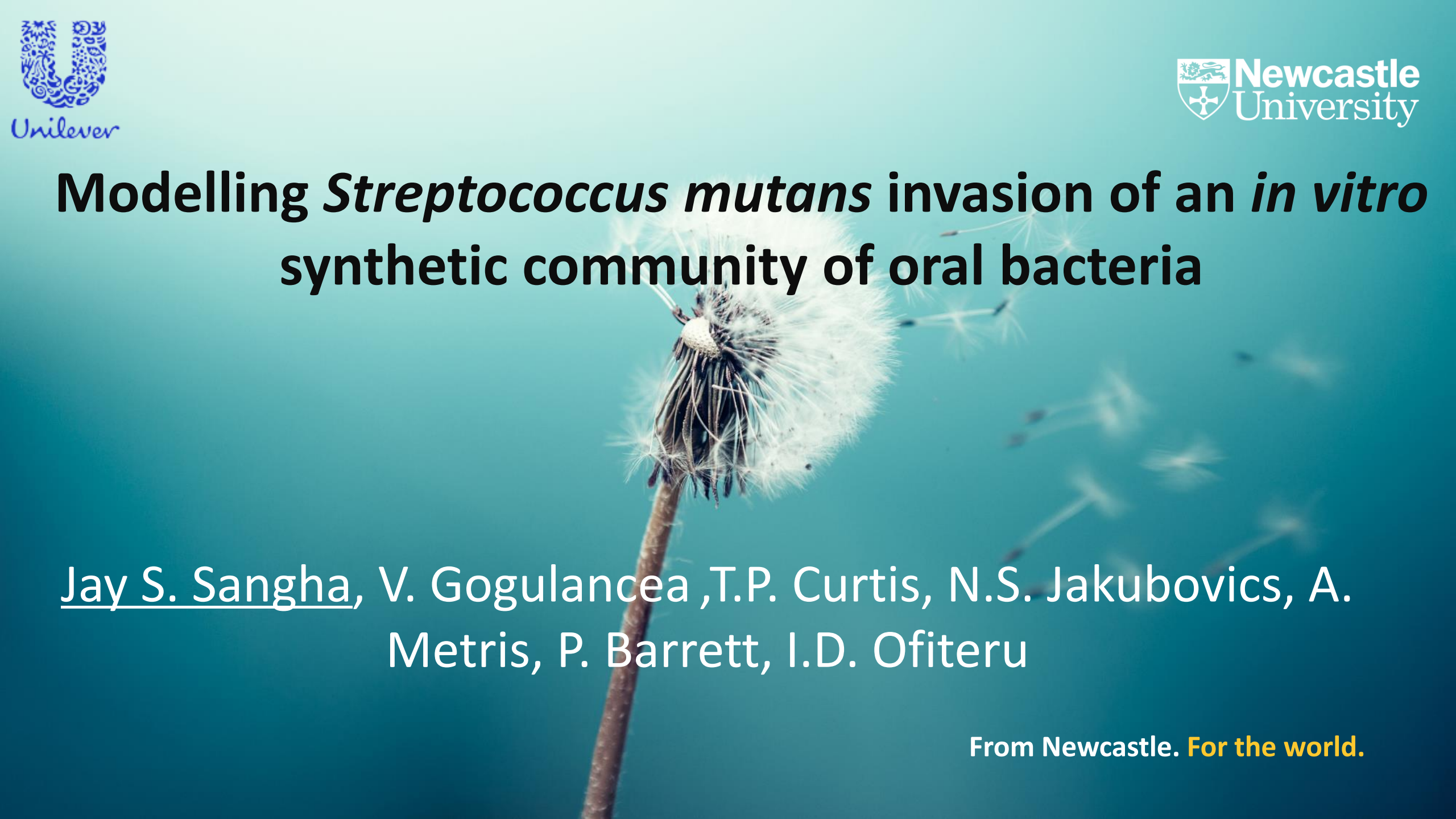


Modelling *Streptococcus mutans* invasion of an *in vitro* synthetic community of oral bacteria

Jay S. Sangha, V. Gogulancea ,T.P. Curtis, N.S. Jakubovics, A. Metris, P. Barrett, I.D. Ofiteru

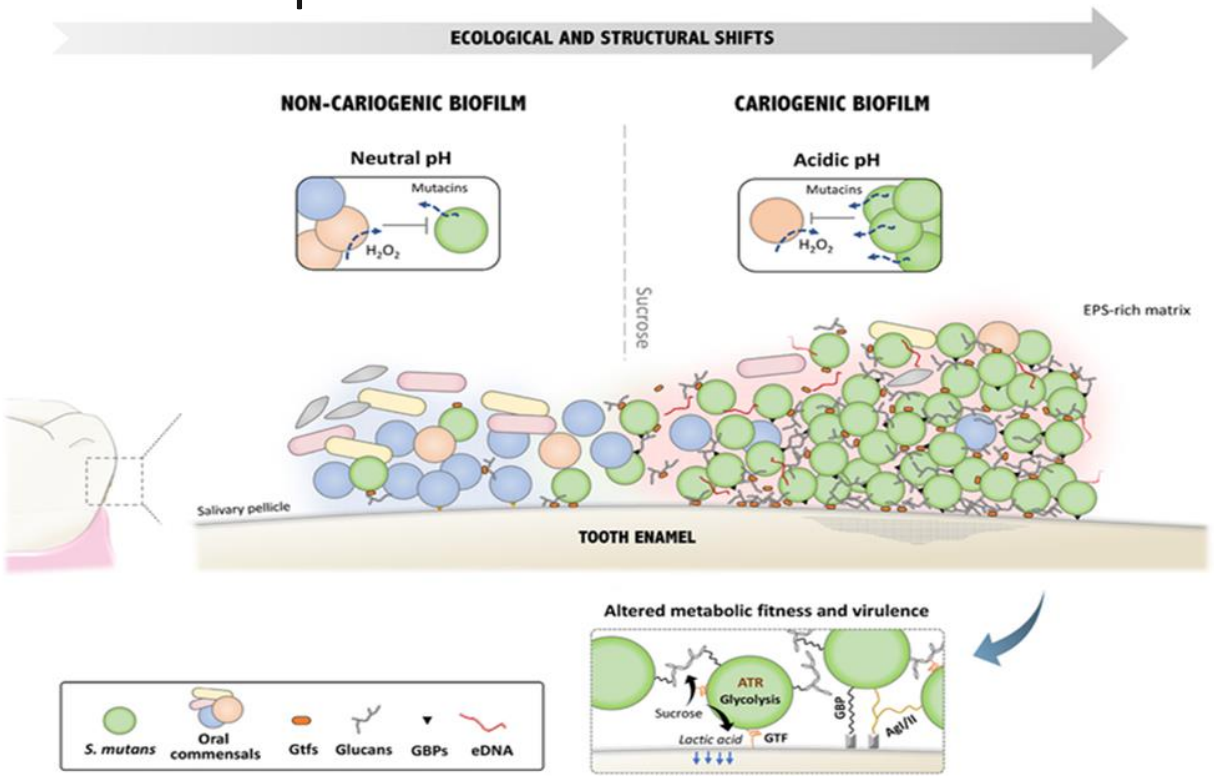
From Newcastle. For the world.

Dental caries & the oral microbiome

Carious lesion

(Armstrong et al., 2005)

Cariogenic biofilm development



(Lemos et al., 2018)

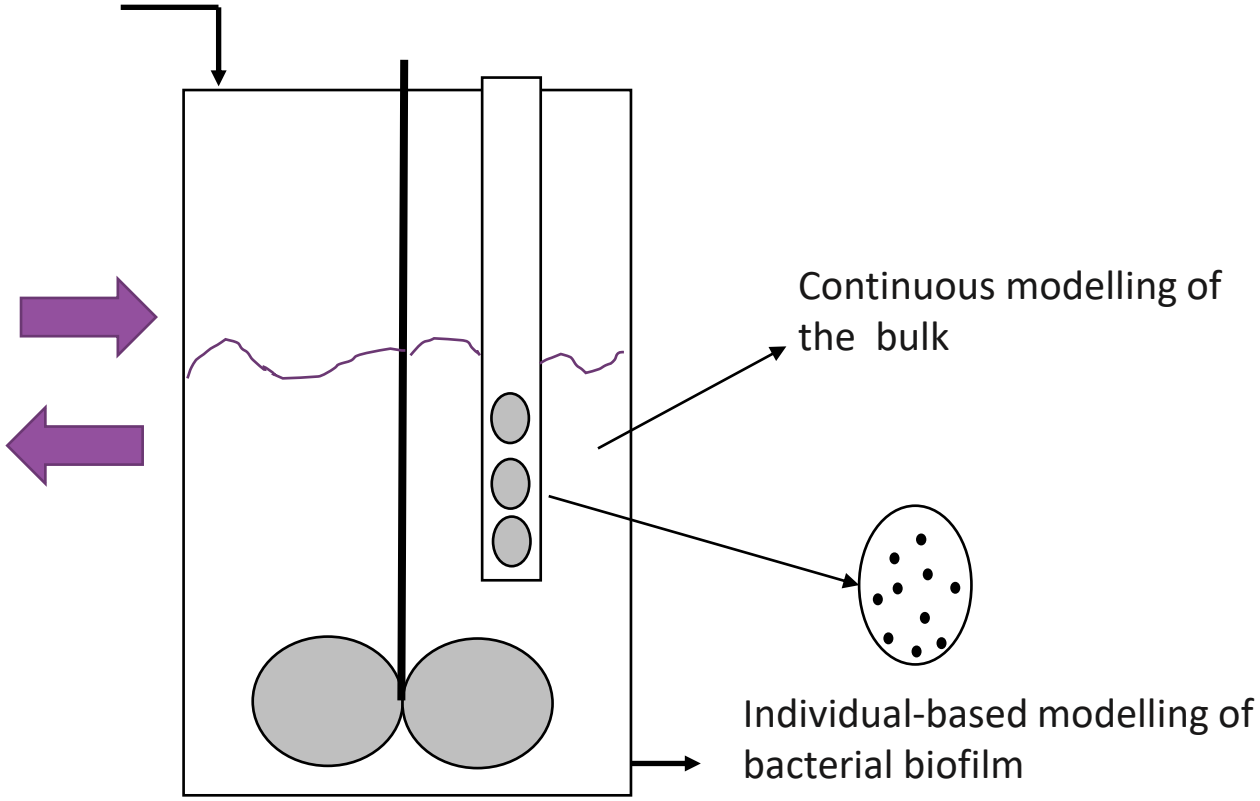
Safe products

(Figure created using www.Biorender.com)

Modelling the oral microbiome & aims

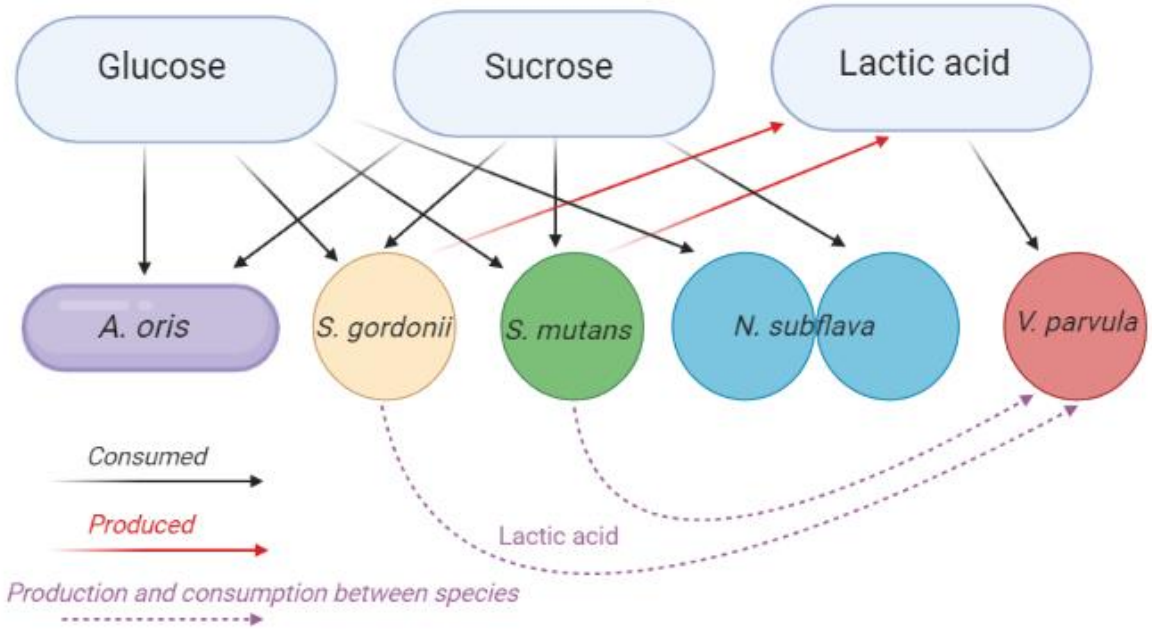
Develop modelling approaches to characterise *Streptococcus mutans* invasion to drive safe product development and risk assessment

In vitro (CDC reactors)



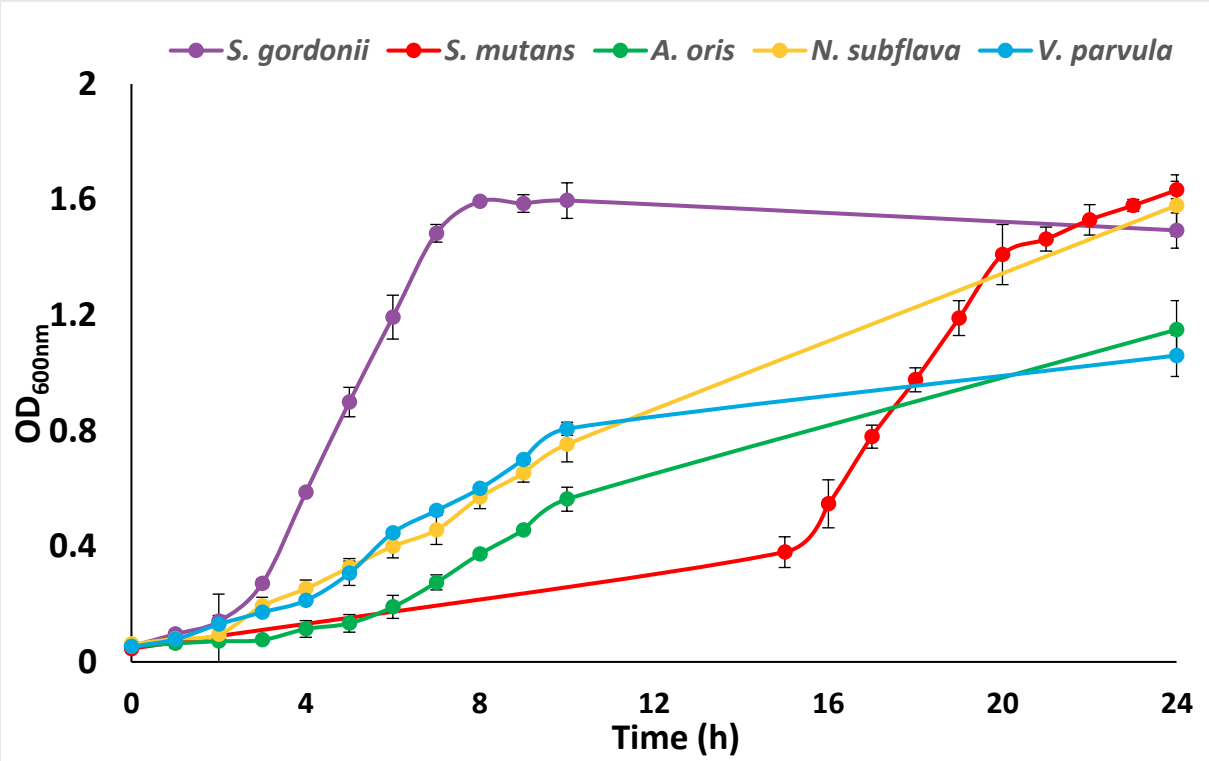
In silico

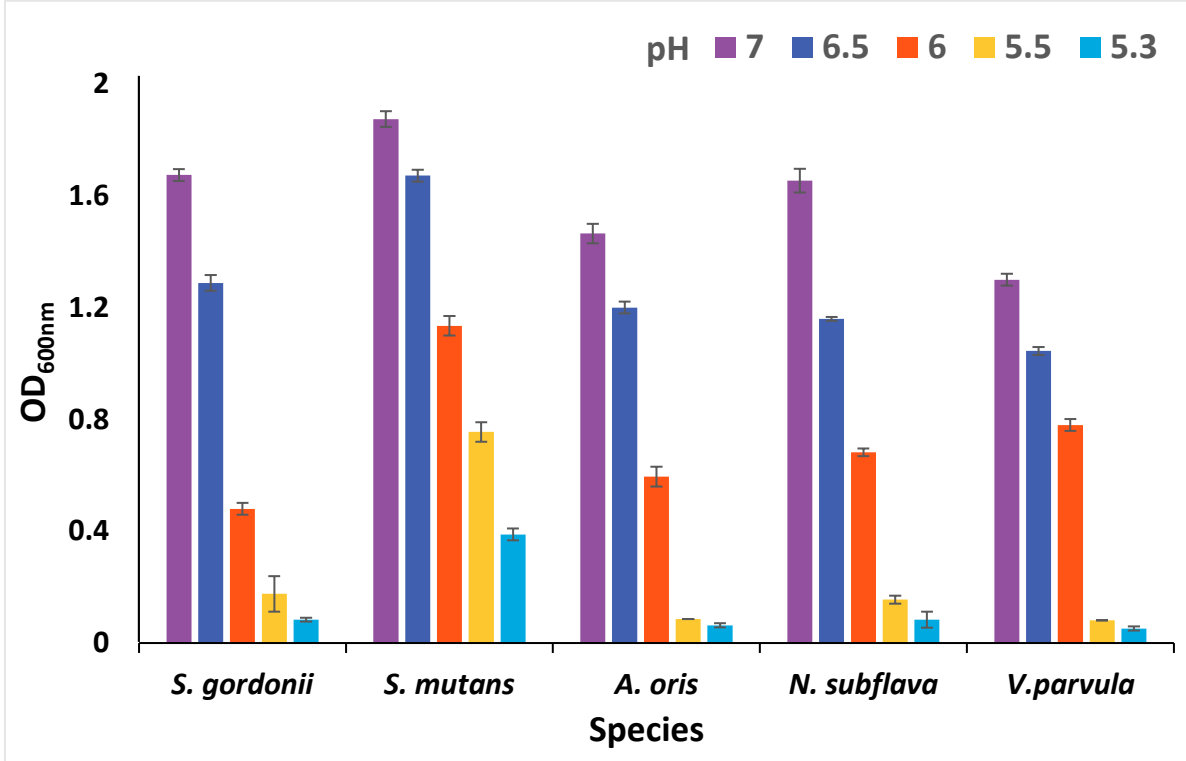
Synthetic community



Bacterial strain	Role in oral microbiome
***Streptococcus gordonii* DL1**	Pioneering coloniser
***Veillonella parvula* DSM2008**	Present in progression stages of oral biofilm development
***Actinomyces oris* MG1**	Early coloniser of freshly cleaned teeth
***Neisseria subflava* DSM17610**	Commensal, part of normal flora
***Streptococcus mutans* UA159**	Cariogenic species, more abundant in caries progression

Synthetic community characterisation





μmax for synthetic community species (h^{-1})				
S. gordonii	*S. mutans*	*A. oris*	*N. subflava*	*V. parvula*
0.492	0.406	0.227	0.261	0.246

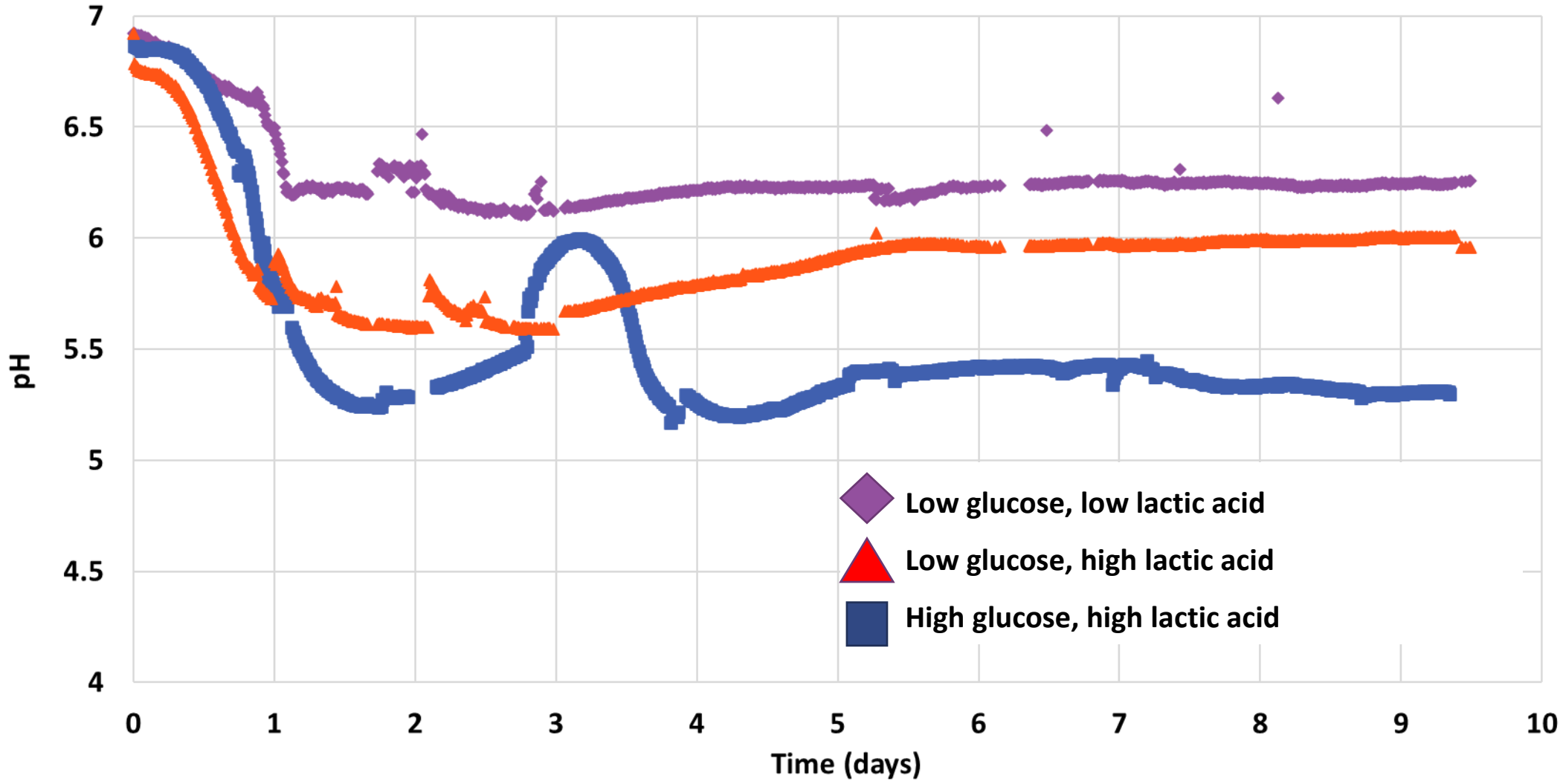
Ks values (mmol L^{-1})				
S. gordonii	*S. mutans*	*A. oris*	*N. subflava*	*V. parvula*
6.60	5.55	7.78	5.55	26.90

In vitro modelling of *S. mutans* colonisation

Continuous flow of 0.4 mL min^{-1}. Temperature maintained at 37 °C

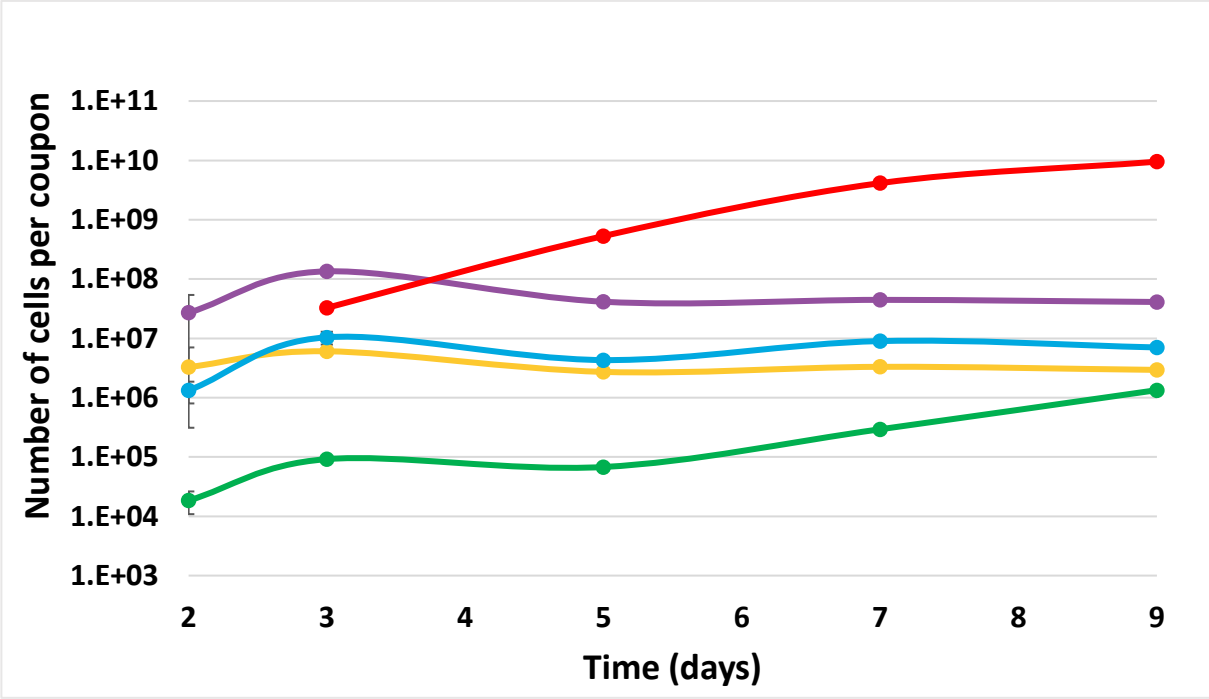
Inoculation (day)	Species
0	*Actinomyces oris*
1	*Streptococcus gordonii* *Neisseria subflava* *Veillonella parvula*
2	*Streptococcus mutans*

pH variation in the bulk

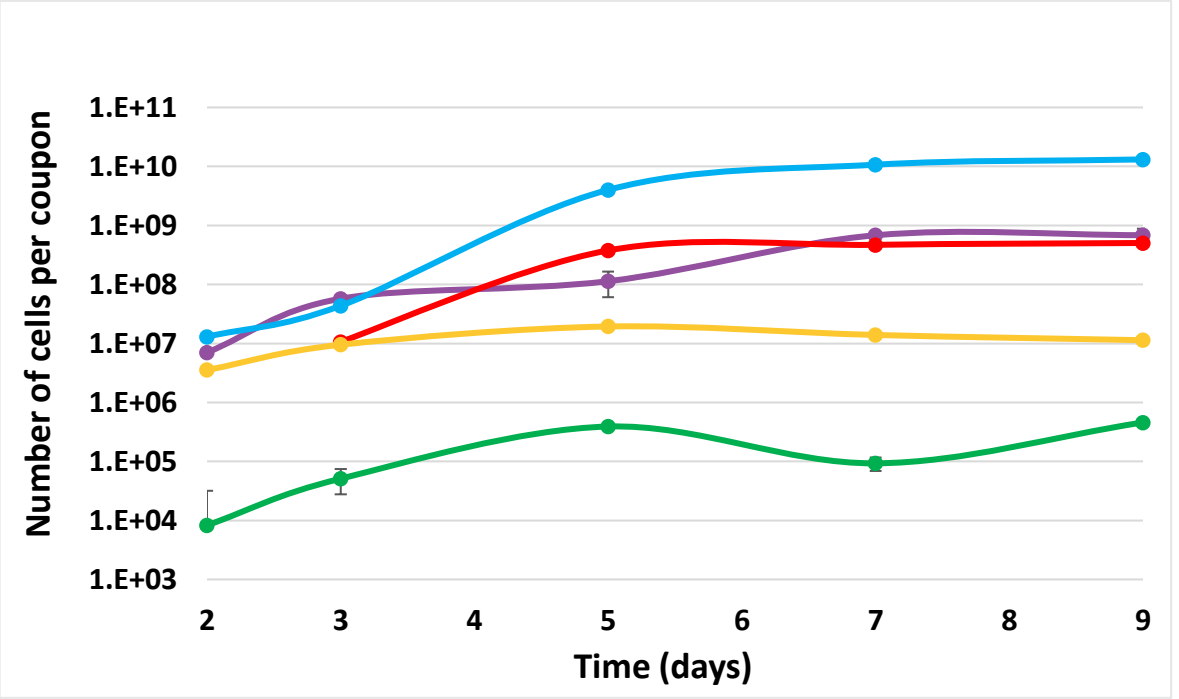


qPCR abundance in the biofilm (coupons)

High glucose

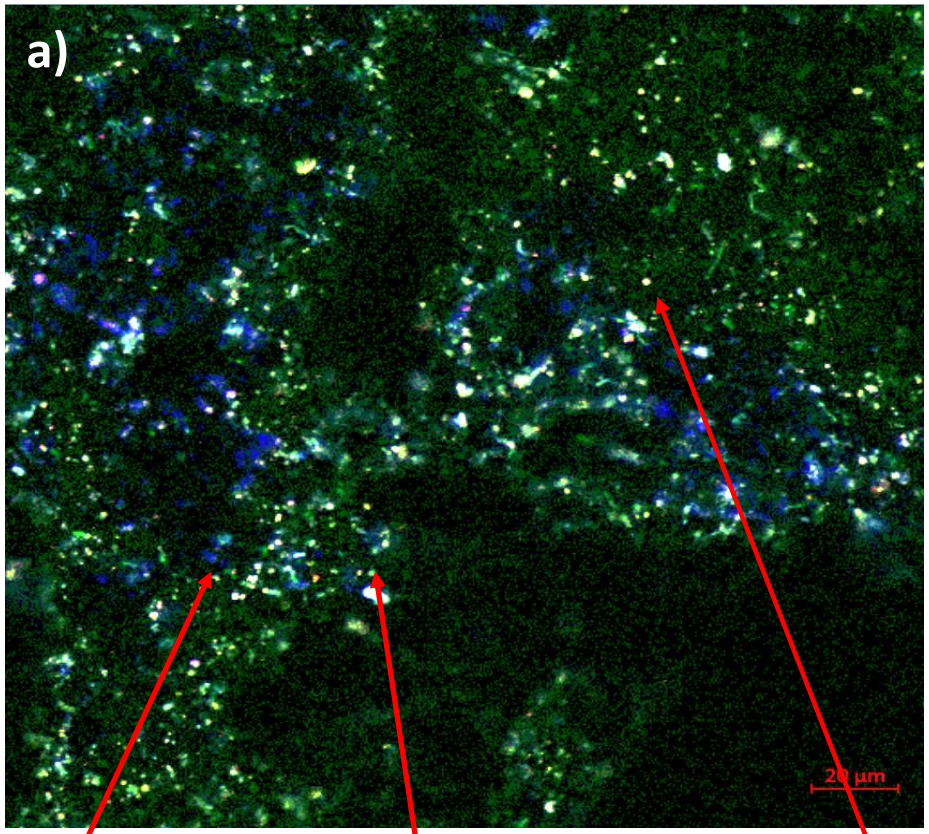


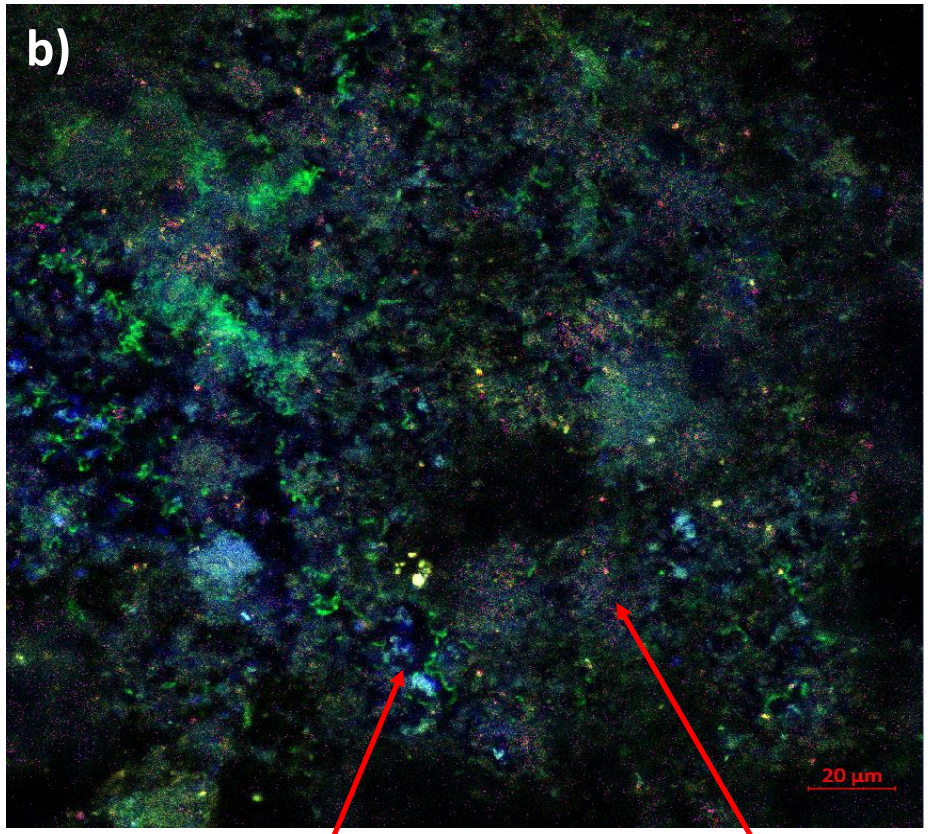
Low glucose



S. gordonii
N. subflava
S. mutans
V. parvula
A. oris

Visualisation of the biofilm on the coupons (FISH images)





a) High glucose b) Low glucose

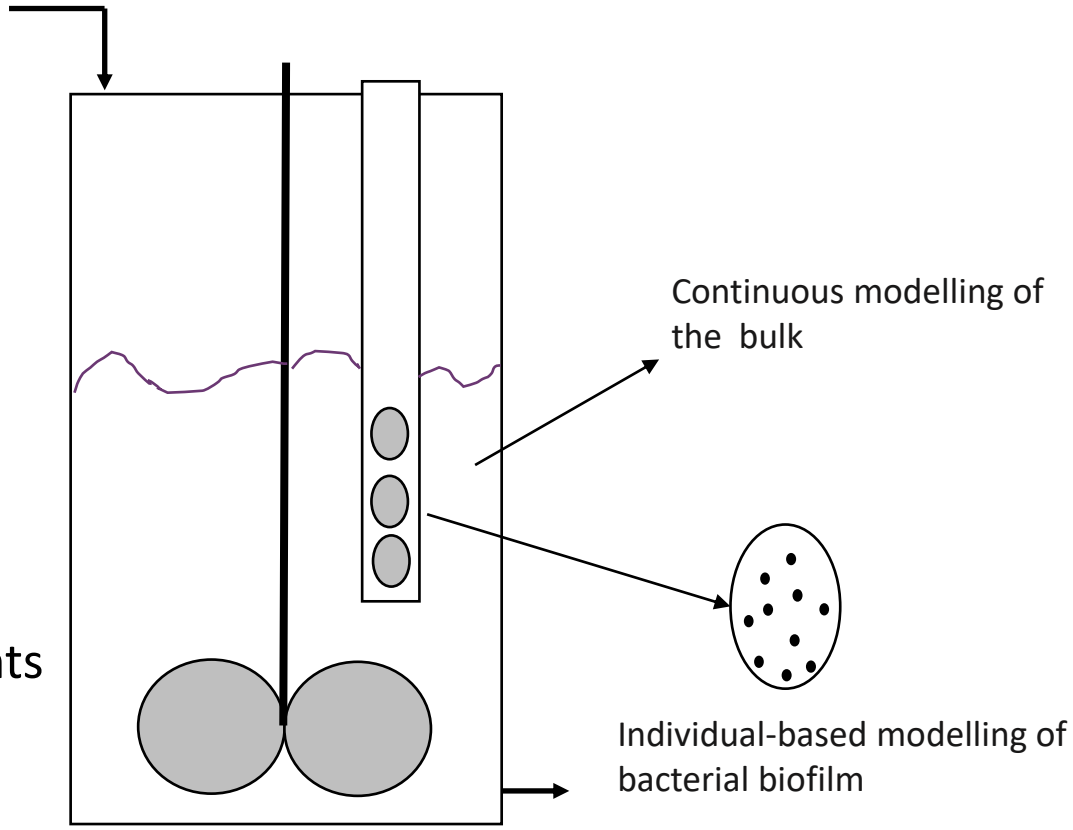
Mathematical modelling of the oral microbiome

The bulk:

- Continuous stirred-tank reactor model
- Yield calculated based on stoichiometry of bacterial species
- Comparison of the relative abundance and pH of bulk to that of *in vitro* model

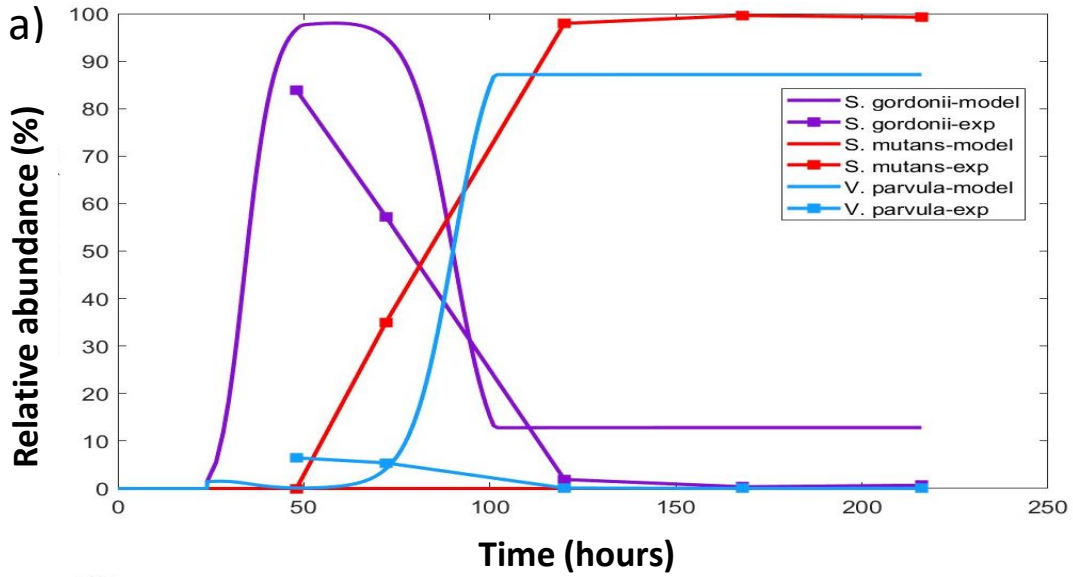
The biofilm:

- Cells modelled as own agent
- Bacteria affected by local pH environment and nutrients
- Allows comparison of the relative abundance to qPCR results and simulates local pH environment

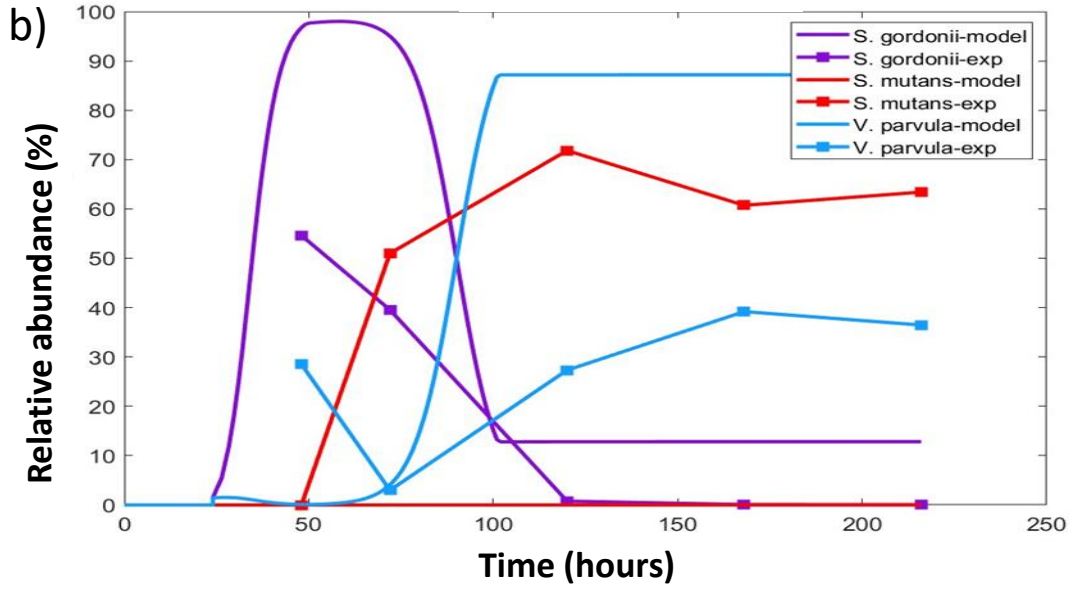


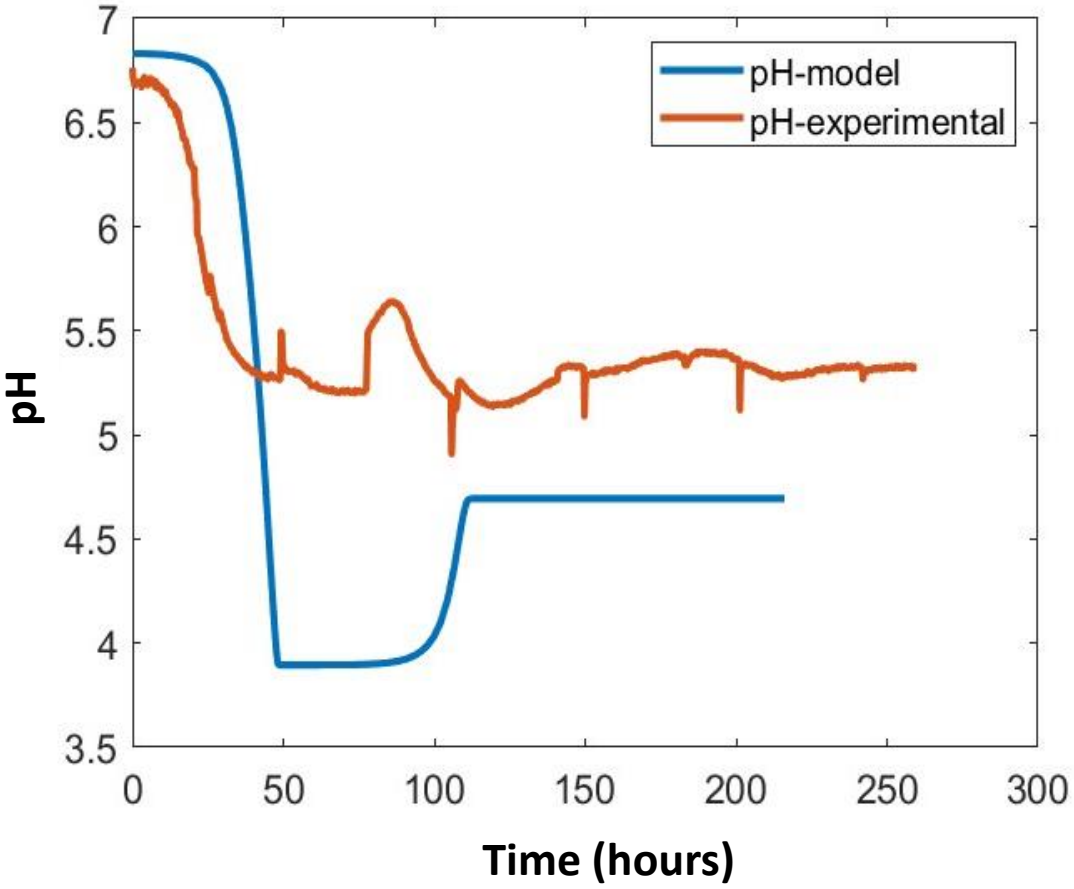
Continuous modelling bulk-relative abundance and pH

a)



b)

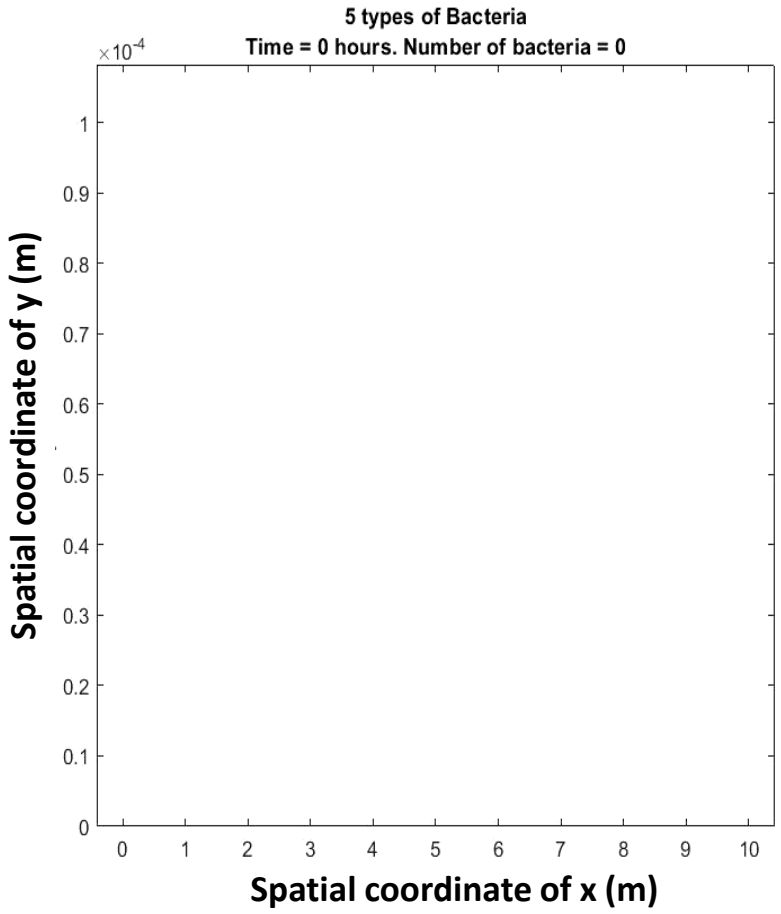


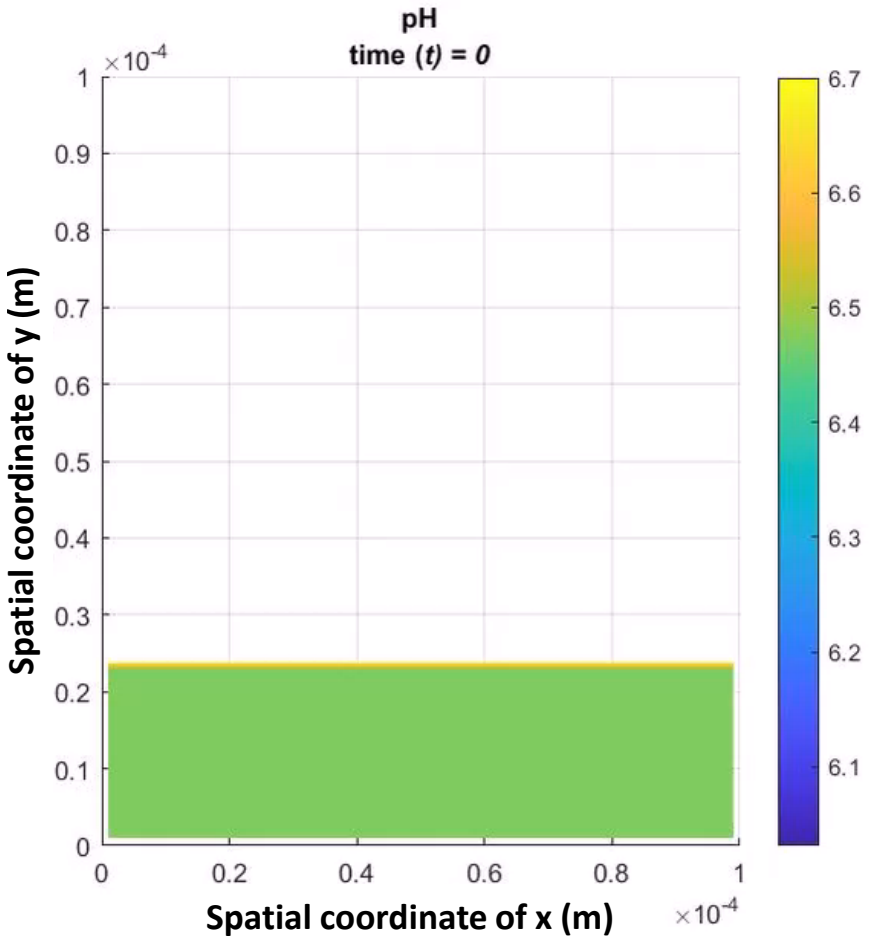


a) High glucose b) Low glucose

IbM. Example of biofilm growth and pH profile

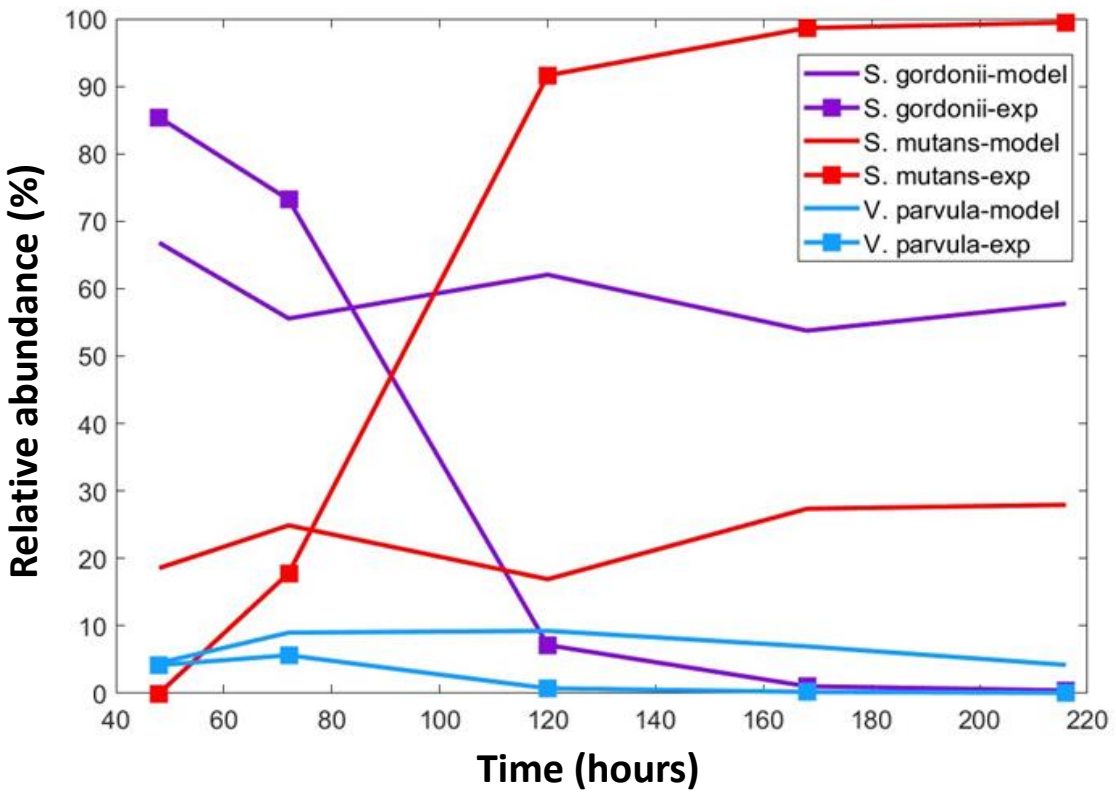
- *S. gordonii*
- *S. mutans*
- *A. oris*
- *N. subflava*
- *V. parvula*



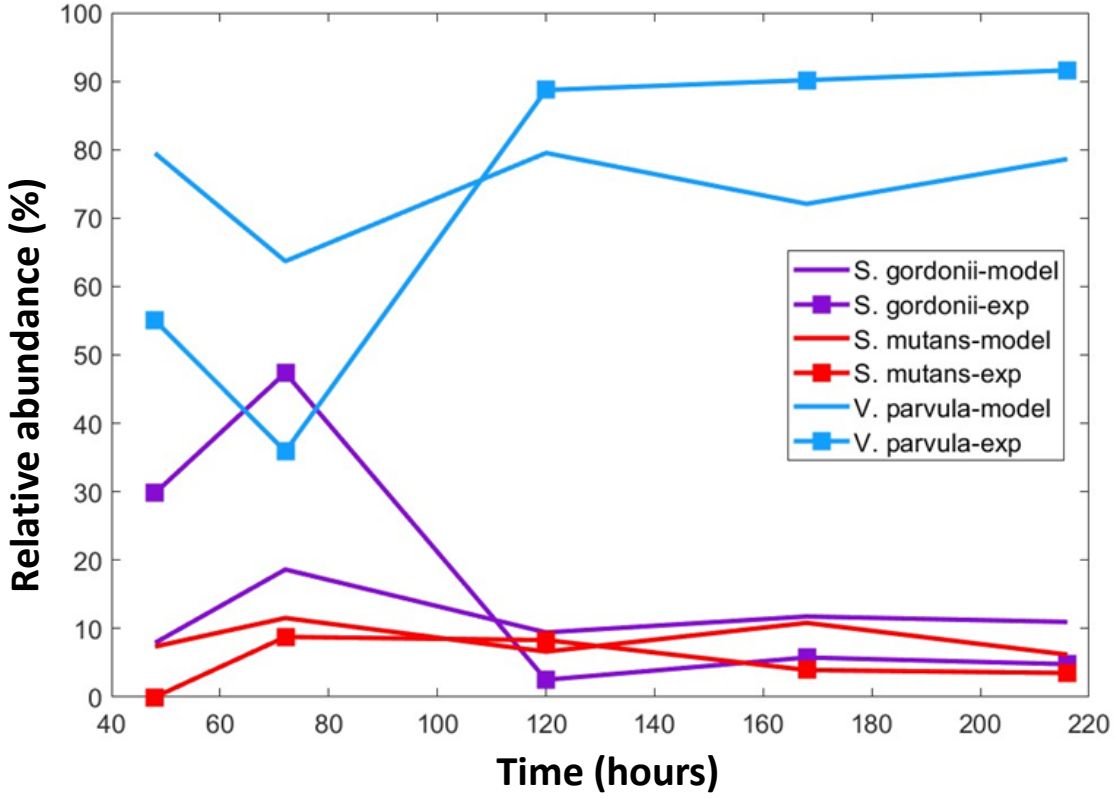


IbM. Biofilm growth and species relative abundance

High glucose



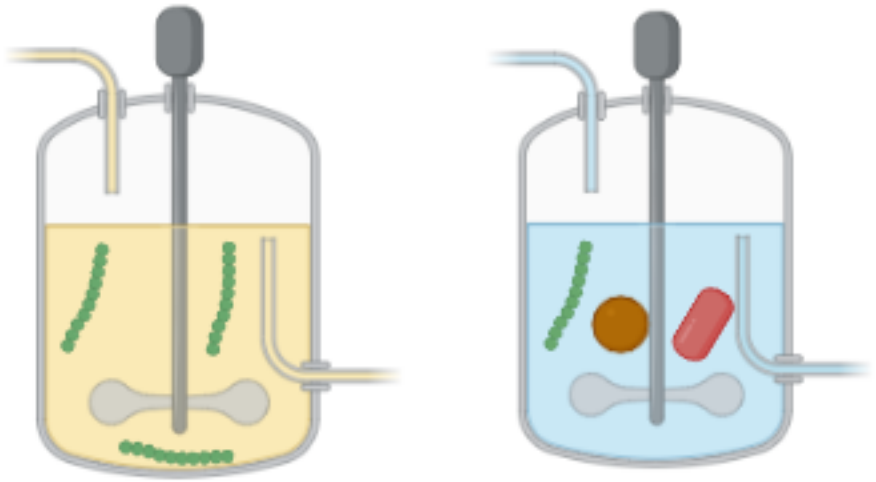
Low glucose

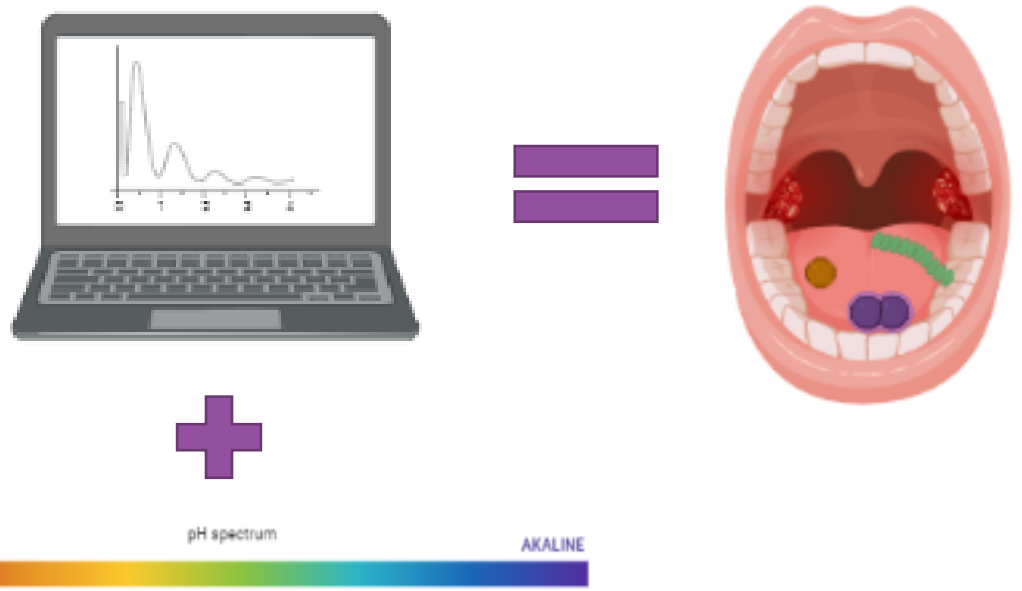


Conclusions

High glucose → Low pH

Low glucose → High pH





(Figures created using www.Biorender.com)

Future work

(Figures created using www.Biorender.com)

Acknowledgements

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