The first detection of the sequence of bacteria from the Simkaniaceae family in surface waters in Poland

M. Pawlikowska-Warych1,2, W. Deptula1,2
1Department of Microbiology, Faculty of Biology, University of Szczecin, Poland
2Molecular Biology and Biotechnology Center, Faculty of Biology, University of Szczecin, Felczaka 3c, 71-412 Szczecin, Poland

Abstract

Bacteria from the Simkaniaceae family are intracellular parasites belonging to the Chlamydiales order, detected in surface waters, drinking water, chlorine water, and in wastewater. Its main representative, Simkania negevensis, is pathogenic to humans and animals, especially fishes, as it principally causes respiratory tract diseases. Bacteria from this family are also capable of surviving and existing in free-living amoebas, omnipresent in the natural environment, which makes them an additional risk for human and animal health. The aim of the present study was to search for representatives of this family in freshwaters from the Odra River and two municipal lakes (Rusalka and Goplana). Out of 100 water samples analysed, the sequence of bacteria of Simkaniaceae family was found just in 1 percent, because phylogenetic analysis revealed that the obtained OdraWCh30 sequence shows 93% similarity to Simkania negevensis strain Z as well as 87% similarity to Candidatus Syngnamydia salmonis isolate Ho-2008 and Candidatus Syngnamydia salmonis isolate VS10102006 and 84-85% similarity to endosymbiont of Xenoturbella westbladi, Simkaniaceae bacterium clone SM081012-5s and Candidatus Syngnamydia venezia strain Pi3-2. This is the first case of detecting sequence of bacteria of Simkaniaceae family in the aquatic environment in Poland.

Key words: Simkaniaceae, surface water, phylogenetic analysis, OdraWCh30 sequence, Poland

Introduction

Bacteria from the Simkaniaceae family with classic chlamydia (the Chlamydiaceae family) and 9 families referred to as CLO – chlamydia-like organisms or environmental chlamydia belong to the Chlamydiales order (Pierle et al. 2015, Bou Khalil et al. 2016, Pizzetti et al. 2016, Pawlikowska-Warych and Deptula 2016). A prototype for this family is the identified in 1993 S. negevensis, isolated as contamination from cell cultures (Kahane et al. 1993). Its classification among the Chlamydiales order is conditioned by identical ribosomal genes, at the level of 80-90% (Everett et al. 1999) and characteristic of chlamydia two-phase but long