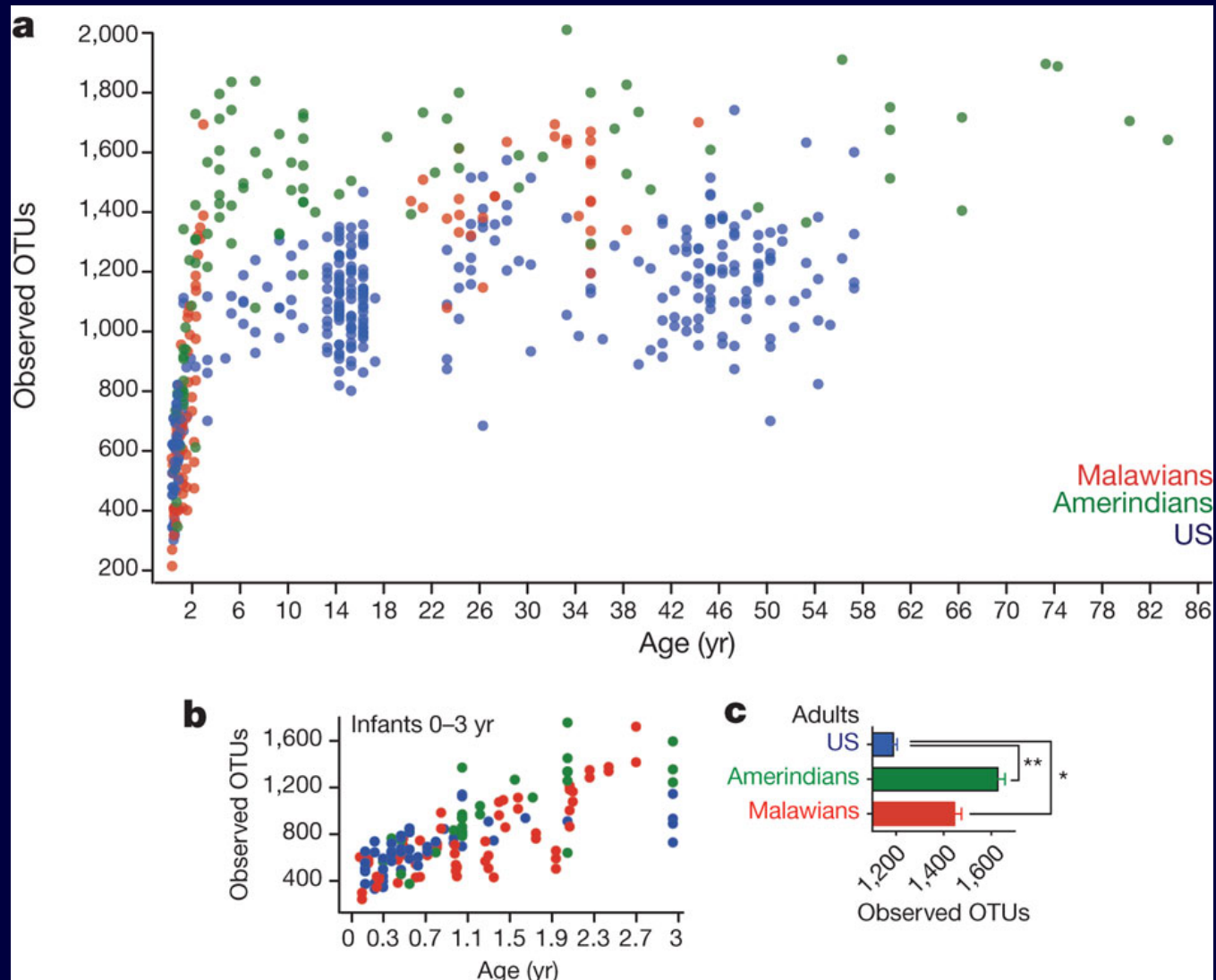


Microbiota, metabolism and immunity:  
the potential for early-life intervention.

Mick Bailey

Professor of Comparative Immunology,  
Bristol University

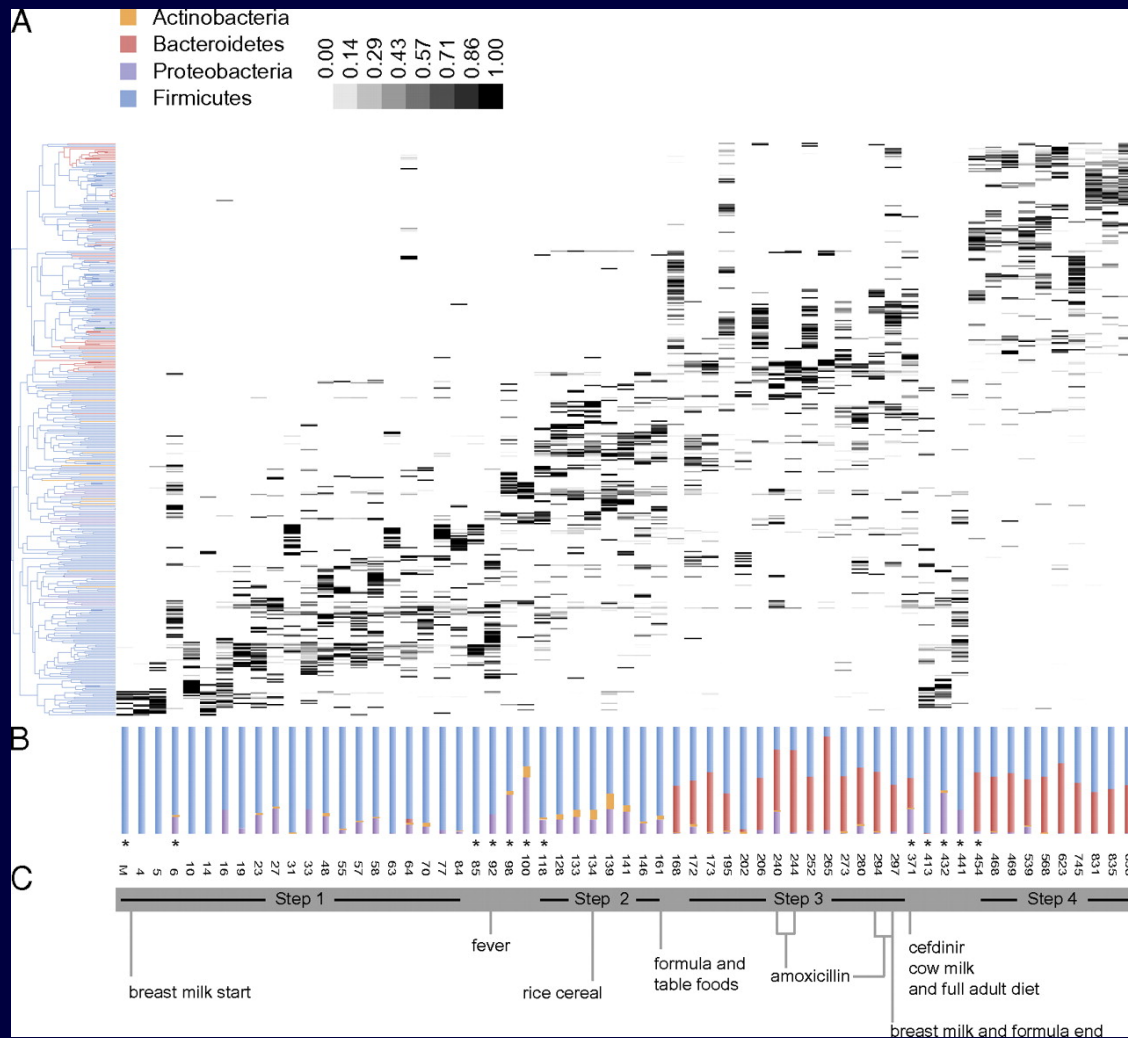
# Bacterial diversity increases with age in human populations.



T Yatsunenko *et al.* *Nature* **000**, 1-7 (2012) doi:10.1038/nature11535

nature

# Succession of microbial communities: OTU-based community structure and composition in the human gut microbiota changes with age, rather than just becomes more complex.



Koenig J E et al. PNAS 2011;108:4578-4585

# The ‘hygiene hypothesis’

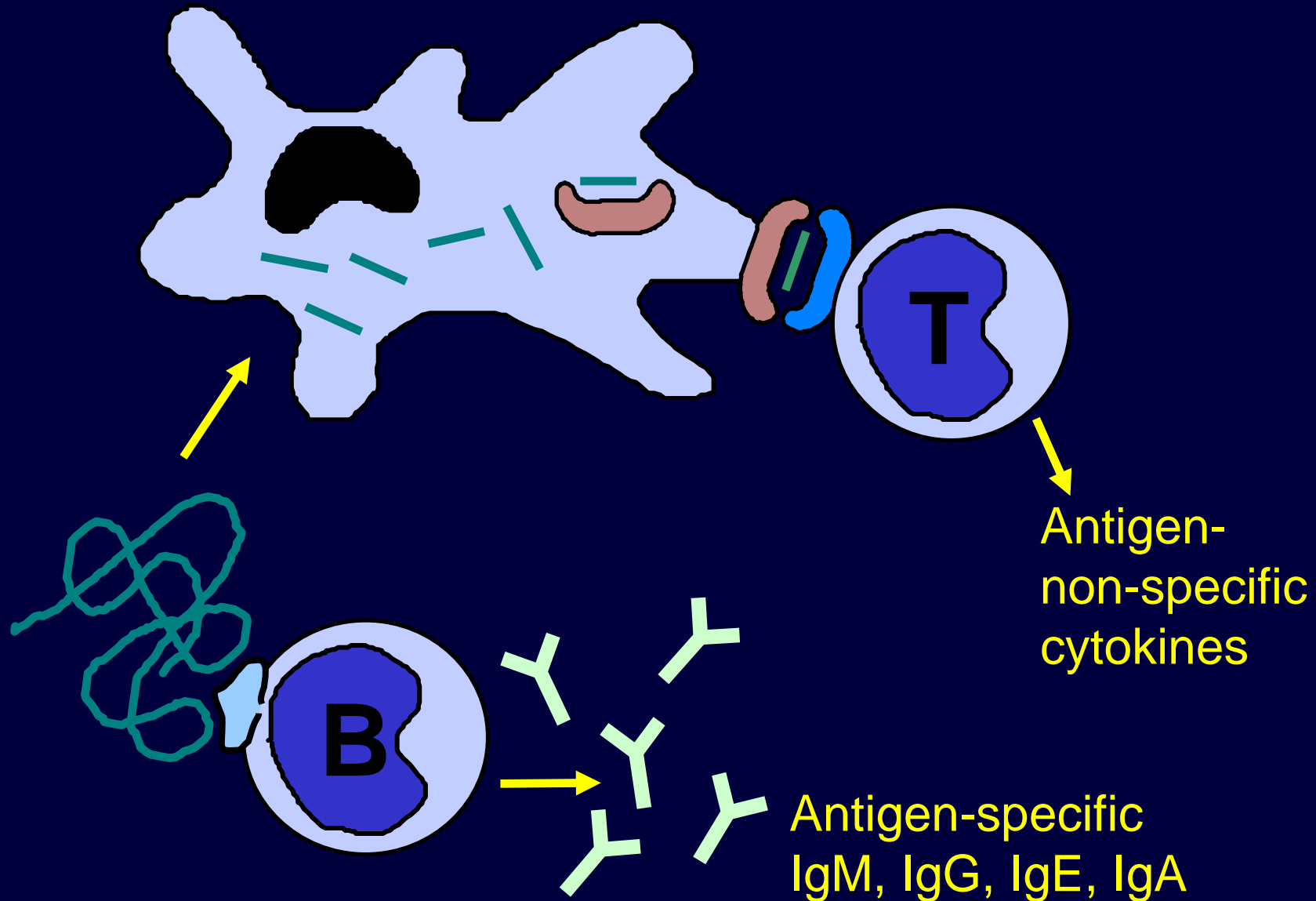
- Species co-evolve with their microbiota.
- The immune system requires interactions with commensal microbiota and with pathogens for it to express appropriate function (‘enteric health’).
- The absence of appropriate interactions predisposes to diseases of immune dysfunction (allergies, autoimmunity, unusual susceptibility to infectious diseases).
- Similarly, appropriate interactions with gut microbiota are required for development of normal metabolic systems.
- The ‘wrong’ interactions can predispose to metabolic disease in later life.

# The 'hygiene hypothesis'

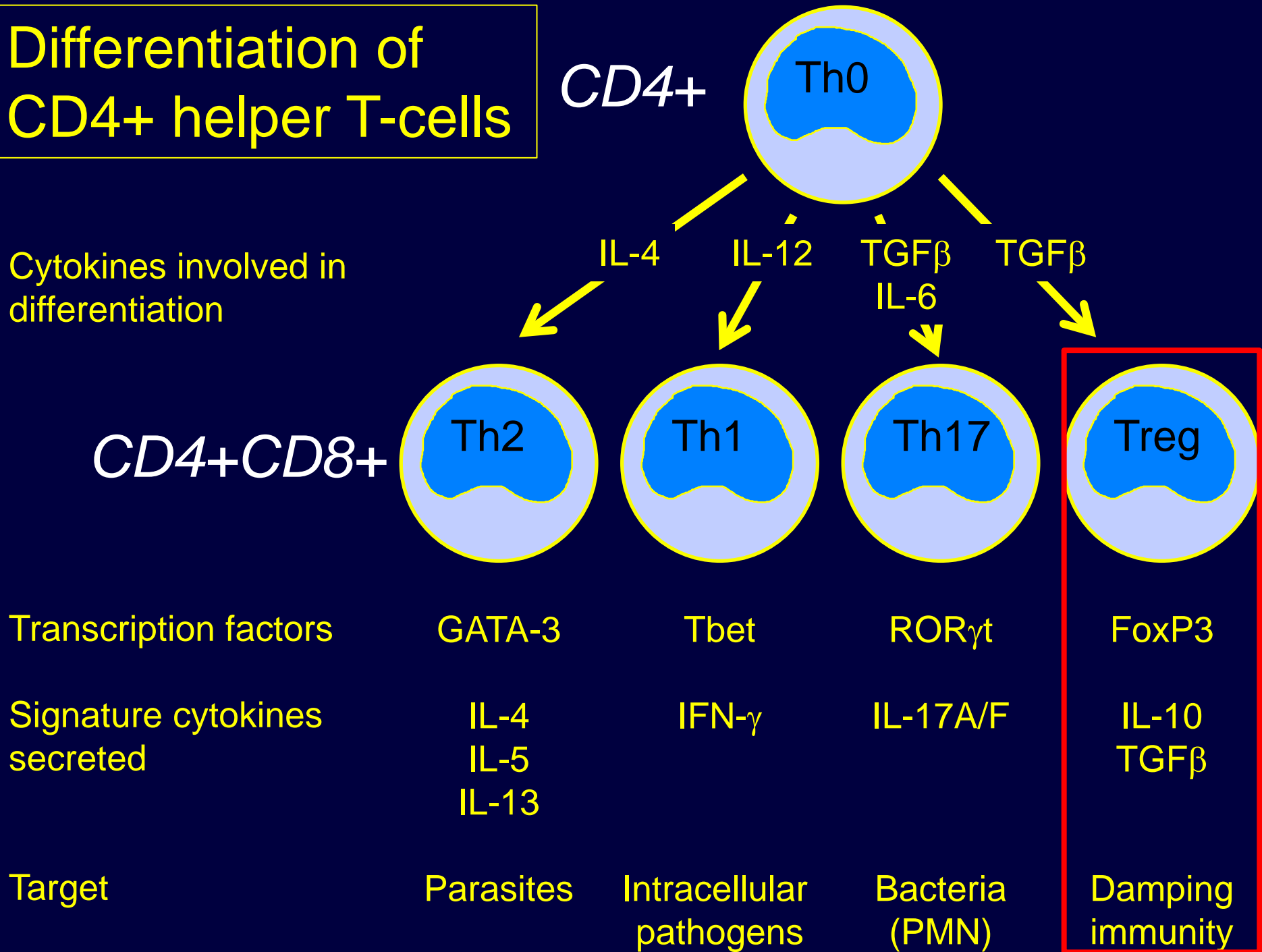
- **Early-life colonisation by microbiota can have long-lasting effects on immunity and metabolism, which may be categorised as 'beneficial' or 'detrimental' under particular circumstances.**
- **This is as relevant to our domesticated species as to humans.**



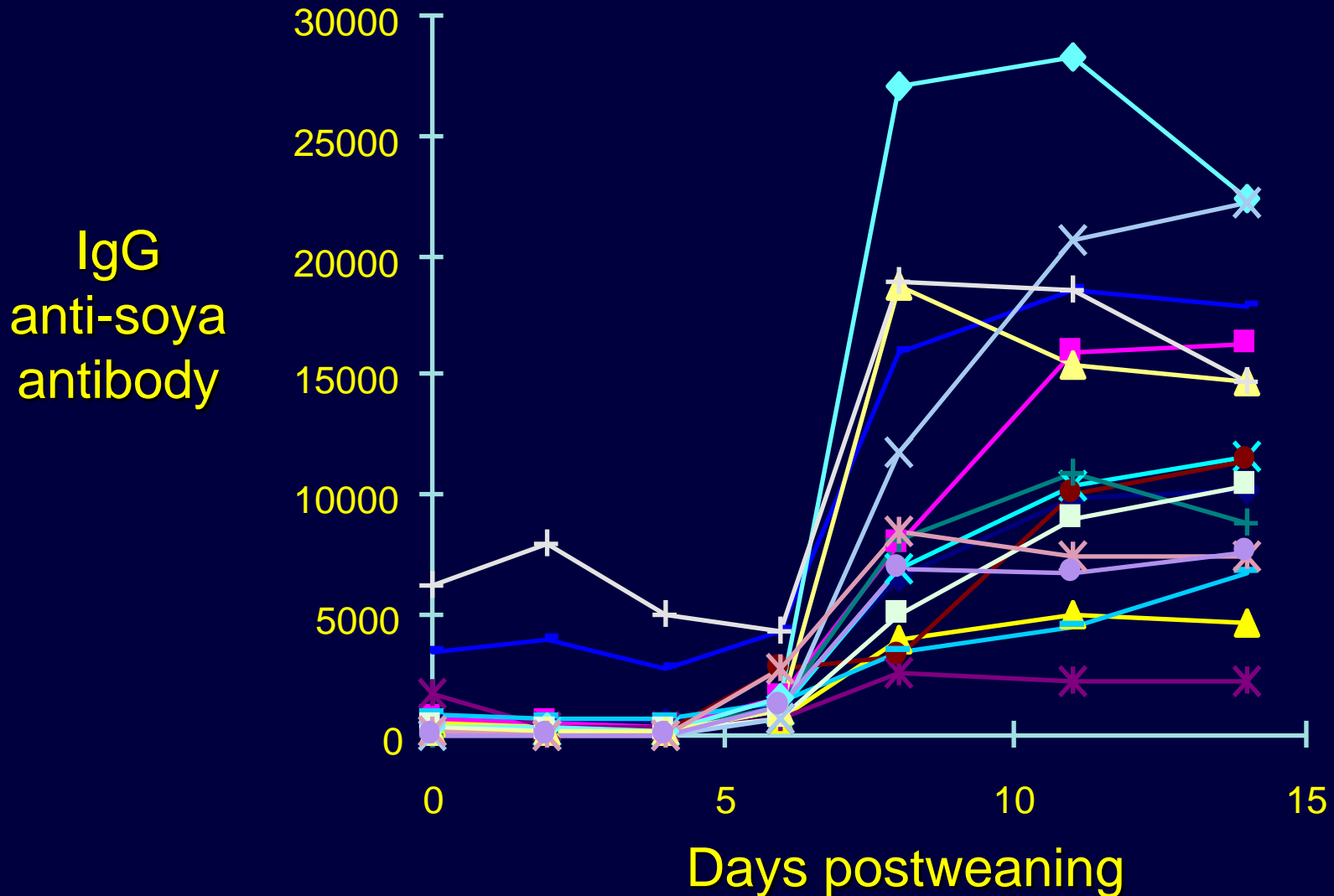
# CD4+ helper T cells require MHCII-restricted presentation of peptides



# Differentiation of CD4+ helper T-cells



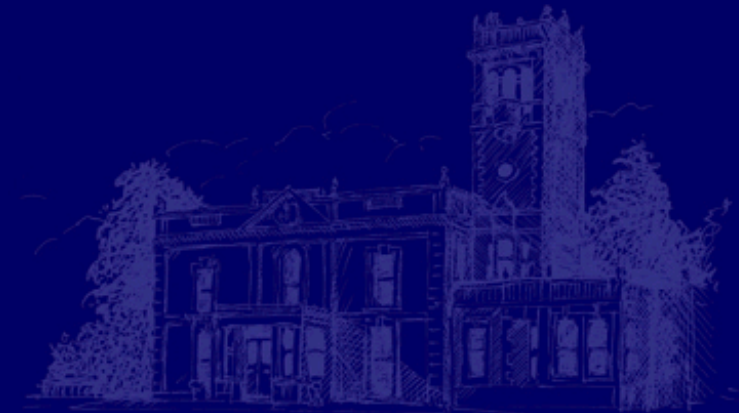
# Novel food proteins trigger inappropriate immune responses in early-weaned piglets

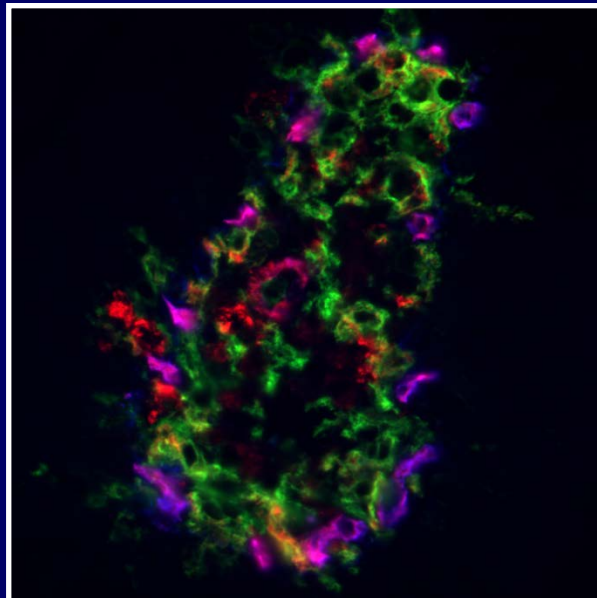
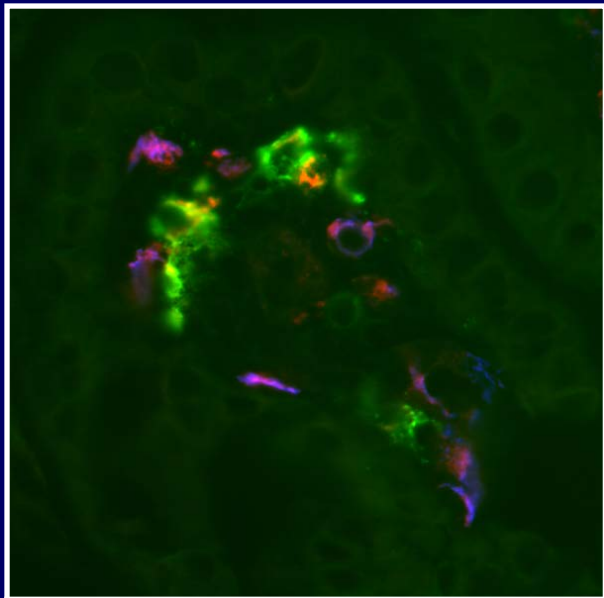




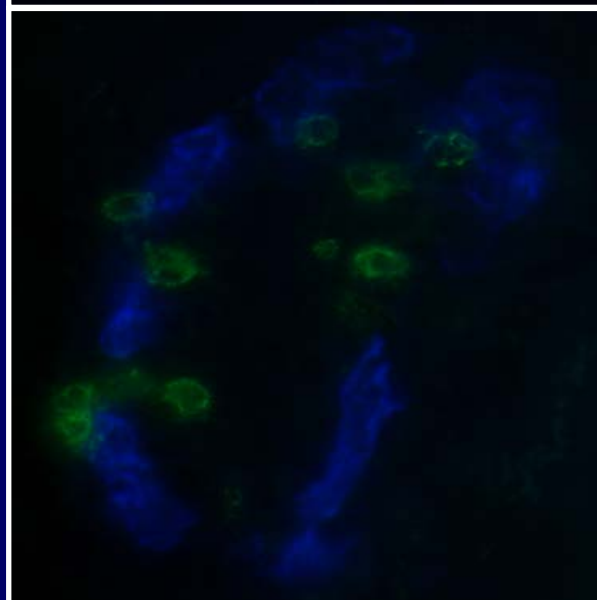
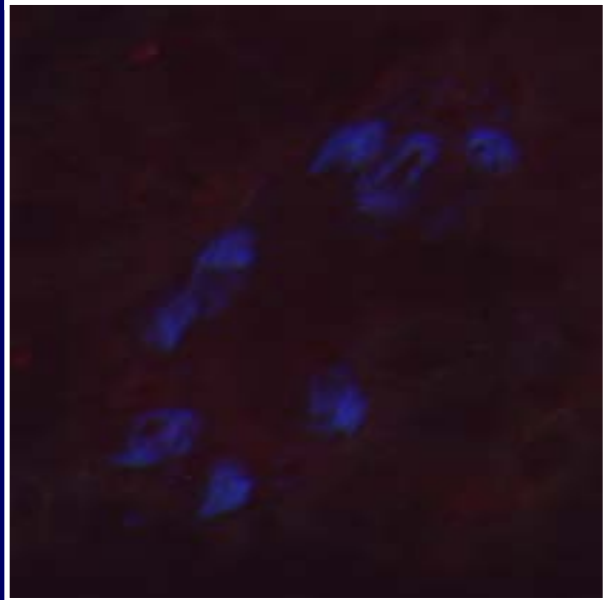
The ability to mount appropriate responses is critical for ‘enteric health’ – IgG, IgE or IgA; Th<sub>1</sub>, Th<sub>2</sub>, Th<sub>17</sub> or T<sub>reg</sub>

The structure of the mucosal immune system determines the efficiency of responses to food, pathogen and commensal microbiota.





MHC II  
CD16  
MIL11



CD8  
CD4  
MIL11

Day 0

Day 28



# Stages in the development of the mucosal immune system of the pig

1. Rudimentary Peyers patches, essentially no mucosal T cells. Limited B-cell repertoire. Few dendritic cells but MHCII on endothelial cells. The newborn pig.

2. Non-specific expansion of B-cells and Peyers patches. Appearance of early, activated T-cells, influx of MHCII+ cells. 1 days to 2 weeks.

3. Appearance of CD4+ T cells. 2 weeks to 4 weeks.

4. Antigen-specific B-cell responses. Appearance of CD8+ T cells. 4 weeks to 6 weeks.



Most of this expansion of the adaptive immune system is driven by microbiota.

Colonisation of newborn, gnotobiotic piglets with defined microbiota results in expansion of the mucosal immune system which replicates, approximately, that in conventional pigs.

Inman et al, 2012 PLoS One; Laycock et al, 2012 Vet Immunol Immunopathol

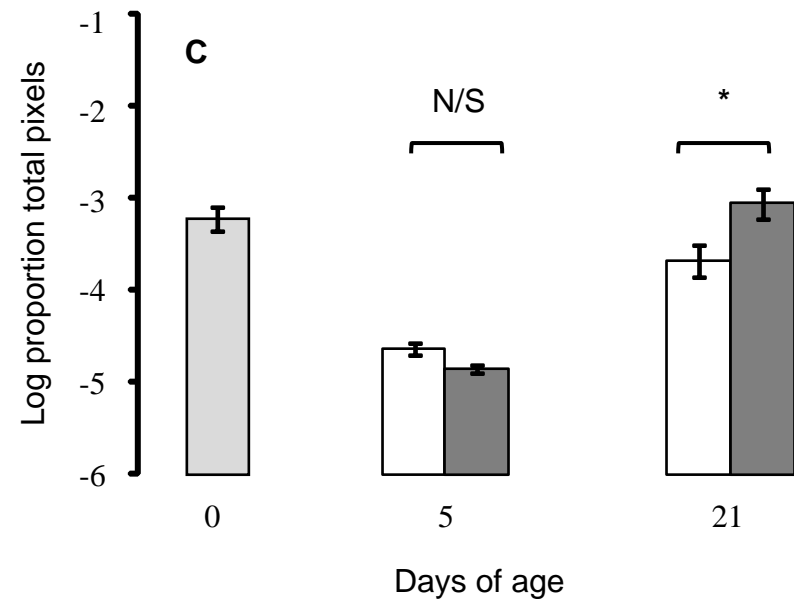
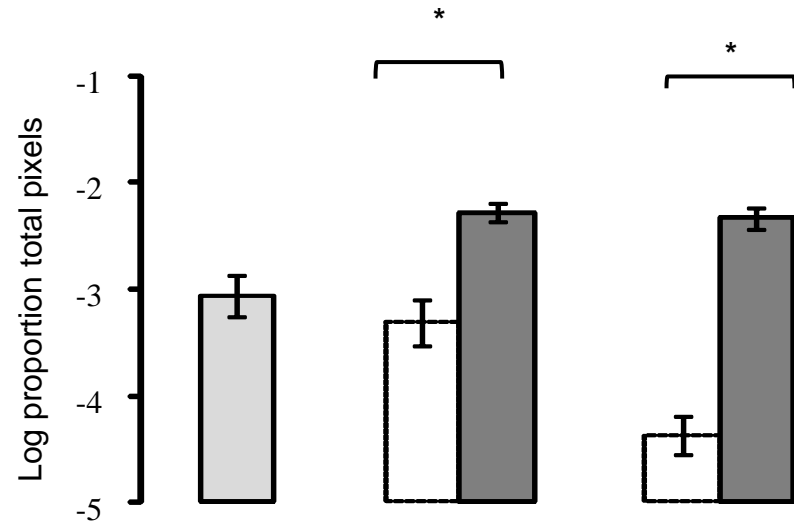




**SIRP $\alpha^+$   
CD11R1-  
CD16-  
MHCII+**

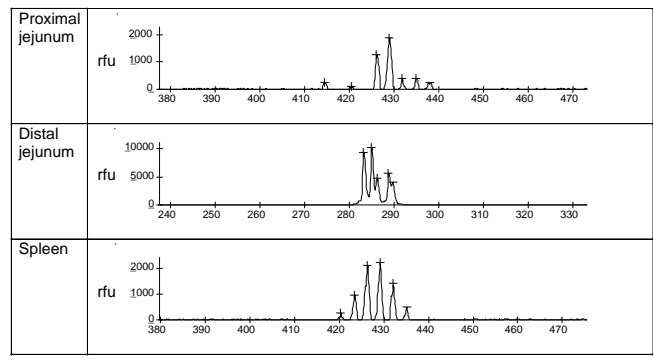
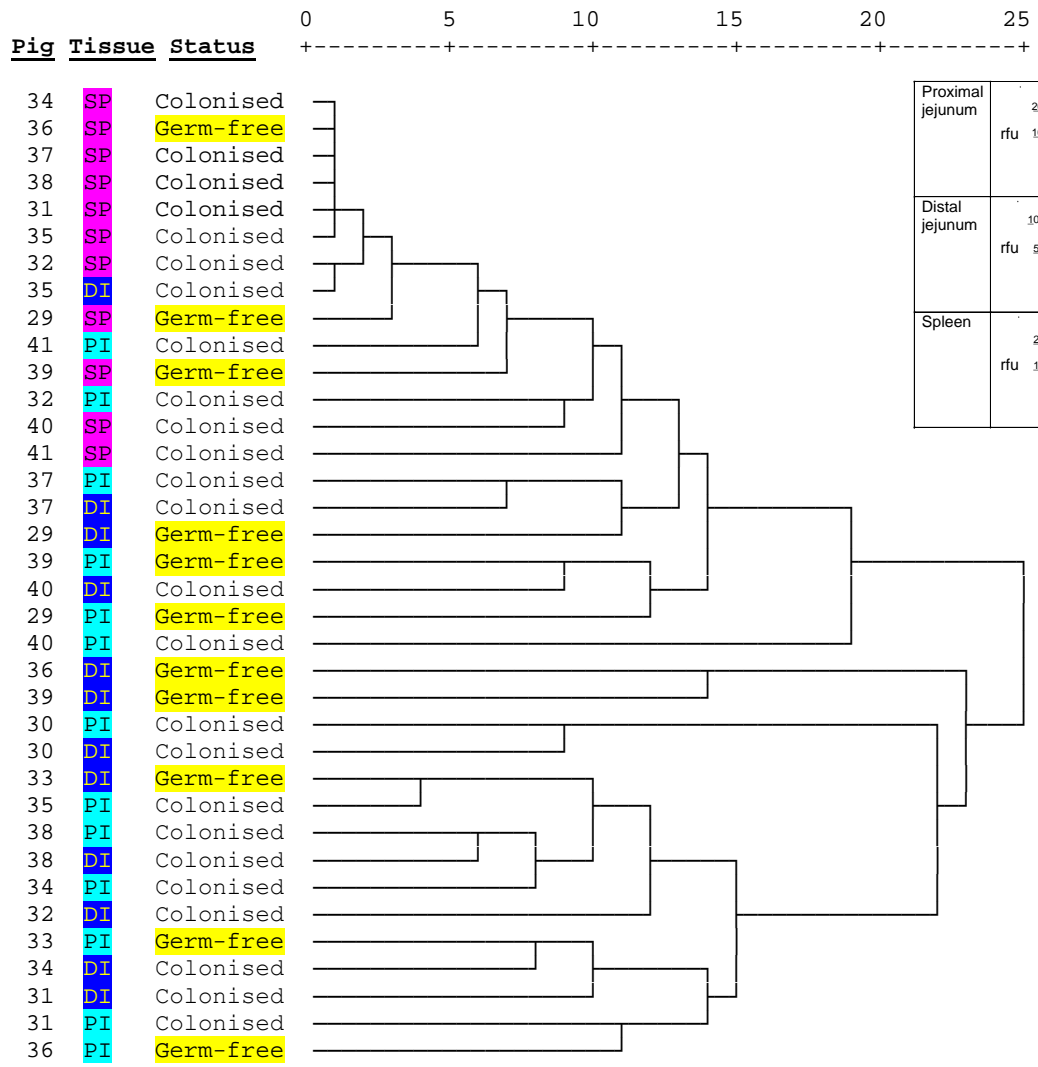
Defined colonisation  
of gnotobiotic piglets  
expands mucosal  
SIRP $\alpha^+$  DC first,  
then CD4 $^+$  T-cells  
(Inman, 2012, PLoS  
One)

 Colonised  
 Germ-free



# T-cell receptor repertoire is not skewed in fully MHC-inbred, colonised, gnotobiotic piglets

Rescaled Distance Cluster Combine



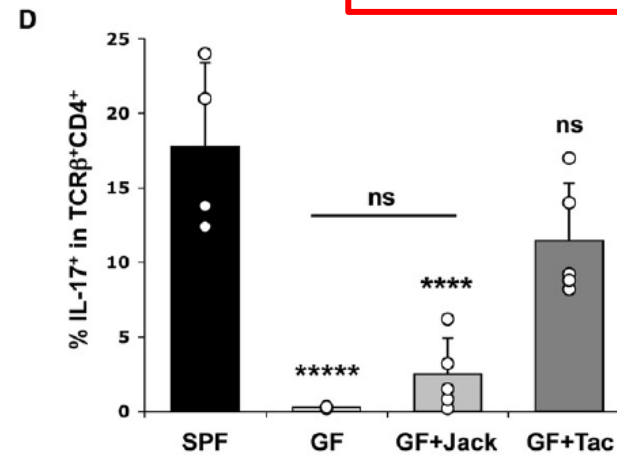
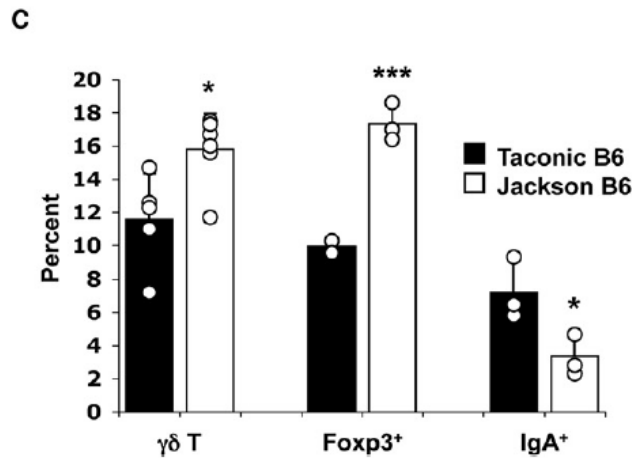
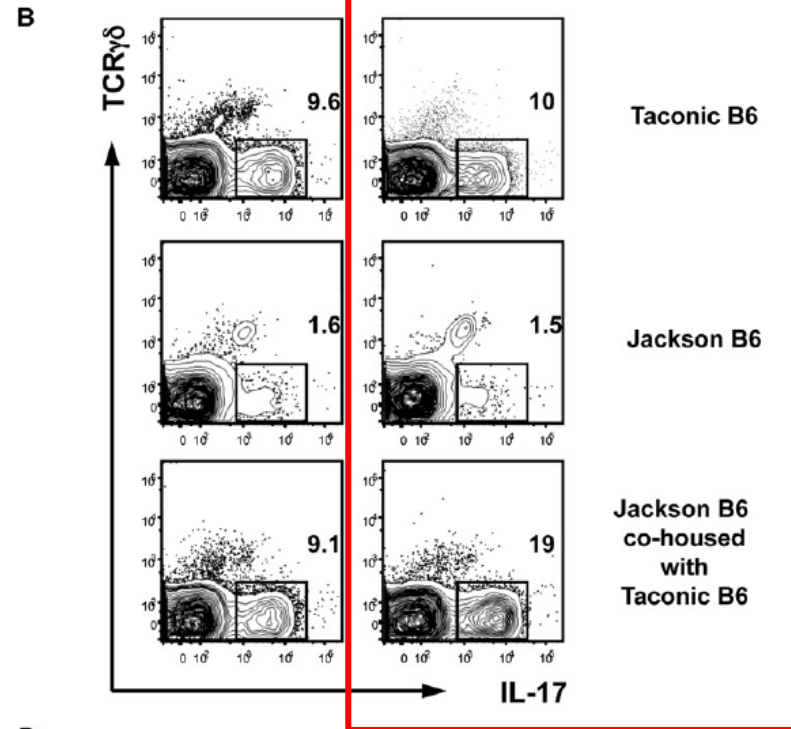
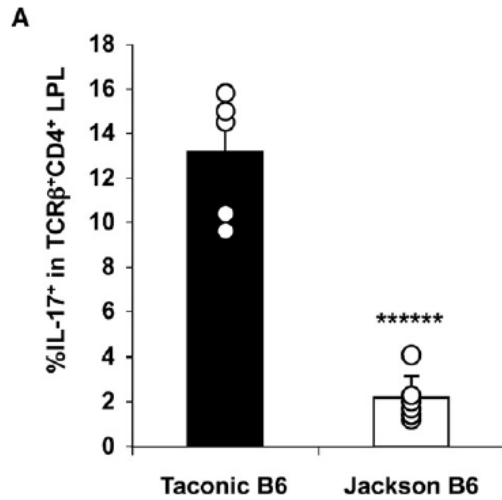
Inman et al, 2012, PLoS One



Are studies in gnotobiotic mice and piglets relevant to anything that looks vaguely like the real thing?



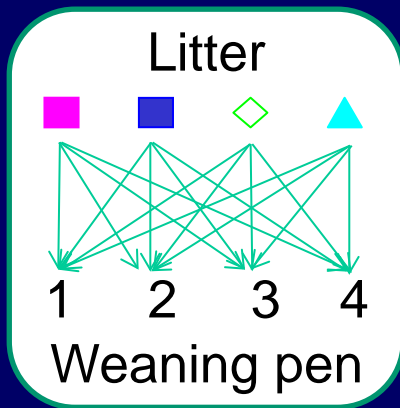
# Is it important? Genetically identical mice from different suppliers have different immune systems dependant on their microbiota





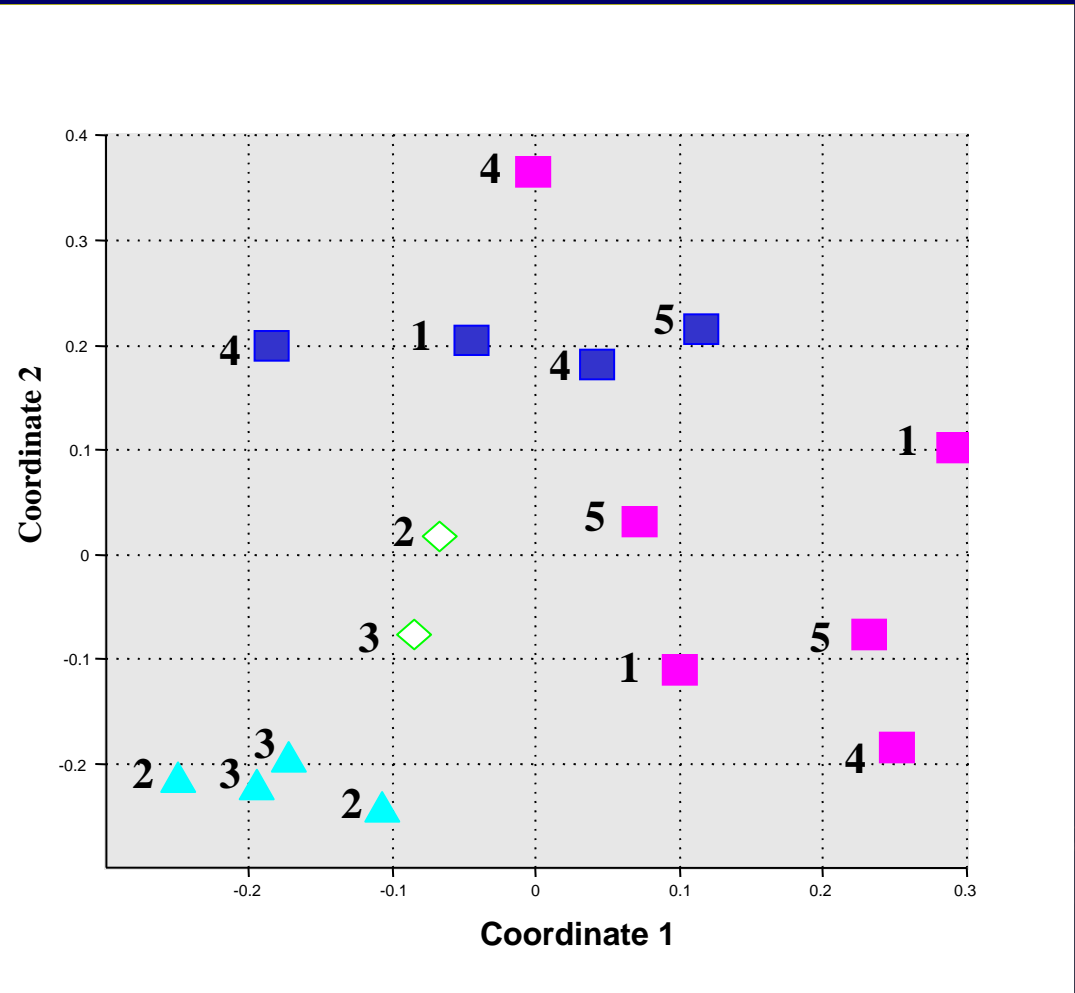
# Is it important? Microbiota is 'imprinted' before weaning in neonatal piglets

4 different litters (weaning + 21 days)



Non-metric,  
multidimensional scaling  
analysis

Tighter clustering for  
siblings than pen mates



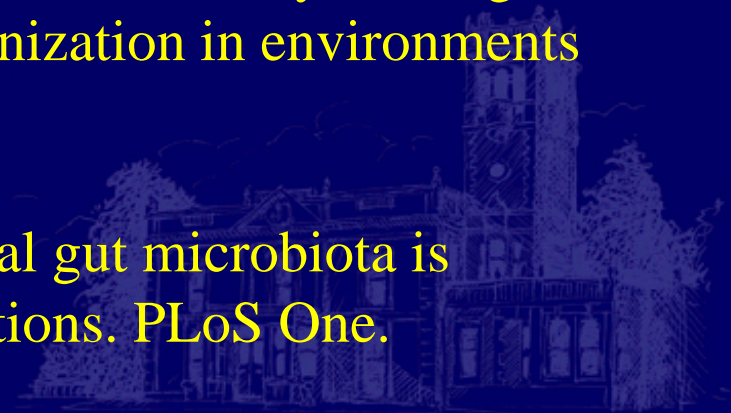
# Is it important? Manipulation of the microbiota and the mucosal immune system by rearing macro-environment (GUTWEAN)

Mulder et al (2009). Environmentally-acquired bacteria influence microbial diversity and natural innate immune responses at gut surfaces. *BMC Biology* (7).

Inman et al (2010). Rearing environment affects development of the immune system in neonates. *Clinical and Experimental Immunology* 160: 431-439

Mulder et al (2011) Restricting microbial exposure in early life negates the immune benefits associated with gut colonization in environments of high microbial diversity. *PLoS One*.

Schmidt et al, (2011) Establishment of normal gut microbiota is compromised under excessive hygiene conditions. *PLoS One*.



# Is it important? Variation between commercial farms in development of the immune system may also be attributable to farm-specific microbiota

Appearance of memory/effector T-cells (CD4+CD8+) with age (Griksen, Banks, Haverson, Bailey)

Tests of Between-Subjects Effects

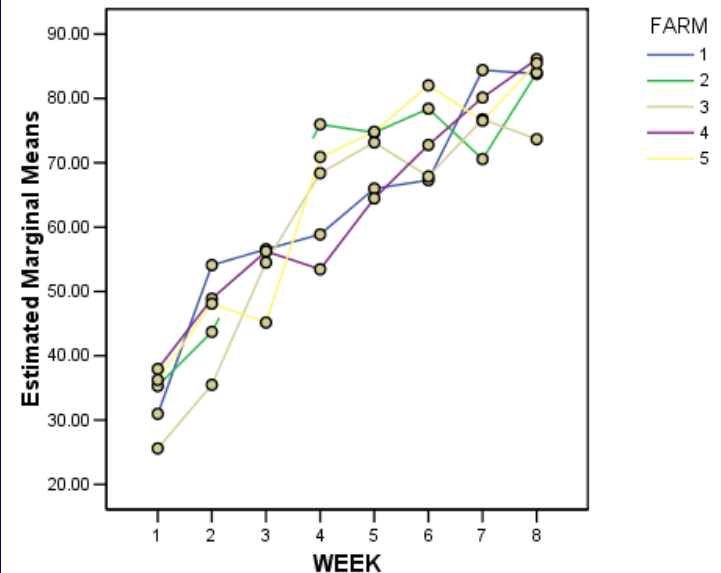
Dependent Variable: CD4+CD8+ / All CD4+

Source	Type IV Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	145383.169 <sup>a</sup>	38	3825.873	26.416	.000
Intercept	1872181.253	1	1872181.253	12926.805	.000
WEEK	121856.891 <sup>b</sup>	7	17408.127	120.197	.000
FARM	462.841 <sup>b</sup>	4	115.710	.799	.526
WEEK * FARM	14587.177	27	540.266	3.730	.000
Error	68504.300	473	144.829		
Total	2297958.454	512			
Corrected Total	213887.469	511			

a. R Squared = .680 (Adjusted R Squared = .654)

b. The Type IV testable hypothesis is not unique.

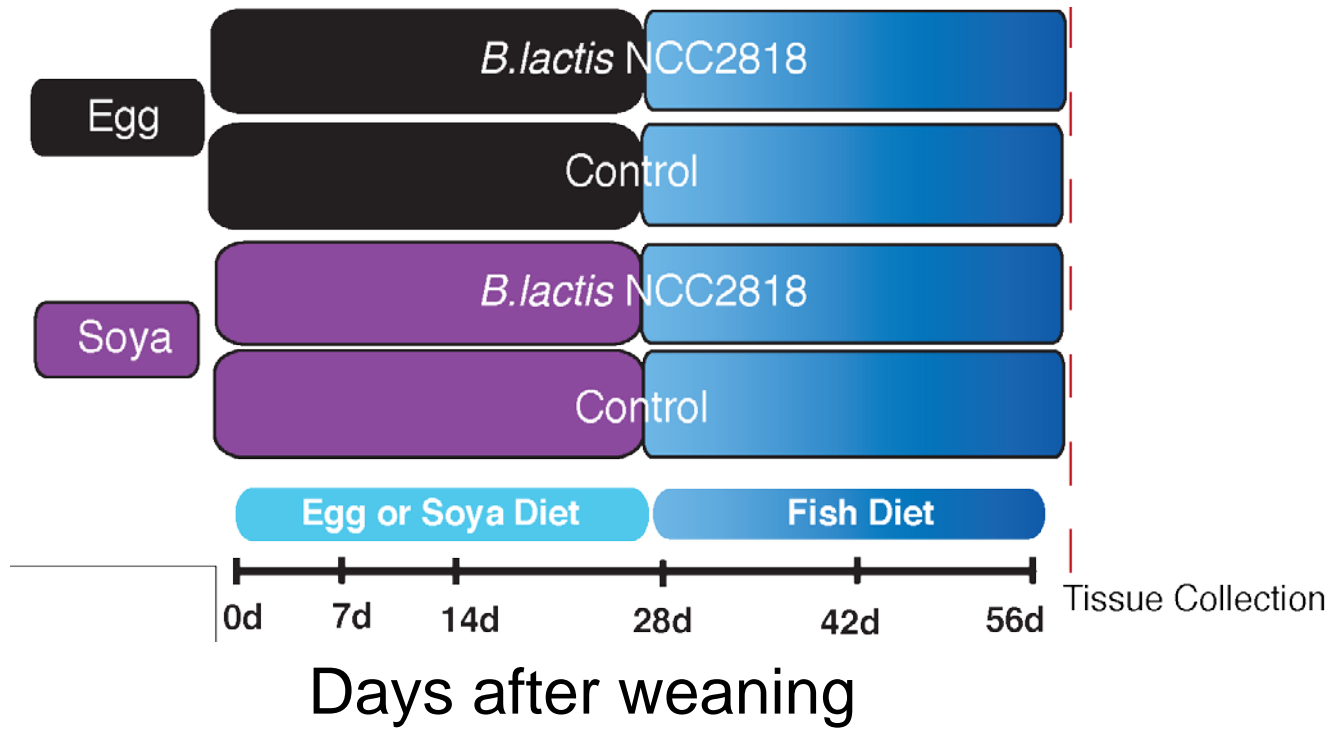
Estimated Marginal Means of CD4+CD8+ / All CD4+



Non-estimable means are not plotted

Can we manipulate this directly in conventional animals with complex, highly variable microbiota?

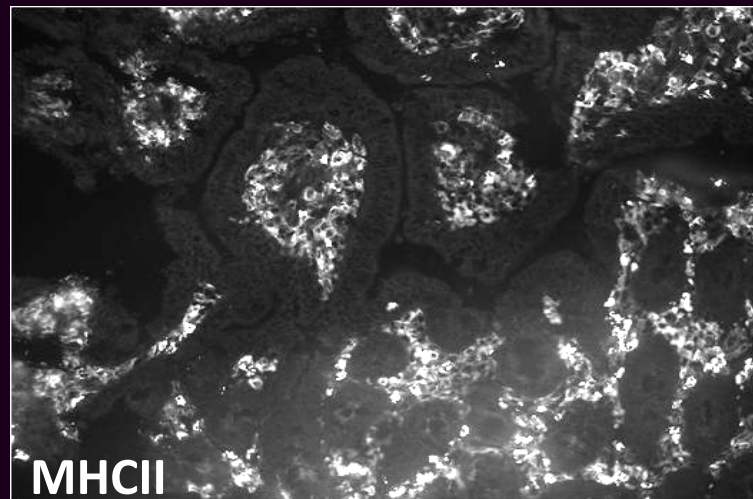
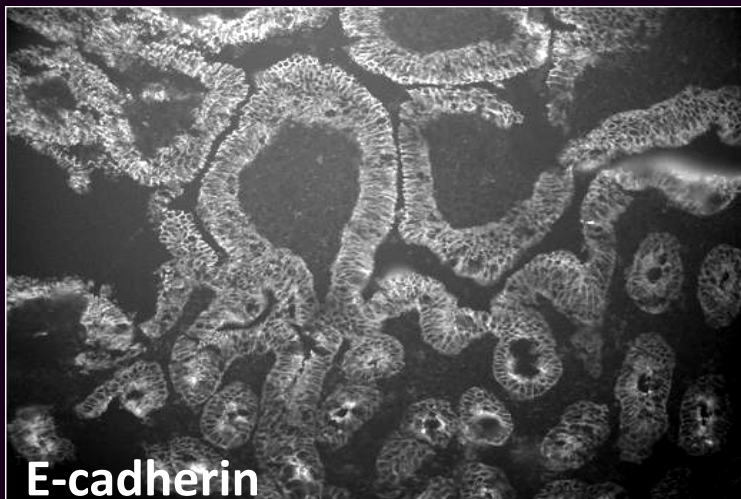
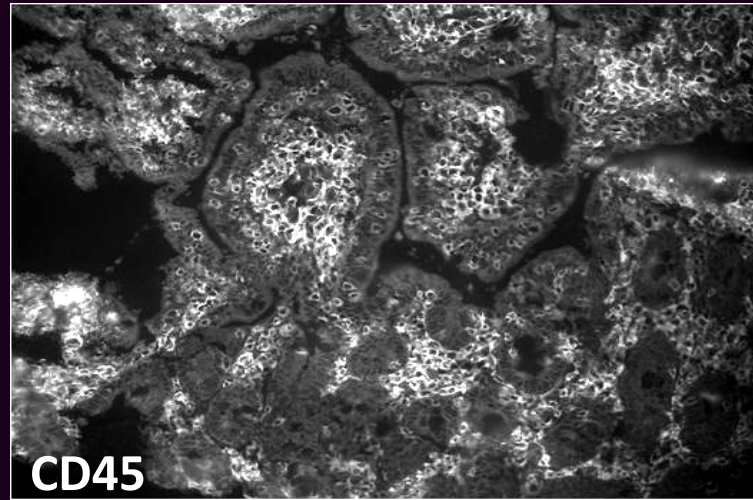
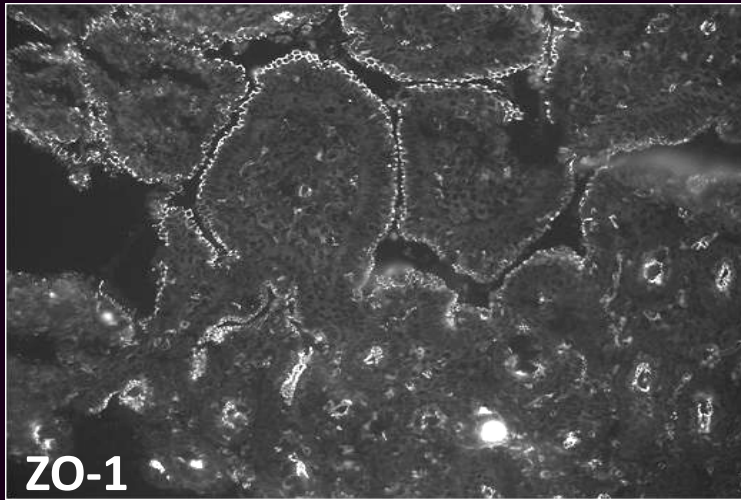




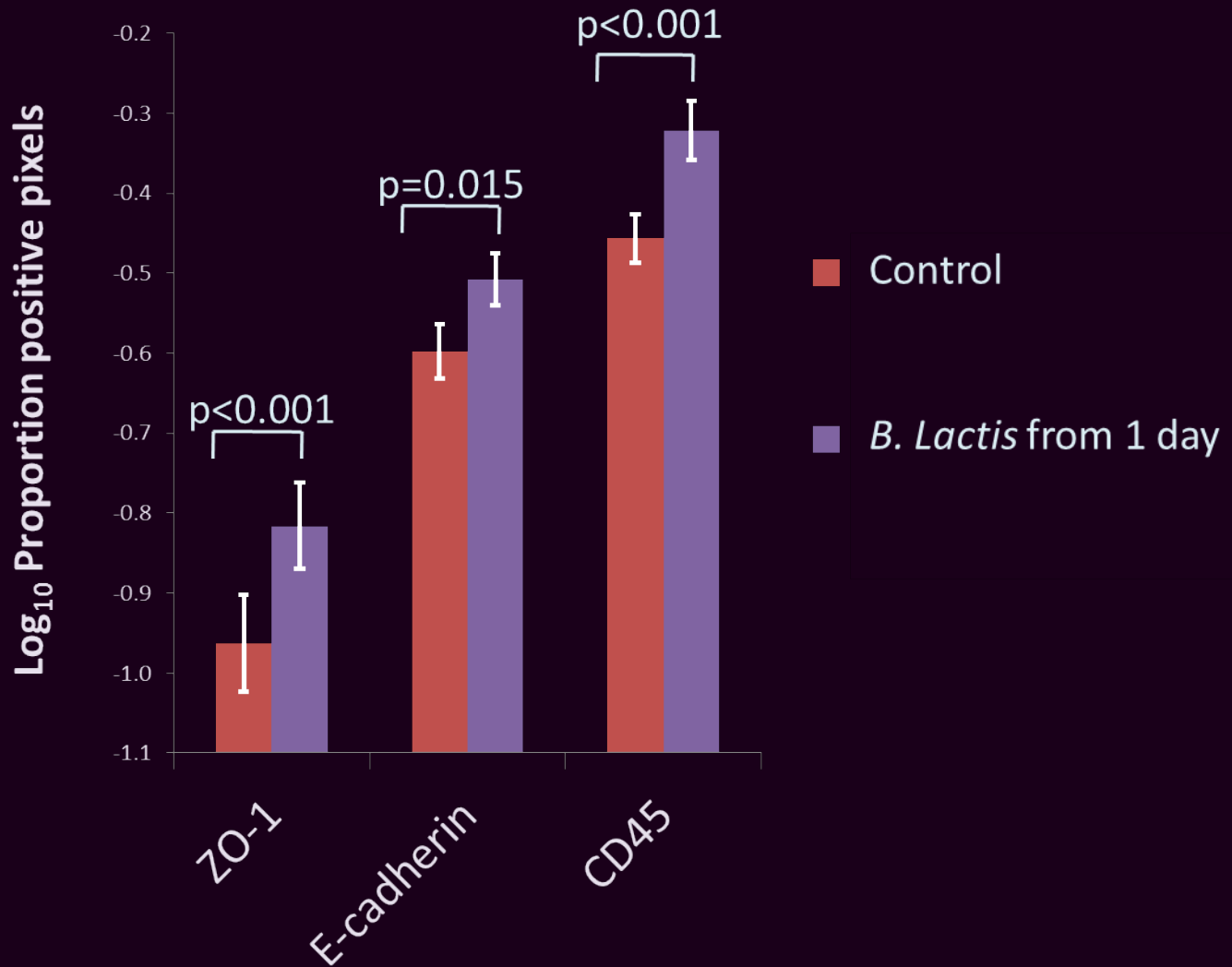
Merrifield, Lewis, et al, 2013, Gut (in press)



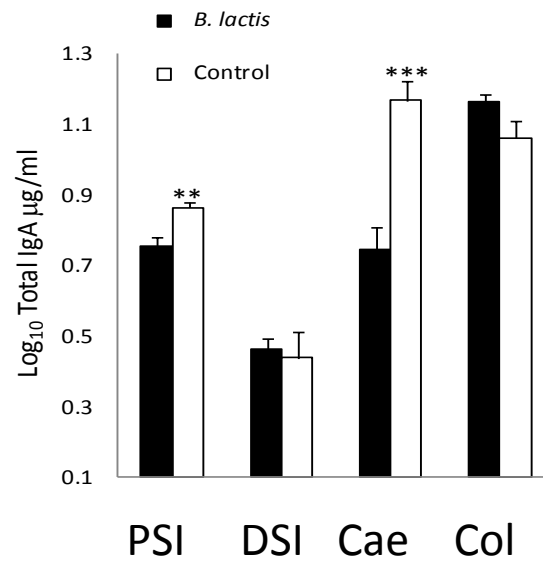
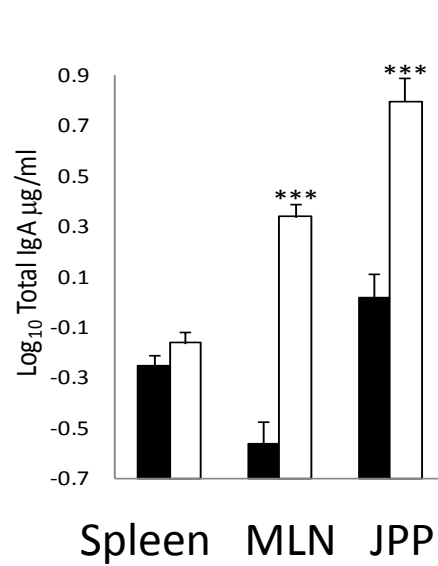
# Intestinal Barrier Function



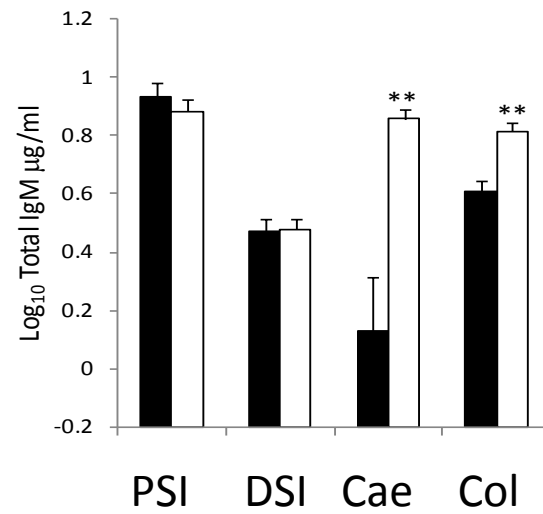
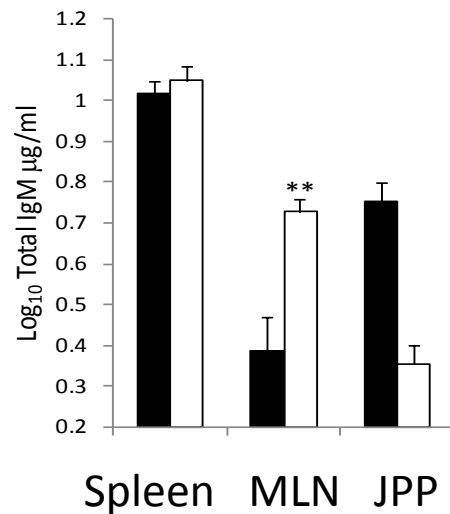
# Increased epithelial barrier function after 'probiotic' administration



# Decreased local IgA and IgM synthesis after 'probiotic' administration



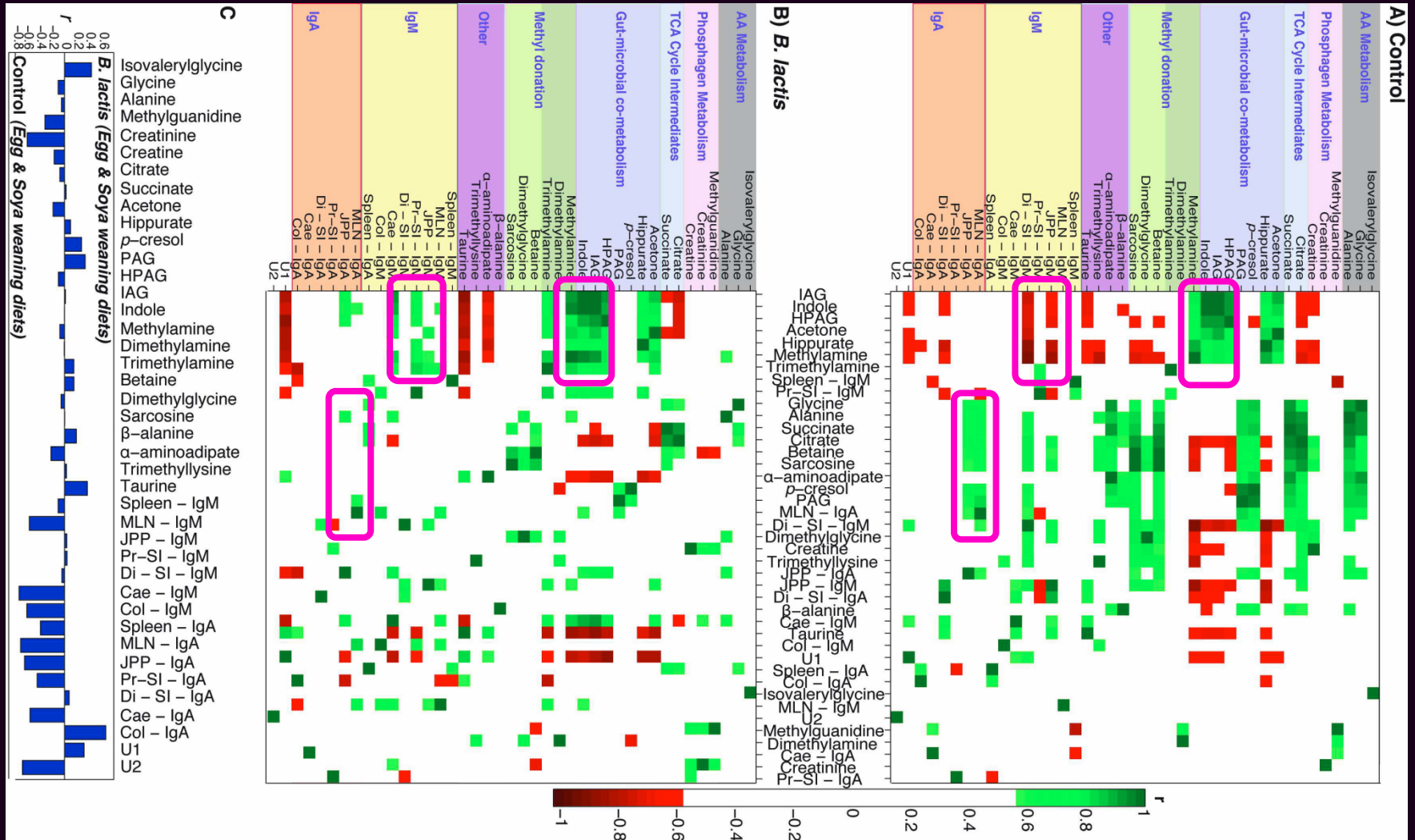
MLN – mesenteric lymph node  
JPP – jejunal Peyers patch  
PSI – upper jejunum  
DSI – lower jejunum  
Cae – caecum  
Col - colon



(Lewis et al, in press, BJJ)



# Probiotic supplementation changes the structure of immuno-metabolic correlations.



***B. lactis***

**Control**

A

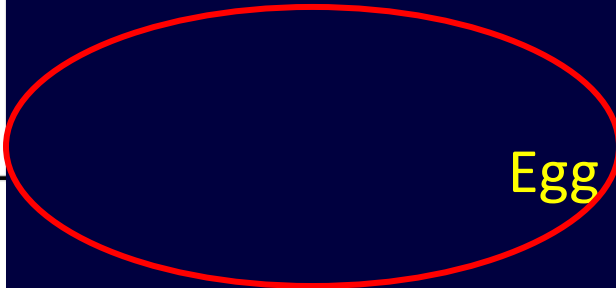
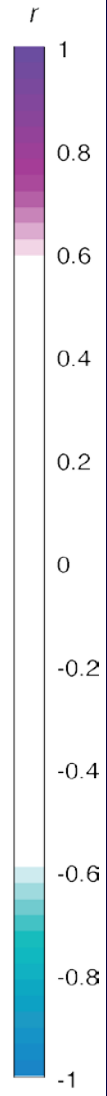
Q<sup>2</sup>Y: 0.59  
R<sup>2</sup>Y: 0.88  
R<sup>2</sup>X: 0.23

Spleen – IgM  
Spleen – IgA  
MLN – IgM  
MLN – IgA  
Pr-SI – IgM  
Pr-SI – IgA  
Di – SI – IgM  
Di – SI – IgA  
JPP – IgM  
JPP – IgA  
Cae – IgM  
Cae – IgA  
Col – IgM  
Col – IgA

Originally weaned  
onto  
**Soya V Egg**

Soya

+ *B. lactis*



Egg

- *B. lactis*

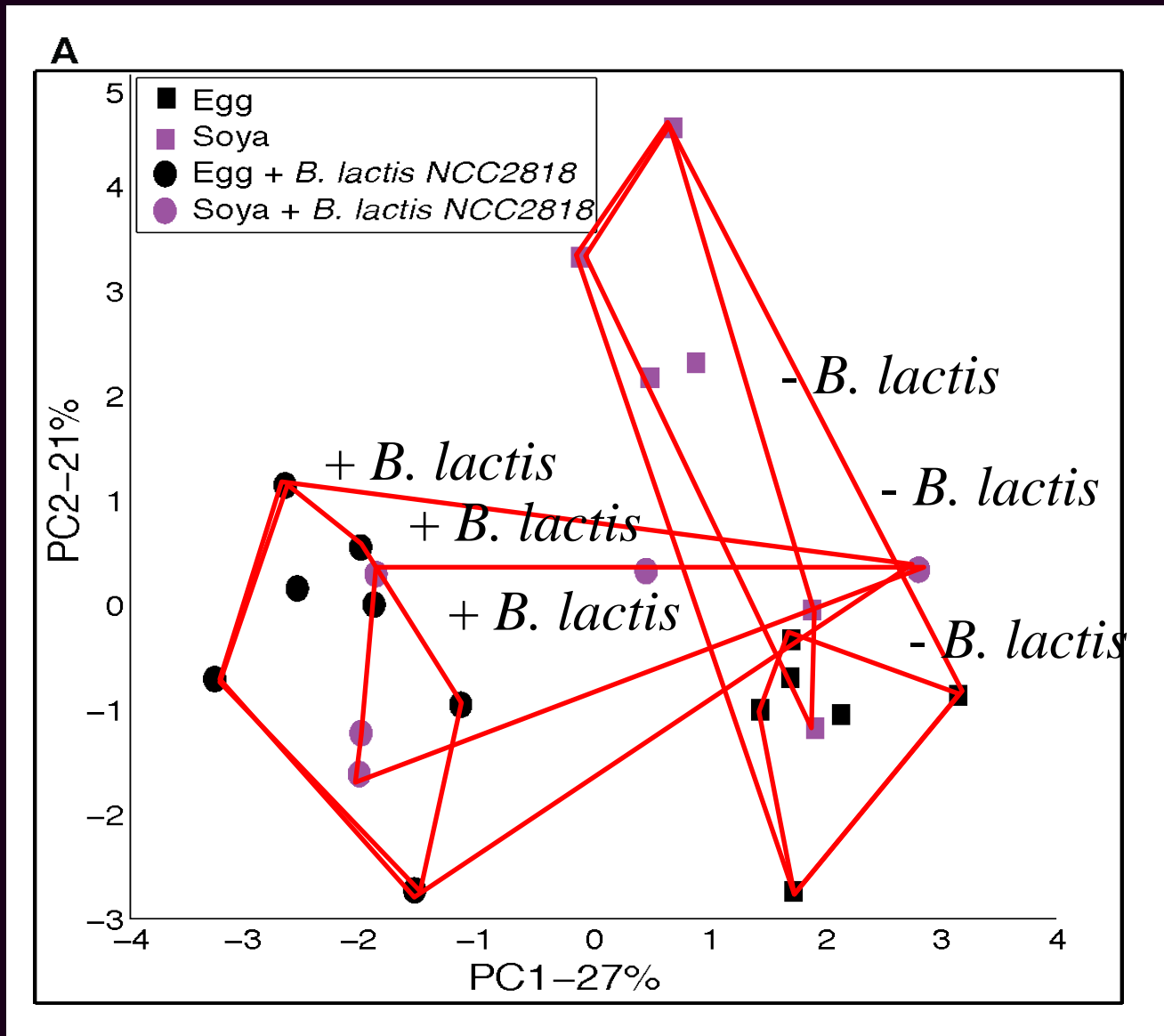
Mucosal synthesis of immunoglobulins is linked both to probiotic and to weaning diet.

The effect of probiotic is different between diets.

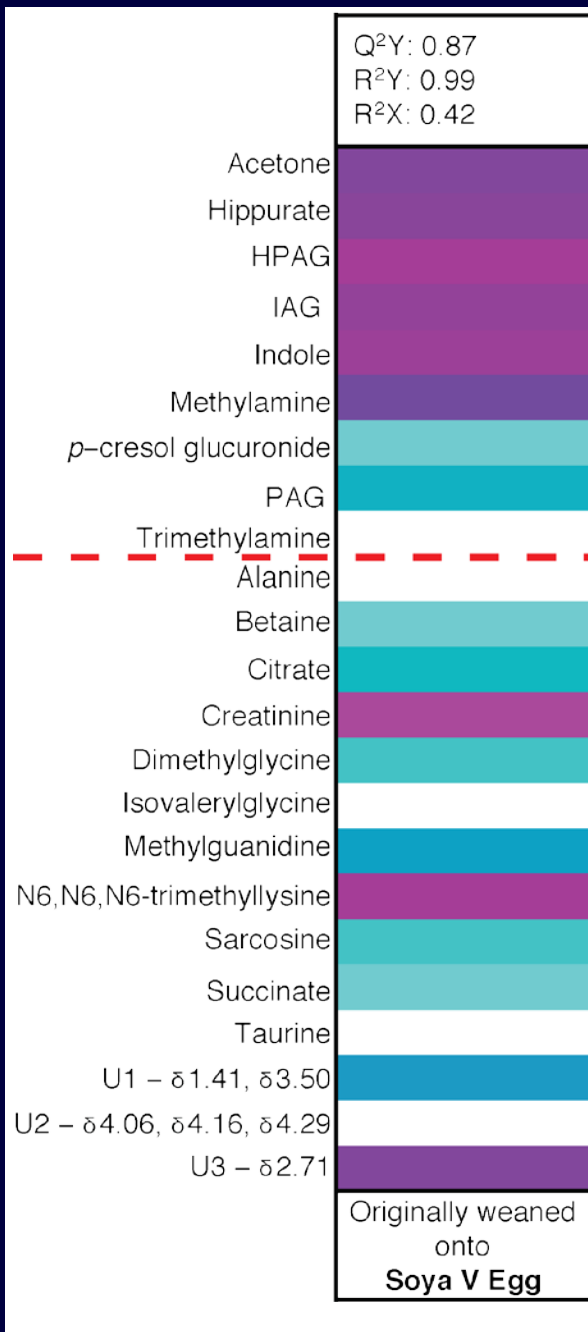
Merrifield et al, Gut, in press.

# *B. lactis*, diet and Ig synthesis

Merrifield et al, Gut, in press



A



Soya

+ *B. lactis*

The effect of probiotic on urinary metabolites also differs between diets.

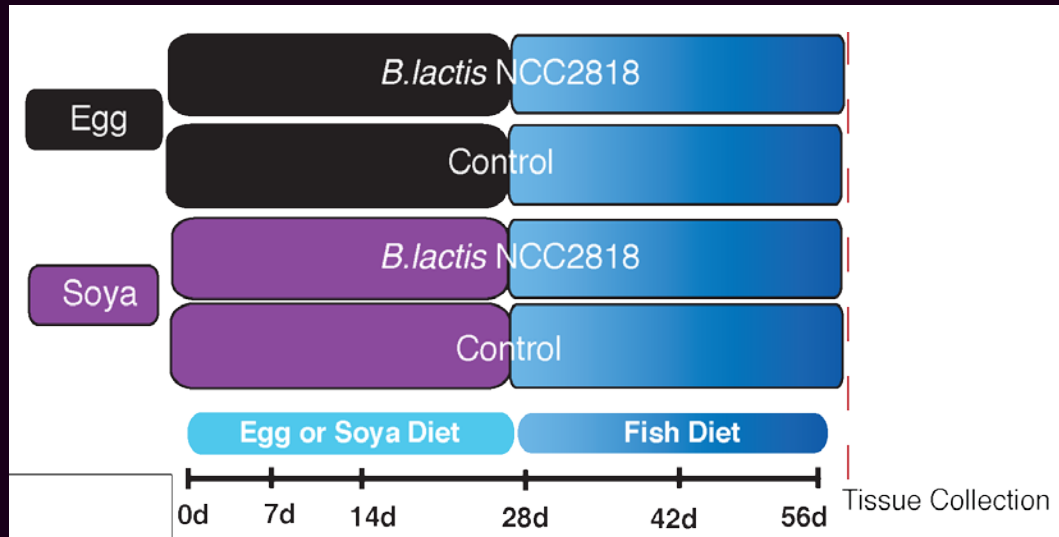
Merrifield et al, Gut, in press.

Egg

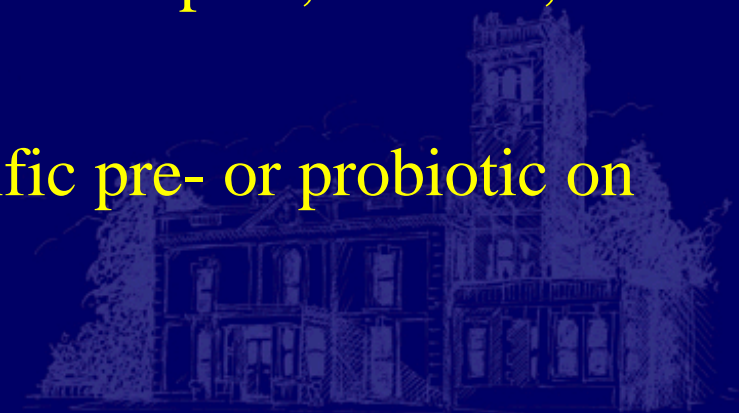
- *B. lactis*

The effects of this probiotic on metabolic and immune function differ between weaning diets:

- The effect is far more obvious on piglets weaned onto egg than those weaned onto soya.
- This is despite the fact that egg and soya were fed for only 4 weeks after weaning.
- At time of sampling (12 weeks old), all piglets had been on the same diet, based on fishmeal, for 4 weeks.



1. Microbiota drives establishment of the architecture of the mucosal immune system.
2. (Different patterns of colonisation, as a consequence of different rearing environments, drive development of different mucosal immune systems.)
3. This can be manipulated by diet and/or probiotic (and/or prebiotic) in early life
4. Birth and weaning seem to be times of particular susceptibility to changes.
5. However, the patterns of change are complex, interact, and are affected by multiple factors.
6. At present, the effects of any specific pre- or probiotic on specific farms are hard to predict.



### Bristol University

Mick Bailey	Chris Stokes
Paul Bland	Karin Haverson
Tom Humphrey	Frieda Jurgenson
Steve Cose	Bevis Miller
Ross Harley	<b>Zoe Christoforidou</b>
<b>Charlotte Inman</b>	<b>Marie Lewis</b>

### Paniotis Turlomousis

Jenny Bailey	Chelsea Hicks
Phil Jones	Cecilia Harris
Christine Whiting	Steve Wilson
Philippa Lait	<b>Georgina Laycock</b>
Martin Kenny	Ben Bradley
<b>Sakon Singha</b>	Andy Weale
Anusha Edwards	Martin Birchall
Louisa Rees	Emma Barker
John Tarleton	

### Wageningen University

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	Sergei Konstantinov

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Jeremy Morgan	Adrian Smith
Mark Stevens	Pauline Vandiemmen

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<b>Claire Merrifield</b>	Olivier Cloarec

### Roslin Institute

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Mary Clapperton	Alan Archibald

### Aberdeen University

Denise Kelly	Imke Mulder
Bettina Schmidt	

### Nestec

Adrian Zuercher	Swantje Duncker
Annick Mercenier	

### J.S.R.

Annabelle Hoste