

Unexpected host dependency of Antarctic Nanohaloarchaeota

Joshua N. Hamm^a, Susanne Erdmann^{a,1}, Emiley A. Eloë-Fadrosch^b, Allegra Angeloni^a, Ling Zhong^c, Christopher Brownlee^d, Timothy J. Williams^a, Kirston Barton^e, Shaun Carswell^e, Martin A. Smith^{e,f}, Sarah Brazendale^{a,2}, Alyce M. Hancock^{a,3}, Michelle A. Allen^a, Mark J. Raftery^c, and Ricardo Cavicchioli^{a,4}

^aSchool of Biotechnology and Biomolecular Sciences, University of New South Wales, Sydney, NSW 2052, Australia; ^bDepartment of Energy, Joint Genome Institute, Walnut Creek, CA 94598; ^cBioanalytical Mass Spectrometry Facility, University of New South Wales, Sydney, NSW 2052, Australia; ^dBiological Resources Imaging Laboratory, University of New South Wales, Sydney, NSW 2052, Australia; ^eKinghorn Centre for Clinical Genomics, Garvan Institute of Medical Research, Darlinghurst, NSW 2010, Australia; and ^fSt. Vincent's Clinical School, University of New South Wales, Sydney, Darlinghurst, NSW 2010, Australia

Edited by Norman R. Pace, University of Colorado Boulder, Boulder, CO, and approved June 5, 2019 (received for review March 25, 2019)

In hypersaline environments, Nanohaloarchaeota (Diapherotrites, Parvarchaeota, Aenigmarchaeota, Nanoarchaeota, Nanohaloarchaeota [DPANN] superphylum) are thought to be free-living microorganisms. We report cultivation of 2 strains of Antarctic Nanohaloarchaeota and show that they require the haloarchaeon *Halorubrum lacusprofundi* for growth. By performing growth using enrichments and fluorescence-activated cell sorting, we demonstrated successful cultivation of *Candidatus Nanohaloarchaeum antarcticus*, purification of *Ca. Nha. antarcticus* away from other species, and growth and verification of *Ca. Nha. antarcticus* with *Hrr. lacusprofundi*; these findings are analogous to those required for fulfilling Koch's postulates. We use fluorescent in situ hybridization and transmission electron microscopy to assess cell structures and interactions; metagenomics to characterize enrichment taxa, generate metagenome assembled genomes, and interrogate Antarctic communities; and proteomics to assess metabolic pathways and speculate about the roles of certain proteins. Metagenome analysis indicates the presence of a single species, which is endemic to Antarctic hypersaline systems that support the growth of haloarchaea. The presence of unusually large proteins predicted to function in attachment and invasion of hosts plus the absence of key biosynthetic pathways (e.g., lipids) in metagenome assembled genomes of globally distributed Nanohaloarchaeota indicate that all members of the lineage have evolved as symbionts. Our work expands the range of archaeal symbiotic lifestyles and provides a genetically tractable model system for advancing understanding of the factors controlling microbial symbiotic relationships.

archaea | symbiont | DPANN

Recent exploration into the genomic landscape of the domain Archaea has shed light on the ecological and evolutionary prominence of uncultivated lineages (1). The Nanohaloarchaea were first identified from metagenomic data as a class of uncultivated halophilic archaea composed of 6 clades (2) and were subsequently placed in the phylum Nanohaloarchaeota within the Diapherotrites, Parvarchaeota, Aenigmarchaeota, Nanoarchaeota, Nanohaloarchaeota (DPANN) superphylum (3). The lineage has since been identified in data from a range of hypersaline environments including: Australian thalassohaline lake (2, 4), Spanish saltern (5), Russian soda brine (6), Californian saltern (7), and Chilean halite (8). From these data, 1 complete metagenome-assembled genome (MAG; *Candidatus [Ca.] Nanopetramus SG9*) (8) and 12 incomplete MAGs have been generated. Nanohaloarchaeal cells in environmental samples appear as small cocci with an average diameter of ~0.6 μ m (0.1 to 0.8 μ m size range) (2, 4) and a genome size smaller (e.g., 1.1 Mb for *Ca. Nanopetramus SG9*) (8) than haloarchaea (phylum Euryarchaeota, class Halobacteria; ~3 to 4 Mb).

Despite the monophyly of the DPANN superphylum being called into question (9), members, such as *Candidatus Nanoarchaeum equitans* (0.4- μ m diameter, <0.5 Mb) (10), *Candidatus Nanopusillus*

acidilobi (<0.3- μ m diameter, ~0.6 Mb) (11), *Candidatus Parvarchaeum acidophilus* (0.6- μ m diameter, <1 Mb) (12), and *Candidatus Mancarchaeum acidophilum* (~1- μ m diameter, ~1 Mb) (13), have all been shown to possess small cell and genome sizes; these are traits that have been proposed to be typical of all DPANN phyla (3). Due to their reduced genomic capacity, these Nanoarchaeota and Parvarchaeota require cell-cell contact with larger (10–12) or similarly (13) sized hosts to proliferate and can be described as ectoparasites (11). The DPANN *Candidatus* Huberarchaeum crystalense has also been described as a possible epibiotic symbiont of *Candidatus Altiarchaeum* sp. (14). Although most DPANN genomes lack some biosynthetic pathways required for autonomous growth, it has been reasoned that certain genetic traits (diversity generating retroelements) may enhance the ability of DPANN lineages (e.g., Pacearchaeota and Woesearchaeota) to

Significance

We demonstrate that *Candidatus Nanohaloarchaeum antarcticus* requires *Halorubrum lacusprofundi* for growth, illustrating that Nanohaloarchaeota require a host rather than being free living as previously proposed. Developing the means of cultivating Nanohaloarchaeota in the laboratory provides the capacity to advance understanding of how archaea interact and the factors that control their symbiotic relationship (e.g. mutualism, commensalism, antagonism). Our findings amplify the view that Antarctic lakes are a treasure trove for the discovery of microbes with previously unknown properties.

Author contributions: J.N.H. and R.C. designed research; J.N.H., S.E., A.A., L.Z., C.B., K.B., S.C., M.A.S., S.B., A.M.H., and M.J.R. performed research; J.N.H., E.A.E.-F., T.J.W., M.A.A., and R.C. analyzed data; and J.N.H., S.E., E.A.E.-F., A.A., L.Z., C.B., T.J.W., K.B., S.C., M.A.S., S.B., A.M.H., M.A.A., M.J.R., and R.C. wrote the paper.

The authors declare no conflict of interest.

This article is a PNAS Direct Submission.

This open access article is distributed under [Creative Commons Attribution License 4.0 \(CC BY\)](#).

Data deposition: The mass spectrometry data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with project name Cultivation of an Antarctic Nanohaloarchaea (accession no. [PXD010625](#)). Integrated Microbial Genomes identification numbers are [3300005925](#), [2643221421](#), [3300028663](#), [3300028522](#), [2791354821](#), and [3300031914](#).

¹Present address: Department of Microbiology, Max Planck Institute for Marine Microbiology, 28359 Bremen, Germany.

²Present address: Private address, Pegarah, TAS 7256, Australia.

³Present address: University of Tasmania Institute of Marine and Antarctic Studies, Antarctic Gateway Partnership and Antarctic Climate & Ecosystem Research Centre, Battery Point, TAS 7004, Australia.

⁴To whom correspondence may be addressed. Email: r.cavicchioli@unsw.edu.au.

This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1905179116/-DCSupplemental.

Published online June 28, 2019.

have dynamic interactions with their hosts that possibly enable shifts between mutualism, predation, and parasitism (15).

In contrast to host dependence, analyses of an ~1.24-Mb single amplified genome of *Candidatus Iainarchaeum andersonii* (Diapherotrites) (16) and ~1.2-Mb metagenome assemblies of *Candidatus Nanosalina* sp. J07AB43 and *Candidatus Nanosalarum* sp. J07AB56 (Nanohaloarchaea) (2) have drawn the conclusion that these DPANN members could be capable of autonomous growth. The Nanohaloarchaea were predicted to be free living based on their genome size being larger than other known DPANN representatives and nanohaloarchaeal cells not being observed to associate with potential host cells in environmental samples (2). The view that Nanohaloarchaeota may be capable of leading an independent lifestyle is reflected in the current literature (17).

Here, we report the cultivation of Antarctic strains of nanohaloarchaea (proposed as *Candidatus Nanohaloarchaeum antarcticus*) from 2 different hypersaline lakes and show that an Antarctic haloarchaeon, *Halorubrum lacusprofundi*, is required for growth. Examination of the nanohaloarchaea–haloarchaea interactions and analysis of available MAGs of nanohaloarchaea lead us to conclude that Nanohaloarchaeota have evolved as symbionts requiring hosts rather than as free-living cells.

Cultivation of Antarctic Nanohaloarchaeota

Enrichment cultures were previously established using hypersaline water from Rauer 1 Lake, East Antarctica, resulting in the isolation of *Hrr. lacusprofundi* strain R1S1 (18) (SI Appendix, Table S1). Metagenome data of an enrichment culture revealed high relative abundance of *Hrr. lacusprofundi* (47%) and Nanohaloarchaeota (43%) (SI Appendix, Fig. S1A and Table S1). From guanine-cytosine (GC) binning, iterative assembly, and additional PCR sequencing, 2 scaffolds resolved representing a MAG for Rauer 1 Nanohaloarchaeota, herein referred to as *Ca. Nha. antarcticus* R1 (“Nha-R1”). Transmission electron microscopy (TEM) of the enrichment culture (SI Appendix, Fig. S1A–D) and 0.22- μ m filtrate (SI Appendix, Fig. S1E and F) revealed small cocci (0.3 to 1.0 μ m) resembling the morphology of nanohaloarchaea (2, 4), including small cocci associated with larger, pleomorphic rod-shaped cells characteristic of *Hrr. lacusprofundi* (SI Appendix, Fig. S1A and C) (18–20).

While Nha-R1 grew in liquid enrichment and on solid medium, multiple attempts to propagate Nha-R1 using the 0.22- μ m filtrate in liquid or on solid medium were unsuccessful (Materials and Methods). Isolation attempts included the use of spent media from the Nha-R1 enrichment, fresh medium supplemented with a cell extract of the enrichment, and a diffusion chamber inoculated with the Nha-R1 filtrate and placed into a growing enrichment culture. The growth experiments provided nutrients from the enrichment community while preventing Nha-R1 from having physical contact with other species, indicating that cell–cell contact was required for Nha-R1 to proliferate.

To confirm the cultivability of Nanohaloarchaeota and obtain a second MAG, an enrichment culture was established using water from Club Lake, East Antarctica (see Fig. 2). TEM revealed morphologies similar to those from the Rauer 1 Lake enrichment (SI Appendix, Fig. S2). After metagenome sequencing (SI Appendix, Table S1), a single scaffold was obtained, which had >99% average nucleotide identity (ANI) and an identical 16S ribosomal ribonucleic acid (rRNA) gene sequence to the Nha-R1 MAG, indicating that the enrichments contain strains of the same Nanohaloarchaeota species. The Club Lake Nanohaloarchaeota *Ca. Nha. antarcticus* C is referred to as “Nha-C,” and its metagenome “Nha-Ce” denotes *Ca. Nha. antarcticus* Club Lake enrichment (SI Appendix, Table S1). *Hrr. lacusprofundi* (41%) and Nanohaloarchaeota (26%) were the 2 most abundant taxa in the enrichment (SI Appendix, Fig. S1B and Table S1).

Growth of Nha-C with *Hrr. lacusprofundi* ACAM34-hmgA

In the enrichments from both lakes, *Hrr. lacusprofundi* was the most abundant species (Fig. 1A and B), indicating that it could be the host. The up-regulated 3-hydroxy-3-methylglutaryl coenzyme A reductase gene (*hmgA*) gene in plasmid pJWID1 confers resistance to 2.5 μ g mL^{−1} pravastatin in *Hrr. lacusprofundi* ACAM34 (21). Pravastatin inhibits HmgA and hence, lipid synthesis via the mevalonate pathway, which is absent from the *Ca. Nha. antarcticus* MAGs (see below). To inhibit the growth of other archaea in the enrichment, the transformed ACAM34 strain was grown with an aliquot of the Club Lake enrichment in pravastatin (2.5 μ g mL^{−1}) and bacterial antibiotic (ampicillin 100 μ g mL^{−1}, chloramphenicol 25 μ g mL^{−1}, kanamycin 50 μ g mL^{−1}, tetracycline 10 μ g mL^{−1}) containing media (Fig. 2). To provide stronger selection pressure for *Hrr. lacusprofundi* ACAM34, after several rounds of growth, pravastatin concentration was increased up to 10 μ g mL^{−1}, and additional archaeal antibiotics were added (mevinolin 0.02 μ g mL^{−1}, simvastatin 0.01 μ g mL^{−1}). This resulted in selection of a strain (ACAM34-hmgA) where the *hmgA* gene from the plasmid (flanked by *Hrr. lacusprofundi* transposases) relocated into the chromosome, and all other plasmid genes were lost or rendered nonfunctional (SI Appendix, Fig. S3).

The metagenome of cultures (grown with 10 μ g mL^{−1} pravastatin) harvested during midlog phase growth showed a high relative abundance of Nha-C (30%) and *Hrr. lacusprofundi* (56%), with a relatively low abundance of *Natrinema* (8%) and bacterial *Marinobacter* (6%) (SI Appendix, Fig. S1C and Table S1). The *Ca. Nha. antarcticus* MAG is referred to as “Nha-CHI,”

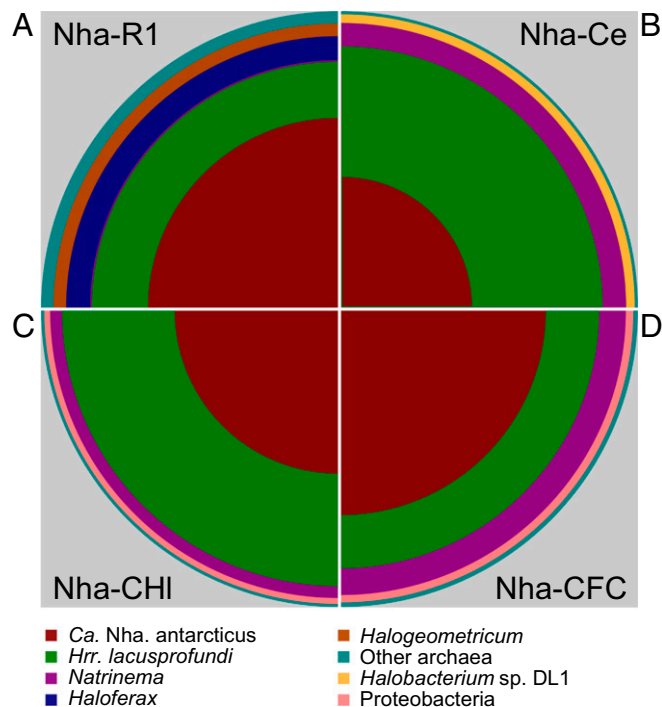
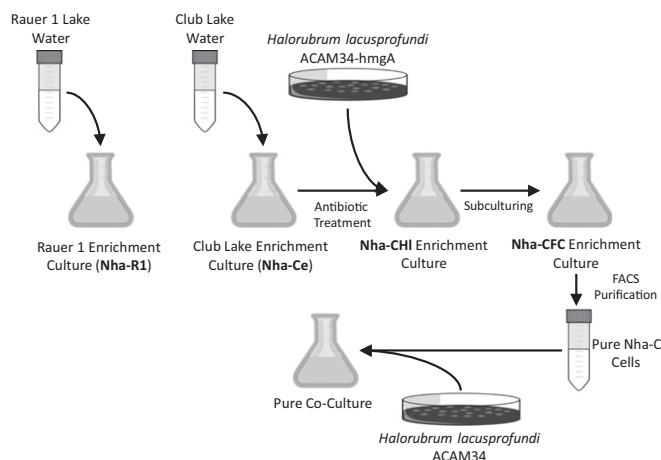


Fig. 1. Relative abundances of the major taxa present in *Ca. Nha. antarcticus* enrichment cultures. Metagenomes for Nha-R1 (A), Nha-Ce (B), Nha-CHI (C), and Nha-CFC (D). Quadrants show relative abundances of the major taxa identified in each enrichment metagenome. Abundances were calculated using average read depth across a set of universally distributed single-copy genes. Area of the colored sections is directly proportional to the relative abundance of each taxonomic unit. The only taxa identified in all 4 metagenomes were *Ca. Nha. antarcticus* (Nha-R1: 41%; Nha-Ce: 19%; Nha-CHI: 30%; Nha-CFC: 47%), *Hrr. lacusprofundi* (Nha-R1: 28%; Nha-Ce: 59%; Nha-CHI: 56%; Nha-CFC: 29%), and *Natrinema* sp. (Nha-R1: 1%; Nha-Ce: 14%; Nha-CHI: 8%; Nha-CFC: 16%).



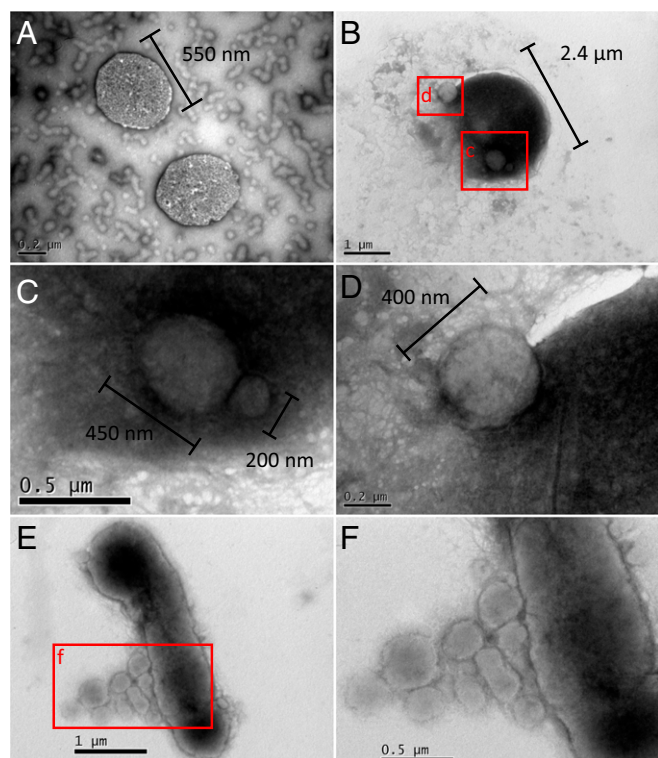


Fig. 6. TEM of Nha-C FACS cells with *Hrr. lacusprofundi* ACAM34. Small individual cells consistent with being Nha-C (A). A single and “budded” cell (putative Nha-C) intimately associated with a larger cell (putative *Hrr. lacusprofundi*) (B–D). The budded structure may arise from cell division occurring while Nha-C cells are attached to *Hrr. lacusprofundi* (D). Multiple small cells (putative Nha-C) seem to be associated with a larger cell (putative *Hrr. lacusprofundi*) surrounded by possible extracellular material (E and F). The appearance of extracellular material occurred in other images of FACS cultures (SI Appendix, Fig. S14), including in an image of a large cell (putative *Hrr. lacusprofundi*) that appears to have lysed (SI Appendix, Fig. S14E).

Possible Molecular Mechanisms of Interaction

The most distinctive feature of nanohaloarchaeal genomes is the existence of genes encoding very long (up to 8,553 amino acids) “SPEARE” proteins, which contain serine protease, adhesion, and restriction endonuclease domains (Fig. 7A and SI Appendix, Table S2). The *Ca. Nha. antarcticus* SPEARE protein is 5,998-amino acids long, with *Ca. Nanopetramus* SG9 possessing 8,553-, 4,057-, 3,315-, and 655-amino acid versions (Fig. 7B). Matches to SPEARE proteins were also identified in 3 incomplete assemblies (~1 Mbp, PSG99524.1, halite; 27 kbp, PSG99792.1, halite; 9 kbp, RLG14629.1, deep sea hydrothermal vent sediments), and a high identity match was identified in the Lake Tyrrell metagenome that the assemblies derived from (Fig. 7B) (2). The *Ca. Nanopetramus* SG9 8553 amino acid protein is the second largest protein described for Archaea, exceeded only by halomucin, a sugar binding protein from *Haloquadratum walsbyi* (~9,000 amino acids) (27). The 4 *Ca. Nanopetramus* SG9 SPEARE genes combined represent 4% of the genome.

Most of the SPEARE proteins are predicted to have the majority of their length extracytoplasmic, with a transmembrane domain toward the C terminus anchoring the protein to the membrane and the C-terminal region positioned inside the cytoplasm (Fig. 7A). The domain structure of the 3,315-amino acid *Ca. Nanopetramus* SG9 protein is reversed, and the transmembrane domain is toward the N terminus (Fig. 7B).

The most conserved region of the SPEARE proteins is the intracellular portion, which contains domains characteristic of

type III restriction enzymes, suggesting a role in DNA degradation. Similar sequences were identified in assemblies of the DPANN lineages Woesearchaeota, Aenigmarchaeota, and Micrarchaeota as well as Altiarchaeales (SI Appendix, Fig. S17 and Table S3) but not in Nanoarchaeota or Parvarchaeota.

The extracytoplasmic portions of the SPEARE proteins display more sequence variation, but all extracytoplasmic portions possess at least 1 laminin-G domain and multiple other adhesion domains (Fig. 7B and SI Appendix, Table S2). The *Ca. Nha. antarcticus* protein contains distinct serine protease (amino acids 1 to 1,500) and bacteriotoxin (3,300 to 4,800) domains (Fig. 7A). Tertiary structure of the toxin domain is predicted to be similar to the bacterial BC toxin subunit of the ABC toxin complex that mediates formation of pores in the membrane of targeted cells (28). The highest identity (25 to 35%) was to predicted adhesion proteins from several bacterial genomes. Notably, many of the bacterial lineages (*Bacteriovorax*, Elusimicrobia, members of the Candidate Phyla Radiation) are characterized by or predicted to have lifestyles in which they attach to and parasitize other organisms (29–31).

Proteomic analysis demonstrated that the Nha-C SPEARE protein was synthesized (SI Appendix, Table S4). The protein was most abundant in polyacrylamide gel fractions >315 kDa, with mass spectrometry (MS) analysis detecting 81 unique peptides (18% sequence coverage) of the ~550-kDa extracytoplasmic portion of the protein (SI Appendix, Fig. S18). Peptides to the transmembrane and cytoplasmic portions were identified only in size fractions <315 kDa (SI Appendix, Fig. S18). The presence of the cytoplasmic and transmembrane-extracytoplasmic portions in distinct size ranges may be the result of posttranslational processing or the protein preparation protocol (bead beating).

Knowing that the protein is synthesized and remains largely (or fully) intact prompts speculation about its possible function. The adhesion domains could facilitate physical interactions, with the host’s S layer degraded through serine protease activity. The anchoring domain may help position the bacterial toxin-like domain correctly to form a pore that enables transport in and/or out of the cytoplasm. Transfer of genetic material into the nanohaloarchaeal cell could be degraded by the intracellular restriction enzyme domain. Such activity may serve to reduce possible negative impacts of taking up DNA (e.g., mutation via recombination) and/or provide a source of nucleotides for replication and energy conservation.

In addition to the SPEARE protein, proteins annotated as subunits FlaI, FlaJ, and archaellin were identified in the Nha-C proteome (SI Appendix, Table S4). By themselves, these subunits are not sufficient to form a functional archaellum, and the other requisite subunits are not present in the *Ca. Nha. antarcticus* MAG. The genes are homologous to type IV pilus proteins (PilB, PilC, and pilin), and adhesion domains (immunoglobulin folds and polycystic kidney disease domains) are present in the “archaellum.” Other DPANN lineages (Woesearchaeota and Diapherotrites) also possess these putative pilus-like structures, indicating that they may play a role in mediating the interactions between DPANN archaea and their hosts.

Metabolic and Cellular Capacity of Nanohaloarchaeota

Strong evidence for Nanohaloarchaeota host dependency relates to the absence of key biosynthetic pathways for essential compounds, such as lipids, amino acids, nucleotides, and cofactors (SI Appendix, SI Text). The mevalonate pathway genes for lipid precursor synthesis are conserved and recognizable in Archaea (32), and therefore, their absence is strong evidence that Nanohaloarchaeota are incapable of synthesizing phospholipids. The genomic and proteomic data are indicative of *Ca. Nha. antarcticus* having an aerotolerant, heterotrophic, fermentative metabolism as inferred previously for Nanohaloarchaeota (2), and a total of 458 proteins were detected in the proteome (38%

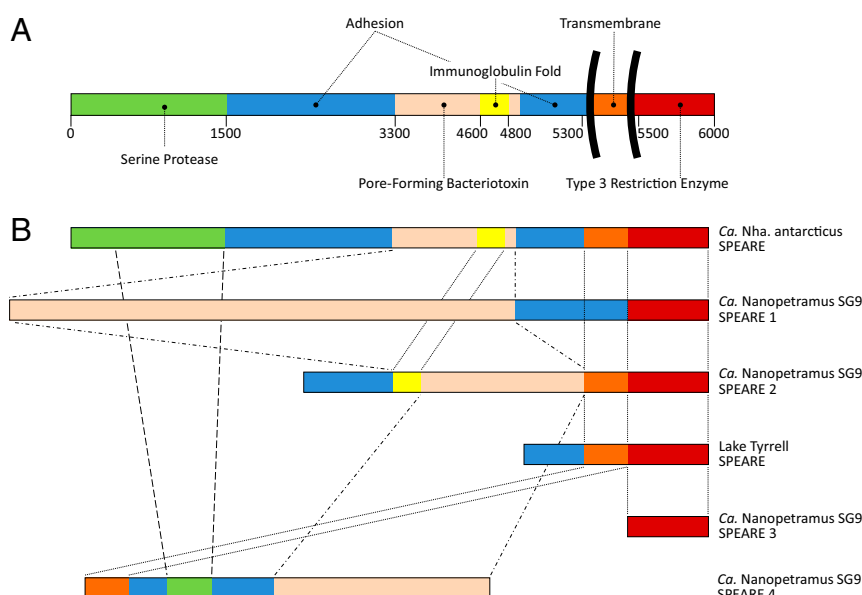


Fig. 7. Domain structure of SPEARE proteins. (A) Protein domains predicted for the 5,998 amino acid *Ca. Nha. antarcticus* SPEARE protein (IMG gene identification no. 2643306914; locus tag: NAR1_1133). (B) Domain structure comparison of SPEARE proteins from Nha-R1, *Ca. Nanopetramus* SG9 (8), and Lake Tyrrell metagenome data (2) depicted approximately to scale. *Ca. Nanopetramus* SG9 SPEARE 1 (8,553 amino acids; hypothetical protein AOV86_04780; accession no. AOV94740.1). *Ca. Nanopetramus* SG9 SPEARE 2 (4,057 amino acids; hypothetical protein AOV86_02335; accession no. AOV95205.1). Lake Tyrrell SPEARE (717 amino acids; IMG gene identification no. LTJ07AB_218510; locus tag: LTJ07AB_218510). *Ca. Nanopetramus* SG9 SPEARE 3 (3,315 amino acids; hypothetical protein AOV86_02330; accession no. AOV94739.1).

of protein-encoding genes) (*SI Appendix, Table S4*). Overall, the proteome is consistent with the genomic evidence that *Ca. Nha. antarcticus* can synthesize its own carbohydrates (including for storage) but otherwise, has extremely limited biosynthetic capabilities (*SI Appendix, SI Text*). Thus, *Ca. Nha. antarcticus* would require certain biopolymers from its host, including polypeptides and nucleic acids as sources of amino acids and nucleotides, respectively. Conceivably, *Ca. Nha. antarcticus* could gain access to essential metabolic products when it is attached to hosts, with surplus carbon stored as polysaccharides that could be mobilized when cells are nonattached. It is possible that *Hrr. lacusprofundi* may gain some benefit from by-products produced by *Ca. Nha. antarcticus* that the latter apparently cannot assimilate, such as ammonium or acetate (33, 34).

Genome Variation and Evolution of Nanohaloarchaeota

Metagenome read and contig mapping identified Nanohaloarchaeota in 2 Vestfold Hills lakes (Deep Lake and Club Lake) and 4 Rauer Island lakes (3, 6, 11, 13) (*SI Appendix, Figs. S19–S21*). The samples from Deep Lake represented 37 metagenomes spanning 8 y (December 2006 to January 2015) and covering a seasonal cycle (December 2013 to January 2015) and depth profile (2008: surface and 5, 13, 24, and 36 m) (26). Read coverage across the Deep Lake metagenomes was ~0.5%, similar to Club Lake, with the Rauer Island lakes having more variable coverage, and highest overall coverage (3.5%) was from Rauer 3 Lake (*SI Appendix, Fig. S19*). All of the lakes with Nanohaloarchaeota contained high levels of haloarchaea, with the highest representation in the Vestfold Hills lakes (26).

Contig and read coverage were high (average genome coverage 68%), although the relative abundance of Nanohaloarchaeota was low ($\leq 3.5\%$), and contigs had high identity ($>99\%$), illustrating that little genomic variation existed within the nanohaloarchaeal populations (*SI Appendix, Figs. S19–S21*). Short regions existed with high read depth (*SI Appendix, Figs. S20 D–G and S21*) and contained mobile elements (e.g., transposases) with high identity to Antarctic haloarchaea (e.g., 100% match to Halorubraceae

IS5-like element) (*SI Appendix, Table S5*), indicating that they arose through sharing with haloarchaea. Gaps between contigs (~270, 930, and 1,025 kb) coincided with low read recruitment (*SI Appendix, Figs. S20 D–G and S21*) and contained similar types of sequences (transposases, viral genes, hypothetical proteins), most of which had best matches to haloarchaea. Of note was a complete type 5 Bacteriophage Exclusion (BREX) system that was absent in Nha-CHI but present in Nha-R1 (*SI Appendix, Fig. S20C and Table S5*). BREX functions by inhibiting viral replication (35). One additional gene was present (2643307549) downstream from the BREX genes, which is annotated as conserved Nanohaloarchaeota hypothetical protein and may possibly be a Nanohaloarchaeota-specific BREX gene. The BREX cluster was flanked by a gene annotated as a viral integrase (2643307539 integrated microbial genomes [IMG] gene identification), with average coverage indicating that the BREX cluster itself may be part of a mobile element. The read depth coverage across all lake metagenomes was ~25% of average, indicating that the BREX-containing phylotype was present throughout all of the lakes in approximately 1/4 of the Nanohaloarchaeota population.

While genomic variation across the Antarctic Nanohaloarchaeota is minimal, the genomes of non-Antarctic Nanohaloarchaeota have much lower similarity ($\leq 70\%$ ANI, $<90\%$ 16S rRNA gene identity) (*SI Appendix, Fig. S22*), indicating that the other known nanohaloarchaeal lineages represent distinct genera from a range of diverse types of hypersaline environments. This level of diversity (i.e., genera) is similar to the diversity present within haloarchaea (36) and may arise within the Nanohaloarchaeota as a result of host specificity. If coevolution occurs, each lineage of Nanohaloarchaeota would be expected to interact with a specific lineage of haloarchaea. In this regard, we predict that a host for some of the Lake Tyrrell Nanohaloarchaeota is *Hqr. walsbyi*, as it is an abundant species of haloarchaea in the lake, and nanohaloarchaea appear in FISH images associated with square-shaped cells (figure 2 in ref. 2).

Concluding Remarks

Cultivation of *Ca. Nha. antarcticus* with its host *Hrr. lacusprofundi* represents successful laboratory cultivation of a member of the Nanohaloarchaeota. In defining a host, the study corrects the view that Nanohaloarchaeota are likely to be free living and have a nonhost-associated lifestyle (2). We propose that members of the haloarchaea, which are present in all environments in which Nanohaloarchaeota have been identified, are the hosts. The phylogenetic diversity of Nanohaloarchaeota seems to be equivalent to that of the haloarchaea (2). The existence of distinct clades of Nanohaloarchaeota may reflect specialization to hosts from specific clades of haloarchaea.

The main species of haloarchaea in Deep Lake are known to support a high level of intergenera gene exchange that is counterbalanced by niche adaptation, thereby maintaining sympatric speciation (36, 37). In searching for mechanisms of gene exchange between the dominant Antarctic species, *Hrr. lacusprofundi* R1S1 was found to harbor a plasmid (pR1SE) that packages into specialized membrane vesicles and disseminates like a virus (18). Identifying *Hrr. lacusprofundi* as a host for *Ca. Nha. antarcticus* adds to the known physiological capacity of this species and suggests that it is particularly receptive to internal (pR1SE) and external (*Ca. Nha. antarcticus*) stimuli that invoke major changes to its membrane. Other than *Ca. Nha. antarcticus*, the cultivated DPANN superphyla are the hyperthermophilic *Ca. Nanoarchaeum equitans* (10), *Ca. Nanopusillus acidilobii* (11), and *Ca. Nanocleptia minutus* (38) and the acid mine drainage *Ca. Micrarchaeota* (ARMAN-1) A_DKE (17, 39) and *Ca. Mancarchaeum acidophilum*, which is no longer cultivatable (13). The *Hrr. lacusprofundi*–*Ca. Nha. antarcticus* model provides a useful experimental system that includes the ability to genetically manipulate *Hrr. lacusprofundi* (20) for advancing understanding of how archaea interact and the factors that control their symbiotic relationship (e.g., mutualism, commensalism, antagonism).

Materials and Methods

Cultivation of Nanohaloarchaeota. Enrichment cultures were grown using water collected from Rauer 1 Lake, Filla Island, Rauer Island group, East Antarctica (–68.8081667, 77.8550500) in September 2014 and Club Lake, Vestfold Hills, East Antarctica (–68.5417333, 78.2467667) in November 2014. Descriptions of the systems, metagenomes, and/or isolation of haloarchaea from these lakes were previously described (18, 26). Lake water was inoculated into a range of concentrations of modified David Burns cultivation media 2 (DBCM2) medium [DBCM2 (40) supplemented with 1 g L^{−1} peptone and 0.1 g L^{−1} yeast extract] or artificial Deep Lake vitamin broth (ADLVB) (19) in glass flasks shaken at 100 to 120 rpm at 16 °C to 20 °C, and the cultures were monitored for the presence of small cells using TEM (see below). From MAGs of Nha-R1 (see below), specific primer sets were designed (SI Appendix, Fig. S23 and Table S6, primer pairs SB1, SB2, and NHA-FISH). To monitor the community composition of enrichment cultures, PCR sequencing was performed using these primers plus 16S rRNA gene primers specific to Bacteria (SI Appendix, Table S6, primer pair Bacterial 16S) and Archaea (SI Appendix, Table S6, primer pair Archaeal 16S) (41). Subculturing the enrichment culture onto ADLVB agar plates (16.5 g L^{−1} agar, 20 °C) produced single colonies, which were subsequently inoculated into ADLVB (10 mL), grown at 100 rpm at 16 °C for 1 wk, and then, transferred into 40 mL ADLVB medium, and growth was continued.

To attempt to purify Nha-R1 away from other species, a culture was filtered through a 0.22-μm pore filter (Corning Filter Systems), and the filtrate was examined by TEM to assess the presence of *Ca. Nha. antarcticus*-sized cells. Fresh ADLVB media (30 mL) were inoculated with the filtrate (10 mL) and grown for 4 wk (100 rpm, 16 °C). To provide Nha-R1 with the compounds present in the enrichment culture, spent media were obtained by sequential filtration through 0.8-, 0.22-, and 0.1-μm filters. Spent media (30 mL) were inoculated with Nha-R1 inoculum (10 mL) and grown for 4 wk (16 °C, 100 rpm). Cell extract supplemented media were used to provide Nha-R1 with any compounds present in the enrichment culture that would not pass through the filtration steps used for producing spent media. Cell extracts from the enrichment culture, a pure *Hrr. lacusprofundi* ACAM34 culture, and a pure culture of a halophilic Antarctic bacterium *Halomonas* sp. isolated from the enrichment culture were obtained by sonication or

autoclaving. Cells harvested by centrifugation at 6,800 × g for 30 min were sonicated using a Q500 Sonicator (Qsonica) at an output intensity of 30% with 3 bursts each of 1 min, or pellets were resuspended in media and autoclaved at 121 °C for 20 min. For growth experiments, cell extracts were added to stock ADLVB media to a concentration proportional to the volume of the culture from which the extract was acquired (i.e., 100 mL of cell extract was harvested from 1 L of culture, and therefore, 10 mL of cell extract was added for every 90 mL of stock media). Cultures were inoculated with the Nha-R1-enriched inoculum and grown for 3 wk (40 mL, 100 rpm, 16 °C). Diffusion chambers were used to attempt to accurately emulate nutrient flux and provide an ongoing supply of nutrients to Nha-R1. Diffusion chambers were made from Vivaspin 20 columns (1 million-molecular weight cutoff; Sartorius Stedim) or from a 14-kDa dialysis tube (Millipore Sigma). Both types of chambers were inoculated with 10 mL of 0.22 μm filtered culture, with an additional 10 mL of fresh ADLVB media added to the dialysis tubing or 40 mL of fresh ADLVB added to the Vivaspin unit, and the chambers were submerged in the enrichment culture and left to grow for 3 wk (100 rpm, 16 °C). All growth experiments were performed at least 3 times each. To obtain a pure culture of the *Natrinema* sp. present in the enrichment, a selective medium was designed using the inferred capacity of this *Natrinema* sp. to utilize gluconate as a sole carbon source and nitrite as a sole nitrogen source. Growth of the Nha-R1 enrichment in *Natrinema* isolation media [3.1 M NaCl, 813 mM MgCl₂ 6H₂O, 62 mM MgSO₄ 7H₂O, 50 mM KCl, 510 nM gluconate, 1.5 μM NaNO₂, 100 mM CaCl₂, 0.01× Vitamin Mix (40)] yielded a pure culture of the *Natrinema* sp. that was then used for additional growth experiments as a potential host.

Growth of *Ca. Nha. antarcticus* with *Hrr. lacusprofundi* ACAM34. *Hrr. lacusprofundi* ACAM34 was transformed with plasmid pJWID1 as described previously (21) and grown to an optical density (OD)₆₀₀ of 1.0 in modified DBCM2 medium. The *Hrr. lacusprofundi* ACAM34 pJWID1 and Nha-Ce enrichment cultures were centrifuged at 8,000 × g for 20 min, and pellets were resuspended and combined in 1 mL total of fresh DBCM2 media. The mixture was incubated in a 2-mL microfuge tube at room temperature for 2 h and then used to inoculate 4 flasks of modified DBCM2 media containing 2.5 μg mL^{−1} of pravastatin and bacterial antibiotics (ampicillin 100 μg mL^{−1}, chloramphenicol 25 μg mL^{−1}, kanamycin 50 μg mL^{−1}, tetracycline 10 μg mL^{−1}). Cultivation of the enrichment, referred to as Nha-CHI, was continued by diluting cultures when they had reached OD₆₀₀ of 1.0 to 0.05 using fresh modified DBCM2 medium supplemented with 10 μg mL^{−1} pravastatin, 0.02 μg mL^{−1} mevinolin, 0.01 μg mL^{−1} simvastatin, and bacterial antibiotics as described previously (100 mL, 100 rpm, 22 °C). Treatment of the enrichment with this combination of antibiotics resulted in selection of an *Hrr. lacusprofundi* strain in which pJWID1 had integrated into the genome, losing all genes with the exception of the up-regulated *hmgA* gene; the strain is referred to as *Hrr. lacusprofundi* ACAM34-hmgA. Cultures were incubated for prolonged periods (up to 3 mo) and routinely assessed for taxonomic composition, and *Ca. Nha. antarcticus* abundance was evaluated using PCR and microscopy. Microscopy of a replicate of the Nha-CHI culture that had high relative abundance of *Ca. Nha. antarcticus* was subjected to metagenome sequencing, confirming its abundance. This culture is referred to as Nha-CFC and was used for FACS experiments.

Transmission Electron Microscopy. TEM was performed as described previously (18). Samples were diluted to OD₆₀₀ of 0.2 to 0.5, fixed with 2.5% glutaraldehyde, incubated overnight at 4 °C, mounted onto formvar-coated copper grids, negatively stained with uranyl acetate (2%) for 2 min, and dried overnight. Imaging was performed at 100 kV using a JEOL JEM-1400 electron microscope at the Electron Microscopy Unit at the University of New South Wales, Sydney, Australia.

Fluorescence Microscopy. The 16S rRNA probes conjugated with fluorophores were designed using ARB (42), screened for specificity using ProbeCheck (43), and synthesized by Integrated DNA Technologies Inc. *Ca. Nha. antarcticus* probes were conjugated with Cy5, and *Hrr. lacusprofundi* was conjugated with Cy3 (SI Appendix, Fig. S23 and Table S6). Samples were fixed with 2.5% glutaraldehyde, incubated overnight at 4 °C, and dehydrated using an ethanol series (50, 80, 100% [vol/vol]; 3 min for each concentration). Hybridization conditions were optimized at 46 °C for 3 h as previously described (44). Samples were counterstained with DAPI (ThermoFisher Scientific) as per the manufacturer's instructions. Samples were mounted onto glass slides along with SlowFade Gold antifade reagent (ThermoFisher Scientific). Images of the emission spectrum of each dye were acquired separately in grayscale at 100× magnification on an Olympus BX61 microscope using cellSens v2.2 software (Olympus Corporation). Images were assigned color

postacquisition to maximize contrast, and images were combined to form composite images of all 3 dyes for each field of view.

Flow Cytometry and Cell Growth. Sorting was performed on a BD Influx Cell Sorter (BD). Software used for sorting was the BD FACS Software version 1.2.0.117, Valcomp 7.5.1.3.16, on a Utopex server, build 1.2.0.107. Sorting was done into a 2-tube holder and was carried out using a piezo amplitude of 0.18 with a drop delay of 45.8111. Mode used was 1.5 Drop Pure with a drop envelope of 1.5 drops and an objective of purify. The phase mask was 16/16, with extra coincidence bits of 4 and a drop frequency of 38.40 kHz. Size regions for sorting were established using 4,000 series monosized particles of sizes 300 nm, 500 nm, 800 nm, and 1 μ m (ThermoFisher Scientific). Two gates for sorting were drawn around regions representing ~400 and ~600 nm, respectively. A second gate was drawn using fluorescence for Cy5, with an unstained sample used as a negative control and FISH-stained cells used as a positive control. Cell sizes were estimated by summing the total number of cells recorded in each size range equating to the standard size beads and taking the average across all 3 size ranges that were expected to capture Nha-C cells (300, 500, and 800 nm), resulting in an average cell size estimate of 340 nm in diameter. The average cell size for Nha-C cells from TEM was calculated from the diameter of 30 cells across a number of fields of view, including both attached and nonattached cells, resulting in an average cell size estimate of 400 nm. Based on these estimates, there is minimal difference (60 nm) between flow cytometry and TEM estimates of cell size.

Sorted Nha-C cells (500 μ L) from each size range (~400 and ~600 nm in diameter), equating to ~320,000 and 160,000 cells, respectively, were each added to 500 μ L (~5 \times 10⁶ cells) of *Hrr. lacusprofundi* ACAM34 or *Natrinema* sp. or 500 μ L of fresh DBCM2 media. A total of 4 replicates, 2 for each size range used in sorting (i.e., total of 8), were performed for each incubation of Nha-C with *Hrr. lacusprofundi* ACAM34 or *Natrinema* sp., and 2 replicates were performed for Nha-C with fresh media. All cultures were incubated for 1 d static at 18 °C before fresh media were added to bring cultures to a final volume of 10 mL. Cultures were incubated at 18 °C shaking at 100 rpm and monitored for up to 130 d.

Metagenomes and MAGs of Enrichment Cultures. Enrichment culture biomass was harvested by centrifugation at 5,000 \times g, and DNA was isolated using a QIAGEN DNeasy Blood and Tissue Kit following the manufacturer's instructions. To obtain the Nha-R1 MAG, DNA was sheared to 300 bp using the Covaris LE220 and size selected using SPRI beads (Beckman Coulter). The fragments were treated with end repair, A tailing, and ligation of Illumina compatible adapters (IDT, Inc.) using the KAPA-Illumina library creation kit (KAPA Biosystems). qPCR was used to determine the concentration of the libraries before sequencing on the Illumina HiSeq-2500 to yield 150-bp paired end reads at the Department of Energy (DOE) Joint Genome Institute. Quality-filtered metagenomic sequences were assembled with Megahit (version 1.0.6) (45). Assembly of the enrichment culture metagenome yielded 28,529 scaffolds (maximum length = 136,362 bp, scaffold N50 = 53,057 bp), which derived from 2 main taxa: *Hrr. lacusprofundi* 670-fold average read depth (28% relative abundance) and Nanohaloarchaeota 983-fold average read depth (41% relative abundance). GC binning identified reads belonging to a low-GC (40%) archaeon, which resolved after iterative assembly using SPAdes (version 3.5.0) into 3 scaffolds representing a single incomplete MAG for Nha-R1, and contigs were uploaded and annotated by the IMG pipeline (46). To close gaps in the Nha-R1 MAG, contigs from the Rauer 1 Lake enrichment metagenome (IMG genome identification no. 3300005925) were aligned to the 3 Nha-R1 scaffolds using Burrows-Wheeler Aligner (BWA) (47) and manually assessed to identify overlapping sequences. A metagenomic contig was identified that aligned to both scaffolds 2 and 3, indicating that the 2 could be concatenated. PCR primers were designed (SB1 and SB2 in *SI Appendix, Table S6*), and PCR amplification of the region was performed. Sanger sequencing of the product confirmed that scaffolds 2 and 3 could be concatenated, resulting in gap closure and removal of ~5.8 kbp of sequence from scaffold 2.

To obtain MAGs for Nha-C, Nanopore sequencing was performed according to the manufacturer's instructions on a GridION release v17.11.4 with the following alterations. The SQK-LSK108 1D Genomic DNA by ligation kit was used to prepare 1.4 μ g of DNA from the Club Lake enrichment (Nha-Ce) and 2.3 μ g of DNA from the Club Lake enrichment grown with *Hrr. lacusprofundi* ACAM34 (Nha-CHI). The formalin-fixed, paraffin embedded (FFPE) repair and end prep steps were combined into a single reaction with the following components: DNA in 48 μ L water, 3.5 μ L FFPE DNA Repair Buffer, 2 μ L NEBNext FFPE DNA repair mix, 3.5 μ L Ultra II End-prep reaction buffer, and 3 μ L Ultra II End-prep enzyme mix. The reaction was incubated at 20 °C for 5 min and 65 °C for 5 min. After end repair, the DNA was purified by adding Ampure XP beads at a

1:1 ratio (Beckman Coulter A63880) and rotating on a Hula mixer for 5 min. The beads were pelleted on a magnet, washed twice with 200 μ L of fresh 70% ethanol, and resuspended in 31 μ L of nuclease-free water. After the final elution, 408 or 660 ng of adapted DNA was loaded onto 2 FLO-MIN106 flow cells with 1,407 and 1,560 pores each for samples Nha-Ce and Nha-CHI, respectively. The sequencing ran for a total of 48 h for each run. The most up to date Oxford Nanopore software available at the time of the run was used. For Nha-Ce, MinKNOW acquisition software version 1.10.24 and Guppy base calling software version 0.3.0 were used. For Nha-CHI, MinKNOW version 1.13.5 and Guppy version 1.4.3 were used.

De novo assembly was carried out on the Nanopore data using a combination of miniasm version 0.2-r168-dirty (parameter flags: -f), minimap version 2.9 (parameter flags: -Sw5 -L100 -m0 -t16) (48), and racon version 1.2.0 as described previously (49). Contigs were uploaded and annotated using the IMG pipeline. Taxonomic classification was assigned based on best basic local alignment search tool (BLAST) hit, interpreted through the MEGAN 6.12.0 software, and manually reviewed for accuracy. Raw reads were aligned to the polished contigs using the BWA-mem algorithm, and coverage data were calculated using the pileup.sh script within the bbmap package. Relative abundances were calculated by taking the average fold coverage across a set of universally distributed single-copy genes (50). Genes were manually identified using IMG annotations, and taxonomy was assigned based on best blast hit. Raw reads were aligned, and coverage was calculated as above. Abundances were averaged across all genes identified for each taxonomic unit. Metagenome statistics were calculated using the stats.sh script from the bbmap package. *Ca. Nha. antarcticus* contigs in the Nha-Ce and Nha-CHI metagenomes were identified by aligning all contigs against the reference Nha-R1 MAG using BWA-mem. Identified Nha-Ce and Nha-CHI contigs were aligned to each other to establish a consensus sequence and determine the level of heterogeneity in the Nha-Ce and Nha-CHI metagenomes. This process yielded a single contiguous sequence representing the complete genome of *Ca. Nha. antarcticus* from the Nha-CHI metagenome, referred to as the Nha-CHI MAG.

The Nha-R1 MAG contained the 53 housekeeping genes identified as signature sequences for archaeal genomes (2). Metabolic pathways were reconstructed using IMG and manual analysis. Hypothetical proteins and the SPEARE protein were manually annotated as described previously (51). Sequence similarity to known proteins was assessed using BLAST (52), conserved domains using InterProScan (53), signal peptides using SignalP (54), prediction of cellular location using TMHMM (55), protein alignments by HMM-HMM (hidden Markov model) comparison using HHpred (56), and tertiary structure prediction using Swiss Model (57). In addition for the SPEARE protein, phylogenetic tree construction was performed using the maximum likelihood method based on the Jones Taylor Thornton (JTT) matrix-based model (58) using MEGA7 (59). Tertiary structure and function prediction was also performed using I-TASSER (60) with a 1,500-amino acid sliding window. Potential functional domains within the SPEARE protein were subjected to small-scale structural modeling using I-TASSER (60).

For contig recruitment to replicons, contigs \geq 1 kb from each metagenome were compared with the Nha-Ce contig (Ga0309993_1030) using nucmer from the MUMMER 3 toolkit (61). Only hits spanning at least 5 kb and with \geq 80% nucleotide identity were considered. The percentage of genome covered by metagenome contigs was calculated based on the hits identified by nucmer cumulated over the entire genome. The corresponding read coverage was calculated by summing the number of reads mapped to all contigs with a nucmer hit to the replicon and expressed as a percentage of the total number of reads mapped to all contigs. In addition, unassembled reads for each lake sampling time point were pooled together and mapped to the Nha-Ce contig (Ga0309993_1030) using Bowtie2 (62). The resulting alignments were then analyzed using Samtools (63) to generate total read mapping and read depth values using the idxstats and depth options, respectively. Read depth was plotted for each pooled set of reads using a 5-kb moving average. ANI between the 6 nanohaloarchaeal genomes (Nha-R1, Nha-CHI, *Ca. Nanopetramus*, *Ca. Nanosalina*, *Ca. Nanosalinarum*, and *Ca. Haloredivivus*) was calculated using the JSpeciesWS ANIb tool (64).

Proteomics. Proteomics was performed based on methods previously used for the analysis of proteins from Antarctic haloarchaea (18, 20). Biomass for proteomics was collected from an Nha-CHI enrichment culture in which *Ca. Nha. antarcticus* appeared (by microscopy) to be the most abundant taxon. Cells were centrifuged at 20,000 \times g for 30 min and resuspended in 400 μ L of radioimmunoprecipitation assay buffer containing 2 μ L proteinase inhibitor mixtures (Sigma) and 2 scoops of silica beads (BioSpec, 0.5 mm). Bead beating was performed for 30 s at 5,000 rpm and repeated 4 times. The sample was maintained on ice between pulses. After the bead beating, the

sample was incubated at 37 °C for 5 min followed by centrifugation at $19,083 \times g$ at 4 °C for 10 min. The supernatant was transferred to a new tube, and the protein concentration was measured using a 2-D Quant kit (GE Healthcare) as per the manufacturer's instructions. For in-solution digestion of proteins, ~40 µg of protein was reduced in 5 mM dithiothreitol (DTT) at 37 °C for 30 min, alkylated in 10 mM iodoacetic acid at room temperature for 30 min, and digested with trypsin (1 µg; sequencing grade; Promega) overnight. The digest (5 µg) was desalted using an SCX Stage Tip (Thermo Scientific) before mass spectrometry analysis. For analysis of the SPEARE protein, protein samples (23 to 43 µg), 5 µL color-coded prestained protein marker, high range (Cell Signaling Technology), and 5 µL PageRuler prestained protein marker (Thermo Fisher) were loaded onto 3 to 8% NuPAGE Tris-Acetate Mini Gels (Thermo Fisher Scientific) and electrophoresed at 150 V following the manufacturer's instructions. The gel was stained using a mass spectrometry-compatible silver staining method as described previously (65). Silver-stained sections were digested by incubation of the gel bands with 40 µL DTT (10 mM) in NH_4HCO_3 (50 mM) for 30 min at 37 °C. After removal of the solvent, the bands were incubated with 40 µL iodoacetamide (25 mM) in NH_4HCO_3 (50 mM) for 30 min at 37 °C. The bands were washed twice with 50 µL of acetonitrile for 10 min each, 40 µL trypsin (~100 ng) in NH_4HCO_3 (20 mM) was added, and the solution was incubated at 37 °C for 14 h. The bands were washed with 50 µL deionized water plus 1% (vol/vol) formic acid and 100 µL of acetonitrile for 15 min. The extracted peptides were dried and dissolved in 10 µL deionized water with 0.05% (vol/vol) heptafluorobutyric acid and 0.1% (vol/vol) formic acid.

Peptides from in-solution and in-gel digestions were separated by nano-liquid chromatography using an Ultimate nanoRSLC UPLC and autosampler system (Dionex). Samples (2.5 µL) were concentrated and desalted onto a micro-C18 precolumn (300 µm \times 5 mm; Dionex) with $\text{H}_2\text{O}:\text{CH}_3\text{CN}$ (98:2; 0.1% trifluoroacetic acid) at 15 µL min⁻¹. After a 4-min wash the solvent flow through from the precolumn was changed (Valco 10 port UPLC valve, Valco) to allow the trapped peptides to elute onto a fritless nanocolumn (75 µm \times ~15 cm) containing C18AQ media (1.9 µm, 120 Å; Dr Maisch). Peptides were eluted using a linear gradient of $\text{H}_2\text{O}:\text{CH}_3\text{CN}$ (98:2; 0.1% formic acid) to $\text{H}_2\text{O}:\text{CH}_3\text{CN}$ (64:36; 0.1% formic acid) at 200 nL min⁻¹ over 30 min. High voltage of 2,000 V was applied to low-volume Titanium union (Valco), and the tip was positioned ~0.5 cm from the heated capillary ($T = 275$ °C) of a Orbitrap Fusion Lumos (Thermo Electron) mass spectrometer. Positive ions were generated by electrospray and the Fusion Lumos operated in data-dependent acquisition mode. A survey scan m/z 350 to 1,750 was acquired in the orbitrap (resolution = 120,000 at m/z 200, with an accumulation target value of 400,000 ions) and lockmass enabled (m/z 445.12003). Data-dependent tandem MS analysis was performed using a top-speed approach (cycle time of 2 s). Mass spectrometry stage 2 spectra were fragmented by higher-energy collisional dissociation (normalized collision energy = 30) activation mode, and the ion trap was selected as the mass analyzer. The intensity threshold for

fragmentation was set to 25,000. A dynamic exclusion of 20 s was applied with a mass tolerance of 10 ppm. Peak lists were generated using Mascot Daemon/Mascot Distiller (Matrix Science) using default parameters, and submitted to the database search program Mascot (version 2.5.1; Matrix Science). Search parameters were precursor tolerance 4 ppm and product ion tolerances ± 0.5 Da, Met (O) carboxyamidomethyl-Cys specified as variable modification; enzyme specificity was trypsin, and 1 missed cleavage was possible. A custom database containing predicted protein coding sequences from *Ca. Nha. antarcticus*, proteins encoded by the host genome, and a database of common contaminant proteins were searched at the same time. A total of 458 proteins with 2 or more unique peptides were identified, of which 279 (~61%) were annotated with clusters of orthologous genes identifications: 155 information processing and storage (B, J, K, L); 72 metabolism (C, E, F, G, H, I, P, Q); 32 general cellular processes and signaling (D, M, N, O, T, U, V, W, Y, Z). The remaining 179 proteins included 89 hypothetical proteins, of which 62 had no BLAST hits outside of the Nanohaloarchaeota. The mass spectrometry data have been deposited to the ProteomeXchange Consortium via the Proteome Identification (PRIDE) partner repository with Project Name: Cultivation of an Antarctic Nanohaloarchaea and Project accession no. PXD010625.

ACKNOWLEDGMENTS. We thank Kate Montgomery and Belinda Ferrari for assistance with FISH; Nicole Shapiro, Simon Roux, and Alicia Clum for assistance with managing and analyzing metagenome data; Jocelyne DiRuggiero for providing access to *Ca. Nanopetramus* SG9 data; Rhiannon Kuchel, Sigrid Fraser, and Nicholas Ariotti for assistance with electron microscopy; the Helicopter Resources crew, 2014 Rauer Traverse Team, and other expeditioners at Davis Station during the 2014 winter and 2014/2015 summer for their assistance in collecting water samples; and the Australian Antarctic Division for technical and logistical support during the expedition. DNA sequencing of PCR products was performed at the Ramaciotti Centre for Genomics (University of New South Wales, Sydney), and computational analyses were performed on the computational cluster Katana supported by the Faculty of Science (University of New South Wales, Sydney). Mass spectrometry results were obtained at the Bioanalytical Mass Spectrometry Facility, and electron microscopy was at the Electron Microscope Unit, both within the Analytical Centre of the University of New South Wales. Subsidized access to the Bioanalytical Mass Spectrometry Facility is acknowledged. The authors thank the PRIDE team and ProteomeXchange for efficiently processing and hosting the mass spectrometry data. This work was supported by Australian Research Council Grant DP150100244 and Australian Antarctic Science Program Project 4031. The work conducted by the US DOE Joint Genome Institute, a DOE Office of Science User Facility, is supported by Office of Science of the US DOE Contract DE-AC02-05CH11231. S.E. was supported by European Molecular Biology Organization Long-Term Fellowship ALTF 188-2014, which is cofunded by European Commission Grants EMBOCOFUND2012 and GA-2012-600394 and supported by Marie Curie Actions.

1. A. Spang, E. F. Caceres, T. J. G. Ettema, Genomic exploration of the diversity, ecology, and evolution of the archaeal domain of life. *Science* **357**, eaaf3883 (2017).
2. P. Narasingarao *et al.*, *De novo* metagenomic assembly reveals abundant novel major lineage of *Archaea* in hypersaline microbial communities. *ISME J.* **6**, 81–93 (2012).
3. C. Rinke *et al.*, Insights into the phylogeny and coding potential of microbial dark matter. *Nature* **499**, 431–437 (2013).
4. K. Andrade *et al.*, Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. *ISME J.* **9**, 2697–2711 (2015).
5. R. Ghai *et al.*, New abundant microbial groups in aquatic hypersaline environments. *Sci. Rep.* **1**, 135 (2011).
6. C. D. Vavourakis *et al.*, Metagenomic insights into the uncultured diversity and physiology of microbes in four hypersaline soda lake brines. *Front. Microbiol.* **7**, 211 (2016).
7. O. Zhaxybayeva, R. Stepanauskas, N. R. Mohan, R. T. Papke, Cell sorting analysis of geographically separated hypersaline environments. *Extremophiles* **17**, 265–275 (2013).
8. A. Crites-Christoph *et al.*, Functional interactions of archaea, bacteria and viruses in a hypersaline endolithic community. *Environ. Microbiol.* **18**, 2064–2077 (2016).
9. M. Aouad *et al.*, Extreme halophilic archaea derive from two distinct methanogen Class II lineages. *Mol. Phylogenet. Evol.* **127**, 46–54 (2018).
10. H. Huber *et al.*, A new phylum of *Archaea* represented by a nanosized hyperthermophilic symbiont. *Nature* **417**, 63–67 (2002).
11. L. Wurch *et al.*, Genomics-informed isolation and characterization of a symbiotic Nanoarchaeota system from a terrestrial geothermal environment. *Nat. Commun.* **7**, 12115 (2016).
12. B. J. Baker *et al.*, Enigmatic, ultrasmall, uncultivated *Archaea*. *Proc. Natl. Acad. Sci. U.S.A.* **107**, 8806–8811 (2010).
13. O. V. Golyshtina *et al.*, 'ARMAN' archaea depend on association with euryarchaeal host in culture and *in situ*. *Nat. Commun.* **8**, 60 (2017).
14. A. J. Probst *et al.*, Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. *Nat. Microbiol.* **3**, 328–336 (2018).
15. B. G. Paul *et al.*, Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. *Nat. Microbiol.* **2**, 17045 (2017).
16. N. H. Youssef *et al.*, Insights into the metabolism, lifestyle and putative evolutionary history of the novel archaeal phylum 'Diapherotrites'. *ISME J.* **9**, 447–460 (2015).
17. N. Dombrowski, J. H. Lee, T. A. Williams, P. Offre, A. Spang, Genomic diversity, lifestyles and evolutionary origins of DPANN archaea. *FEMS Microbiol. Lett.* **366**, fnz008 (2019).
18. S. Erdmann, B. Tschitschko, L. Zhong, M. J. Raftery, R. Cavicchioli, A plasmid from an Antarctic haloarchaeon uses specialized membrane vesicles to disseminate and infect plasmid-free cells. *Nat. Microbiol.* **2**, 1446–1455 (2017).
19. P. D. Franzmann *et al.*, *Halobacterium lacusprofundi* sp. nov., a halophilic bacterium isolated from Deep Lake, Antarctica. *Syst. Appl. Microbiol.* **11**, 20–27 (1988).
20. T. J. Williams *et al.*, Cold adaptation of the Antarctic haloarchaea *Halohasta litchfieldiae* and *Halorubrum lacusprofundi*. *Environ. Microbiol.* **19**, 2210–2227 (2017).
21. Y. Liao *et al.*, Developing a genetic manipulation system for the Antarctic archaeon, *Halorubrum lacusprofundi*: Investigating acetamidase gene function. *Sci. Rep.* **6**, 34639 (2016).
22. K. Schwank *et al.*, An archaeal symbiont-host association from the deep terrestrial subsurface. *ISME J.* **10**, 1038/s41396-019-0421-0 (2019).
23. L. R. Comolli, B. J. Baker, K. H. Downing, C. E. Siegerist, J. F. Banfield, Three-dimensional analysis of the structure and ecology of a novel, ultra-small archaeon. *ISME J.* **3**, 159–167 (2009).
24. L. R. Comolli, J. F. Banfield, Inter-species interconnections in acid mine drainage microbial communities. *Front. Microbiol.* **5**, 367 (2014).
25. T. Heimerl *et al.*, A complex endomembrane system in the archaeon *Ignicoccus hospitalis* tapped by *Nanoarchaeum equitans*. *Front. Microbiol.* **8**, 1072 (2017).
26. B. Tschitschko *et al.*, Genomic variation and biogeography of Antarctic haloarchaea. *Microbiome* **6**, 113 (2018).

27. D. G. Burns *et al.*, Haloquadrum walsbyi gen. nov., sp. nov., the square haloarchaeon of Walsby, isolated from saltern crystallizers in Australia and Spain. *Int. J. Syst. Evol. Microbiol.* **57**, 387–392 (2007).
28. J. N. Busby, S. Panjikar, M. J. Landsberg, M. R. H. Hurst, J. S. Lott, The BC component of ABC toxins is an RHS-repeat-containing protein encapsulation device. *Nature* **501**, 547–550 (2013).
29. H. Chen, S. Young, T. K. Berhane, H. N. Williams, Predatory *Bacteriovorax* communities ordered by various prey species. *PLoS One* **7**, e34174 (2012).
30. D. P. R. Herlemann, O. Geissinger, A. Brune, The termite group I phylum is highly diverse and widespread in the environment. *Appl. Environ. Microbiol.* **73**, 6682–6685 (2007).
31. L. A. Hug *et al.*, A new view of the tree of life. *Nat. Microbiol.* **1**, 16048 (2016).
32. Y. Koga, H. Morii, Biosynthesis of ether-type polar lipids in archaea and evolutionary considerations. *Microbiol. Mol. Biol. Rev.* **71**, 97–120 (2007).
33. T. J. Williams *et al.*, Microbial ecology of an Antarctic hypersaline lake: Genomic assessment of ecophysiology among dominant haloarchaea. *ISME J.* **8**, 1645–1658 (2014).
34. B. Tschitschko *et al.*, Ecophysiological distinctions of haloarchaea from a hypersaline Antarctic lake determined using metaproteomics. *Appl. Environ. Microbiol.* **82**, 3165–3173 (2016).
35. T. Goldfarb *et al.*, BREX is a novel phage resistance system widespread in microbial genomes. *EMBO J.* **34**, 169–183 (2015).
36. M. Z. DeMaere *et al.*, High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. *Proc. Natl. Acad. Sci. U.S.A.* **110**, 16939–16944 (2013).
37. R. Cavicchioli, Microbial ecology of Antarctic aquatic systems. *Nat. Rev. Microbiol.* **13**, 691–706 (2015).
38. E. St John *et al.*, A new symbiotic nanoarchaeote (*Candidatus Nanocleptia minutus*) and its host (*Zestosphaera tikiterensis* gen. nov., sp. nov.) from a New Zealand hot spring. *Syst. Appl. Microbiol.* **42**, 94–106 (2019).
39. S. Krause, A. Bremges, P. C. Münch, A. C. McHardy, J. Gescher, Characterisation of a stable laboratory co-culture of acidophilic nanoorganisms. *Sci. Rep.* **7**, 3289 (2017).
40. M. Dyall-Smith, "The Halohandbook—Protocols for Haloarchaeal Genetics." (2009). https://haloarchaea.com/wp-content/uploads/2018/10/Halohandbook_2009_v7.3mds.pdf. Accessed 10 November 2017.
41. S. Takahashi, J. Tomita, K. Nishioka, T. Hisada, M. Nishijima, Development of a prokaryotic universal primer for simultaneous analysis of *Bacteria* and *Archaea* using next-generation sequencing. *PLoS One* **9**, e105592 (2014).
42. W. Ludwig *et al.*, ARB: A software environment for sequence data. *Nucleic Acids Res.* **32**, 1363–1371 (2004).
43. A. Loy *et al.*, ProbeCheck—A central resource for evaluating oligonucleotide probe coverage and specificity. *Environ. Microbiol.* **10**, 2894–2898 (2008).
44. J. Pernthaler, F. Glöckner, W. Schönhuber, R. Amann, Fluorescence *in situ* hybridization (FISH) with rRNA-targeted oligonucleotide probes. *Methods Microbiol.* **30**, 201–210 (2001).
45. D. Li *et al.*, MEGAHIT v1.0: A fast and scalable metagenome assembler driven by advanced methodologies and community practices. *Methods* **102**, 3–11 (2016).
46. I. A. Chen *et al.*, IMG/M: Integrated genome and metagenome comparative data analysis system. *Nucleic Acids Res.* **45**, D507–D516 (2017).
47. H. Li, Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. *arXiv:1303.3997v2* (16 March 2013).
48. H. Li, Minimap and miniasm: Fast mapping and de novo assembly for noisy long sequences. *Bioinformatics* **32**, 2103–2110 (2016).
49. R. Vaser, I. Sović, N. Nagarajan, M. Šikić, Fast and accurate de novo genome assembly from long uncorrected reads. *Genome Res.* **27**, 737–746 (2017).
50. C. J. Creevey, T. Doerks, D. A. Fitzpatrick, J. Raes, P. Bork, Universally distributed single-copy genes indicate a constant rate of horizontal transfer. *PLoS One* **6**, e22099 (2011).
51. M. A. Allen *et al.*, The genome sequence of the psychrophilic archaeon, *Methanococcoides burtonii*: The role of genome evolution in cold adaptation. *ISME J.* **3**, 1012–1035 (2009).
52. S. F. Altschul, W. Gish, W. Miller, E. W. Myers, D. J. Lipman, Basic local alignment search tool. *J. Mol. Biol.* **215**, 403–410 (1990).
53. P. Jones *et al.*, InterProScan 5: Genome-scale protein function classification. *Bioinformatics* **30**, 1236–1240 (2014).
54. T. N. Petersen, S. Brunak, G. von Heijne, H. Nielsen, SignalP 4.0: Discriminating signal peptides from transmembrane regions. *Nat. Methods* **8**, 785–786 (2011).
55. A. Krogh, B. Larsson, G. von Heijne, E. L. L. Sonnhammer, Predicting transmembrane protein topology with a hidden markov model: Application to complete genomes. *J. Mol. Biol.* **305**, 567–580 (2001).
56. L. Zimmermann *et al.*, A completely reimplemented MPI bioinformatics toolkit with a new HHpred server at its core. *J. Mol. Biol.* **430**, 2237–2243 (2018).
57. A. Waterhouse *et al.*, SWISS-MODEL: Homology modelling of protein structures and complexes. *Nucleic Acids Res.* **46**, W296–W303 (2018).
58. D. T. Jones, W. R. Taylor, J. M. Thornton, The rapid generation of mutation data matrices from protein sequences. *Comput. Appl. Biosci.* **8**, 275–282 (1992).
59. S. Kumar, G. Stecher, K. Tamura, MEGA7: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol. Biol. Evol.* **33**, 1870–1874 (2016).
60. J. Yang *et al.*, The I-TASSER suite: Protein structure and function prediction. *Nat. Methods* **12**, 7–8 (2015).
61. S. Kurtz *et al.*, Versatile and open software for comparing large genomes. *Genome Biol.* **5**, R12 (2004).
62. B. Langmead, S. L. Salzberg, Fast gapped-read alignment with Bowtie 2. *Nat. Methods* **9**, 357–359 (2012).
63. H. Li *et al.*, 1000 Genome Project Data Processing Subgroup, The sequence alignment/map format and SAMtools. *Bioinformatics* **25**, 2078–2079 (2009).
64. M. Richter, R. Rosselló-Móra, F. Oliver Glöckner, J. Peplies, JSpeciesWS: A web server for prokaryotic species circumscription based on pairwise genome comparison. *Bioinformatics* **32**, 929–931 (2016).
65. E. Mortz, T. N. Krogh, H. Vorum, A. Görg, Improved silver staining protocols for high sensitivity protein identification using matrix-assisted laser desorption/ionization-time of flight analysis. *Proteomics* **1**, 1359–1363 (2001).