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CHARACTERIZATION OF EXTREMOTOLERANT MICROALGES ISOLATED FROM THE ATACAMA DESERT

Javiera Collao[2], **Manuel Zapata Arcos**[1,2], Maricarmen Ruiz-Domínguez[2], Alejandro Maureira[2], Mariella Rivas A.[1,2]

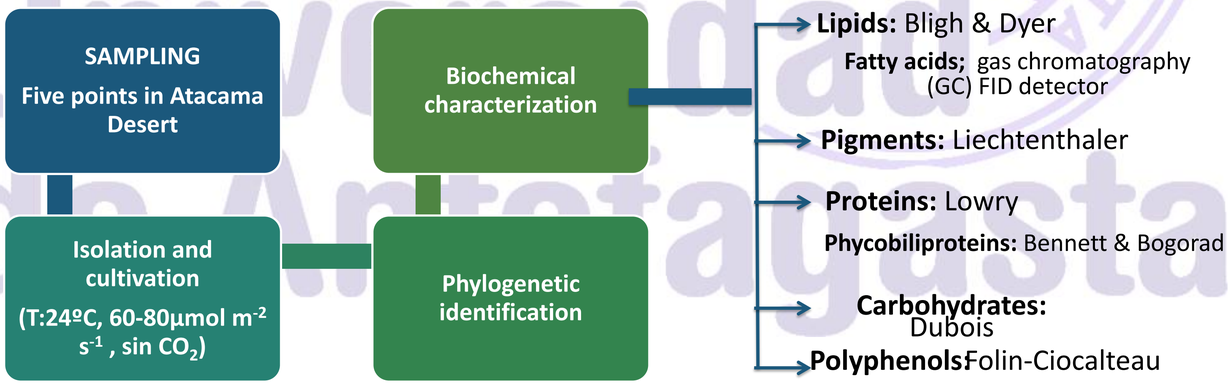
E-mail: mzarcos@gmail.com & mariella.rivas@uantof.cl

1. INTRODUCTION

The Atacama Desert is an environment with extreme characteristics unique in the world, presents high solar radiation, salinity, temperature fluctuation during the day, high altitude above sea level and also areas with high presence of pollutants and heavy metals such as, lead, mercury and arsenic (1). These physicochemical characteristics favor the growth of microalgae species with unique physiological properties compared to other species, since they are able to survive extreme environmental conditions through the production of metabolites and / or bioactive compounds (2,3,4).

The main objective of this work was to isolate and characterize microalgae with high functional diversity from different lagoons of the Atacama Desert in order to obtain products of great biotechnological interest. This study presents the phylogenetic identification of isolated microalgae by sequencing rDNA16S and rDNA18S ribosomal genes, along with growth curves, total fatty acid content, pigments, proteins, carbohydrates and total polyphenols.

2. METHODOLOGY



3. RESULTS

3.1 Isolation

Table 1. Isolation and origin of the 11 strains obtained.

Nº	Strain	Sampling site	Origin
1	37.1	Peine3	Microbial mat
2	42.2	Peine3	Water column
3	42.4	Peine3	Water column
4	42.6	Peine3	Water column
5	44.2	Jere Valley	Sediment
6	44.3	Jere Valley	Sediment
7	46.1	Salar de Tara	Sedimento
8	47.1	Los Flamencos	Water column
9	47.2	Los Flamencos	Water column
10	47.3	Los Flamencos	Water column
11	51.3	Los Flamencos	Water column

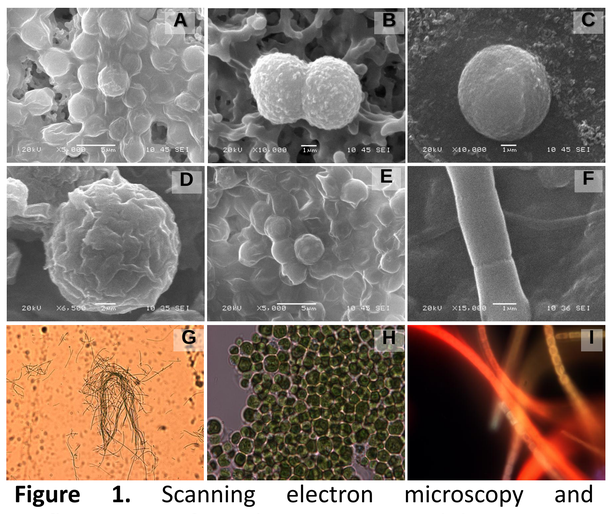


Figure 1. Scanning electron microscopy and epifluorescence for isolates: strain 42,2 (A), strain 42,4 (B) and strain 42,6 (C), strain 44,2 (D) and strain 44,3 (E), strain 46,1 (F) and (I), strain 37,1 (G) strain 47,2 (H).

3.2 Phylogenetic identification

Table 2. Phylogenetic identification of the 11 strains isolated from the Atacama Desert through the use of BlastN.

Strains	Homology hit	Similarity %
37.1	*Leptolyngbya* sp.	98%
42.4	*Cyanothece* sp.	96%
42.6	*Cyanothece* sp.	98%
46.1	*Oscillatoria* sp.	100%
42.2	*Micractinium inermun*	99%
44.2	*Micractinium inermun*	99%
44.3	*Micractinium inermum*	99%
47.1	*Chlorella* sp.	99%
47.2	*Chlorella* sp.	96%
47.3	*Chlorella* sp.	99%
51.3	*Chlorococcum* sp.	99%

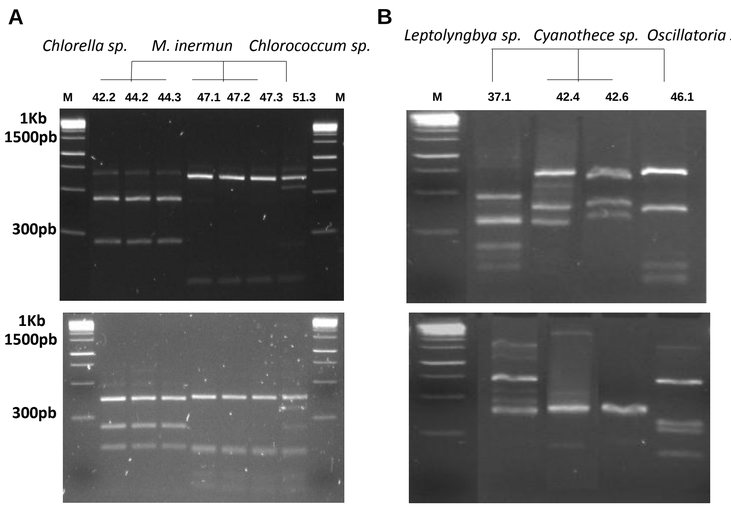


Figure 2. RFLP analysis for ribosomal gene 18S rRNA and 16S rRNA in A and B respectively. In the upper part the enzyme AluI and HaeIII is shown and in the inferior, HpaI and HhaI.

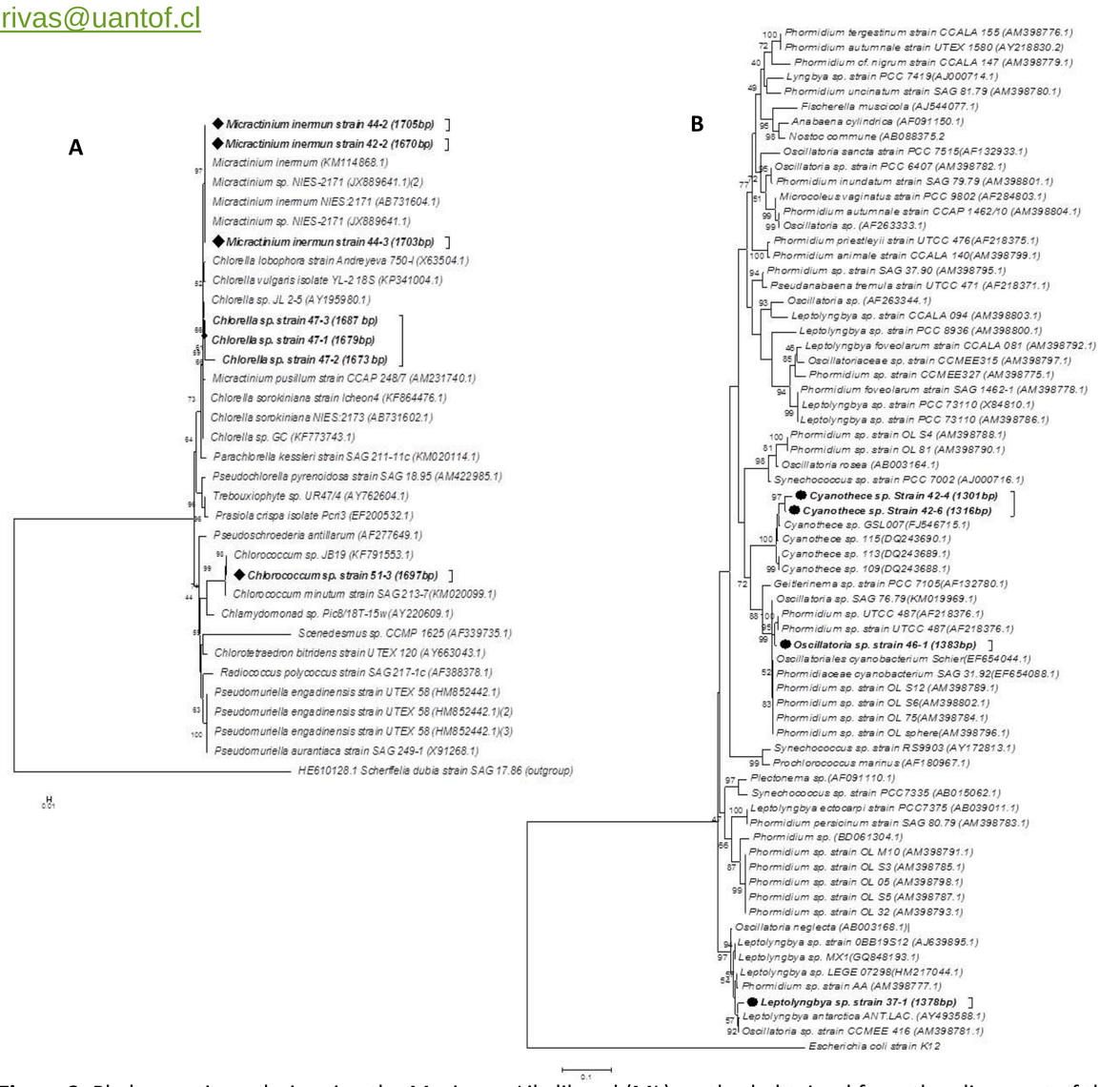


Figure 3. Phylogenetic analysis using the Maximum Likelihood (ML) method obtained from the alignment of the sequences of the rDNA18S (A) and rDNA16S (B) genes. The analysis was carried out using ClustalW and MEGA 6 with 1000 boostrap.

3.3 Characterization of growth and productivity

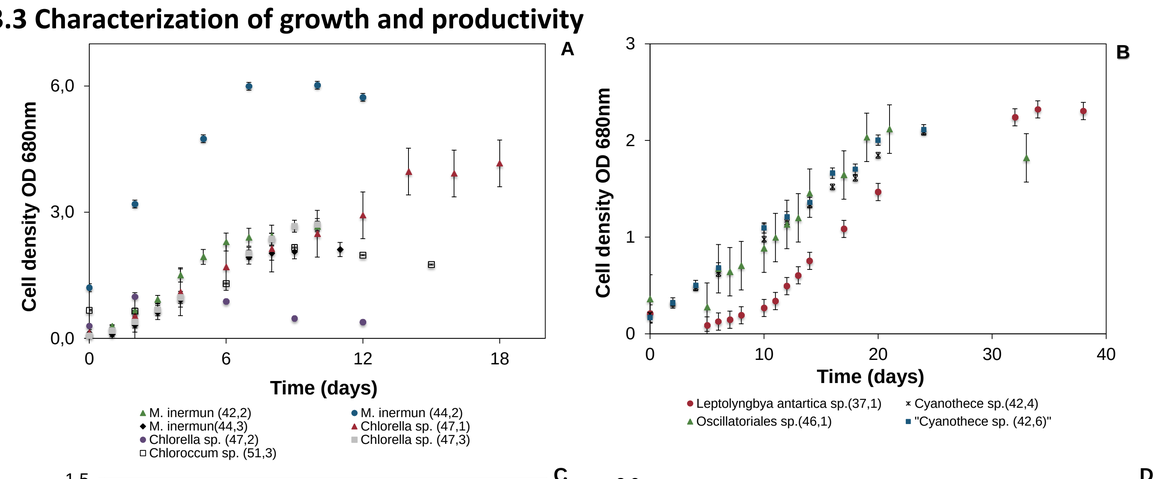


Figure 4. Growth curves. Optical density at 680nm and dry weight (g·L^{-1}) with respect to time (days) for Chlorophyta (A) and (C) species, and for Cyanophyta (B) and (D) species.

3.4 Determination of the biochemical composition

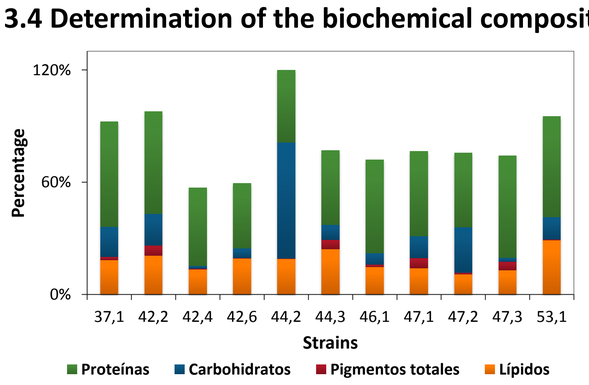


Figure 5. Biochemical determination of isolated strains.

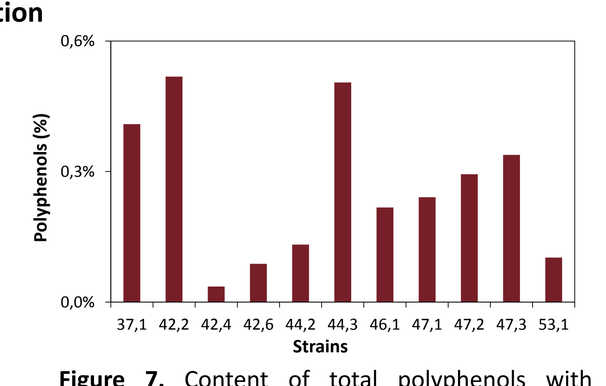


Figure 7. Content of total polyphenols with respect to dry biomass for the 11 isolated strains.

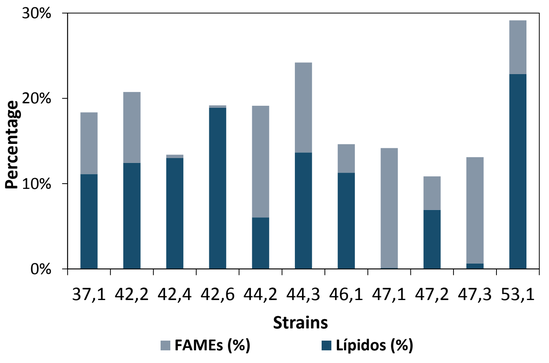


Figure 6. Content of FAMEs with respect to total lipids.

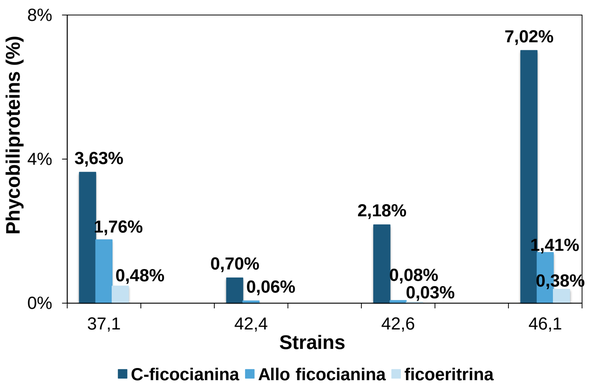


Figure 8. Determination of phycobiliproteins of the cyanobacteria group, with respect to their biomass.

4. CONCLUSIONS

- Eleven species of microalgae identified as *Leptolyngbya* sp., *Cyanothece* sp., *Oscillatoria* sp. *Micractinium inermun*, *Chlorella* sp. and *Chlorococcum* sp.
- The species *Oscillatoria* sp. strain 46.1 had higher productivity (805 mg·L^{-1}·d^{-1}). In addition this strain had a higher content of c-phycocyanin, 7% with respect to its dry biomass.
- Strain 53.1 had the highest lipid content with 29% g·g biomass^{-1}.

5.REFERENCES

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6. FINANCING

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1. Bioenergía y Sustentabilidad Ambiental, Centro de Investigación Científico Tecnológico para la Minería CICITEM, Avda. José Miguel Carrera 1701, Antofagasta.
2. Laboratorio de Biotecnología Algal y Sustentabilidad, Facultad de Ciencias del Mar y Recursos Biológicos, Universidad de Antofagasta, Avda. Angamos 601, Antofagasta.
3. Laboratorio de Microalgas, Facultad de Ciencias del Mar y Recursos Biológicos, Universidad de Antofagasta, Avda. Angamos 601, Antofagasta.