Diurnal variation in bacterioplankton composition and DNA damage in the microbial community from an Andean oligotrophic lake

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Abstract
Laguna Azul is an oligotrophic lake situated at 4,560 m above sea level and subject to a high level of solar radiation. Bacterioplankton community composition (BCC) was analysed by denaturing gradient gel electrophoresis and the impact of solar ultraviolet radiation was assessed by measuring cyclobutane pyrimidine dimers (CPD). Furthermore, pure cultures of Acinetobacter johnsonii A2 and Rhodococcus sp. A5 were exposed simultaneously and CPD accumulation was studied. Gel analyses generated a total of 7 sequences belonging to Alpha-proteobacteria (1 band), Beta-proteobacteria (1 band), Bacteroidetes (2 bands), Actinobacteria (1 band), and Firmicutes (1 band). DGGE profiles showed minimal changes in BCC and no CPD was detected even though a high level of damage was found in biodosimeters. A. johnsonii A2 showed low level of DNA damage while Rhodococcus sp. A5 exhibited high resistance since no CPD were detected under natural UV-B exposure, suggesting that the bacterial community is well adapted to this highly solar irradiated environment.

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Variación diurna de la composición bacterioplanctónica y daño en el ADN de la comunidad microbiana de una laguna oligotrófica de los Andes

Resumen
La Laguna Azul es un ambiente oligotrófico localizado a 4560 m de altura y sometido a elevados niveles de radiación solar. La composición de su comunidad bacterioplanctónica fue analizada empleando la técnica de electroforesis en gradiente desnaturalizante y se investigó el impacto de la radiación ultravioleta cuantificando los dimeros de pirimidina (CPD). Además, se expusieron simultáneamente cultivos puros de Acinetobacter johnsonii A2 y Rhodococcus sp. A5 para estudiar la acumulación de CPD. El análisis de los geles mostró siete secuencias pertenecientes a Alpha-proteobacteria (1 banda), Beta-proteobacteria (1 banda), Bacteroidetes (2 bandas), Actinobacteria (1 banda) y Firmicutes (1 banda). A lo largo del día se observaron cambios mínimos en la composición de la comunidad y no se detectaron CPD. A. johnsonii A2 presentó un daño bajo mientras que Rhodococcus sp. A5 no presentó daño en su ADN, sugiriendo que la comunidad bacteriana está muy bien adaptada a este ambiente altamente irradiado.

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A template for re-amplification using primers 2 and 3 and PCR products were sequenced in Macrogen Korea.

Gel analysis gave a total of 15 predominant bands, defined by intensity and frequency of appearance. The 16S rRNA gene sequence of DGGE bands obtained at all sampling times belonged to Alpha and Beta-proteobacteria (Roseobacter sp. and uncultured Beta-proteobacterium), CFB (an uncultured Bacteroidetes), HGC (Agrococcus sp.) and LGC (Staphylococcus sp.). Minor modifications in the community structure were observed throughout the day. Uncultured Beta-proteobacteria (band A3), Agrococcus sp. (band A1) and uncultured bacteria (band A4) were present at all sampling times. Bands that disappeared with increasing solar radiation doses were related to Bacteroidetes (bands A6 and A7). Finally, a band that emerged during solar exposition was related to Roseobacter sp. (band A2) and Staphylococcus sp. (band A5) (Table 1).

The amount of CPD was determined by using the method proposed by Boelen et al. employing a primary antibody (H3, Affitech, Oslo) directed mainly to thymine dimers. CPD detection was done using ECL detection reagents (Amersham) in combination with photosensitive films (Amersham Hyperfilm ECL). Films were scanned and analysed using an image analyser (Gel Doc 2000 Bio Rad). Each blot contained two dilution series of standard DNA with known amounts of CPD, allowing the estimation of absolute amounts of CPD.

No damage in the DNA was detected in the planktonic community during exposure to solar radiation. A. johnsonii A2 showed 21.6±2.55 CPD Mb⁻¹ at the end of the exposure and no CPD were detected in Rhodococcus sp. A5 saline suspension exposure to natural radiation. However, 1,763±174.44 CPD Mb⁻¹ were detected in the calf thymus DNA at the end of the experiments.

The present study contributes to our knowledge of the bacterial diversity of a remote and rather unexplored habitat and the effect of natural radiation in this microbial community. The microbial community in Laguna Azul was similar to those from other Argentinean and Chilean high-altitude wetlands where Bacteroidetes and Proteobacteria were predominant. As it was observed in Laguna Vilama, a HAAW where similar experiments were carried out, no significant changes in the bacterioplankton community composition throughout a day were detected (Table 2). The bands recovered in Laguna Azul revealed sequences shared with Laguna Vilama such as Agrococcus sp. and Roseobacter sp. In both lakes, the uncultured Agrococcus band remained stable during solar exposure while in Laguna Azul, the Roseobacter sp. band increased its intensity during solar exposure.

With regard to the band related to Staphylococcus, an increase in its intensity was observed during natural solar exposure in Laguna Azul. In a previous work, this genus was described as UV-resistant since long-term exposure of water samples from this lake showed that a Staphylococcus-related isolate had high resistance to artificial UV-B radiation. A similar response was observed in other HAAW where long-term water exposure to UV-B showed that a strain related to Staphylococcus was one of the most resistant in the assay conditions.
Andean lakes

Contrary to Laguna Vilama, no damage in the DNA in plankton from Laguna Azul was detected (Table 2). However the high amount of CPD detected in biodosimeters in Laguna Azul would indicate the presence of efficient protection systems in the planktonic community from this environment.

In early works Rhodococcus sp. A5 strain was identified as Nocardia sp. A5 but deep physiological and genetic studies allowed to reassign it to the genus Rhodococcus and renamed it as Rhodococcus sp. A5\textsuperscript{14}. In agreement with previous works high resistance to artificial UV-B radiation

### Table 1  Identification of DGGE bands from Laguna Azul and changes during one-day exposure

<table>
<thead>
<tr>
<th>Phylum</th>
<th>DGGE Band</th>
<th>Closest phylogenetic affiliation (Accession number)</th>
<th>Similarity (%)</th>
<th>Accession number</th>
<th>Local hour</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>11:00</td>
</tr>
<tr>
<td><strong>Proteobacteria</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>a-proteobacteria</strong></td>
<td>A2</td>
<td>Uncultured Roseobacter sp. (DQ659416.1)</td>
<td>99</td>
<td>HE603975</td>
<td>–</td>
</tr>
<tr>
<td><strong>β-proteobacteria</strong></td>
<td>A3</td>
<td>Uncultured β-proteobacterium (EF471681.1)</td>
<td>96</td>
<td>HE603970</td>
<td>+</td>
</tr>
<tr>
<td><strong>CFB</strong></td>
<td>A6</td>
<td>Uncultured Bacteroidetes bacterium (AY862775.2)</td>
<td>96</td>
<td>HE603971</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>A7</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Actinobacteria</strong></td>
<td>A1</td>
<td>Uncultured Agrococcus sp. (DQ870712.1)</td>
<td>99</td>
<td>HE603972</td>
<td>+</td>
</tr>
<tr>
<td><strong>Firmicutes</strong></td>
<td>A5</td>
<td>Uncultured Staphylococcus sp. (HM103367.1)</td>
<td>96</td>
<td>HE603973</td>
<td>+</td>
</tr>
<tr>
<td><strong>Environmental bacteria</strong></td>
<td>A4</td>
<td>Uncultured bacterium (EF443749.1)</td>
<td>95</td>
<td>HE603974</td>
<td>+</td>
</tr>
</tbody>
</table>

+ presence, – absence of band.

### Table 2  Summary of similar parameters measured in Laguna Azul and Laguna Vilama

<table>
<thead>
<tr>
<th>Wetland</th>
<th>Laguna Azul</th>
<th>Laguna Vilama\textsuperscript{a}</th>
</tr>
</thead>
<tbody>
<tr>
<td>Location</td>
<td>Catamarca</td>
<td>Jujuy</td>
</tr>
<tr>
<td>Altitude (m)</td>
<td>4,560</td>
<td>4,660</td>
</tr>
<tr>
<td>Max. UVR registered (Wm\textsuperscript{2})</td>
<td>3.3 (UV-B)\textsuperscript{b}</td>
<td>8.94 (UVR)\textsuperscript{c}</td>
</tr>
<tr>
<td>Changes in bacterial composition</td>
<td>Minor</td>
<td>Minor</td>
</tr>
<tr>
<td>DNA damage (CPD Mb\textsuperscript{-1})</td>
<td>Minor</td>
<td>Minor</td>
</tr>
<tr>
<td>Plankton community</td>
<td>0</td>
<td>320</td>
</tr>
<tr>
<td>Pure cultures</td>
<td>A. johnsonii A2: 21.6</td>
<td>No damage in Pseudomonas sp. V1 or Brachybacterium sp. V5</td>
</tr>
<tr>
<td>Biodosimeters</td>
<td>1,763</td>
<td>625</td>
</tr>
</tbody>
</table>

\textsuperscript{a} Farías et al., 2009.

\textsuperscript{b} ELDONET Radiometer.

\textsuperscript{c} Radiometer 09811-56, Cole Parmer Instrument Company.
was described\textsuperscript{3,4,14,15}, both \textit{A. johnsonii} A2 and \textit{Rhodococcus} sp. A5 showed high UV-B resistance in their native environment since low or no damage were detected in their DNA.

In conclusion, DNA damage over the total microbial community as well as in individual strains from Laguna Azul showed that microorganisms living in such condition have developed efficient DNA protection systems to overcome irradiation stress. Currently, metagenomic studies are carried out in order to reveal the genetic mechanisms related to DNA repair.

**Ethical disclosures**

Protection of human and animal subjects. The authors declare that no experiments were performed on humans or animals for this study.

Confidentiality of data. The authors declare that no patient data appear in this article.

Right to privacy and informed consent. The authors declare that no patient data appear in this article.

Conflicts of interest

The authors declare that they have no conflicts of interest.

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**References**


