

Antibiotic resistance profiles of environmental isolates from Mhlathuze River, KwaZulu-Natal (RSA)

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Abstract

One hundred and thirteen enteric bacteria were isolated from the Mhlathuze River during February 2001 to January 2002. The antibiotic resistance patterns (ARPs) of these identified isolates showed that 94.7% were resistant to at least one class of antibiotic while 75.2% were multi-resistant. All isolates were sensitive to gentamicin. The levels of resistance exhibited by isolates to specific antibiotics are as follows: penicillin, 72.6%; rifampicin, 69.2%; novobiocin, 52.1%; ampicillin, 43.6% and cephalothin, 28.2%. The antibiotic resistance gene pool especially that for β -lactamase is likely to be widely available in the environment. The ARPs for *E. coli* and non-*E. coli* groups were very similar. The enteric bacteria isolated from downstream, which is a mainly urban and industrial area, were more resistant to several antibiotics than those from upstream which is predominantly rural. The results suggest that environmental, industrial and/or human activities impact on the level of antibiotic resistance in the environment. The strong correlation ($r=0.97$) between the ARPs of the clinical and the environmental isolates may suggest a link between diarrhoeal incidence and the water quality in the region. It is thus imperative that the determination of antibiotic susceptibility/resistance patterns of isolated microbes is a part of the microbial monitoring process of the water.

Keywords: antibiotic resistance profile, Mhlathuze, environmental, *Enterobacteriaceae*

Introduction

The increase of faecal pollution in source water is a problem in developing as well as in developed countries (American Society for Microbiology (ASM) Colloquium Report, 1999). Water-borne bacterial pathogens such as *E. coli* 0157, *Salmonella* spp., *Shigella* spp. and *Vibrio cholerae* can lead to diarrhoeal outbreaks that may have serious medical and economic implications (WHO, 2000; WHO, 1996). This problem is further compounded by the increasing incidence of pathogens with antibiotic and/or drug resistance (DePaola et al., 1995; Ogan and Nwiika, 1993). Exposure to environmental pollutants and changes in nutrient composition may lead to selective pressures favoring certain organisms or genotypes. Recent studies demonstrated positive correlations between industrial pollution and the spatial distribution of antibiotic resistance (Goñi-Urriza et al., 2000; McArthur and Tuckfield, 2000). Heavy use of antibiotics for medical and veterinary purposes (Balagué and García Vescovi, 2001; White et al., 2000) as well as the domestic and agricultural use of pesticides and related compounds (Balagué and García Vescovi, 2001) caused significant antibiotic contamination of the natural environment and consequent development of resistance in communities. Antibiotic and drug resistance in medicine generates significant health and economic impacts (ASM Colloquium Report, 1999).

A recent study (Ash et al., 2002) showed that several rivers in the United States of America have become a major reservoir for antibiotic-resistant microbes. With global travel and widespread commerce, drug- and antibiotic-resistant microbes can spread to all parts of the world.

Similar to that for antibiotics, heavy metal contamination is also a severe environmental problem due to the increase in human and industrial activities (ASM Colloquium Report, 1999). Heavy metals such as lead, mercury, cadmium and nickel are metabolically poisonous at low concentrations. They inhibit the activities of certain enzymes involved in the metabolic process (Midigan et al., 2003). At high concentrations these metals form unspecific complex compounds in the micro-organism, which leads to toxic effects (Nies, 1999). Bacterial accumulation of and resistance to toxic heavy metals is a widespread phenomenon. The mechanisms of heavy metal resistance have been reported to enhance the antibiotic resistance ability of microorganisms (Davidson, 1999; Edlund et al., 1996).

The Mhlathuze catchment sustains various agricultural and industrial communities. This water system also serves as a main source of water to the large rural population which resides in this region (Steyl et al., 2000). The results from monitoring physico-chemical and microbiological quality of the Mhlathuze River (Lin et al., 2004a; Bezuidenhout et al., 2002) indicated a high contamination of faecal coliform and heavy metals in this water system. The industrial and intensive farming activities in this region might also contribute to the selection of antibiotic resistance genes in bacteria that colonize humans and animals. Therefore in this study we focused on the level of antibiotic and metal resistances of enteric bacteria in this water system.

Materials and methods

Isolation of bacteria

All water samples were collected every two weeks from 5 different sites namely KwaDlangezwa, Dlangubo, Richards Bay estuary, Mhlathuze pumping station and Felixton, along the Mhlathuze

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