

# Coupling of diversification and pH adaptation during the evolution of terrestrial Thaumarchaeota

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Edited by Edward F. DeLong, University of Hawaii, Manoa, Honolulu, HI, and approved June 11, 2015 (received for review October 7, 2014)

**The Thaumarchaeota is an abundant and ubiquitous phylum of archaea that plays a major role in the global nitrogen cycle. Previous analyses of the ammonia monooxygenase gene *amoA* suggest that pH is an important driver of niche specialization in these organisms. Although the ecological distribution and eco-physiology of extant Thaumarchaeota have been studied extensively, the evolutionary rise of these prokaryotes to ecological dominance in many habitats remains poorly understood. To characterize processes leading to their diversification, we investigated coevolutionary relationships between *amoA*, a conserved marker gene for Thaumarchaeota, and soil characteristics, by using deep sequencing and comprehensive environmental data in Bayesian comparative phylogenetics. These analyses reveal a large and rapid increase in diversification rates during early thaumarchaeotal evolution; this finding was verified by independent analyses of 16S rRNA. Our findings suggest that the entire Thaumarchaeota diversification regime was strikingly coupled to pH adaptation but less clearly correlated with several other tested environmental factors. Interestingly, the early radiation event coincided with a period of pH adaptation that enabled the terrestrial Thaumarchaeota ancestor to initially move from neutral to more acidic and alkaline conditions. In contrast to classic evolutionary models, whereby niches become rapidly filled after adaptive radiation, global diversification rates have remained stably high in Thaumarchaeota during the past 400–700 million years, suggesting an ongoing high rate of niche formation or switching for these microbes. Our study highlights the enduring importance of environmental adaptation during thaumarchaeotal evolution and, to our knowledge, is the first to link evolutionary diversification to environmental adaptation in a prokaryotic phylum.**

archaea | ammonia oxidation | phylogeny | diversification | Thaumarchaeota

**A**mmonia oxidation, the first and rate-limiting step in nitrification, is central to the global nitrogen cycle. Ammonia-oxidizing archaea (AOA) and ammonia-oxidizing bacteria (AOB) perform this biochemical transformation, converting as much as 70% of the 100 Tg of nitrogen fertilizer applied annually (1) and generating significant nitrous oxide (2). Although only distantly related, AOA and AOB perform similar ecosystem functions by catalyzing the conversion of ammonia to nitrite (via hydroxylamine) by using ammonia monooxygenase, a multimeric enzyme comprising the subunits AmoA, AmoB, and AmoC (3). Although AOA were initially classified as Crenarchaeota, improvements in phylogenetic methods and genomic sampling of uncultured archaeal diversity led to their placement within a new archaeal phylum, the Thaumarchaeota (4, 5). These organisms are ubiquitous, with archaeal *amoA* genes frequently outnumbering those of AOB (6). Furthermore, AOA are the principal drivers of ammonia oxidation in many soils, particularly those with low pH (7, 8). Environmental pH is a major factor affecting the distribution of AOA in terrestrial ecosystems (3, 9), and most terrestrial Thaumarchaeota can be phylogenetically assigned to one

of five pH-adapted lineages, two being acidophilic, two alkaliphilic, and one neutrophilic (9).

Despite great progress in understanding of thaumarchaeotal ecology and physiology (10), little is known about the evolutionary mechanisms that have generated their great diversity in nature. In multicellular eukaryotes, the fossil record can provide insight into evolutionary processes over geological timescales, but such approaches are not possible for many prokaryotes because of the lack of an informative fossil record. In this context, recently developed probabilistic methods geared toward reconstructing the dynamics of species diversification and trait evolution using molecular phylogenies (11–13) have great potential. A recent Bayesian method that explicitly aims to characterize and quantify heterogeneity in evolutionary rates (13–15) holds particular promise for modeling prokaryotic evolution, whereby features such as massive population size, frequent lateral gene transfer (LGT), and fast growth all facilitate rapid increases in diversity, suggesting that complex evolutionary regimes may be the norm. Here, we apply these recently developed methods to test a key hypothesis about the ecological drivers of thaumarchaeotal diversification through deep evolutionary time. Based on the documented importance of soil pH in structuring modern AOA communities (9), we tested the hypothesis that adaptation to pH is an important driver of diversification in the Thaumarchaeota by comparing associations between pH and a

## Significance

**The link between species diversification and adaptation has long interested biologists working on multicellular eukaryotes, but remains poorly understood in prokaryotes, in which diversity is much greater. We tested the hypothesis that diversification is associated with environmental adaptation in Thaumarchaeota, an ancient and abundant microbial group and key player in the global nitrogen cycle. We provide evidence that the Thaumarchaeota underwent a major radiation event hundreds of millions of years ago that coincided with a major period of pH adaptation. Subsequently, these microbes have maintained high rates of diversification, potentially because of the high rate at which new terrestrial niches arise. This study provides a framework for comparing dynamics of evolutionary processes across the tree of life.**

Author contributions: C.G.-R. and D.J.M. designed research; C.G.-R., C.K., and D.J.M. performed research; A.C.M. contributed new reagents/analytic tools; C.G.-R., T.A.W., A.C.M., T.M.E., J.I.P., and D.J.M. analyzed data; and C.G.-R., T.A.W., T.M.E., J.I.P., and D.J.M. wrote the paper.

The authors declare no conflict of interest.

This article is a PNAS Direct Submission.

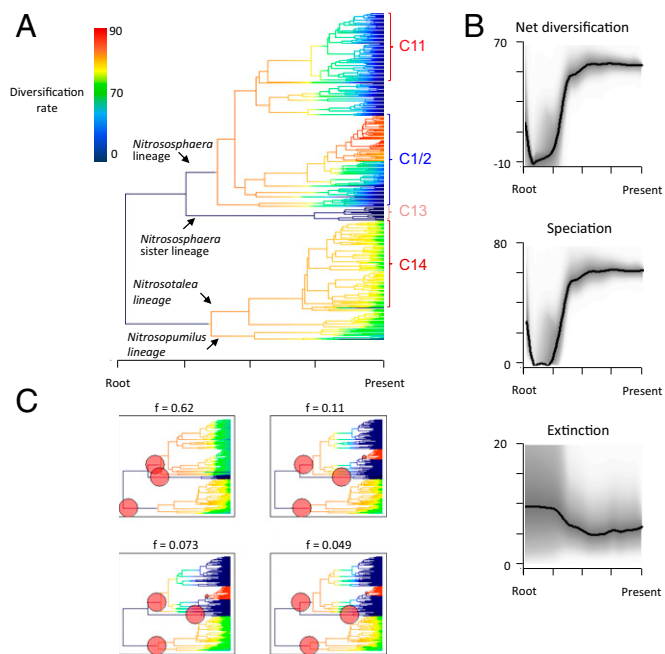
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Data deposition: The alignment files and phylogenetic trees in this paper have been deposited in the Dryad Digital Repository, [datadryad.org \(10.5061/dryad.0nv00\)](http://datadryad.org/10.5061/dryad.0nv00).

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This article contains supporting information online at [www.pnas.org/lookup/suppl/doi:10.1073/pnas.1419329112/-DCSupplemental](http://www.pnas.org/lookup/suppl/doi:10.1073/pnas.1419329112/-DCSupplemental).





**Fig. 2.** Evolutionary heterogeneity in diversification rates in terrestrial Thaumarchaeota inferred from the 370-sequence *amoA* tree within the BMM framework. (A) Phylorate plot illustrating the heterogeneity in diversification rates along each branch of the phylogeny. The different color regimes depicted represent the mean of the marginal posterior density of diversification rates for distinct segments of the tree. (B) Plots of net diversification rate, speciation rate, and extinction rate (y axis) through time during thaumarchaeotal evolution. Shaded areas denote 90% Bayesian credibility intervals. (C) Plots of the four most probable diversification rate-shift configurations along with their individual contributions to the posterior distribution of all sampled BMM models. All four plots include similar positive rate shifts (indicated by red filled circles).

global diversification rate and associated rate shifts at the base of the *amoA* phylogeny were robust to these sampling assumptions (*SI Appendix, Fig. S5*). However, the stability in diversification rate across the latter half of thaumarchaeotal evolution was affected. Specifically, when <90% of sampling diversity was assumed to be recaptured, a slow, steady increase in diversification rate was observed during the same time period (*SI Appendix, Fig. S5*). However, this change was invariably less rapid and of a lesser magnitude than the initial increase (*SI Appendix, Fig. S5*). As an independent measure of confidence, we merged our 454 *amoA* sequence dataset with the complete diversity of non-redundant published *amoA* sequences. This led to an alignment of 613 unique sequences with better representation of *Nitrosotalea* and *Nitrosopumilus*, presumably recapturing known diversity from marine and estuarine environments that was not sampled in our soil study. These sequences were used in Bayesian phylogenetic analyses, and the resulting tree was used in a BMM diversification analysis, which was highly congruent with results based on 454 data only (*SI Appendix, Fig. S6*).

To further test the robustness of our findings, we repeated the BMM analysis by using a 16S rRNA dataset (508 aligned sequences) combining a comprehensive nonredundant representation of published sequence diversity with a 454 dataset we had recently generated (27). To provide the most direct comparison between 16S rRNA and *amoA*, we used a phylogenetic approach to ensure that the included 16S rRNA genes were sampled from lineages in which *amoA* genes are known to be present (*SI Appendix, SI Materials and Methods*). In striking support of the *amoA* findings, the 16S rRNA analysis also suggested an initial rapid increase in global diversification rate that was associated with similar major rate shifts

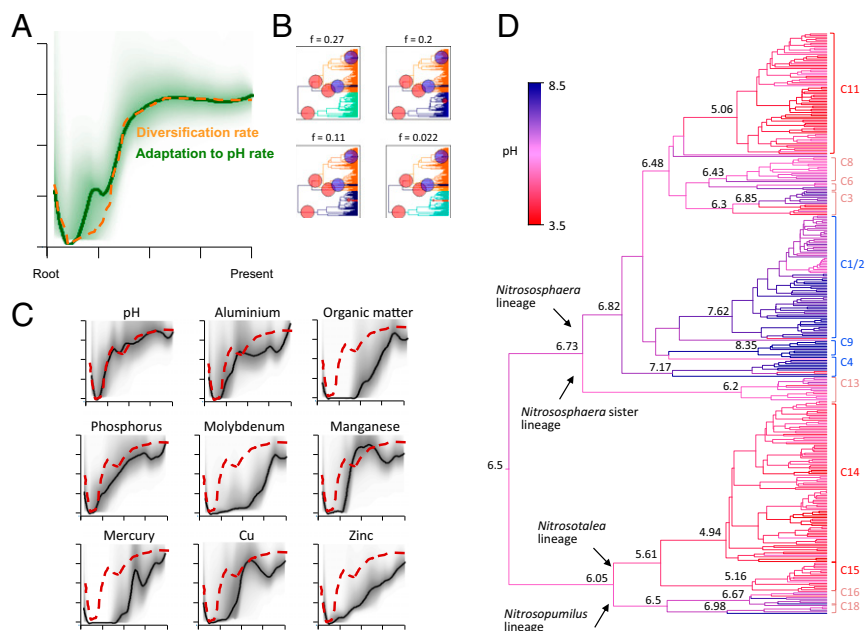
toward higher diversification at the base of the thaumarchaeotal radiation (*SI Appendix, Fig. S7*). Again, the 16S rRNA analysis provides support for an initial radiation event that was followed by maintenance of relatively high diversification rates across the remainder of thaumarchaeotal evolution (*SI Appendix, Fig. S7B*). In slight contrast to *amoA*, the 16S rRNA analysis also supported a modest decrease in diversification rate approaching the present day (*SI Appendix, Fig. S7B*). However, if we assume that less global diversity was represented (<0.75; *SI Appendix, Fig. S8*), the diversification rate is inferred to be stable or slightly increasing, as observed for *amoA*. This scenario is likely true, in view of the reduced sequencing depth used in the 16S rRNA 454 approach (these primers also targeted non-AOA thaumarchaeotal groups and, to a lesser extent, some Euryarchaeota) (27), reducing the present AOA diversity obtained and thereby undersampling the true modern diversity.

Thus, with the use of independent gene markers, there is support for an early radiation within Thaumarchaeota, with stably high subsequent diversification rates over hundreds of millions of years of evolution.

**Coupling of Environmental Adaptation to Diversification.** As pH has a major impact on the ecology of extant Thaumarchaeota (9), we postulated that this environmental variable contributed to the thaumarchaeotal diversification regime. We therefore reconstructed rates of pH adaptation across thaumarchaeotal evolution in the BMM framework (13–15). Our reconstructions of adaptation were based on estimates of pH preference of extant Thaumarchaeota, considered as the pH of the soil from which the *amoA* sequences were isolated. This approach requires the assumptions that the organisms are most likely to be present in soils with pH close to their optimal pH for growth and that the fitness of sampled organisms is reflected in *amoA* sequence abundance; in other words, *amoA* sequences that represent free DNA or dormant cells should be highly underrepresented in comparison with well-adapted replicating organisms. Further, we assumed that the high level of sampling sufficiently reduced the significance of potential effects of spatial and temporal heterogeneity in soil pH.

Remarkably, with the 370-sequence *amoA* dataset, our BMM analyses indicated that the rate of change of pH adaptation was tightly coupled to thaumarchaeotal diversification, including the same three basal rate shifts described earlier (Fig. 3 *A* and *B* and *SI Appendix, Fig. S3B*). However, it is important to note that pH and a number of environmental factors may be interdependent, potentially confounding inferences surrounding the role of pH per se. For 181 of the 370 *amoA* sequences in our dataset, a broader range of quantitative environmental data were available that are potentially linked to pH (*SI Appendix, Table S2*). These sequences were spread across the *amoA* tree, enabling us to test the hypothesis that pH adaptation rates are more tightly coupled with diversification rates than other environmental variables by performing additional BMM analyses on this reduced 181-sequence phylogeny. Importantly, the diversification and pH adaptation analyses were congruent across the 181- and 370-sequence trees, indicating that the removal of modern diversity from the larger tree did not affect the observed association between diversification and pH adaptation (Fig. 3C). Although all other tested environmental factors also showed an increase in the rate of putative adaptation across the period of thaumarchaeotal evolution, none tracked diversification rate as clearly as pH (Fig. 3C). For several factors, including organic matter, manganese, molybdenum, copper, and mercury, a rapid period of phenotypic change is inferred, but, unlike pH, this occurred long after the initial thaumarchaeotal radiation event (Fig. 3C). For aluminum, phosphorus, and zinc, rates of phenotypic adaptation initially increase at the same time as the onset of the initial radiation, but at much lower rates than pH, which closely matched the rate of diversification (Fig. 3C).





**Fig. 3.** Evolutionary heterogeneity in rates of environmental adaptation in terrestrial Thaumarchaeota inferred from the *amoA* 370-sequence tree within the BAMM framework. There is evidence that diversification (Fig. 2) is coupled to pH adaptation at two levels: (A) comparing the global rate of pH adaptation through time (green line) to the equivalent data for diversification rates (orange dotted line; taken from Fig. 2B) and (B) comparing the most probable phenotypic rate-shift configurations with equivalent diversification rate-shift data (Fig. 2C). (C) Equivalent analyses were performed for eight additional environmental factors on a smaller *amoA* tree of 181 sequences. (D) Ancestral pH preferences are shown for the 370-sequence *amoA* tree based on a ridge regression approach (28), with estimates of ancestral pH provided at key nodes.

Interestingly, although not as clearly correlated with diversification as pH, rates of phenotypic evolution linked to aluminum and phosphorus levels tracked the global diversification rate across thaumarchaeotal evolution (Fig. 3C).

**Changes in pH Specialization at the Base of the Thaumarchaeotal Radiation.** To further explore the hypothesis of a link between pH adaptation and diversification, we reconstructed ancestral soil pH adaptation across the 370-sequence *amoA* tree with the use of a recently developed method that models phenotypic evolution for every branch in a tree by using ridge regression, an extension of ordinary least-squares regression that accounts for phylogenetic structure (28). This analysis suggests that the thaumarchaeotal common ancestor was adapted to a pH of approximately 6.5 and that there were early shifts toward lower and higher pH preferences in the respective ancestors of the *Nitrosotalea/Nitrosopumilus* and *Nitrososphaera* lineages (Fig. 3D). Further, these results suggest that the specialized acidophilic and alkaliphilic clusters (9) arose independently from neutrophilic ancestors more recently in thaumarchaeotal evolution (Fig. 3D).

## Discussion

It is clearly important to understand the evolutionary processes contributing to the long-term ecological success of microbes and their associated ecosystem functions. Experimental evolution and population genomics are providing new insights into how mutation, selection, and drift shape microbial evolution over short timescales, but these approaches have less to say about long-term evolutionary dynamics over geological timescales, or the microbial equivalents of the patterns that paleontologists trace in the fossil record. In this work, we integrated recently developed Bayesian comparative phylogenetic approaches with contemporary environmental data on soil composition to test a key hypothesis about thaumarchaeotal evolution. Modern AOA communities are structured accordingly to environmental pH (9), raising the hypothesis that pH was an important factor in the long-term

evolution of terrestrial Thaumarchaeota, one of the most abundant of the 10 currently recognized archaeal phyla (29).

Our results support this hypothesis as, of nine environmental factors tested, pH adaptation was the only one strikingly coupled to the rate of diversification (Fig. 3). This is consistent with a scenario in which pH adaptation was a positive factor contributing to an early radiation during thaumarchaeotal evolution. However, our results cannot eliminate the possibility that other physiological innovations arose at a similar time that promoted diversification that were correlated to or unrelated to pH. Indeed, our comparative phylogenetic analyses point to periods of environmental adaptation involving several factors theoretically linked to pH, although these periods were invariably more detached from the major initial thaumarchaeotal radiation (Fig. 3). It is important to note here that our sampling was designed to represent a wide range of soil pH, presumably recapturing a broad range of physiological adaptation to pH. Conversely, for the other factors tested, the range of environmental variation in our samples might be suboptimal for the detection of adaptation. Therefore, further work that more fully explores the environmental drivers of thaumarchaeotal evolution would be a welcome addition to the present findings focused on pH.

Looking more deeply at the hypothesis that pH was an important factor promoting thaumarchaeotal diversification, our results suggest that the lineage ancestor was a neutrophile that initially split into two major lineages that showed preferences toward acid (*Nitrosopumilus/Nitrosotalea*) and alkaline (*Nitrososphaera*) conditions (Fig. 3D). Subsequently, pH adaptation was inferred to have occurred rapidly, which may have promoted niche exploitation and allopatric isolation and hence new lineage formation. Interestingly, as two other archaeal phyla likely arose at near-neutral pH (*Euryarchaeota*; pH  $\geq 6$ ) or in moderately acidic environments (*Crenarchaeota*; pH 4–6) (30), we can now infer that the common ancestor of archaea was probably a hyperthermophile (31, 32) with neutral pH preference.

As these analyses represent one of the first applications of Bayesian modeling of long-term evolutionary processes in prokaryotes, it is important to keep associated caveats in mind. In particular, our analyses may have been affected by biased or incomplete sampling of extant thaumarchaeotal diversity, although independent approaches suggested this was not a major concern. Sensitivity analyses (*SI Appendix*, Fig. S5) suggested that our main findings were robust to random incomplete sampling. In addition, our conclusions were consistent across diversification analyses performed on a full range of sequences available within public databases using two independent phylogenetic markers: archaeal *amoA* (*SI Appendix*, Fig. S6), which is unique to ammonia oxidizing archaea; and 16S rRNA (*SI Appendix*, Figs. S7 and S8). Nevertheless, certain environments (e.g., hyperthermophilic, halophilic, or heavy metal-contaminated) may contain additional uncharacterized AOA diversity. A second potential caveat concerns variation in extinction rates during thaumarchaeotal evolution. Extinction rates are difficult to model on phylogenetic trees, even for multicellular eukaryotes, for which extinction is a frequent and reasonably well-characterized process (33, 34). This is compounded by our poor understanding of extinction in the prokaryotic world, which may be less frequent because of large population sizes, propensity for LGT, fast evolutionary rates, ease of dispersal, and the ability to form dormant or resistant states (e.g., ref. 35). Further, we currently lack a quantitative understanding of the factors that might influence extinction rates and how they vary among prokaryotic groups or between prokaryotes and eukaryotes. Importantly, the Bayesian methods we used provide a natural framework for incorporating uncertainty about these rates, and indeed the large credibility intervals surrounding these parameter estimates (Fig. 2B) suggest that our inferences were robust to a large range of extinction rates. Nevertheless, we cannot exclude the possibility that high extinction rates during early thaumarchaeotal evolution impacted the shape of our *amoA* phylogeny and therefore the inference of diversification rates through time. Nonetheless, it seems less likely that these issues would have affected reconstructions of environmental adaptation, which also strongly depend on contextual data measured within extant lineages.

Our analyses stand in contrast to the limited number of previous studies that examined diversification in microorganisms. Analyses that used the  $\gamma$ -statistic (36) suggest that diversification rates have decreased during the evolution of many free-living bacteria and archaea (37). Another approach, the likelihood of branching times, suggested a rapid early diversification followed by a decrease in rate for the obligate endosymbiont *Borrelia burgdorferi* clade (38). Such results suggest that previously available niches have been filled by microorganisms, a situation recaptured in experimental evolution studies with bacteria (39, 40). This is akin to the classic adaptive radiation model described in multicellular eukaryotes, whereby an initial burst of speciation is followed by declining diversification through time as new niches become exhausted (41, 42). The analyses that used *amoA* sequences invariably suggested that diversification rates have remained stable or even steadily increased from the apex rates of the original radiation event (43) (Fig. 1, *Inset*, Fig. 2B, and *SI Appendix*, Figs. S5 and S6). Although 16S rRNA analysis did imply a minor decrease in diversification rate, this result was likely a product of undersampling (*SI Appendix*, Figs. S7 and S8). With realistic sampling assumptions for 16S rRNA, our results were entirely congruent with the pattern observed for *amoA* (*SI Appendix*, Fig. S6). Such long-term maintenance of high diversification rates does not support a classical model of niche filling (44) and may reflect a higher rate at which niches become available for prokaryotes. Given the long-term co-occurrence of high diversification and apparent environmental adaptation rates after early radiation (Fig. 3), our data lend support to this idea in terms of terrestrial niches associated with variable ecological

characteristics. Another interesting possibility is that high ongoing diversification rates in Thaumarchaeota are associated with high levels of niche switching without extensive specialization, which has been suggested for certain eukaryotes (45–47), or high levels of energy source switching by assimilating different substrates such as inorganic or organic nitrogen compounds (48, 49). Our work therefore demonstrates how approaches that combine contemporary molecular and environmental data can be used to compare evolutionary processes between prokaryotes and eukaryotes, and raises important questions about the similarities and differences in the long-term drivers of diversification across the tree of life.

## Materials and Methods

**Phylogenetic Analyses.** Because very few thaumarchaeotal genomes have been published, we used the Roche 454 platform to sequence thaumarchaeotal *amoA* (9) and 16S rRNA diversity (27) from a range of UK soils. These data were used to generate three separate sequence alignments, two for *amoA* (370 and 613 sequences; both with 388 aligned nucleotide sites) and one for 16S rRNA (508 sequences; 568 aligned nucleotide sites). These alignments were built from the 454 data used alone (*amoA* 370-sequence alignment) or after merging with a wider representation of nonredundant sequences available from GenBank or the Silva database (50) (*amoA* 613-sequence alignment and 16S rRNA alignment; *SI Appendix*). Separate *amoA* alignments were necessary because downstream analyses required environmental data unavailable in the public datasets. Before phylogenetic analysis, redundant sequences were dereplicated at defined cutoffs by using Uclust (51) (*SI Appendix*), and the presence of recombination was checked with RDP4 (52) before recombinant sequences were removed if necessary. A recombination event was accepted in RDP4 when statistically significant ( $P < 0.01$ ) in three of the four following methods: RDP, GENECONV, MaxChi, and Bootscan. Bayesian relaxed molecular clock phylogenetic analysis were performed in BEAST (Bayesian Evolutionary Analysis Sampling Trees) version 1.7 (53) after screening alignments for mutational saturation (54) and selecting the best substitution model in PartitionFinder (55). For *amoA*, the third codon position (CP) was excluded because of evidence of saturation, and CP1 and CP2 were separately modeled under GTR+G with equal base frequencies. The 16S rRNA was modeled under GTR+G+I with equal base frequencies. A Yule speciation prior (56) and uncorrelated lognormal relaxed clock model (20) was set, and two Markov chain Monte Carlo (MCMC) chains were run for between 100 and 500 million steps, sampling every 10,000 steps. Convergence was confirmed by using Tracer version 1.5 ([tree.bio.ed.ac.uk/software/tracer/](http://tree.bio.ed.ac.uk/software/tracer/)), and effective sample sizes exceeded 200 for all parameters after the first 10% of steps were removed. Maximum clade credibility trees from converged MCMC runs were generated by using TreeAnnotator version 1.7 (53).

The pH specialization of phylogenetic clusters was characterized as described previously (9) using generalized additive modeling with the mgcv package (57) in R (58).

**Comparative Phylogenetics.** A lineage-through-time plot and  $\gamma$ -statistic analysis were performed with the 370-sequence *amoA* tree using LASER (59) in R (58). Four separate phylogenetic trees were then analyzed by using the BMM program (13, 14). This included the three trees described earlier (i.e., 370- and 613-sequence *amoA* tree and 508-sequence 16S rRNA tree) and an additional *amoA* tree generated by pruning the 370-sequence tree. For the original 370-sequence *amoA* tree derived from 454 sequencing (9), the pH of soil samples was evenly distributed across the full range (pH 3.48–8.74), but this was not the case for samples on which the 613-sequence *amoA* and 508-sequence 16S rRNA trees were based. In addition, for 181 sequences embedded within the 370-sequence *amoA* tree, a wider range of environmental data were available from the same sampled soils (quantitative measures of organic matter and aluminum, phosphorus, molybdenum, manganese, mercury, copper, and zinc levels; *SI Appendix*, Table S2). Therefore, a new 181-sequence *amoA* tree was obtained by removing tips with missing environmental data, which were distributed across the whole tree. Separate BMM analyses of diversification rates were performed for all four trees and phenotypic evolutionary rates for the 370- and 181-sequence *amoA* trees, using the full range of contemporary environmental data available. All phenotypic rate analyses were based on soil mean values defined for each tip of the tree based on dereplicated sequences. MCMC simulations in BMM were run for 100 million and 1,000 million steps for diversification and phenotypic analyses, respectively, sampling parameters every 10,000 or 100,000 steps, respectively. A series of scripts was used to analyze the MCMC data and confirm convergence of the chains within the

R package BAMMtools (60). pH preferences were reconstructed at each node of the 370-*amoA* tree using the RidgeRace algorithm (28), a method that explicitly allows heterogeneity in phenotypic rates across all branches in a tree.

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