

Microbiota Associated With the Larval Culture of Red Cusk Eel *Geniptyerus Chilensis* in Chile

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Abstract : The culture of the marine fish red cusk eel *Geniptyerus chilensis* is currently considered a priority for Chilean aquaculture which is a Chilean native species of high gastronomic demand and market value. The microbiota was analyzed in terms of diversity and structure using massive Illumina sequencing. The analysis of alpha diversity was performed in samples of *G. chilensis* larvae of 6, 18 and 32 dph (days post-hatching) and it was observed that there were significant differences ($P = 0.05$) between the days of culture for the Chao1 index, being the larvae of 18 dph the one with the highest index followed by the larvae of 6 dph, The lowest value for this index was presented in larvae of 32 dph. There were no significant differences in larvae between the days of culture for the Shannon ($P=0.0857$) and Simpson ($P=0.0714$) indices. In general, the larvae of *G. chilensis* have high rates of diversity. When analyzing the beta diversity, a differentiation between the bacterial communities is observed depending on the day of the culture of the larvae. Considering the PCoA elaborated from the unweighted UniFrac statistic, the explained variance was 46.2% (PC1 29.2% and PC2 17.0%) and in the case of the PCoA elaborated with the weighted UniFrac statistic; the explained variance was 65.5% (PC1 41.8% and PC2 23.7%) these differences were significant based on the Permanova statistical analysis ($P= 0.002$ and 0.037 respectively). When analyzing the taxonomic composition of the microbiota of the larvae in the different days of culture it was observed that at the phyla level the most abundant in the larvae of 6 dph were Proteobacteria (57%) Verrucomicrobia (24%) and Firmicutes (14%), for the larvae of 18 dph the predominant phyla were Proteobacteria (90%), Dependientiae (5%), Actinobacteria (2%) and Plactomyces (2%), for the larvae of 32 dph the phyla that presented the highest relative abundance were Proteobacteria (57%), Firmicutes (29%), Verrucomicrobia (5%) and Actinobacteria (5%), when comparing the larvae between the days it was observed that the phylum Proteobacteria was the most abundant in the samples of larvae of 6, 18 and 32 dph being the larvae of 18 dph those that present the highest relative abundance, the larvae of 6 dph were those that presented the highest relative abundance for the phylum Verrucomicrobia and in the larvae of 32 dph was observed greater abundance of the phylum Firmicutes compared to the other days of larval culture. At the level of genera, those with the highest relative abundance in larvae of 6 dph were Rubritalea (30%), Psychrobacter (28%), staphylococcus (17%) and Ralstonia (10%), for the larvae of 18 dph the genera with the highest abundance were Psychrobacter (47%), Litoreibacter (13%), Nautella (9%) and Cohesibacter (8%), for the larvae of 32 dph the most abundant genera were Alloiococcus (25%), Dialister (14%), Neptunomonas (13%) and Piscirickettsia (11%). When observing the taxonomic composition of the larvae between the days of larval culture, it is observed that there are differences between them.

Keywords : microbiota, diversity, *G. Chilensis*, larvae

Conference Title : ICAAA 2023 : International Conference on Aquaculture and Aquatic Animals

Conference Location : Toronto, Canada

Conference Dates : July 10-11, 2023