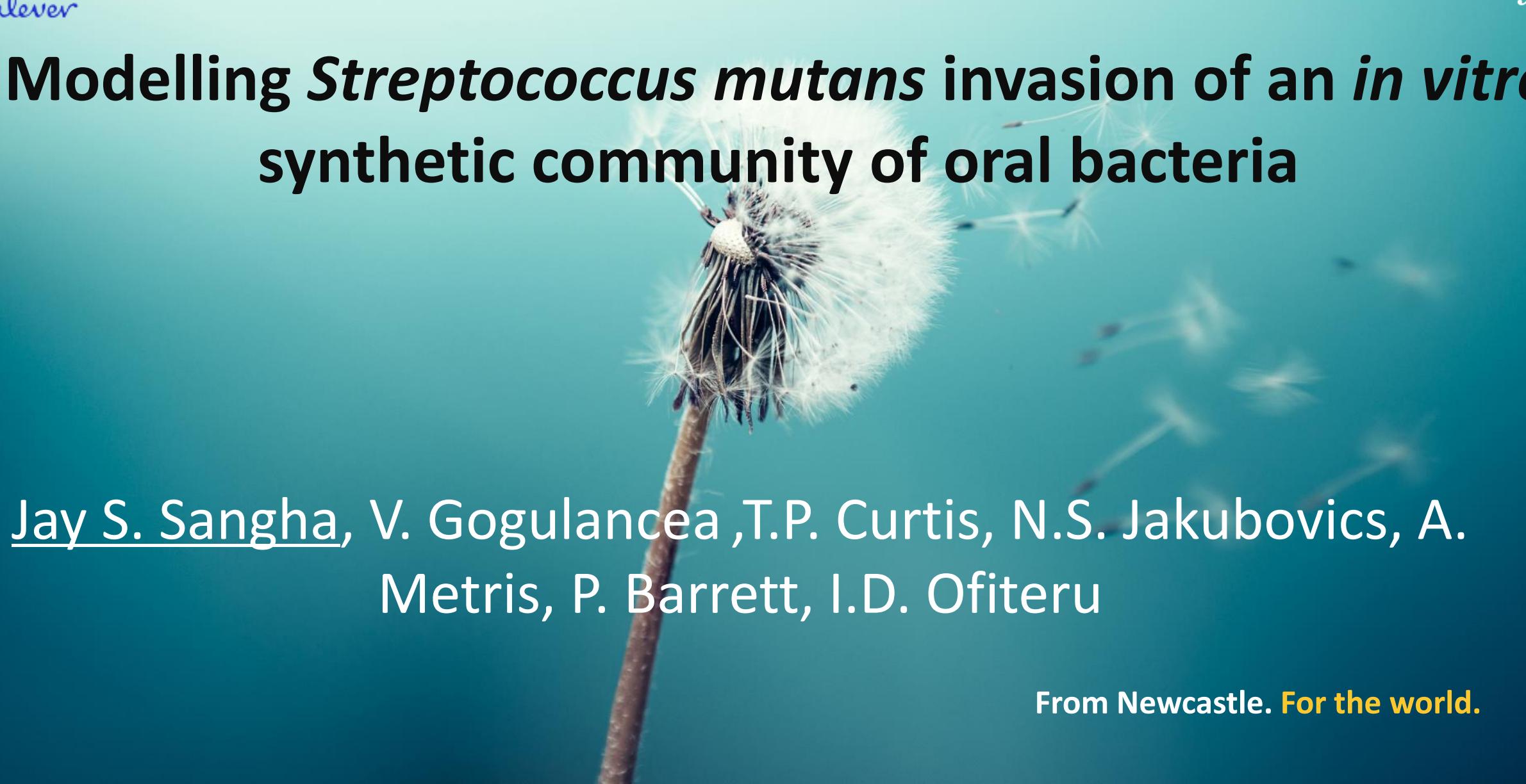


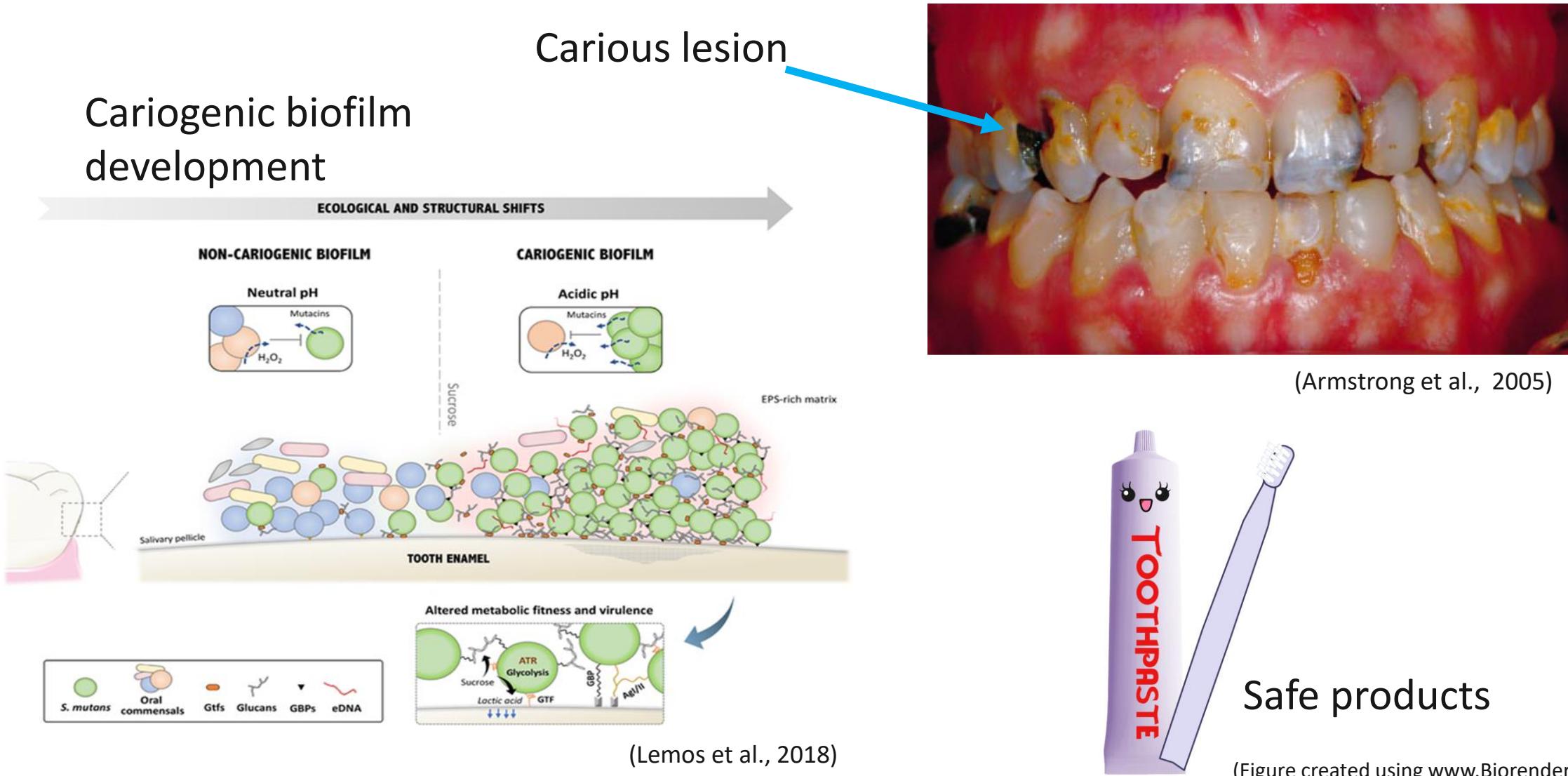
# Modelling *Streptococcus mutans* invasion of an *in vitro* synthetic community of oral bacteria



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

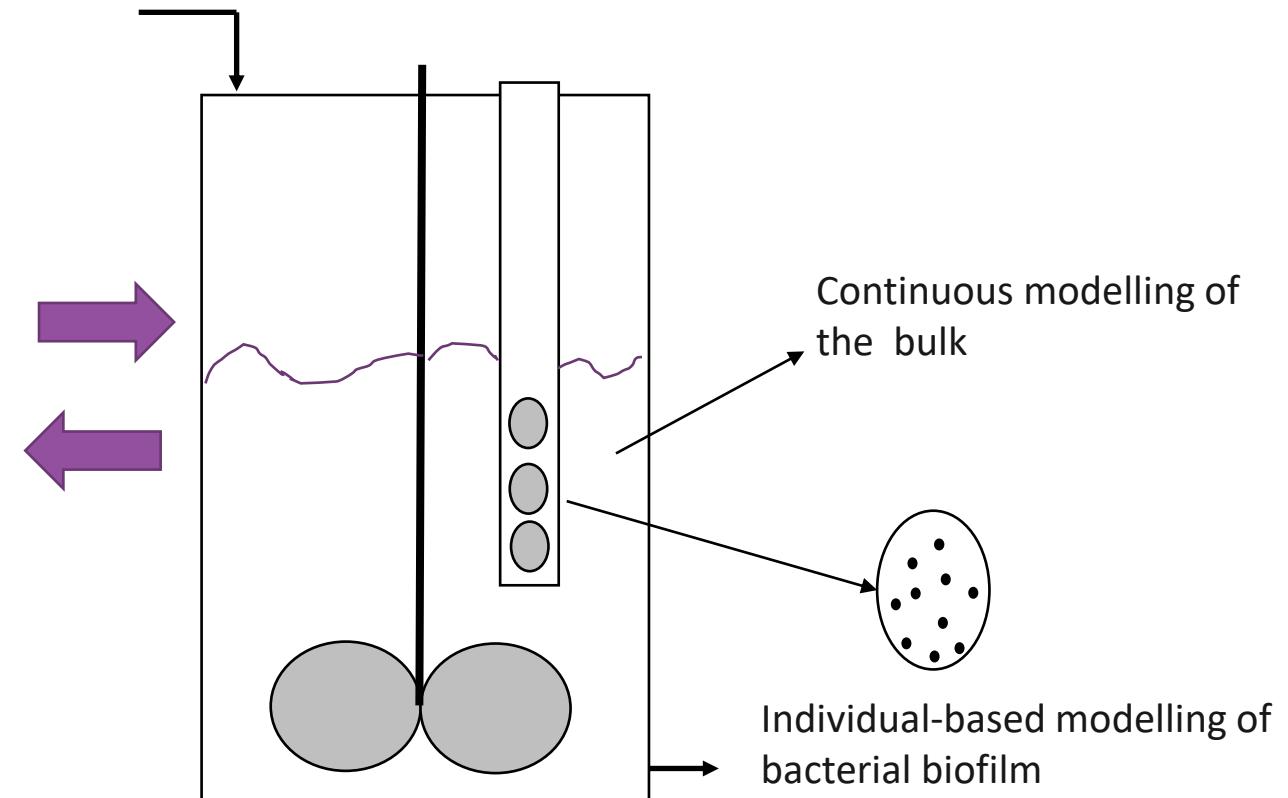


# Modelling the oral microbiome & aims

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

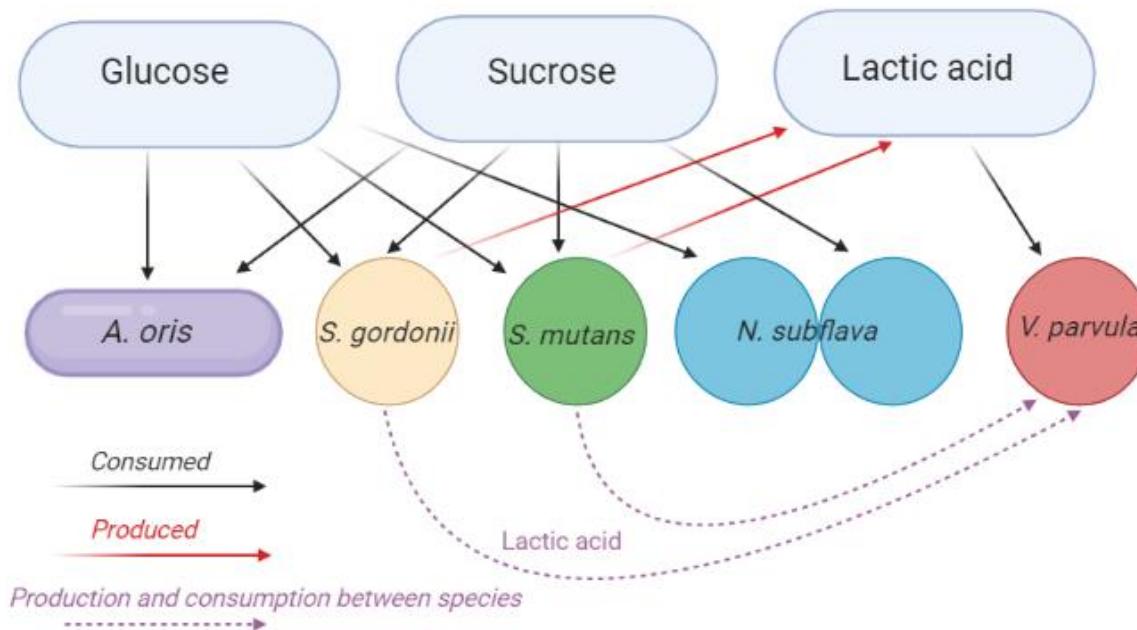


*In vitro* (CDC reactors)



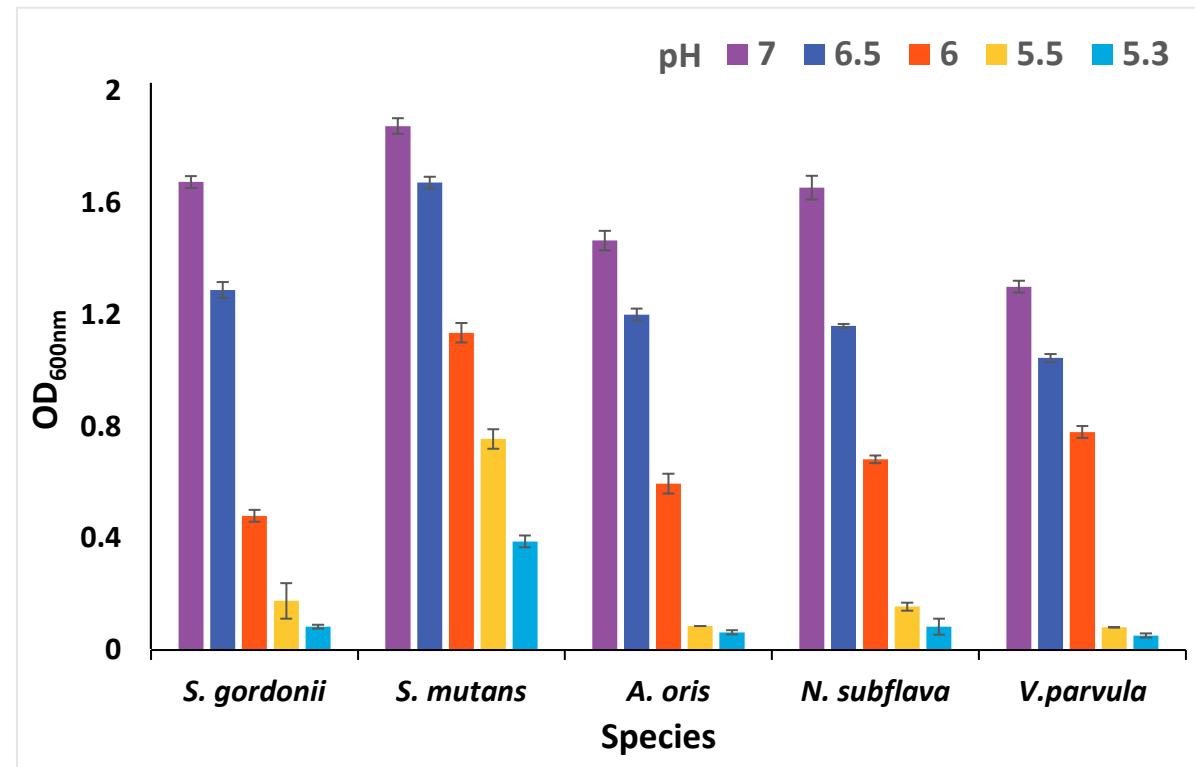
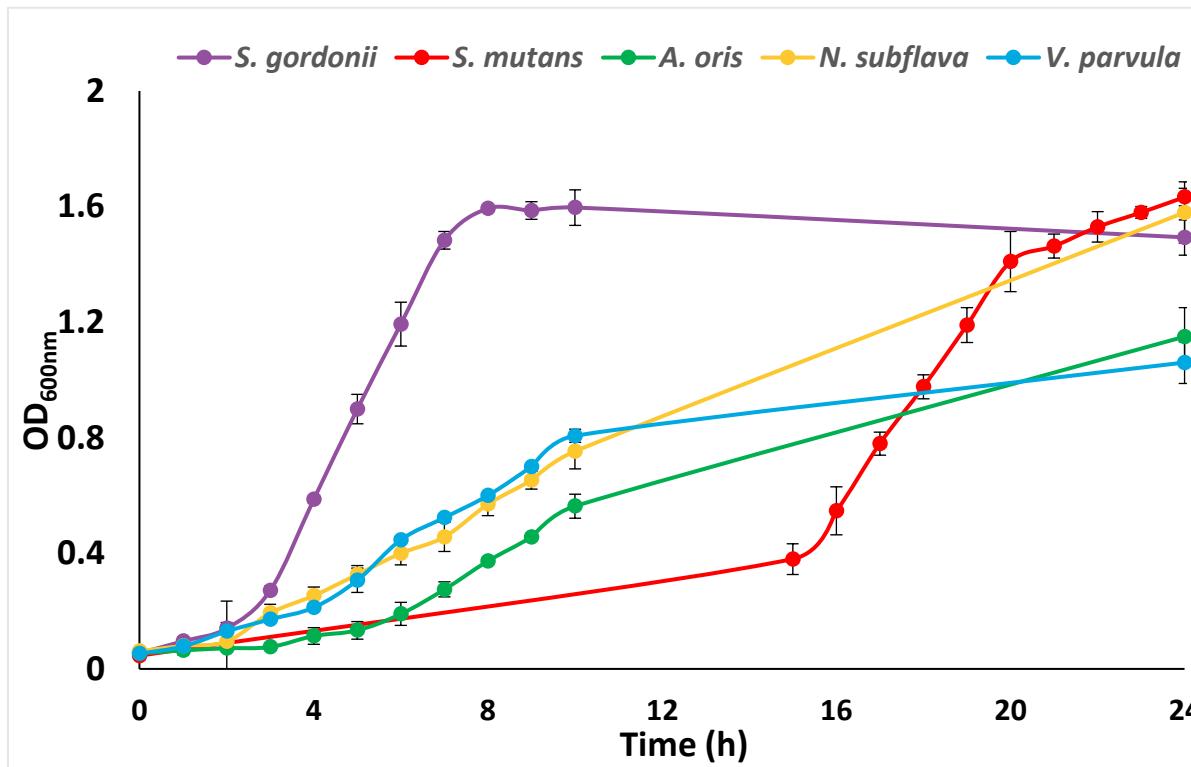
*In silico*

# Synthetic community



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

# Synthetic community characterisation



μmax for synthetic community species (h <sup>-1</sup> )				
<i>S. gordonii</i>	<i>S. mutans</i>	<i>A. oris</i>	<i>N. subflava</i>	<i>V. parvula</i>
0.492	0.406	0.227	0.261	0.246

Ks values (mmol L <sup>-1</sup> )				
<i>S. gordonii</i>	<i>S. mutans</i>	<i>A. oris</i>	<i>N. subflava</i>	<i>V. parvula</i>
6.60	5.55	7.78	5.55	26.90

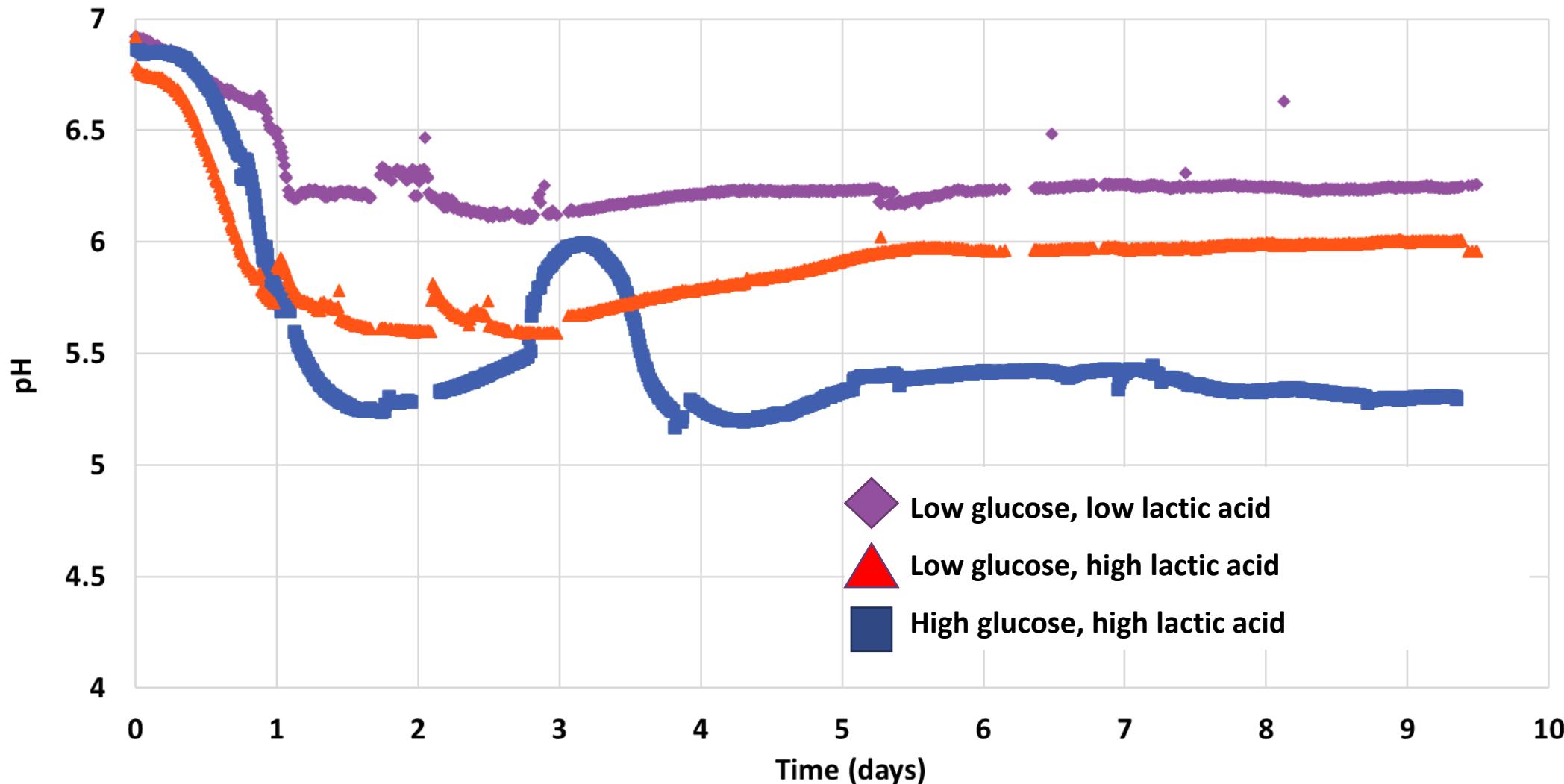
# *In vitro* modelling of *S. mutans* colonisation

Continuous flow of 0.4 mL min<sup>-1</sup>. Temperature maintained at 37 °C

Inoculation (day)	Species
0	<i>Actinomyces oris</i>
1	<i>Streptococcus gordonii</i> <i>Neisseria subflava</i> <i>Veillonella parvula</i>
2	<i>Streptococcus mutans</i>

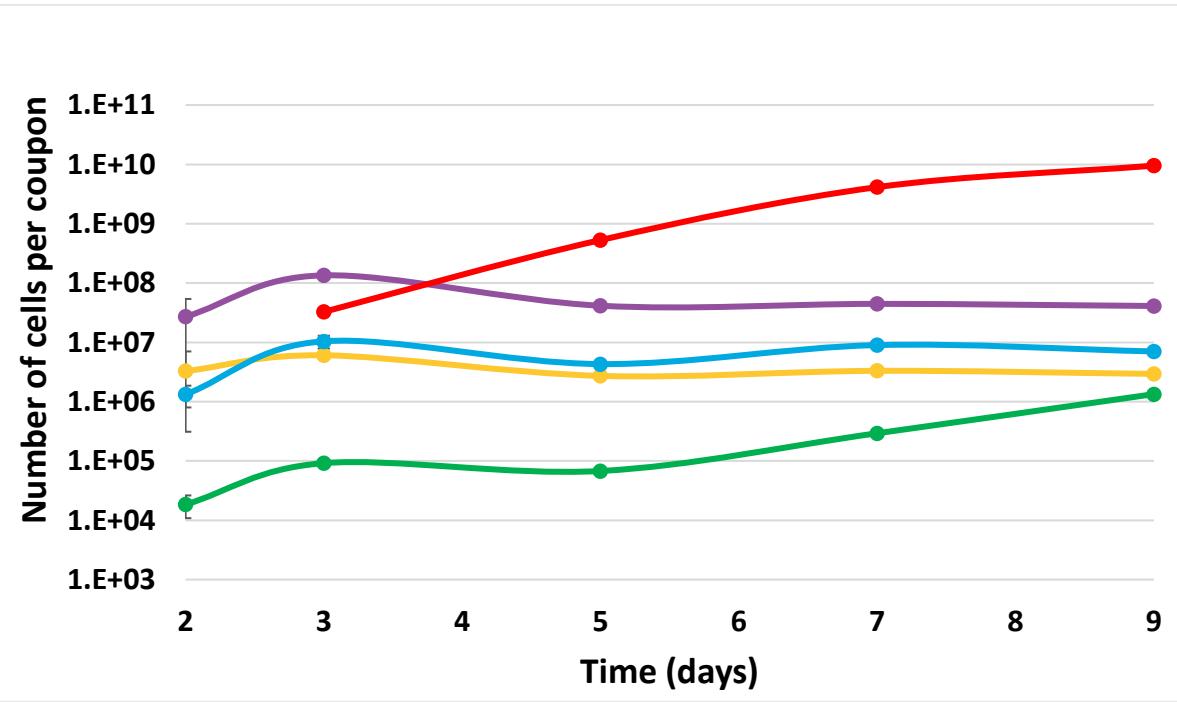


# pH variation in the bulk

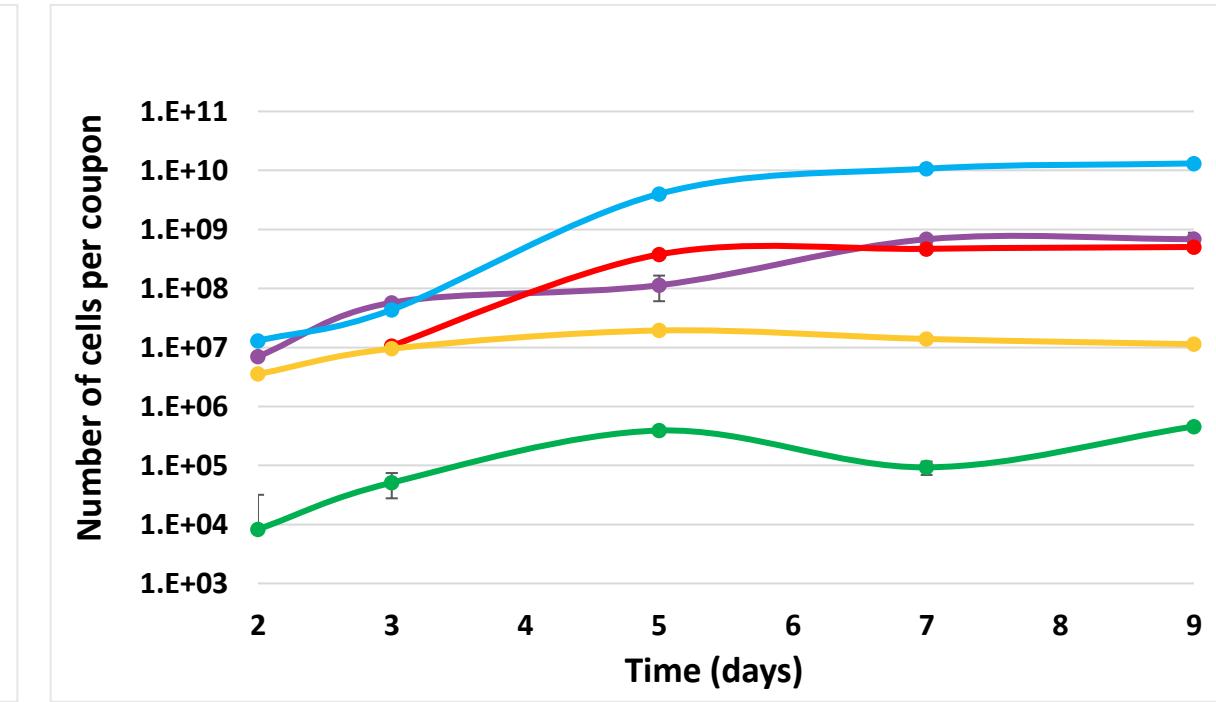


# qPCR abundance in the biofilm (coupons)

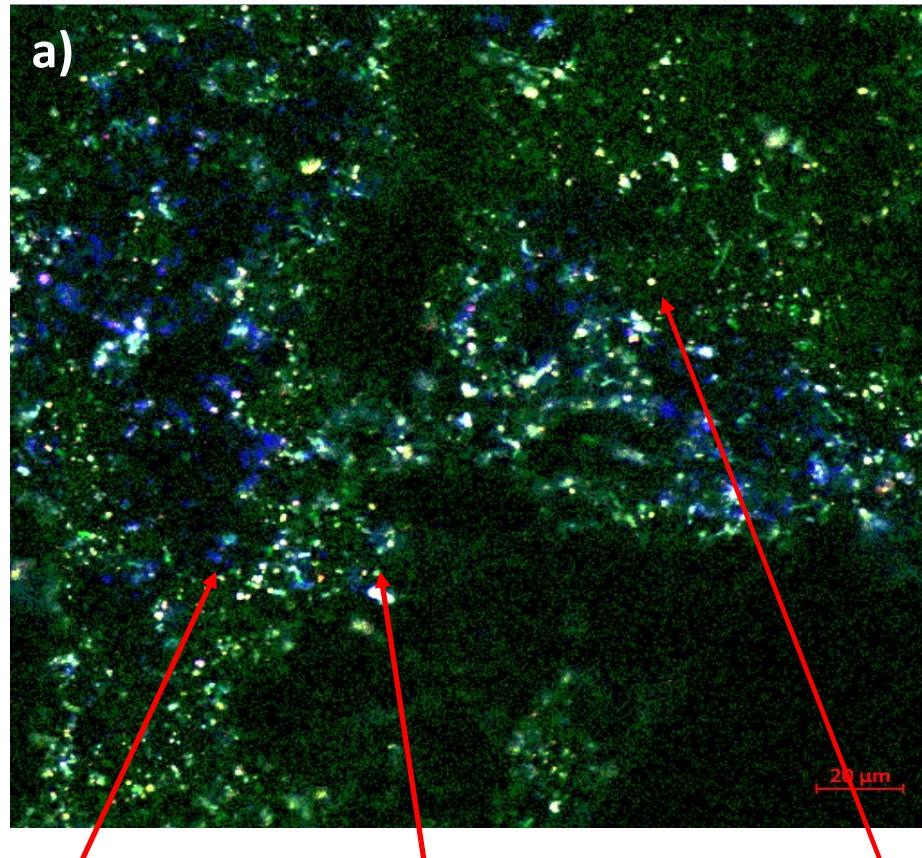
High glucose



Low glucose



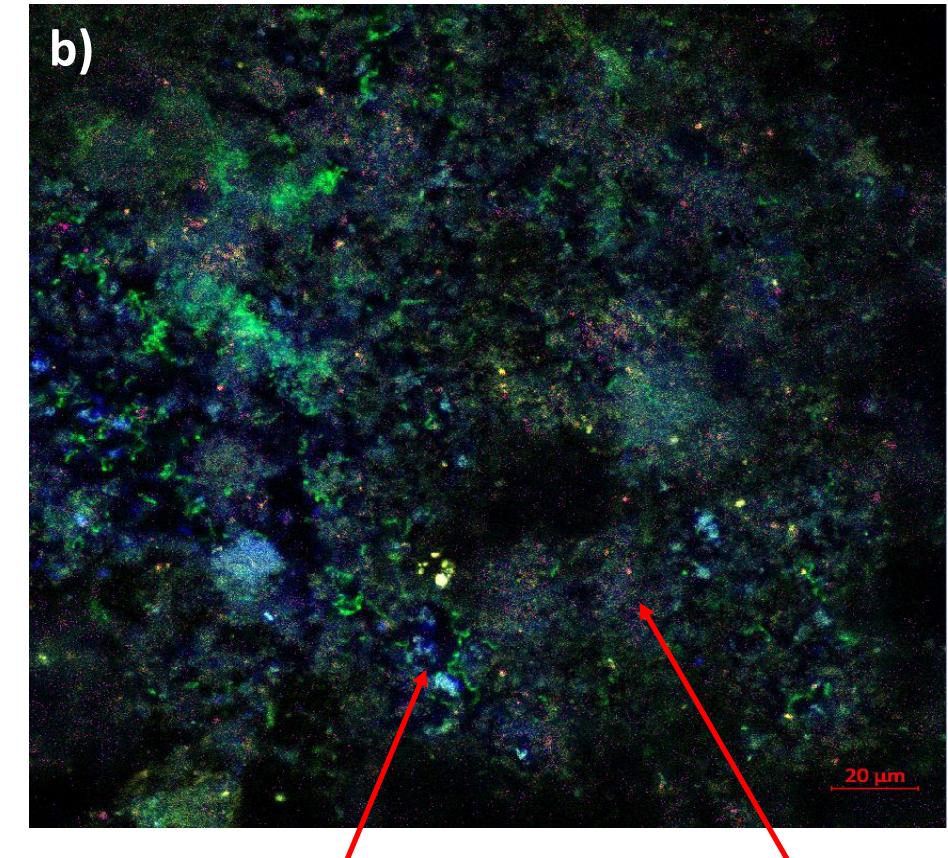
—●— *S. gordonii*    —○— *N. subflava*  
 —●— *S. mutans*    —●— *V. parvula*  
 —●— *A. oris*



*S. gordonii*

*S. mutans*

*A. oris*



*N. subflava*

*V. parvula*

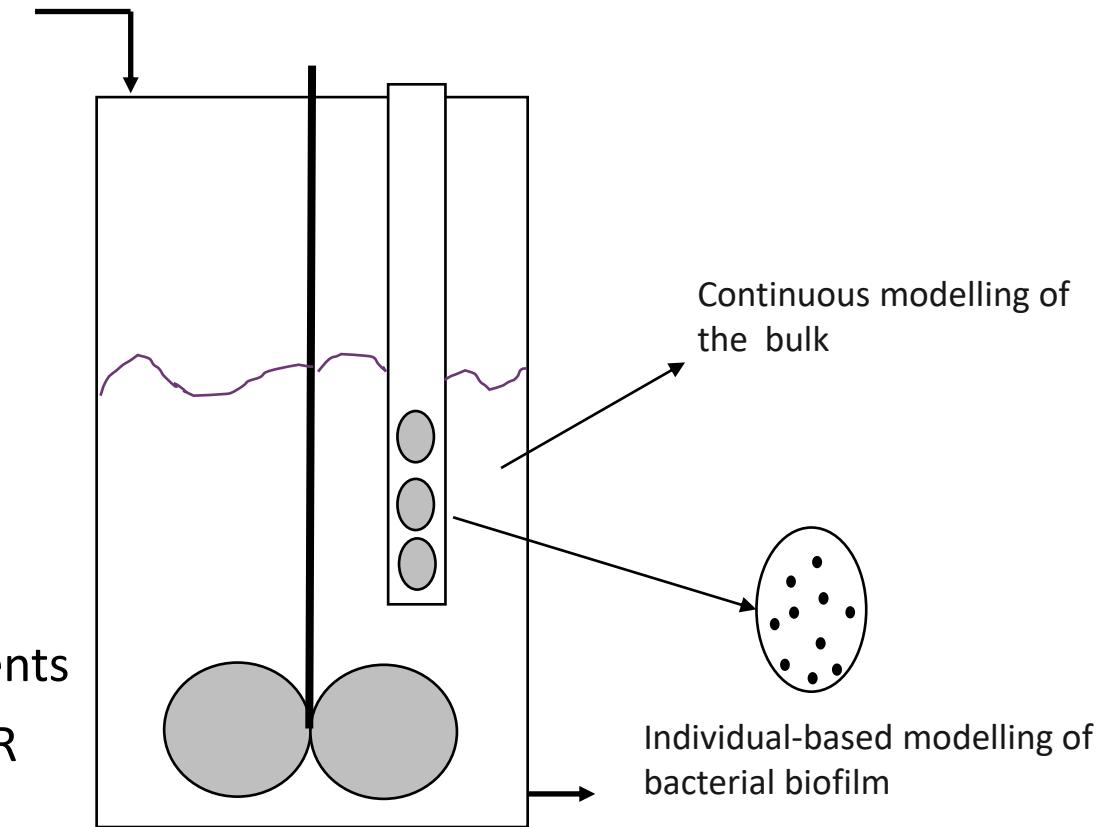
a) High glucose    b) Low glucose

## The bulk:

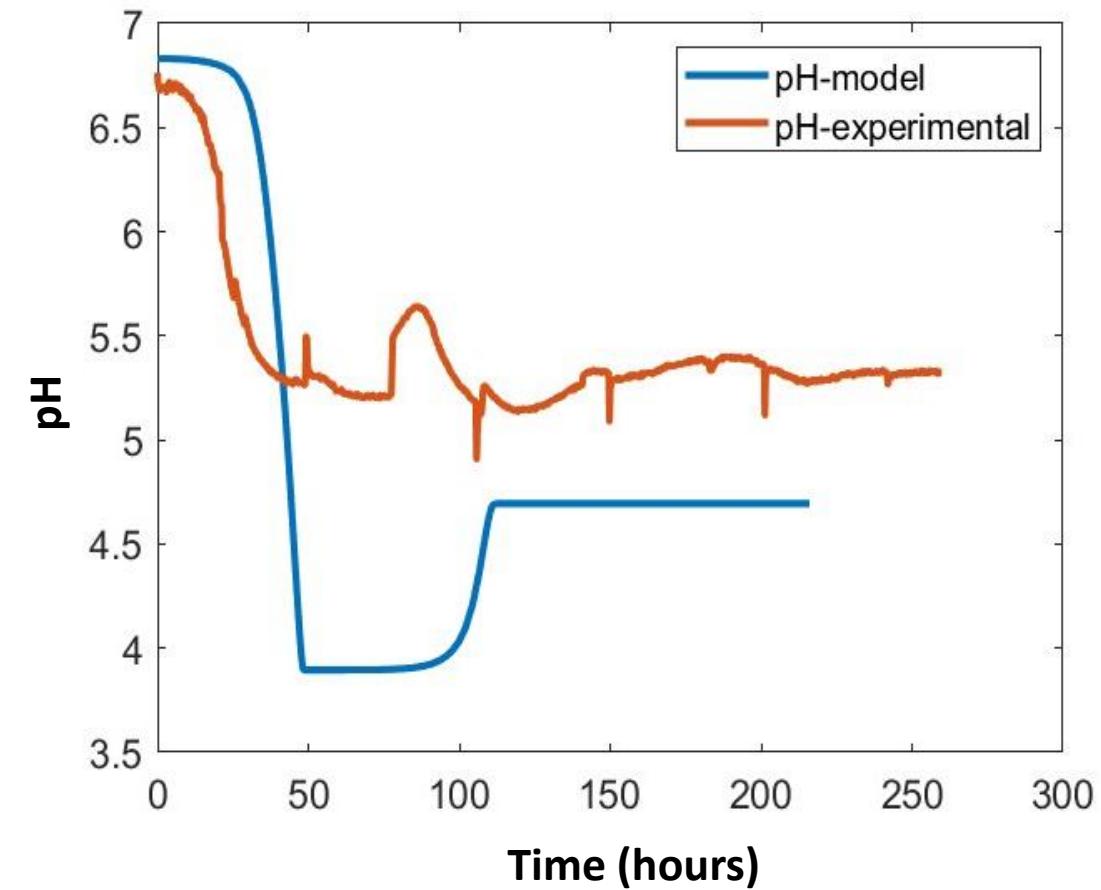
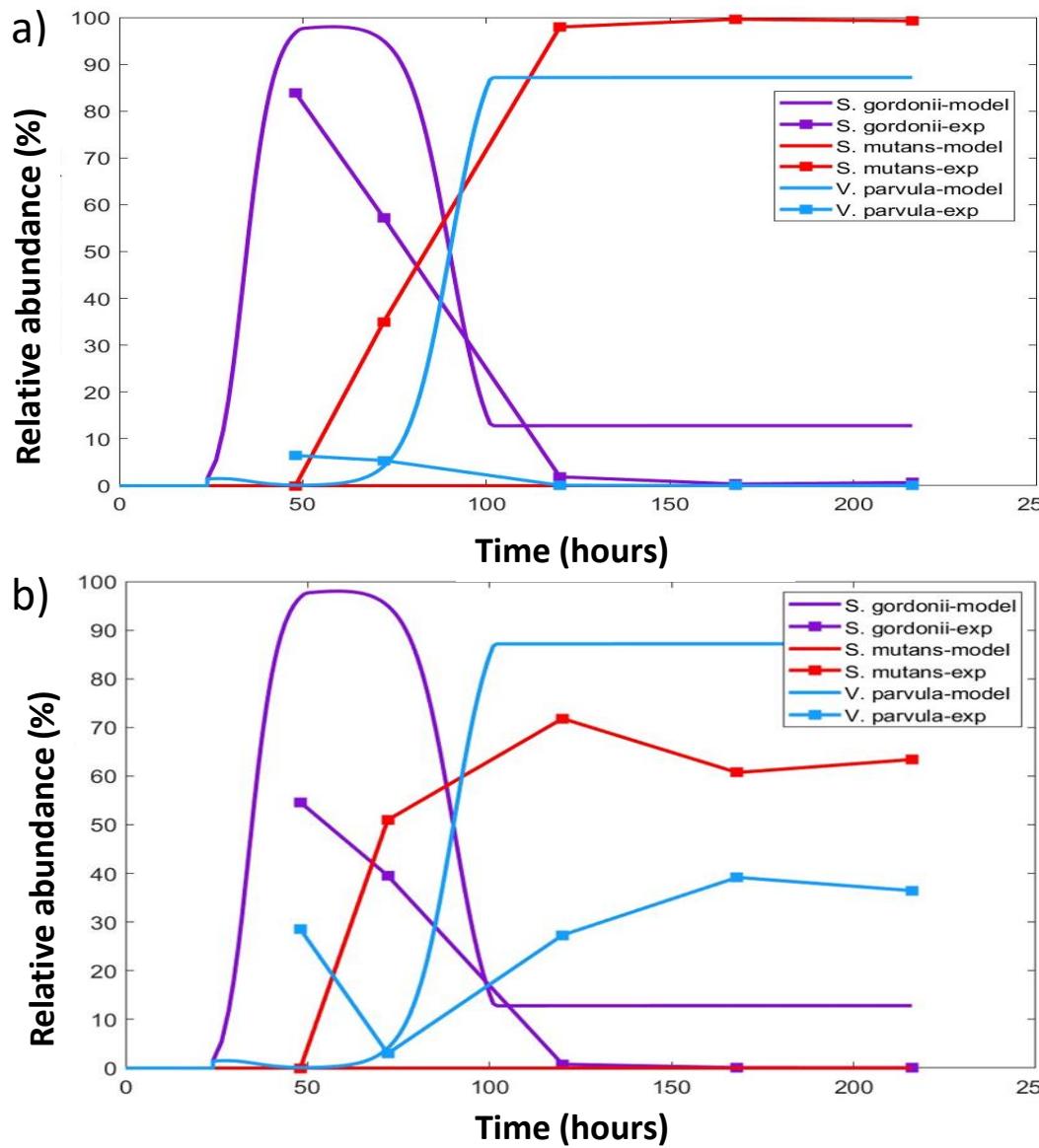
- Continuous stirred-tank reactor model
- Yield calculated based on stoichiometry of bacterial species
- Comparison of the relative abundance and pH of bulk to that of *in vitro* model

## 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



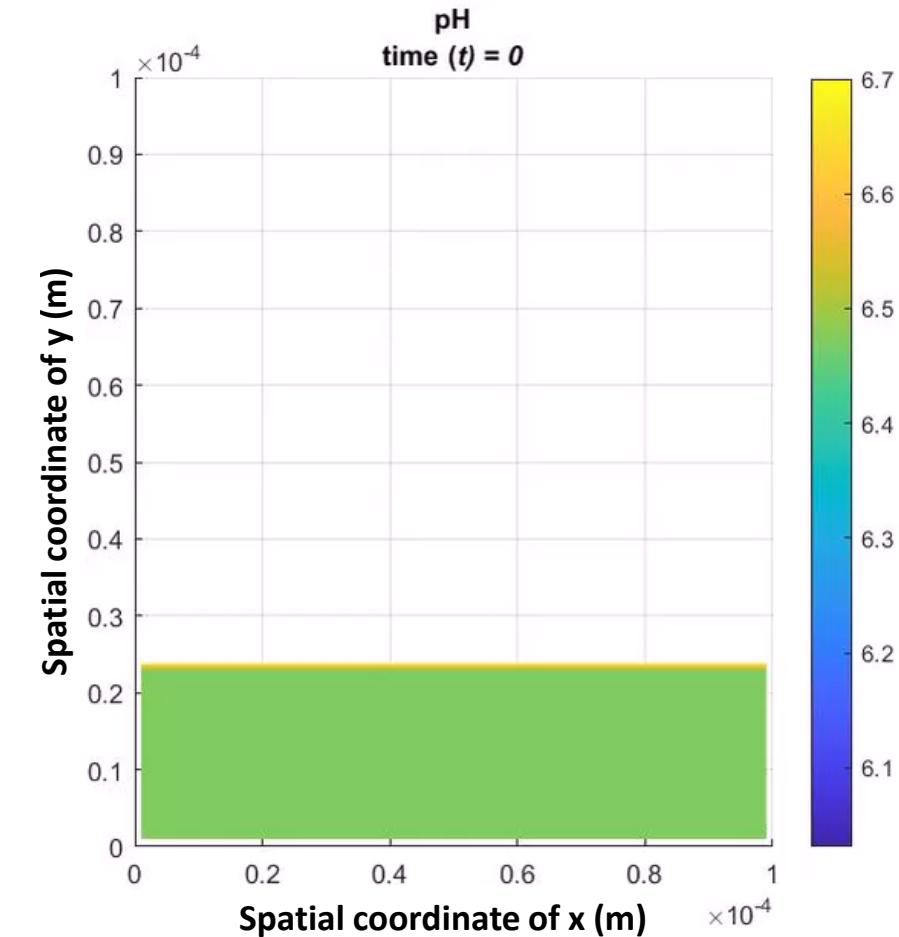
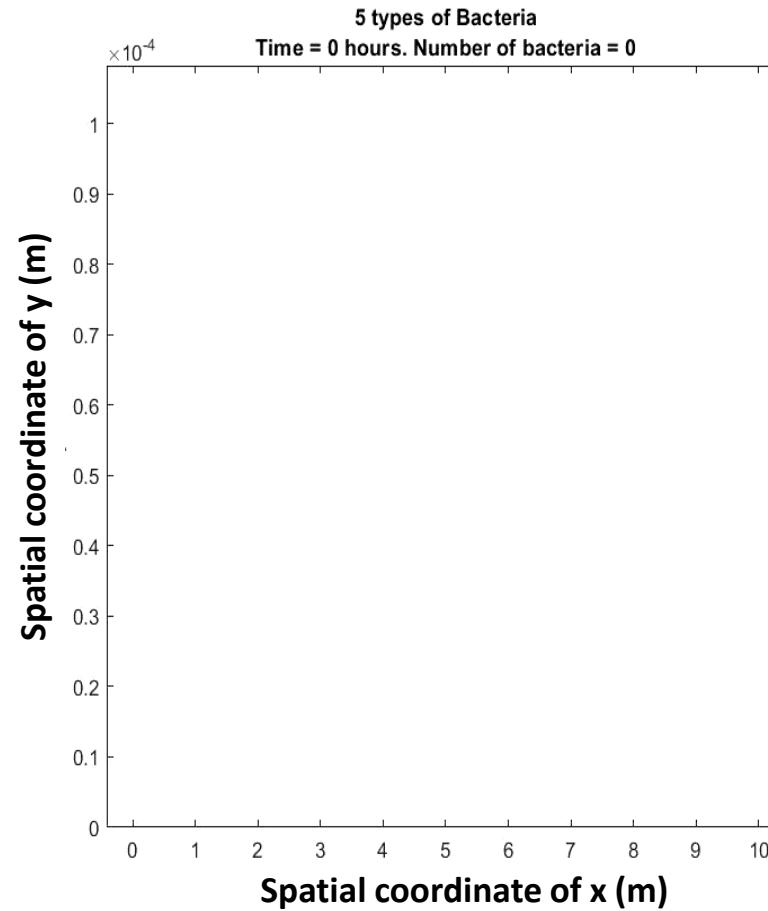
# Continuous modelling bulk-relative abundance and pH



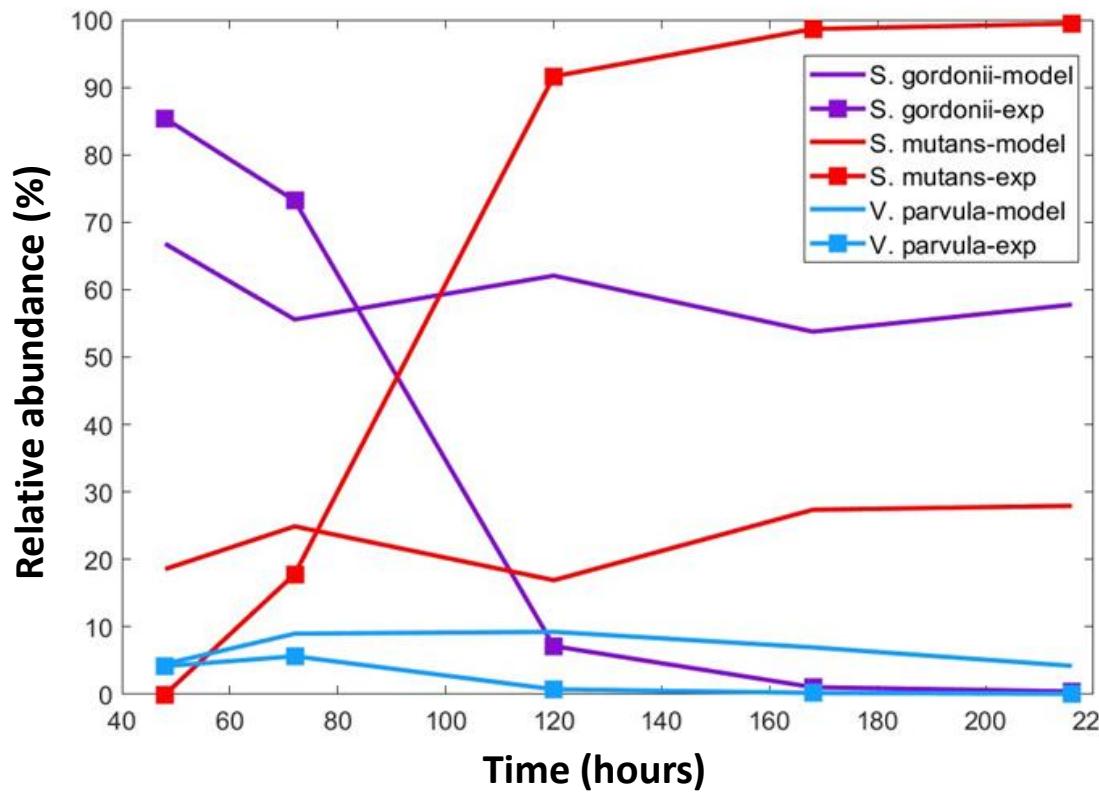
a) High glucose    b) Low glucose

## IbM. Example of biofilm growth and pH profile

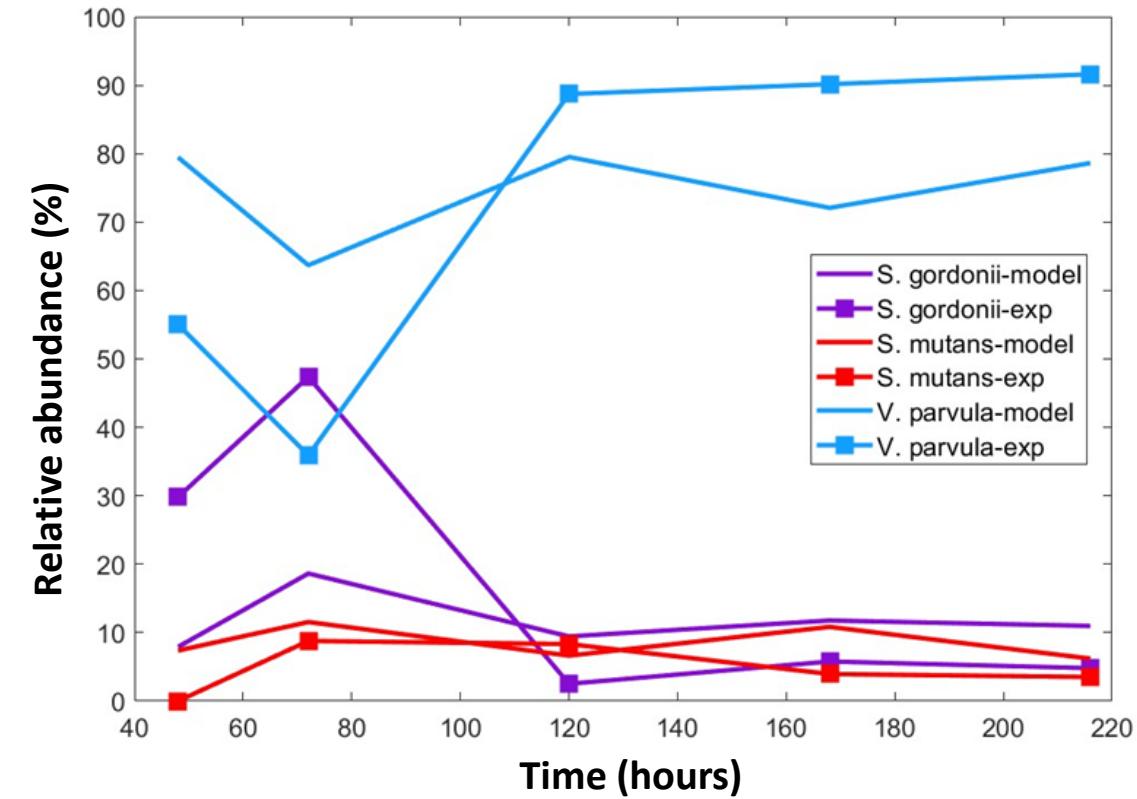
- *S. gordonii*
- *S. mutans*
- *A. oris*
- *N. subflava*
- *V. parvula*



## High glucose



## Low glucose

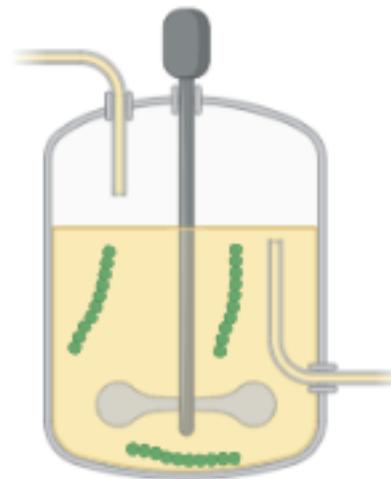


# Conclusions

High glucose



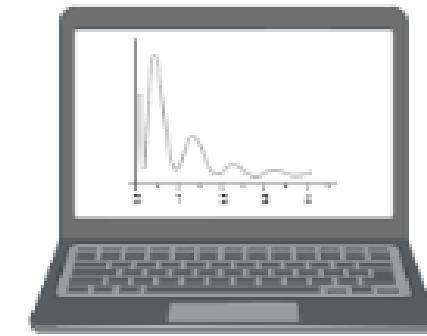
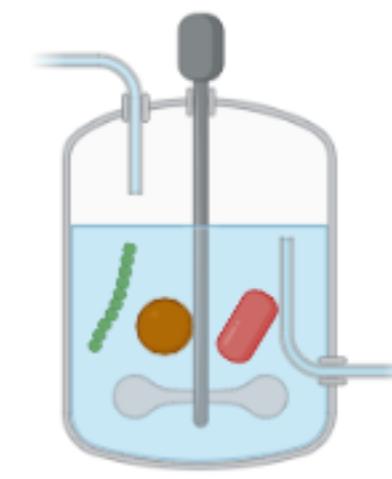
Low pH



Low glucose



High pH



ACID



pH spectrum

ALKALINE

(Figures created using [www.Biorender.com](http://www.Biorender.com))

# Future work



# Acknowledgements



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Safety and Environmental Assurance Centre , Unilever



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Research Council



Unilever

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