Antimicrobial use in aquaculture re-examined: its relevance to antimicrobial resistance and to animal and human health

Felipe C. Cabello,* 1 Henry P. Godfrey, 2 Alexandra Tomova, 1 Larisa Ivanova, Humberto Dölz, 3 Ana Millanao, 3 Alejandro H. Buschmann 4

Departments of 1 Microbiology and Immunology and 2 Pathology, New York Medical College, Valhalla, NY 10595, USA. 3 Instituto de Farmacia, Facultad de Ciencias, Universidad Austral de Chile, Valdivia, Chile. 4 Centroënmar, Universidad de Los Lagos, Puerto Montt, Chile.

August, 01 2013

The worldwide growth of aquaculture has been accompanied by a rapid increase in therapeutic and prophylactic usage of antimicrobials including those important in human therapeutics. Approximately 80% of antimicrobials used in aquaculture enter the environment with their activity intact where they select for bacteria whose resistance arises from mutations or more importantly, from mobile genetic elements containing multiple resistance determinants transmissible to other bacteria. Such selection alters biodiversity in aquatic environments and the normal flora of fish and shellfish. The commonality of the mobilome (the total of all mobile genetic elements in a genome) between aquatic and terrestrial bacteria together with the presence of residual antimicrobials, biofilms, and high concentrations of bacteriophages where the aquatic environment may also be contaminated with pathogens of human and animal origin can stimulate exchange of genetic information between aquatic and terrestrial bacteria. Several recently found genetic elements and resistance determinants for quinolones, tetracyclines, and beta-lactamases are shared between aquatic bacteria, fish pathogens, and human pathogens, and appear to have originated in aquatic bacteria. Excessive use of antimicrobials in aquaculture can thus potentially negatively impact animal and human health as well as the aquatic environment and should be better assessed and regulated.

This abstract was excerpted from the original paper, which was published in Environmental Microbiology. 2013, Vol. 15. Issue 7: 1917-1942