



Atacama Database: a platform of the microbiome of the Atacama Desert

Carolina A. Contador · Luis Veas-Castillo · Emilio Tapia · Marcela Antipán · Noemi Miranda · Benjamín Ruiz-Tagle · Jonathan García-Araya · Barbara A. Andrews · Mauricio Marin · Cristina Dorador · Juan A. Asenjo

Received: 15 May 2019 / Accepted: 7 September 2019 / Published online: 18 September 2019
© Springer Nature Switzerland AG 2019

Abstract The Atacama Desert is one of the oldest and driest places on Earth. In the last decade, microbial richness and diversity has been acknowledged as an important biological resource of this region. Owing to the value of the microbial diversity apparent in potential biotechnology applications and conservation purposes, it is necessary to catalogue these microbial communities to promote research activities and help to preserve the wide range of ecological niches of the Atacama region. A prototype Atacama Database has been designed and it provides a description of the rich microbial diversity of the Atacama Desert, and helps to visualise available

literature resources. Data has been collected, curated, and organised into several categories to generate a single record for each organism in the database that covers classification, isolation metadata, morphology, physiology, genome and metabolism information. The current version of Atacama Database contains 2302 microorganisms and includes cultured and uncultured organisms retrieved from different environments within the desert between 1984 and 2016. These organisms are distributed in bacterial, archaeal or eukaryotic domains, along with those that are unclassified taxonomically. The initial prototype of the Atacama Database includes a basic search and taxonomic and advanced search tools to allow identification and comparison of microbial populations, and space distribution within this biome. A geolocation search was implemented to visualise the microbial diversity of the ecological niches defined by sectors and extract general information of the sampling sites. This effort will aid understanding of the microbial ecology of the desert, microbial population dynamics, seasonal behaviour, impact of climate change over time, and reveal further biotechnological applications of these microorganisms. The Atacama Database is freely available at: <https://www.atacamadb.cl>.

C. A. Contador (✉) · M. Antipán · N. Miranda · B. A. Andrews · J. A. Asenjo
Centre for Biotechnology and Bioengineering (CeBiB),
Department of Chemical Engineering, Biotechnology and
Materials, University of Chile, Beauchef 851,
8370456 Santiago, Chile
e-mail: ccontad@ing.uchile.cl

L. Veas-Castillo · E. Tapia · B. Ruiz-Tagle · M. Marin
Centre for Biotechnology and Bioengineering (CeBiB),
Departamento de Ingeniería Informática (DIINF),
Universidad de Santiago de Chile, Santiago, Chile

J. García-Araya · C. Dorador
Centre for Biotechnology and Bioengineering (CeBiB),
Laboratorio de Complejidad Microbiana y Ecología
Funcional, Instituto Antofagasta & Departamento de
Biotecnología, Facultad de Ciencias del Mar y Recursos
Biológicos, Universidad de Antofagasta, Antofagasta,
Chile

Keywords Atacama Desert · Chile · Microbial database · Microbial diversity

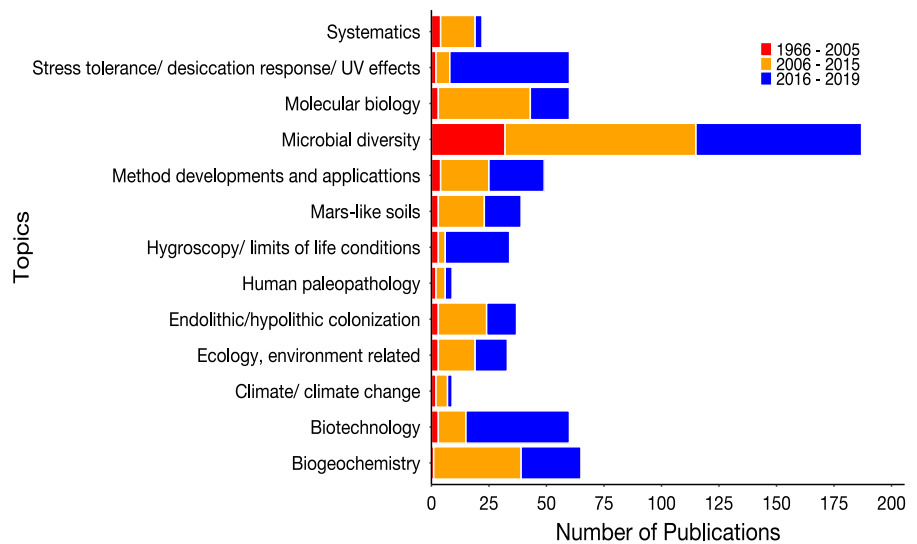
Introduction

The Atacama Desert is located in the north of Chile from 19°S to 30°S along the Pacific coast of South America and from east to west extending from the Andean Cordillera to the coast. It encompasses 105,000 sq km with an altitude ranging from sea level to over 3500 m above (Dorador 2007; Azua-Bustos et al. 2017; Bull et al. 2018). Arid conditions in the region date back 150 million years making this desert one of the oldest and driest places on earth (Hartley et al. 2005; Clarke 2006). The Atacama Desert exhibits semi-arid to extreme hyper-arid environments that are characterised by low water availability and variable levels of organic carbon content. The ecological niches of the zone are very diverse comprising sectors with conditions considered to be at the dry limit for life (Connon et al. 2007; Schulze-Makuch et al. 2018), caves in the Coastal range, geyser fields, and the high Andean plateau (Altiplano) where different water bodies with a wide range of salinity (from freshwater to saturated saltwater), and peatland (bofedales) can be found (Demergasso et al. 2004, 2010; Dorador et al. 2013). It is notable that several of these sectors are extremely sensitive to climate change and anthropogenic disturbances (Bull et al. 2016). For decades, the Atacama Desert has been known as a rich resource of minerals with an intense mining activity present in the region and heavy use of natural resources for those purposes, especially water extraction (Scheihing and Tröger 2018). During the last decade, microbiological research has grown substantially in this hyper-arid desert covering different topics from microbial diversity and ecology studies to biogeochemistry and Mars-like environments as shown in Fig. 1 (Bull et al. 2016). Thanks to these research efforts and their findings, the microbial richness and diversity of the Atacama Desert is evident. In general, these studies establish what microbes are present, what type of niches they colonise and the tolerance mechanisms to extreme physical and chemical conditions, amongst others (Azua-Bustos et al. 2012; Bull et al. 2016; Idris et al. 2017a; Pérez et al. 2017; Schulze-Makuch et al. 2018). Bioprospecting studies of microorganisms isolated from the extremely arid zone of the Atacama have shown promising results with the isolation of novel species, and new chemical structures with biological activity such as antibiotics and anticancer agents

(Schulz et al. 2011; Santhanam et al. 2012a, b; Idris et al. 2017b; Wichner et al. 2017). Indeed, several new *Streptomyces* strains have been isolated and described. For example, *Streptomyces leeuwenhoekii* produces previously described metabolites, but also synthesises novel antibiotics, chaxamycins and chaxalactins, and chaxapeptin (Elsayed et al. 2015; Gomez-Escribano et al. 2015; Castro et al. 2018). At present, specialised metabolite producers are of particular interest to help with the growing problem of antimicrobial resistant strains (Mohammadipanah and Wink 2016). In addition, many studies have been carried out in the arid region of the Atacama Desert since it has been compared to Mars soil, with increased attention on astrobiology applications (Navarro-Gonzalez 2003; Davila and Schulze-Makuch 2016; Azua-Bustos et al. 2018).

The microbial diversity of the Atacama Desert is of great importance due to its current and potential biotechnological applications. It is important to highlight their functional role regarding trophic web interactions (Dorador et al. 2018), C and N biogeochemical cycles (Thiel et al. 2010; Molina et al. 2018a) and greenhouse gas production (Molina et al. 2018b). Previous studies have demonstrated the high microbial diversity in different habitats of the Atacama Desert independent of the applied technique (Demergasso et al. 2004; Dorador et al. 2013; Idris et al. 2017a). Therefore, a catalogue of these microbial communities is necessary to promote its diversity, protect these endemic resources and their environment, and as an educational resource about the value of these microorganisms. These microbial communities are important natural resources whose environment is mostly without protection. For instance, there is no protection for areas of the core of the hyper-arid desert that are known to be vulnerable to perturbation by mining, recreational (e.g. Rally) and other activities. Most of the microbial diversity of the Atacama Desert has been described from either the hyper-arid desert or high altitude saline wetlands (locally called 'salares'), some of which are included in national reserves and national parks. To obtain samples from protected areas it is imperative to have permission from CONAF (National Forest Corporation, Ministry of Agriculture) following strict regulations. Some of these areas are managed by local indigenous communities (e.g. Atacameños). The area covered by the database described here includes some protected areas

Fig. 1 Enumeration of microbial research publications by topics from 1966 to 2019. Figure adapted and updated from data by Bull et al. (2016)



such as Los Flamencos National Reserve (Salar de Atacama, Salar de Tara, Salar de Pujsa) and Lullail-laco National Park. Nevertheless, most of the microbiological studies performed in the Atacama Desert have been carried out in unprotected areas. Furthermore, the knowledge about microbial diversity of these ecosystems is mostly unknown to the local and national community.

Over the past 20 years, several efforts have been made to create microbial diversity databases to promote the understanding of microbial communities within the context of their habitats (Stoner et al. 2001; Majhi et al. 2013; Wu et al. 2013). Stoner et al. (2001) were pioneers with their development of The Yellowstone Microbial Database and Map server. This database integrates microbiological data with environmental, geographical and ecological data to improve the understanding of the microbial communities and provides a scheme to implement maps of microbial diversity. Using these previous studies as a base, the prototype Atacama Database seeks to make visible the microbiological research done in the region during the last 50 years in order to value and preserve the unique and native microbial diversity of the Atacama Desert. It compiles the published resources available to facilitate information retrieval from primary literature to create a comprehensive source of microbial information. The prototype Atacama Database currently houses data relating to 2302 strains. These organisms include archaea, bacteria, fungi, microalgae, and taxonomically unidentified

microorganisms. Data stored have an emphasis on taxonomic and isolation metadata information. Morphology, physiology, genome and metabolism information were included in the cases in which these data were available. Data were collected from open access sources and articles published in peer-reviewed journals. Data were processed and stored in a document storage system built using MongoDB (<https://www.mongodb.com/>). The current version of the Atacama Database Platform includes tools to access the data such as a quick search by typing entries and taxonomic and advance search tools where filters can be used to identify specific microorganisms. A geolocation search was implemented to help with the visualisation of ecological niches and extract physical and chemical parameters of the sampling sites. When this database is fully developed, it will help to promote the study of the microbial ecology of the desert, microbial population dynamics, biogeography, seasonal behaviour, impact of climate change over time, and reveal further biotechnological applications of local microorganisms.

Materials and methods

Data sources and database structure

The Atacama Database contains information from literature sources including more than 100 publications and open access sources such as the US National

Library of Medicine (Pubmed) (NCBI Resource Coordinators 2017), and Genomes Online Database (GOLD) (Bernal et al. 2001). Links to external databases were added to facilitate access to primary data. By the end of March 2018, the Atacama Database contained information on 2302 organisms isolated from 135 different sampling sites. The sampling sites cover diverse ecological niches from lakes and foggy sites to extreme and hyper-arid desert areas ranging from 0 to 5916 [m above sea level]. The data collected are continually evolving, but preliminary statistics show that the catalogue includes representatives of 32 phyla, 50 classes, 75 orders, 90 families, 104 genera and 70 species. To date, the number of validly named species isolated from the Atacama Desert is low and a general taxonomic rank is usually provided in most of the published studies. The number of microorganisms associated with each phylum present in the catalogue is shown in Fig. 2a.

Data were collected, curated and organised into six main categories: taxonomy, isolation metadata, morphology, physiology, genome and metabolism. These categories encompass the major characteristics of these organisms and the available information has been added to each respective attribute. Taxonomy includes information related to general classification, NCBI taxonomy ID, accession numbers to different databases and literature information. Isolation metadata provides information such as isolation environment, environment features, sample type, collection site, geographical location (latitude and longitude in decimal format), altitude and physical and chemical characteristics of the sample and/or sites. Morphology describes cell size, cell shape, motility and spore morphology while the physiology section provides growth requirements such as pH and O₂ requirements. The data related to genomes includes genomic features such as genome size and digital DNA G + C composition. Metabolic products data associated with pharmacological/biotechnological applications has been included such as compound type and PubChem Compound ID (CID). Figure 2b shows the available data for each category.

A single record was generated for each organism where a unique Organism ID was assigned to each organism to link all its attributes in a Microsoft Excel Open XML Format Spreadsheet file (XLSX file extension). This file includes a reference for metabolic information that was saved in a separate XLSX file.

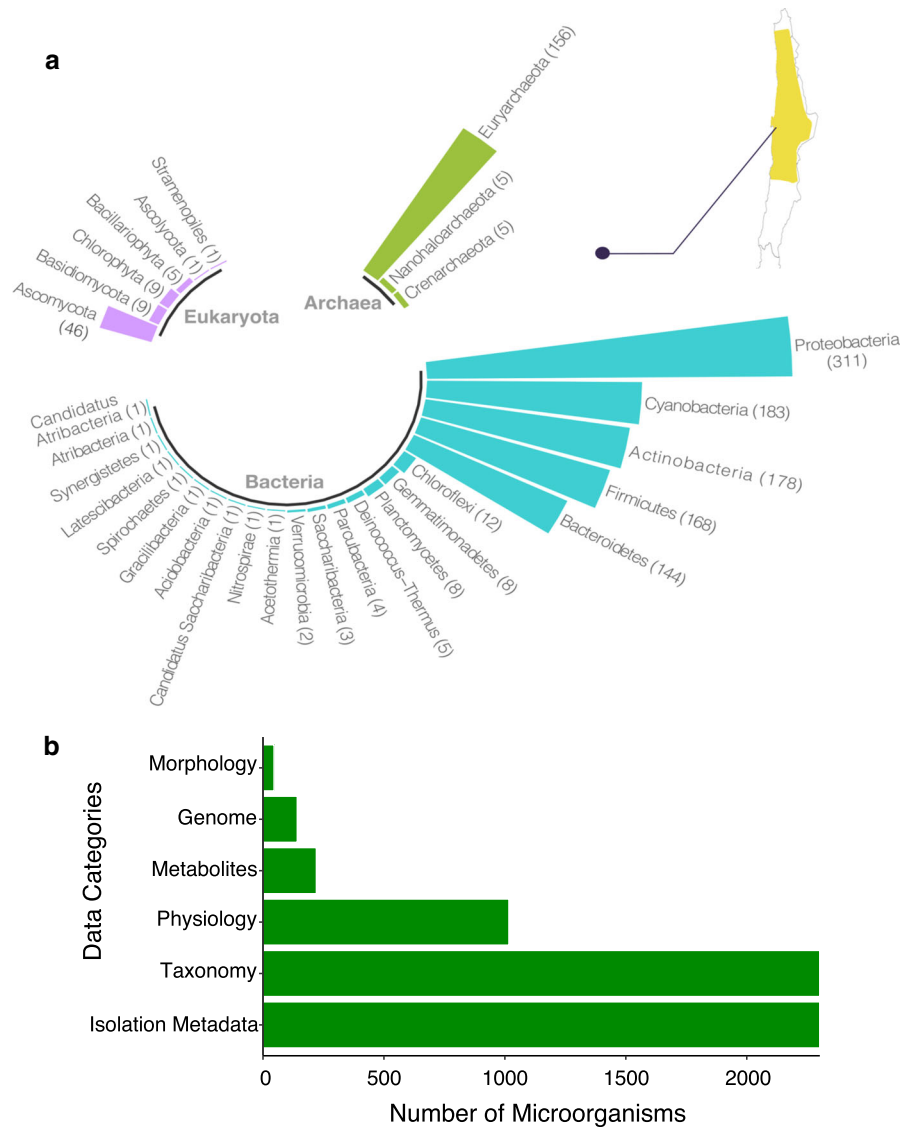
Relevant geographic areas were stored in a similar way. Data were processed with an application developed in Java programming language, which stores it in a document database system using MongoDB. The platform was built using a Web Service Layer (API REST architecture), the back-end was implemented using Golang programming language (<https://golang.org/>) and the front-end was built using a JavaScript framework (Vue.js framework (<https://vuejs.org/>)) to visualise the data. Geolocation was implemented with the help of the Google Maps JavaScript API (<https://developers.google.com/maps/>). Several indexes were constructed with the stored documents to allow taxonomic, advanced, and geographic searches in an efficient and scalable way. Figure 3a summarises the organisation of data and database structure in the Atacama Database and Fig. 3b shows the internal structure of data saved in the database.

Results and discussion

Database features

The prototype version of Atacama Database offers access to a catalogue of microorganisms of the Atacama Desert through a web interface. It was implemented using a non-structured database where data was stored using a document-oriented approach in MongoDB and the Vue.js JavaScript framework for interacting with the data. This configuration allows scalability and easy modification of fields or attributes of the information. Currently, the data present in this database has an emphasis on taxonomic and isolation metadata and specific information about each organism is continually added as it becomes available. The Atacama Database homepage gives easy access to the main querying options: basic search, taxonomy tree search, advanced search, and geolocation search. Graphs with the distribution of organisms by domain and phylum, and by the different levels of the phylogenetic tree, are provided to reflect the diversity of the organisms in the database and acquisition of data into Atacama Database. The Atacama Database gives support for users that require assistance or would like to submit suggestions about the data after registration. Registration is free and gives access to the Database content. Additionally, a brief tutorial is included in the Help section.

Fig. 2 a Distribution of microorganisms by Phylum in the database. Numbers in parenthesis indicate total number of microorganisms in each phylum. **b** Number of microorganisms associated with each data category in the Atacama Database



Basic search

A basic or simple search option can be performed to query the database from the homepage. Microorganism name or ID are used to request information from the database under this option. Query results are displayed as a list with organism ID and organism description fields. Specific data can be retrieved after selecting an organism. Data is displayed in a table with different sections: taxonomy, isolation metadata, morphology, physiology, genome, and metabolism. Links to other databases are provided to access additional information. Also, links to the respective

publications in which the microorganism was identified are provided.

Taxonomic tree viewer

A taxonomic search was implemented through a phylogenetic tree. A phylogenetic tree containing the microorganisms for each domain was constructed to organise the data. Graphs describing the taxonomic distribution are provided. Microorganisms are listed on the basis of their classification. All data associated with a specific organism can be retrieved after selecting it. Information regarding any specific

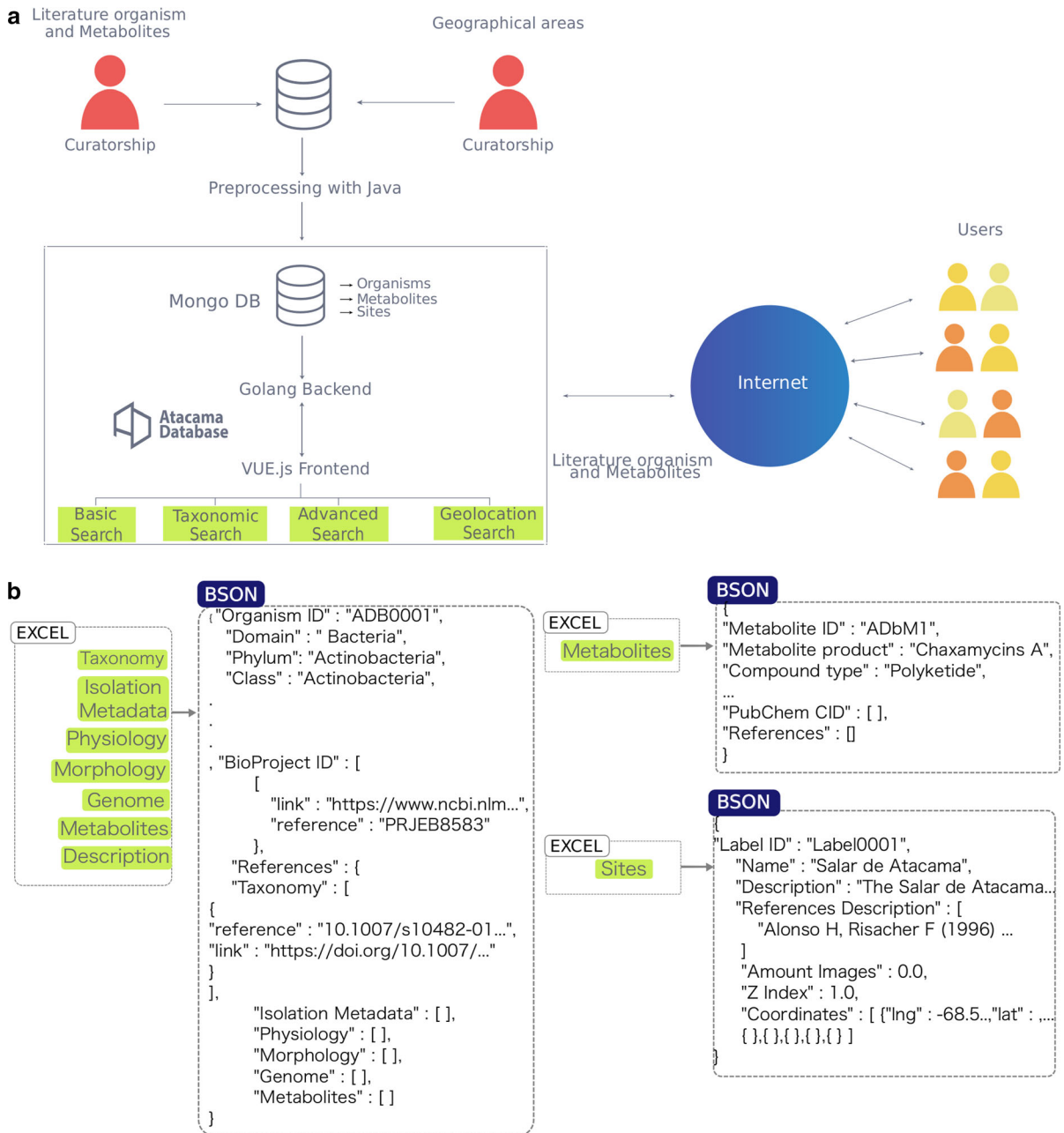


Fig. 3 **a** Workflow describing the organisation of data and the database structure used in the Atacama Database. **b** Internal data structure. Single records of each organism are stored in the form

microorganism can be inspected using the same display format from Basic Search. A summary of the search can be downloaded in CSV format.

of JSON style documents using MongoDB. Several querying options and display formats have been implemented allowing users to apply filters to refine searches

Advanced search

An advanced search tool is available to query the database for specific information. The filters of the advanced search allow the user to narrow down the results, explore the data in Atacama Database and look

Table 1 Geolocations in Atacama Database

Sector	Number of microorganisms	Environment
Salar de Atacama	185	Hyper-arid zone
Salar Punta Negra	7	Athalassohaline wetland
Salar Grande	42	Hyper-arid zone
Death Valley	252	Saline soil zone
Laguna Tebenquiche	190	Athalassohaline lake water
Valle de la Luna	42	Hyper-arid and extreme hyper-arid zones
Salar de Aguas Calientes	17	Salt flat with saturated salt waters
Salar de Huasco	230	Altiplano
Salar de Ascotán	320	Hyperhaline lake
Laguna Chaxa	99	High-altitude salt lake
Yungay	245	Extreme hyper-arid zone
Maria Elena South	26	Extreme hyper-arid zone
Lomas Bayas	22	Extreme hyper-arid zone
El Tatio	8	Geothermal geyser field
Cerro Chajnantor	29	Arid zone
Lomas de Tilocalar	6	Hyper-arid zone
Sairecabur volcano	7	Sulfur-rich soil
Simba summit lake	13	High-altitude lake with acid pH
Laguna Miscanti	5	Brackish water lake
Laguna Lejia	26	Oligohaline shallow lake
Pozo Almonte	10	Arid zone
La Portada	2	Atacama coast
Laguna de Piacota	27	Freshwater lake
Lago Chungara	55	Polymictic cold lake
Laguna Brava	2	Extreme conditions
Salar de Llamara	137	Hyper-arid zone
Salar de Tara	14	Salt flat
Licancabur summit lake	11	High-altitude lake with alkaline pH
Llullaillaco volcano lake	1	High-altitude lake
Burro Muerto lake	3	Athalassohaline water body
Altamira	27	Arid zone with heavy fog events
Salar Soronal	4	Hyper-arid zone
Llano de la Paciencia	33	Hyper-arid zone
Bofedal de Parinacota	45	Wetland
Cordillera de Domeyko	32	Mountain range

for organisms with specific characteristics. The Database can be explored by taxa classification (domain, phylum, class, order, family, genus and species); collection site features such as isolation environment, environment feature, sample type; and strains with specific characteristics such as type strain, Gram stain, oxygen requirements, and metabolic products. Results are listed by organism ID and description. Specific microorganism data can be

accessed using the display format described above. An overview of the query results can be retrieved in CSV format.

Geolocation search

Since the Atacama Desert has many different ecological niches, a geolocation search was implemented to display organisms by their sample collection sites data

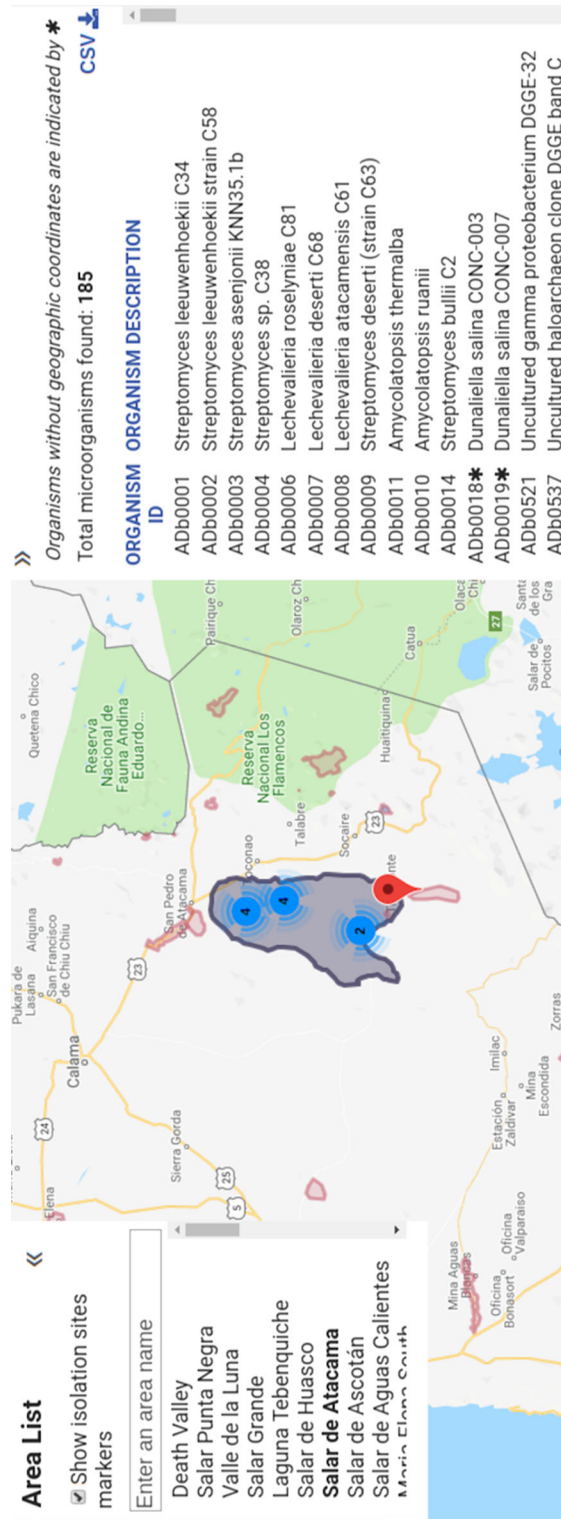


Fig. 4 Geolocation search in the Atacama Database to visualise microorganisms and extract physical and chemical parameters of the sampling sites; isolated markers can be displayed by isolation environment to narrow down the search. Markers are clustered by distance: blue, yellow and red markers indicate less than 10 sites, more than 10 sites and 100 or more sites, respectively. Number indicates the number of sites in that set. Area list includes thirty-five isolation sectors. The selected area is highlighted in the map. (Color figure online)

using Google Maps JavaScript API. Organisms are grouped by polygons and markers in the Atacama Desert map. The search by polygons is defined by thirty-five areas that include salt lakes (salares), lakes, lagoons and volcanoes among others. Table 1 summarises the geolocations available in the database. These areas were selected since they cluster the prime collection sites. Areas are highlighted and listed on the map to facilitate selection, location and retrieval of information. A description of the areas and a list with the organisms associated with each sector are provided. On the other hand, information on latitude and longitude was used to display collection site locations by markers on the map. An example of the geolocation search is shown in Fig. 4.

Future steps

Since 2000, several Microbial Observatory projects have established to help and support research into microbial communities over time and across environmental gradients. These observatories have had a key role in the study and understanding of microbial diversity (Countway et al. 2010; Edgcomb et al. 2011; Cardace et al. 2013) and in efforts to describe new species of bacteria and archaea. Although the Atacama Database is still in the early stages of development, this project provides a preliminary interface to describe the phylogenetic diversity derived from the Atacama Desert and compile a library of the primary literature. The Database will continue to grow and information related to proteins, genes and metabolic pathways will be incorporated in the next stages. Also, the Geolocation search tool will be improved to include additional information related to the environmental and geological context. Isolation metadata provides data from published studies and it includes general information such as sample type, sample collection date, collection site information and physical and chemical properties of the sites. However, this data is scarce or not always available. Additional data related to the geological and geochemical habitats will help the study of ecosystems, microbial population dynamics and seasonal behaviour.

The current version of Atacama Database is mainly directed to the academic sector. A public version of Atacama Database is being developed to reach the general community since it is important to educate the

public about the value of these endemic resources and the necessity of protecting their environment.

Conclusions

Many studies have been done in the arid region of the Atacama Desert with the first findings of bacterial presence dating back to the 1960's (Cameron et al. 1966), but in general the information is sparse and did not reveal the complexity of this ecosystem. Despite the growing interest in the microbiology of the Atacama Desert, there is a low number of validly named microbial species that have been first isolated from the Atacama. In this study, a platform for the valorisation of the microbial diversity of the Atacama Desert was developed. The Atacama Database will help to promote research, provide a comprehensive data collection of the Atacama Desert microorganisms and find further biotechnology applications for its microorganisms.

Acknowledgements We would like to thank Mervyn Bibb, and Marcel Jaspars for their valuable help and suggestions to improve the design of the Atacama Database website; and Felipe Maturana, Luis Riquelme and Diego Arenas for their support in the software development process.

Author's contribution Conceiving the study: CAC and CD. PIs of project that support this research: CD, MM, BAA, and JAA. Data acquisition and Curation: CAC. Curation Location: CAC and JGA. Database Design: MA, NM, BRT, LVC, ET and CAC. Development of database and webpages: LVC, ET and BRT. Define database queries: LVC, ET, CAC, MA and NM. Manuscript drafting: CAC, BAA, and JAA. All authors read and approved the final manuscript.

Funding This work was supported by the Conicyt Basal Centre Grant for the CeBiB (FB0001).

Data availability Atacama Database is freely available at <https://www.atacamadb.cl>. Recommended web browsers are Chrome, Firefox and Safari.

Compliance with ethical standards

Conflict of interest The authors have declared no conflict of interest.

References

Azua-Bustos A, Urrejola C, Vicuña R (2012) Life at the dry edge: microorganisms of the Atacama Desert. *FEBS Lett*

- 586:2939–2945. <https://doi.org/10.1016/J.FEBSLET.2012.07.025>
- Azua-Bustos A, González-Silva C, Corsini G (2017) The hyperarid core of the Atacama Desert, an extremely dry and carbon deprived habitat of potential interest for the field of carbon science. *Front Microbiol* 8:993. <https://doi.org/10.3389/FMICB.2017.00993>
- Azua-Bustos A, Fairén AG, González-Silva C, Ascaso C, Carrizo D, Fernández-Martínez MÁ, Fernández-Sampedro M, García-Descalzo L, García-Villadangos M, Martín-Reondo MP, Sánchez-García L, Wierzchos J, Parro V (2018) Unprecedented rains decimate surface microbial communities in the hyperarid core of the Atacama Desert. *Sci Rep* 8:16706. <https://doi.org/10.1038/s41598-018-35051-w>
- Bernal A, Ear U, Kyrpides N (2001) Genomes OnLine Database (GOLD): a monitor of genome projects world-wide. *Nucleic Acids Res* 29:126–127
- Bull AT, Asenjo JA, Goodfellow M, Gómez-Silva B (2016) The Atacama Desert: technical resources and the growing importance of novel microbial diversity. *Annu Rev Microbiol* 70:215–234. <https://doi.org/10.1146/annurev-micro-102215-095236>
- Bull AT, Andrews BA, Dorador C, Goodfellow M (2018) Introducing the Atacama Desert. *Antonie Van Leeuwenhoek* 111(8):1269–1272. <https://doi.org/10.1007/s10482-018-1100-2>
- Cameron R, Gensel D, Blank C (1966) Soil studies desert microflora. XII. Abundance of microflora in soil samples from the Chile Atacama Desert. *Space Progr Summ IV*:140–147
- Cardace D, Hoehler T, McCollom T, Schrenk M, Carnevale D, Kubo M, Twing K (2013) Establishment of the Coast Range ophiolite microbial observatory (CROMO): drilling objectives and preliminary outcomes. *Sci Drill* 16:45–55. <https://doi.org/10.5194/sd-16-45-2013>
- Castro JF, Razmilic V, Gomez-Escribano JP, Andrews B, Asenjo J, Bibb M (2018) The ‘gifted’ actinomycete *Streptomyces leeuwenhoekii*. *Antonie Van Leeuwenhoek* 111(8):1433–1448. <https://doi.org/10.1007/s10482-018-1034-8>
- Clarke JDA (2006) Antiquity of aridity in the Chilean Atacama Desert. *Geomorphology* 73:101–114. <https://doi.org/10.1016/j.entcs.2005.12.035>
- Connon SA, Lester ED, Shafaat HS, Obenhuber DC, Ponce A (2007) Bacterial diversity in hyperarid atacama desert soils. *J Geophys Res* 112:G04S17. <https://doi.org/10.1029/2006JG000311>
- Countway PD, Vigil PD, Schnetzer A, Moorthi SD, Caron DA (2010) Seasonal analysis of protistan community structure and diversity at the USC microbial observatory (San Pedro Channel, North Pacific Ocean). *Limnol Oceanogr* 55:2381–2396. <https://doi.org/10.4319/lo.2010.55.6.2381>
- Davila AF, Schulze-Makuch D (2016) The last possible outposts for life on mars. *Astrobiology* 16:159–168. <https://doi.org/10.1089/ast.2015.1380>
- Demergasso C, Casamayor EO, Chong G, Galleguillos P, Escudero L, Pedrós-Alió C (2004) Distribution of prokaryotic genetic diversity in athallassohaline lakes of the Atacama Desert, Northern Chile. *FEMS Microbiol Ecol* 48:57–69. <https://doi.org/10.1016/j.femsec.2003.12.013>
- Demergasso C, Dorador C, Meneses D, Blamey J, Cabrol N, Escudero L, Chong G (2010) Prokaryotic diversity pattern in high-altitude ecosystems of the Chilean Altiplano. *J Geophys Res* 115:G00D09. <https://doi.org/10.1029/2008JG000836>
- Dorador CI (2007) Microbial communities in high altitude altiplanic wetlands in northern Chile: phylogeny, diversity and function. Ph.D. Thesis, Max Planck Institute for Evolutionary Biology
- Dorador C, Vila I, Witzel K-P, Imhoff JF (2013) Bacterial and archaeal diversity in high altitude wetlands of the Chilean Altiplano. *Fundam Appl Limnol/Arch für Hydrobiol* 182:135–159. <https://doi.org/10.1127/1863-9135/2013/0393>
- Dorador C, Fink P, Hengst M, Icaza G, Villalobos AS, Vejar D, Meneses D, Zadjelovic V, Burmann L, Moelzner J, Harrod C (2018) Microbial community composition and trophic role along a marked salinity gradient in Laguna Puilar, Salar de Atacama. Chile *Antonie van Leeuwenhoek* 111(8):1361–1374. <https://doi.org/10.1007/s10482-018-1091-z>
- Edgcomb V, Orsi W, Bunge J, Jeon S, Christen R, Leslin C, Holder M, Taylor GT, Suarez P, Varela R, Epstein S (2011) Protistan microbial observatory in the Cariaco Basin, Caribbean. I. Pyrosequencing vs Sanger insights into species richness. *ISME J* 5:1344–1356. <https://doi.org/10.1038/ismej.2011.6>
- Elsayed SS, Trusch F, Deng H, Raab A, Prokes I, Busarakam K, Asenjo JA, Andrews BA, Van West P, Bull AT, Goodfellow M, Yi Y, Ebel R, Jaspars M, Rateb ME (2015) Chaxapeptin, a Lasso Peptide from Extremotolerant *Streptomyces leeuwenhoekii* Strain C58 from the Hyperarid Atacama Desert. *J Org Chem* 80:10252–10260. <https://doi.org/10.1021/acs.joc.5b01878>
- Gomez-Escribano JP, Castro JF, Razmilic V, Chandra G, Andrews B, Asenjo JA, Bibb MJ (2015) The *Streptomyces leeuwenhoekii* genome: de novo sequencing and assembly in single contigs of the chromosome, circular plasmid pSLE1 and linear plasmid pSLE2. *BMC Genom* 16:485. <https://doi.org/10.1186/s12864-015-1652-8>
- Hartley AJ, Chong G, Houston J, Mather AE (2005) 150 million years of climatic stability: evidence from the Atacama Desert, northern Chile. *J Geol Soc Lond* 162:421–424. <https://doi.org/10.1144/0016-764904-071>
- Idris H, Goodfellow M, Sanderson R, Asenjo JA, Bull AT (2017a) Actinobacterial rare biospheres and dark matter revealed in habitats of the Chilean Atacama Desert. *Sci Rep* 7:1–11. <https://doi.org/10.1038/s41598-017-08937-4>
- Idris H, Nouioui I, Asenjo JA, Bull AT, Goodfellow M (2017b) *Lentzea chajnantorensis* sp. nov., an actinobacterium from a very high altitude Cerro Chajnantor gravel soil in northern Chile. *Antonie Van Leeuwenhoek* 110:795–802. <https://doi.org/10.1007/s10482-017-0851-5>
- Majhi MC, Behera AK, Kulshreshtha NM, Kumar R, Kumar A (2013) ExtremeDB : a unified web repository of extremophilic archaea and bacteria. *PLoS ONE* 8:e63083. <https://doi.org/10.1371/journal.pone.0063083>
- Mohammadipanah F, Wink J (2016) Actinobacteria from arid and desert habitats: diversity and biological activity. *Front Microbiol* 6:1541. <https://doi.org/10.3389/fmicb.2015.01541>

- Molina V, Dorador C, Fernández C, Bristow L, Eissler Y, Hengst M, Hernandez K, Olsen LM, Harrod C, Marchant F, Anguita C, Cornejo M (2018a) The activity of nitrifying microorganisms in a high-altitude Andean wetland. *FEMS Microbiol Ecol* 94:1–13. <https://doi.org/10.1093/femsec/fiy062>
- Molina V, Eissler Y, Cornejo M, Galand PE, Dorador C, Hengst M, Fernandez C, Francois JP (2018b) Distribution of greenhouse gases in hyper-arid and arid areas of northern Chile and the contribution of the high altitude wetland microbiome (Salar de Huasco, Chile). *Antonie Van Leeuwenhoek* 111(8):1421–1432. <https://doi.org/10.1007/s10482-018-1078-9>
- Navarro-Gonzalez R (2003) Mars-like soils in the Atacama Desert, Chile, and the dry limit of microbial life. *Science* 80(302):1018–1021. <https://doi.org/10.1126/science.1089143>
- NCBI Resource Coordinators (2017) Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res* 45:D12–D17. <https://doi.org/10.1093/nar/gkw1071>
- Pérez V, Hengst M, Kurte L, Dorador C, Jeffrey WH, Wattiez R, Molina V, Matallana-Surget S (2017) Bacterial survival under extreme UV radiation: a comparative proteomics study of *Rhodobacter* sp., isolated from high altitude wetlands in Chile. *Front Microbiol* 8:1–16. <https://doi.org/10.3389/fmicb.2017.01173>
- Santhanam R, Okoro CK, Rong X, Huang Y, Bull AT, Weon HY, Andrews BA, Asenjo JA, Goodfellow M (2012a) *Streptomyces atacamensis* sp. nov., isolated from an extreme hyper-arid soil of the Atacama Desert. *Chile Int J Syst Evol Microbiol* 62:2680–2684. <https://doi.org/10.1099/ijs.0.038463-0>
- Santhanam R, Okoro CK, Rong X, Huang Y, Bull AT, Andrews BA, Asenjo JA, Weon HY, Goodfellow M (2012b) *Streptomyces deserti* sp. nov., isolated from hyper-arid Atacama Desert soil. *Antonie Van Leeuwenhoek* 101:575–581. <https://doi.org/10.1007/s10482-011-9672-0>
- Scheihing K, Tröger U (2018) Local climate change induced by groundwater overexploitation in a high Andean arid watershed, Lagunillas basin, northern Chile. *Hydrogeol J* 26:705–719. <https://doi.org/10.1007/s10040-017-1647-4>
- Schulz D, Beese P, Ohlendorf B, Erhard A, Zinecker H, Dorador C, Imhoff JF (2011) Abenquines A-D: aminoquinone derivatives produced by *Streptomyces* sp. strain DB634. *J Antibiot (Tokyo)* 64:763–768. <https://doi.org/10.1038/ja.2011.87>
- Schulze-Makuch D, Wagner D, Kounaves SP, Mangelsdorf K, Devine KG, de Vera J-P, Schmitt-Kopplin P, Grossart H-P, Parro V, Kaupenjohann M, Galy A, Schneider B, Airo A, Frösler J, Davila AF, Arens FL, Cáceres L, Solís Cornejo F, Carrizo D, Dartnell L, DiRuggiero J, Flury M, Ganzert L, Gessner MO, Grathwohl P, Guan L, Heinz J, Hess M, Keppler F, Maus D, McKay CP, Meckenstock RU, Montgomery W, Oberlin EA, Probst AJ, Sáenz JS, Sattler T, Schirmack J, Sephton MA, Schloter M, Uhl J, Valenzuela B, Vestergaard G, Wörmer L, Zamorano P (2018) Transitory microbial habitat in the hyperarid Atacama Desert. *PNAS* 115:2670–2675. <https://doi.org/10.1073/pnas.1714341115>
- Stoner DL, Geary MC, White LJ, Lee RD, Brizzee JA, Rodman AC, Rope RC (2001) Mapping microbial biodiversity. *Appl Environ Microbiol* 67:4324–4328. <https://doi.org/10.1128/AEM.67.9.4324>
- Thiel V, Tank M, Neulinger SC, Gehrman L, Dorador C, Imhoff JF (2010) Unique communities of anoxygenic phototrophic bacteria in saline lakes of Salar de Atacama (Chile): evidence for a new phylogenetic lineage of phototrophic Gammaproteobacteria from pufLM gene analyses. *FEMS Microbiol Ecol* 74:510–522. <https://doi.org/10.1111/j.1574-6941.2010.00966.x>
- Wichner D, Idris H, Houssen WE, McEwan AR, Bull AT, Asenjo JA, Goodfellow M, Jaspars M, Ebel R, Rateb ME (2017) Isolation and anti-HIV-1 integrase activity of lentzeosides A-F from extremotolerant *lentzea* sp. H45, a strain isolated from a high-altitude Atacama Desert soil. *J Antibiot (Tokyo)* 70:448–453. <https://doi.org/10.1038/ja.2016.78>
- Wu L, Sun Q, Sugawara H, Yang S, Zhou Y, McCluskey K, Vasilenko A, Suzuki K, Ohkuma M, Lee Y, Robert V, Ingsriswang S, Guissart F, Phillippe D, Ma J (2013) Global catalogue of microorganisms (gcm): a comprehensive database and information retrieval, analysis, and visualization system for microbial resources. *BMC Genom* 14:933

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.