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Toxic effects of a single sulfonamide antibiotic on two indicator organisms

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Abstract

The widespread use of antibiotics leads to more and more serious pollution of antibiotics in the environment, which has become a global ecological environment problem. Antibiotic pollution will affect the normal life activities of organisms and threaten human health through the food chain. In order to investigate the toxic effects of antibiotic pollution on different indicator organisms, Scenedesmus obliquus and Vibrio qinghaiensis sp-Q67 were used as indicator organisms. Eight widely used sulfonamides antibiotics (SAs), namely, sulfapyridine (SPY), sulfamethazine (SMR), sulfadimethazine (SM2), sulfamethoxazine (SMP), sulfamethoxazole (SMZ), sulfaquinoxaline (SQ), sulfamethoxine (SMM), sulfamethoxine (SMM), and sulfamethoxine (SMM), were studied by microplate toxicity test. The growth inhibition toxicity of sulfamide chloropyrazine sodium (2-SPZ) and its binary mixture to Cyanobacteria obliqua (96h) and Vibrio Qingqingensis Q67 (15min acute and 1h chronic); Based on the actual environmental concentration of SAs in Huixian wetland of Guilin, two groups of six-element mixtures were designed to study their combined toxicity to two different indicator organisms.

Keywords

Toxic effects, single sulfonamide antibiotic.

1. Introduction

With the increasing severity of antibiotic pollution, people pay special attention to the situation of antibiotic pollution. Only a small part of SAs can be metabolized in living organisms, most of which enter the natural environment in the form of maternal compounds or metabolites, although the concentration in the environment is low, but also affect the normal life activities of animals, plants and other organisms, thus threatening human health. In this chapter, eight common SAs(sulfapyridine, sulfamethazine, sulfadimethazine, sulfamethoxazole, sulfamethoxazole, sulfaquinoxaline, sulfamethoxine and sulfachlorpyrazine sodium) were selected to study their toxic effects on Chloropyrazine and Vibrio Qinghaiensis.

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2. Physicochemical properties of sulfonamides antibiotics

The eight SAs include sulfapyridine (SPY), sulfamethazine (SMR), Sulfadimethazine (SM2), Sulfamethoxazine (SMP), Sulfamethoxazole (SMZ), Sulfaquinoxaline (SQ), sulfamethoxine (SMM), sulfachlorpyrazine sodium (2-SPZ), sulfamethoxazole (SMM), sulfamethoxine (SMM), sulfachlorpyrazine sodium (2-SPZ), sulfamethoxazole (SMM), and sulfamethoxazine. All purchased from Cato Research Chemicals Inc., USA, with purity greater than 98%.

3. Results and discussion

3.1. Toxicity of a single sulfonamide antibiotic to Alga obliqua

The biological toxicity of SAs was measured by the inhibition rate of the algae at 96 h. For the specific toxicity test methods of the algae, see Chapter 2, 2.2.2.

The concentrate-effect data of the eight SAs species on the alga tillosa can all be fitted by Weibull function or Logit function. The fitting model parameters (regression α and β values, statistical parameters R2 and RMSE) are shown in Table 3.2. The R2 values of the eight SAs fitting curves range from 0.944 to 0.997, and are all greater than 0.94. The RMSE values of the fitted curves ranged from 0.008 to 0.033, and were all less than 0.03 (except 2-SPZ), which indicated that the model fitting results were accurate and reliable. Figure 3.2 shows the concentration-effect-number fitting curves (CRCs) for eight SAs, all of which appear as classical S-shapes. Taking pEC50 as the toxicity index, the higher the value of pEC50, the higher the toxicity [94], then the toxicity sequence of the eight tested SAs to the clavicularia is as follows: SQ(pEC50=5.31) > SPY(pEC50=3.76) > SMZ(pEC50=3.75) > SMP(pEC50=3.68) > SMM(pEC50=3.66) > SM2(pEC50=3.09) > 2-SPZ(pEC50=2.98) > SMR(pEC 50=2.60); It can be seen that SQ is the most toxic, followed by SPY and SMR is the smallest.

Chen Qiong et al. [88] took Chlorella proteinucleus as the test organism to investigate the toxic effects of five kinds of SAs, and the results showed that the toxic effects of SAs on Chlorella proteinucleus were not very obvious, and the toxicity levels among SAs could not be compared. The results showed that the alga obclina was more sensitive to SAs than Chlorella proteinucleus.

3.2. Toxicity of a single sulfonamide antibiotic to Vibrio Q67

Vibrio Qinghaiensis Q67 was used as the indicator organism to test the biotoxicity of SAs, and the inhibition rate of Vibrio Qinghaiensis Q67 in 15min and 1h was used to indicate the toxicity of SAs. For specific toxicity test methods of Vibrio Qinghaiensis Q67, see Chapter 2 2.3.2.

The dose-effect data of eight SAs for 15min acute toxicity of Vibrio Qinghai Q67 could all be fitted by Logit function. The fitting model parameters (regression α and β values, statistical parameters R2 and RMSE) were shown in Table 3.3. The R2 values of the eight SAs fitting curves ranged from 0.902 to 0.997 and were all greater than 0.90. The RMSE values of the fitted curves ranged from 0.003 to 0.010, all of which were less than 0.01 (except SMZ), indicating that the model fitting results were accurate and reliable. Figure 3.3 shows the CRCs of the eight SAs, all presented as the classic S-type. Taking pEC50 as the toxicity index, the greater the pEC50 value, the greater the toxicity, then the 15min acute toxicity sequence of the eight SAs tested against Vibrio Q67 was as follows: SQ(pEC50=2.76) > SPY(pEC50=2.54) > 2-SPZ(pEC50=2.44) > SMZ(pEC50=2.36) > SMM(pEC50=2.22) > SMR(pEC50=2.04) > SMP(pEC50=2.00) > SM2(pEC 50=1.85); It can be seen that SQ is the most toxic, followed by SPY and SM2 is the least. The dose-effect data of 1h chronic toxicity of eight SAs to Vibrio Qinghai Q67 could all be fitted by Logit function. The fitting model parameters (regression α and β values, statistical parameters R2 and RMSE) were shown in Table 3.4. The R2 values of the eight SAs fitting curves ranged from 0.901 to 0.973, and were all greater than 0.90. The RMSE value of the fitted curve is 0.002～

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All of them are smaller than 0.03, which indicates that the model fitting results are accurate and reliable. Figure 3.4 shows the CRCs of the eight SAs, all presented as the classic S-type. Taking pEC50 as the toxicity index, the higher the value of pEC50, the higher the toxicity, then the 1h chronic toxicity sequence of the eight SAs tested against Vibrio Q67 was as follows: SQ(pEC50=4.02) > SPY(pEC50=3.14) > SMM(pEC50=3.07) > SMP(pEC50=2.90) > SM2(pEC50=2.89) > SMZ(pEC50=2.81) > SMR(pEC50=2.39) > 2-SPZ(pEC 50=2.27); It can be seen that SQ is the most toxic, followed by SPY and 2-SPZ is the smallest.

Compared with the experimental results of Ding Tingting et al. [87], it was found that the pEC50 of SPY to Vibrio Q67 of Qinghai was 3.41, which was close to the results of this experiment (3.14). Compared with the experimental results of Chen Qiong et al. [88], it was found that the pEC50 of SM2 toxicity to Vibrio Q67 of Qinghai was 3.12, which was also close to the results of this experiment (2.89).

3.3. Toxicity difference analysis of sulfonamides antibiotics to two indicator organisms

The pEC50 values of eight SAs for two indicator organisms are shown in Table 3.5. As can be seen from Table 3.5, the toxicity levels of the eight SAs species to P. obvialis and Vibrio Qinghai Q67 were different. Among them, the toxicity levels to P. obvialis 96h were in the order of SQ > SPY > SMZ > SMP > SMM > SM2 > 2-SPZ > SMR. The order of 15min acute toxicity to Vibrio Q67 was SQ > SPY > 2-SPZ > SMZ > SMM > SMR > SMP > SM2. The order of 1h chronic toxicity to Vibrio Q67 was SQ > SPY > SMM > SMP > SM2 > SMZ > SMR > 2-SPZ. The results of 15min acute toxicity and 1h chronic toxicity of SAs to Vibrio Q67 showed that the chronic toxicity was higher than the acute toxicity, and the toxicity of SAs to Vibrio Q67 increased with the increase of time. According to pEC50, the sensitivity of the eight SAs was higher than that of Vibrio Q67.

For the two indicator organisms, the two SAs with the highest toxicity are SQ and SPY, which are far greater than the other six SAs, and the difference in toxicity of each SAs may be related to its molecular structure. The more -CH3 groups in the side R group, the lower the toxicity [80]. As can be seen from Figure 3.1, there is no -CH3 group in the R group of SQ and SPY, which is the possible reason why SQ and SPY are more toxic to the two indicator organisms than other SAs. Although 2-SPZ has no CH3 group in the side R group, its toxicity to the two indicator organisms is not strong, which may be related to the presence of chlorine atoms in its structure.

4. Conclusion

The toxicity levels of the eight SAs species to P. obvialis and Vibrio Q67 were different. Among them, the toxicity levels to P. obvialis 96h were in the order of SQ > SPY > SMZ > SMP > SMM > SM2 > 2-SPZ > SMR. The order of 15min acute toxicity to Vibrio Q67 was SQ > SPY > 2-SPZ > SMZ > SMM > SMR > SMP > SM2. The order of 1h chronic toxicity to Vibrio Q67 was SQ > SPY > SMM > SMP > SM2 > SMZ > SMR > 2-SPZ. The results of 15min acute toxicity and 1h chronic toxicity of SAs to Vibrio Q67 showed that the chronic toxicity was higher than the acute toxicity, and the toxicity of SAs to Vibrio Q67 increased with the increase of time. According to pEC50, the sensitivity of the eight SAs was higher than that of Vibrio Q67.

For the two indicator organisms, the two SAs with the highest toxicity are SQ and SPY, and they are far greater than the other six SAs. There is no -CH3 group in the R group of SQ and SPY, which may be the reason why SQ and SPY are more toxic to the three indicator organisms than the other SAs. Although 2-SPZ has no CH3 group in the side R group, its toxicity to the three indicator organisms is not strong, which may be related to the presence of chlorine atoms in its structure.

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