SEARCH FOR SUITABLE MOLECULAR MARKERS FOR SPECIES DIFFERENTIATION OF ENTEROCOCCI

BOBKOVA, S.; BAUDISOVA, D.

National Institute of Public Health

Keywords: *Enterococcus* — faecal contamination — molecular markers — microbial source tracking (MST)

Enterococci, together with representatives of the species *Escherichia coli*, belong to the so-called indicators of faecal pollution, which are used in the evaluation of the microbiological quality of bathing waters. Their determination is governed by the Decree of the Ministry of Health No. 238/2011 Coll. and performed by culture on selective agar media. It is known that not all types of enterococci are of fecal origin and are therefore directly related to fecal water pollution. To properly assess the quality of bathing water, it would be useful to know the origin of these bacteria. For tracing the origin of these microorganisms (so-called microbial source tracking) the molecular biology methods can be used. Using PCR method, different types of enterococci can be distinguished by amplification of molecular markers (ie specific parts of DNA). There are many publications dealing with this topic, however, in most studies, only one marker is analyzed for species differentiation, and this may not always be sufficient when working with natural samples. For reliable species identification in natural samples, it would be more advantageous to use a combination of several markers. At the same time, it would be appropriate to apply the knowledge gained from experiments with pure cultures to natural samples of bathing water, both pure and faecally polluted. For practice, it would be also important to use procedures enabling PCR from a mixed natural sample, without the need for pre-cultivation on selective media, in order to minimize the time for which the result is known.

The aim of this paper is to summarize the published molecular markers for the identification of both enterococci and related microorganisms, and to evaluate their possible use in water microbiology for the rapid classification of Enterococcus species into species during the analysis of natural samples.