The B-vitamin biosynthesis capabilities of the human gut microbiome. By S. Magnusdottir and I. Thiele, *Luxembourg Centre for Systems Biomedicine, University of Luxembourg, 7, avenue des Hauts-Fourneaux, L-4362 Esch-sur-Alzette, Luxembourg*

Introduction

B-vitamins are necessary cofactors for our metabolism. Human cells are not capable of producing B-vitamins, and must acquire them instead from the diet. In addition to the diet, the human gut microbiota is known to supply its host with several nutrients, including B-vitamins (1). However, we still do not know sufficiently about which microbes can supply us with these vitamins, and which ones compete with our cells for resources from the vitamin pool in our intestine.

To assess the question of which microbes are capable of providing our cells with B-vitamins, we looked at the genomes of 259 known human gut microbes. We examined each genome for the genome annotations that are related to B-vitamin *de novo* biosynthesis, and from there predicted the vitamin biosynthesis capabilities of each organism in the list.

Results

The five major abundant phyla in the gut microbiome, Actinobacteria, Bacteroidetes, Firmicutes, Fusobacteria, and Proteobacteria were represented in the genome collection. For each of the phyla, we calculated the ratio of organisms that were predicted to be producers of each B-vitamin tested. The results are shown in Figure 1.

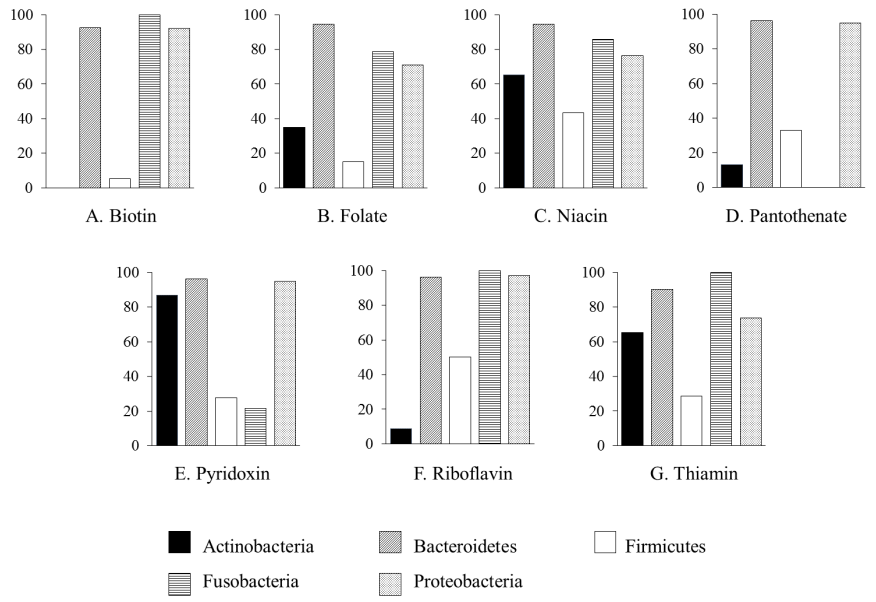

Figure 1. The ratio of predicted producers of each vitamin per phyla. Values are presented as percentages.

Our results indicate that B-vitamins are being supplied to our cells mainly from Bacteroidetes and Proteobacteria, where over 75% of the organisms are predicted to be able to produce all seven vitamins. Fusobacteria are predicted to be able to produce all vitamins except or pantothenate and pyridoxin.

The gram-positive phyla Actinobacteria and Firmicutes have the least

abilities to produce vitamins. 85% of

Table 1. Comparison of genomic predictions and experimental evidence. Filled circles represent that predictions and data agree, empty circles represent mismatches.

Organism	B	F	N	P	B6	R	T	Ref
Akkermansia muciniphila	●	●	●	●	●	●	●	(2)
Bacteroides fragilis NCTC 9343	●	●	●	●	●	●	●	(3)
Bacteroides thetaiotaomicron VPI-5482	●	●	●	●	●	●	●	(3)
Bacteroides vulgatus ATCC 8482	●	●	●	●	●	●	●	(3)
Bifidobacterium breve	●	●	●	●	●	○	●	(4)
Bifidobacterium longum	●	○	●	●	●	○	●	(4)
Clostridium difficile CD196	●	●	●	●	●	●	●	(5)
Escherichia coli str. K-12 substr. MG1655	●	●	●	●	●	●	●	(6)
Faecalibacterium prausnitzii	●	●	●	●	●	●	○	(7)
Helicobacter pylori 26695	●	●	●	●	●	●	○	(8)
Klebsiella pneumoniae 1162281	●	●	●	●	●	●	●	(9)
Lactobacillus plantarum WCFS1	○	○	●	●	●	●	○	(10)
Listeria monocytogenes	●	●	●	●	●	●	●	(11)
Salmonella enterica subsp. *Enterica* Typhimurium	●	●	●	●	●	●	●	(12)

B: biotin, F: folate, N: niacin, P: pantothenate, B6: pyridoxin, R: riboflavin, T: thiamin, Ref: references.

Actinobacteria have the ability to produce pyridoxin, and 65% can produce niacin and thiamin. For the remaining four vitamins, less than 40% of the Actinobacteria genomes have the ability to produce them. In the case of Firmicutes, less than 50% have the ability to produce the seven vitamins, where most can produce riboflavin and niacin.

In order to assess the reliability of our predictions, we compared our results with experimental data available on 14 organisms in our list. Out of 98 predictions, 92% matched the experimental evidence found in literature (Table 1).

Discussion

The information of which microorganisms can produce which B-vitamins is especially useful for the metabolic modelling of the human gut microbiota. The gut microbes are known to be involved in several diseases, and modelling the metabolic interactions between the human cells

and the microbiota could give us information on how the relationship between diet, microbiota, and human cells can result in diseased states of the host.

Since the human gut is estimated to have over 1000 species present, experimentally identifying all the possible interactions is today an infeasible task, and we must rely on data from alternative sources to produce biologically relevant microbial models. The presented B-vitamin biosynthesis genome analysis provides new biochemical information about the 259 inspected genomes, which could be included in metabolic models of the respective organisms. The analysis can be further applied to other subsystems of metabolism as well.

It is important to note that in most of the presented cases, the predictions we have made have not yet been validated. However, in the cases where we did find experimental evidence, the prediction success rate was high, and we would therefore not expect many false predictions for the rest of the organisms in our list. Nevertheless, in the case of false predictions the metabolic models could easily be refined later on as experimental data becomes available.

Methods

The presence of B-vitamin biosynthesis related genome annotations were analyzed using the PubSEED platform (13).

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