

Impact of climate change on spread of antibiotic-resistant bacteria in wastewater treatment plants for water reuse in agricultural irrigation

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Reuse of treated wastewater for non-potable purpose such as irrigation, ground water recharge after proper treatment has a widespread significance. So the aim of the present investigation was to isolate, identify and characterize lytic bacteriophages against multi-drug resistant strains of *Pseudomonas aeruginosa* and *Enterococcus faecalis* from wastewater. Plaque size, transmission electron microscopy (TEM), virulence factors, and in vitro lytic activity of bacteriophage isolates were investigated. The sewage water was collected from wastewater treatment plants (WTs) in El-Sharkia Governorate, Egypt. *E. faecalis* and *P. aeruginosa* were the predominant pathogenic bacteria from wastewater. The highest percentage of multi-antibiotic resistance bacteria (MAR) in all sewage water samples were *P. aeruginosa* and *E. faecalis* (84%). The results showed that the presence of bacteriophages for *P. aeruginosa* strains named (PP1, PP2 and PP3) while phages infect *E. faecalis* strains named (EP1, EP2 and EP3). Isolated phages examined by TEM and their morphological shapes were detected. The bacteriophages had an isometric head and long-contractile tail and another phage with short tail with varying their dimensions from length, diameter of head and length, diameter of tail. They are belonging to Myoviridae and Siphoviridae families. TEM confirmed *P. aeruginosa* and *E. faecalis* bacteriophages belonging to the family Myoviridae. Among *P. aeruginosa* and *E. faecalis* bacteriophages with broad host range, 18 isolates (66.7%) did not harbor any *P. aeruginosa* and *E. faecalis* virulence factors. Therefore, they are considered potential candidates for controlling the contamination of *P. aeruginosa* and *E. faecalis* in water or other applications.