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GENOME SEQUENCES

Genomic Islands in the Full-Genome Sequence of an NAD-Hemin-Independent *Avibacterium paragallinarum* Strain Isolated from Peru

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ABSTRACT Here, we report the full-genome sequence of an NAD-hemin-independent *Avibacterium paragallinarum* serovar C-2 strain, FARPER-174, isolated from layer hens in Peru. This genome contained 12 potential genomic islands that include ribosomal protein-coding genes, a *nadR* gene, hemocin-coding genes, sequences of fagos, an *rtx* operon, and drug resistance genes.

Avibacterium paragallinarum is the etiologic agent of infectious coryza, an acute respiratory disease of chickens, which is globally distributed and causes serious economic losses in the poultry production industry. It is a Gram-negative, nonmotile, capsulated, facultative anaerobe belonging to the family *Pasteurellaceae* and is classified in 9 serovars distributed in 3 serogroups (A, B, and C) (1, 2). The study of its genome and virulence factors (hemagglutinin antigen, capsule, lipopolysaccharide, and RTX toxin) is important to better understand the pathogenesis of infectious coryza (3–6). Usually, virulence factor-coding genes are located in genomic islands (GIs) comprising clusters of genes suspected to have a horizontal origin (integrons, transposons, integrative and conjugative elements, and prophages) (7–9).

The strain FARPER-174 was isolated from nasal secretions of the paranasal sinuses of layer hens from an infectious coryza outbreak from the central rainforest region of Peru during 2015 and was grown in blood culture medium with X-(hemin) and V-(NAD) factors (10). FARPER-174 was subsequently cultured in brain heart infusion (BHI) agar without any factors at 37°C in a candle jar for 24 hours. The strain was identified as *A. paragallinarum* serovar C-2 using the morphology of the colony, biochemical tests (catalase test, oxidase test, urease test, peptone test, and carbohydrate fermentation, such as that of maltose, mannitol, lactose, and sorbitol) (11), specific PCR (12), and hemagglutination inhibition (HI) (13). The disk diffusion test (14) revealed resistance to colistin, ampicillin, sulfamethoxazole-trimethoprim, penicillin, neomycin, lincomycin, oxacillin, enrofloxacin, and gentamicin. The strain was susceptible to amoxicillin-clavulanic acid, doxycycline, streptomycin, florfenicol, tiamulin, levofloxacin, and gatifloxacin.

DNA was extracted from the fresh bacterial culture (500 ml of BHI without factors at 37°C with agitation at 180 rpm for 24 hours) centrifuged at 5,000 × *g* for 15 min. The pellet was resuspended in phosphate-buffered saline (PBS) for DNA isolation using the phenol-chloroform protocol (15). The genome was sequenced on the PacBio RS II platform (Pacific Biosciences, CA) using P6-C4 chemistry and assembled with Hierarchical Genome Assembly Process (HGAP) version 3.0 (16) with default parameters by Macrogen, Inc. (South Korea). A total of 92,198 reads (average length, 8,615 bp; N_{50}, 12,231 bp) generated a closed circular genome of 2,425,949 bp, with a G+C content of 40.87% and 147× average depth of coverage, and no plasmids.

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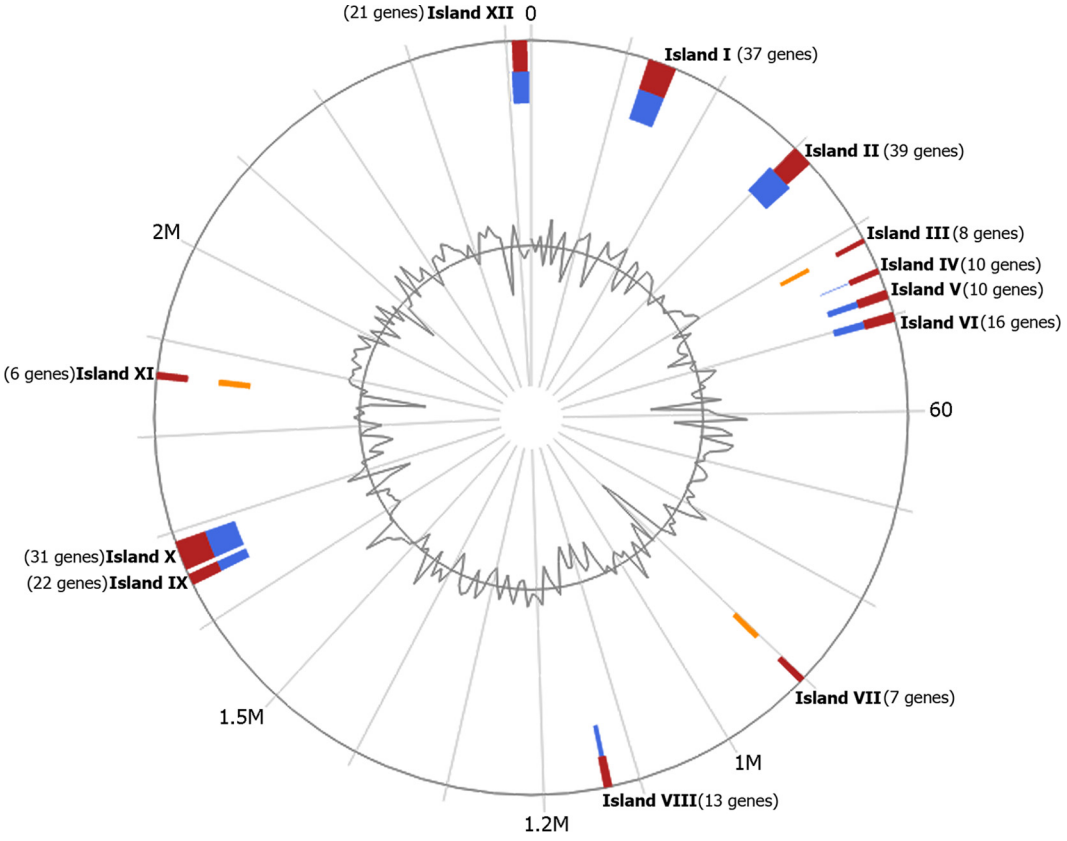

FIG 1 Genomic islands of strain FARPER-174 predicted by IslandViewer 4. The outer circle shows the scale line in megabase pairs. Predicted genomic islands are colored based on methods, as follows: red, integrated; blue, IslandPath-DIMOB; and orange, SIGI-HMM. The center circle represents the G+C content (%).

The FARPER-174 strain genome was annotated with the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP v4.7) (17). Some hypothetical proteins were similar to coding DNA sequences (CDSs) of *A. paragallinarum* previously published in GenBank; the annotations were, therefore, manually improved in this version.

A total of 2,327 genes, 2,248 CDSs, 106 pseudogenes, and 79 RNA genes, which included 56 tRNAs, 19 rRNAs (5S, 16S, and 23S), 1 transfer-messenger RNA (tmRNA), and 3 noncoding RNAs (ncRNAs), were identified. Six 16S rRNA genes compared by BLASTn with the 16S rRNA database of NCBI are from 97% to 98% similar to those of *A. paragallinarum* strain NCTC 11296 (GenBank accession number NR_042932). Genomic islands were predicted by submitting the PGAAP-generated GenBank file to the IslandViewer 4 tool (18). In total, 12 genetic islands, namely, I to XII, which include 220 genes (Fig. 1), were found.

Data availability. The complete *Avibacterium paragallinarum* strain FARPER-174 genome sequence is available in GenBank under the accession number CP034110. Raw data are available in SRA under BioSample number SAMN10471982 and SRA run number SRR8506728.

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We declare no competing interests.

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