


Analysing the effect of dietary prebiotics and probiotics on gut bacterial richness and diversity of Asian snakehead fingerlings using T-RFLP method

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Abstract

This study was designed to evaluate the effects of three prebiotics (β -glucan, galacto-oligosaccharide [GOS], mannan-oligosaccharide [MOS]) and two probiotics (*Saccharomyces cerevisiae*, *Lactobacillus acidophilus*) on the microbiome of snakehead during growth of fingerlings. In addition, the experiment evaluated the capacity of *Channa striata* fingerlings to retain the benefits derived from these supplements after withdrawal. Throughout the study, it was observed that supplementation with dietary prebiotics and probiotics led to significant ($p < 0.05$) change in gut bacterial profile and improvement in gut morphology. Terminal restriction fragment length polymorphism (T-RFLP) was used for the comparative analysis of gut communities and all 46 of the T-RFLP detected phylotypes were present in the *Lactobacillus* supplemented fish, while significantly fewer were detected in controls and other experimental supplement regimes. Histological studies and electron microscopy revealed that both the prebiotic and probiotic treated fish had significantly longer and wider villi and deeper crypts compared to the controls. The microvilli length, as evaluated with electron microscopy, was also longer in all treated fish compared to controls. Furthermore, this study is the first to report the absence of differences in sustaining the efficacies attained after intake of β -glucan, GOS, MOS and live yeast upon post-feeding with an unsupplemented feed, over a prolonged period.

KEYWORDS

gut bacterial richness and diversity, prebiotics, probiotics, snakehead fingerlings, terminal restriction fragment length polymorphism

1 | INTRODUCTION

Analysing the intestinal bacterial profile is one of the important factors in fish nutrition studies (Daniel et al., 2014; Lara-Flores, Olvera-Novoa, Guzmán-Méndez, & López-Madrid, 2003; Moen, Saeed, Mohammad, & Faranaz, 2011). The gastrointestinal (GI) tract of fish is known as the ecological niche (Austin & Austin, 1987; Cahill, 1990; Denev, Staykov, Moutafchieva, & Beev, 2009; Holben et al., 2002; Kim, Brunt, & Austin, 2007; Llewellyn, Boutin,

Hoseinifar, & Derome, 2015; Ringø et al., 2000; Ringø, Sperstad, Myklebust, Mayhew, & Olsen, 2006; Ringø, Strøm, & Tabachek., 1995) for a group of diverse selected beneficial bacteria derived from the surrounding aquatic environment, including water sediment and feed. The abundance of beneficial bacteria in the fish intestine is expected to influence fish growth and health (Cahill, 1990; Hoseinifar Khalili, & Sun, 2016; Hoseinifar, Ahmadi, et al., 2016; MacFarlane, McLaughlin, & G. Bullock., 1986). Moreover, a