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Distribution and antibiotic susceptibility profiles of *Aeromonas* spp. from different aquatic environments in north Lebanon

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Abstract

Introduction: Bacteria of Aeromonas genus are ubiquitous organisms in aquatic environments. This work aims to explore the presence of four clinically relevant species in Lebanese waters and to study their susceptibility to antibiotics.

Methododogy: One hundred water samples are collected in northern Lebanon from different sources (river, springs, wells, ponds, sea, chlorinated water and sewage) and analyzed by culture methods. The isolates were identified at genus level by a PCR assay targeting *gcat* gene. The presence of four species (*A. hydrophila*, *A. caviae*, *A. media* and *A. veronii*) was investigated by a multiplex PCR. The antibiotic susceptibility was also studied.

Results: *Aeromonas* spp. was detected in 28% of investigated samples. In total, 38 isolates were identified as *Aeromonas* spp (10 out of 7 river water samples, 9 out of 35 spring, 9 among 26 wells, 5 out of 4 sewage samples, 2 out of 5 ponds, 2 out of 8 seawater samples and 1 out of 15 chlorinated water samples). *Aeromonas hydrophila* was the predominant species (19 isolates; 50%). The 3 other species were found to a lesser extent: *A. caviae* (3 isolates; 7.9%), *A. veronii* (2 isolates; 5.3%) and *A. media* (2 isolates; 5.3%). 12 other isolates (31.5%) remained unidentified by the used multiplex PCR technique. All isolates were resistant to more than one antibiotic. The most common resistance concerned beta-lactams.

Conclusion: This study highlighted the interesting distribution of these species in aquatic biotopes in Lebanon and the threat of potential transmission of these resistant strains to humans.

Key words: Aeromonas, antibiotic susceptibility, aquatic environments, identification, north Lebanon.

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