

7. Dietary supplementation of non-starch polysaccharides affects growth of Pacific white shrimp (*Litopenaeus vannamei*) and microbial compositions in biofloc system

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The experiment compared two diets differing in the NSP level: high (NSP) and low (CON) on *Litopenaeus vannamei* reared in biofloc system (BFT). NSP diet was formulated by 40% dilution of CON diet using wheatbran. Shrimp was fed isoproteinic for 42 days. To measure the contribution of natural biota on shrimp growth shrimp were also grown in a RAS system (RAS) as control. The NSP diet increased the carbon to nitrogen (CN) ratio of the shrimp feces from 11.8 in CON treatment to 20.5. The NSP diet had a lower apparent digestibility coefficient (ADC) of dry matter, protein, energy, carbohydrate, and minerals ($P < 0.05$). The experimental diet did not show any effect on the shrimp production ($P > 0.05$), but shrimp weight harvested from BFT was higher than from the RAS system ($P < 0.05$). The percentage of biofloc contribution on DM, N, and energy was statistically similar between the diets ($P < 0.05$), ranging 42.6-43.5% for CON and 31.1-32.0% for NSP diet. No significant effect was found on the biofloc formation and nutritional quality ($P < 0.05$). The accumulation of NO_x ($\text{NO}_2 + \text{NO}_3$) and total organic N were higher in CON diet than in NSP diet ($P < 0.05$), meanwhile the NH_4 concentration was similar ($P > 0.05$). The alpha-diversity of the prokaryotic microbial communities in the BFT samples, did not revealed significant changes between the diet treatments, but time showed a decrease in richness and increase in diversity. On the contrary, for eukaryotic and fungal communities, both richness and diversity decreased over time, while no significant effect of the diet was found. In the prokaryotic communities, the most abundant microbial phyla was *Chloroflexi*, followed by *Proteobacteria*, *Planctomycetota*, *Bacteroidota* and *Cyanobacteria*. With regard to genera, a large portion of the microbial communities was not assigned to a genus (60%), while the most abundant genus was *Candidatus Nitrosopumilus*, followed by *Maricauda*, *Calorithrix* and *Pleurocapsa*. In the eukaryotic communities, *Chlorophyta* phylum occupied more than 75% of the relative abundance, followed by *Nematoda* and *Rotifera*. Among the *Chlorophyta* phylum, *Nannochloropsis* was the most abundant genera. In the fungal communities, two main groups were detected: *Ascomycota* and *Basidiomycota*, while a high percentage was not assigned to any group (25-50%). At the genus level, *Penicillium*, *Trichosporon* and *Engyodontium* were amongst the most abundant, although the abundance was changing over time.