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Short Communication

Draft genome sequence of *Pseudoalteromonas piscicida* strain 36Y_RITHPW, a hypersaline seawater isolate from the south coast of Sonora, Mexico

Ricardo Sánchez-Díaz[a], Zinnia Judith Molina-Garza[a], Lucía Elizabeth Cruz-Suárez[a], Joseph Selvin[b], George Seghal Kiran[c], José Cuauhtémoc Ibarra-Gámez[d], Bruno Gómez-Gil[e], Lucio Galaviz-Silva[a,*]

[a] *Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Ave. Universidad SN, Cd. Universitaria, San Nicolás de los Garza, Nuevo León, Mexico*
[b] *Department of Microbiology, Pondicherry University, Puducherry, India*
[c] *Department of Food Science and Technology, Pondicherry University, Puducherry, India*
[d] *Departamento de Ciencias Agronómicas y Veterinarias, Instituto Tecnológico de Sonora, Ciudad Obregón, Sonora, Mexico*
[e] *CIAD, Mazatlán Unit for Aquaculture and Environmental Management, Mazatlán, Sinaloa, Mexico*

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ABSTRACT

Objectives: This study reports the draft genome sequence of *Pseudoalteromonas piscicida* strain 36Y_RITHPW, a marine Gammaproteobacteria that synthesises bioactive compounds with antagonistic activity against *Vibrio parahaemolyticus*, a multidrug-resistant strain that is the causative agent of acute hepatopancreatic necrosis disease (AHPND), reported in shrimp farm outbreaks from Asia to Mexico with mortality rates of 80–100%.

Methods: The genome of *P. piscicida* 36Y_RITHPW was sequenced with an Ion Torrent™ Personal Genome Machine™ (PGM) platform. A total of 606 805 reads were constructed for a 308.48 Mbp and 33.5 × coverage. A high-quality draft assembly and ordering of contigs was obtained with Mauve. The annotation was obtained with RAST and antiSMASH.

Results: The genome size consists of 5.15 Mbp, with a total of 4548 genes, 4217 protein-coding sequences and a GC content of 43.3%. Several resistance genes as well as other genes involved in the production of bacteriocins and ribosomally synthesised antibacterial peptides are also present.

Conclusions: Mining of this draft genome provides valuable information to explain the antagonistic capacity of *P. piscicida* 36Y_RITHPW, a useful strain as a potential probiotic in shrimp aquaculture against pathogenic *V. parahaemolyticus*.

The genus *Pseudoalteromonas* (Gammaproteobacteria) is ubiquitous in the marine environment and includes Gram-negative, heterotrophic and aerobic non-spore-forming rods with a polar flagellum [1]. It can be found in polar regions, seawater, sediments and on the surfaces of marine organisms [2]. *Pseudoalteromonas* is a prominent genus involved in the biosynthesis of marine bioactives and hydrolytic enzymes with antibacterial, antifouling and antibiofilm activities. Considering its anti-infective activity and probiotic nature, this genus is promising in shrimp health management. This marine bacterium has been used as probiotic in aquaculture systems to inactivate pathogens and to prevent disease outbreaks [3].

General features of *Pseudoalteromonas piscicida* strain 36Y_RITHPW and minimum information about the genome sequence (MIGS) are summarised in Table 1. This strain synthesises antimicrobial compounds that show inhibitory and antibiofilm activity against shrimp pathogenic *Vibrio* spp., including *Vibrio parahaemolyticus* that causes acute hepatopancreatic necrosis disease (AHPND) in shrimp culture [4].

Total genomic DNA was sequenced with an Ion Torrent™ Personal Genome Machine™ (PGM) platform (Thermo Fisher Scientific, Waltham, MA). A total of 606 805 reads were obtained for 308.48 Mbp (33.5 × coverage). Sequence reads were assembled with Newbler v.2.6, obtaining 226 contigs (N_{50} value of 83.97 Kbp) for a 5 154 709-bp genome with a GC

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[*] Corresponding author.
E-mail address: lucio.galavizsl@uanl.edu.mx (L. Galaviz-Silva).

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Table 1
General features of *Pseudoalteromonas piscicida* strain 36Y_RITHPW and minimum information about the genome sequence (MIGS) mandatory information [8].

Item	Description
General features	
Current classification	Domain: Bacteria Phylum: Proteobacteria Class: Gammaproteobacteria Order: Alteromonadales Family: Pseudoalteromonadaceae Genus: *Pseudoalteromonas* Species: *piscicida*
Gram stain	Negative
Cell shape	Rod
Pigmentation	Pigmented
Sporulation	Non-spore-forming
Temperature	10–40 °C
Optimum temperature	28 °C
Salinity	Required
pH range	7.0–8.5
Carbon source	Varied
Energy source	Chemoorganotrophic
Oxygen	Aerobic
Motility	Motile
MIGS data	
Investigation type	Bacteria_archaea
Project name	Antagonistic bacteria against *Vibrio parahaemolyticus* (AHPND)
Collection date	5 September 2014
Country	Mexico
Coordinates	26.783083 1N, 109.807222 W
Depth	15 cm
Altitude/elevation	NA
Environment	Estuary with hypersaline seawater
Number of replicons	NA
Reference biomaterial	**SAMN07269797** (BioSample accession no.)
Biotic relationship	Free-living
Trophic level	Heterotroph
Oxygen requirement	Aerobe
Sequencing method	Ion Torrent
Genome coverage	33.5×
Assembly method	Newbler (v.2.6)
Estimated size	5 154 709 bp
Finishing strategy	Draft

AHPND, acute hepatopancreatic necrosis disease.

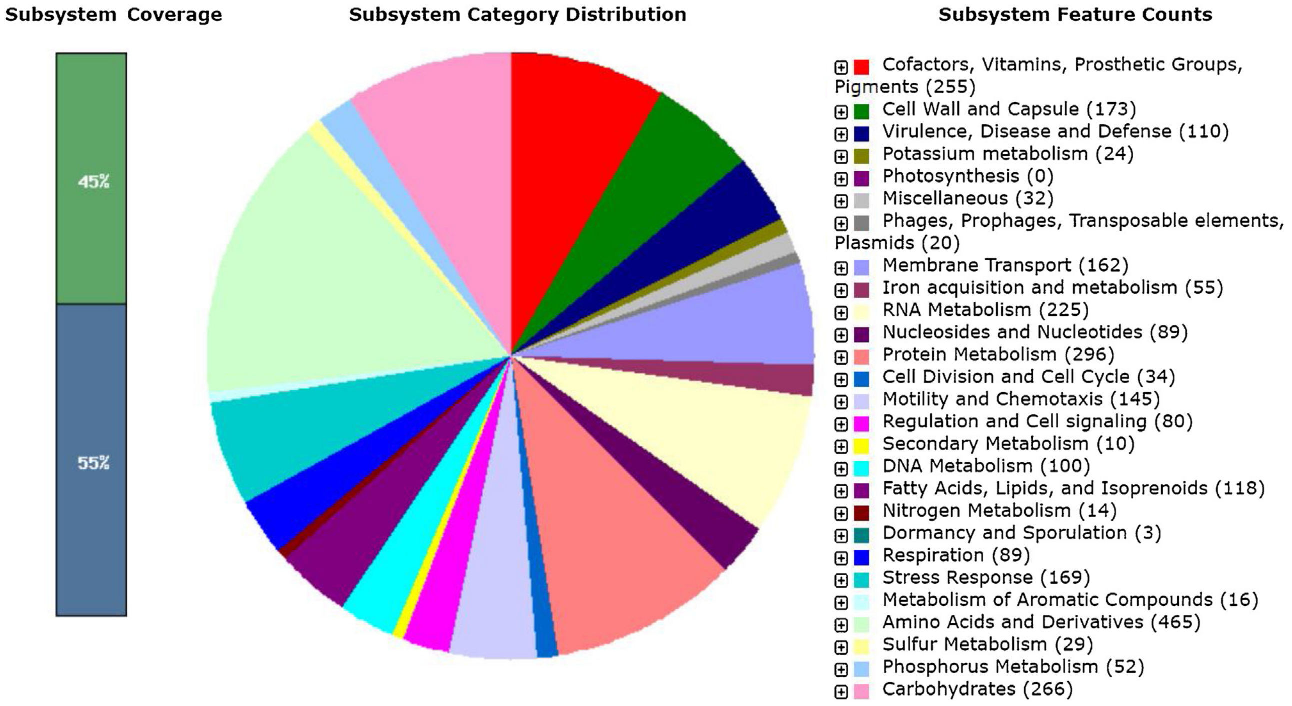
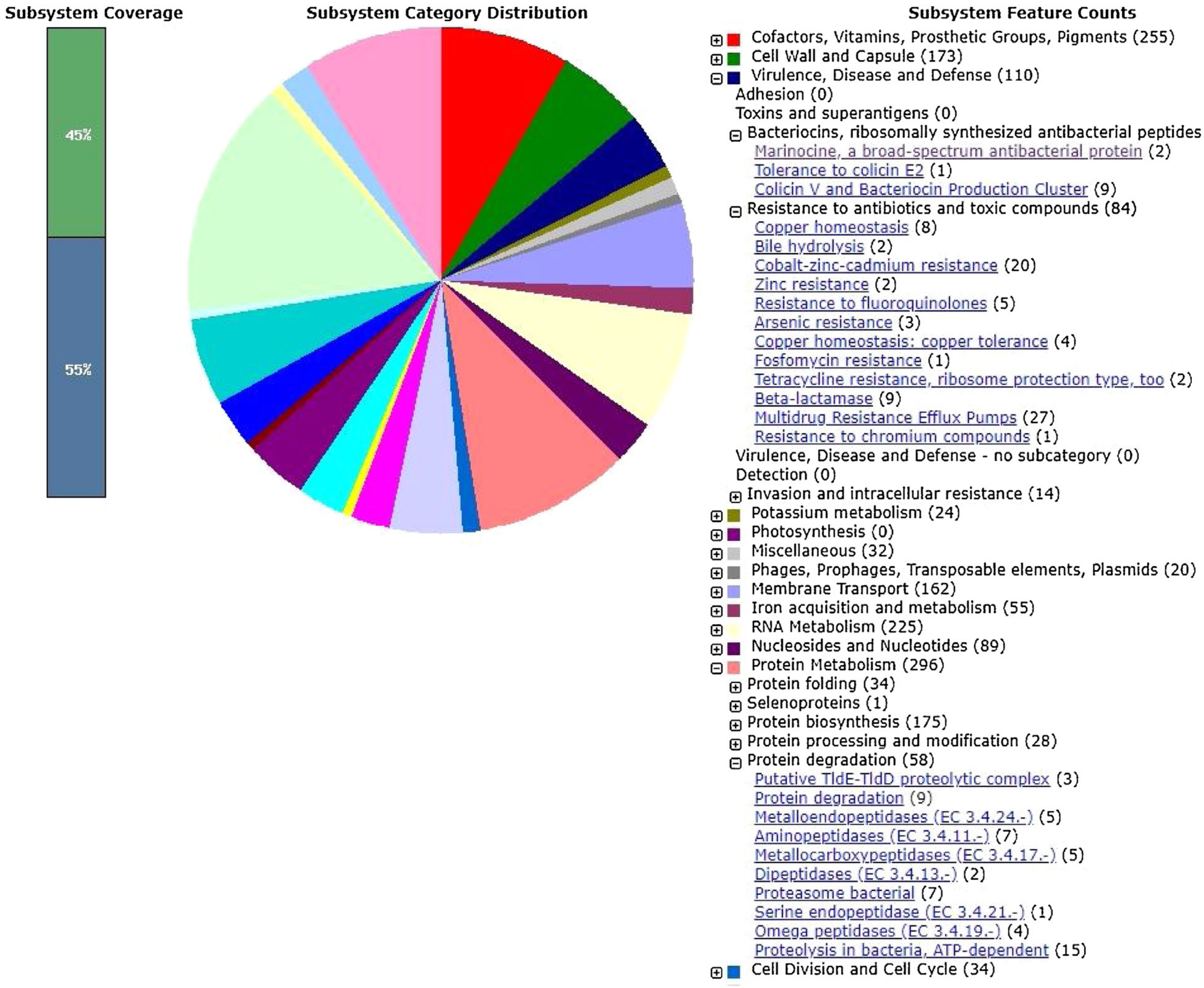


Fig. 1. Subsystems category distribution of *Pseudoalteromonas piscicida* strain 36Y_RITHPW revealed by Rapid Annotation using Subsystem Technology (RAST) annotation. The subsystem distribution is indicated in the pie graph, with each colour representing a subsystem category (gene group with functional roles) and the feature counts listed on the right side.


Subsystem Coverage

Subsystem Category Distribution

Subsystem Feature Counts

⊞ ■ Cofactors, Vitamins, Prosthetic Groups, Pigments (255)
⊞ ■ Cell Wall and Capsule (173)
⊟ ■ Virulence, Disease and Defense (110)
  Adhesion (0)
  Toxins and superantigens (0)
  ⊟ Bacteriocins, ribosomally synthesized antibacterial peptides (12)
    Marinocine, a broad-spectrum antibacterial protein (2)
    Tolerance to colicin E2 (1)
    Colicin V and Bacteriocin Production Cluster (9)
  ⊟ Resistance to antibiotics and toxic compounds (84)
    Copper homeostasis (8)
    Bile hydrolysis (2)
    Cobalt-zinc-cadmium resistance (20)
    Zinc resistance (2)
    Resistance to fluoroquinolones (5)
    Arsenic resistance (3)
    Copper homeostasis: copper tolerance (4)
    Fosfomycin resistance (1)
    Tetracycline resistance, ribosome protection type, too (2)
    Beta-lactamase (9)
    Multidrug Resistance Efflux Pumps (27)
    Resistance to chromium compounds (1)
  Virulence, Disease and Defense - no subcategory (0)
  Detection (0)
  ⊞ Invasion and intracellular resistance (14)
⊞ ■ Potassium metabolism (24)
⊞ ■ Photosynthesis (0)
⊞ ■ Miscellaneous (32)
⊞ ■ Phages, Prophages, Transposable elements, Plasmids (20)
⊞ ■ Membrane Transport (162)
⊞ ■ Iron acquisition and metabolism (55)
⊞ ■ RNA Metabolism (225)
⊞ ■ Nucleosides and Nucleotides (89)
⊟ ■ Protein Metabolism (296)
  ⊞ Protein folding (34)
  ⊞ Selenoproteins (1)
  ⊞ Protein biosynthesis (175)
  ⊞ Protein processing and modification (28)
  ⊟ Protein degradation (58)
    Putative TldE-TldD proteolytic complex (3)
    Protein degradation (9)
    Metalloendopeptidases (EC 3.4.24.-) (5)
    Aminopeptidases (EC 3.4.11.-) (7)
    Metallocarboxypeptidases (EC 3.4.17.-) (5)
    Dipeptidases (EC 3.4.13.-) (2)
    Proteasome bacterial (7)
    Serine endopeptidase (EC 3.4.21.-) (1)
    Omega peptidases (EC 3.4.19.-) (4)
    Proteolysis in bacteria, ATP-dependent (15)
⊞ ■ Cell Division and Cell Cycle (34)

Fig. 1. (Continued)

content of 43.3%. A draft assembly and ordering of contigs were constructed with Mauve Genome Alignment v.2.4.0. Annotation was performed with Rapid Annotation using Subsystem Technology (RAST). A total of 4548 genes, 4217 protein-coding sequences and 71 RNA sequences (4 rRNAs, 63 tRNAs and 4 ncRNAs) were found. Annotation revealed 84 genes involved in resistance to antimicrobials such as fluoroquinolones, fosfomycin and tetracycline as well as a group of multidrug resistance efflux pumps and β-lactamase genes; resistance genes to toxic compounds such as copper, zinc, arsenic, chromium and cadmium; 12 genes involved in the production of bacteriocins and ribosomally synthesised antibacterial peptides (marinocine and colicin V); 80 genes involved in regulation (orphan) and cell signalling (cAMP); 10 genes involved in secondary metabolism, such as lanthionine synthetases, paerucumarin (a novel cumarin) and auxin biosynthesis; and an integron gene related with transposable elements mechanisms. Annotation also revealed the presence of coding regions for protein degradation (metalloendopeptidases, aminopeptidases, dipeptidases, omega peptidases and proteolysis in bacteria ATP-dependent, among others) (Fig. 1). Using antiSMASH v.3.0.5, two bacteriocin-type clusters were identified, including one lantipeptide gene, 4 type I polyketide synthase/non-ribosomal peptide synthase (PKS/NRPS) and one aryl-polyene/NRPS hybrid cluster, and one type I PKS and 7 NRPS cluster [5].

Strain DE2-B of *P. piscicida* is similar to 36Y_RITHPW, since the former is somewhat larger with a genome size of 5 317 048 bp (two chromosomes of 4 128 210 bp and 1 188 838 bp), a GC content of 43.44%, and a genome containing a large number of genes (4722 plus 322 pseudogenes), but with 4258 predicted protein genes, 31 rRNAs and 107 tRNAs. Also, DE2-B has putative proteases, including 11 serine proteases and 7 metalloproteases [6,7].

This whole genome shotgun project has been deposited at DDBJ/ENA/GenBank under accession no. **NKHF00000000**. The version described in this paper is the first version, **NKHF01000000**.

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Competing interests

None declared.

Ethical approval

Not required.

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