

Interactive comment on “Correlations between total cell concentration, total adenosinetri-phosphate concentration and heterotrophic plate counts during microbial monitoring of drinking water” by E. Siebel et al.

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General comments:

The aim of the paper is clear and straightforward: comparison of two newly available, rapid and accurate detection methods and a conventional method for quantification of bacterial biomass in drinking water. The methods and results are described in a clear and concise way. ATP and flow cytometry are relatively new methods in drinking water research; drinking water companies hesitate to use these in routine application because the relation with the conventional methods is still unclear. This makes the

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topic of this applied research relevant and it should be published. The scope is quite limited, however, from a scientific point of view. For example, it would be interesting to include other new methods (e.g. Q-PCR) and conventional methods (e.g. microscopic cell counts) to provide a more general comparison of methods. The results should be discussed in a broader light (see specific comments below)

Specific comments:

-The two new methods show good correlation, and therefore the authors recommend to use these in a complementary way. The conventional HPC method only shows a very small fraction of the total number of bacteria in the water. This raises the question how results of the new methods, showing much higher cell numbers, should be interpreted in terms of the drinking water guidelines? Are historical data (100 years is mentioned in the paper) useless, or should the HPC method be continued to be carried out as well?

-The fundamental questions that are raised by this work should be discussed in more detail. E.g. What is the effect of cell cycle and growth rate on ATP level per cell? Which fraction of ATP originates from intact cells, and which fraction is dissolved in the bulk water? Is the fraction of culturable cells stable? This should add to a more fundamental understanding of the relations between conventional and new methods.

-On p.77 line 14, regrowth is mentioned as a reason for increase of cell count in the distribution system. Is anything known about the finished water of the treatment plant to prove this point?

-Separation of low (LNA) and high (HNA) nucleic acid clusters comprises a substantial part of the discussion, but this does is not mentioned in the abstract.

Technical corrections:

-The use of the term significantly throughout the text is confusing, because it is not strictly used in its statistical meaning (for example compare in the abstract p. 72 line 4 and 15)

-Throughout the results section ranges are given with average values (e.g. p.76 line

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3). Please specify what these represent: standard deviation, standard deviation of the mean or confidence interval?

-p.73 line 12-14: include reference to back up the statement that a huge discrepancy exists between HPC and TCC methods.

-p.76 line 21: Deininger et al. 2001 should be Deininger and Lee 2001

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