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Draft Genome Sequence of *Bacillus azotoformans* MEV2011, a (Co-) Denitrifying Strain Unable to Grow with Oxygen

Supplementary Tables

Table S1. Overview of the genomic inventory for dissimilatory nitrogen transformations in *Bacillus azotoformans* MEV2011 (according to the IMG autoannotation).

Function	Gene	Locus Tag	Gene Coordinates	GenBank Identifier (pBLAST best hit)	% ID
Cytoplasmic dissimilatory nitrate reduction	*narG1*	M670_00379	330131..333814(3684bp)	WP_003331056.1 *Bacillus azotoformans* LMG9581	99
	narH1	M670_00378	328591..330141(1551bp)	WP_003331055.1 *Bacillus azotoformans* LMG9581	99
	narJ1	M670_00377	328056..328604(549bp)	WP_003331054.1 *Bacillus azotoformans* LMG9581	99
	narI1	M670_00376	327296..328012 (717bp)	WP_003331053.1 *Bacillus azotoformans* LMG9581	97
	narJ2	M670_03226	120251..120832 (582bp)	YP_001124780.1 *Geobacillus thermodenitrificans* NG80-2	36
	narG2	M670_03224	15014..118781 (3768bp)	YP_516567.1 *Desulfitobacterium hafniense* Y51	70
	narH2	M670_03225	118771..120288 (1518bp)	YP_003242070.1 *Paenibacillus sp.* Y412MC10	70
	narI2	M670_03227	120835..121515 (681bp)	YP_252572.1 *Staphylococcus haemolyticus* JCSC1435	56
	narJ3	M670_04859	10048..10602 (555bp)	WP_003331449.1 *Bacillus azotoformans* LMG9581	98
	narH3	M670_04860	10048..10602 (1467bp)	WP_003331450.1 *Bacillus azotoformans* LMG9581	98
	narI3	M670_04858	9362..10051 (690bp)	WP_003331448.1 *Bacillus azotoformans* LMG9581	100
	narG3	M670_04861	2138..15821(3684bp)	WP_003331451.1 *Bacillus azotoformans* LMG9581	98

Function	Gene	Locus Tag	Gene Coordinates	GenBank Identifier (pBLAST best hit)	% ID
Periplasmic dissimilatory nitrate reduction	*napB*	M670_01957	102803..103222 (420bp)	WP_003332435.1 *Bacillus azotoformans* LMG9581	99
	napG1	M670_01955	99581..100177 (597bp)	WP_003332433.1 *Bacillus azotoformans* LMG9581	99
	napA	M670_01956	100253..102790 (2538bp)	WP_003332434.1 *Bacillus azotoformans* LMG9581	100
	napD	M670_01958	103267..103524 (258bp)	WP_003332436.1 *Bacillus azotoformans* LMG9581	97
	napG2	M670_01959	103530..104099 (570bp)	WP_003332437.1 *Bacillus azotoformans* LMG9581	99
	napH	M670_02517	30733..31632 (900bp)	WP_003332276.1 *Bacillus azotoformans* LMG9581	99
	moa	M670_01954	98302..99333 (1032bp)	WP_003332432.1 *Bacillus azotoformans* LMG9581	99

Function	Gene	Locus Tag	Gene Coordinates	GenBank Identifier (pBLAST best hit)	% ID
Dissimilatory reduction to NO	*nirK*	M670_01705	69499..70560 (1062bp*)*	WP_003329883.1 *Bacillus azotoformans* LMG9581	99

Function	Gene	Locus Tag	Gene Coordinates	GenBank Identifier (pBLAST best hit)	% ID
Dissmilatory nitrite reduction to ammonium	*nrfH*	M670_01133	104203..104718 (516bp)	WP_003329814.1 *Bacillus azotoformans* LMG9581	100
	nrfA	M670_01132	102744..104201 (1458bp)	WP_003329815.1 *Bacillus azotoformans* LMG9581	100

Function	Gene	Locus Tag	Gene Coordinates	GenBank identifier (pBLAST best hit)	% ID
Dissimilatory quinol-dependent nitric oxide reduction	*qnorB1*	M670_01459	65358..67619 (2262bp)	WP_003329195.1 *Bacillus azotoformans* LMG9581	99
	qnorB2	M670_00384	335562..337925 (2364bp)	WP_003331062.1 *Bacillus azotoformans* LMG9581	99

Dissimilatory menaquinol/cytc-dependent nitric oxide reduction (Type I)	*cbaB1*	M670_03526	55005..55523 (519bp)	WP_003330136.1 *Bacillus azotoformans* LMG9581	99
	cbaA1	M670_03525	53497..54978 (1482bp)	WP_003330135.1 *Bacillus azotoformans* LMG9581	99
	senC1	M670_03524	52899..53504 (606bp)	WP_003330134.1 *Bacillus azotoformans* LMG9581	99
	cbaD1	M670_03523	52309..52872 (564bp)	WP_003330133.1 *Bacillus azotoformans* LMG9581	88
Dissimilatory menaquinol/cytc-dependent nitric oxide reduction (Type II)	*cbaC2*	M670_04975	4839..5411 (573bp)	WP_003330503.1 *Bacillus azotoformans* LMG9581	98
	senC2	M670_04974	4204..4839 (636bp)	WP_003330502.1 *Bacillus azotoformans* LMG9581	98
	cbaB2	M670_04972	1938..2399 (462bp)	WP_003330500.1 *Bacillus azotoformans* LMG9581	96
	cbaA2	M670_04973	2414..4117 (1704bp)	WP_003330501.1 *Bacillus azotoformans* LMG9581	94

Function	**Gene**	**Locus Tag**	**Gene Coordinates**	**GenBank Identifier (pBLAST best hit)**	% ID
Dissimilatory nitrous oxide reduction	*nosF*	M670_01450	54548..55465 (918bp)	WP_003329185.1 *Bacillus azotoformans* LMG9581	98
	nosY	M670_01449	53709..54551 (843bp)	WP_003329184.1 *Bacillus azotoformans* LMG9581	99
	nosL	M670_01448	53225..53734 (510bp)	WP_003329183.1 *Bacillus azotoformans* LMG9581	96
	nosD	M670_01447	51885..53228 (1344bp)	WP_003329182.1 *Bacillus azotoformans* LMG9581	96
	nosZ	M670_01444	49300..51150 (1851bp)	WP_003329179.1 *Bacillus azotoformans* LMG9581	99
	nosC	M670_01443	48814..49275 (462bp)	WP_003329178.1 *Bacillus azotoformans* LMG9581	94
	nosC	M670_03087	131955..132401 (447bp)	WP_003330275.1 *Bacillus azotoformans* LMG9581	95

	nosZ	M670_03086	130050..131930 (1881bp)	WP_003330276.1 *Bacillus azotoformans* LMG9581	99
	nosD	M670_03084	128108..129433 (1326bp)	WP_003330278.1 *Bacillus azotoformans* LMG9581	99
	nosD	M670_00060	54903..56246 (1344bp)	WP_003332806.1 *Bacillus azotoformans* LMG9581	100
	nosL	M670_00059	54421..54906 (486bp)	WP_003332807.1 *Bacillus azotoformans* LMG9581	99
	nosY	M670_00058	53550..54380 (831bp)	WP_003332808. *Bacillus azotoformans* LMG9581	97
	nosF	M670_00057	52814..53560 (747bp)	WP_003332809.1 *Bacillus azotoformans* LMG9581	97
	nosL	M670_00056	51729..52448 (720bp)	WP_003332811.1 *Bacillus azotoformans* LMG9581	97
	nosC	M670_00026	24574..25008 (435bp)	WP_003332840.1 *Bacillus azotoformans* LMG9581	99
	nosZ	M670_00025	22681..24558 (1878bp)	WP_003332841.1 *Bacillus azotoformans* LMG9581	100
	nosD	M670_00023	20637..22052 (1416bp)	WP_003332843.1 *Bacillus azotoformans* LMG9581	99
	nosY	M670_00022	19840..20637 (798bp)	WP_003332844.1 *Bacillus azotoformans* LMG9581	100
	nosF	M670_00021	19172..19843 (672bp)	WP_003332845.1 *Bacillus azotoformans* LMG9581	100

Function	**Gene**	**Locus Tag**	**Gene Coordinates**	**GenBank identifier (pBLAST best hit)**	**% ID**
Nitrate/Nitrite transporter	*narK*	M670_03223	113794..115014 (1221bp)	WP_019240754.1 *Bacillus massilioanorexius*	75
	nirC	M670_04679	22520..23290 (771bp)	WP_003331452 *Bacillus azotoformans* LMG9581	97

Table S2. Overview of the genomic inventory for enzymatic reduction of O_2 and ATP synthase in *Bacillus azotoformans* MEV2011 (according to the IMG autoannotation). Genes encoding complex I-IV in the electron transport chain and an ATPase were identified. In addition, genes were found encoding an alternative terminal oxidase.

Locus Tag	**Gene Product Name**	**Gene Coordinates**	**pBLAST best hit**	
	Complex I		**GenBank Identifier**	**%ID**
M670_02616	NADH dehydrogenase subunit A [EC: 1.6.5.3]	119047...119421 (375bp)	WP_003333358.1 *Bacillus azotoformans* LMG9581	100
M670_02617	NADH dehydrogenase subunit B [EC: 1.6.5.3]	119412…119933 (522bp)	WP_003333357.1 *Bacillus azotoformans* LMG9581	99
M670_02618	NADH dehydrogenase subunit C [EC: 1.6.5.3]	119961…121145 (1185bp)	WP_003333355.1 *Bacillus azotoformans* LMG9581	97
M670_02619	NADH dehydrogenase subunit D [EC: 1.6.5.3]	121149…122252 (1104bp)	WP_003333354.1 *Bacillus azotoformans* LMG9581	100
M670_02620	NADH dehydrogenase subunit H [EC: 1.6.5.3]	122252…123256 (1005bp)	WP_017756590.1 *Bacillus* sp. ZYK	83
M670_02621	NADH dehydrogenase subunit I [EC: 1.6.5.3]	123299…123718 (420bp)	WP_003333353.1 *Bacillus azotoformans* LMG9581	100
M670_02622	NADH dehydrogenase subunit J [EC: 1.6.5.3]	123715…124230 (516bp)	WP_003333352.1 *Bacillus azotoformans* LMG9581	96
M670_02623	NADH dehydrogenase subunit K [EC: 1.6.5.3]	124223…124537 (315bp)	WP_003333351.1 *Bacillus azotoformans* LMG9581	100
M670_02624	NADH dehydrogenase subunit L [EC: 1.6.5.3]	124556…126454 (1899bp)	WP_003333350.1 *Bacillus azotoformans* LMG9581	99
M670_02625	NADH dehydrogenase subunit M [EC: 1.6.5.3]	126451…127959 (1509bp)	WP_003333349.1 *Bacillus azotoformans* LMG9581	99
M670_02626	NADH dehydrogenase subunit N [EC: 1.6.5.3]	127966…19486 (1521bp)	WP_003333348.1 *Bacillus azotoformans* LMG9581	99
M670_00090	NADH dehydrogenase, FAD-containing subunit [EC: 1.6.99.3]	77922…79145 (1224bp)	WP_003332777.1 *Bacillus azotoformans* LMG9581	99

Locus Tag	**Gene Product Name**	**Gene Coordinates**	**pBLAST best hit**	
	Complex II		**GenBank Identifier**	**%ID**
M670_01296	succinate dehydrogenase subunit B [EC: 1.3.99.1]	268315…269070 (756bp)	WP_003331006.1 *Bacillus azotoformans* LMG9581	99
M670_01297	succinate dehydrogenase subunit A [EC: 1.3.99.1]	269073…270863 (1791bp)	WP_003331007.1 *Bacillus azotoformans* LMG9581	98
M670_01298	succinate dehydrogenase subunit C [EC: 1.3.5.1]	271108..271737 (630bp)	WP_003331008.1 *Bacillus azotoformans* LMG9581	100

Locus Tag	**Gene Product Name**	**Gene Coordinates**	**pBLAST best hit**	
	Complex III		**GenBank Identifier**	**%ID**
M670_00552	menaquinol-cytochrome c reductase cytochrome b/c subunit	458363...459136 (774bp)	WP_003331133.1 *Bacillus azotoformans* LMG9581	100
M670_00553	menaquinol-cytochrome c reductase cytochrome b subunit	459168...459842 (675bp)	WP_003331134.1 *Bacillus azotoformans* LMG9581	100
M670_00554	Rieske Fe-S protein [EC: 1.10.2.-]	459857...460354 (498bp)	WP_003331135.1 *Bacillus azotoformans* LMG9581	99

Locus Tag	**Gene Product Name**	**Gene Coordinates**	**pBLAST best hit**	
	Complex IV (cytochrome c oxidase)		**GenBank Identifier**	**%ID**
M670_04800	cytochrome c oxidase assembly factor CtaG	3158...4060 (903bp)	WP_003329986.1 *Bacillus azotoformans* LMG9581	95
M670_04801	cytochrome c oxidase, subunit IVB [EC: 1.9.3.1]	4101…4433 (333bp)	WP_003329987.1 *Bacillus azotoformans* LMG9581	99
M670_04802	Heme/copper-type cytochrome/quinol oxidase, subunit 3 [EC: 1.9.3.1]	4439…5059 (621bp)	WP_003329988.1 *Bacillus azotoformans* LMG9581	100
M670_04803	Heme/copper-type cytochrome/quinol oxidases, subunit 1 [EC: 1.9.3.1]	5059…6930 (1872bp)	WP_003329990.1 *Bacillus azotoformans* LMG9581	99
M670_04804	cytochrome c oxidase, subunit II [EC: 1.9.3.1]	6947…7990 (1044bp)	WP_003329991.1 *Bacillus azotoformans* LMG9581	99
M670_04805	cyoE protoheme IX farnesyltransferase [EC:2.5.1.-]	8424...9167(744bp)	WP_003329992.1 *Bacillus azotoformans* LMG9581	99

Locus Tag	**Gene Product Name**	**Gene Coordinates**	**pBLAST best hit**	
	Complex IV (alternative terminal oxidase)		**GenBank Identifier**	**%ID**
M670_01069	cytochrome aa3-600 menaquinol oxidase subunit IV [EC:1.10.3.12]	49816..50109 (294bp)	WP_003331328.1 *Bacillus azotoformans* LMG9581	98
M670_01068	cytochrome aa3-600 menaquinol oxidase subunit III [EC:1.10.3.12]	49217...49813 (597bp)	WP_003331327.1 *Bacillus azotoformans* LMG9581	100
M670_01067	cytochrome aa3-600 menaquinol oxidase subunit I [EC:1.10.3.12]	47268...49217 (1950bp)	WP_003331326.1 *Bacillus azotoformans* LMG9581	99
M670_01066	cytochrome aa3-600 menaquinol oxidase subunit II [EC:1.10.3.12]	46351...47265 (915bp)	WP_003331325.1 *Bacillus azotoformans* LMG9581	98

Locus Tag	**Gene Product Name**	**Gene Coordinates**	**pBLAST best hit**	
	ATPase		**GenBank Identifier**	**%ID**
M670_04237	ppk polyphosphate kinase [EC:2.7.4.1]	21328…23442 (2115bp)	WP_003330039.1 *Bacillus azotoformans* LMG9581	99
M670_00299	pyrophosphatase PpaX [EC:3.6.1.1]	247358…248005 (648bp)	WP_003330763.1 *Bacillus azotoformans* LMG9581	99
M670_02607	atpB F-type H+-transporting ATPase subunit a [EC:3.6.3.14]	111451…112161 (711bp)	WP_003333362.1 *Bacillus azotoformans* LMG9581	99
M670_02608	ATP synthase F0 subcomplex C subunit [EC:3.6.3.14]	112216…112434 (219bp)	WP_003333365.1 *Bacillus azotoformans* LMG9581	100
M670_02609	ATP synthase F0 subcomplex B subunit [EC:3.6.3.14]	112693…113223 (531bp)	WP_003333364.1 *Bacillus azotoformans* LMG9581	100
M670_02610	ATP synthase F1 subcomplex delta subunit [EC:3.6.3.14]	113220…113765 (546bp)	WP_003333363.1 *Bacillus azotoformans* LMG9581	100
M670_02611	ATP synthase F1 subcomplex alpha subunit [EC:3.6.3.14]	113783…115291 (1509bp)	WP_003333362.1 *Bacillus azotoformans* LMG9581	100
M670_02612	ATP synthase F1 subcomplex gamma subunit [EC:3.6.3.14]	115374…115234 (861bp)	WP_003333361.1 *Bacillus azotoformans* LMG9581	99
M670_02613	ATP synthase F1 subcomplex beta subunit [EC:3.6.3.14]	116337…117749 (1413bp)	WP_003333360.1 *Bacillus azotoformans* LMG9581	99
M670_02615	ATP synthase F1 subcomplex epsilon subunit [EC:3.6.3.14]	117977…118378 (402bp)	WP_003333359.1 *Bacillus azotoformans* LMG9581	99
M670_00902	type III secretion system ATPase, FliI/YscN [EC: 3.6.3.15]	272821…274131 (1311bp)	WP_003332537.1 *Bacillus azotoformans* LMG9581	99

Table S3. Overview of the genomic inventory for the detoxification of reactive oxygen species in *Bacillus azotoformans* MEV2011 (according to the IMG autoannotation).

Locus Tag	**Gene Product Name**	**Gene Coordinates**	**pBLAST best hit**	
			GenBank Identifier	**%ID**
M670_04927	SOD2 superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	11018…11629 (612bp)	WP_003332388.1 *Bacillus azotoformans*	100
M670_01567	Cu2+/Zn2+ superoxide dismutase SOD1	156379…157017 (639bp)	WP_003331991.1 *Bacillus azotoformans*	99
M670_01373	tpx thiol peroxidase, atypical 2-Cys peroxiredoxin [EC:1.11.1.15]	346493…34993 (501bp)	WP_003347404.1 *Bacillus methanolicus*	86
M670_04941	glutathione peroxidase [EC:1.11.1.9]	6177…6740 (564bp)	WP_003331960.1 *Bacillus azotoformans*	97
M670_00605	Mn-containing catalase	503460..504029 (570bp)	WP_017755616.1 *Bacillus* sp. ZYK	91