

Draft Genome Sequence of *Buttiauxella* sp. Strain A111, Which Converts 2-Azahypoxanthine to 2-Aza-8-Oxohypoxanthine

メタデータ	言語: eng 出版者: 公開日: 2019-10-04 キーワード (Ja): キーワード (En): 作成者: Choi, Jae-Hoon, Moriuchi, Ryota, Sukprasitchai, Apirati, Tokuyama, Shinji, Kawagishi, Hirokazu, Dohra, Hideo メールアドレス: 所属:
URL	http://hdl.handle.net/10297/00026844



Draft Genome Sequence of *Buttiauxella* sp. Strain A111, Which Converts 2-Azahypoxanthine to 2-Aza-8-Oxohypoxanthine

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ABSTRACT We report here the draft genome sequence of *Buttiauxella* sp. strain A111, isolated on the basis of bioconversion activity of the plant growth-regulating compound 2-azahypoxanthine to 2-aza-8-oxohypoxanthine. The genome contains 4,388 protein-coding sequences, including several genes possibly involved in the metabolism of the plant growth-regulating compound.

The efficient production method of 2-aza-8-oxohypoxanthine (AOH), a strong plant growth stimulator (1), is limited to bioconversion from 2-azahypoxanthine (AHX) by incubation with resting cells of *Burkholderia contaminans* CH-1 (2). We isolated a *Buttiauxella* sp. bacterium (designated strain A111) from forest soil in Hokkaido, Japan, by screening based on the bioconversion activity from AHX to AOH. The genus *Buttiauxella* is a member of the family *Enterobacteriaceae*, which contains an endophytic bacterium, *Buttiauxella* sp. strain SaSR13, that improves the growth of a plant of the genus *Crassulaceae* (3).

Genomic DNA of *Buttiauxella* sp. strain A111 was extracted using a DNeasy blood and tissue kit and fragmented using a Covaris acoustic solubilizer. A library constructed using a TruSeq DNA PCR-free library preparation kit was sequenced using the Illumina MiSeq platform to generate 301-bp paired-end reads. The raw reads were cleaned up as described previously (4) using Trimmomatic ver. 0.36 (5). The resultant 1,592,778 high-quality read pairs totaling 918 Mb and representing 187.8-fold coverage of the genome were assembled using SPAdes ver. 3.13.0 (6), with the same parameters as reported previously (4). The assembly generated 37 contigs (>200 bp), with a longest sequence of 1,350,757 bp and an N_{50} value of 643,281 bp. The draft genome sequence of *Buttiauxella* sp. strain A111 consisted of 4,889,549 bp, with a G+C content of 50.3%. The genome was annotated using the DFAST-core ver. 1.2.0 (7). The genome contains 4,388 protein-coding sequences, 4 rRNA genes, and 79 tRNA genes. Although the 16S rRNA gene of strain A111 showed a high similarity (99.8%) to that of *Buttiauxella gaviniae* (GenBank accession number [NR_025330](https://.ncbi.nlm.nih.gov/nucl/NC_025330)), average nucleotide identity (ANI) analysis (8, 9) showed the highest ANI value (86.42%) with the *Buttiauxella ferrugutiae* ATCC 51602 genome (GenBank accession number [LXEQ00000000](https://.ncbi.nlm.nih.gov/nucl/LXEQ00000000)). This ANI value was significantly lower than the species threshold of 95% (8), suggesting that *Buttiauxella* sp. strain A111 was a novel species belonging to the genus *Buttiauxella*. The proteomes of *Buttiauxella* sp. strain A111 and *B. contaminans* CH-1 (GenBank accession numbers [AP018357](https://ncbi.nlm.nih.gov/nucl/AP018357) to [AP018360](https://ncbi.nlm.nih.gov/nucl/AP018360)) (4) were annotated using KofamKOALA (10) to compare xanthine dehydrogenase (XDH) homologs as candidate enzymes involved in the conversion of AHX to AOH. The *Buttiauxella* sp. strain A111 genome contains two gene clusters coding for XDHs, XdhABC (BSPA111_02450 to 02430) (Fig. 1A), and the xanthine dehydrogenase family protein

Citation Choi J-H, Moriuchi R, Sukprasitchai A, Tokuyama S, Kawagishi H, Dohra H. 2019. Draft genome sequence of *Buttiauxella* sp. strain A111, which converts 2-azahypoxanthine to 2-aza-8-oxohypoxanthine. *Microbiol Resour Announc* 8:e00664-19. <https://doi.org/10.1128/MRA.00664-19>.

Editor Julie C. Dunning Hotopp, University of Maryland School of Medicine

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Received 6 June 2019

Accepted 27 June 2019

Published 18 July 2019

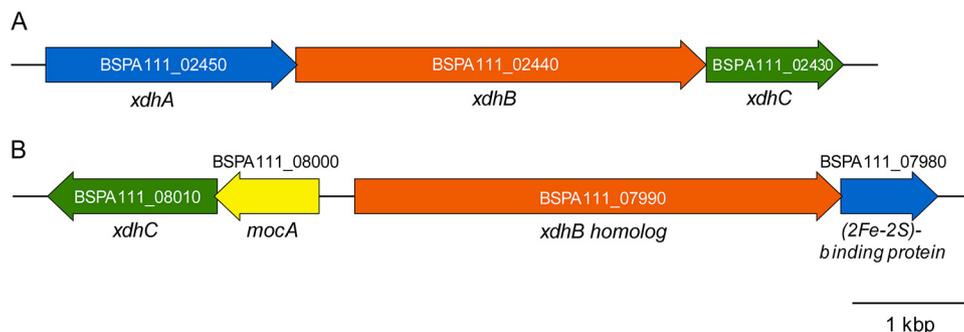


FIG 1 Gene clusters coding for xanthine dehydrogenases of *Buttiauxella* sp. strain A111. (A) The xanthine dehydrogenase *xdhABC* gene cluster. (B) The gene cluster encoding putative xanthine dehydrogenase homologs. Genes *xdhA*, *xdhB*, *xdhC*, and *mocA* encode xanthine dehydrogenase small subunit, xanthine dehydrogenase large subunit, xanthine dehydrogenase accessory factor, and molybdenum cofactor cytidyltransferase, respectively. Note that the gene coding for the 2Fe-2S-binding protein is shorter than *xdhA* because its product lacks flavin adenine dinucleotide (FAD)-binding and carbon monoxide (CO) dehydrogenase flavoprotein C-terminal domains.

molybdopterin-binding subunit (BSPA111_07990) and (2Fe-2S)-binding protein (BSPA111_07980) (Fig. 1B). Unlike *B. contaminans* CH-1, molybdenum cofactor cytidyltransferase *MocA* (BSPA111_08000) and xanthine dehydrogenase accessory protein *XdhC* (BSPA111_08010) were encoded adjacent to the upstream area of the latter gene cluster in the *Buttiauxella* sp. strain A111 genome (Fig. 1B) and have been reported to be involved in the cytidylation of molybdenum cofactor (11) and insertion of the cofactor into XDH (12), respectively. It remains to be elucidated whether the high conversion activity in *Buttiauxella* sp. strain A111 is due to the cytidylation of the cofactor. The genome information of *Buttiauxella* sp. strain A111 would be expected to provide important clues as to the biosynthetic pathways and functions of the plant growth-regulating compounds.

Data availability. The raw reads of *Buttiauxella* sp. strain A111 have been deposited in the DDBJ Sequence Read Archive under the accession number [DRA008321](https://www.ncbi.nlm.nih.gov/sra/DRA008321). The draft genome sequence has been deposited in DDBJ/ENA/GenBank under the accession number [BJFN00000000](https://www.ncbi.nlm.nih.gov/genbank/BJFN00000000).

ACKNOWLEDGMENTS

This work was partially supported by JSPS KAKENHI grants number 16H06192 (to J.-H. Choi) and 17H06402 (to H. Kawagishi), Grants-in-Aid for Young Scientists A 16H06192 (JSPS) (<https://kaken.nii.ac.jp/en/grant/KAKENHI-PROJECT-16H06192/>) to J.-H. Choi, and the Grant-in-Aid for Scientific Research on Innovative Areas 17H06402 (JSPS) (<https://kaken.nii.ac.jp/en/grant/KAKENHI-PLANNED-17H06402/>) to H. Kawagishi.

REFERENCES

- Choi JH, Ohnishi T, Yamakawa Y, Takeda S, Sekiguchi S, Maruyama W, Yamashita K, Suzuki T, Morita A, Ikka T, Motohashi R, Kiriwa Y, Tobina H, Asai T, Tokuyama S, Hirai H, Yasuda N, Noguchi K, Asakawa T, Sugiya S, Kan T, Kawagishi H. 2014. The source of “fairy rings”: 2-azahypoxanthine and its metabolite found in a novel purine metabolic pathway in plants. *Angew Chem Int Ed* 53:1552–1555. <https://doi.org/10.1002/anie.201308109>.
- Choi JH, Kikuchi A, Pumkiao P, Hirai H, Tokuyama S, Kawagishi H. 2016. Bioconversion of AHX to AOH by resting cells of *Burkholderia contaminans* CH-1. *Biosci Biotechnol Biochem* 80:2045–2050. <https://doi.org/10.1080/09168451.2016.1189314>.
- Wu K, Luo J, Li J, An Q, Yang X, Liang Y, Li T. 2018. Endophytic bacterium *Buttiauxella* sp. SaSR13 improves plant growth and cadmium accumulation of hyperaccumulator *Sedum alfredii*. *Environ Sci Pollut Res Int* 25:21844–21854. <https://doi.org/10.1007/s11356-018-2322-6>.
- Choi JH, Sugiura H, Moriuchi R, Kawagishi H, Dohra H. 2017. High-quality draft genome sequence of *Burkholderia contaminans* CH-1, a Gram-negative bacterium that metabolizes 2-azahypoxanthine, a plant growth-regulating compound. *Genome Announc* 5:e01148-17. <https://doi.org/10.1128/genomeA.01148-17>.
- Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- Tanizawa Y, Fujisawa T, Nakamura Y. 2018. DFAST: a flexible prokaryotic genome annotation pipeline for faster genome publication. *Bioinformatics* 34:1037–1039. <https://doi.org/10.1093/bioinformatics/btx713>.
- Goris J, Konstantinidis KT, Klappenbach JA, Coenye T, Vandamme P, Tiedje JM. 2007. DNA-DNA hybridization values and their relationship to

- whole-genome sequence similarities. *Int J Syst Evol Microbiol* 57:81–91. <https://doi.org/10.1099/ijs.0.64483-0>.
9. Rodriguez-R LM, Konstantinidis KT. 2016. The enveomics collection: a toolbox for specialized analyses of microbial genomes and metagenomes. *PeerJ PrePrints* 4:e1900v1. <https://doi.org/10.7287/peerj.preprints.1900v1>.
 10. Aramaki T, Blanc-Mathieu R, Endo H, Ohkubo K, Kanehisa M, Goto S, Ogata H. 2019. KofamKOALA: KEGG ortholog assignment based on profile HMM and adaptive score threshold. *bioRxiv* <https://doi.org/10.1101/602110>.
 11. Neumann M, Mittelstädt G, Seduk F, Iobbi-Nivol C, Leimkühler S. 2009. MocA is a specific cytidylyltransferase involved in molybdopterin cytosine dinucleotide biosynthesis in *Escherichia coli*. *J Biol Chem* 284: 21891–21898. <https://doi.org/10.1074/jbc.M109.008565>.
 12. Leimkuhler S, Klipp W. 1999. Role of XDHC in molybdenum cofactor insertion into xanthine dehydrogenase of *Rhodobacter capsulatus*. *J Bacteriol* 181:2745–2751.