ANALYSIS OF THE INTESTINAL MICROBIOTA OF RAINBOW TROUT (*Oncorhynchus mykiss*, WALBAUM) AND THE AQUATIC ENVIRONMENT IN THE MOUNTAIN REGION OF THE STATE OF RIO DE JANEIRO

ANÁLISE DA MICROBIOTA INTESTINAL DE TRUTA ARCO-ÍRIS (*Oncorhynchus mykiss*, WALBAUM) E SEU AMBIENTE AQUÁTICO NA REGIÃO SERRANA DO ESTADO DO RIO DE JANEIRO

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Abstract

Truticulture is an activity widely developed activity in the South and Southeast regions of Brazil, including the mountain region of the state of Rio de Janeiro, the target of this study. Antibiotic therapy is used for the prophylaxis and treatment of bacterial diseases. However, these drugs act on commensal and pathogenic bacteria in the intestinal microbiota of healthy and sick fish, which increases the presence of residues in the environment if used indiscriminately, favoring the selective pressure for bacterial resistance to antimicrobials and increasing horizontal transfer of resistance genes among several bacterial populations. The objective of this study was to carry out a survey of cultivable commensal and pathogenic microorganisms in the intestinal content of rainbow trout (Oncorhynchus mykiss) and the aquatic environment for identification of bacteria resistant to antimicrobials and circulating pathogenic factors in the region. Five trout farms were visited. Nine samples of water from the active tanks and 50 fish of the species O. mykiss were collected from July to October and submitted to zootechnical evaluation including the parameters body mass (MC), total length (CT) and standard length (CP). The mean values were 307.15±149.65, 25.79±3.71 and 22.85±3.45, respectively. From the total samples, 222 bacterial isolates were obtained, and the susceptibility profile to antimicrobials was evaluated. Of the total of isolates, 54.5% (n = 121) showed Gram-negative bacteria, especially species from the Enterobacteriaceae, Aeromonaceae and Pseudomonadaceae families; and 45.5% (n = 101) Gram-positive, especially species of the genera Staphylococcus, Enterococcus, Lactococcus, Streptococcus, Kocuria and Gemella. We observed that 65.3% (n = 79) of Gram-negative bacteria and 82.2% (n = 83) of Gram-positive bacteria showed resistance to at least one antimicrobial, and a multidrug resistance profile was observed in 7.4% (n = 9) and 36.6% (n = 37), respectively. Both groups had statistically significant ($P<0,05$) resistance to beta-lactam antibiotics ($p = 0.000$; $p = 0.045$) according to Fisher's exact test. Cephalothin (45.5%), amoxicillin/clavulanic Acid (27.3%), ampicillin (26.5%) and cefoxitin (24,0%) for Gram-negative; amoxicillin and oxacillin (48.5%), ampicillin (42.6%), penicillin G (39.6%), clindamycin (33.7%), gentamicin (28.7%) and tetracycline (27.7%) for Gram-positive. In the molecular analysis, strains of coagulase-negative Staphylococcus spp. (n = 51) were submitted to the PCR technique to detect the methicillin-resistant mecA gene and to detect staphylococcal enterotoxins A, C and D, with the following results: 33.3% (n = 17) positive for the presence of the mecA gene; 98.0% (n = 50) for the sea gene; 9.8% (n = 5) for the sec gene; and 13.7% (n = 7) for the sed gene. Considering the microbiological diversity, resistance profile to antimicrobials associated with virulence factors, it is important to advise producers about adoption of sustainable practices in truticulture, in order to prevent the spread of resistant genes and the consequences to the environment and public health.

Keywords

Rainbow trout; Intestinal microbiota; Multi-resistance to antimicrobials.

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