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# Influence of Gut Microbiota on Growth and Development of Fishes

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**Abstract:** *Fishes are the main component of aquaculture market belongs to diverse community of vertebrates. Microbes colonize inside the gut of the animals including fishes. Micro-flora or microbiota harbours inside the fishes have direct effect on fish health by stimulating immune system, aids in the nutrient acquisition and compete with the pathogenic microbes. The gut microflora also involved in development of gastro-intestine, production and provision of vitamins, enhancement nutrient uptake with the help of enzymatic activity. Along with the availability of nutrients, gut flora also helps in the maintenance of mucosal tolerance, disease resistance, and secretion of therapeutic compounds such as anti-cancerous and anti-inflammatory agents. These microbes inside the animals controls diverse metabolic functions such as physiology to immunological processes. The group of microbes involved in the gut flora are Firmicutes, Bacteroidetes, and Actinobacteria and these plays diverse role in health of fishes.*

*This investigation aims at role of gut microflora on the health of fishes. The interactions of gut microbes with the physiology and metabolism. The major effect brought by the microbes on growth and development of fishes are also investigated in this article.*

**Keywords:** Gut flora, Fish Biology, microbial interactions, Fish health

## I. INTRODUCTION

Fishes are the diverse group of animals, which includes poikilothermic aquatic animals, belongs to vertebrates and invertebrates. Fish have special place as the dietary component as it contents several necessary elements such as I, Mg, Zn, K, Ca, P, omega-3 fatty acids, vitamins $B_2$, vitamins D, essential minerals, etc. Since 19th century demand of fish as dietary components tremendously increased. Among all, the Teleost is having special place in aquaculture industry.

Fishes exposed to microbes through surrounding water and soil and these microbes get colonize on external surface and in internal organs. Diverse group of microbes and symbionts harbours inside the fish having favourable ecological niche and regulates nutrition, environment and age of fishes (Syvokienė et al., 2011). These microbes produces bioactive agents inside the fishes like tetrodotoxin, eicosapentaenoic acid, biotin, vitamin B12 and antimicrobial compounds which helps in benefits of fishes such as pool of enzymes for enhanced digestions (Bairagi et al., 2004). Microbes inside the gastrointestinal region colonize, survive and multiply in this region. These gut flora helps to prevent colonization of pathogens inside the gut (Gomez-Gil et al., 2000; Ringø et al., 2005), improved digestion with the release of diverse enzymes (Ringo and Birkbeck, 1999); increased uptake of nutrient and organic material (Moriarty, 1996) and immune-stimulations (Rengpipat et al.,2000; Bhat et.al. 2024).

Fishes are important dietary element of human food as it provides micro and macronutrients necessary for the growth and development of human beings (Mishra 2020a). The catfishes are having demand fish market because of high medicinal value and they are highly nutritious (Mishra, 2020b). The diet and food habits are the important parameters towards availability of natural resources (Kido, 1996). The biochemical estimations of gut content helps in tracking food and feeding habits of fish's results in good management practice of fisheries (Agbabiaka, 2012; Mishra, 2020c). The analysis of food habit reveals type of prey frequently consumed, quantify rate of ingestion and type of individual food

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types to get the better idea of fish nutrition (Kariman et al., 2009). The diet of fishes helps to find their position in the food web of ecosystem (Padmakumar et al., 2009), prey-predator size relationship, habitat selection and diet shift during ontogeny (Chipps and Garvey, 2007; Mishra, 2020d).

Fishes often exposed to microbes through water and in sediments. These microbes influence the colonization on external surfaces along with gills. The water and food also taken up by the digestive tract, full of microbes. Microbial colonization commenced at the egg or larval stage until the complete maturity of the fish (Olafsen, 2001). The flora inside the developing fishes depends on the microbial density in the eggs, larvae, food and water. This flora manipulated by addition of probiotic, which can colonize the fishes for shorter or longer period as per the need (Austin, 2002; Robertson et.al. 2000).

Till date there were three chances of microbial exposure to fishes recorded; a) Organisms around the fishes came in close contact with microbes or growth of microbes at wound sites; b) Microbes went inside of fishes with water or food and colonize alimentary canal; and c) microbes present fish's surfaces interfered by antibiotics or natural inhibitory compounds or resident microflora (Austin and Austin, 1987).

## II. AUTOCHTHONOUS AND ALLCHTONOUS MICROBIOTA

The microbial colonization or microbiota inside the fish's gut categorize into Autochthonous and Allchtonous Microbiota. The microflora can be termed as autochthonous when microbes adheres to epithelia of fish's gut while allchtonous are unable to colonize on GI tract. Allchtonous these groups of microbes enter inside the gut for some time but rejected for their colonization inside the gut (Ringø & Birkbeck 1999; Ringø et al. 2003; Kim et al. 2007; Merrifield et al. 2011). In some reports, it recorded that these microbes can colonize in between the microvilli under stress or same sort of special conditions (Olsen et.al. 2005). Autochthony microflora can be identified with particular criteria such as a) colonize in healthy fishes, b) colonize during early stages of host and persist for long time, c) can be cultured in free-living and hatchery-culture, d) can survive in anaerobic conditions, and e) colonization can be observed near stomach, proximal or distal intestine on their epithelial mucosa. The microbial colonization inside the fish gut depends on gastric acidity, digestive enzymes, bile salts, peristalsis, immune response and natural inhibitory compounds present near the fishes (Ringø et al. 2003; Ray et.al. 2012).

## III. COMPOSITION AND DIVERSITY OF THE GUT MICROBIOME

Diverse group of microbes survive inside the fish's gut in symbiotic fashion. These microbes belong to four major phyla such as Firmicutes, Bacteroidetes, Actinobacteria and Proteobacteria. The first group of microbes are Firmicutes (e.g. Clostridium, Lactobacillus, Faecalibacterium, etc.) involved in degradation of dietary fibers, produces short-chain fatty acids (SCFAs) and promotes gut health of fish (Jandhyala, 2015). The groups helps in maintenance of intestinal barrier and immune-modulations. The second group of microbes are Bacteroidetes, plays important role energy release by the breakdown of complex carbohydrates (Talapko et.al., 2022). Altogether in balanced ratio these two phyla Bacteroidetes and Firmicutes maintained healthy gut while in absence it will cause obesity or inflammatory bowel disease (Vishwakarma,et.al. 2025).

Because of the different environmental conditions, composition gut microbiota is different in Marine and freshwater fishes (Li et al. 2017). Major phyla observed in both habitat are Fusobacteria and Proteobacteria (Givens et al. 2015, Li et al. 2017, Deb et al. 2020). The most common Proteobacteria observed in freshwater fishes are Aeromonas, Pseudomonas, and Enterobacter. In case of marine fishes, common gut flora includes Vibrio, Photobacterium, and Shewanella, etc. The member Firmicutes include Lactobacillus and Streptococcus, Actinobacteria, including Micrococcus, and Bacteroidetes such as Flavobacterium and Chryseobacterium (Sullam et al. 2012, Wu et al. 2012, Llewellyn et al. 2014, Givens et al. 2015, Deb et al. 2020). Firmicutes in marine species contains Bacillus and Clostridium, and Bacteroidetes such as Cytophaga (Llewellyn et al. 2014, Givens et al. 2015, Egerton et al. 2018, Ou et al. 2021, Uniacke-Lowe et al. 2024; Singh et.al. 2025).

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- **Factors Affecting Fish Gut Microbiome**

The factors responsible for colonization inside the gut can summarized as, a) random dispersal of microbes at the intestinal community, b) selective microbe-microbe or microbe host interactions. Microbial seeding occurred developing larvae from surrounding environment, persists until maturity reached through the non-neutral processes (Yan et.al. 2016; Burns et.al. 2016). The most phenomenal colonization inside the gut is deterministic cause of microbe-microbe or host-microbe specific interactions (Talwar et.al. 2018).

- **Gnotobiotic models of marine fish**

Gnotobiotic model, in which fishes reared in one type of microbial species or reared in axenic culture (Pham et.al. 2008). This sort of technique used to find out sensitivity of organs against diverse group of microbes and to find out benefit aspects of this microbiota. The fish used as the ideal gnotobiotic model is zebrafish as it has particular characters like transparent body, high fecundity, large brood size, external fertilization, rapid external development, and abundant genomic information (Leulier et al. 2017; Pham et al. 2008). The correlation of microflora of gut, environmental factor and health benefits of fish can be established using gnotobiotic model (Weihao et.al. 2021).

- **Gut microbiota of freshwater fish**

Diversification in the gut microbiota of the freshwater and marine water fishes recorded by several authors (Izvekova et al. 2007). Because of different environmental conditions, gutflora also varies in composition from marine water e.g. Acinetobacter, Aeromonas, Flavobacterium, Lactococcus, Pseudomonas, obligate anaerobes (Bacteroides, Clostridium and Fusobacterium) and members of family Enterobacteriaceae (Gómez and Balcazar, 2008; Uma et.al. 2020).

- **Effects of the microbiota on fish health**

Pathogenic microbes as the fish microbiomes are not always cause diseases. Prevalence of pathogens are more in case of mammals and plants whenever balance commensal microbes of fishes is disturbs, this process is also known as dysbiosis. The dominance of pathogenic microbes is suppressed in case of healthy fishes as in case of largemoth bronze gudgeons (Coreius guichenoti) prevalence of Aeromonas is detected but its present is more dominated in case of furunculosis-infected fish (Kumari, 2020).

The development effect such as life span and shape the body are the resultant of interaction between host and microbiota, leads to popularization of term holobiont and the hologenome (Bordenstein and Theis, 2015; Foster et.al. 2017; McFall-Ngai et.al., 2013). The mechanism involved in the host-microbiome interactions plays pivotal role in the functions of holobionts (Simon et al., 2019; Diwan et.al. 2013). Recent years, the microbiome concept is getting more attention as the healthy gut is maintain by the altered microbes through the prevention and treatment of the disease, an important advantage governed by holobiont. Healthy microbiota of fish’s gut maintained by probiotics, prebiotics, and synbiotics. It is also recommended by the many author to use biofloc system for checking disease spreads among cultivable organisms and promotes healthy conditions during the aquaculture farming (Diwan et.al., 2021; Rajeev et.al., 2020; Van Doan et.al., 2020; Wang et.al., 2019).

Gut microbiome plays important role in development and physiological functions of the host. The host-microbiome interactions controls growth, breeding and immune system. The surrounding environment is the major factor which can be responsible for the any sort disease outbreak in aquatic environment (Diwan et.al., 2021; Sun et.al. 2019).

- **Development of gut microbiota in fish**

The first feed to growing larvae responsible for microbial colonizations. The dominant microbiota reported in the fish eggs most often are Cytophaga, Flavobacterium, and Pseudomonas (Austin, 1982; Yoshimizu et al., 1986), variation among the species observed (Hansen and Olafsen, 1989; Romero and Navarrete, 2006; McIntosh et al., 2008). The most prevalent microbes in the primary developmetal stages are species-specific because of variation in binding glycoproteins on the egg surface (Larsen, 2014). The population of eggs controlled by the influence of surrounding environment. The freshly hatched larvae possess the first colonisers as the chorion-associated microbes, which colonize at the developing GI tract. Once the larvae begin to eat and drink, the microbial composition becomes diversified (Hansen and Olafsen, 1989; Korsnes et al., 2006; Reid et al., 2009; Lauzon et al., 2010).

Diversification in microbiota of captive state of fishes observed in freshwater samples (Bucio et al., 2006) and marine fishes (Nelson et al., 2013). In case of captured fishes, the microbiota influenced by the climate and diets. The microbiota manipulated in captive fish breeding and rearing. Antibiotics at industry levels during the farming controls the microbial diversity in aquaculture systems (Navarrete et al., 2008; Lozano et al., 2018).

- **Gut microbiota in fresh water, brackish water and marine fish**

The most dominant colonisers in the Gut of fishes are fungi, protists, viruses, and bacteria. Bacteria (Rombout et al., 2011) dominate the intestinal regime. Microbiota among the different trophic level from same sources are restricted to distinguish. Trophic level has great influence on microbial composition. In an investigation from the same water sample diverse group of microbes were recorded in different trophic levels such as herbivorous (e.g. Megalobrama amblycephala and Ctenopharyngodon idellus), carnivorous (e.g. Siniperca chuatsi and Culteral burnus) and omnivorous (e.g. Cyprinuscarpio and Carassius auratus and filter-feeder Hypophthalmichthys molitrix and H. nobil) (Liu et al., 2016). Microbiota associated with herbivorous fishes involved in fermentative digestions e.g. marine fishes, such as flatfish (Liston, 1956), salmon (Yoshimizu and Kimura, 1976), and sea chub (Rimmer and Wiebe, 2006). Very rate information is available on microbiota associated with brackishwater fishes. Brackishwater fishes possesses the microbiota, which belongs to both sort of sources like freshwater as well as marine water. This microbiota having potential cellulolytic and amylolytic activity (Rani et.al. 2012).

- **Factors affecting fish gut microbiome (FGM)**

The Fish Gut Microbiome dependes on two factors such as intrinsic and extrinsic factors. The intrinsic factors contains gender, immunity and genetics while extrinsic factor composed of water quality, feed and antibiotics (Figure 1).

The environmental factor as if salinity, climate and geographical location have great impact on the bacterial communities (e.g free living and symbiotic bacteria) (Ray, 2016; Zhang et al., 2016). The most factor influence microbial composition is diet of the fishes. Microbiome composition can change along with alteration of diet in controlled environmental conditions (Desai et al., 2012; Ingerslev et al., 2014a,b; Estruch et al., 2015; Schmidt et al., 2017). Habitat and microbial composition is significant but reason behind still not clear. With respect to diverse environmental conditions like freshwater and marine water, the microbial composition in the fish's gut shown great variations (Herlemann et al., 2011; Ghanbari et al., 2015). In comparison to diet, the environmental factors responsible contaminants in food and dietary elements often neglected.

The composition of microbes in FGM have shown taxonomical and regional differences. The animal health affected by stress. The exposure of stress to the fishes most probably caused by water quality, high pollutants content, inadequate photoperiod, oxygen levels, temperature, dense population, under-nourishment, storage and handling (Cantas et al., 2012). Several authors investigated the microbial composition during ontogenetic growth (Romero and Navarrete, 2006; Ingerslev et al., 2014a,b; Bledsoe et al., 2016; Stephens et al., 2016).

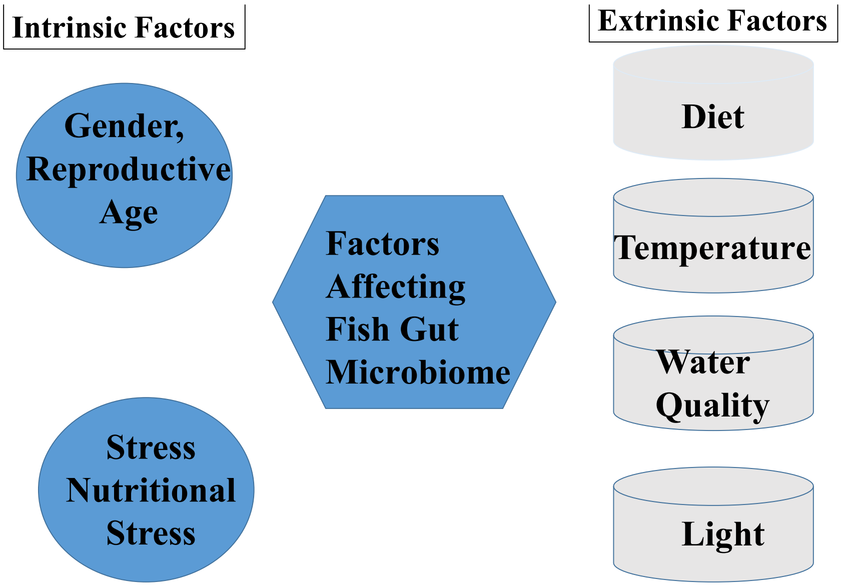

**Figure 1: Factors affecting the fish gut microbiome (Intrinsic and Extrinsic factors)**

- **Fishmeal in Aquaculture Farming**

The FGM are colonize together with other microbes in symbiotic or endosymbiosis fashion (e.g. Escherichia coli, Salmonella, Listeria inhabiting the GI tract) (Vine et al., 2006). The aquatic feed formulations provides enriched diet to the fishes containing protein-rich components with balanced amino acids and high palatability. Often shortage of fishmeal suggests that the fishmeal cannot compete with the current demand of the aquaculture market. The major component of fishmeal is soybean meal obtained as the byproduct during soybean oil extraction. The nutritional value of soybean meal constrained by some unnecessary factors like phytate, tannins, and soybean lectins (Francis et al., 2001), responsible for poor feed intake and palatability (Zhang et al., 2013) and reduction in the growth performance (Kumar et al., 2012; Xinru et.al., 2026).

The portion of FM can be replace by animal-byproduct and make it cheaper (Forster et al., 2003; Hernandez ´ et al., 2008; Davis et al., 2002). The regular use of animal byproduct is restricted because of lower protein digestion and utilization level, lack of balanced amino acids (deficiency in methionine) (Tan et al., 2005). The enzymatic hydrolysis can convert large complex protein molecules into good amino acid balance and bioactive peptides (antioxidant, anti-hypertensive, immunomodulatory, and antimicrobial peptides (Chalamaiah et al., 2012, Javaherdoust et al.,2020b). The Hydrolyzed porcine mucosa (HPM) and enzymatic chicken liver powder (ECLM) are rich source of protein containing small peptides and free amino acids. The HPM more often used in case of piglets (Cho et al., 2010; Figueroa et al., 2016; Myers et al., 2014). HPM helps in the improment meat quality (Yang et al., 2022). The growth performance of tilapia affected by the replacement of FM with chicken liver meal and dried porcine solubles (Wu et.al. 2021a; Hongjie et.al. 2023. Diverse microbes with good enzymatic activities detected in GI tract of rohu, catla, mrigal, bata, murrel, orange-fin labeo, Nile tilapia, and climbing perch (Mondal et al., 2010).

## IV. CONCLUSION

The microbiota resides in GI tract influence the growth and development of host. The enzymatic secretions helps in the digestion of complex food molecules for the easily available food molecules. The prevalence of microbiota during the early stages of ontogenic development shown species-specific. Later on after the maturity, the prevalence of microbes increase and diversified with the intake of water and food molecules. The understanding of fish microbiota helps in the understanding of sensitivity and growth effects. This portion reveals the feed controls can manipulate microbiota and alter physiological effects.

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