A chemically-defined growth medium for a model human gut microbiome

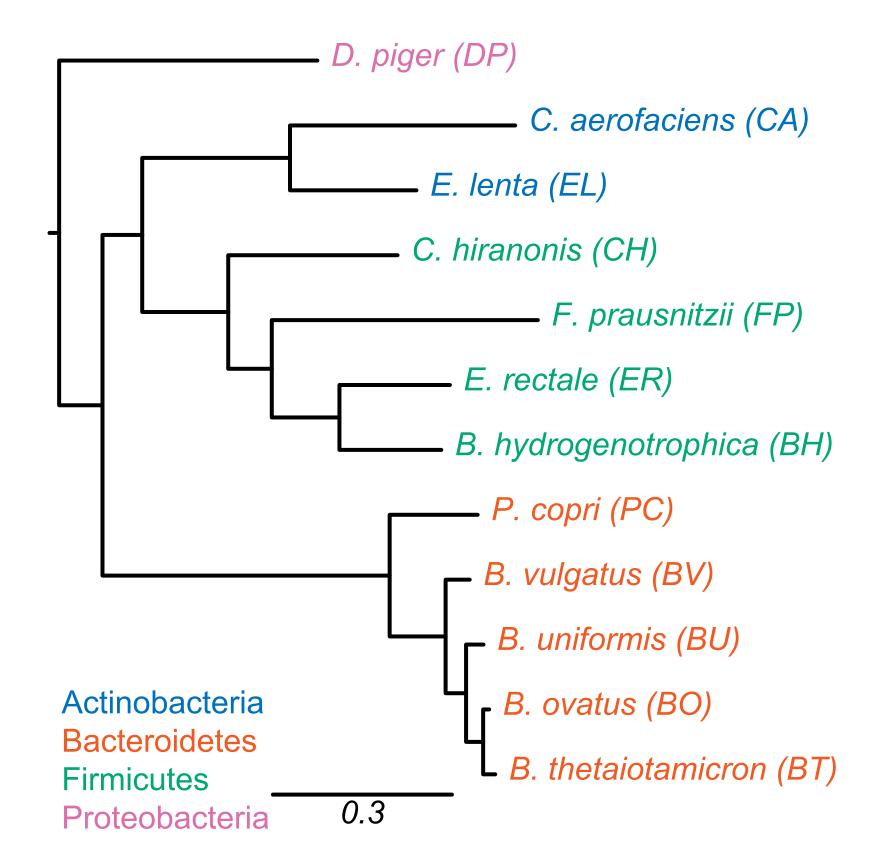
Joshua J. Hamilton¹, Ryan L. Clark¹, Emma S. Groblewski¹, and Ophelia S. Venturelli^{1,2,3}

¹Department of Biochemistry, ²Department of Bacteriology, ³Department of Chemical and Biological Engineering, University of Wisconsin-Madison

A Model Human Gut Microbiome

Microorganisms rarely exist in isolation, but instead form complex communities, or microbiomes. Interactions among microbes are ubiquitous in these communities, and microbial interactions major determinants of microbiome function. These interactions are especially important in the human gut, where the microbiome plays diverse roles, including preventing diséase and enhancing digestion. In-vitro, culture-based model microbiomes are necessary to interrogate the mechanisms of interspecies interaction.

previously developed a model microbiome containing 12 species that together encompass the functional and phylogenetic diversity of the natural human gut microbiome¹. Here, we present a chemically defined culture medium that supports the growth of 11 of 12 members of this community. Growth experiments on a series of defined media enabled us to characterize the nutritional preferences and biosynthetic capabilities of these microbes, as well as identify specific metabolites that enhance or inhibit growth.



PROSPECTUS

Development of a chemically-defined medium enables mechanistic investigations of interspecies interactions, such as identifying cross-fed metabolites.

Media composition can be used to alter monospecies abundance, and possibly control community composition.

Our defined medium serves as a resource refinement of genome-scale, computational metabolic models.

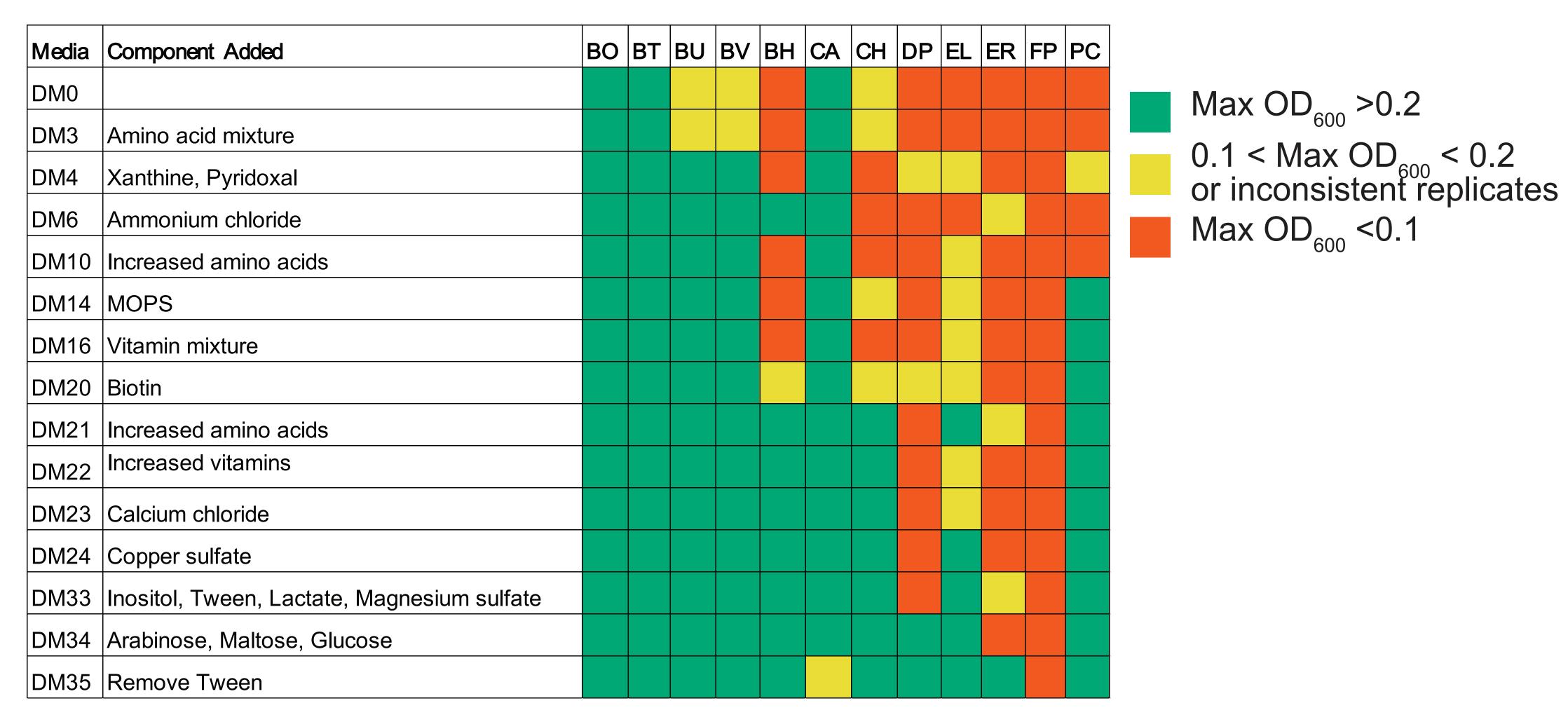
ACKNOWLEDGEMENTS

This research was supported by the UW-Madison Microbiome Initiative and the Office of the Vice Chancellor for Research and Graduate Education.

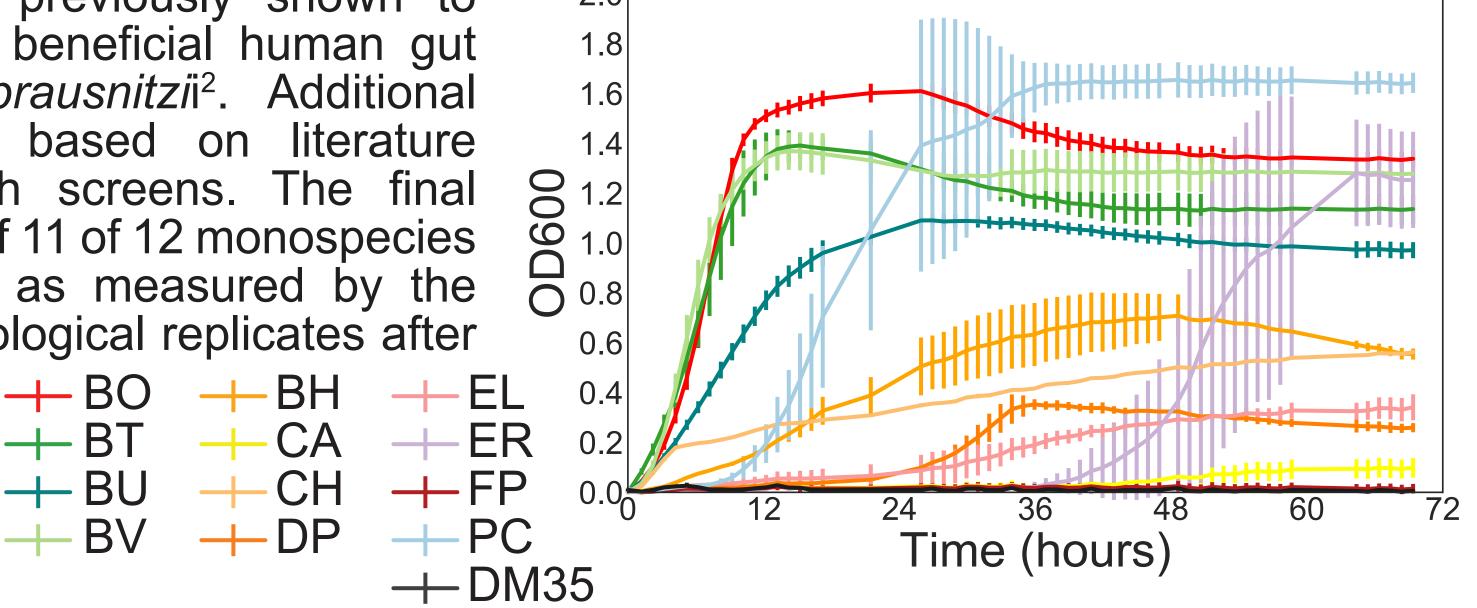
REFERENCES

- 1. Venturelli OS, Carr AC, Fisher G, Hsu RH, Lau R, et al. (2017). bioRxiv.
- 2. Heinken A, Khan MT, Paglia G, Rodionov DA, Harmsen HJM, et al. (2014). J Bacteriol 196: 3289–3302.

Developing a Chemically-Defined Growth Medium (DM35)



We began with a media previously shown to support the growth of the beneficial human gut microbe *Faecalibacterium prausnitzi*i². Additional components were added based on literature review and *in-vitro* growth screens. The final medium supported growth of 11 of 12 monospecies in our model microbiome, as measured by the maximum OD₆₀₀ of three biological replicates after 72 hours. +BO +BH +EL



Modeling the Effect of Media Composition on Growth

+BV +DP

DM35 contains all 20 amino acids and four sugars. All monospecies were grown in titrations of amino acid and sugar mixtures for 48 hours. A growth model was fit to the data, and linear regression was used to explore how the growth rate and carrying capacity of each monospecies change with media composition.

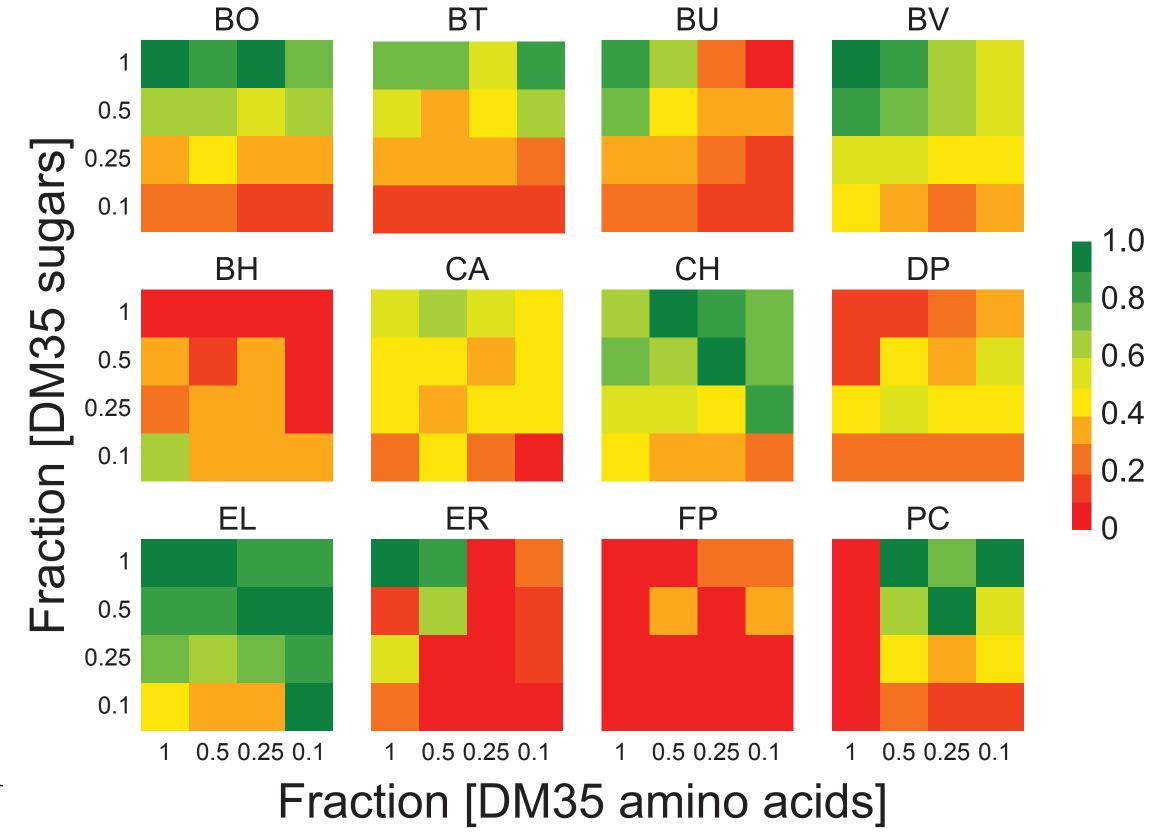
Growth model:

$$\frac{dx}{dt} = x(\mu - \alpha x)$$

x: abundance

 μ : growth rate

 α : self-interaction term



Maximum OD₆₀₀

At steady-state: $x_{\text{steady state}} = \frac{\mu}{2} = \text{carrying capacity}$

Regression model: $x_{steady\ state} = \beta f_s + \gamma f_{aa} + x_0$ f_s : fraction of [DM35 sugars] (0 to 1)

$$\mu = \epsilon f_s + \zeta f_{aa}$$

 $f_a a$: fraction of [DM35 amino acids] (0 to 1)

 x_0 : initial abundance

Model results for carrying capacity

	β	γ	x_0	\mathbb{R}^2
BO	0.64	0.04	0.11	0.91
BT	0.49	0.05	0.08	0.88
BU	0.37	0.29	-0.02	0.60
BV	0.35	0.19	0.25	0.75
BH	0.35	-0.37	0.13	0.65
CA	0.28	-0.12	0.28	0.64
CH	0.50	0.02	0.33	0.78
DP	0.43	-0.10	-0.11	0.18
EL	0.44	0.05	0.39	0.68
PC	0.44	0.64	-0.64	0.69

Model results for growth rate

	ϵ	ζ	\mathbb{R}^2
BO	0.90	2.71	0.62
BT	-0.25	1.35	0.46
BU	-0.90	2.42	0.61
BV	0.40	4.65	0.56
BH	1.12	0.21	0.68
CA	0.02	0.27	0.71
CH	0.47	0.25	0.73
DP	0.43	0.03	0.74
EL	0.36	0.46	0.55
PC	0.44	-0.02	0.51