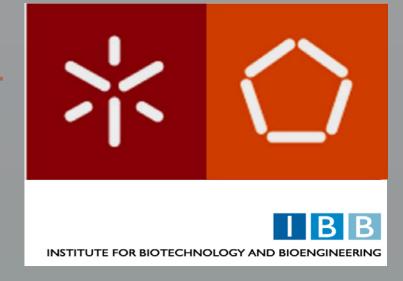


Genome-scale metabolic network of the central carbon metabolism of Enterococcus faecalis



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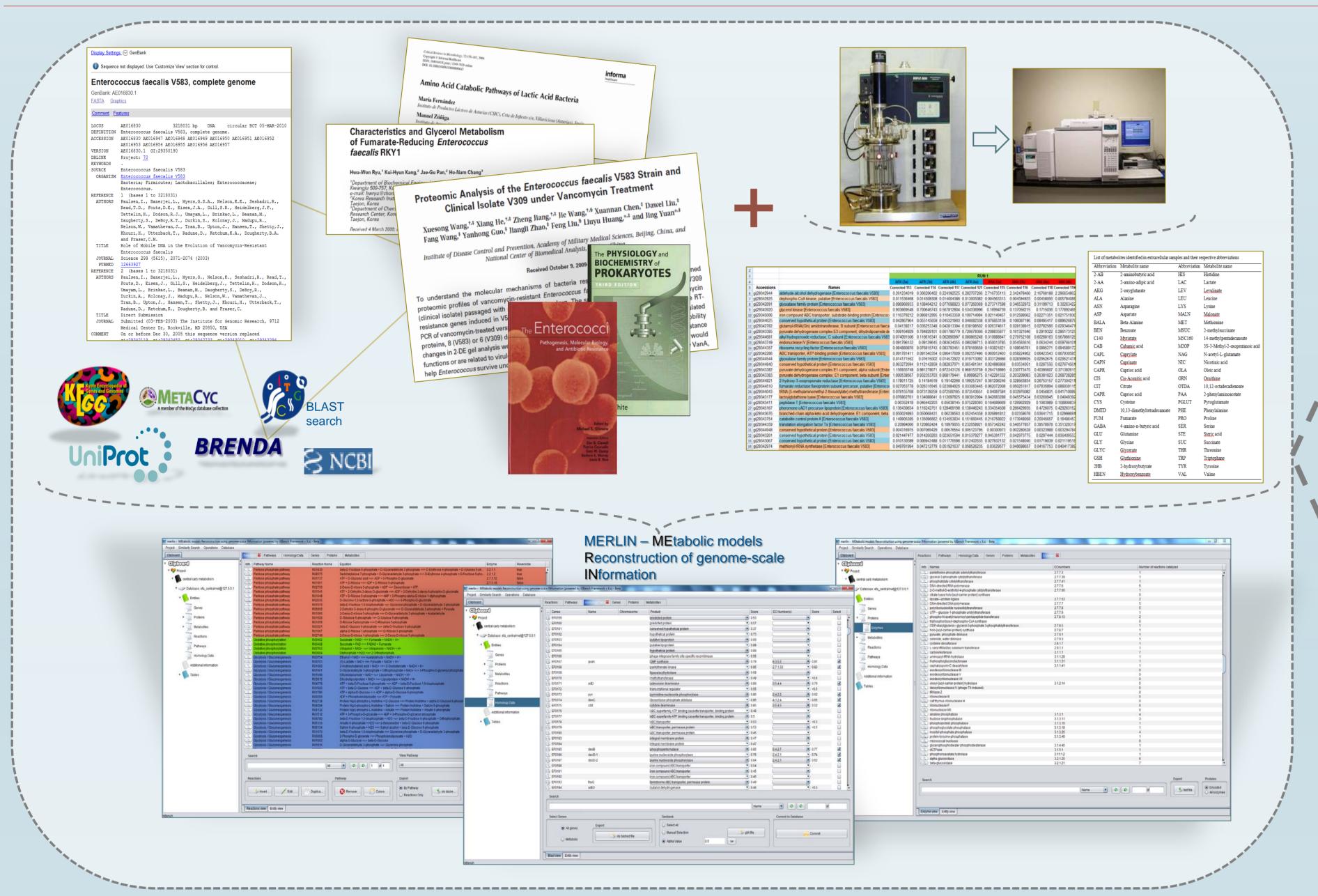
Introduction

E. faecalis is a gram-positive bacterium that is getting more We propose to reconstruct the genome scale metabolic attention due to its "two-face" behavior. This natural inhabitant of network of the central carbon metabolism of *E. faecalis*. the mammalian gastrointestinal tract is also an opportunist pathogen responsible for urinary tract infections, nosocomial infections, bacteremia and infective endocarditis. Its intrinsic physiological properties such as inherent antibiotic resistance and exceptional ability to adapt to harsh conditions provide this databases and literature research. organism with an enormous advantage in the infection processes.

Objectives

The model will support the interpretation and better understanding of the metabolomic and proteomic data. The reconstruction will be based initially on the genome sequencing information available as well as online

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H96 A B 73 R00782 R_00122 L-Cysteine + H2O <=> Hydrogen sulfide + Pyruvate + NH3 74 R00801 R_00113 Sucrose + H2O <=> D-Fructose + D-Glucose 3.2.1.20 75 R00802 R_00071 Sucrose + H2O <=> beta-D-Fructose + alpha-D-Glucose 3.2.1.20 76 R00811 R_00202 Sucrose + Protein N(pi)-phospho-L-histidine <=> Sucrose-6-phosphate + Protein histidine 2.7.1.69 77 R00835 R 00052 D-Glucose 6-phosphate + NADP+ <=> D-Glucono-1.5-lactone 6-phosphate + NADPH + H+ 1.1.1.49 78 R00863 R_00190 3-Sulfino-L-alanine <=> L-Alanine + Sulfur dioxide 4.1.1.12 79 R00895 R_00262 L-Cysteine + 2-Oxoglutarate <=> Mercaptopyruvate + L-Glutamate Merlin, metabolomic data, book Alanine, aspartate and aspargine met 80 R00897 R_00099 O-Acetyl-L-serine + Hydrogen sulfide <=> L-Cysteine + Acetate 2.5.1.47 book Alanine, aspartate and aspargine metabolism in m.o, microbiolo 81 R00927 R_00088 Propanoyl-CoA + Acetyl-CoA <=> CoA + 2-Methylacetoacetyl-CoA 2.3.1.9 2 R00945 R 00225 5,10-Methylenetetrahydrofolate + Glycine + H2O <=> Tetrahydrofolate + L-Serine 2.1.2.1 TRUE R00959 R_00156 D-Glucose 1-phosphate <=> alpha-D-Glucose 6-phosphate 5.4.2.2 84 R00996 R 00240 L-Threonine <=> 2-Oxobutanoate + NH3 4.3.1.19 TRUE 85 R00999 R 00265 O-Succinyl-L-homoserine + H2O <=> 2-Oxobutanoate + Succinate + NH3 2.5.1.48 TRUE Proteomics analysis of the efa V583 and clinical isolate under vancomy 86 R01000 R_00222 2-Hydroxybutanoic acid + NAD+ <=> 2-Oxobutanoate + NADH + H+ 1.1.1.27 87 R01001 R_00270 L-Cystathionine + H2O <=> L-Cysteine + NH3 + 2-Oxobutanoate 4.4.1.1 88 R01015 R 00074 D-Glyceraldehyde 3-phosphate <=> Glycerone phosphate 5.3.1.1 4.2.3.3 89 R01016 R_00187 Glycerone phosphate <=> Methylglyoxal + Orthophosphate 90 R01049 R_00172 ATP + D-Ribose 5-phosphate <=> AMP + 5-Phospho-alpha-D-ribose 1-diphosphate 2.7.6.1 91 R01051 R_00069 ATP + D-Ribose <=> ADP + D-Ribose 5-phosphate 2.7.1.15 92 R01056 R_00008 D-Ribose 5-phosphate <=> D-Ribulose 5-phosphate 5.3.1.6 93 R01057 R_00257 alpha-D-Ribose 1-phosphate <=> D-Ribose 5-phosphate 5.4.2.7 94 R01061 R_00062 D-Glyceraldehyde 3-phosphate + Orthophosphate + NAD+ <=> 3-Phospho-D-glyceroyl phosphate + NADH + H+ 1.2.1.12 95 R01066 R_00137 2-Deoxy-D-ribose 5-phosphate <=> D-Glyceraldehyde 3-phosphate + Acetaldehyde 4.1.2.4 TRUE 4.1.2.13 96 R01070 R_00169 beta-D-Fructose 1,6-bisphosphate <=> Glycerone phosphate + D-Glyceraldehyde 3-phosphate 97 R01072 R_00145 L-Glutamine + 5-Phospho-alpha-D-ribose 1-diphosphate + H2O <=> 5-Phosphoribosylamine + Diphosphate + L-Glutamate 2.4.2.14 98 R01083 R_00141 N6-(1,2-Dicarboxyethyl)-AMP <=> Fumarate + AMP 4.3.2.2 99 R01090 R 00041 I-Leucine + 2-Ovoglutarate <=> 4-Methyl-2-ovonentanoate + I-Glutamate 2.6.1.42 TRUE

Figure 2: Metabolic network of the central carbon metabolism in an Excel spreadsheet

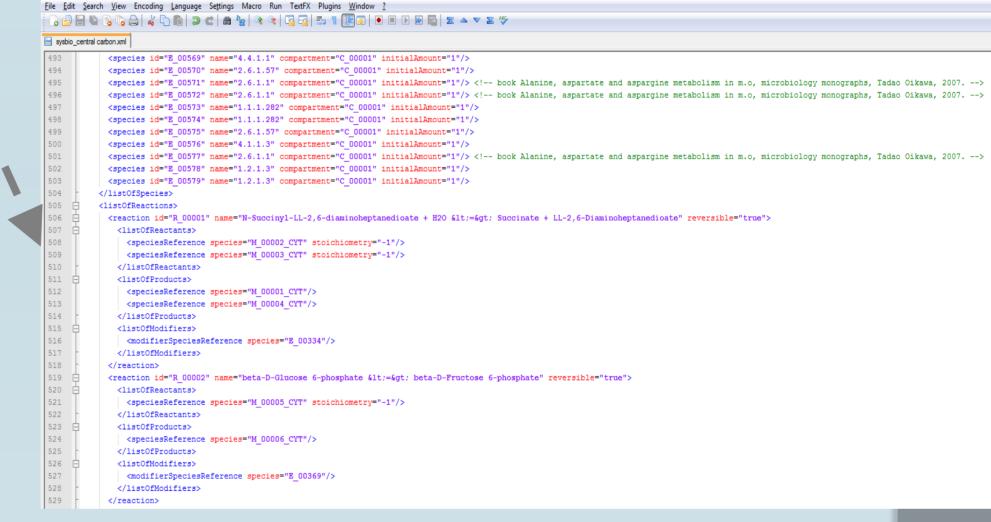


Figure 3: Metabolic network of the central carbon metabolism in an XML formal - SBML

Figure 1: Data integration of different levels of information.

Results

cytosol extracelular sugars aminoacids peptides

Figure 4: Graphical representation of the cental carbon metabolism of Enterococcus faecalis metabolic network - Cell designer

Future directions

On-going activities are the addition of:

- Membrane transport reactions (of extracelular compounds to the inside of the cell)
- Metabolism products (that are secreted by the cell)
- Biomass equation

Simulations:

- Optimization of growth
- Minimal nutrient requirements
- Gene deletion

Extend model for full metabolic network



A metabolic network reconstruction is practically and endless process that may lead to even more accurate predictions of cell metabolism.

Conclusions

The metabolic model generated for this bacterium will allow the correlation of metabolite levels and fluxes, enabling identification of key control points in its metabolism. Additionally, the metabolomic data already generated by our group allowed the identification of key compounds/reactions in E. faecalis metabolism that were still unclear. As it has been previously shown for other organisms, the metabolic network reconstruction may serve as a valuable tool to predict the phenotypic behaviour under various genetic and environmental conditions as well as to perform metabolic engineering simulations (e.g. gene deletion experiments).

