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Title (English) Development of a diagnostic method for <i>Legionella</i> species based on the RNase P RNA-gene <i>rnpB</i>		
Title (Swedish)		
Abstract Legionnaires' disease is caused by <i>Legionella</i> bacteria and can be lethal for immune suppressed persons. The bacteria live in water habitats and can be numerous in manmade water systems like thermostats and whirlpools. The <i>Legionella</i> genus comprises at least 48 species of which <i>L. pneumophila</i> is most common in clinical isolates. In this project a new two step method based on the RNase P RNA-gene (<i>rnpB</i>) for <i>Legionella</i> detection has been evaluated. An initial real-time PCR identifies <i>Legionella</i> and <i>L. pneumophila</i> . Additional pyrosequencing of PCR fragments enable differentiation of <i>Legionella</i> species due to sequence differences. This study indicates that species identification is possible, but it seems impossible to create a genus specific PCR for <i>Legionella</i> based on <i>rnpB</i> .		
Keywords <i>Legionella</i> , legionnaires' disease, RNase P, <i>rnpB</i> , real-time PCR		
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