawytscha*) health and growth performance in freshwater recirculating aquacultivation systems. Frontiers in Microbiology, 14, 1065823.

Zhou, J. & Ning, D. (2017). Stochastic community assembly: Does it matter in microbial ecology? Microbiology and Molecular Biology Reviews, 81(4), e00002-17. https://doi.org/10.1128/MMBR.00002-17

Zhu, Z., Xu, Y. M., Liang, J. H., Huang, W., Chen, J. D., Wu, S. T., Huang, X. H., Huang, Y. H., Zhang, X. Y., Sun, H. Y., & Qin, Q. W. (2023). Relationship of environmental factors in pond water and dynamic changes of gut microbes of sea bass *Lateolabrax japonicus*. Frontiers in Microbiology, 14, 1086471

Zhu, C. Z., Li, D., Chen, W. J., & Ban, S. N. (2021). Effects of dietary host-associated *Lactococcus lactis* on growth performance, disease resistance, gutal

UNIVERSITAS
GADJAH MADA
**Dinamika Komposisi dan Diversitas Bakteri di Usus Ikan Lele (Clarias sp.) pada Berbagai Tahapan Budidaya**
Samsuri Djamal, Prof. Dr. Ir. Murwantoko, M.Si.; Dr. Ir. Triyanto, M.Si.
**Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/**

morphology and gutal microbiota of mandarin fish *(Siniperca chuatsi)*. Aquacultivation, 540, 736702.

Ziab, M., Chaganti, S. R., Heath, D. D. (2023). The effects of host quantitative genetic architecture on the gut microbiota composition of Chinook salmon (*Oncorhynchus tshawytscha*). Heredity (Edinb) 131, 43–55. https://doi.org/10.1038/s41437-023-00620-x