

Sulfonamides degradation and microbial responses in Riverbank Filtration(RBF) system: a laboratory column study

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Contamination of drinking water sources by pharmaceutical activated compounds is emerging recently in the urban water cycle, which is an important issue related to human health, ecological effects (Benner et al. 2013). Antibiotic resistance genes (ARGs) are also increasingly regarded as emerging environmental contaminant.

the other hand, bank filtration has long been recognized as an effective and sustainable technique for pathogenic microbes and organic micro pollutants removal around the world (Tufenkji, Ryan and Elimelech 2002). River bank area which is characterized by gradients in light, temperature, redox potential, pH, oxygen, and carbon source, controls the intensity of biodegradation. It is frequently reported that the most significant biochemical changes related to microbial activity occurs in the early stages of bank infiltration process (Kedziorek, Geoffriau and Bourg 2008, Zhang et al. 2015, Ma et al. 2015).

The changing redox conditions in natural groundwater system would enhance a change in microbial activity, which is the main incentive of biodegradation intensity (Richter et al. 2009). In the biodegradation process of antibiotics in the environment, redox condition as long as carbon source supply controls the microbial activity, and are the main factors controlling the intensity (García-Galán et al. 2008). Benno et al. proved that sulfamethoxazole was more effectively degraded under aerobic than under anoxic conditions and the availability of DOC fosters SMX removal (Baumgarten et al. 2011). Raffaella et al. noticed an increasing degradation rate of p-TSA in groundwater due to the microbial adaption to the change of redox condition (anoxic to oxic) (Meffe et al. 2012). Doreen et al. also found out p-TSA and o-TSA were redox-sensitive compounds and preferably degraded in the presence of O₂ (Richter et al. 2009). Jette et al. studied direct metabolism of three sulfonamides (sulfanilamide (SAA), sulfadimethoxine (SDT), and sulfapyridine (SPY)) through enzymatic catalysis by the fungal laccase from *Trametes versicolor* in soil. So it is imperative that we improve understanding of the processes and environmental factors that govern the fate of sulfonamides in the riverbank filtration process (Mohatt et al. 2011).

In this paper, two independent RBF soil column pilots (3 columns and 7 columns) were constructed and five sulfonamides including Sulfapyridine, Sulfadiazine, Sulfamethoxazole, Sulfamethazine and Sulfaquinoxaline were selected as the target antibiotics. The object of this research include: 1) contrasting the attenuation dynamic and migration behavior of sulfonamides in monitored RBF system under different redox condition and retention time, 2) examining microbial community structure dynamic in porous aquifer media and its effect on sulfonamides removal rate, 3) investigating sulfonamides resistance gene (sul1, sul2) abundance and accumulation mechanisms during riverbank filtration and the risk posted on drinking water safety. By analyzing the different attenuation behavior of sulfonamides in two pilot systems, and the microbial responses to this environment pressure, we can further deduce the effect of hydrological retention time, redox condition and microbial activity and community structure had on sulfonamides degradation during MAR process.

Keywords: River bank filtration, Antibiotics, Antibiotics resistance genes