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Impact of selected NSAIDs on performances, microbial activity and microbial community in sequencing batch reactors

The non-steroidal anti-inflammatory drugs (NSAIDs) are the most commonly used drugs worldwide. Among them, diclofenac (DCF), ibuprofen (IBP) and naproxen (NPX) were frequently detected in the environment as the trace emerging contaminants. The growing production and application of these three NSAIDs raises the risk of discharging them into wastewater treatment plants (WWTPs). In the last few decades, concern is growing over the determination and occurrence of the NSAIDs in the environment and WWTPs. In accordance with their observations, the NSAIDs were usually detected at ng L^{-1} to ug L^{-1} levels in the WWTPs. In most instances, municipal WWTPs are biological wastewater treatment processes to remove nitrogen, phosphorus and organic pollutants where microbial component of activated sludge drive the key processes. Figure 1 was the table of content of this study, providing a brief summary on experiment design and results.

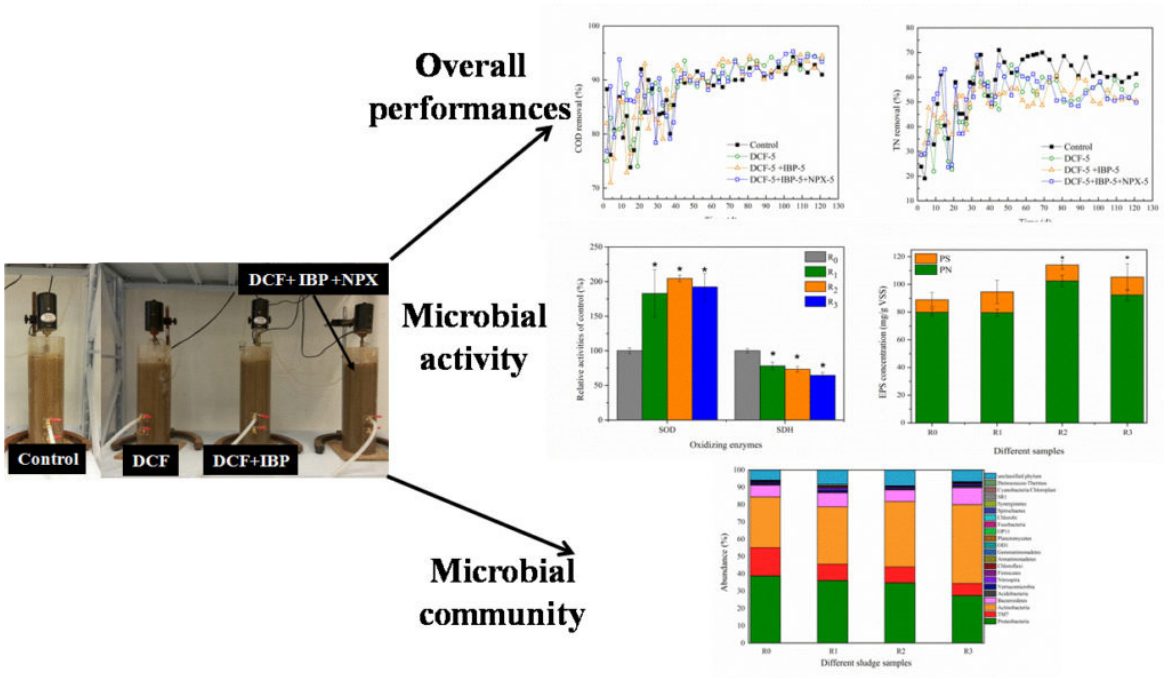

Fig. 1. Table of content of this study.

Overall performance: COD and NH_4^+-N removals were all over 90% in three samples ($p > 0.05$), but the removals of TN decreased from 64.04% to 53.19% ($p < 0.05$) and there was no obvious difference in reactors of TN removal ($p > 0.05$). The results indicated that the selected NSAIDs of environmental concentration had little effect on COD and NH_4^+-N removals, but decreased TN removal. It seems that TN removal was easier to be affected than COD removal. A possible explanation of unchanged COD removal is that the sum of heterotrophs responsible for organic matter removal were not affected with the addition of

selected NSAIDs of environmental concentration, and the decreased TN removal might be caused by the decrease of denitrifying microorganisms.

Microbial activity of activated sludge: the results indicated that environmentally relevant concentration of selected NSAIDs stimulated the superoxide dismutase activity, suggesting that the three NSAIDs could induce the oxidative stress of microorganisms in activated sludge. Succinate dehydrogenase existing in many prokaryotic cells is an important enzyme in the tricarboxylic acid cycle. The increase of extracellular polymeric substances content with the combination of selected NSAIDs indicated that the mixtures of selected NSAIDs might improve the toxicity to microorganisms, which could stimulate microorganisms to produce more extracellular polymeric substances content.

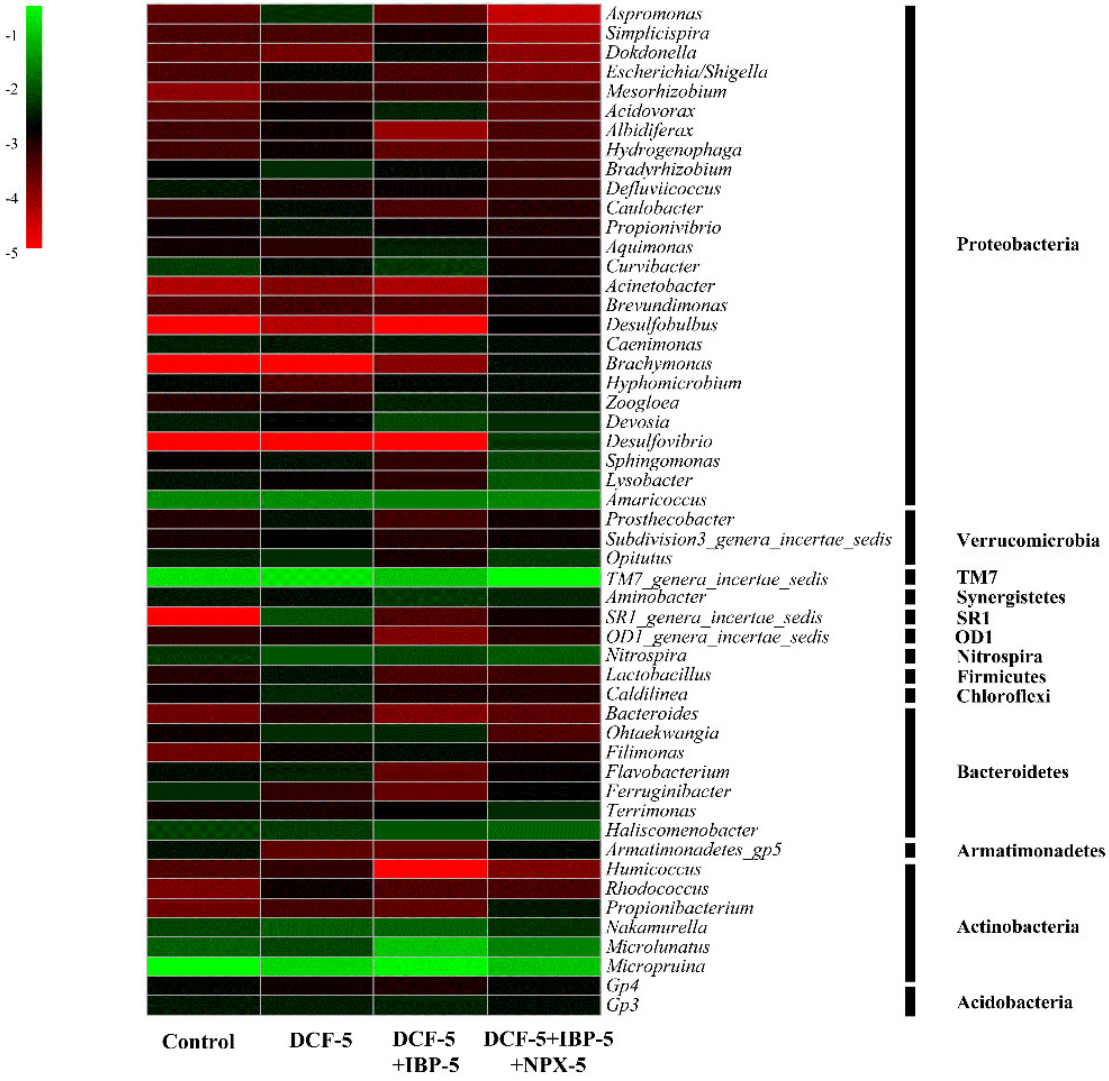

Fig. 2. Heat map of genera occurring at >0.2% abundance in at least one sludge sample.

Microbial community of activated sludge: the heat map of bacterial abundance at genus level is shown in Figure 2. The results indicated that the microbial composition was affected by adding the NSAIDs and the mixtures of selected NSAIDs had greater influence on microbial community. *Micropruina* accounted for a large part in activated sludge, which kept the decreasing trendy from 29.53% to 14.90%, 14.21% and 9.50% in R_0-R_3, respectively. *Nakamurella*, also affiliated to Actinobacteria phylum, decreased from 1.31% (R_0) to 0.46% (R_3). *TM7_genera_incertae_sedis, Amaricoccus, Haliscomenobacter* and *Microlunatus* were the dominant genera in all sludge samples, which increased with the addition of pharmaceuticals. The abundance of *Zoogloea,* affiliated with Proteobacteria phylum, had an augmentation under the pressure of pharmaceuticals, increasing from 0.08% (R_0) to 0.33% (R_3). The abundances of *Desulfovibrio* and *Desulfobulbus* were 0.01% in the control (R_0), increasing to 0.53% and 0.17% in R_3. TM 7 and Bacteroidetes were the dominant species in the activated sludge. Actinobacteria and Bacteroidetes were enriched with the presence of selected NSAIDs.

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Characterization of microbial community and antibiotic resistance genes in activated sludge under tetracycline and sulfamethoxazole selection pressure.
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