INTRODUCTION

The aim of the project was to isolate different bacteria from Lake Geneva and determine the species using molecular biology methods.

OBSERVATIONS AND RESULTS

We isolated bacteria from water and sediment of Lake Geneva (Fig. 1). We processed the samples (Fig. 2) and enriched the bacteria on different media. We observed all kind of different bacterial colonies (Fig. 3).

Afterwards we isolated single colonies on rich media plates. These bacteria were first stained following the method of Gram to get a first impression of their shape and kind. The corresponding microscopy images are shown in Fig. 4.

To find out which specific kind of bacteria we have, we isolated their genomic DNA (Fig. 5A). This genomic DNA we used as template for polymerase chain reaction (PCR) to amplify the 16S rRNA gene (Fig. 5B). This ribosomal RNA is present in all bacteria and can be used for bacterial identification due to hypervariable regions.

Based on the obtained sequences we isolated *Bacillus cereus* (S-P-LB1), *Aeromonas veronii* (C-F-MC1) and *Aeromonas popoffii* (T-LB).

DISCUSSION AND CONCLUSION

Even though we cannot see them, microorganisms are widely spread in the environment. Most of them are not amenable to laboratory culture conditions but a minority is. We made use of this fact and successfully isolated bacteria from Lake Geneva. Luckily we neither found bacteria in tap nor fountain water.

In summary we used traditional microbiological methods combined with modern molecular biology techniques. Based on the 16S rRNA sequence we were able to specify the bacterial isolates. Using bioinformatic tools we compared our isolates to well-known species and assembled a phylogenetic tree (Fig. 6).