ABSTRACT

The spread of antibiotic resistance in aquaculture is an increasing public health concern, as farmed fish are thought to be potential reservoirs of resistant bacteria and genes. The current study was conducted to isolate identify, and characterize *Salmonella*, from farmed rainbow trout with a focus on determining their antibiotic resistance profiles. Initial enrichment was carried out in buffered peptone water and Brain Heart Infusion broth, followed by selective isolation on MacConkey and XLD agar. The spread of antibiotic resistance in aquaculture is an increasing public health concern, as farmed fish are thought to be potential reservoirs of resistant bacteria and genes.

Out of thirty samples, seven were observed to revealed typical *Salmonella* colonies, which were confirmed through Gram staining, biochemical testing, and molecular screening with genus-specific primers targeting the invA gene (284 bp). In the present study the prevalence of *salmonella* was 23.33% (n = 7/30) of commercial trout. Antibiotic susceptibility tests found that all isolates were susceptible to tetracycline, cefoperazone, and gentamycin. However, considerable levels of resistance were detected against amoxicillin (85.7%), vancomycin (71.5%), erythromycin (57.1%), ciprofloxacin (42.9%), and chloramphenicol (28.6%). Molecular detection indicated the presence of resistance genes such as *CTX-M, catA, vanA, ermB,* and *qnrB*, with a high correlation (r= 0.9721) between phenotypic and genotypic resistance profiles. These findings highlight the rise of multidrug-resistant (MDR) *Salmonella* in aquaculture environments, indicating the importance of strict antibiotic management and the use of alternative treatments like probiotics and vaccination in fish farming systems.