Supplementary Material

Table S1. Genomic features of *Methylobacter* BlB1.

Traits	Values
Genome size	4.86584 Mb
G+C content	51.3 %
N50	50,157
Proteins (according to NCBI)	4319
tRNA, nc RNA	38, 4
rRNA	3
Contigs	240
Bioproject number	PRJNA675424
Sequencing platform used	Illumina Hiseq, 2*150 paired-end sequencing
NCBI Accession number	JADMKV01

Table S2. Blastp analysis of the annotated protein list of the BlB1 genome. (The table contains the name of the enzyme, protein name and amino acid length, NCBI annotated accession number, closest affiliate along with percent similarity and the affiliate accession number).

Enzyme/ Protein	Accession number	Current closest relative with percent similarity	Accession no. of the closest current relative
Methane metabolism			
Methane monooxygenase			
Methane monooxygenase/ ammonia monooxygenase subunit C (250 aa)	WP_194968270.1	*Methylobacter luteus* IMV-B-3098 97.60%	WP_027159169.1
Methane monooxygenase/ ammonia monooxygenase subunit B (414 aa)	WP_194968272.1	*Methylobacter luteus* IMV-B-3098 96.38%	WP_027159171.1
Methane monooxygenase/ ammonia monooxygenase subunit A (247 aa)	WP_194968271.1	*Methylobacter luteus* IMV-B-3098 98.79%	WP_027159170.1
Methanol dehydrogenase			
Methanol/ethanol family PQQ-dependent dehydrogenase (617 aa)	WP_194969372.1	*Methylobacter luteus* IMV-B-3098 98.06%	WP_027156973.1
Methanol/ethanol family PQQ-dependent dehydrogenase (587 aa)	WP_194970903.1	*Methylobacter luteus* IMV-B-3098 98.63%	WP_027158520.1
Zinc-dependent alcohol dehydrogenase family protein (330 aa)	WP_194969024.1	*Methylobacter luteus* IMV-B-3098 90.61%	WP_027156944.1
Zinc-dependent alcohol dehydrogenase family protein (341 aa)	WP_194972107.1	*Methylobacter luteus* IMV-B-3098 89.74%	WP_027158154.1
NAD(P)-dependent alcohol dehydrogenase (354 aa)	WP_194969379.1	*Methylobacter tundripaludum* 21/22 80.52%	WP_027149771.1
Methanol dehydrogenase [cytochrome c] MoxF (94 aa)	WP_027158517.1	*Methylobacter marinus* A45 94.62%	WP_020158035.1
Methanol oxidation system protein MoxJ (295 aa)	WP_194970898.1	*Methylobacter* sp. BBA5.1 94.24%	WP_081917930.1
Formaldehyde dehydrogenase			
glutathione-dependent formaldehyde dehydrogenase (390 aa)	WP_194969551.1	*Methylobacter luteus* IMV-B-3098 94.87%	WP_027157143.1

aldehyde dehydrogenase family protein (506 aa)	WP_194969126.1	*Methylobacter luteus* IMV-B-3098 94.27%	WP_027158760.1
aldehyde dehydrogenase family protein (476 aa)	WP_194972017.1	*Methylobacter luteus* IMV-B-3098 87.61%	WP_036242998.1
Methylenetetrahydromethanopterin dehydrogenase (302 aa)	WP_194969028.1	*Methylobacter luteus* IMV-B-3098 97.34%	WP_027156940.1
Methylenetetrahydromethanopterin dehydrogenase (301 aa)	WP_194969029.1	*Methylobacter luteus* IMV-B-3098 98.01%	WP_027156939.1
formylmethanofuran dehydrogenase subunit B (419 aa)	WP_194971419.1	*Methylobacter luteus* IMV-B-3098 94.27%	WP_027157051.1
formylmethanofuran dehydrogenase subunit A (555 aa)	WP_194971420.1	*Methylobacter marinus* A45 95.68%	WP_020160238.1
formylmethanofuran dehydrogenase subunit C (271 aa)	WP_194971422.1	*Methylobacter luteus* IMV-B-3098 95.56%	WP_027157054.1
Formate dehydrogenase			
formate dehydrogenase subunit delta (65 aa)	WP_194971613.1	*Methylobacter luteus* IMV-B-3098 90.77%	WP_027159490.1
formate dehydrogenase accessory sulfurtransferase FdhD (282 aa)	WP_194971614.1	*Methylobacter luteus* IMV-B-3098 94.33%	WP_027159491.1
formate dehydrogenase subunit alpha (945 aa)	WP_194971615.1	*Methylobacter luteus* IMV-B-3098 97.35%	WP_027159492.1
formate dehydrogenase (517 aa)	WP_194971616.1	*Methylobacter luteus* IMV-B-3098 94.78%	WP_027159493.1
formate dehydrogenase subunit gamma (158 aa)	WP_194971617.1	*Methylobacter luteus* IMV-B-3098 94.94%	WP_027159494.1
NAD-dependent formate dehydrogenase (401 aa)	WP_194971647.1	*Methylobacter whittenburyi* ACM 3310 97.5%	WP_036298316.1
Carbon dioxide fixation			
LysR family transcriptional regulator (CbbR) of RubisCO operon (301 aa)	WP_194969243.1	*Methylobacter luteus* IMV-B-3098 97.34%	WP_036243303.1
Nitrogen metabolism			
Cyanate hydrolysis (cyanate → ammonium)			
Cyanate hydratase/ cyanase CynS	WP_194971646.1	*Methylosarcina lacus* LW14 92.52%	WP_024299829.1
Nitrogen fixation (Nitrogen → Ammonia)			
nitrogenase molybdenum-iron protein alpha chain NifD (494 aa)	WP_194972098.1	*Methylobacter whittenburyi* ACM 3310 99.19%	WP_036299212.1
nitrogenase molybdenum-iron protein subunit beta NifK (523 aa)	WP_194972097.1	*Methylobacter luteus* IMV-B-3098 95.98%	WP_027158572.1
nitrogenase iron protein NifH (290 aa)	WP_194972099.1	*Methylobacter luteus* IMV-B-3098 97.24%	WP_027158574.1

nitrogenase cofactor biosynthesis protein NifB (495 aa)	WP_194968538.1	*Methylobacter luteus* IMV-B-3098 97.38%	WP_027159369.1
nitrogenase-associated protein (145 aa)	WP_194968540.1	*Methylobacter luteus* IMV-B-3098 86.3%	WP_051299967.1
nitrogenase-stabilizing/protective protein NifW (104 aa)	WP_194968567.1	*Methylobacter whittenburyi* ACM 3310 94.23%	WP_036299321.1
nitrogenase iron-molybdenum cofactor biosynthesis protein NifE (464 aa)	WP_194971348.1	*Methylobacter luteus* IMV-B-3098 98.49%	WP_027159440.1
nitrogenase iron-molybdenum cofactor biosynthesis protein NifN (463 aa)	WP_194971349.1	*Methylobacter luteus* IMV-B-3098 97.19%	WP_027159439.1
nitrogen fixation negative regulator NifL (532 aa)	WP_194968536.1	*Methylobacter luteus* IMV-B-3098 90.06%	WP_027159366.1
nitrogen fixation protein NifQ (191 aa)	WP_194968541.1	*Methylobacter luteus* IMV-B-3098 82.72%	WP_027159371.1
nitrogen fixation protein NifZ (95 aa)	WP_194968559.1	*Methylobacter marinus* A45 80%	WP_020159837.1
nitrogen fixation protein NifZ (159 aa)	WP_194968568.1	*Methylobacter luteus* IMV-B-3098 91.14%	WP_027159398.1
nitrogen fixation protein NifM (292 aa)	WP_194968569.1	*Methylobacter luteus* IMV-B-3098 88.32%	WP_036243252.1
putative nitrogen fixation protein NifT (72 aa)	WP_194971325.1	*Methylobacter luteus* IMV-B-3098 97.22%	WP_027158571.1
nitrogen fixation protein NifX (161 aa)	WP_194971350.1	*Methylobacter luteus* IMV-B-3098 96.5%	WP_081679246.1
NifX-associated nitrogen fixation protein (157 aa)	WP_194971351.1	*Methylobacter marinus* A45 93.63%	WP_020159891.1
Nitrite reductase			
nitrite reductase small subunit NirD (111 aa)	WP_194970424.1	*Methylobacter luteus* IMV-B-3098 83.78%	WP_027159987.1
nitrite reductase large subunit NirB (846 aa)	WP_194970425.1	*Methylobacter luteus* IMV-B-3098 94.33%	WP_027159986.1
nitrite/sulfite reductase (550 aa)	WP_194968231.1	*Methylobacter luteus* IMV-B-3098 95.45%	WP_027159113.1
Denitrification			
nitric oxide reductase subunit B NorB / cbb3-type cytochrome c oxidase subunit I	WP_194970783.1	*Methylobacter luteus* IMV-B-3098 95.56%	WP_155920718.1
nitric oxide reductase NorC subunit/ c-type cytochrome	WP_194970782.1	*Methylobacter luteus* IMV-B-3098 94.95%	WP_027157716.1
Nitrosative stress			
Quinol-dependent nitric oxide reductase subunit B (qNorB)/ cbb3-type cytochrome c oxidase subunit I	WP_194968830.1	*Rugosibacter* sp. 72.85%	TAJ22755.1

Anaerobic nitric oxide reductase transcriptional regulator NorR (511 aa)	WP_194971240.1	*Methylobacter luteus* IMV-B-3098 89.04%	WP_027158752.1
Anaerobic nitric oxide reductase transcriptional regulator NorR (514 aa)	WP_194971405.1	*Methylobacter luteus* IMV-B-3098 90.47%	WP_081679063.1
Hemerythrin metabolic protein			
Bacteriohemerythrin (338 aa)	WP_194968436.1	*Methylobacter luteus* IMV-B-3098 68.28%	WP_027157247.1
hemerythrin family protein (132 aa)	WP_194968504.1	*Methylobacter luteus* IMV-B-3098 92.42%	WP_027159334.1
hemerythrin domain-containing protein (131 aa)	WP_194971595.1	*Methylobacter luteus* IMV-B-3098 82.52%	WP_027160007.1
hemerythrin domain-containing protein (182 aa)	WP_194970353.1	*Methylobacter luteus* IMV-B-3098 81.62%	WP_027157941.1

Whole genome sequencing details and data analysis

DNA of strain BlB1 was extracted using the GenElute™ Bacterial Genomic DNA isolation Kit (Sigma-Aldrich, India) using the protocol for Gram negative cells. The DNA quality was checked using Nanodrop machine and by loading on the gel. Additionally, the 16S rRNA gene using this DNA was amplified and sequenced. The pure 16S rRNA gene sequence of BlB1 was obtained which indicated that there was no contamination of any other bacteria. Then, the DNA was sent to Medgenome Labs, Bangalore, India for whole genome sequencing. The whole-genome sequencing was done using the Illumina HiSeqX platform (150*2) at Medgenome laboratory, Bangalore, India as per standard protocols. The library preparation was done according to the standard protocols developed for the platform.

Quality check on the raw fastq files was done using the *FASTQC* toolkit to check for base quality, base composition and GC content. Low-quality sequence reads are excluded from the analysis. The Paired-end reads were quality filtered using cutadapt [1.18]. The NEB adapters were filtered using cutadapt. After adapter trimming, human, fungi and other contamination reads are filtered. The *De novo* assembly was performed with hash length of 53 using SPADES *De novo* assembler. The assembly was optimized using SSPACE-basic assembler to obtain high quality genome assembly.

The Kmer frequencies were calculated using in-house scripts to identify the most frequent Kmer in the data. The SPADES default parameters (--12 for interleaved paired-end reads). Read participation in the assembly was assessed by mapping filtered paired-end reads on the assembled scaffolds.

The assembled contigs were submitted to NCBI prokaryotic genome annotation pipeline PGAP (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/) and also uploaded in RAST (http://rast.nmpdr.org/) for genome annotation. To construct the metabolic pathways, the amino-acid file of the BlB1 genome was uploaded in KEGG (https://www.kegg.jp/blastkoala/).