Susceptibility of Ammonia-Oxidizing Bacteria to Nitrification Inhibitors

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Activity of nitrification inhibitors to several typical ammonia-oxidizing bacteria isolated recently, \textit{i.e.} \textit{Nitrosococcus}, \textit{Nitrosolobus}, \textit{Nitrosomonas}, \textit{Nitrosospira} and \textit{Nitrosovibrio} species was assayed using 2-amino-4-methyl-6-trichloromethyl-1,3,5-triazine (MAST), 2-amino-4-trichloromethyl-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 > MAST > other inhibitors. Two \textit{Nitrosomonas} strains, \textit{N. europaea} ATCC25978 and \textit{N. sp. B2}, were extremely susceptible to Br-MAST, exhibiting a \( p_{I50} \approx 6.40 \). 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 \textit{Nitrosomonas} was 94% to 100% of \textit{Nitrosomonas europaea}, although those of the less susceptible 3 strains of ammonia-oxidizing bacteria, \textit{Nitrosococcus oceanus} C-107 ATCC19707, \textit{Nitrosolobus} sp. PJA1 and \textit{Nitrosolobus multiformis} ATCC25196, were 77.85, 91.53 and 90.29, respectively. However, no clear correlation has been found yet between \( p_{I50}\)-values and percent similarity of 16S rRNA gene sequence among ammonia-oxidizing bacteria.

\textit{Key words:} Ammonia-Oxidizing Bacteria, Susceptibility to Nitrification Inhibitors, Nitrapyrin