frontiers in MICROBIOLOGY

REVIEW ARTICLE
published: 02 June 2014
doi: 10.3389/fmicb.2014.00207

# Teleost microbiomes: the state of the art in their characterization, manipulation and importance in aquaculture and fisheries

**Martin S. Llewellyn[1,2†], Sébastien Boutin[1†], Seyed Hossein Hoseinifar[3†] and Nicolas Derome[1*†]**

[1] *Département de Biologie, Institut de Biologie Intégrative et des Systèmes, Université Laval, Québec, QC, Canada*
[2] *Molecular Ecology and Fisheries Genetics Laboratory, School of Biological Sciences, University of Wales, Bangor, UK*
[3] *Department of Fisheries, Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran*

***Edited by:***
*David Georges Biron, Centre National de la Recherche Scientifique, France*

***Reviewed by:***
*Ryan J. Newton, University of Wisconsin-Milwaukee, USA*
*Jaime Romero, Universidad de Chile, Chile*

***Correspondence:**
*Nicolas Derome, Département de Biologie, Institut de Biologie Intégrative et des Systèmes, Université Laval, Pavillon Alexandre-Vachon, 1045, av. de la Medecine, Local 3058, Québec, QC G1V 0A6, Canada*
*e-mail: nicolas.derome@bio.ulaval.ca*

*† These authors have contributed equally to this work.*

Indigenous microbiota play a critical role in the lives of their vertebrate hosts. In human and mouse models it is increasingly clear that innate and adaptive immunity develop in close concert with the commensal microbiome. Furthermore, several aspects of digestion and nutrient metabolism are governed by intestinal microbiota. Research on teleosts has responded relatively slowly to the introduction of massively parallel sequencing procedures in microbiomics. Nonetheless, progress has been made in biotic and gnotobiotic zebrafish models, defining a core microbiome and describing its role in development. However, microbiome research in other teleost species, especially those important from an aquaculture perspective, has been relatively slow. In this review, we examine progress in teleost microbiome research to date. We discuss teleost microbiomes in health and disease, microbiome ontogeny, prospects for successful microbiome manipulation (especially in an aquaculture setting) and attempt to identify important future research themes. We predict an explosion in research in this sector in line with the increasing global demand for fish protein, and the need to find sustainable approaches to improve aquaculture yield. The reduced cost and increasing ease of next generation sequencing technologies provides the technological backing, and the next 10 years will be an exciting time for teleost microbiome research.

**Keywords: fish, microbiota, probiotics, aquaculture, fisheries**

## INTRODUCTION

The bacteria that colonize the internal and external epidermal surfaces of metazoans are thought to outnumber their host cells by at least 10 to 1 (Human Microbiome Project, 2012). Adult humans contain over a kilogram of such organisms (Ley et al., 2008; Human Microbiome Project, 2012; Karlsson et al., 2013). The emergence and evolution of metazoan organisms has undoubtedly involved close partnership with bacterial life. As such, the relationship that exists between vertebrates and their bacterial colonists dates back hundreds of millions of years (Ley et al., 2008). The microbial metagenome dwarfs that of their hosts (Qin et al., 2010). Numerous metabolic processes vital for host fitness and survival may be assigned to, or facilitated by, their microbial community.

Definition of the services provided by a host microbiome depends on our ability to establish its composition and functional capacity. Furthermore, functional stability in space and time may provide clues to recruitment and host fitness constraints on community structure (Costello et al., 2009; Turnbaugh et al., 2009a). Next-generation sequencing techniques, including amplicon and shot-gun approaches, and associated bioinformatic tools have revolutionized our ability to count and classify commensal bacteria. Concurrently, DNA database development for reliable classification of taxonomy (e.g., GreenGenes, Silva), and functionality (e.g., UniProt, Swiss-prot) has facilitated data interpretation. Large-scale multi-partner projects, particularly the Human Microbiome Project (2012), have driven much of the tool development in this area and are also responsible for the instigation of standard operating procedures to facilitate comparisons between samples, centers, and studies. As such, sophisticated hypotheses across large and dispersed cohorts of individuals can be addressed including the impacts of lifestyle, (e.g., Turnbaugh et al., 2006), disease (Morgan et al., 2012), and antibiotic treatment (Perez-Cobas et al., 2013). Studies frequently document perturbations in meta-community structure that accompany these phenomena as well as perturbations that may have a predictive value for certain metabolic diseases (collectively called dysbiosis) (Karlsson et al., 2013). More important still is to establish a causal link between dysbiosis (imbalance in the microbiome) and pathology. In proving causality, "forward microbiomics" are highly attractive (introducing artificial or transplanting microbiomes into naïve hosts). Humanized germ free (gnotobiotic) mouse models, transplanted with human fecal microbiomes, have corroborated dietary microbiome shifts observed in the clinic (Turnbaugh et al., 2009b). Furthermore, transplantation of "obese" human microbiomes into germ-free animals can modulate mouse metabolism toward adiposity and increased body mass (Ridaura et al., 2013).