

**TITLE:** GENOME SEQUENCING OF THREE *Bacillus* STRAINS ISOLATED IN PERU AND SEARCH OF GENES RELATED TO CYANIDE METABOLISM

**AUTORS:** ZAPATA SIFUENTES, DANIELA<sup>1</sup>; JUSTO ARÉVALO, SANTIAGO<sup>1,2</sup>; PIERRY, PAULO MARQUES<sup>2</sup>; MORAIS, CARLOS<sup>2</sup>; QUIÑONES AGUILAR, MAURO<sup>1</sup>; PINEDA CHAVARRÍA, ROBERTO<sup>1</sup>; SETUBAL, JOÃO CARLOS<sup>2</sup>; DA SILVA, ALINE MARIA<sup>2</sup>.

**INSTITUTION:** 1. LABORATORIO DE BIOTECNOLOGÍA AMBIENTAL. FACULTAD DE CIENCIAS BIOLÓGICAS. UNIVERSIDAD RICARDO PALMA; 2. DEPARTAMENTO DE BIOQUÍMICA, INSTITUTO DE QUÍMICA. UNIVERSIDADE DE SÃO PAULO

**ABSTRACT**

Cyanide is used in several industrial processes due to its high affinity for metals. This same property makes cyanide a toxic compound by inhibiting enzymes such as cytochrome oxidase causing cellular asphyxia and death in most aerobic organisms. Therefore, industries must reduce the concentration of cyanide in their effluents before their final disposal. Various methodologies have been used for this purpose but not one of them meets all the desired characteristics: efficiency, low cost, environmentally friendly. Bioremediation processes are environmentally friendly and have low costs, but have not yet met the required efficacy. This is partially due to lack of knowledge on the cyanide degradation metabolic pathways and their regulation in response to cyanide. Here we present the draft genome sequences of three *Bacillus* strains (*B. pumilus* PER-URP-08, *B. licheniformis* PER-URP-12, *B. subtilis* PER-URP-17) that can degrade cyanide *in vitro* and were isolated from mining drainage in Casapalca - Lima, Peru. Genomic DNA was prepared using Promega Wizard DNA purification kit, subjected to indexed DNA fragment libraries preparation using the Illumina Nextera XT Library Prep Kit and sequenced using the Illumina MiSeq V2 500-cycle reagent kit. The quality of the paired-end reads was checked in FastQC prior to assembly with Discover (*B. pumilus*) and A5 (*B. licheniformis* and *B. subtilis*). Genome scaffolding was performed with the program MeDuSa. The draft genomes were submitted to NCBI and IMG for automatic annotation. Initial analyses revealed that *B. pumilus* strain presented the cyanide dihydratase CynD (pFAM 00795). The genomes of *B. pumilus*, *B. licheniformis* and *B. subtilis* strains encode respectively, six, seven and three CDSs with a rhodanese-like domain (pFAM 00581) that can convert cyanide into thiocyanate. In addition, the genomes of *B. pumilus* and *B. licheniformis* strains encode, respectively, one and two amidases, which together with nitrile hydratases could form nitrile degradation systems. Our observations warrant further investigation to evaluate expression level of these CDSs upon exposition of the three strains to cyanide.

**Keywords:** Genome sequencing; *Bacillus*; Cyanide

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