

SUPPLEMENTARY MATERIALS

Genome-resolved multi-omics analysis of *Lentilactobacillus buchneri* subsp. *silagei* strain AGA55 reveals metabolic versatility and probiotic potential

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Table S1. Horizontal gene transfer verification results of the detected resistome found on the genome of the *Llb. buchneri* sp. *silagei* strain AGA55.

Antibiotic	BV-BRC ID/ JGI-IMG-MER ID	Gene	Product	Source organism based on Protein-BLAST result	Acession	Identity	E-value
Elfamycins	fig 1581.157.peg.1526	<i>EF-Tu</i>	Translation elongation factor Tu	<i>Lentilactobacillus buchneri</i>	WP_013727577.1	100.00%	0.0
Fosfomycin	fig 1581.157.peg.1766	<i>MurA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	<i>Lentilactobacillus buchneri</i>	WP_013728364.1	100.00%	0.0
Streptomycin	fig 1581.157.peg.324	<i>GdpD</i>	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	<i>Lentilactobacillus buchneri</i>	WP_014940020.1	100.00%	0.0
Fosfomycin	fig 1581.157.peg.710	<i>S12p</i>	SSU ribosomal protein S12p (S23e)	MULTISPECIES: 30S ribosomal protein S12 [<i>Lentilactobacillus</i>]	WP_013728508.1	100.00%	5e-93
Fosfomycin	fig 1581.157.peg.1562	<i>MurA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	<i>Lentilactobacillus buchneri</i>	WP_014939815.1	100.00%	0.0
daptomycin	fig 1581.157.peg.573	<i>PgsA</i>	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	<i>Lentilactobacillus buchneri</i>	WP_014939844.1	100.00%	3e-133
isoniazid;triclosan	fig 1581.157.peg.646	<i>kasA</i>	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)	<i>Lentilactobacillus buchneri</i>	WP_013728445.1	100.00%	0.0
fusidic acid	fig 1581.157.peg.708	<i>EF-G</i>	Translation elongation factor G	<i>Lentilactobacillus buchneri</i>	WP_013728506.1	100.00%	0.0
daptomycin	fig 1581.157.peg.712	<i>rpoC</i>	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	<i>Lentilactobacillus buchneri</i>	WP_014940338.1	100.00%	0.0
daptomycin	fig 1581.157.peg.878	<i>GdpD</i>	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	<i>Lentilactobacillus buchneri</i> subsp. <i>silagei</i>	BEJ52847.1	100.00%	2e-157
tetracycline;tigecycline	fig 1581.157.peg.707	<i>S10p</i>	SSU ribosomal protein S10p (S20e)	<i>Lentilactobacillus buchneri</i>	WP_153152373.1	99.02%	6e-66
	fig 1581.157.peg.45	<i>MprF</i>	L-O-lysylphosphatidylglycerol synthase (EC 2.3.2.3)	<i>Lentilactobacillus buchneri</i>	WP_419713231.1	100.00%	0.0
trimethoprim;brodimoprim;tetroxoprim;iclaprim	fig 1581.157.peg.435	<i>folA, Dfr</i>	Dihydrofolate reductase (EC 1.5.1.3)	<i>Lentilactobacillus buchneri</i>	WP_014939942.1	100.00%	4e-117
D-cycloserine	fig 1581.157.peg.599	<i>Ddl</i>	D-alanine--D-alanine ligase (EC 6.3.2.4)	<i>Lentilactobacillus buchneri</i>	WP_014939823.1	100.00%	0.0
isoniazid;ethionamide;trichlosan	fig 1581.157.peg.640	<i>inhA, fabI</i>	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9)	<i>Lentilactobacillus buchneri</i>	WP_013728439.1	100.00%	0.0
rifamycin;daptomycin;rifabutin;rifampin	fig 1581.157.peg.713	<i>rpoB</i>	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	<i>Lentilactobacillus buchneri</i> NRRL B-30929	AEB73983.1	100.00%	0.0
Fluoroquinolones Quinolones Quinolines, Aminocoumarin antibiotics	fig 1581.157.peg.2241	<i>gyrB</i>	DNA gyrase subunit B (EC 5.99.1.3)	<i>Lentilactobacillus buchneri</i>			
Sulfonamides	fig 1581.157.peg.390	<i>folP</i>	Dihydropteroate synthase (EC 2.5.1.15)	<i>Lentilactobacillus buchneri</i>	WP_014939977.1	100.00%	0.0
daptomycin	fig 1581.157.peg.887	<i>GdpD</i>	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	<i>Lentilactobacillus buchneri</i>	WP_014939185.1	100.00%	5e-169
streptomycin	fig 1581.157.peg.1172	<i>gidB</i>	16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.170)	<i>Lentilactobacillus buchneri</i>	WP_014939544.1	100.00%	5e-178
mycinamicin;tylosin;lincomosamides	fig 1581.157.peg.1451	<i>RlmA(II)</i>	23S rRNA (guanine(748)-N(1))-methyltransferase (EC 2.1.1.188)	<i>Lentilactobacillus buchneri</i>	WP_014939612.1	100.00%	0.0
mupirocin (pseudomonic acid)	fig 1581.157.peg.1470	<i>Iso-tRNA</i>	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	<i>Lentilactobacillus buchneri</i>	WP_014939626.1	100.00%	0.0
D-cycloserine	fig 1581.157.peg.1757	<i>Alr</i>	Alanine racemase (EC 5.1.1.1)	<i>Lentilactobacillus buchneri</i>	WP_014940239.1	100.00%	0.0
Fluoroquinolones Quinolones Quinolines	fig 1581.157.peg.2242	<i>gyrA</i>	DNA gyrase subunit A (EC 5.99.1.3)	<i>Lentilactobacillus buchneri</i>	WP_419713160.1	99.88%	0.0
Beta-lactam resistance	8131219588	<i>oppA</i>	oligopeptide transport system substrate-binding protein	<i>Lentilactobacillus buchneri</i>	WP_014940071.1	100.00%	0.0
Beta-lactam resistance	8131219591	<i>penP</i>	beta-lactamase class A	<i>Lentilactobacillus buchneri</i>	WP_014940069.1	100.00%	5e-180
Beta-lactam resistance	8131219671	<i>pbp2A</i>	penicillin-binding protein 2A	<i>Lentilactobacillus buchneri</i>	WP_014940059.1	100.00%	0.0
Beta-lactam resistance	8131219738	<i>oppA</i>	oligopeptide transport system substrate-binding protein	<i>Lentilactobacillus buchneri</i>	WP_136838251.1	100.00%	0.0
Beta-lactam resistance	8131219826	<i>mrcA</i>	penicillin-binding protein 1A	<i>Lentilactobacillus buchneri</i>	WP_014939963.1	100.00%	0.0
Beta-lactam resistance	8131220231	<i>oppF</i>	oligopeptide transport system ATP-binding protein	<i>Lentilactobacillus buchneri</i>	WP_014940411.1	100.00%	0.0
Beta-lactam resistance	8131220232	<i>oppD</i>	oligopeptide transport system ATP-binding protein	<i>Lentilactobacillus buchneri</i>	WP_013728598.1	100.00%	0.0
Beta-lactam resistance	8131220233	<i>oppC</i>	oligopeptide transport system permease protein	<i>Lentilactobacillus buchneri</i>	WP_013728599.1	100.00%	0.0
Beta-lactam resistance	8131220234	<i>oppB</i>	oligopeptide transport system permease protein	MULTISPECIES: oligopeptide ABC transporter permease [<i>Lentilactobacillus</i>]	WP_014940412.1	100.00%	0.0
Beta-lactam resistance	8131220235	<i>oppA</i>	oligopeptide transport system substrate-binding protein	<i>Lentilactobacillus buchneri</i>	WP_014940413.1	100.00%	0.0
Beta-lactam resistance	8131220236	<i>oppA</i>	oligopeptide transport system substrate-binding protein	<i>Lentilactobacillus buchneri</i>	WP_014940414.1	100.00%	0.0
Beta-lactam resistance	8131220289	<i>oppA</i>	oligopeptide transport system substrate-binding protein	<i>Lentilactobacillus buchneri</i>	WP_149315620.1	100.00%	0.0
Beta-lactam resistance	8131220314	<i>oppA</i>	oligopeptide transport system substrate-binding protein	<i>Lentilactobacillus buchneri</i>	WP_014939186.1	100.00%	0.0
Beta-lactam resistance	8131220396	<i>oppA</i>	oligopeptide transport system substrate-binding protein	<i>Lentilactobacillus buchneri</i>	WP_014939257.1	100.00%	0.0

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Antibiotic	BV-BRC ID/ JGI-IMG-MER ID	Gene	Product	Source organism based on Protein-BLAST result	Acession	Identity	E-value
Beta-lactam resistance	8131220423	<i>oppA</i>	oligopeptide transport system substrate-binding protein	<i>Lentilactobacillus buchneri</i>	WP_014939279.1	100.00%	0.0
Beta-lactam resistance	8131220758	<i>oppA</i>	oligopeptide transport system substrate-binding protein	<i>Lentilactobacillus buchneri</i>	WP_014939279.1	100.00%	0.0
Beta-lactam resistance	8131221441	<i>oppA</i>	oligopeptide transport system substrate-binding protein	<i>Lentilactobacillus buchneri</i>	KRK69441.1	100.00%	0.0
Beta-lactam resistance	8131221529	<i>oppA</i>	oligopeptide transport system substrate-binding protein	<i>Lentilactobacillus buchneri</i>	WP_014939310.1	100.00%	0.0
Beta-lactam resistance	8131221867	<i>AbcA</i>	ATP-binding cassette, subfamily B, bacterial AbcA/BmrA	<i>Lentilactobacillus buchneri</i>	WP_014940594.1	100.00%	0.0
Vancomycin resistance	8131220017	<i>Ddl</i>	D-alanine-D-alanine ligase	<i>Lentilactobacillus buchneri</i>	WP_014939823.1	100.00%	0.0
Vancomycin resistance	8131220845	<i>VanX</i>	zinc D-Ala-D-Ala dipeptidase	<i>Lentilactobacillus buchneri</i> subsp. <i>silagei</i>	AFR99804.1	100.00%	0.0
Vancomycin resistance	8131220886	<i>mraY</i>	phospho-N-acetylmuramoyl-pentapeptide-transferase	<i>Lentilactobacillus buchneri</i>	WP_014939621.1	100.00%	0.0
Vancomycin resistance	8131220888	<i>MurG</i>	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	<i>Lentilactobacillus buchneri</i>	WP_014939621.1	100.00%	0.0
Vancomycin resistance	8131221200	<i>alr</i>	alanine racemase	<i>Lentilactobacillus buchneri</i>	WP_014940239.1	100.00%	0.0
Vancomycin resistance	8131221203	<i>MurF</i>	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	<i>Lentilactobacillus buchneri</i>	WP_014940241.1	100.00%	0.0
Transporter	fig 1581.157.peg.2417	<i>3.A.1.117.2</i>	Efflux ABC transporter, permease/ATP-binding protein, The Drug Exporter-2 (DrugE2) Family	<i>Lentilactobacillus buchneri</i>	WP_014940594.1	100.00%	0.0
Transporter	fig 1581.157.peg.2164	<i>2.A.1.2.93</i>	Uncharacterized MFS-type transporter	<i>Lentilactobacillus buchneri</i>	KRK66659.1	99.54%	0.0

Table S2. Putative antioxidant and oxidative-stress-related genes identified in the AGA55 genome

BV-BRC ID	Gene	Predicted protein/function	Probable relevance
>fig 1581.157.peg.184	<i>ohrR</i>	Organic hydroperoxide resistance transcriptional regulator	Regulates response to organic hydroperoxides and peroxide stress
>fig 1581.157.peg.274	<i>trxA</i>	Thioredoxin	Maintains intracellular redox balance
>fig 1581.157.peg.551	<i>trxA</i>	Thioredoxin	Redox homeostasis and oxidative-stress protection
>fig 1581.157.peg.100	<i>trxB</i>	Thioredoxin reductase	Regenerates reduced thioredoxin
>fig 1581.157.peg.1258	<i>trxB</i>	Thioredoxin reductase	Supports thioredoxin-dependent antioxidant activity
>fig 1581.157.peg.52	<i>nrdH</i>	Glutaredoxin-like protein NrdH	Thiol-disulfide redox regulation
>fig 1581.157.peg.587	<i>tpx</i>	Thiol peroxidase, Tpx-type	Detoxification of peroxides
>fig 1581.157.peg.744	<i>npx</i>	NADH peroxidase	Detoxification of hydrogen peroxide
>fig 1581.157.peg.758	<i>npx</i>	NADH peroxidase	Peroxide detoxification and redox balance
>fig 1581.157.peg.1730	<i>gpx / tpx</i>	Glutathione peroxidase / thioredoxin peroxidase	Detoxification of organic and inorganic peroxides
>fig 1581.157.peg.906	<i>nox</i>	NADH:flavin oxidoreductase / NADH oxidase	Oxygen metabolism and redox balance
>fig 1581.157.peg.733	<i>azoR</i>	FMN-dependent NADH-azoreductase	Redox-active oxidoreductase
>fig 1581.157.peg.77	<i>ndh</i>	NAD(P)H dehydrogenase quinone	Electron transfer and redox balancing
>fig 1581.157.peg.849	<i>ndh2</i>	NAD(P)H dehydrogenase quinone 2	Quinone reduction and redox homeostasis
>fig 1581.157.peg.829	<i>pntB</i>	NAD(P) transhydrogenase subunit beta	Maintains NADH/NADPH balance
>fig 1581.157.peg.830	<i>pntA</i>	NAD(P) transhydrogenase alpha subunit, C-domain	NADPH generation
>fig 1581.157.peg.831	<i>pntA</i>	NAD(P) transhydrogenase alpha subunit, N-domain	NADPH-dependent antioxidant support
>fig 1581.157.peg.383	<i>msrB</i>	Peptide-methionine R-sulfoxide reductase	Repairs oxidized methionine residues
>fig 1581.157.peg.384	<i>msrA</i>	Peptide-methionine S-sulfoxide reductase	Repairs oxidized methionine residues
>fig 1581.157.peg.591	<i>fRMsr / msrC</i>	Free methionine-R-sulfoxide reductase	Repairs oxidized free methionine
>fig 1581.157.peg.910	<i>dps</i>	DNA protection during starvation protein	Protects DNA against oxidative damage
>fig 1581.157.peg.893	<i>mntH</i>	Manganese transport protein MntH	Mn uptake and oxidative-stress protection
>fig 1581.157.peg.731	<i>mntR</i>	Mn-dependent transcriptional regulator	Regulates manganese homeostasis
>fig 1581.157.peg.778	<i>copA</i>	Heavy metal/copper-translocating P-type ATPase	Metal detoxification
>fig 1581.157.peg.938	<i>copA</i>	Heavy metal/copper-translocating P-type ATPase	Metal ion homeostasis
>fig 1581.157.peg.939	<i>copA</i>	Copper-transporting ATPase	Copper detoxification
>fig 1581.157.peg.940	<i>copA</i>	Copper-transporting ATPase	Copper homeostasis
>fig 1581.157.peg.1669	<i>copZ</i>	Copper chaperone	Copper trafficking and detoxification
>fig 1581.157.peg.1797	<i>cydC</i>	Glutathione/L-cysteine efflux ABC transporter CydC	Thiol transport and redox protection
>fig 1581.157.peg.1798	<i>cydD</i>	Glutathione/L-cysteine efflux ABC transporter CydD	Redox-associated stress protection
>fig 1581.157.peg.1799	<i>cydB</i>	Cytochrome d ubiquinol oxidase subunit II	Oxygen metabolism
>fig 1581.157.peg.1800	<i>cydA</i>	Cytochrome d ubiquinol oxidase subunit I	Oxygen metabolism
>fig 1581.157.peg.944	<i>pox</i>	Pyruvate oxidase	Redox metabolism
>fig 1581.157.peg.1155	<i>pox</i>	Pyruvate oxidase	Redox metabolism
>fig 1581.157.peg.1386	<i>pox</i>	Pyruvate oxidase	Redox metabolism
>fig 1581.157.peg.1596	<i>pox</i>	Pyruvate oxidase	Redox metabolism
>fig 1581.157.peg.632	<i>gfo / idh-like</i>	Gfo/Idh/MocA-family oxidoreductase	General redox metabolism
>fig 1581.157.peg.813	<i>putative oxr</i>	Putative oxidoreductase	Possible antioxidant/redox-associated enzyme
>fig 1581.157.peg.976	<i>akr</i>	Aldo/keto reductase-family oxidoreductase	Detoxification of reactive carbonyls
>fig 1581.157.peg.1016	<i>sdr</i>	Short-chain dehydrogenase/reductase	Redox metabolism
>fig 1581.157.peg.1219	<i>sdr</i>	Short-chain dehydrogenase/reductase	Redox-active enzyme

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BV-BRC ID	Gene	Predicted protein/function	Probable relevance
>fig 1581.157.peg.1221	<i>akr</i>	Aldo/keto reductase-family oxidoreductase	Carbonyl detoxification
>fig 1581.157.peg.1313	<i>akr</i>	Aldo/keto reductase-family oxidoreductase	Detoxification of aldehydes/ketones
>fig 1581.157.peg.1404	<i>sdr</i>	Short-chain dehydrogenase/reductase	General redox metabolism
>fig 1581.157.peg.1842	<i>sdr</i>	Short-chain dehydrogenase/reductase	Redox-associated metabolism
>fig 1581.157.peg.2001	<i>sdr</i>	Short-chain dehydrogenase/reductase	Redox-associated metabolism

Table S3. Putative bile tolerance and cholesterol-assimilation-related genes identified in the AGA55 genome.

BV-BRC ID	Gene	Predicted protein/function	Probable relevance
>fig 1581.157.peg.979	<i>cbh</i>	Choloylglycine hydrolase	Bile salt deconjugation
>fig 1581.157.peg.417	<i>mvaK1</i>	Mevalonate kinase	Mevalonate/isoprenoid metabolism
>fig 1581.157.peg.418	<i>mvaD</i>	Diphosphomevalonate decarboxylase	Mevalonate pathway
>fig 1581.157.peg.419	<i>mvaK2</i>	Phosphomevalonate kinase	Mevalonate pathway
>fig 1581.157.peg.522	<i>mvaS / hmgS</i>	Hydroxymethylglutaryl-CoA synthase	HMG-CoA/mevalonate metabolism
>fig 1581.157.peg.1790	<i>mvaA / hmgR</i>	Hydroxymethylglutaryl-CoA reductase	Mevalonate pathway
>fig 1581.157.peg.433	<i>lip / gdl</i>	Lipase/acylhydrolase with GDSL-like motif	Possible lipid interaction
>fig 1581.157.peg.943	<i>abh</i>	Alpha/beta-fold hydrolase	Possible lipid/ester hydrolase activity
>fig 1581.157.peg.1267	<i>abh</i>	Alpha/beta-fold hydrolase	Possible lipid/ester hydrolase activity
>fig 1581.157.peg.1251	<i>putative csh</i>	Putative cell-surface hydrolase	Possible cholesterol binding contribution
>fig 1581.157.peg.1728	<i>putative csh</i>	Cell-surface hydrolase	Cell-envelope-associated interaction
>fig 1581.157.peg.1068	<i>glpQ-like</i>	Membrane-anchoring domain / glycerophosphoryl diester phosphodiesterase	Membrane lipid metabolism
>fig 1581.157.peg.878	<i>glpQ</i>	Glycerophosphoryl diester phosphodiesterase	Phospholipid metabolism
>fig 1581.157.peg.887	<i>glpQ</i>	Glycerophosphoryl diester phosphodiesterase	Membrane lipid metabolism
>fig 1581.157.peg.324	<i>glpQ</i>	Glycerophosphoryl diester phosphodiesterase	Membrane lipid metabolism
>fig 1581.157.peg.874	<i>fadB</i>	3-hydroxyacyl-CoA dehydrogenase	Fatty-acid metabolism
>fig 1581.157.peg.1117	<i>hbd / fadB</i>	3-hydroxybutyryl-CoA dehydrogenase	Fatty-acid and lipid-associated metabolism
>fig 1581.157.peg.1990	<i>hbd / fadB</i>	3-hydroxybutyryl-CoA dehydrogenase	Fatty-acid metabolism
>fig 1581.157.peg.1686	<i>acd</i>	Acyl-CoA dehydrogenase	Fatty-acid metabolism
>fig 1581.157.peg.946	<i>sdr</i>	Short-chain dehydrogenase	Possible sterol/lipid-associated redox activity
>fig 1581.157.peg.1016	<i>sdr</i>	Short-chain dehydrogenase/reductase	Possible sterol-associated transformation
>fig 1581.157.peg.1219	<i>sdr</i>	Short-chain dehydrogenase/reductase	Possible sterol-associated redox activity
>fig 1581.157.peg.1404	<i>sdr</i>	Short-chain dehydrogenase/reductase	Redox/lipid-associated metabolism
>fig 1581.157.peg.1842	<i>sdr</i>	Short-chain dehydrogenase/reductase	Redox/lipid-associated metabolism
>fig 1581.157.peg.2001	<i>sdr</i>	Short-chain dehydrogenase/reductase	Redox/lipid-associated metabolism

Table S4. Putatively identified adhesion, aggregation, and cell-surface-associated genes in the AGA55 genome.

BV-BRC ID	Gene	Predicted protein/function	Probable relevance
>fig 1581.157.peg.1286	<i>apf</i>	Aggregation-promoting factor	Auto-aggregation and persistence
>fig 1581.157.peg.1763	<i>srtA</i>	Sortase A, LPXTG-specific	Anchoring of surface proteins
>fig 1581.157.peg.23	<i>lytR / cpsA / psr</i>	LytR-CpsA-Psr family cell-envelope protein	Cell-wall architecture
>fig 1581.157.peg.137	<i>tagH</i>	Teichoic acid export ATP-binding protein	Cell-wall teichoic acid export
>fig 1581.157.peg.477	<i>tagG</i>	Teichoic acid translocation permease	Teichoic acid export
>fig 1581.157.peg.601	<i>ltaS</i>	Lipoteichoic acid synthase Type IIa	Lipoteichoic acid biosynthesis
>fig 1581.157.peg.1255	<i>ltaS</i>	Lipoteichoic acid synthase Type IIb	Lipoteichoic acid biosynthesis
>fig 1581.157.peg.602	<i>lafC</i>	Integral membrane protein LafC	Glycolipid and LTA synthesis
>fig 1581.157.peg.603	<i>lafB</i>	Glycosyltransferase LafB	Gal-Glc-DAG formation
>fig 1581.157.peg.604	<i>ugtP</i>	1,2-diacylglycerol 3-glucosyltransferase	Glycolipid biosynthesis
>fig 1581.157.peg.623	<i>bglT / gtf</i>	Bactoprenol glucosyltransferase	Cell-wall glycan synthesis
>fig 1581.157.peg.1439	<i>gtf</i>	Glycosyltransferase	Surface polysaccharide synthesis
>fig 1581.157.peg.1441	<i>wzx-like</i>	Putative sugar translocase	Surface polysaccharide formation
>fig 1581.157.peg.482	<i>ami</i>	N-acetylmuramoyl-L-alanine amidase	Cell-wall remodeling
>fig 1581.157.peg.671	<i>ami</i>	N-acetylmuramoyl-L-alanine amidase	Cell-wall remodeling
>fig 1581.157.peg.955	<i>atl</i>	Bifunctional autolysin Atl	Adhesion and cell-wall turnover
>fig 1581.157.peg.1630	<i>ami</i>	N-acetylmuramoyl-L-alanine amidase	Cell-wall remodeling
>fig 1581.157.peg.1954	<i>atl</i>	Bifunctional autolysin Atl	Cell-wall remodeling
>fig 1581.157.peg.996	<i>pgdA</i>	Peptidoglycan N-acetylglucosamine deacetylase	Cell-wall modification
>fig 1581.157.peg.1249	<i>p45</i>	Peptidoglycan lytic protein P45	Cell-wall remodeling
>fig 1581.157.peg.1915	<i>p45</i>	Peptidoglycan lytic protein P45	Cell-wall remodeling
>fig 1581.157.peg.1251	<i>putative csh</i>	Putative cell-surface hydrolase	Cell-surface interaction
>fig 1581.157.peg.1728	<i>putative csh</i>	Cell-surface hydrolase	Adhesion/cell-envelope interaction
>fig 1581.157.peg.132	<i>spyDAC-associated</i>	Uncharacterized secreted protein associated with spyDAC	Possible secreted/surface-associated protein
>fig 1581.157.peg.402	<i>lspA</i>	Lipoprotein signal peptidase	Processing of surface lipoproteins
>fig 1581.157.peg.97	<i>lgt</i>	Prolipoprotein diacylglyceryl transferase	Lipoprotein maturation
>fig 1581.157.peg.666	<i>camS</i>	Putative pheromone cAM373 precursor lipoprotein	Surface/lipoprotein-associated function
>fig 1581.157.peg.1805	<i>isdE</i>	Heme transporter IsdDEF, lipoprotein IsdE	Surface-associated transport

Table S5. Putative acid-tolerance and gastrointestinal survival genes detected in the AGA55 genome.

BV-BRC ID	Gene	Predicted protein/function	Probable relevance
>fig 1581.157.peg.128	<i>nhaC</i>	Na ⁺ /H ⁺ antiporter	Intracellular pH regulation
>fig 1581.157.peg.303	<i>nhaC</i>	Na ⁺ /H ⁺ antiporter	Acid and ion stress tolerance
>fig 1581.157.peg.827	<i>napA</i>	Na ⁺ /H ⁺ antiporter NapA	pH homeostasis
>fig 1581.157.peg.1151	<i>napA</i>	Na ⁺ /H ⁺ antiporter NapA	pH and sodium stress adaptation
>fig 1581.157.peg.1264	<i>nhaC</i>	Na ⁺ /H ⁺ antiporter	Intracellular pH regulation
>fig 1581.157.peg.1864	<i>nhaC</i>	Na ⁺ /H ⁺ antiporter	pH homeostasis
>fig 1581.157.peg.854	<i>gadC</i>	Glutamate/GABA antiporter	Acid resistance
>fig 1581.157.peg.855	<i>gadB</i> / <i>gadA</i>	Glutamate decarboxylase	Proton-consuming acid-resistance mechanism
>fig 1581.157.peg.860	<i>arcD</i>	Arginine/ornithine antiporter	Acid resistance
>fig 1581.157.peg.1275	<i>arcD</i>	Arginine/ornithine antiporter	Acid-stress adaptation
>fig 1581.157.peg.1353	<i>arcD</i>	Arginine/ornithine antiporter	Acid-stress adaptation
>fig 1581.157.peg.967	<i>cadA</i> / <i>ldc-like</i>	Lysine decarboxylase family protein	Possible acid-resistance contribution
>fig 1581.157.peg.1564	<i>atpC</i>	ATP synthase epsilon chain	Proton extrusion and pH homeostasis
>fig 1581.157.peg.1565	<i>atpD</i>	ATP synthase beta chain	Proton extrusion under acid stress
>fig 1581.157.peg.1566	<i>atpG</i>	ATP synthase gamma chain	pH homeostasis
>fig 1581.157.peg.1567	<i>atpA</i>	ATP synthase alpha chain	pH homeostasis
>fig 1581.157.peg.1569	<i>atpF</i>	ATP synthase F0 sector subunit b	Proton translocation
>fig 1581.157.peg.1570	<i>atpE</i>	ATP synthase F0 sector subunit c	Proton translocation
>fig 1581.157.peg.1571	<i>atpB</i>	ATP synthase F0 sector subunit a	Proton translocation

Table S6. Putative stress-tolerance and general probiotic fitness genes identified in the AGA55 genome.

BV-BRC ID	Gene	Predicted protein/function	Probable relevance
>fig 1581.157.peg.108	<i>clpP</i>	ATP-dependent Clp protease proteolytic subunit	Protein quality control
>fig 1581.157.peg.714	<i>clpC</i>	ATP-dependent Clp protease ATP-binding subunit	Stress-induced protein refolding/degradation
>fig 1581.157.peg.608	<i>clpE</i>	ATP-dependent Clp protease ATP-binding subunit	Stress tolerance
>fig 1581.157.peg.1528	<i>clpX</i>	ATP-dependent Clp protease ATP-binding subunit	Protein quality control
>fig 1581.157.peg.1860	<i>clpE</i>	ATP-dependent Clp protease ATP-binding subunit	Stress response
>fig 1581.157.peg.459	<i>clpB</i>	Chaperone protein ClpB	Refolding of aggregated proteins
>fig 1581.157.peg.492	<i>dnaJ</i>	Chaperone protein DnaJ	Protein folding under stress
>fig 1581.157.peg.493	<i>dnaK</i>	Chaperone protein DnaK	Heat- and acid-stress tolerance
>fig 1581.157.peg.494	<i>grpE</i>	Heat-shock protein GrpE	DnaK co-chaperone
>fig 1581.157.peg.71	<i>groES</i>	Heat-shock protein GroES	Protein folding
>fig 1581.157.peg.72	<i>groEL</i>	Heat-shock protein GroEL	Protein folding and stress protection
>fig 1581.157.peg.1743	<i>hslO</i>	33 kDa chaperonin HslO	Stress protection
>fig 1581.157.peg.375	<i>hslV</i>	ATP-dependent protease subunit HslV	Protein degradation
>fig 1581.157.peg.376	<i>hslU</i>	ATP-dependent Hsl protease ATP-binding subunit	Protein quality control
>fig 1581.157.peg.1517	<i>lon</i>	Lon-like protease with PDZ domain	Stress-related proteolysis
>fig 1581.157.peg.1744	<i>ftsH</i>	ATP-dependent zinc metalloprotease FtsH	Membrane/protein quality control
>fig 1581.157.peg.544	<i>gsp</i>	General stress protein	General stress adaptation
>fig 1581.157.peg.1547	<i>gsp13</i>	General stress protein 13	General stress protection
>fig 1581.157.peg.595	<i>uspA</i>	Universal stress protein	Stress adaptation
>fig 1581.157.peg.1366	<i>uspA</i>	Universal stress protein	Stress adaptation
>fig 1581.157.peg.1680	<i>uspA</i>	Universal stress protein	Stress adaptation
>fig 1581.157.peg.359	<i>asp</i>	Putative alkaline-shock protein	pH-stress response
>fig 1581.157.peg.1859	<i>csp</i>	Cold-shock protein	Cold adaptation and RNA stabilization
>fig 1581.157.peg.485	<i>relA / spoT</i>	ppGpp synthetase/hydrolase	Stringent response
>fig 1581.157.peg.190	<i>lexA</i>	SOS-response repressor and protease	DNA damage response
>fig 1581.157.peg.521	<i>lexA</i>	SOS-response repressor and protease	DNA damage response
>fig 1581.157.peg.29	<i>radA</i>	DNA repair protein Rada	DNA repair
>fig 1581.157.peg.345	<i>recN</i>	DNA repair protein RecN	Double-strand break repair
>fig 1581.157.peg.361	<i>recG</i>	ATP-dependent DNA helicase RecG	DNA repair
>fig 1581.157.peg.446	<i>recQ</i>	ATP-dependent DNA helicase RecQ	DNA repair
>fig 1581.157.peg.467	<i>recO</i>	DNA recombination and repair protein RecO	DNA repair
>fig 1581.157.peg.571	<i>recA</i>	RecA protein	DNA repair and SOS response
>fig 1581.157.peg.57	<i>recR</i>	Recombination protein RecR	DNA repair
>fig 1581.157.peg.668	<i>uvrD / pcrA</i>	ATP-dependent DNA helicase	DNA repair
>fig 1581.157.peg.1297	<i>alkA</i>	DNA alkylation repair enzyme	DNA damage repair