



Impact of submerged aquatic macrophytes on 3-dim current systems and hydrodynamic transport processes in Lake Constance

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According to the assessment criteria of the European water framework directive Lake Constance is having a good water quality. Nevertheless upcoming criteria using environmental quality measures show that there are still problems with respect to micropollutants.

In fact, we observe significantly enhanced concentrations of micropollutants close to river mouths and in the areas of shallow water zones within Lake Constance compared to deep water concentrations. These findings are caused by river water plumes which can flow over distances of kilometers in the lake without being diluted or mixed only weakly with the surrounding lake water body. Besides, in the area of interest exist large populations of submerged aquatic macrophytes (SAM). There is only little knowledge, how these influence the distribution and transport processes of micropollutants.

In order to assess the impact and distribution of river water plumes in different areas of the lake we implemented a 3-dim hydrodynamic model using DELFT3D-FLOW on a locally refined numerical grid which enables to cover different process scales of the distribution of river water bodies ranging from a few meters up to basin wide scales in the order of a few kilometers. We used numerical tracers (conservative and non-conservative) in order to quantify the impact of different abstract substance classes which are distinguished by their decay rates. In order to assess the influence of SAM populations on current field and transport processes we used a special simulation technique – the trachytopo concept.

The results of our 3-dim hydrodynamic model showed significantly changed current velocities, residence times and age of water parameters within the SAM areas compared to the control simulation without SAM. By simulating the propagation of coliform bacteria using numerical tracers with spatially and temporarily variable decay rates, we found complex impact pattern of the SAM on the distribution of these potentially harmful microorganisms.