Phylogenetic Analysis of Ammonia Monooxygenase (amoA) Genes From Desert Caves

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Nitrification is the process by which ammonia is oxidized to nitrate, and is an important biogeochemical reaction in the global nitrogen cycle. This process is catalyzed by ammonia monooxygenase (AMO), which is encoded by the amoA gene. Both bacteria (ammonia-oxidizing bacteria, or AOB) and archaea (ammonia-oxidizing archaea, or AOA) are capable of carrying out ammonia oxidation. This project focuses on the phylogenetic analysis of novel amoA genes from microorganisms found in caves. Through this project, amoA genes from two new metagenomes from Lehman Caves in Nevada and Lechuguilla Cave in New Mexico are being analyzed. Other amoA sequences used for phylogenetic comparison are being compiled from the scientific literature, including amoA studies that go back more than 23 years, as well as from metagenomes from other cave systems. At least one bacterial and one archaeal amoA have been identified so far, and preliminary BLAST analysis showed that these likely originated from close relatives of known ammonia oxidizers, including Nitrosomonas spp., and an unknown archaea. Detailed phylogenetic analysis shows that the amoA from the ammonia-oxidizing bacterium is most closely related to Nitrosomonas spp. and to amoA recovered from other caves, as well as several pmoA sequences, indicating potential use of trace methane. We are now performing additional phylogenetic analyses to further classify these new amoA sequences and explore the evolution of ammonia-oxidizing microorganisms in caves, as well as to further explore the potential use of trace methane as an energy resource in desert caves. The work from this project will be used in future research aimed at uncovering new ammonia-oxidizing cave microorganisms and exploring their role in the subterranean nitrogen cycle.

Keywords:
ammonia monooxygenase, bacteria, cave, amoA, phylogenetics


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