



## Genome Announcements

# Draft genome sequence of *Exiguobacterium aurantiacum* strain PN47 isolate from saline ponds, known as “Salar del Huasco”, located in the Altiplano in the North of Chile

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## ABSTRACT

In this report, we present a draft genome of 2,886,173 bp of an *Exiguobacterium aurantiacum* strain PN47 isolate from the sediment of a saline pond named “Salar del Huasco” in the Altiplano in the North of Chile. Strain PN47 encodes adaptive characteristics enabling survival in extreme environmental conditions of high heavy metal and salt concentrations and high alkalinity.

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The *Exiguobacterium* genus is comprised of 17 species, including several strains that come from extreme habitat.<sup>1-5</sup> The “Salar del Huasco” is a saline pond located at an altitude of 3778 m in the Andes Mountains of northern Chile. The average temperature of this pond is 5 °C with high UV irradiation (>1100 W m<sup>2</sup>), alkaline pH (8–10) and sediments with high Arsenic and Boron concentrations.<sup>6,7</sup> In this extreme environment, a rich community of microorganisms, including the *Exiguobacterium* genus have been described.<sup>8-11</sup> To

understand the bacterial mechanism involved in this natural adaptation, the *Exiguobacterium aurantiacum* strain PN47 was isolated (20°19'29.69"S, 68°51'8.85"O), and its genome was sequenced and analyzed.

The PN47 strain is a Gram-positive, non-spore forming bacteria with orange colony on Luria-Bertani agar plate and capability of growth at alkaline pH in the presence of heavy metals and saline conditions. Whole-genome sequencing was performed using 300 bp pair-end reads on the Illumina MiSeq

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platform. A total of 14.2 million reads were obtained with an average length of 178 nucleotides. Reads were filtered by quality (at least 20) and assembled using A5 pipeline (2015 version 2015 year for linux).<sup>12</sup> Open reading frame prediction and annotation was performed using Prokka software version 1.11.<sup>13</sup>

The PN47 strain exhibits 83% homology with the genome of *E. aurantiacum* DSM 6208 (accession number JN1Q0000000), covering 91% of the genome according to BLAST microbe analysis (National Center for Biotechnology Information). In addition, 16S rRNA genes comparison showed a 99% identity match with *E. aurantiacum* strain Q20 (accession number KU933354.1), thereby confirming species identity. Using the RNAmmer Prediction Server (Technical University of Denmark) and tRNA analysis by ARAGORN,<sup>14</sup> 10 copies of 5S rRNA, a single copy of 16S and 23S rRNA gene, and a total of 65 tRNAs sequences were identified.

Using the RAST-NMPDR server,<sup>15</sup> the genome was observed to include 2927 coding sequence (CDS) spread in 392 subsystems, including lipid, fatty acid and isoprenoid metabolism pathways probably related with the synthesis of the orange pigment. In addition, PN47 strain has genes related with hot and cold temperature stress in accordance with atmospheric temperature changes commonly described in this area (22 to  $-8^{\circ}\text{C}$ ). The presence of *ars* operon and arsenite oxidase genes are probably associated with an arsenic resistance mechanism, but the classical *atr1*, *van1* or *bor* genes described for boron resistance mechanisms were absent. One possibility is that a putative cross-stress resistance mechanism produces boron tolerance,<sup>16</sup> through their own copper and salt stress response genes. Among salt resistance genes, several proton/anti-porters were found, which along with genes of choline-glycine betaine transport and synthesis, could contribute to salt tolerance and facilitate growth in alkaline conditions.<sup>17-19</sup>

In light of this report, future genomic comparisons will contribute to understanding the flexibility of *E. aurantiacum* species to survive in diverse environmental conditions. Strains of PN47 that more closely match the genome described in this study are those that come from potato processing factories (*E. aurantiacum* DSM 6208)<sup>20</sup> and petroleum contaminated soil (Q20 strain).

Regarding nucleotide sequence accession numbers, this Whole Genome Shotgun project has been deposited at DDBJ/ENA/Embank under the accession MKXO00000000. The version described in this paper is version MKXO01000000.

### Conflicts of interest

The authors declare no conflicts of interest.

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