The Genomic Standards Consortium
Complete genome sequence of Ferrimonas balearica type strain (PATT)

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Ferrimonas balearica Rossello-Mora et al. 1996 is the type species of the genus Ferrimonas, which belongs to the family Ferrimonadaceae within the Gammaproteobacteria. The species is a Gram-negative, motile, facultatively anaerobic, non spore-forming bacterium, which is of special interest because it is a chemoorganotroph and has a strictly respiratory metabolism with oxygen, nitrate, Fe(III)-oxyhydroxide, Fe(III)-citrate, MnO₂, selenate, selenite and thiosulfate as electron acceptors. This is the first completed genome sequence of a member of the genus Ferrimonas and also the first sequence from a member of the family Ferrimonadaceae. The 4,279,159 bp long genome with its 3,803 protein-coding and 144 RNA genes is a part of the Genomic Encyclopedia of Bacteria and Archaea project.

Introduction
Strain PAT (⁴ DSM 9799 = CCM 4581) is the type strain of the species Ferrimonas balearica, which is the type species of its genus Ferrimonas [1,2]. Currently, there are five species in the genus Ferrimonas [3]. The generic name derives from the Latin word ‘ferrum’ meaning ‘iron’ and the Greek word ‘monas’ meaning ‘unit’, referring to an iron(III)-reducing cell. The species epithet is also derived from the Latin word ‘balearica’ meaning ‘of the Balearic Islands’, referring to the place where the strain was isolated [1]. Ferrimonas is the type genus of the family Ferrimonadaceae and one of two genera in the family Ferrimonadaceae [4]. Strain PAT was described in 1995 by Rossello-Mora et al. [1] who isolated the strain from the upper few centimeters of marine sediment of the Palma de Mallorca harbor, Spain [1,5]. Here we present a summary classification and a set of features for F. balearica PAT, together with the description of the complete genomic sequencing and annotation.

Classification and features
The 16S rRNA gene sequence of PAT is 99% identical to four culturable strains, which are reported...
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Two strains, A2A-18 (AB193752) and A3B-47-3 (AB193753), were isolated from marine sand [7]. The culturable strain S8-05 (EU620413) was isolated from Palk Bay sediment in Thondi, India and another strain with accession number AY158002 was isolated from Ala Wai Canal sediment in Honolulu, USA. The 16S rRNA gene of strain PAT shares 93.5-97.4% sequence identity with the sequences of the type strains from the other members of the family Ferrimonadaceae [8]. The environmental samples database (env_nt) contains the marine metagenome clone 1096626783183 (96% sequence identity, AA-CY020355234). The genomic survey sequences database (gss) contains the uncultured bacterium clone BYUP987.b1 (92%, EF996742), isolated from a fecal sample of adult woman who gave birth after 11 months [9]. Altogether, strains belonging to the species F. balearica or the genus Ferrimonas are rather rare in the habitats screened so far (status September 2010).

Figure 1 shows the phylogenetic neighborhood of F. balearica PAT in a 16S rRNA based tree. The sequences of the seven 16S rRNA gene copies in the genome differ from each other by up to five nucleotides, and differ by up to four nucleotides from the previously published sequence (X93021), which contains two ambiguous base calls.

Strain PAT is a Gram-negative, nonspore-forming, facultatively anaerobic bacterium [1]. The cells are straight rods (0.3-0.5 × 1.2-1.5 µm) with rounded ends (Figure 2, Table 1) [1,5] and appear singly, occasionally in pairs or short chains and usually not encapsulated [1,5]. Strain PAT is motile by means of monotrichous flagella (not visible in Figure 2, but 10% of the cells in the original liquid culture were highly motile) [1]. Colonies produce a black iron precipitate when the cells are grown on TSI agar [1]. Although initially isolated using TSI based media this strain grows better on Marine Broth. Colonies are often brown and mucous when the cells are grown under aerobic conditions [5]. Fresh isolates of this species may not form colonies on PYG agar medium, but the colonies are formed after several subcultivations in enrichment medium [1,5]. Resting stages of strain PAT are not known [5]. Cells of the strain undergo autolysis within five days under aerobic conditions [1,5]. Strain PAT does not contain polyhydroxybutyrate (PHB) or other intracellular inclu-
sions [2]. The strain is chemoorganotrophic. Under anaerobic conditions, the reduction of Fe(III)-oxyhydroxide is coupled to the utilization of lactate as the electron donor, which yields magnetite [1,5]. Strain PAT\textsuperscript{T} uses oxygen, nitrate, Fe(III)-oxyhydroxide, Fe(III)-citrate, MnO\textsubscript{2}, selenate, selenite and thiosulfate as electron acceptors [1,5,25]. Strain PAT\textsuperscript{T} requires a minimum of 0.5% NaCl for growth, with a range of NaCl tolerance of 0.5%-7.5% [1]. It does not grow at 5°C or 44°C but does grow at 42°C [1]. The pH range for growth is 6-9 [1]. Enzymatic reactions are positive for catalase, oxidase, phenylalanine deaminase, DNAse and lipase (Tween 20 and Tween 80), but negative for amylase, arginine dihydrolase, gelatinase, lysine decarboxylase, Simmons citrate and urease [1,5]. The strain does not hydrolyze starch [1]. The genus \textit{Ferrimonas} can be distinguished from other strictly respiratory Gram-negative genera of the \textit{Gammaproteobacteria} based on its ability to reduce Fe(III), denitrification, growth at 42°C, presence of phenylalanine deaminase activity, inability to grow in NaCl-free media, lack of gelatinase, urease and a negative reaction of Simmons citrate test [5].

![Figure 2. Scanning electron micrograph of F. balearica PAT\textsuperscript{T}](image)

**Chemotaxonomy**

The quinone profiles of strain PAT\textsuperscript{T} are MK-7 (62.9%), Q-8 (20.4%) and Q-7 (16%) [7]. The presence of both menaquinones and ubiquinones being indicative of the ability of this organism to grow aerobically (with ubiquinones) and anaerobically (with menaquinones). The presence of menaquinones and ubiquinones with different distributions of isoprenoid side chains is a feature also shared by members of the genus \textit{Shewanella} [26-28] and \textit{Paraferrimonas} [29]. The major cellular fatty acids of strain PAT\textsuperscript{T}, when grown on PYG medium, given in the original species description are C\textsubscript{17:1ω8c} (27.5%), iso-C\textsubscript{15:0} (14.5%), C\textsubscript{17:0} (7.8%), iso-C\textsubscript{13:0} (5.8%), C\textsubscript{16:1ω7c} (4.7%), C\textsubscript{15:0} (4.5%), C\textsubscript{14:0} (4.2%), C\textsubscript{18:1ω9c} (4.0%) and C\textsubscript{12:0} 3-OH (1.8%), C\textsubscript{17:1ω6c} (1.6%) and C\textsubscript{18:1ω7c} (1.2%) [1]. More recent data show a somewhat different fatty acid pattern [7], with the fatty acids comprising iso-C\textsubscript{15:0} (9.8%), C\textsubscript{15:0} (1.8%) iso-C\textsubscript{16:1ω9c} (10.4%) iso-C\textsubscript{16:ω7c} (5.2%), C\textsubscript{16:0} (13.4%) iso-C\textsubscript{17:0} (2.1%) C\textsubscript{17:1ω8c} (12.6%) C\textsubscript{17:0} (7.9%) C\textsubscript{18:1ω9c} (17.6%) C\textsubscript{18:1ω7c} (4.9%) and C\textsubscript{18:0} (3.9%). Hydroxylated fatty acids were not reported. Interestingly the fatty acids reported in a subsequent paper [25] that are based on the work of Kasuta et al. [7] omit the iso-C\textsubscript{16:1} fatty acids. The fatty acids reported in the original publication [1] show a number of features also found in members of the genera \textit{Shewanella}.

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and Paraferrimonas [29,30]. Data generated in the DSMZ during the course of this work indicates that the fatty acids comprise, iso-C<sub>13:0</sub> (3.7%), C<sub>13:0</sub> (2.7%), C<sub>12:0</sub> 3OH (2.2%), iso-C<sub>14:0</sub> (1.1%), C<sub>14:0</sub> (1.0%), iso-C<sub>13:0</sub> 3OH (3.7%), C<sub>13:0</sub> 3OH (1.9%), iso-
C<sub>15:0</sub> (16.1%), C<sub>15:1</sub> w<sub>8c</sub> (2.1%), C<sub>15:0</sub> (4.5%), C<sub>14:0</sub> 3-
OH (2.9%), C<sub>16:1</sub> w<sub>9c</sub> (8.1%), C<sub>16:1w7c</sub> (4.9%), C<sub>16:0</sub>
(8.4%), iso-C<sub>15:0</sub> 3OH, (0.9%), iso-C<sub>17:0</sub> (1.4%), C<sub>17:1</sub>
w<sub>8c</sub> (14.7%), C<sub>17:0</sub> (5.6%), C<sub>18:1</sub> w<sub>9c</sub> (7.8%) and C<sub>18:1</sub>
w<sub>7c</sub> (1.4%). These results are more consistent with
those published in the original description [1], but
there are differences that cannot be attributed to
differences in the growth conditions. The com-
plete absence of hydroxylated fatty acids in the
work of Kasuta et al. [7] suggests that no attempt
was made to detect them. The presence of at least
two positional isomers in unsaturated fatty acids
with the same chain length is indicative of the
presence of at least two enzymatic pathways for
introducing the double bonds. A fairly simple po-
lar lipid pattern has been reported for Ferrimonas
futtsuensis, comprising, phosphatidylglycerol,
phosphatidylethanolamine and an unidentified
aminophospholipid [29].

| Table 1. Classification and general features of F. balearica PAT<sup>T</sup> according to the MIGS recommendations [16]. |
| MIGS ID | Property | Term | Evidence code |
|---------|----------|------|---------------|
| MIGS-22 | Oxygen requirement | facultatively anaerobic | TAS [1] |
| MIGS-6  | Habitat     | marine sediment | TAS [1] |
| MIGS-15 | Biotic relationship | free-living | NAS |
| MIGS-14 | Pathogenicity | none | NAS |
| MIGS-4  | Geographic location | Palma de Mallorca harbor, Spain | TAS [1] |
| MIGS-5  | Sample collection time | 1995 or before | TAS [1] |
| MIGS-4.1| Latitude | 39.57 | NAS |
| MIGS-4.2| Longitude | 2.63 | NAS |
| MIGS-4.3| Depth | not report | |
| MIGS-4.4| Altitude | below the sea level | TAS [1,5] |

Evidence codes - IDA: Inferred from Direct Assay (first time in publication); TAS: Traceable Author Statement (i.e., a direct report exists in the literature); NAS: Non-traceable Author Statement (i.e., not directly observed for the living, isolated sample, but based on a generally ac-
cepted property for the species, or anecdotal evidence). These evidence codes are from of the Gene Ontology project [24]. If the evidence code is IDA, then the property was directly ob-
served by one of the authors or an expert mentioned in the acknowledgements.
Genome sequencing and annotation

Genome project history

This organism was selected for sequencing on the basis of its phylogenetic position [31], and is part of the Genomic Encyclopedia of Bacteria and Archaea project [32]. The genome project is deposited in the Genome OnLine Database [14] and the complete genome sequence is deposited in GenBank. Sequencing, finishing and annotation were performed by the DOE Joint Genome Institute (JGI). A summary of the project information is shown in Table 2.

Table 2. Genome sequencing project information

| MIGS ID | Property                      | Term                                              |
|---------|-------------------------------|---------------------------------------------------|
| MIGS-31 | Finishing quality             | Finished                                          |
| MIGS-28 | Libraries used                | Two genomic Sanger libraries: 8 kb pMCL200 library, fosmid (40 kb) library |
| MIGS-29 | Sequencing platforms          | ABI3730                                           |
| MIGS-31.2| Sequencing coverage           | 9.8 x Sanger                                      |
| MIGS-30 | Assemblers                    | Phrap                                             |
| MIGS-32 | Gene calling method           | Prodigal 1.4, GenePRIMP                            |
|         | INSDC ID                      | CP002209                                          |
|         | Genbank Date of Release       | October 1, 2010                                   |
|         | GOLD ID                       | Gc01378                                           |
|         | NCBI project ID               | 30799                                             |
|         | Database: IMG-GEBA            | 2502082106                                        |
| MIGS-13 | Source material identifier    | DSM 9799                                          |
|         | Project relevance             | Tree of Life, GEBA                                 |

Growth conditions and DNA isolation

F. balearica PATT, DSM 9799, was grown in DSMZ medium 514 (Bacto Marine Broth) [33] at 28°C. DNA was isolated from 0.5-1 g of cell paste using Qiagen Genomic 500 DNA Kit (Qiagen, Hilden, Germany) following the standard protocol as recommended by the manufacturer, with modification st/L for cell lysis as described in Wu et al. [32].

Genome sequencing and assembly

The genome was sequenced using the Sanger sequencing platform (6 and 40 kb DNA libraries). All general aspects of library construction and sequencing performed at the JGI can be found at http://www.jgi.doe.gov/. The Phred/Phrap/Consed software package was used for sequence assembly and quality assessment. After the shotgun stage, reads were assembled with parallel phrap (High Performance Software, LLC). Possible mis-assemblies were corrected with Dupfinisher or transposon bombing of bridging clones (Epicentre Biotechnologies, Madison, WI) [34]. Gaps between contigs were closed by editing in Consed, custom primer walk or PCR amplification. A total of 404 additional custom primer reactions were necessary to close gaps and to raise the quality of the finished sequence. The completed genome sequence contains 48,554 reads, achieving an average of 9.8-fold sequence coverage with an error rate less than 1 in 100,000.

Genome annotation

Genes were identified using Prodigal [35] as part of the Oak Ridge National Laboratory genome annotation pipeline, followed by a round of manual curation using the JGI GenePRIMP pipeline [36]. The predicted CDSs were translated and used to search the National Center for Biotechnology Information (NCBI) non-redundant database, UniProt, TIGRFam, Pfam, PRIAM, KEGG, COG, and InterPro databases. Additional gene prediction analysis and functional annotation was performed within the Integrated Microbial Genomes - Expert Review (IMG-ER) platform [37].

Genome properties

The genome consists of a 4,279,159 bp long chromosome with a 60.2% GC content (Table 3 and Figure 3). Of the 3,947 genes predicted, 3,803 were protein-coding genes, and 144 RNAs; twenty one pseudogenes were also identified. The majority of the protein-coding genes (72.5%) were assigned a putative function while the remaining ones were annotated as hypothetical proteins. The distribution of genes into COGs functional categories is presented in Table 4.
Table 3. Genome Statistics

| Attribute                          | Value      | % of Total |
|------------------------------------|------------|------------|
| Genome size (bp)                   | 4,279,159  | 100.00%    |
| DNA coding region (bp)             | 3,842,563  | 89.80%     |
| DNA G+C content (bp)               | 2,576,887  | 60.22%     |
| Number of replicons                | 1          |            |
| Extrachromosomal elements          | 0          |            |
| Total genes                        | 3,947      | 100.00%    |
| RNA genes                          | 144        | 3.65%      |
| rRNA operons                       | 7          |            |
| Protein-coding genes               | 3,803      | 96.35%     |
| Pseudo genes                       | 21         | 0.53%      |
| Genes with function prediction     | 2,860      | 72.46%     |
| Genes in paralog clusters          | 462        | 11.71%     |
| Genes assigned to COGs             | 2,929      | 74.21%     |
| Genes assigned Pfam domains        | 3,089      | 78.26%     |
| Genes with signal peptides         | 1,154      | 29.24%     |
| Genes with transmembrane helices   | 981        | 24.85%     |
| CRISPR repeats                     | 0          |            |

Figure 3. Graphical circular map of the genome. From outside to the center: Genes on forward strand (color by COG categories), Genes on reverse strand (color by COG categories), RNA genes (tRNAs green, rRNAs red, other RNAs black), GC content, GC skew.
Table 4. Number of genes associated with the general COG functional categories

| Code | Value | %age | Description                                                                 |
|------|-------|------|-----------------------------------------------------------------------------|
| J    | 189   | 5.8  | Translation, ribosomal structure and biogenesis                             |
| A    | 1     | 0.0  | RNA processing and modification                                              |
| K    | 213   | 6.5  | Transcription                                                               |
| L    | 138   | 4.2  | Replication, recombination and repair                                         |
| B    | 1     | 0.0  | Chromatin structure and dynamics                                             |
| D    | 35    | 1.1  | Cell cycle control, cell division, chromosome partitioning                   |
| Y    | 0     | 0.0  | Nuclear structure                                                            |
| V    | 61    | 1.9  | Defense mechanisms                                                           |
| T    | 178   | 5.5  | Signal transduction mechanisms                                               |
| M    | 219   | 6.7  | Cell wall/membrane/envelope biogenesis                                       |
| N    | 133   | 4.1  | Cell motility                                                                |
| Z    | 0     | 0.0  | Cytoskeleton                                                                 |
| W    | 0     | 0.0  | Extracellular structures                                                     |
| U    | 128   | 3.9  | Intracellular trafficking and secretion, and vesicular transport              |
| O    | 155   | 4.8  | Posttranslational modification, protein turnover, chaperones                  |
| C    | 238   | 7.3  | Energy production and conversion                                             |
| G    | 105   | 3.2  | Carbohydrate transport and metabolism                                        |
| E    | 248   | 7.6  | Amino acid transport and metabolism                                          |
| F    | 85    | 2.6  | Nucleotide transport and metabolism                                          |
| H    | 167   | 5.1  | Coenzyme transport and metabolism                                            |
| I    | 99    | 3.0  | Lipid transport and metabolism                                               |
| P    | 184   | 6.7  | Inorganic ion transport and metabolism                                       |
| Q    | 53    | 1.6  | Secondary metabolites biosynthesis, transport and catabolism                 |
| R    | 338   | 10.4 | General function prediction only                                             |
| S    | 287   | 8.8  | Function unknown                                                             |
| -    | 1,018 | 25.8 | Not in COGs                                                                  |

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