Multiplex PCR detection of *Staphylococcus spp.* genes *mec*A, 16S rRNA, and *pvl* in sewage from the Greater Nanaimo Pollution Control Center

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The presence of Methicillin-Resistant *Staphylococcus spp*. in the environment could increase the incidence of infections that are difficult to treat among member of the community. Water released from wastewater treatment plant may act as a reservoir of these organisms, as colonized humans would shed these bacteria from the skin and feces; therefore, detection of these bacteria could be used to determine the efficiency of wastewater treatment systems in their elimination. The purpose of this research was to use a multiplex PCR protocol to detect methicillin resistant *Staphylococcus spp.* from influent and effluent water samples from Greater Nanaimo Pollution Control Center (GNPCC). This was accomplished by using primers designed to detect the *mec*A and 16S rRNA genes. In addition, primers for the Panton-Valentine Leukocidin (PVL) gene *pvl* typically associated with *S. aureus* were also used. The protocol used was able to show that the *mec*A and 16S rRNA genes were present in both influent and effluent water samples, while the presence of *pvl* gene was not detected in any of the samples tested. These results suggest that methicillin resistant *Staphylococcus spp.* but not necessarily MRSA is present in the waste waters of Nanaimo.