
عنوان مقاله:

Research Article: Metagenomic analysis of the intestinal flora and antibiotic resistance genes of yellow catfish ((Pelteobagrus fulvidraco

محل انتشار:

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خلاصه مقاله:

High-throughput sequencing of intestinal microbial DNA using the Illumina platform was implemented to clarify the structure and function of intestinal flora and antibiotic resistance genes (ARGs) abundances in yellow catfish (Pelteobagrus fulvidraco). Species annotation and gene function analysis were performed on the metagenomic sequencing data. Intestinal bacteria were isolated and identified by ۱۶sRNA. The results showed that intestinal flora was highly similar in the three P. fulvidraco. A total of ۳۷ phyla and ۷۸۸ genera of intestinal bacteria were identified. Proteobacteria, Streptomyces, and Clostridium are the dominant flora with the average relative abundance of ۲۵.۷۱%, ۱۴.۷۵%, and ۵.۱۵%, respectively. Six strains were successfully isolated and identified in our experiment. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis showed that the primary metabolic pathway is dominated by metabolism and organic systems, while the secondary metabolic pathway is dominated by sensory system, carbohydrate metabolism, replication, and repair. In addition, ۴۹۹ ARGs of ۳۷ resistance types were identified based on Antibiotic Resistance Genes Database. Tetracycline, polypeptide, macrolide, glycopeptide, and multiple drug resistance were highly abundant. The intestinal ARGs of P. fulvidraco were macB, bcrA, and evgS. In general, rich bacterial diversity and many types of ARG were detected in the intestine of P. fulvidraco. Moreover, probiotics are potentially a good alternative to antibiotic abuse in aquaculture industry. Therefore, analysis of intestinal flora, intestinal .flora ARGs and gene functions is beneficial for the artificial farming of P. fulvidraco

کلمات کلیدی:

Pelteobagrus fulvidraco, Metagenome, Intestinal flora, Antibiotic resistance genes

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