Bacterial Relationships in Enteric Disease

August 4th, 2012

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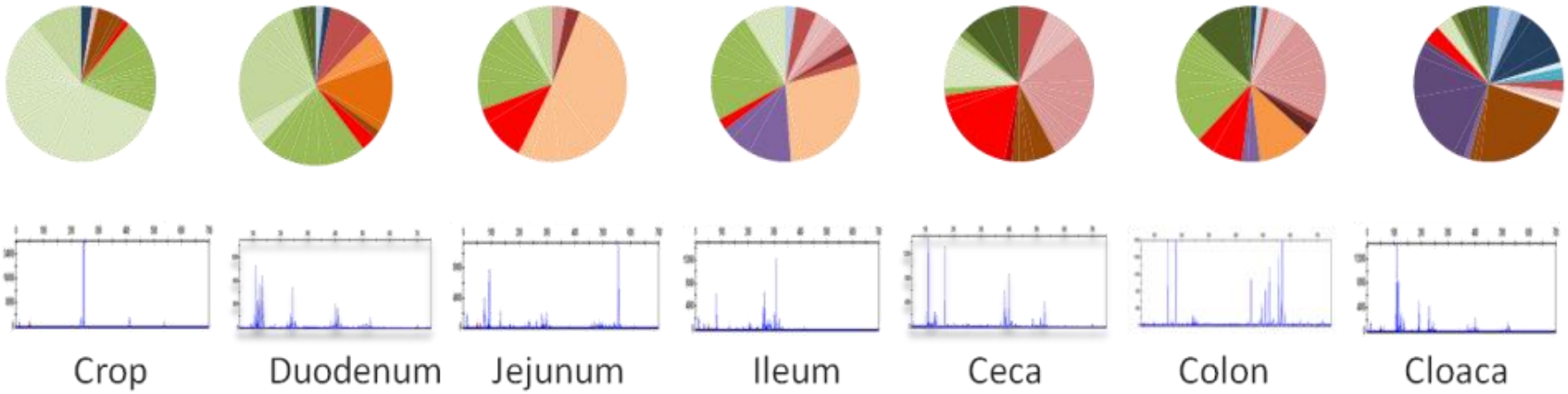
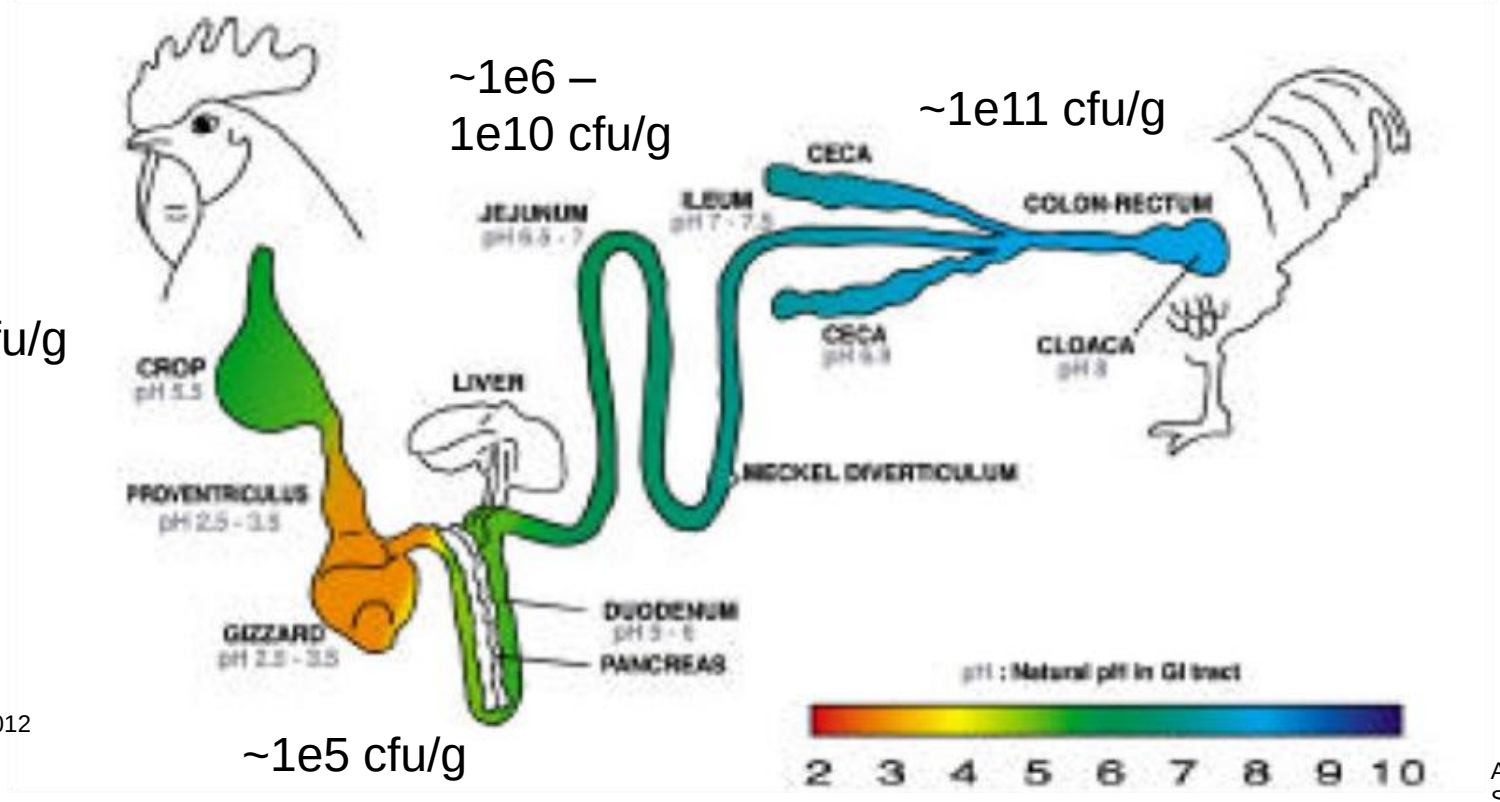


~1e6 – 1e10 cfu/g

~1e11 cfu/g

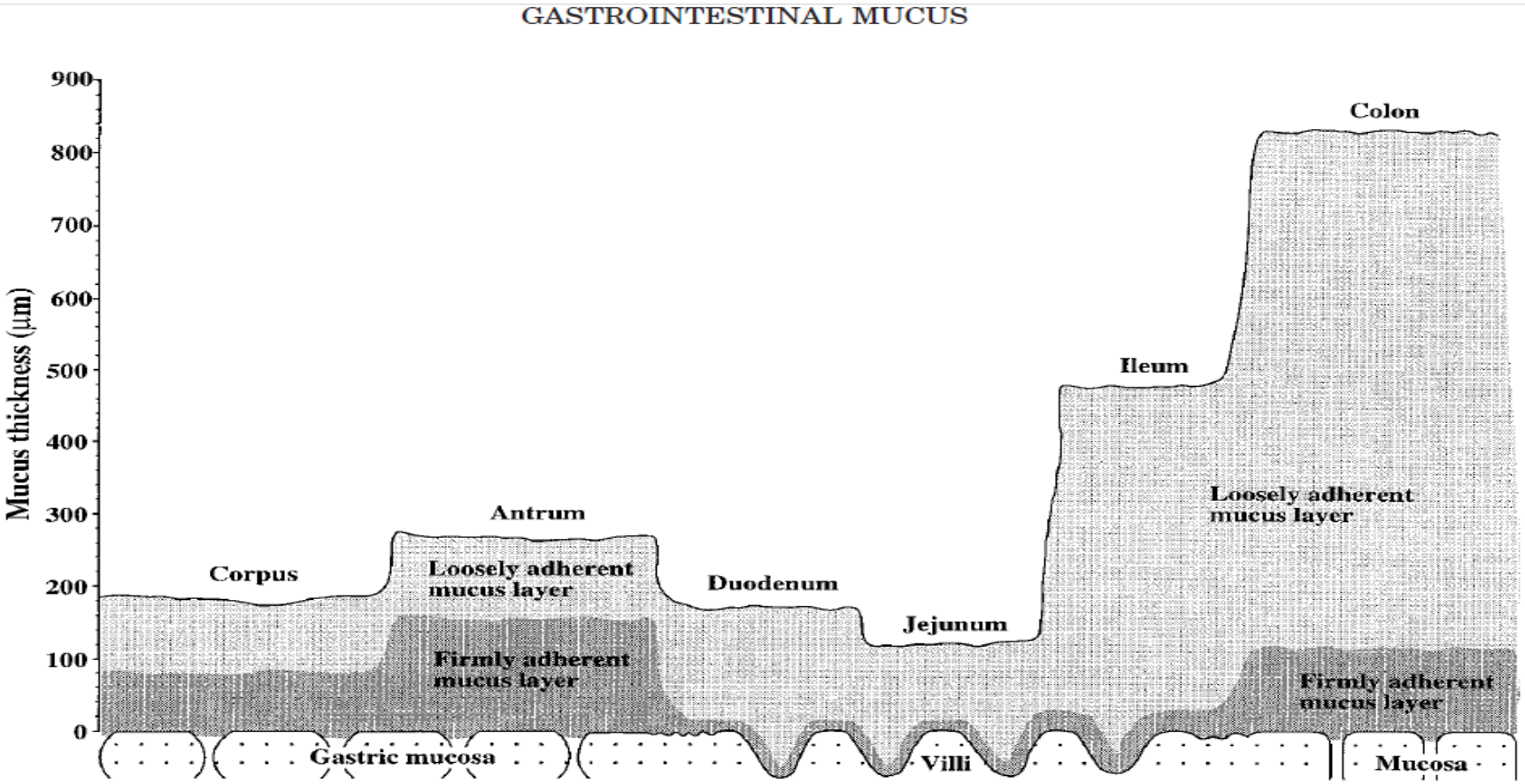
~1e10 cfu/g



~1e5 cfu/g

Adapted from Siragusa *et al.* 2010

Mucosa differences along the GIT

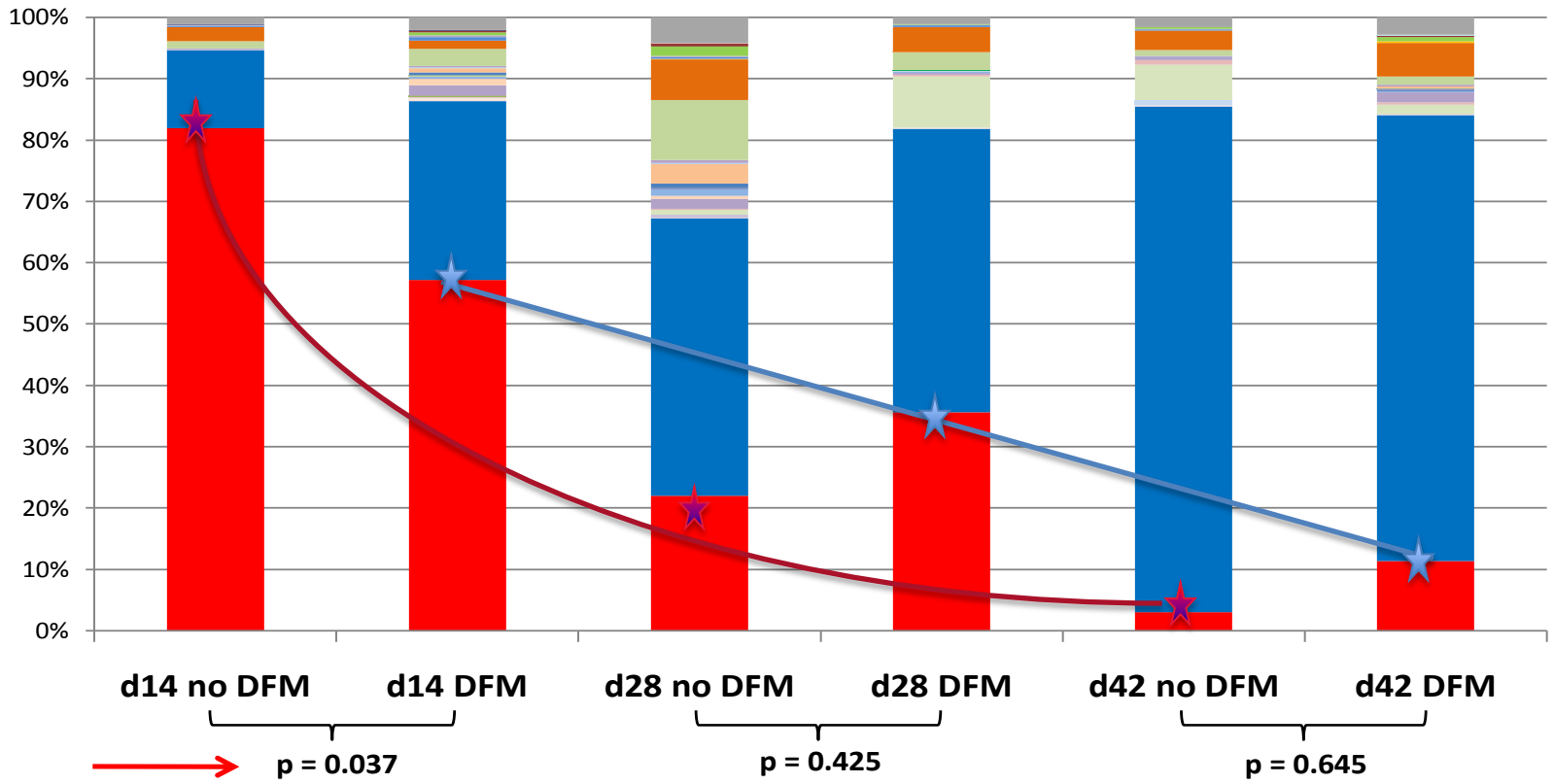


Mean mucus thickness (μm)

Total	189 ± 11	274 ± 41	170 ± 38	123 ± 4	480 ± 47	830 ± 110
Firmly Adherent	80 ± 5	154 ± 16	16 ± 3	15 ± 2	29 ± 8	116 ± 51
Loosely Adherent	109 ± 12	120 ± 38	154 ± 39	108 ± 5	447 ± 47	714 ± 109

Atmua *et al.* 2001

Succession of gut microbiota in healthy broiler chickens



Rough overview of major GIT microbes in the intestine

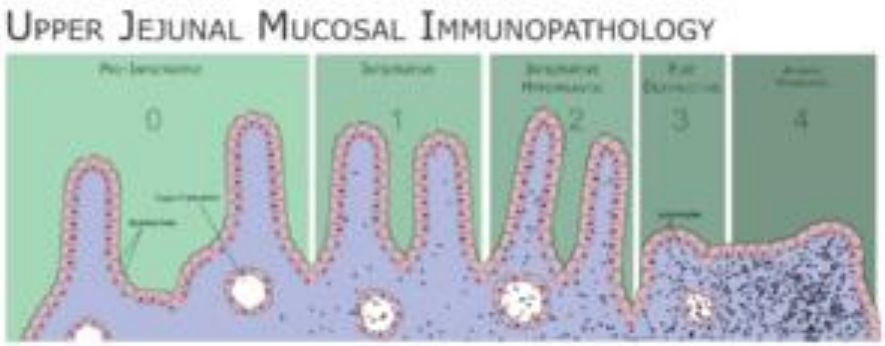
Bacterial species	Beneficial	Harmful	Growth Rate	Degrades	Produces	Sporeformer
LAB	VFA (eg group D *Streptococcus*)	some (eg group A *Streptococcus*)	intermediate	CHO	lactate	no
Enterococcus	VFA, immuno-modulation (*E. facium)*	eg *E. cecorum* (antibiotic resistence)	intermediate	CHO	lactate	no
Lactobacillus	Adherent, Immu-no modulation, *E. coli* antagonist	-	intermediate	CHO	lactate	no
Bifidobacterium	Adherent in SI, VFA	-	slow	lactate	butyrate	no
Propionibacterium	VFA	-	slow	CHO	propionate	no
E. coli	if non-virulent (*E. coli* Nissle)	APEC (adherent, toxins)	fast	CHO	acetate, LPS	no
Clostridium	C. cluster IV	-		soluble fiber	butyrate	yes
	C. cluster XIVa	-		insoluble fiber	butyrate	yes
	-	C. cluster I (*C. perfringens*)	fast	mucus, proteins	entero-toxins, H_2S	yes
Bacteroides, Prevotella	Neutral		slow	fiber	acetate, LPS	no

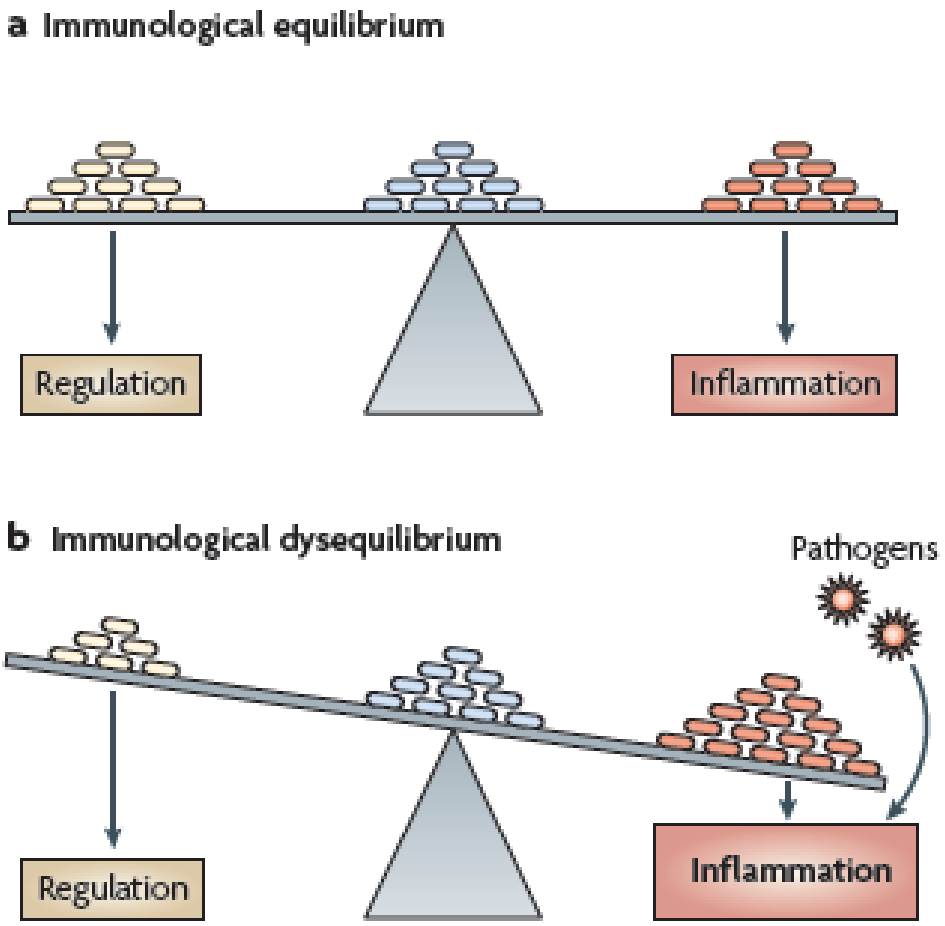
A balanced immune system is necessary for healthy birds

Inflammation is needed to fight pathogens

Excessive inflammation decreases performance

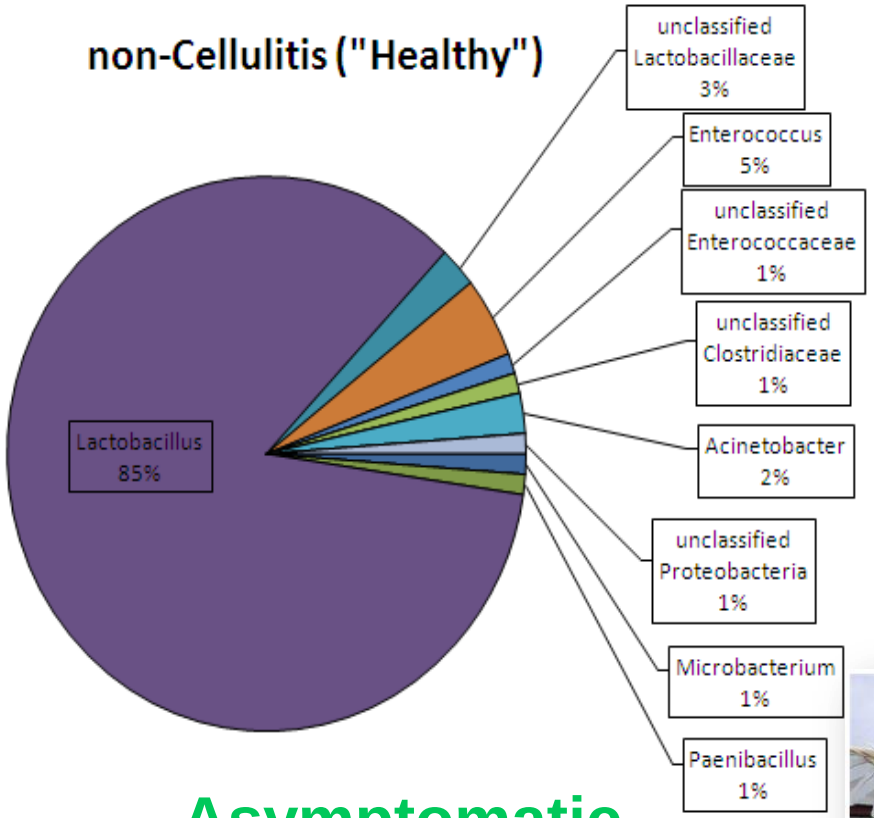
Direct-fed microbials (DFM) can be used to influence the immune system

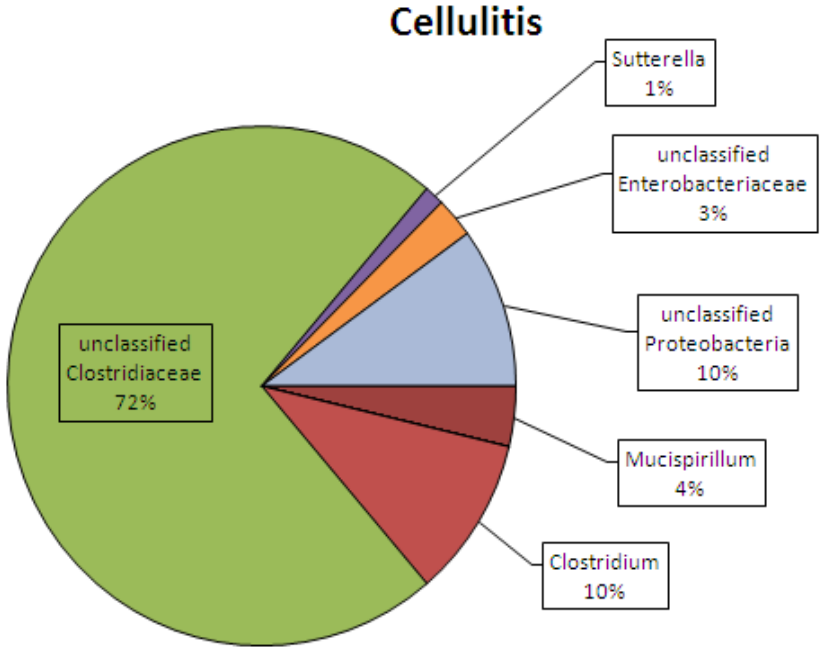




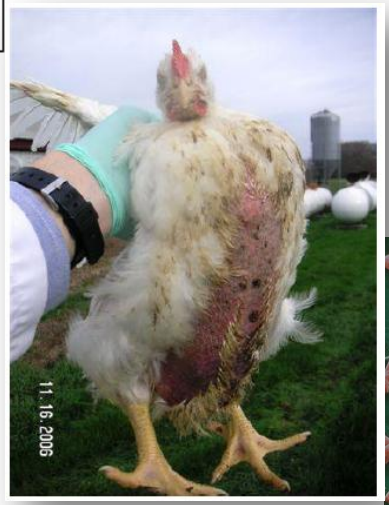
Nature Reviews Immunology, 2009

GD in Broiler Chickens





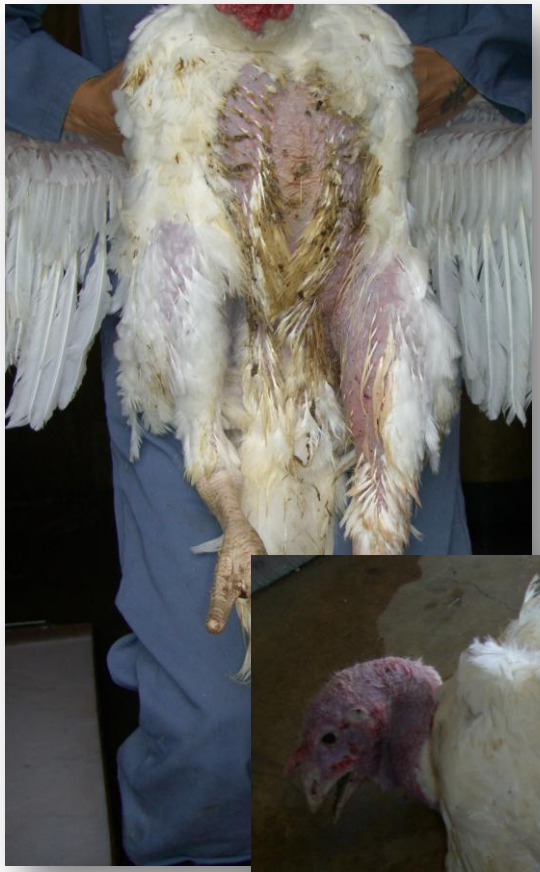
Asymptomatic

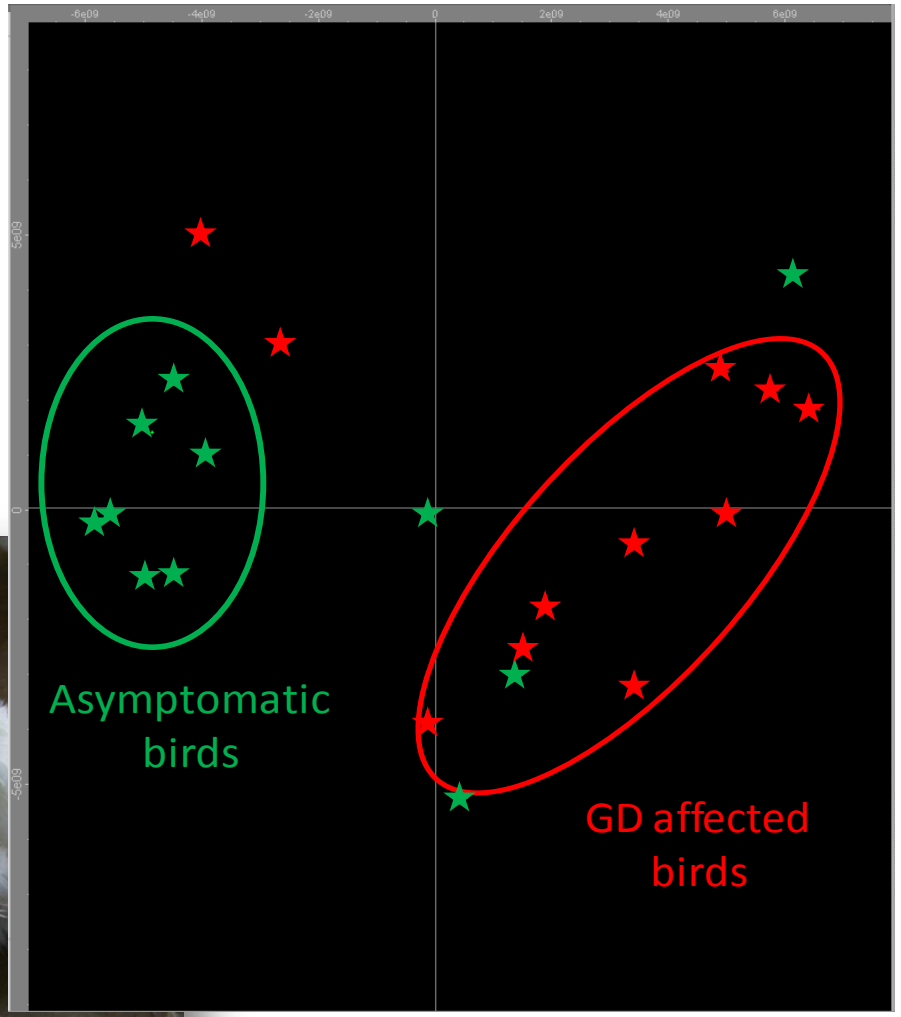


GD Symptomatic

Hibberd *et* al., 2008

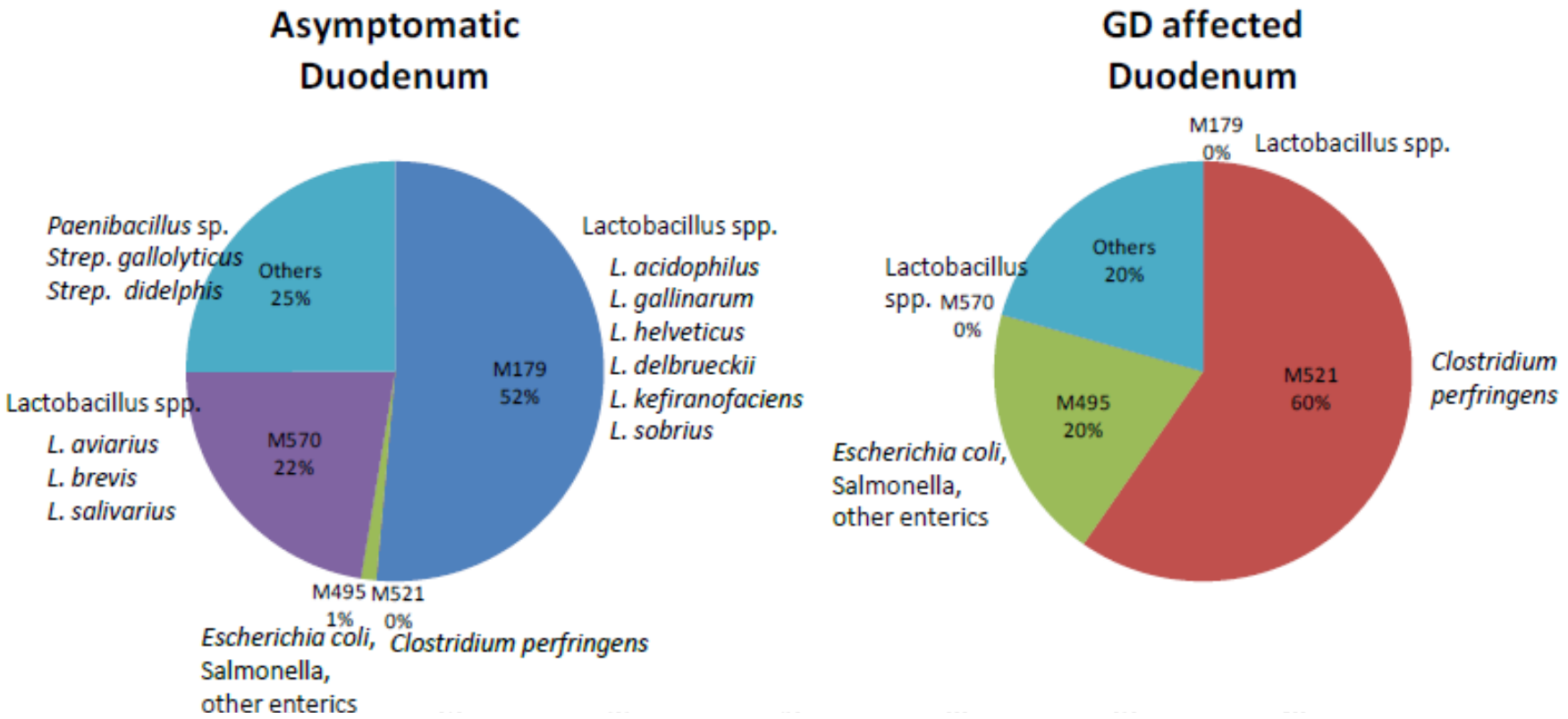
Ileum mucosa microbiota of 11 live capture birds
Principle Component Analysis

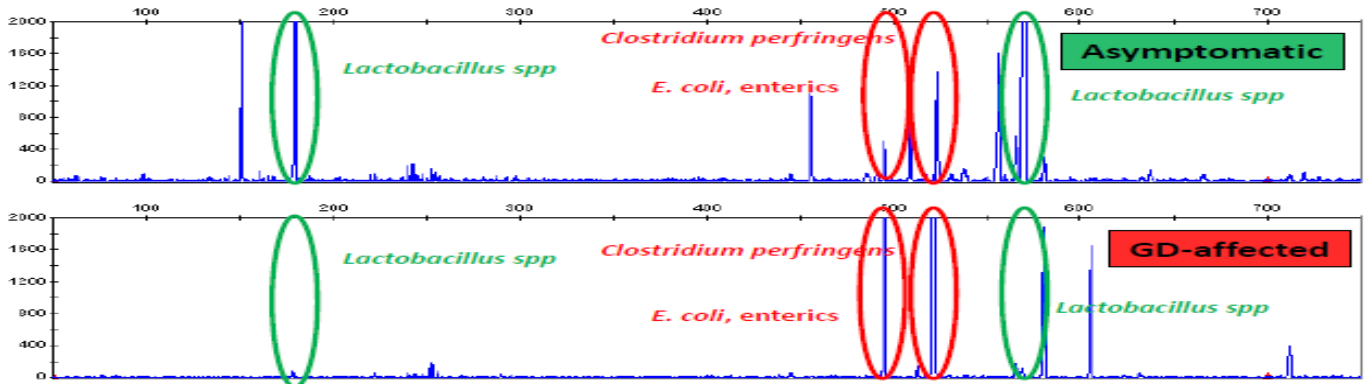




Early *et al.*, 2006

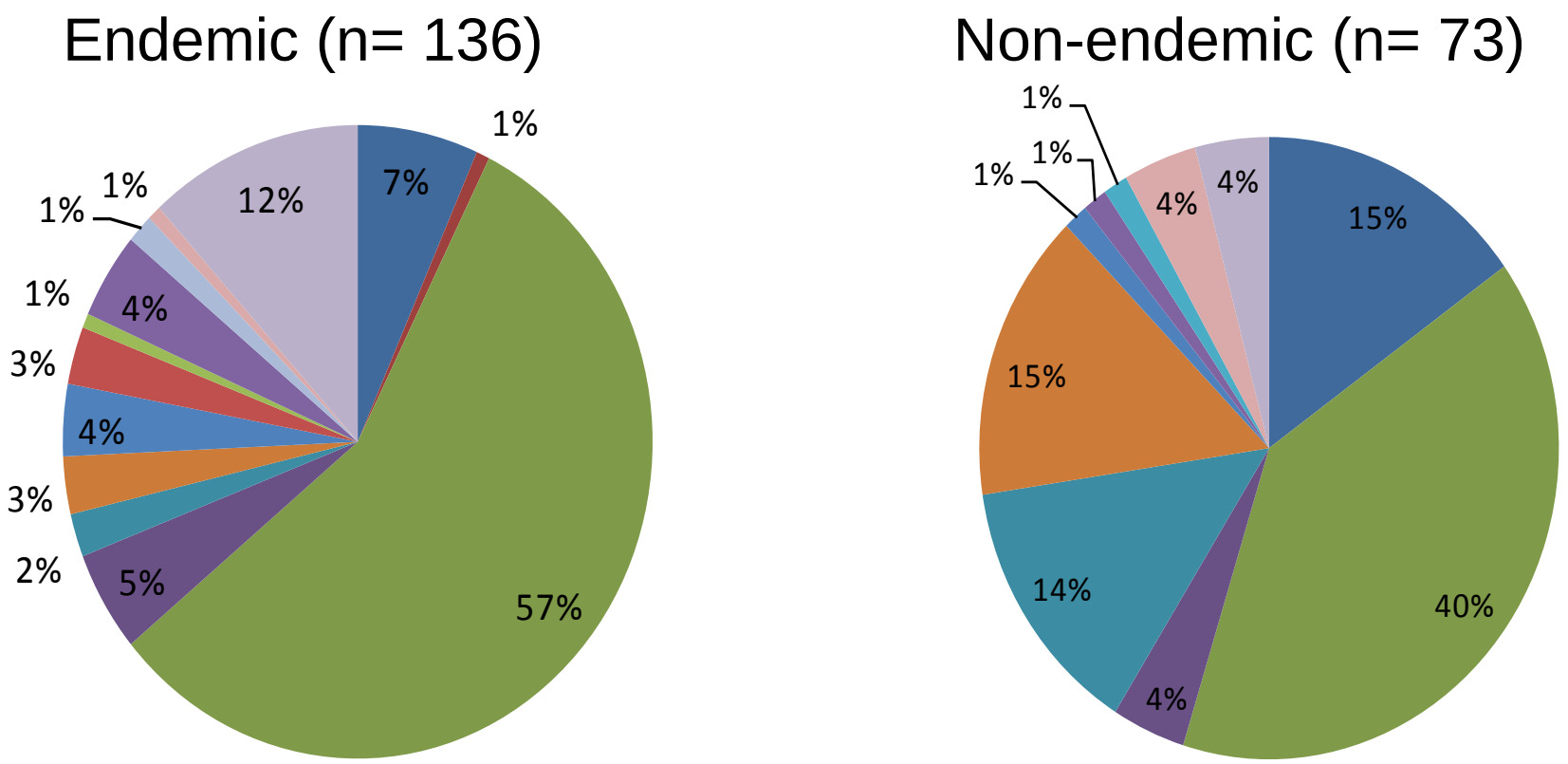
GD in Turkeys - Relative abundance of major MspI TRFs





Benson et al, 2008

Composition of clostridial spores recovered from GD endemic and non-endemic turkey grow-out litter



Early *et al.*, 2006

C. perfringens and *C. septicum* in Turkey Cellulites

Neuman *et al.*, 2007a,b

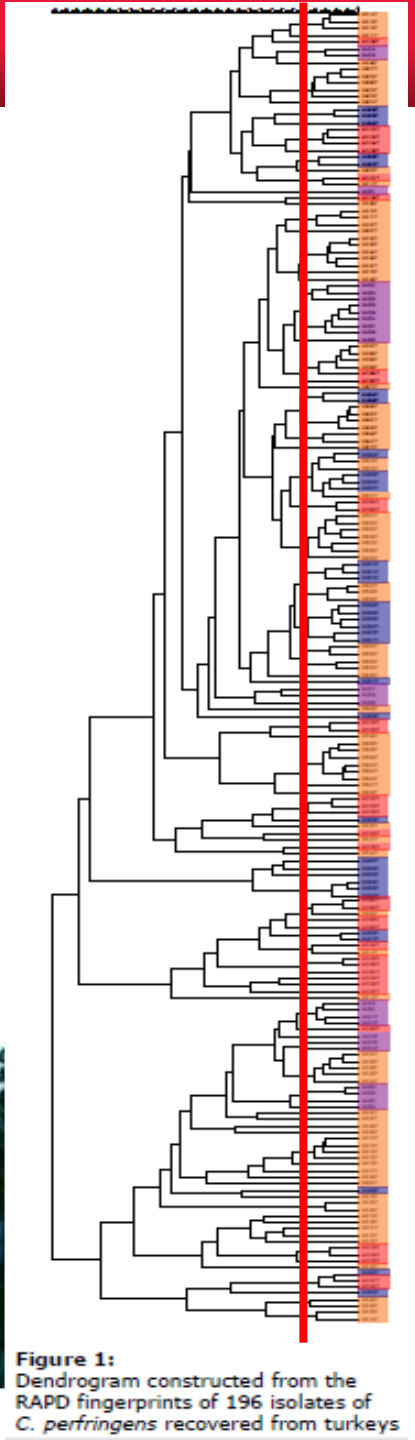


Figure 1:
Dendrogram constructed from the RAPD fingerprints of 196 isolates of *C. perfringens* recovered from turkeys

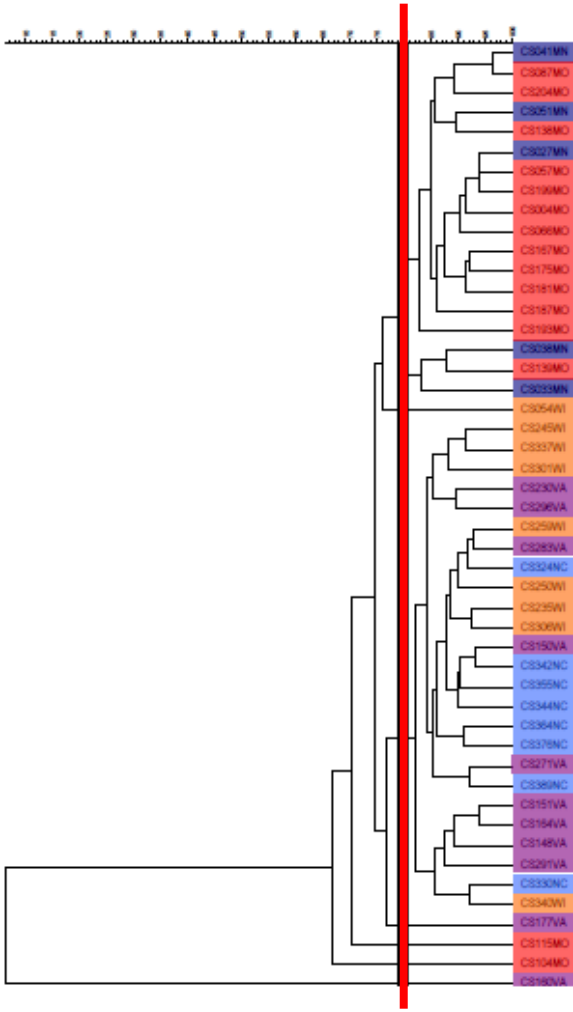
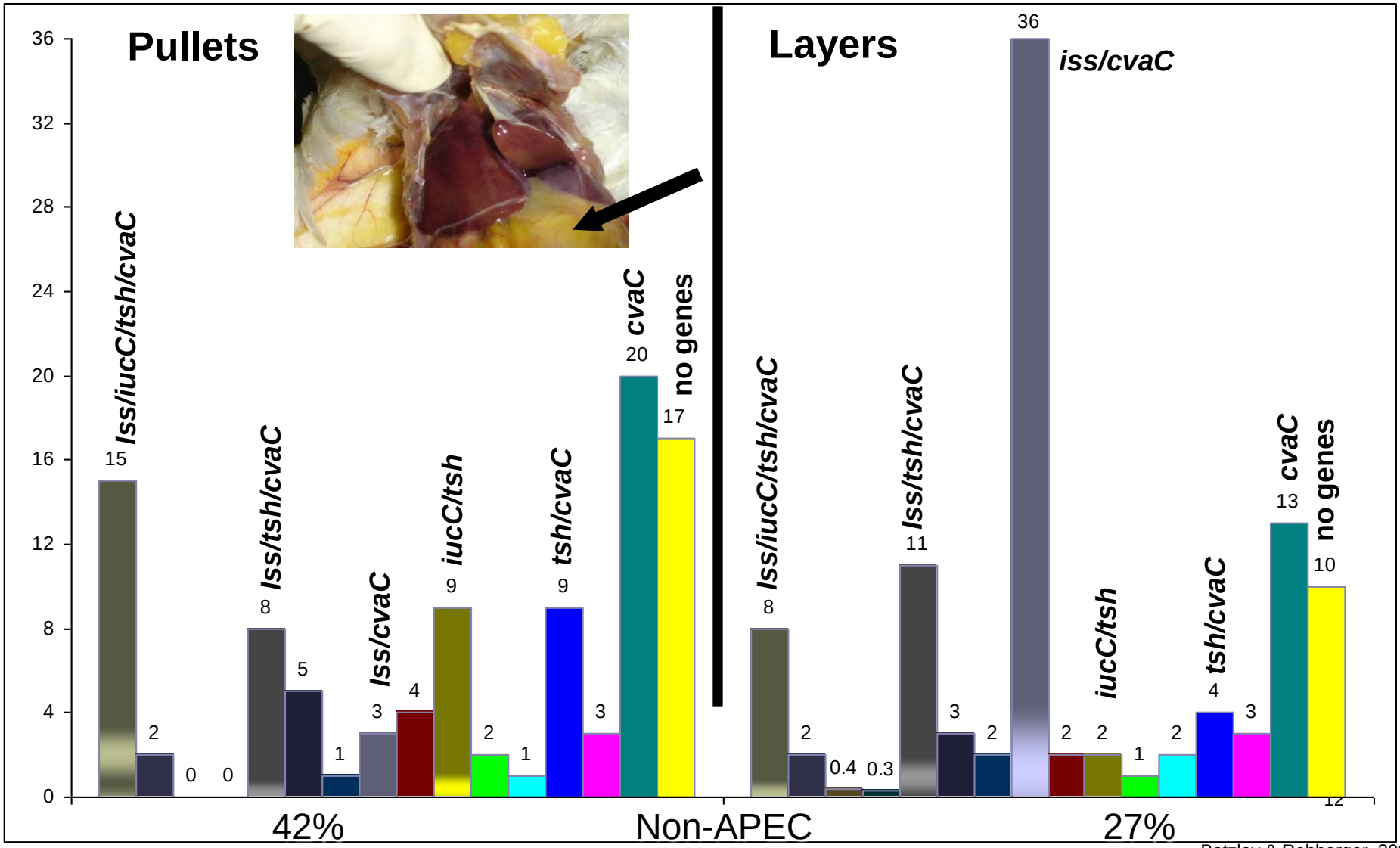


Figure 2
Dendrogram of *C. septicum* isolates recovered from producers in five states; MO (red), MN (indigo), WI (orange), VA (violet) and NC (blue)

Diversity of Avian Pathogenic *E. coli* Toxin Genes in Pullets vs. Laying Hens



Batzley & Rehberger, 2006

Characterization of the duodenal microbiota of commercial layer hens affected by Focal Duodenal Necrosis

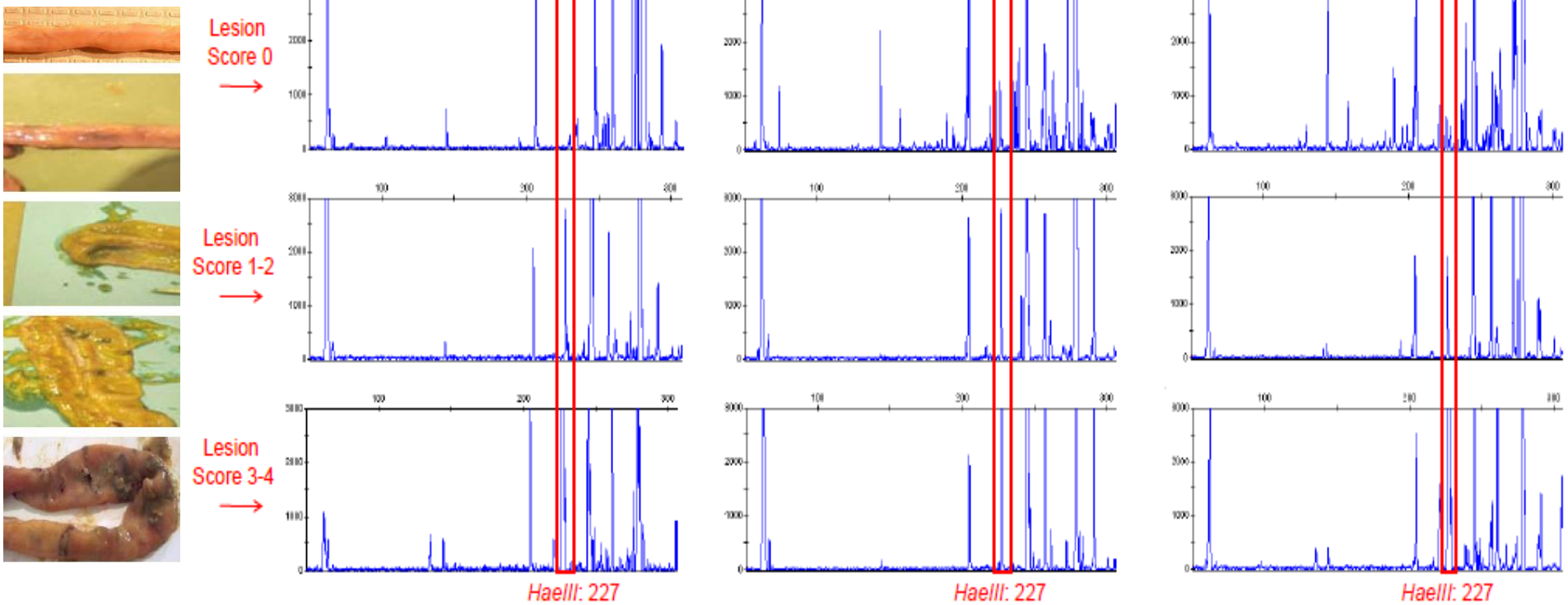


Figure 3. Typical *HaeIII* profiles from layer hens without FDN lesions, with lesion scores of 1-2, and with lesion scores of 3-4. Profiles derived from 3 birds from each health status are shown. Only the first 300 bp of the profile is shown. T-RF *HaeIII*:227, presumptively identified as *C. colinum*, is highlighted by the red boxes.

Benson *et al*., 2009

Characterization of the duodenal microbiota of commercial layer hens affected by Focal Duodenal Necrosis

Table 1. T-RFs correlated with FDN and their possible identifications

Peak	MANOVA Contribution value	Presumptive identification
MspI:470.69	10.598	*Campylobacter* species, *Clostridium paradoxum*
MspI:477	24.632	*Clostridium colinum*
HaeIII:227	34.851	*Clostridium colinum*
HaeIII:312	5.279	*Bacillus* species, *Carnobacterium* species, *Lactococcus garvieae*, *Paenibacillus* species
BstUI:112	25.178	*Clostridium colinum*

Table 2. T-RFs correlated with health and their possible identifications

Peak	MANOVA Contribution value	Presumptive identification
M495	4.86	*E. coli*, *Salmonella*, *Klebsiella*/enterics
M568	24.317	*Enterococcus faecalis*, *Lactobacillus* (*agilis*, *alimentarius*, *animalis*, *aviarius*, *brevis*, *farciminis*, *paralimentarius*, *pentosus*, *plantarum*, *ruminis*, *salivarius*)
H272	8.709	*Helicobacter* species, *Wolinella succinogenes*
H323	15.029	*Lactobacillus* (*acetotolerans*, *alimentarius*, *farciminis*, *intestinalis*, *paralimentarius*, *pentosus*, *plantarum*)
B248	19.229	*Enterococcus faecalis*, *Enterococcus faceium*, *Lactobacillus* (*amylovorus*, *aviarius*, *delbrueckii*, *kefiranofaciens*, *salivarius*, *sobrius*)
B381	11.333	*Helicobacter* species, *Wolinella succinogenes*

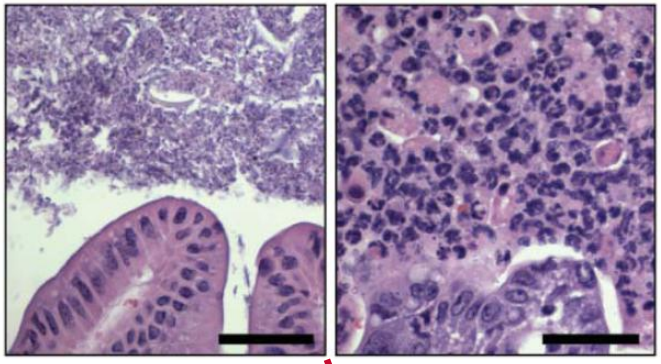
Benson *et al*., 2009

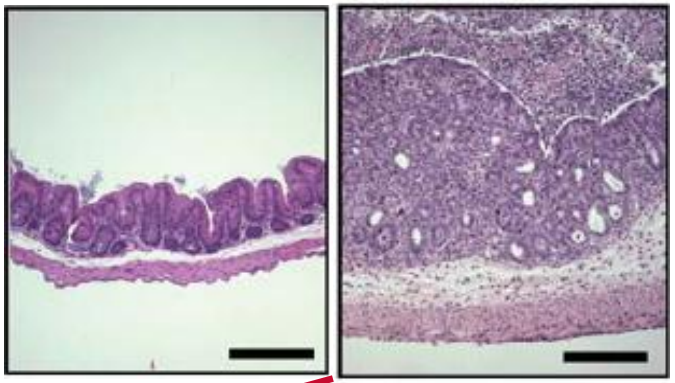
Salmonella infection

Gut inflammation provides a respiratory electron acceptor for *Salmonella*

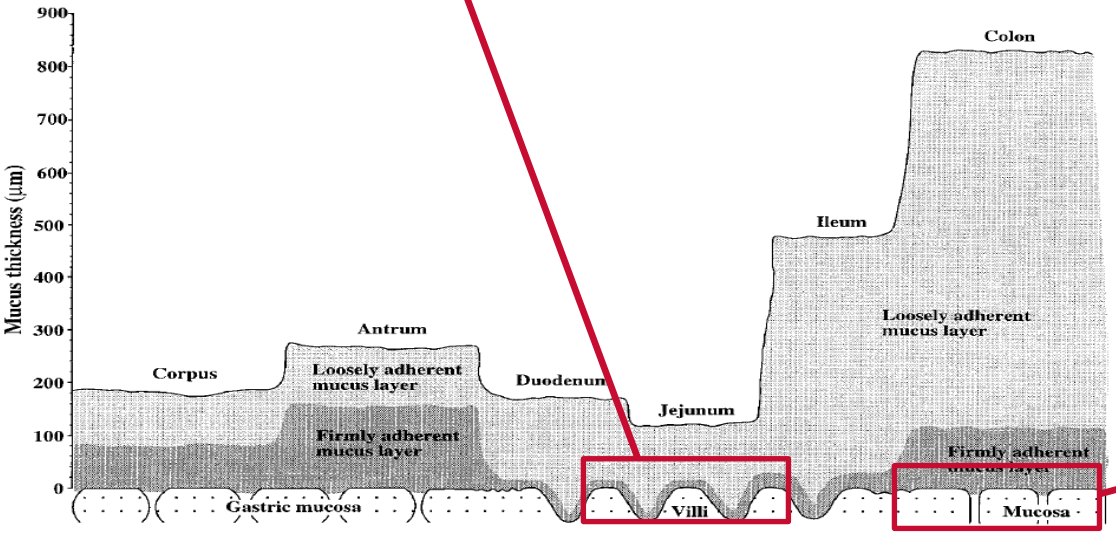
Sebastian E. Winter[1], Parameth Thiennimitr[1,2], Maria G. Winter[1], Brian P. Butler[1], Douglas L. Huseby[3], Robert W. Crawford[1], Joseph M. Russell[1], Charles L. Bevins[1], L. Garry Adams[4], Renée M. Tsolis[1], John R. Roth[3] & Andreas J. Bäumler[1]

Salmonella enterica serotype Typhimurium (*S.* Typhimurium) causes acute gut inflammation by using its virulence factors to invade the intestinal epithelium and survive in mucosal macrophages. The inflammatory response enhances the transmission success of *S.* Typhimurium by promoting its outgrowth in the gut lumen through unknown mechanisms. Here we show that reactive oxygen species generated during inflammation react with endogenous, luminal sulphur compounds (thiosulphate) to form a new respiratory electron acceptor, tetrathionate. The genes conferring the ability to use tetrathionate as an electron acceptor produce a growth advantage for *S.* Typhimurium over the competing microbiota in the lumen of the inflamed gut. We conclude that *S.* Typhimurium virulence factors induce host-driven production of a new electron acceptor that allows the pathogen to use respiration to compete with fermenting gut microbes. Thus the ability to trigger intestinal inflammation is crucial for the biology of this diarrhoeal pathogen.





GASTROINTESTINAL MUCUS



Mean mucus thickness (μm)

	Corpus	Antrum	Duodenum	Jejunum	Ileum	Colon
Total	189 ± 11	274 ± 41	170 ± 38	123 ± 4	480 ± 47	830 ± 110
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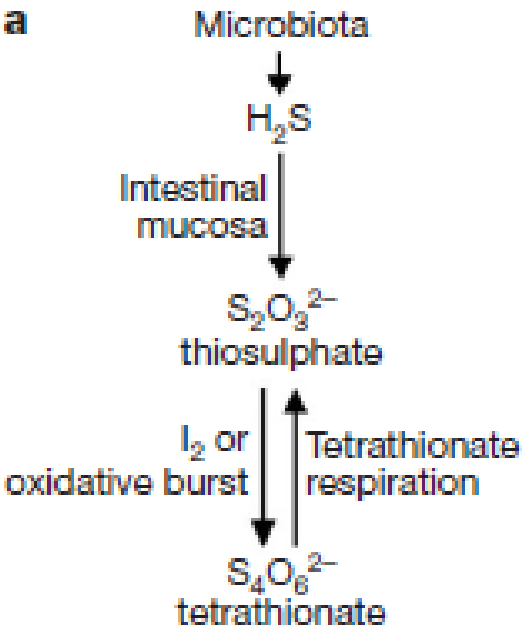

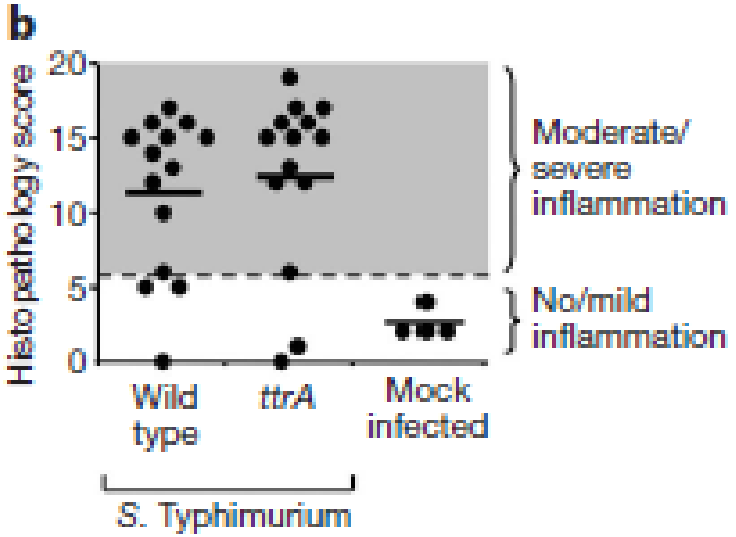

Summary

- In enteric disease, healthy gut microbiota balance is disrupted
- Increased abundance of proteolytic and/or toxin producing Clostridia, specifically *C. perfringens*, is directly or indirectly associated with most enteric diseases
- *C. perfringens* shows high variability on the species level leading to various diseases (NE, GD)
- Enteric disease via Avian Pathogenic *E. coli* is dependent on number of toxin genes present
- Enteric *Salmonella* infection is dependent on previous intestinal disease
- Acute enteric disease is usually accompanied by a decrease in beneficial bacterial populations, for example *Lactobacillus* and group D *Streptococcus*

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