

Draft Genome Sequence of High-Siderophore-Yielding *Pseudomonas* sp. Strain HYS

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We sequenced the genome of the high-siderophore-yielding strain *Pseudomonas* sp. HYS and then analyzed its iron acquisition systems. The 5.6-Mb draft genome sequence has a special pattern of pyoverdine synthesis clusters and contains an *hmuRSTUV* heme uptake cluster, which has a homolog only in some strains of the order *Enterobacteriales*.

Iron is an essential element for bacteria, but free Fe³⁺ is poorly available owing to its low concentration under aerobic conditions. Bacteria secrete siderophores, such as pyoverdine and pyochelin in *Pseudomonas aeruginosa* (4) or enterobactin in *Escherichia coli*, which are ferric-ion-specific ligands that can acquire insoluble iron from the environment effectively (9). The ability of *Pseudomonas* sp. strain HYS, isolated from the water of East Lake of Wuhan, China, to secrete siderophores is approximately 5-fold higher than that of other *Pseudomonas* strains (e.g., *P. fluorescens* CHA0, *P. putida* ATCC 12633, and *P. aeruginosa* PA14), as tested by a universal siderophore detection assay (11). This phenomenon indicates that strain HYS has a special iron acquisition or regulation system. In order to gain insight into such systems, purified genomic DNA was sent to Shenzhen Huada Genomics Institute (BGI) (Shenzhen, China) and sequenced with Solexa paired-end sequencing technology.

Sequencing genomic DNA of *Pseudomonas* sp. HYS yielded 519.18-Mb paired-end sequence reads after adapter and duplication filtering. Raw paired-end reads were *de novo* assembled using the SOAPdenovo alignment tool (<http://soap.genomics.org.cn/index.html#intro2>), which generated 231 contigs, excluding contigs shorter than 200 bp, and were then assembled into 64 scaffolds by paired-end mapping. The total length of the draft genome is 5,639,475 bp, with a mean G+C content of 62.42%. Average nucleotide identity of the draft genome to sequenced genomes of nine *Pseudomonas* species was calculated by using the BLASTN algorithm (2, 7), showing that the strain is closely related to *Pseudomonas entomophila* L48 and *P. putida* GB-1. Protein-coding open reading frames (ORFs) were predicted by using the Glimmer version 3.0 software program (6). All predicted genes were annotated by BLAST (1), with NR, KEGG, COG, Swiss-Prot, and TrEMBL as reference protein databases. The iron acquisition-related genes and clusters were manually analyzed depending on the annotation from all databases.

Pseudomonas sp. HYS has 2 predicted global positive suppressor Fur (ferric uptake regulator)-coding genes, 18 inducing regulator *fecIR*-like gene clusters, and 37 genes encoding outer membrane receptors for heme, pyoverdine, enterochelin, colicins, and other unknown siderophores. Features of these regulators and receptors look similar to those of other bacteria (3). The pattern of pyoverdine synthesis clusters is similar to that for *P. entomophila* L48 (8); *pvdP* and *pvdE* are located in separated clusters, while these two genes are always adjacent to each other in other *Pseudomonas* species (10). *Pseudomonas* sp. HYS has four heme uptake systems, the Phu, Has, Hxu, and Hmu systems. The former two systems are common systems in *Pseudomonas* species, but the Hxu system has been found only in *P. entomophila* L48 and *P. aeruginosa* PA14 (5). The *hmuRSTUV* clus-

ter of the Hmu system is similar to findings for some strains of the order *Enterobacteriales* and has no similarity to any other *Pseudomonas* species by BLAST search with the NR database. The genome sequence of *Pseudomonas* sp. HYS will offer new information on the iron acquisition network related to horizontal gene transfer or evolution in bacteria.

Nucleotide sequence accession numbers. This whole genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AJJP00000000](http://ajjp00000000). The version described in this paper is the first version, [AJJP01000000](http://ajjp01000000).

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