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Metabolic Pathways Reconstruction in Cytophaga through the Exploration of Gene Expression Data Resulting from BIOLOG Substrate Utilization Patterns

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Abstract-A major challenge of systems biology is to provide a complete picture of the cellular capacity of living organisms by integrating genomics, proteomics and metabolomics data. Studies are now being conducted to attribute functions to genes and proteins leading thereby to a better description of regulatory networks underlying metabolic pathways. The goal of these studies is to understand the relationships between the components of an organism's metabolic networks. Recent analyses of the gliding bacteria *Cytophaga hutchinsonii* genome have indicated the presence of a complete Embden-Meyerhof-Parnas pathway. In this study, we used Biolog Ecoplates data for linking metabolic flux to carbohydrate biosynthesis in *Cytophaga* and facilitate post-genomic data integration. Surprisingly, the complete pathway could not be reconstructed with the Biolog data generated, as *Cytophaga* failed to process basic glucose. These findings suggested that the carbon source utilization profiles obtained do not necessarily reflect the functional potential of *Cytophaga* as predicted by its genome. These results will allow us to understand how genomic and metabolic information in *Cytophaga* can be integrated to improve metabolic flux prediction and metabolic network identification, including facilitating the refinement of gene annotations. This will also allow the exploration of genotype-phenotype relationships while developing a framework for multiple sources of data.

Keywords- *Cytophaga, Carbohydrate Utilization, Phenotype-Genotype Interactions, Metabolic Networks, Biolog Ecoplates*

I. Introduction

Cytophaga hutchinsonii is one of the less-studied species in the Bacteroidetes phylum. Among the bacteria belonging to the phylum Bacteroidetes, some genomes have been sequenced and annotated, but studies on *C. hutchinsonii* remain few [1]. *C. hutchinsonii* is a gram-negative bacterium originally isolated from sugarcane piles. This microorganism must therefore produce an array of enzymes allowing it to survive on biomass wastes. *C. hutchinsonii* thus represents a rich source of potentially effective cellulase enzymes that can be harnessed for conversion of biomass to simple sugars [1]. These sugars can then be used as feedstock for ethanol production or other chemical synthesis. However, due to lack of knowledge, most *Cytophaga* based applications are still in infancy. The development of industrial and environmental technologies based on genotype-phenotype relationships is almost non-existent. Several efforts are currently underway, such as the genome sequencing of several other bacteroides, to create a critical mass of knowledge pertaining to *Cytophaga* technologies, including physiological and behavioral studies [1].

The sequencing of *Cytophaga hutchinsonii* ATCC 33406 provided means to investigate the metabolic potential of the *Cytophaga* species, and opened avenues for the development of new biotechnological applications [1, 2]. A whole genome analysis of *C. hutchinsonii* revealed a wealth of genetic determinants that play a role in biocatalysis, such as those for the hyper production of polymers and industrially relevant enzymes [3]. However, despite the clear breakthrough in our understanding of *C .hutchinsonii* through this sequencing effort, the relationship between the genotype and the phenotype cannot be predicted simply from cataloguing and assigning gene functions to the genes found in the genome, and considerable work is still needed before the genome can be translated into a fully functioning metabolic model of value for predicting cell phenotypes. The slow effort of compiling data on the metabolic potential of C. hutchinsonii is partly due to the inherent difficulties in growing these microorganisms under regular laboratory conditions. With this work, we aimed to expand our knowledge in carbon metabolism in *C. hutchinsonii* through the evaluation of its potential to oxidize various carbon sources. By using metabolomics information obtained with Biolog EcoPlates™ we have gained valuable insights into the relationship between genotype and phenotype pertaining carbohydrate catabolism in this bacterium. Our results could be used to improve the production of various industrial and biotechnological compounds including ethanol for renewable energy production.

II. MATERIALS AND METHODS

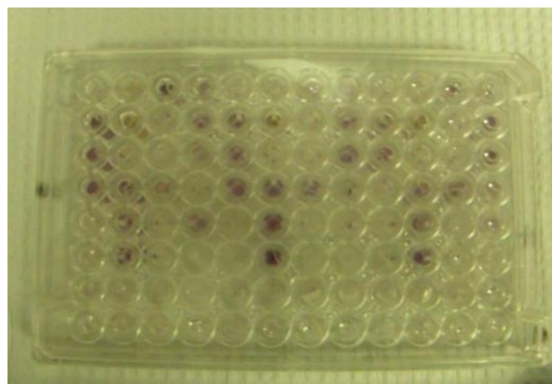
In this study, we evaluated the potential of *C. hutchinsonii* ATCC 33406 in oxidizing various carbon sources by using Biolog Ecoplates following Smalla's and Insam's modified protocols [3, 4]. Bacterial cells suspension was used to inoculate wells of microtiter plates in which each well contains a different carbon source, nutrients, and a tetrazolium dye [4]. The plates were tightly sealed to avoid contamination and then incubated for a suitable period of time while oxidation of the substrates was periodically monitored by measuring the concomitant reduction of the tetrazolium dye. Since it is still generally assumed that the observed profile of carbon sources metabolized reflects the catabolic potential of the inoculum, these 96-wells plates should provide a more or less complete picture of the catabolic potential of *Cytophaga*.

BIOLOG Microbial Community Analysis

EcoPlate™

A1 Water	A2 β-Methyl-D-Glucoside	A3 D-Galactonic Acid γ-Lactone	A4 L-Arginine	A1 Water	A2 β-Methyl-D-Glucoside	A3 D-Galactonic Acid γ-Lactone	A4 L-Arginine	A1 Water	A2 β-Methyl-D-Glucoside	A3 D-Galactonic Acid γ-Lactone	A4 L-Arginine
B1 Pyruvic Acid Methyl Ester	B2 D-Xylose	B3 D-Galacturonic Acid	B4 L-Asparagine	B1 Pyruvic Acid Methyl Ester	B2 D-Xylose	B3 D-Galacturonic Acid	B4 L-Asparagine	B1 Pyruvic Acid Methyl Ester	B2 D-Xylose	B3 D-Galacturonic Acid	B4 L-Asparagine
C1 Tween 40	C2 i-Erythritol	C3 2-Hydroxy Benzoic Acid	C4 L-Phenylalanine	C1 Tween 40	C2 i-Erythritol	C3 2-Hydroxy Benzoic Acid	C4 L-Phenylalanine	C1 Tween 40	C2 i-Erythritol	C3 2-Hydroxy Benzoic Acid	C4 L-Phenylalanine
D1 Tween 80	D2 D-Mannitol	D3 4-Hydroxy Benzoic Acid	D4 L-Serine	D1 Tween 80	D2 D-Mannitol	D3 4-Hydroxy Benzoic Acid	D4 L-Serine	D1 Tween 80	D2 D-Mannitol	D3 4-Hydroxy Benzoic Acid	D4 L-Serine
E1 α-Cyclodextrin	E2 N-Acetyl-D-Glucosamine	E3 γ-Hydroxybutyric Acid	E4 L-Threonine	E1 α-Cyclodextrin	E2 N-Acetyl-D-Glucosamine	E3 γ-Hydroxybutyric Acid	E4 L-Threonine	E1 α-Cyclodextrin	E2 N-Acetyl-D-Glucosamine	E3 γ-Hydroxybutyric Acid	E4 L-Threonine
F1 Glycogen	F2 D-Glucosaminic Acid	F3 Itaconic Acid	F4 Glycyl-L-Glutamic Acid	F1 Glycogen	F2 D-Glucosaminic Acid	F3 Itaconic Acid	F4 Glycyl-L-Glutamic Acid	F1 Glycogen	F2 D-Glucosaminic Acid	F3 Itaconic Acid	F4 Glycyl-L-Glutamic Acid
G1 D-Cellobiose	G2 Glucose-1-Phosphate	G3 α-Ketobutyric Acid	G4 Phenylethyl-amine	G1 D-Cellobiose	G2 Glucose-1-Phosphate	G3 α-Ketobutyric Acid	G4 Phenylethyl-amine	G1 D-Cellobiose	G2 Glucose-1-Phosphate	G3 α-Ketobutyric Acid	G4 Phenylethyl-amine
H1 α-D-Lactose	H2 D,L-α-Glycerol Phosphate	H3 D-Malic Acid	H4 Putrescine	H1 α-D-Lactose	H2 D,L-α-Glycerol Phosphate	H3 D-Malic Acid	H4 Putrescine	H1 α-D-Lactose	H2 D,L-α-Glycerol Phosphate	H3 D-Malic Acid	H4 Putrescine

(a)



(b)

Figure 1. Biolog Ecoplates: (a) experimental design of Biolog Ecoplates showing the various carbon sources present and (b) substrates utilized by *Cytophaga* on the Biolog Ecoplates after 2 weeks of inoculation

The EcoPlates contain 3 replications of 31 different carbon sources and water control wells. Six different classes of substrates, namely amines, amino acids, carbohydrates, carboxylic acids, phenols and polymers were used to grow *Cytophaga* on Biolog Ecoplates (Fig. 1). According to Insam's paper [3], the 6 different classes of known substrates, amines, carbohydrates, carboxylic acids, amino acids, phenols, and polymers were inoculated with 130 µl of *Cytophaga* culture suspension at a cell density of approximately 1×10^8 cells ml−1 [3]. In addition, three flasks with simple glucose were prepared, as the closest substance available on the Biolog plates was glucose-1-Phosphate. The plates and flasks were then incubated at 30◦C (optimum growth temperature for *Cytophaga*) in an incubator, and subsequent color development was measured every 24 hours for 16 days using an automated plate reader at 600nm. Readings was terminated if the average well color density reaches an optical density (OD) of 2. To ensure consistency of the results, the same experiment was repeated 3 times with 3 replications each time and an average OD was calculated as the final working value (Fig. 2).

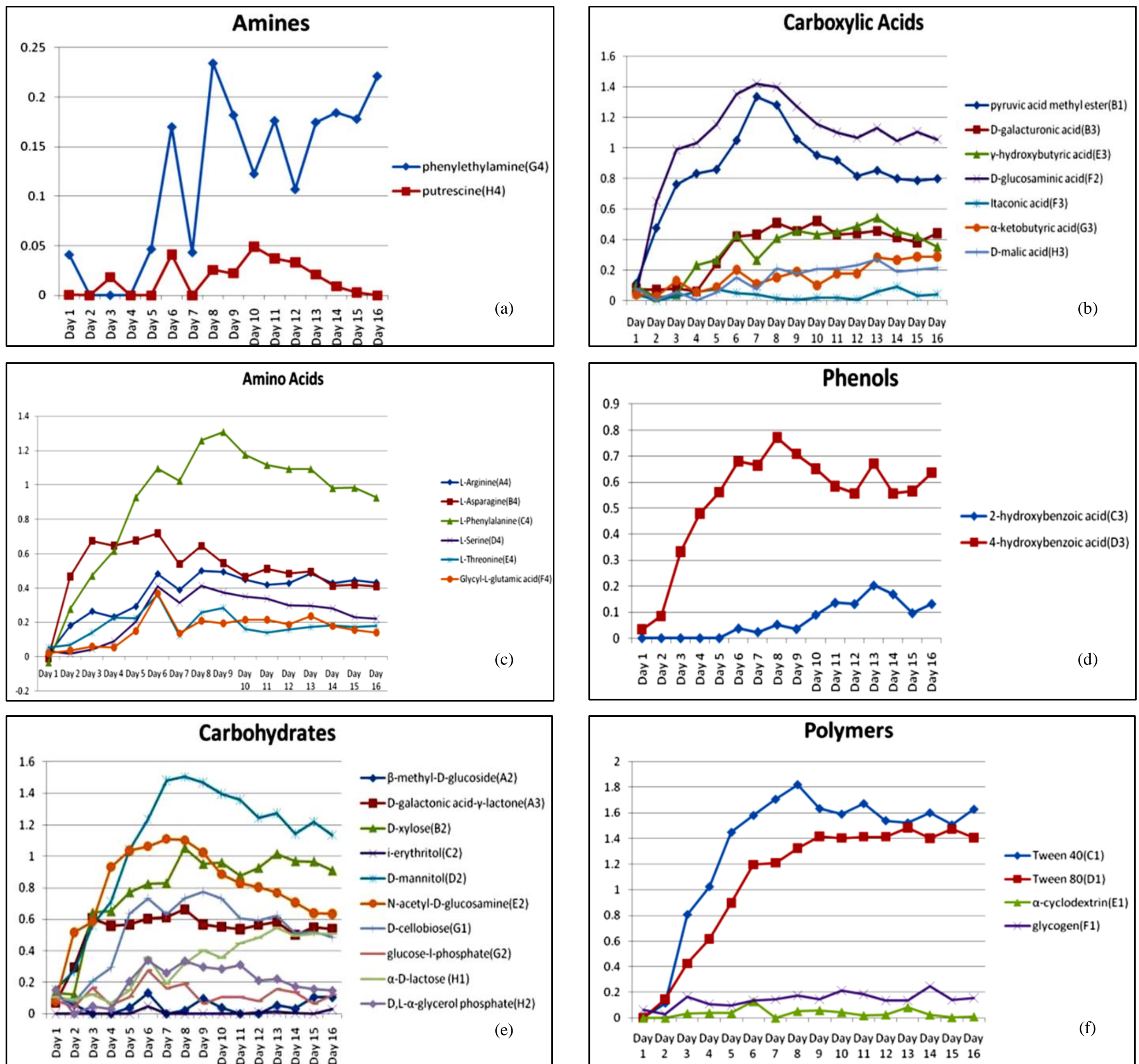


Figure 2. Utilization of the various carbon sources available of the Biolog Ecoplates by *Cytophaga hutchinsonii*

In order to reconstruct the metabolic pathways of *Cytophaga hutchinsonii*, iPath3 was utilized [5]. *Cytophaga*-specific pathways were visualized using orthologous protein information defined in KEGG and derived from the fully-sequenced genome of the organism. Using NCBI Taxonomy ID 269798 [6], Ipath3 was able to display customized versions of *Cytophaga*-specific pathways. The Glycolysis pathway of *C. hutchinsonii* was then compared to the one in *Thermobifida fusca* (Taxonomy ID 269800), a model cellulose degrader, using the same iPath3 interface. A customized map was displayed in the interactive viewer, then it was exported into several graphical formats, both vector such as svg and portable document format (pdf) for inclusion into publications (Fig. 6). In the context of this genome-phenome project, we were able to digest our own data into the customized map generated by iPath3, describing the enzymatic activities of these organisms (Fig. 6).

III. RESULTS

Per our results, *C. hutchinsonii* ATCC 33406 showed a disproportional utilization of the different compounds present on the Biolog Ecoplates (Fig. 1). Among the substrates tested, *C. hutchinsonii* showed the highest affinity for the utilization of the phenylethylamine, L-phenylalanine, D-mannitol, D-glucosaminic acid, D galacturonic acid, 4-hydroxybenzoic acid, and Tween 40 (Fig. 2). As seen on Fig 2, *C. hutchinsonii* showed a high affinity for the utilization of the phenylethylamine, L-phenylalanine, D-mannitol, D-glucosaminic acid, D-galacturonic acid, 4 hydroxybenzoic acid, and Tween 40. This behavior can be partly explained by the higher degree of solubility of some of these compounds, which make them readily available for intake (Table 1).

Despite the solubility of some of these compounds, which can partially explain their utilization by *C. hutchinsonii*, carbohydrates utilization in *Cytophaga* has been reported to be heavily dependent on several regulatory mechanisms at the cell Membrane [7]. Therefore, it is more plausible that the observed phenomenon is due to carrier-mediated soluble nutrient transport mechanisms such as, facilitated diffusion, shock sensitive systems, proton symport, Na+-symport, and the phosphoenolpyruvate phosphotransferase system (PEP-PTS) [8,9]. Some microorganisms are even capable of utilizing several of them [9]. In addition, despite the presence of certain genes in the genome, such as pectinases, *C. hutchinsonii* was unable to process pectin [1]. In several cases, some transporters were lacking, which could explain the inability to hydrolyze certain substrates.

Results from the pathways comparisons in iPath3 are listed in Fig. 4 and Table 2. They revealed a completely different metabolic capacity of *C. hutchinsonii* compared to the model cellulose degrader *Thermobifida fusca*. The Glycolysis pathway of the latter showed 36 genes involved in the process, while *Cytophaga* only has 28 comparatively (Table 2). This difference was also reflected in the way both organisms process carbohydrates. *T. fusca* was more efficient in decomposing biomass compared to *C. hutchinsonii*. However this difference was only noted in liquid growth media, but not on agar plates. As reported in Louime [11], *C. hutchinsonii* has a peculiar way of processing carbohydrates when grown on agar plates. The capabilities of these organisms to process carbohydrates in such a way were partly explained by the lack of cellulose binding domain in their genome. *C. hutchinsonii* inability to release enzymes outside of the cells requires direct contact or attachment to the biomass substrates for efficient processing [1, 11].

TABLE I. WATER SOLUBILITY (AT 20 °C) OF THE DIFFERENT COMPOUNDS FOUND ON THE BIOLOG ECOPLATES

Compounds on the Biolog EcoPlates	Water Solubility
β-methyl-D-glucoside	197.68 mg/mL
glucose-l-phosphate	91g/100 mL
D-galactonic acid-γ-lactone	159 mg/mL
D-xylose	550 mg/mL
Phenylethylamine	40 mg/mL
Putrescine	100 mg/mL
L-erythritol	360 mg/mL
D-mannitol	181.82 mg/mL
N-acetyl-D-glucosamine	50 mg/mL
D-cellobiose	125 mg/mL
α-D-lactose	189.05 mg/mL
D, L-α-glycerol phosphate	50 mg/mL
pyruvic acid methyl ester	10 mg/mL
D-galacturonic acid	100 mg/mL
γ-hydroxybutyric acid	7.11 mg/mL
D-malic acid	558 mg/mL
L-Arginine	148 mg/mL
L-Asparagine	20 mg/mL
L-Phenylalanine	28.57 mg/mL
L-Serine	200 mg/mL
L-Threonine	90 mg/mL
Glycol-L-glutamic acid	8.64 mg/mL
α-cyclodextrin	145 mg/mL
Tween 40	100 mg/mL
Tween 80	5-10 g/100 mL
Glycogen	50 mg/mL
2-hydroxybenzoic acid	2 mg/mL
4-hydroxybenzoic acid	6 mg/mL

As noted, the most striking feature of *C. hutchinsonii* cellulases is the absence of a cellulose-binding domain (CBD), which to date was believed to be imperative in cellulose hydrolysis [11]. This finding is not consistent with the current stand of today's literature on several industrial microorganisms [11]. Most known cellulose degraders have a distinct structure showing a catalytic domain, an adjacent CBM, a Pro/Ser/Thr-rich linker and another CBM [11]. Cellulases genes from *C. hutchinsonii* appear to differ from other cellulose degraders by structurally not having a linker region or any CBM domains. CBM is known to maintain a high concentration of the enzyme near the biomass substrate. Other roles, such as disrupting crystalline cellulose to aid hydrolysis, have been suggested for the CBM [7, 11]. The CBM has been considered as the limiting factor in hydrolysis. Therefore, the question was being raised, in the case of *C. hutchinsonii*, since there is no CBM present, would it be easier to achieve maximum increase in specific activity using *these microorganisms* in an industrial setting? This hypothesis still remains to be tested on a larger scale.

IV. Conclusions

Using genomics data, several fermentation pathways have been elucidated for *Cytophaga,* however metabolomics information is limited concerning the specific transport mechanisms used by these microorganisms for carbohydrates. Genome analysis of *C. hutchinsonii* suggested that, these microorganisms, due to the presence of a complete glycolysis (Fig. 3) and TCA (tricarboxylic acid) cycle, including genes encoding NADH dehydrogenases, should be able to carry out aerobic respiration of glucose [1]. These organisms however, failed to process glucose or glucose 1-phosphate as simple sugars, calling thereby for a reconstruction of the glycolysis pathway (Fig. 6).

In all, Biolog EcoPlates™ seems to provide researchers with a powerful tool to explore microorganisms' metabolic potential [12]. With this tool, microorganisms can be exposed to 95 different carbon sources simultaneously, allowing scientists to accurately characterize bacterial species or communities based on their carbon substrates metabolization patterns [12]. In the study presented here, we have gained some valuable insights into the bacterium *C. hutchinsonii* genotype-phenotype relationship. One can draw on this model to devise metabolic engineering strategies for *Cytophaga* and other Bacteroidetes with the goal of improving production of several classes of biotechnologically useful compounds.

Cytophaga cellulases are not well studied. Being a member of the phylum Bacteroidetes, these organisms are also not closely related to the standard model organism for cellulose utilization. As studies of starch utilization by *Bacteroidetes thetaiotamicron* have revealed many unusual features [13], it is therefore not surprising that these organisms are unique among the studied cellulose degraders. Here we provide in-depth studies of *Cytophaga*, by reporting their carbohydrates utilization patters. These studies produced some intriguing results as basic glucose could not be processed. As previously reported [11], *C. hutchinsonii* was found to produce 80% insoluble sugars, when tested for the production of soluble and insoluble reducing ends, although they lack cellulase binding domain and some of the residues known to be involved in bacterial cellulose decomposition.

The Biolog Ecoplates findings provide indeed a platform to explore *Cytophaga* immense biotechnological potential, as similar compounds are present in plant biomass. By combining available genomics data, one can now systematically integrate information from all these different levels and provide an integrated view of the structural and functional organization of *Cytophaga*. Several studies have demonstrated that metabolic changes are a critical enabler toward understanding mechanisms underlying cellular responses [14,15]. Consequently, targeted manipulations toward improving cellular functions rely heavily on modifications of metabolic networks [16]. We do understand however that there are a large number of interactions involved in biological systems, that one may not be able to capture with a single picture. Therefore, metabolic data must be interpreted with reservations, such as the capacity of microorganisms to perform a certain function under well-defined environmental conditions.

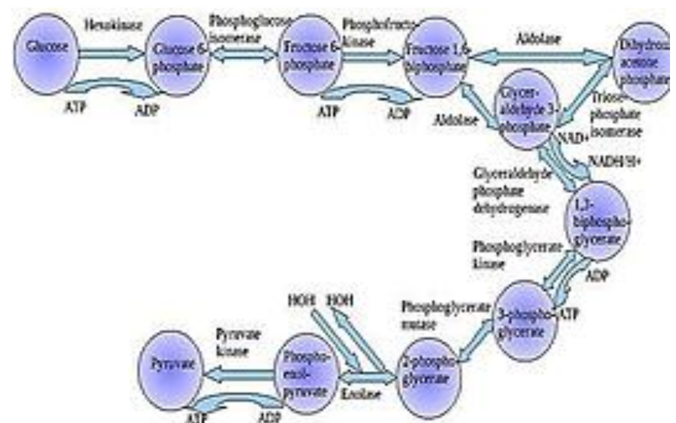


Figure 3. Basic Glycolysis Pathway in *Cytophaga* (however, cellobiose is the most basic carbohydrate processed by *Cytophaga*)

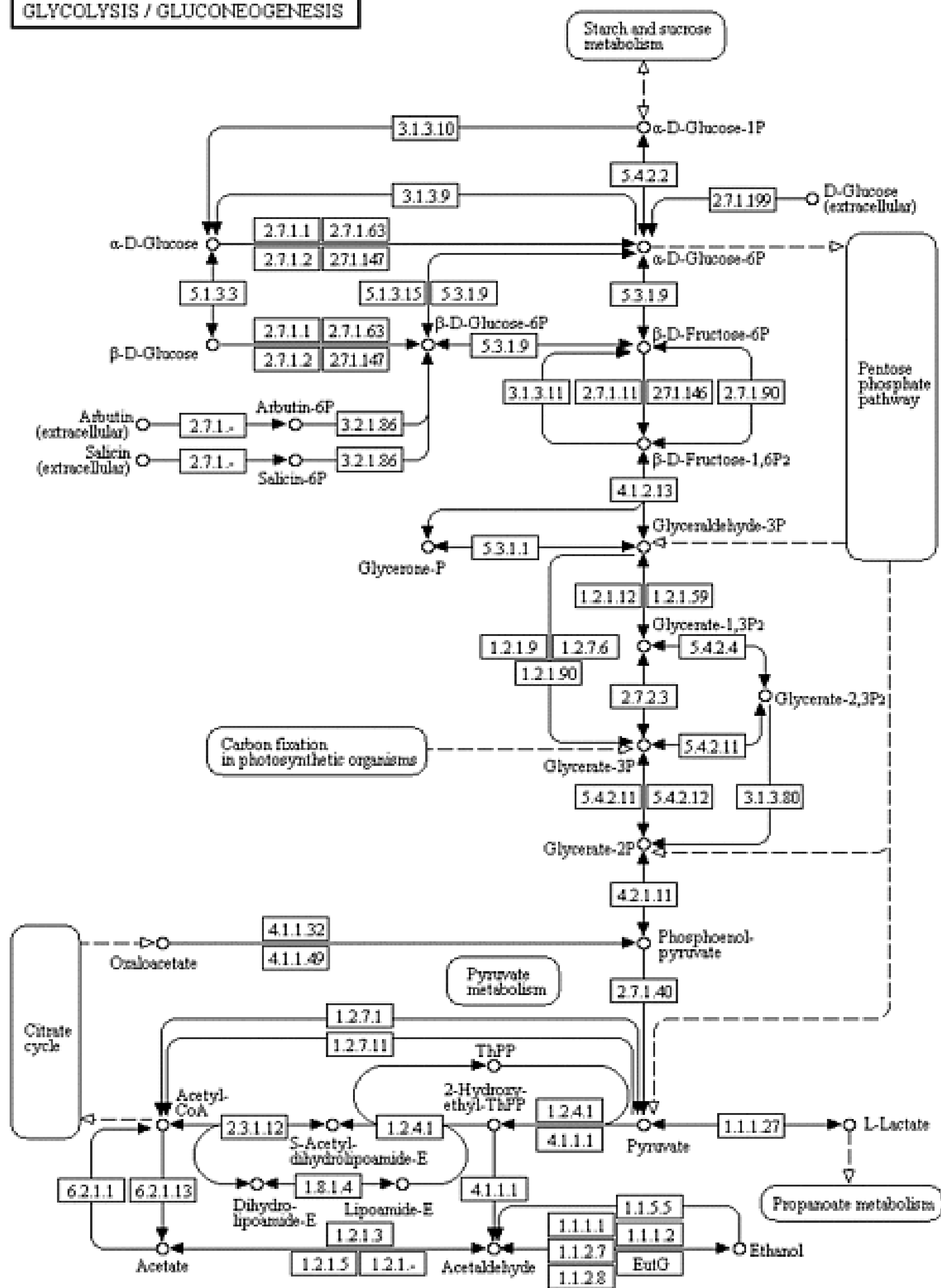


Figure 4. Glycolysis Pathway in *Cytophaga hutchinsonii*

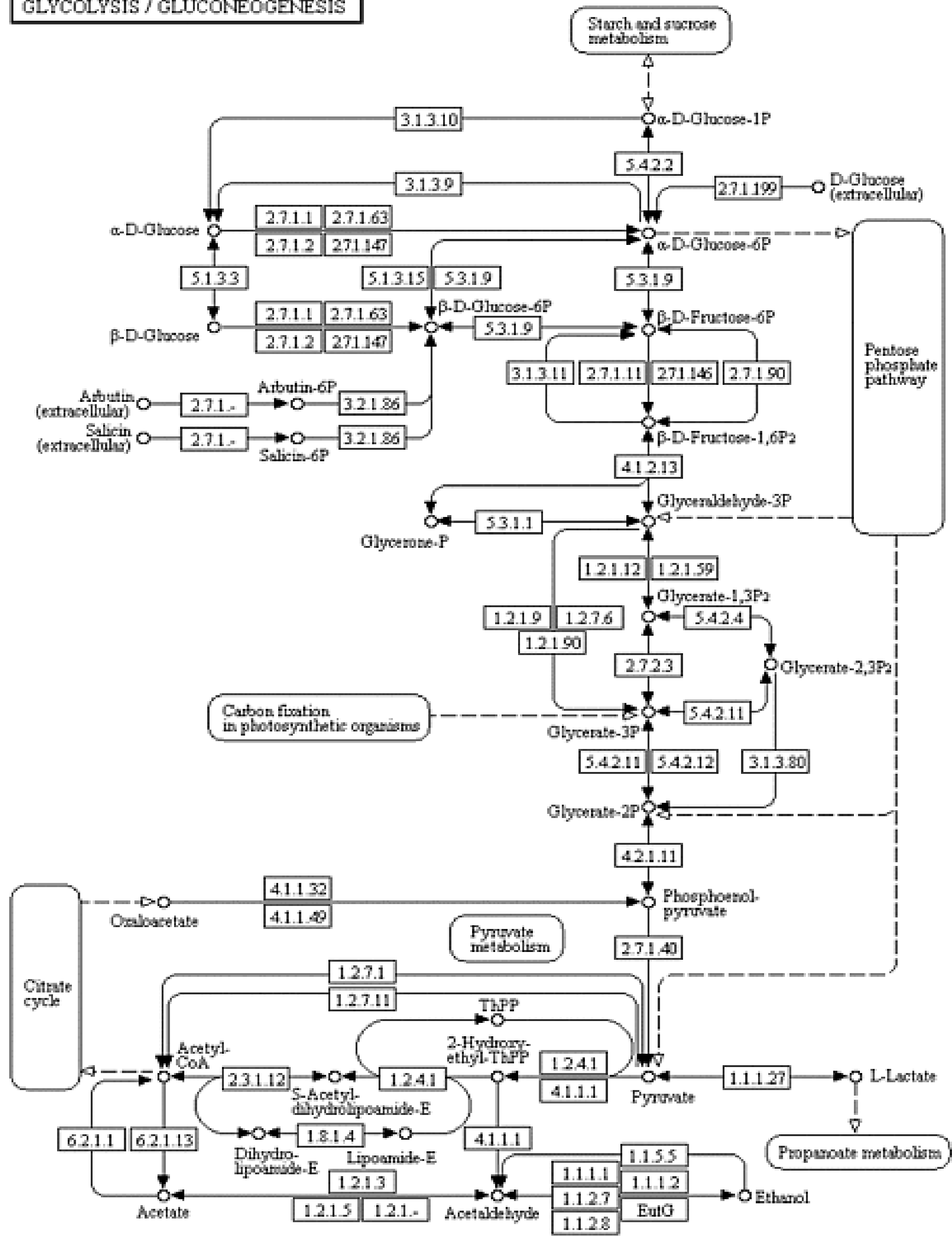


Figure 5. Glycolysis Pathway in *Thermobifida Fusca*

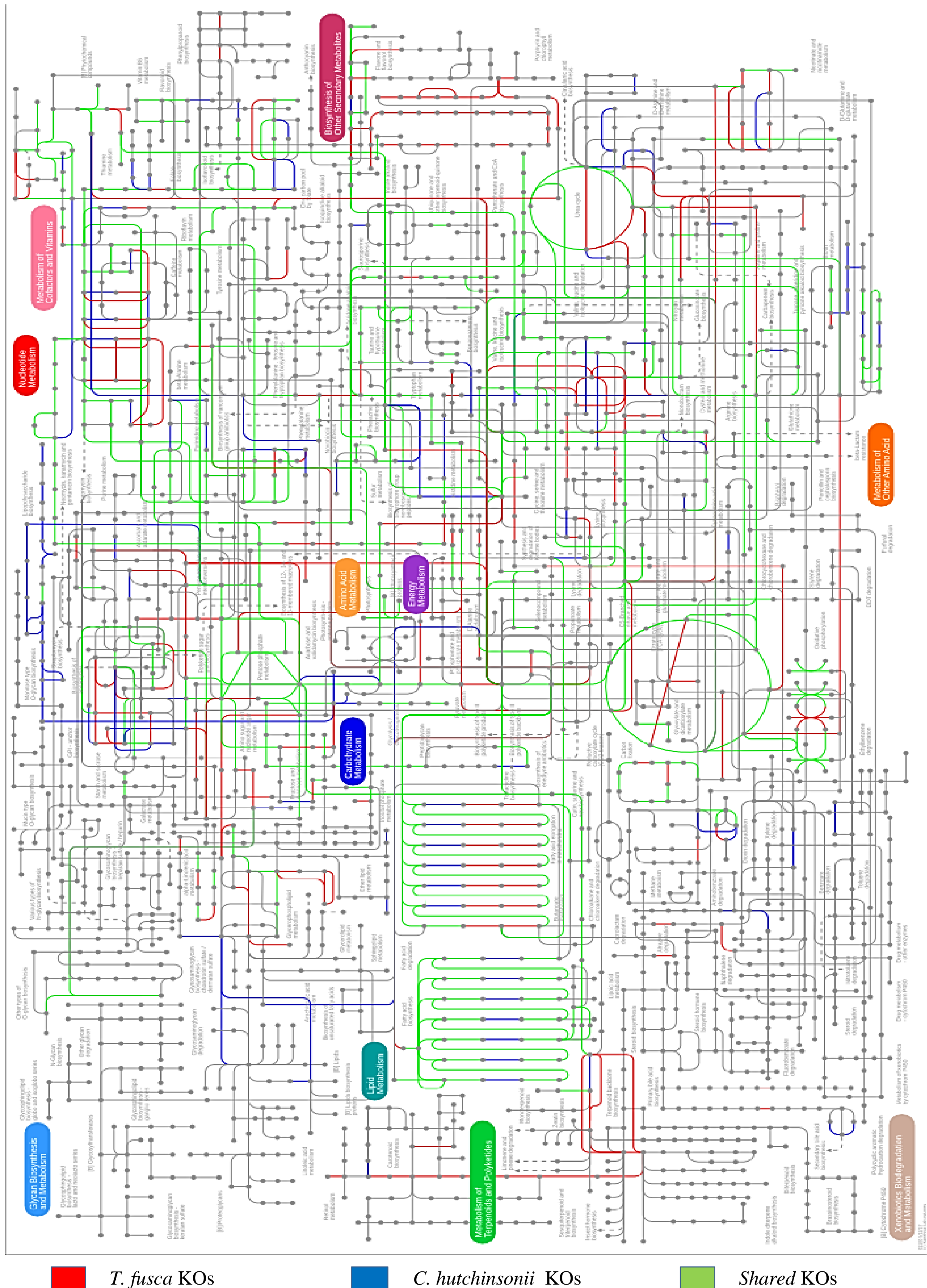


Figure 6. Overlapping of Glycolysis Pathways from Thermobifida fusca and Cytophaga hutchinsonii based on KOs Identifiers (KO - KEGG Orthology)

TABLE II. GENES INVOLVED IN *CYTOPHAGA HUTCHINSONII* GLYCOLYSIS PATHWAY

Organism	*Cytophaga hutchinsonii* [GN:chu]	
28 Genes	CHU_1875	glk; glucokinase [KO:K00845] [EC:2.7.1.2]
	CHU_3060	fbaA; fructose-bisphosphate aldolase, class II [KO:K01624] [EC:4.1.2.13]
	CHU_3277	tpiA; triosephosphate isomerase [KO:K01803] [EC:5.3.1.1]
	CHU_2987	gapA; glyceraldehyde-3-phosphate dehydrogenase [KO:K00134] [EC:1.2.1.12]
	CHU_0251	gap; glyceraldehyde-3-phosphate dehydrogenase [KO:K00134] [EC:1.2.1.12]
	CHU_2229	pgk; phosphoglycerate kinase [KO:K00927] [EC:2.7.2.3]
	CHU_2250	gpmA; phosphoglycerate mutase [KO:K01834] [EC:5.4.2.11]
	CHU_3731	apgM; phosphoglycerate mutase (2,3-bisphosphoglycerate-independent phosphoglycerate mutase) [KO:K15633] [EC:5.4.2.12]
	CHU_3133	eno; enolase [KO:K01689] [EC:4.2.1.11]
	CHU_1400	pykF; pyruvate kinase [KO:K00873] [EC:2.7.1.40]
	CHU_3718	acoA; pyruvate dehydrogenase E1 component alpha subunit [KO:K00161] [EC:1.2.4.1]
	CHU_2680	adhB; pyruvate dehydrogenase E1 component [KO:K00162] [EC:1.2.4.1]
	CHU_1755	pdhC; dihydrolipoyllysine-residue acetyltransferase (dihydrolipoamide S-acetyltransferase) [KO:K00627] [EC:2.3.1.12]
	CHU_3360	lpdA; dihydrolipoyl dehydrogenanse [KO:K00382] [EC:1.8.1.4]
	CHU_1086	adhD; dihydrolipoyl dehydrogenase (dihydrolipoamide dehydrogenase) [KO:K00382] [EC:1.8.1.4]
	CHU_3463	lpdA; pyridine nucleotide-disulfide-related oxidoreductase [KO:K00382] [EC:1.8.1.4]
	CHU_1246	adhP; zinc-type alcohol dehydrogenase [KO:K00001] [EC:1.1.1.1]
	CHU_0053	dhaL; NAD+-dependent aldehyde dehydrogenase [KO:K00128] [EC:1.2.1.3]
	CHU_2982	acs; acetyl-CoA synthetase [KO:K01895] [EC:6.2.1.1]
	CHU_2429	acsA; acetyl-coenzyme A synthetase [KO:K01895] [EC:6.2.1.1]
	CHU_0656	aldose 1-epimerase [KO:K01785] [EC:5.1.3.3]
	CHU_0909	possible haloacid dehalogenase-like hydrolase [KO:K20866] [EC:3.1.3.10]
	CHU_0998	pgm; phosphomannomutase [KO:K01835] [EC:5.4.2.2]
	CHU_0301	gapN; gyceraldehyde-3-phosphate dehydrogenase (NADP+) [KO:K00131] [EC:1.2.1.9]

TABLE III. GENES INVOLVED IN *TERMOBIFIDA FUSCA* GLYCOLYSIS PATHWAY

Organism	*Thermobifida fusca [GN:tfu]*	
34 Genes	Tfu_0273	glucokinase [KO:K00845] [EC:2.7.1.2]
	Tfu_1033	glucokinase [KO:K00845] [EC:2.7.1.2]
	Tfu_2004	glucose-6-phosphate isomerase [KO:K01810] [EC:5.3.1.9]
	Tfu_1037	pyrophosphate-dependent phosphofructokinase [KO:K21071] [EC:2.7.1.90 2.7.1.11]
	Tfu_0464	GlpX [KO:K02446] [EC:3.1.3.11]
	Tfu_3010	fructose-bisphosphate aldolase [KO:K01624] [EC:4.1.2.13]
	Tfu_2015	triosephosphate isomerase [KO:K01803] [EC:5.3.1.1]
	Tfu_2017	glyceraldehyde-3-phosphate dehydrogenase [KO:K00134] [EC:1.2.1.12]
	Tfu_2016	phosphoglycerate kinase [KO:K00927] [EC:2.7.2.3]
	Tfu_2911	phosphoglycerate mutase [KO:K01834] [EC:5.4.2.11]
	Tfu_0428	enolase [KO:K01689] [EC:4.2.1.11]
	Tfu_1179	pyruvate kinase [KO:K00873] [EC:2.7.1.40]
	Tfu_3049	pyruvate dehydrogenase (lipoamide) [KO:K00161] [EC:1.2.4.1]
	Tfu_0180	pyruvate dehydrogenase (lipoamide) [KO:K00161] [EC:1.2.4.1]
	Tfu_0181	putative branched-chain alpha keto acid dehydrogenase E1 beta subunit [KO:K00162] [EC:1.2.4.1]
	Tfu_3050	dehydrogenase complex, E1 component, beta subunit [KO:K00162] [EC:1.2.4.1]
	Tfu_0182	putative dihydrolipoamide acyltransferase component [KO:K00627] [EC:2.3.1.12]
	Tfu_3051	pyruvate dehydrogenase complex, E2 component, dihydrolipoamide acetyltransferase [KO:K00627] [EC:2.3.1.12]
	Tfu_2559	dihydrolipoamide dehydrogenase [KO:K00382] [EC:1.8.1.4]
	Tfu_0994	dihydrolipoamide dehydrogenase [KO:K00382] [EC:1.8.1.4]
	Tfu_2674	2-oxoglutarate ferredoxin oxidoreductase, alpha subunit [KO:K00174] [EC:1.2.7.11 1.2.7.3]
	Tfu_2675	putative oxidoreductase [KO:K00175] [EC:1.2.7.111.2.7.3]
	Tfu_1270	alcohol dehydrogenase class III [KO:K00121] [EC:1.1.1.11.1.1.284]
	Tfu_2771	putative dehydrogenase [KO:K13953] [EC:1.1.1.1]
	Tfu_1489	oxidoreductase [KO:K13953] [EC:1.1.1.1]
	Tfu_0744	aldehyde dehydrogenase (NAD+) [KO:K00128] [EC:1.2.1.3]
	Tfu_2808	putative acetyl-coenzyme A synthetase [KO:K01895] [EC:6.2.1.1]
	Tfu_2856	acetyl-coenzyme A synthetase [KO:K01895] [EC:6.2.1.1]
	Tfu_1546	putative acyl-CoA synthetase [KO:K01895] [EC:6.2.1.1]
	Tfu_1083	putative aldose-1-epimerase [KO:K01785] [EC:5.1.3.3]
	Tfu_1811	Polyphosphate glucokinase [KO:K00886] [EC:2.7.1.63]
	Tfu_0083	phosphoenolpyruvate carboxykinase (GTP) [KO:K01596] [EC:4.1.1.32]
	Tfu_2768	6-phospho-beta-glucosidase [KO:K01222] [EC:3.2.1.86]
	Tfu_2489	putative phosphoenolpyruvate-dependent sugar phosphotransferase [KO:K02777] [EC:2.7.1.]

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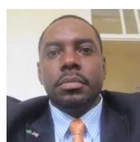

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