p-CRESOL MINERALIZATION AND BACTERIAL POPULATION DYNAMICS IN A NITRIFYING SEQUENTIAL BATCH REACTOR

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Introduction. The sequential batch reactor (SBR) technology can be used for eliminating ammonium from the water through the coupled respiratory processes of nitrification and denitrification. Several studies have reported the ability of nitrifying consortia to oxidize various organic compounds, including phenolic compounds (1). However, knowledge on the oxidation and inhibitory effects of cresols in nitrifying reactors is still limited (2).
Therefore, the aim of this study was to evaluate the ability of a nitrifying sludge to consume *p*-cresol and its intermediates as well as to monitor the population dynamics of the bacterial community throughout the operation cycles in a SBR system.

Methods. Two laboratory-scale SBRs were operated with cycles of 12 h. SBR_A (control) was fed with a lithoautotrophic medium and SBR_B with *p*-cresol. The response variables of nitrification were the ammonium consumption efficiency (E_{NH4}) and the nitrate production yield (Y_{NO3}). The bacterial population dynamics of the consortium were monitored by using denaturing gradient gel electrophoresis (DGGE) and sequencing of DGGE fragments (3).

Results. *p*-Cresol was totally consumed from the SBR_B culture. The SBR system allowed an increase in the metabolic ability of the sludge to oxidize *p*-cresol throughout the cycles (Table 1). *p*-Cresol was first transformed to *p*-hydroxybenzaldehyde and *p*-hydroxybenzoate, which were later mineralized. In spite of the *p*-cresol addition, the nitrification performance did not change significantly in the SBR_B (E_{NH4} = 99.0% ± 0.5 and Y_{NO3} = 0.98 ± 0.07 g NO_3^--N/g NH_4^+-N consumed). This may be related to the high stability observed in the ammonia-oxidizing community (*Nitrosomonas halophila*, Seq 1; uncultured ammonia-oxidizing bacterium, Seq 2; *Nitrosomonas europaea*, Seq 3; *Nitrosomonas oligotropha*, Seq 5) and the nitrite-oxidizing community (*Nitrospira sp*., Seq 7 and *Nitrobacter sp*., Seq 9) (Fig. 1). The ability of the sludge to consume *p*-cresol might be related to the presence of species as *Variovorax paradoxus* (Seq 4) and *Thauera mechernichensis* (Seq 6).

Table 1. Specific rates of *p*-cresol consumption in a nitrifying SBR culture.

Cycles	*p*-Cresol conc. (mg C/L)	Specific rate (mg C/g VSS h)
106	25	30 ± 4
160	50	60 ± 6
226	100	160 ± 10
296	200	10 ± 2
322	200	40 ± 4

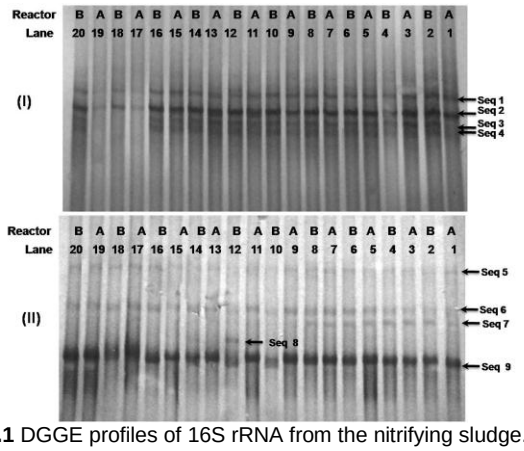

Fig.1 DGGE profiles of 16S rRNA from the nitrifying sludge. I: Gradient 30-38%, II: 45-60%. A: SBR_A without *p*-cresol, B: SBR_B with *p*-cresol. SBR_B: lanes 2 and 4, without *p*-cresol at cycles 1 and 105; lanes 6 and 8, with 25 mg *p*-cresol-C/L at cycles 106 and 159; lanes 10 and 12, with 50 mg C/L at cycles 160 and 225; lanes 14 and 16, with 100 mg C/L at cycles 226 and 295; lanes 18 and 20, with 200 mg C/L at cycles 296 and 322. SBR_A: lanes 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 at cycles: 1, 105, 106, 159, 160, 225, 226, 295, 296, 322.

Conclusions. Results indicate that nitrifying SBR may be a good alternative to eliminate simultaneously NH_4^+ and *p*-cresol from wastewaters, maintaining stable the respiratory process as the bacterial community structure.

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