Susceptibility of Ammonia-Oxidizing Bacteria to Nitrification Inhibitors

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Activity of nitrification inhibitors to several typical ammonia-oxidizing bacteria isolated recently, *i. e. Nitrosococcus*, *Nitrosolobus*, *Nitrosomonas*, *Nitrosospira* and *Nitrosovibrio* species was assayed using 2-amino-4-methyl-6-trichloromethyl-1,3,5-triazine (MAST), 2-amino-4-tribromomethyl-6-trichloromethyl-1,3,5-triazine (Br-MAST), 2-chloro-6-trichloromethyl-pyridine (nitrapyrin) and others, and compared to confirm the adequate control of ammonia-oxidizing bacteria by the inhibitors. The order of activity of the inhibitors to 13 species of ammonia-oxidizing bacteria examined was approximately summarized as Br-MAST ≥ nitrapyrin ≥ MAST > other inhibitors. Two *Nitrosomonas* strains, *N.* europaea ATCC25978 and *N.* sp. B2, were extremely susceptible to Br-MAST, exhibiting a $pI_{50} \geq 6.40$. These values are the position logarithms of the molar half-inhibition concentration. The 16S rRNA gene sequence similarity for the highly susceptible 4 strains of genus *Nitrosomonas* was 94% to 100% of *Nitrosomonas europaea*, although those of the less susceptible 3 strains of ammonia-oxidizing bacteria, *Nitrosococcus oceanus* C-107 ATCC19707, *Nitrosolobus* sp. PJA1 and *Nitrosolobus multiformis* ATCC25196, were 77.85, 91.53 and 90.29, respectively. However, no clear correlation has been found yet between pI_{50}-values and percent similarity of 16S rRNA gene sequence among ammonia-oxidizing bacteria.

Key words: Ammonia-Oxidizing Bacteria, Susceptibility to Nitrification Inhibitors, Nitrapyrin