Mucosal Flora in IBD





Alexander Swidsinski

Supported by Broad Medical Research Program

Mean± SD (x10³ cfu/μL) of Mucosal Bacteria

	Asymptomatic Controls	Self-limiting Colitis	Indeterminate Colitis	UC	CD
	(n=40)	(n=28)	(n=104)	(n=156)	(n=82)
Total anaerobes	0.18±0.3	1.8±5.3 NS	3.41±16 <i>P</i> < 0.08	3.8±11 <i>P</i> < 0.01	9.1±18 <i>P</i> < 0.001
Bacteroides	0.02±0.05	0.26±0.6 NS	0.64±2.1 <i>P</i> < 0.01	1.4±9 <i>P</i> < 0.001	3.1±5.5 <i>P</i> < 0.001
Total aerobes	0.003±0.05	0.08±0.4 NS	0.09±0.5 <i>P</i> < 0.005	0.08±0.6 <i>P</i> <0.05	0.14±0.8 <i>P</i> < 0.001
Enterobacteriaceae	0.002 <u>+</u> 0.05	0.06 ± 0.5 <i>P</i> < 0.06	0.08±0.3 <i>P</i> < 0.005	0.04 ± 0.5 <i>P</i> <0.047	0.090±0.8 <i>P</i> < 0.001

Mucosal bacteria ($x10^3$ cfu/ μ L) and clinical data

A 11	UC (n=156) 3.8	CD (n=82) 9.1	A 11	UC (n=156)	CD (n=82)
All	3.0	9.1	All	3.8	9.1
patients age <25 25-30 30-35 35-40 40-45	2.0 1.7 4.5 3.4 3.2	2.6 9.1 11.9 10.8 4.3	duration of disease in years <5 5-20 >20	3.6 4.6 2.5	10 8.05 1.9
45-50	6.9	4 .5 5.5	f	4.2	12.0
>50	2.6	5.2	m	2.8	4.7
age at the time of manifestation <25 25-30 30-35 35-40 >40	2.6 2.5 3.6 13 1.5	7.5 24.0 14 1.9 3.5 10 5 - 2	7,5	3,5	□ UC ■ Crohn
		0 [1,5	1
			<25 25-30 30-35 35-40	>40	

Mucosal bacteria, disease activity and therapy

Mucosai	Dacter	ia, uis	ease activity and	merapy	/
	UC	CD		UC	CD
	(n=156)	(n=82)		(n=156)	(n=82)
All	3.8	9.1	All	3.8	9.1
	0.0	0.0			
remission	2.9	2.9	no antibiotics in last 12 months	4.6	9.2
activity	4.8	11.0	on antibiotics	0.5	1.4
exacerbated	5.5	8.2	after antibiotics (1-4 weeks)	5.9	27
fistula		20.1	` ′		
no		4.8	no azathioprine	3.1	9.9
no		4.0	azathioprine	5.8	8.3
colonic surgery	2.8	9.0	•		
without surgery	4.6	10.0	corticosteroids	8.2	12.0
			without	3.7	8.7
12]	11				-
10 -			5ASA in gramm		
8 -	8,2		0	4.2	14.9
		■ Remiss	1-2,5	3.7	6.5
6 - 4,8		■ aktiv	3	2.7	3.5
4 - 2,9	2,9	■ Schub	>4	1.4	2.6
2,0	2,9			11.1	2.0
2 -					

UC

Crohn



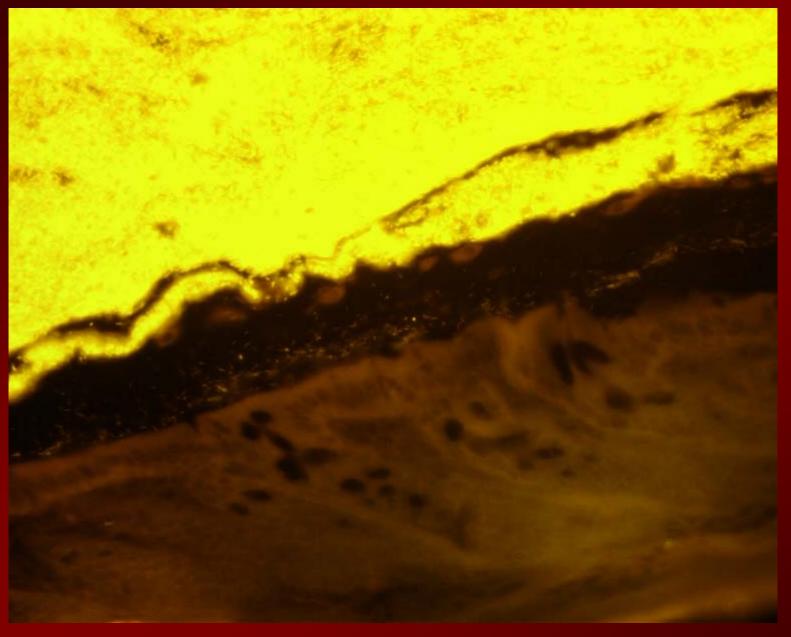
Multicellular bacteria forming stromatolith in Australian salt lakes



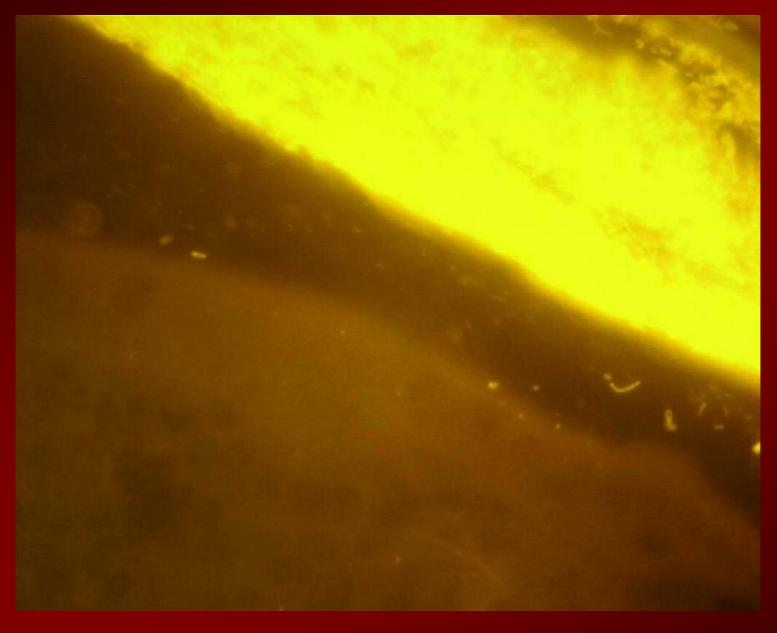
FISH analysis of the mucosal biofilm



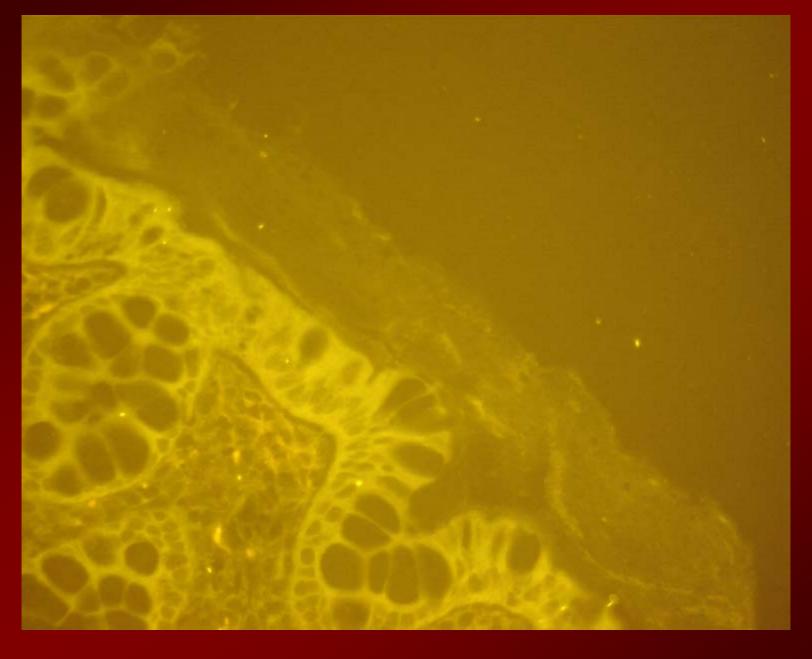
using r-RNA targeted probes



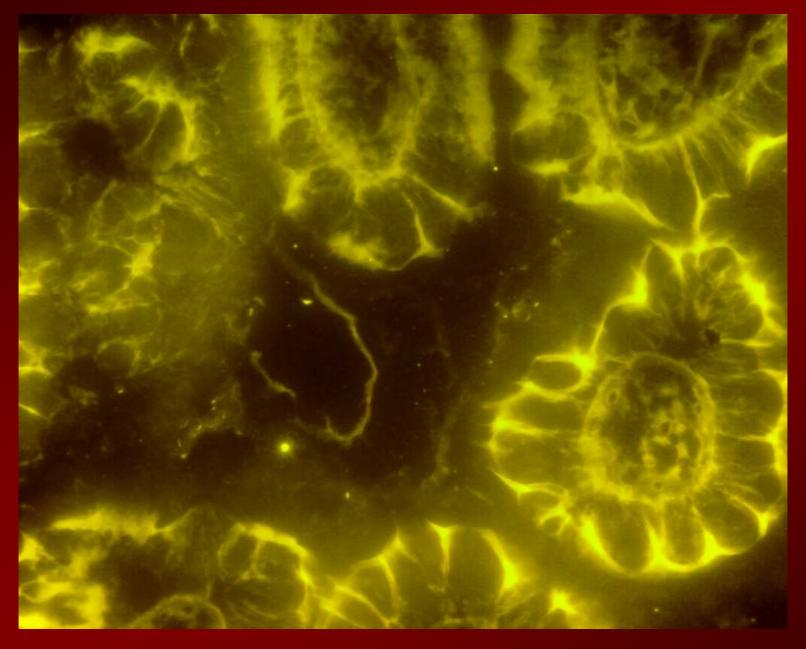
Mucus gap between the colonic wall and feces in healthy mouse



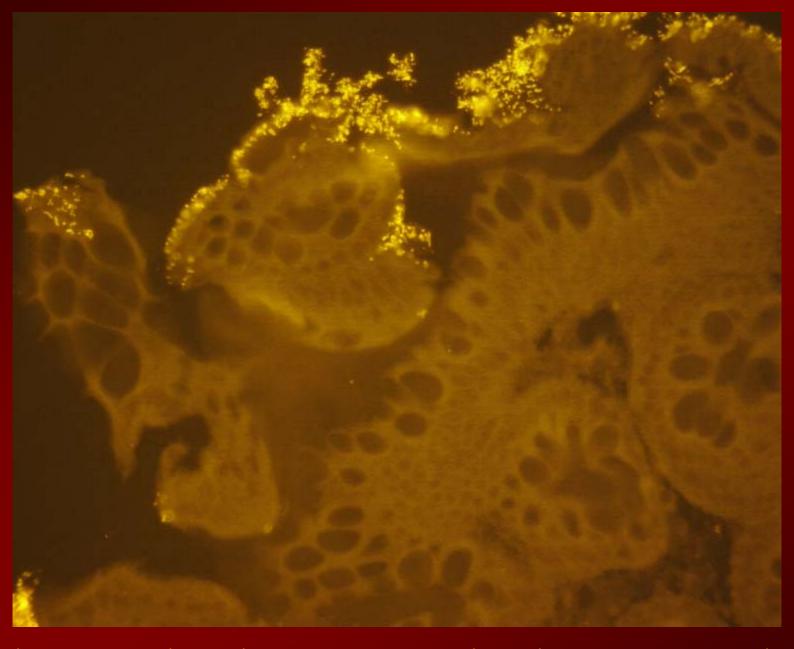
Mucus gap between the colonic wall and feces in healthy mouse



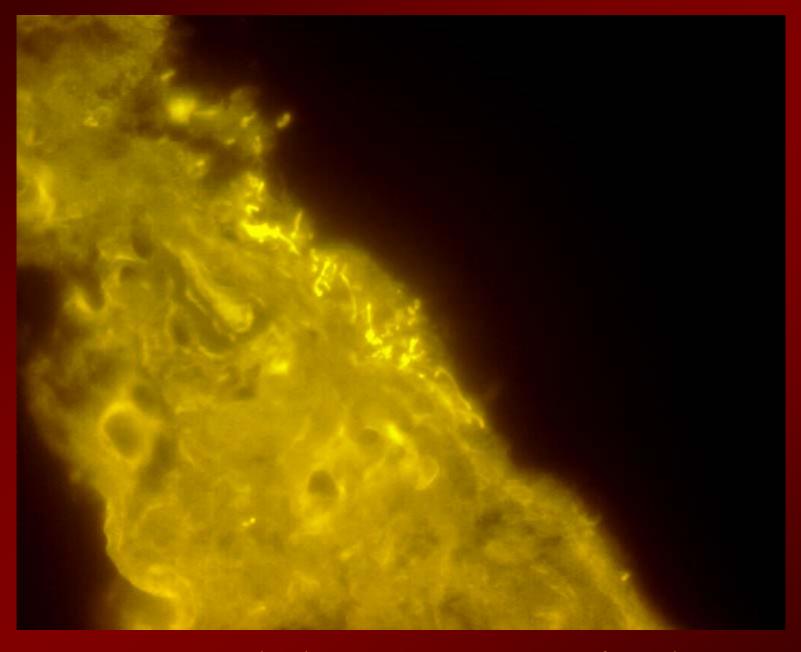
Human colonic wall covered with mucus omitting bacteria



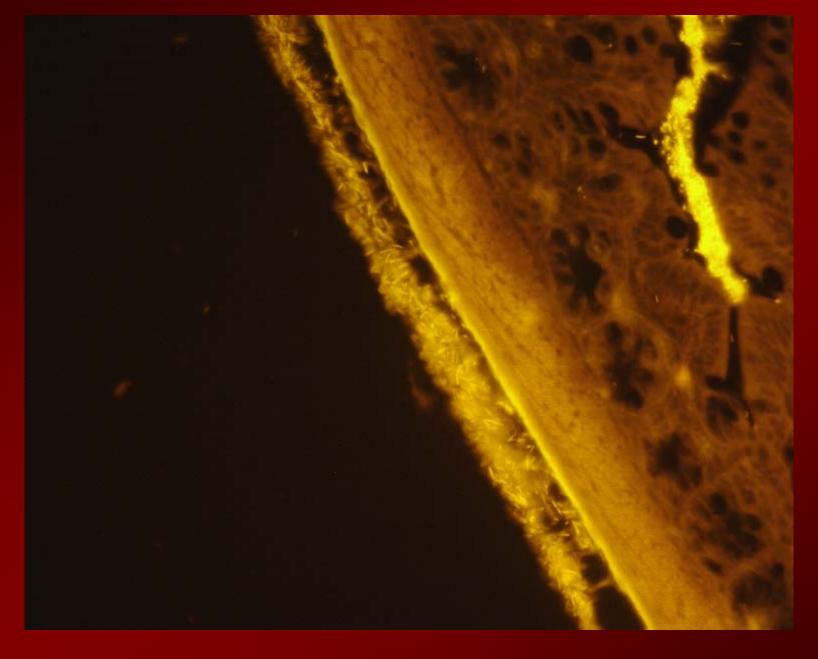
Human ileal wall covered with mucus omitting bacteria



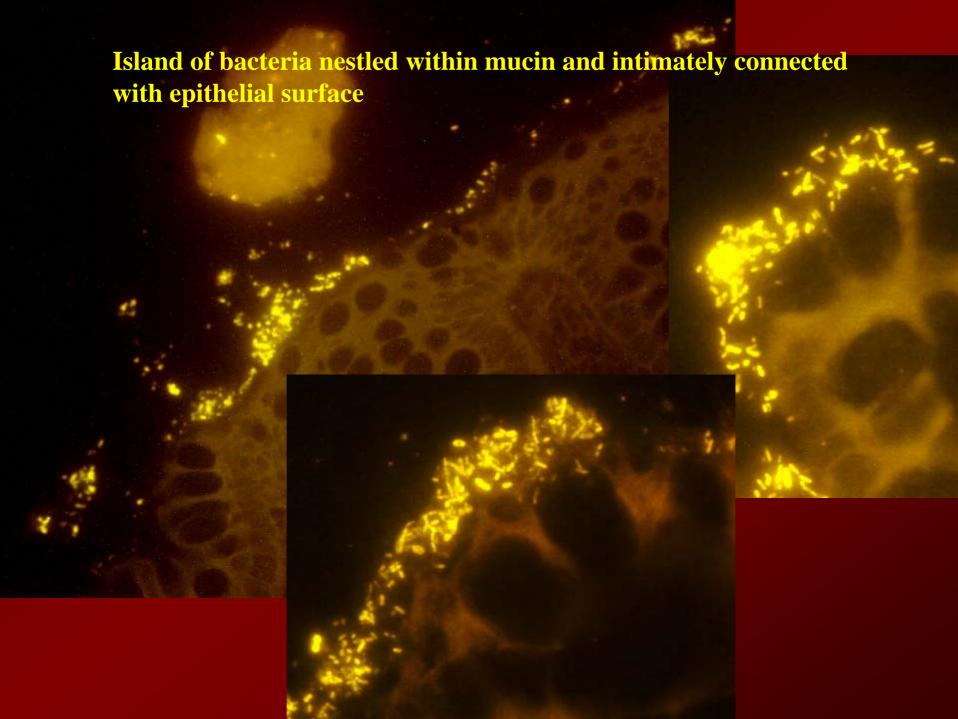
intact mucus is partially denuded, the biopsy is covered by bacteria



Fecal contamination on submucosal parts of the biopsy



bacteria on the peritoneal side of the mouse intestine/ biases

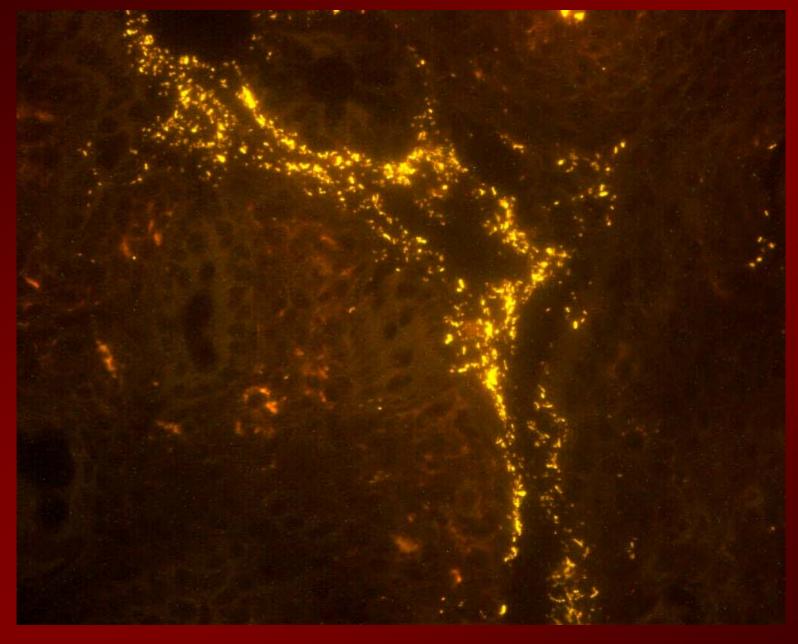




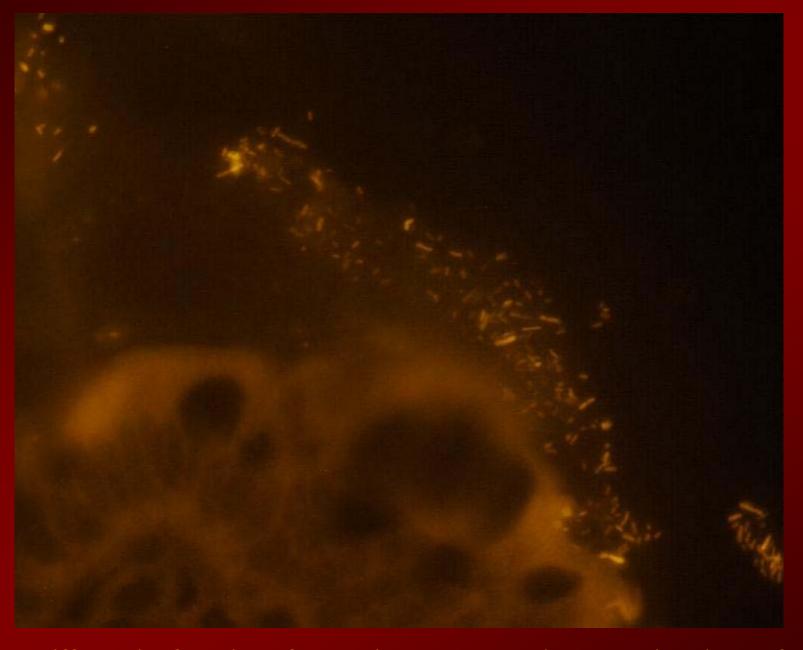




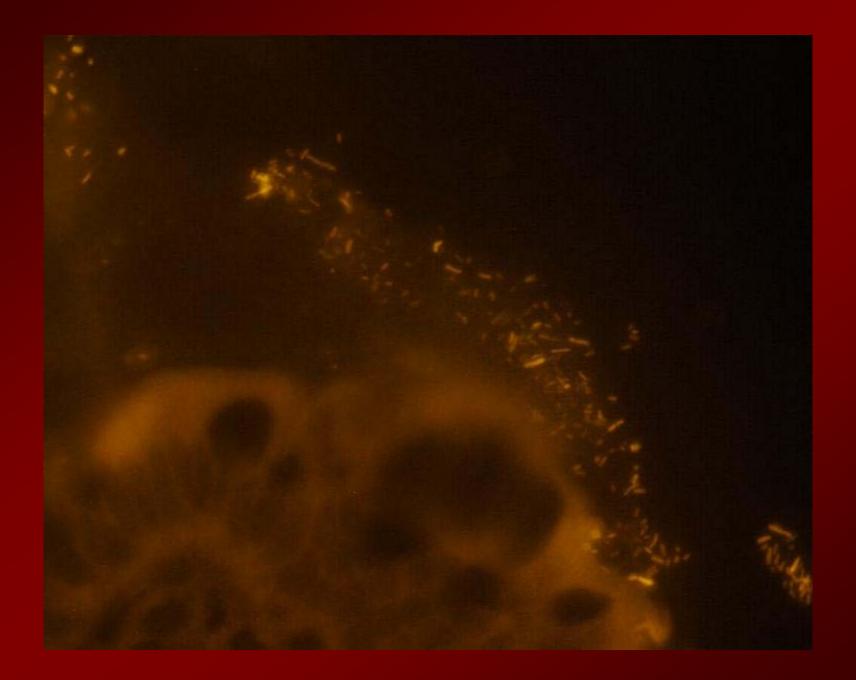




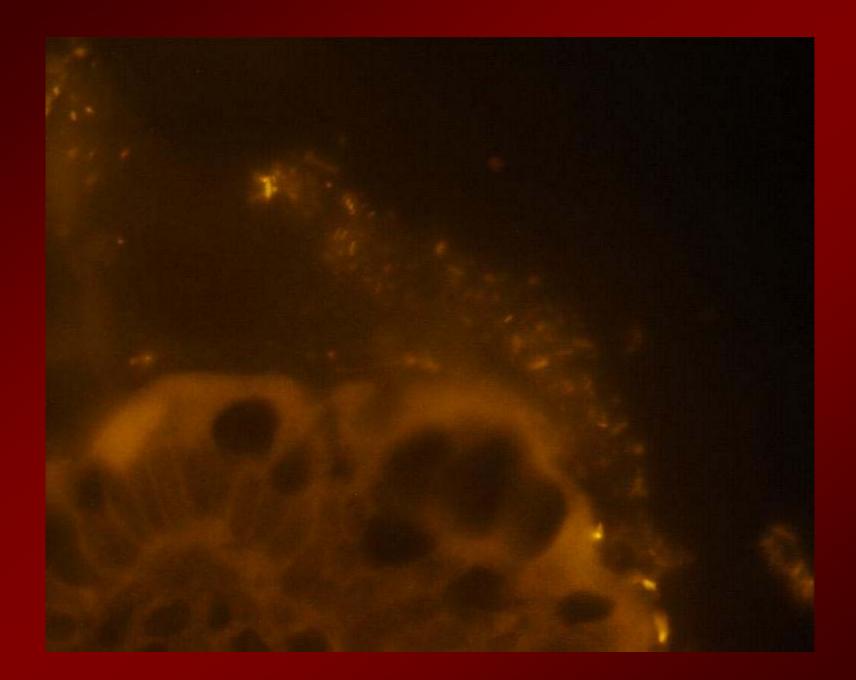
Lawns of bacteria covering the epithelial surface (ileum)

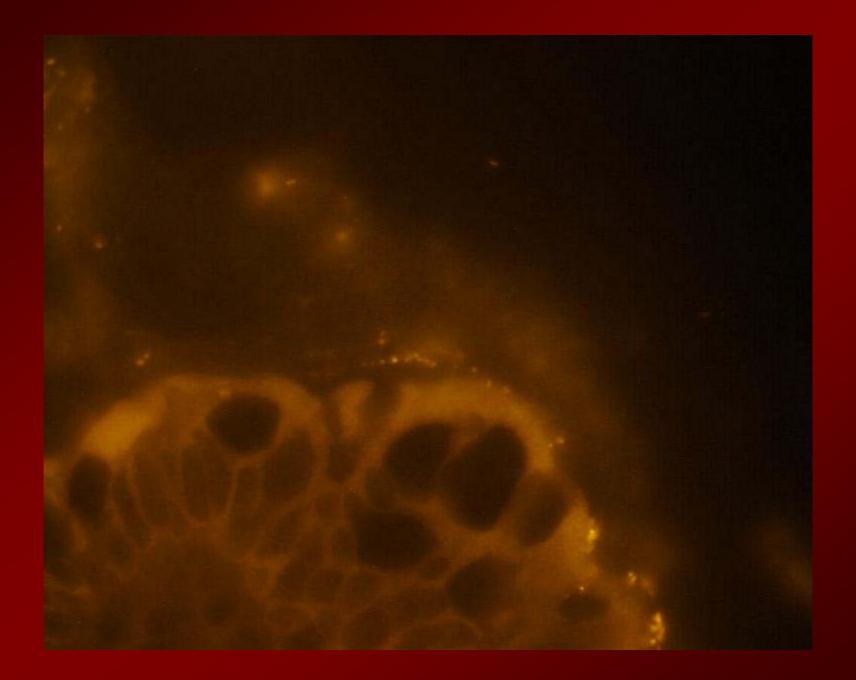


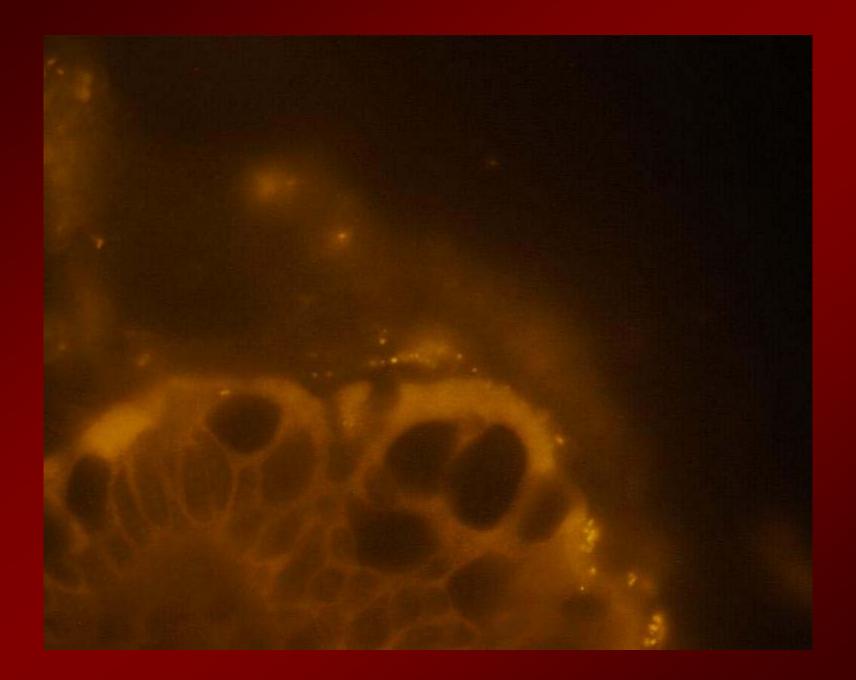
Differential focusing of bacterial lawns covering the epithelial surface

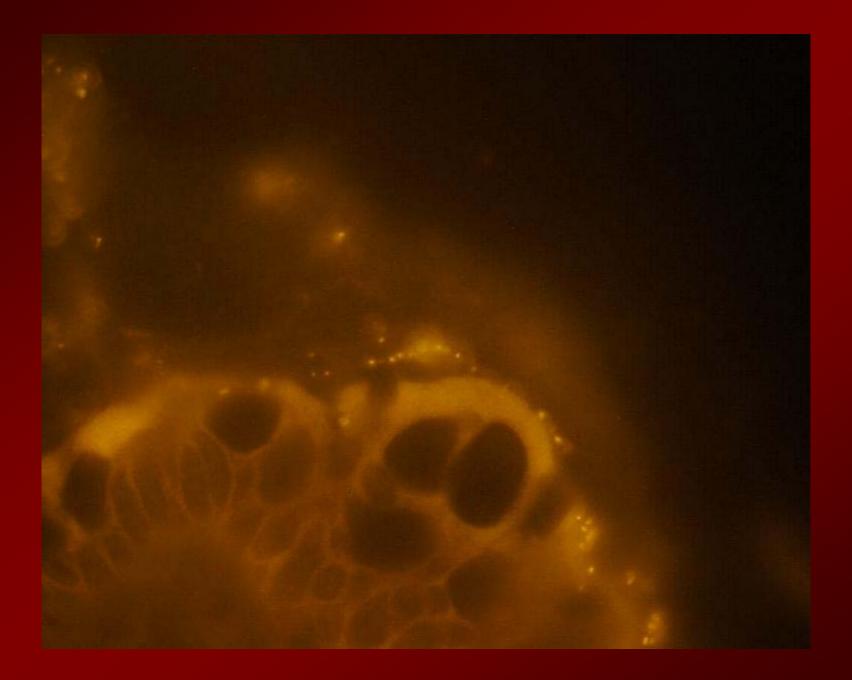


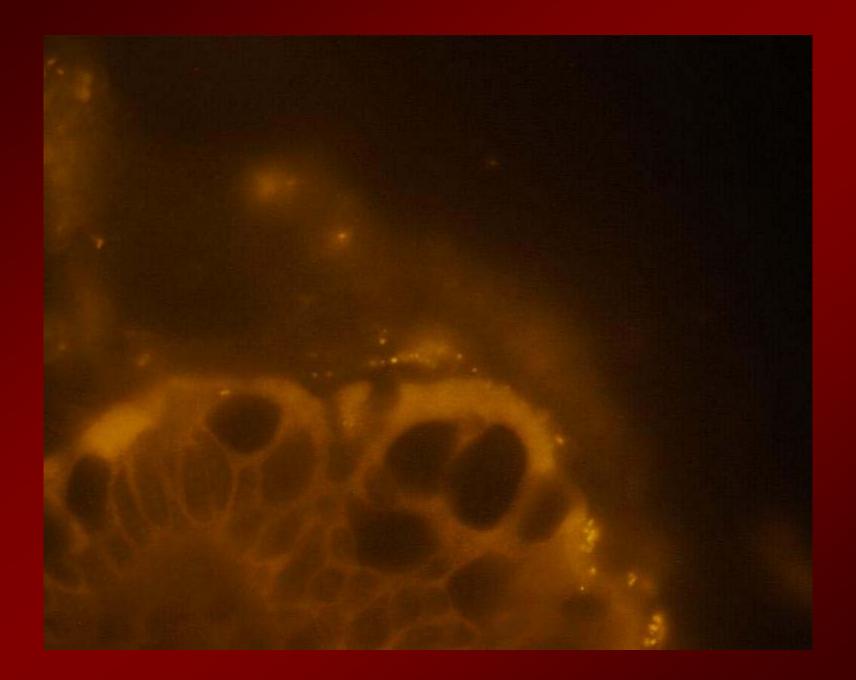


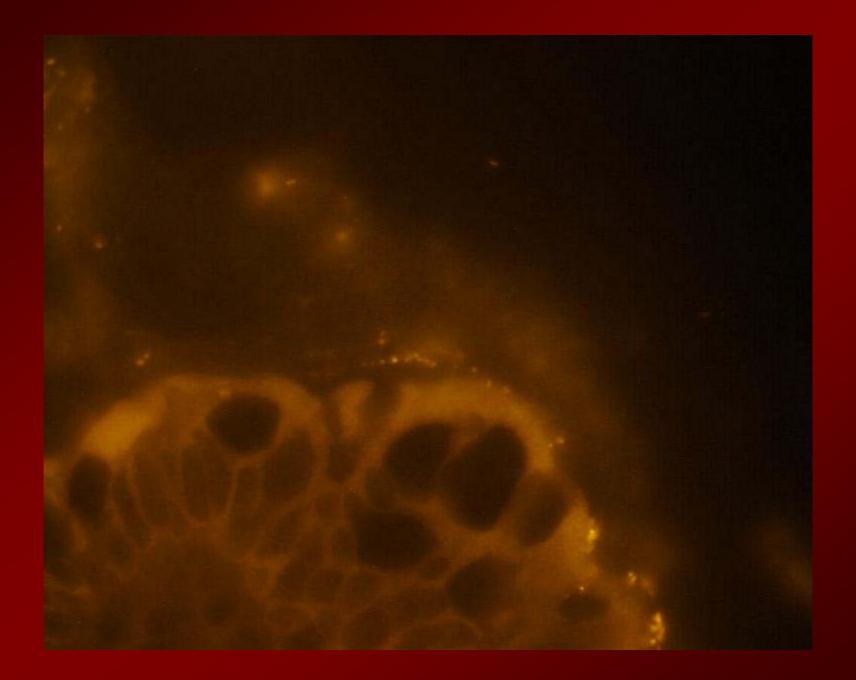


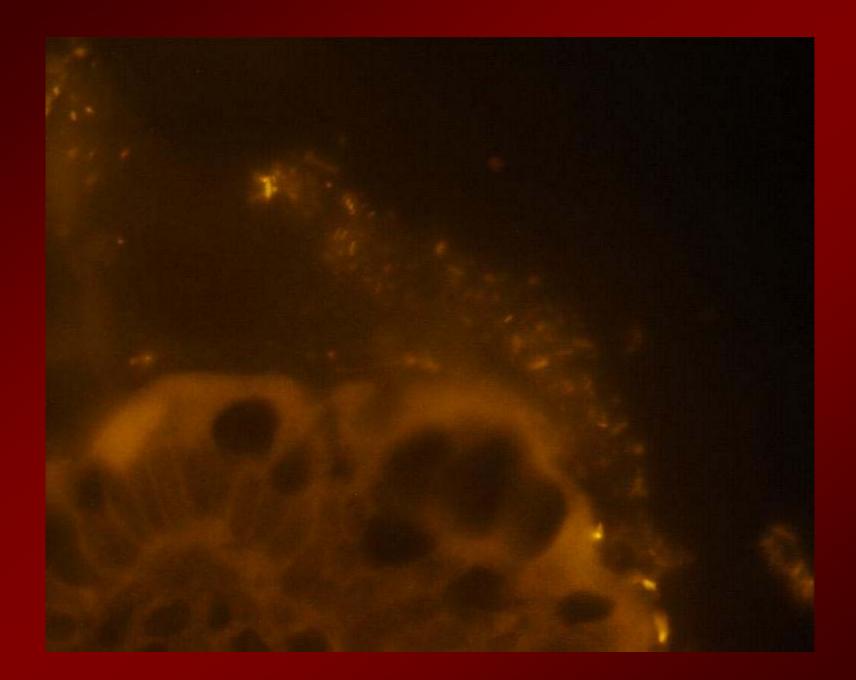


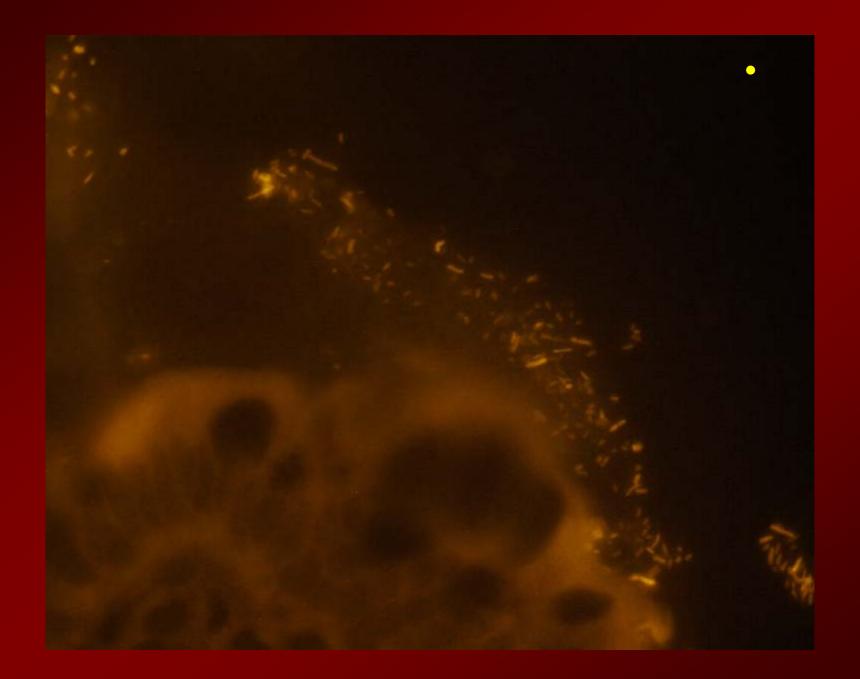


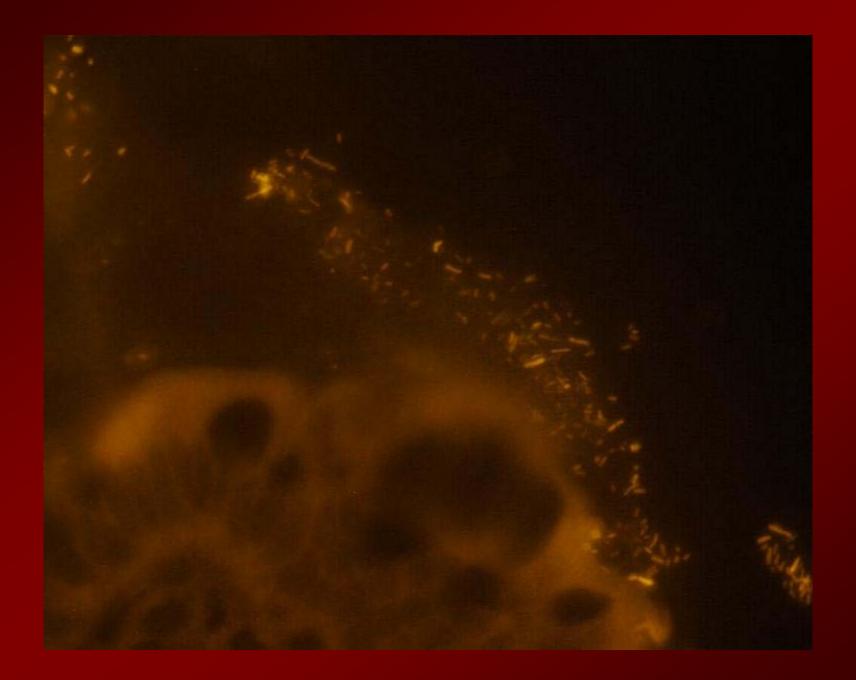




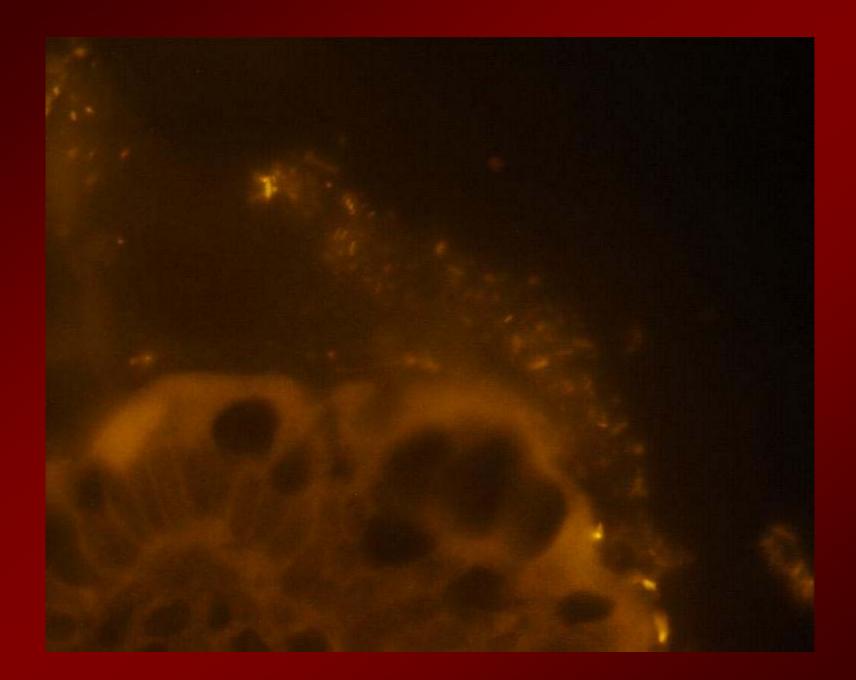


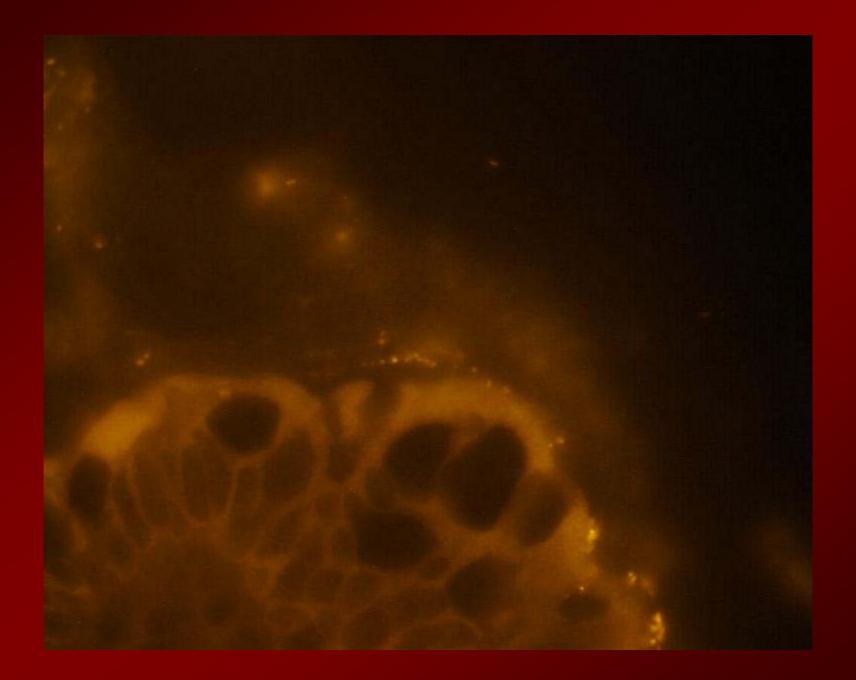


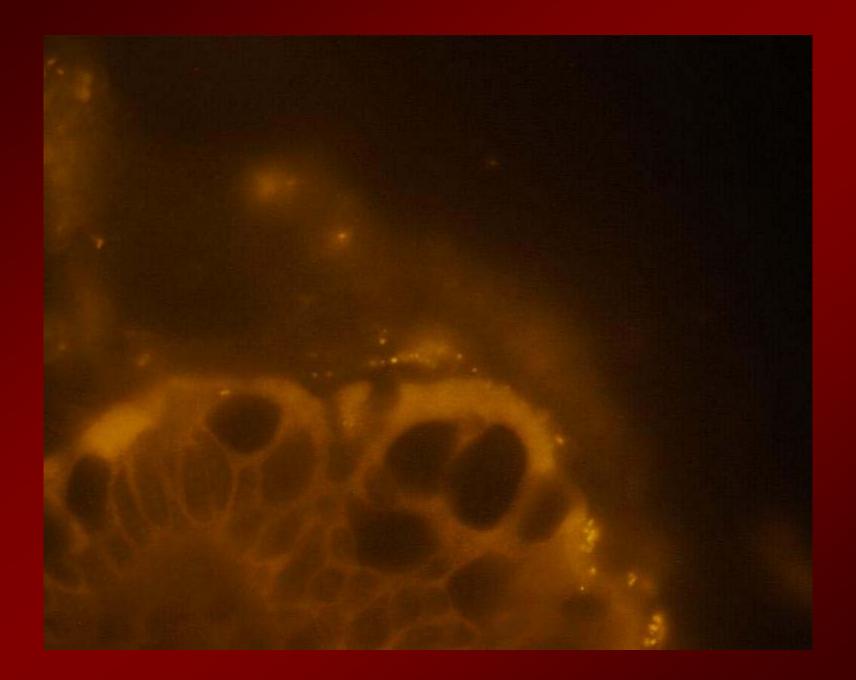


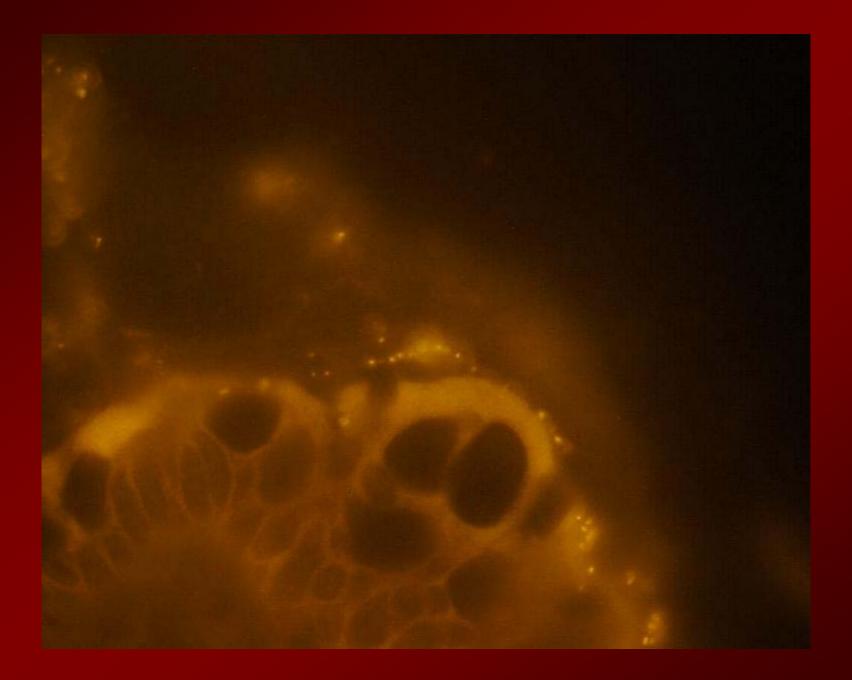


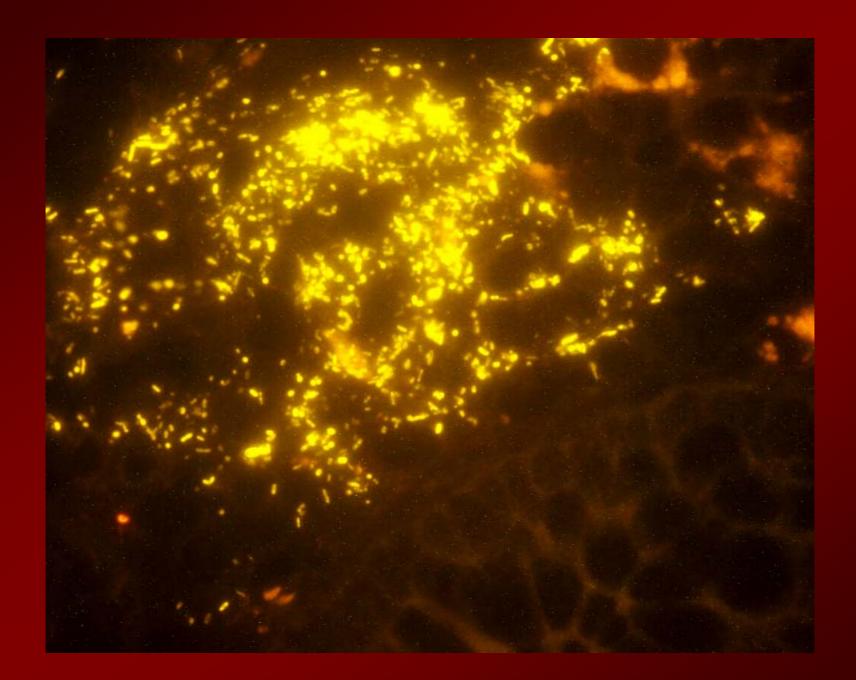


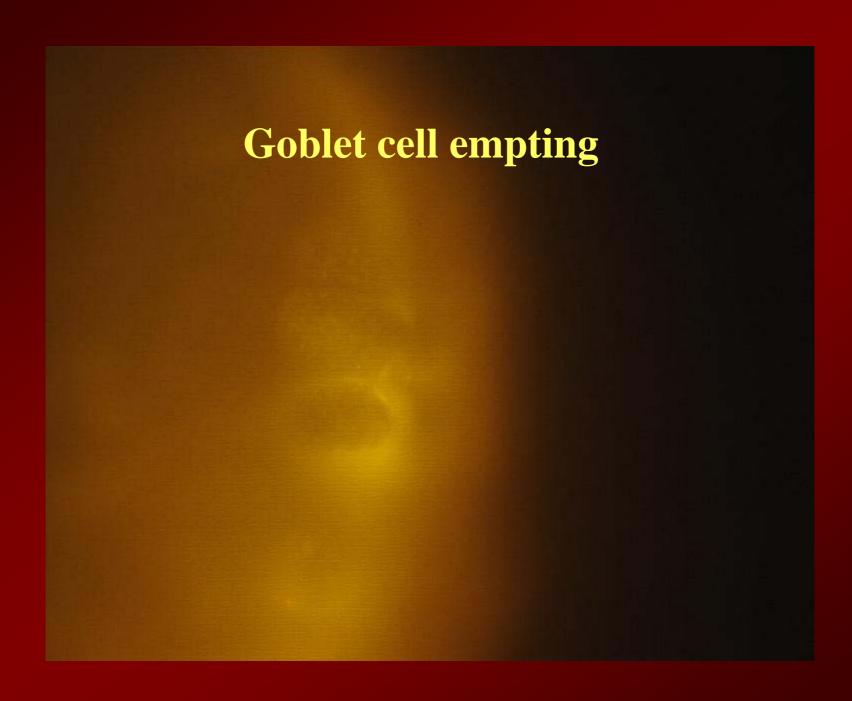


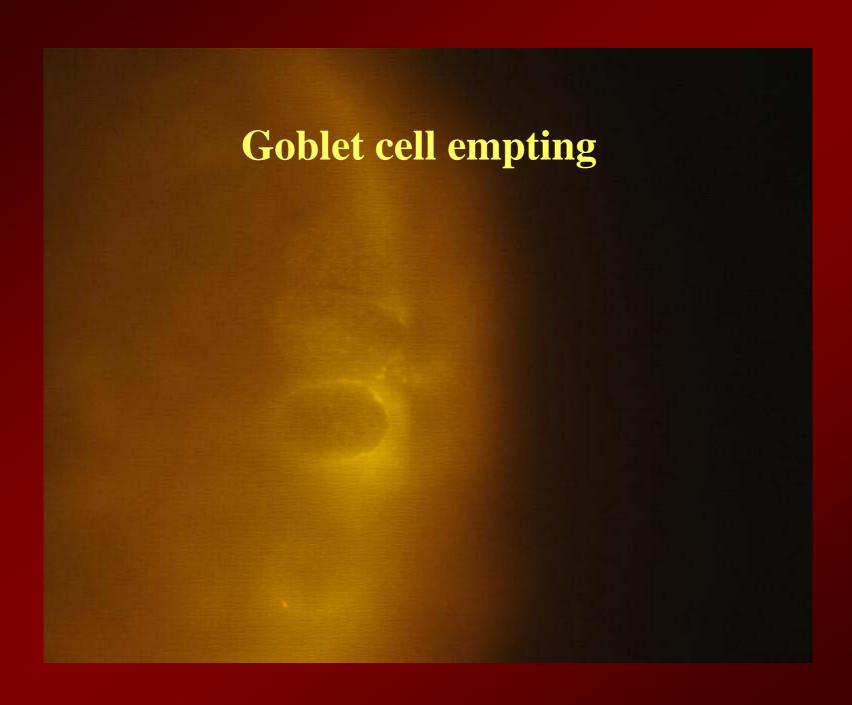


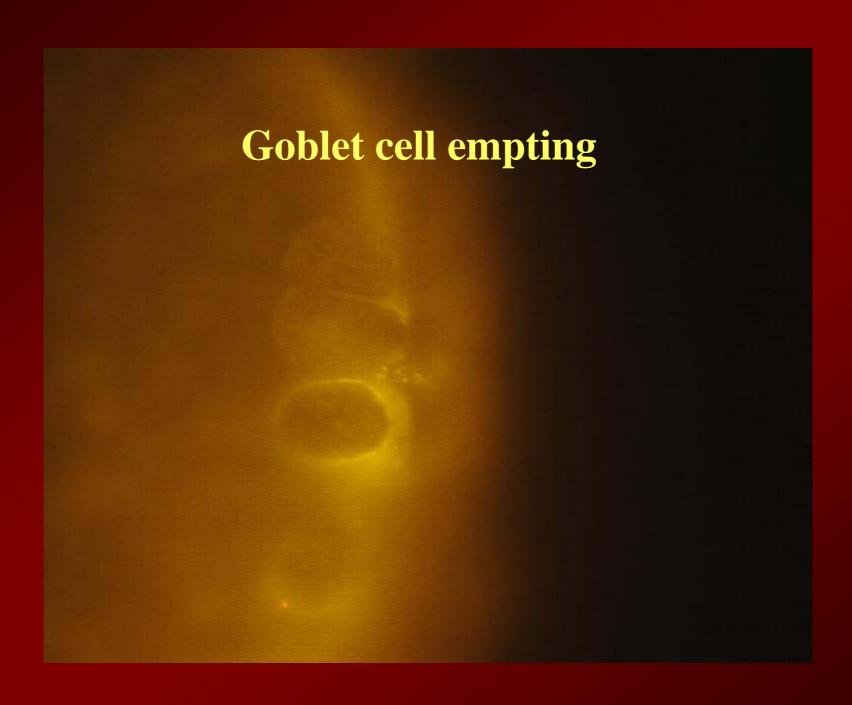


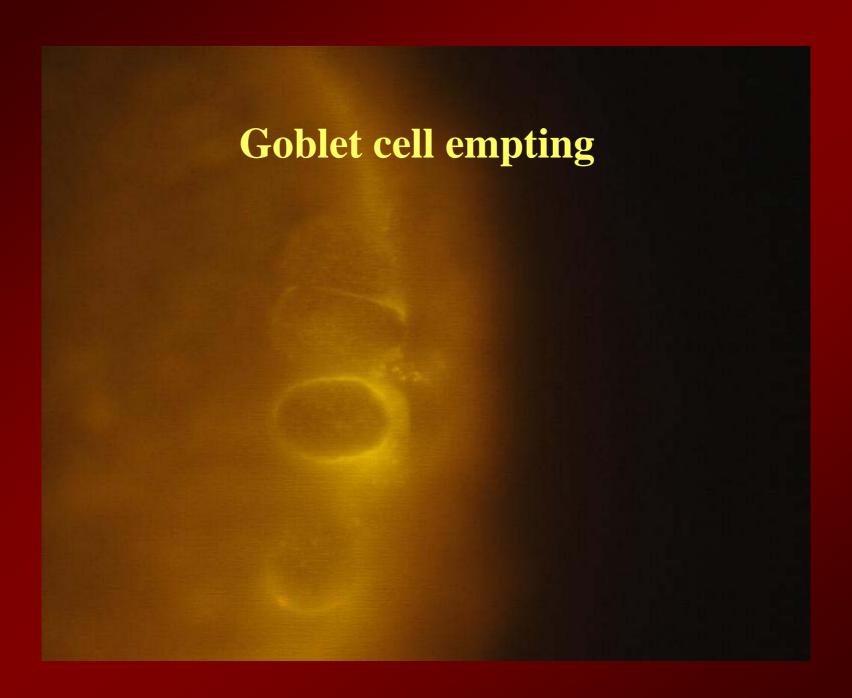


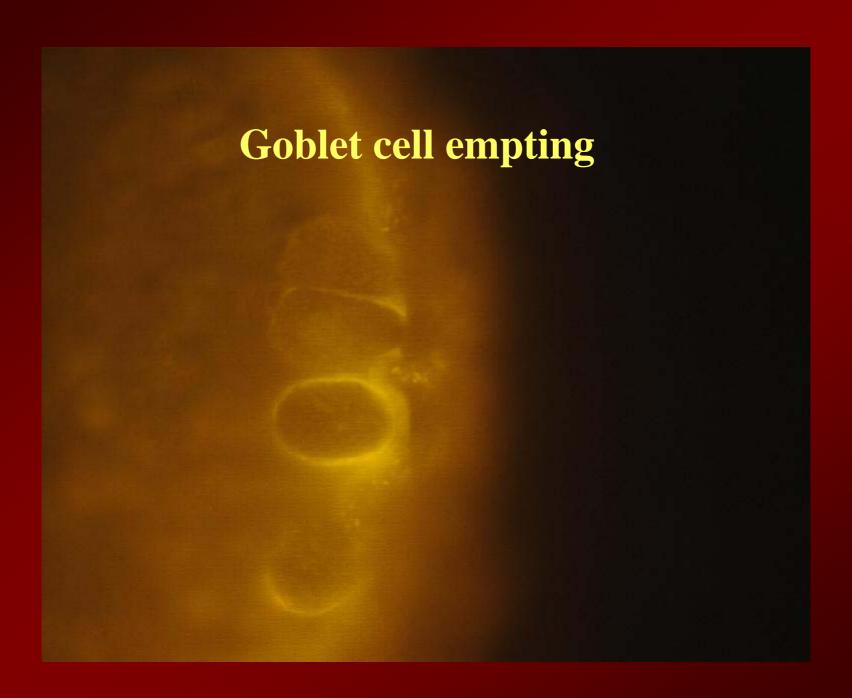


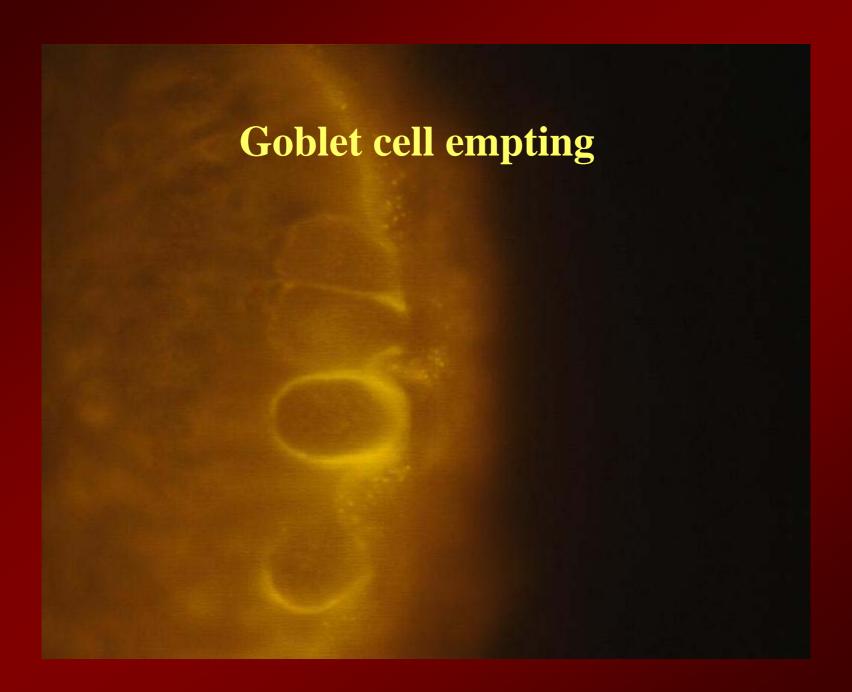


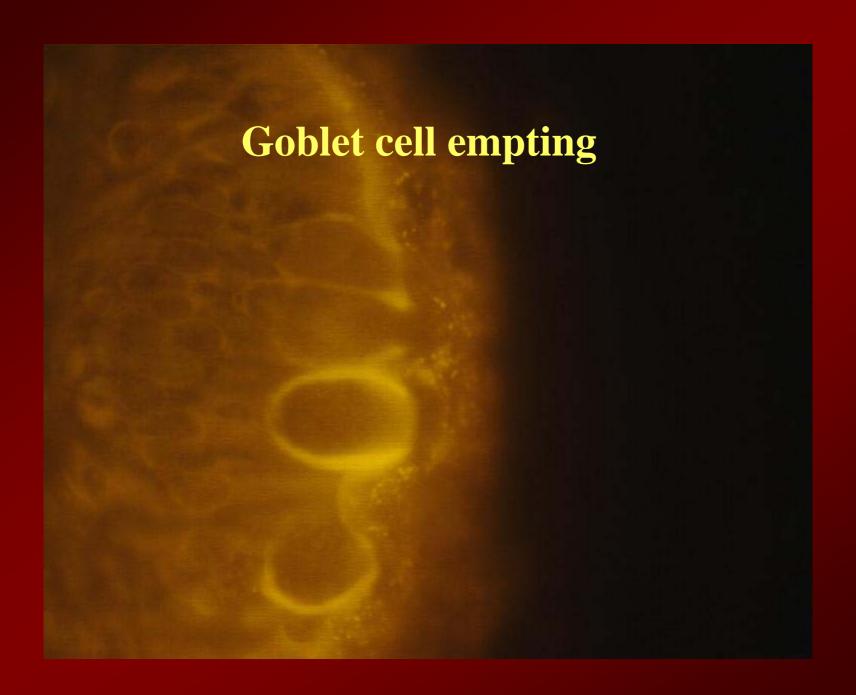


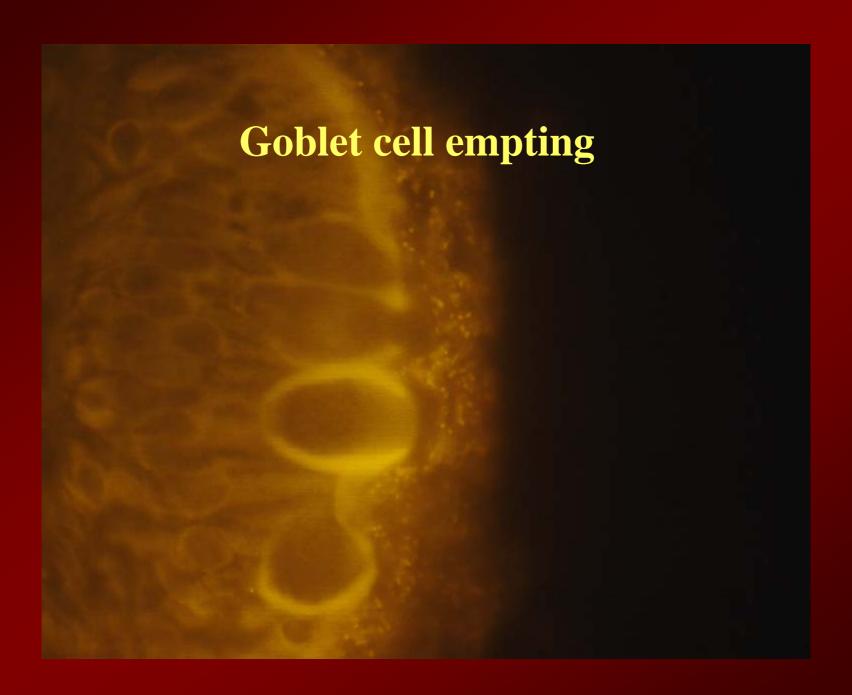


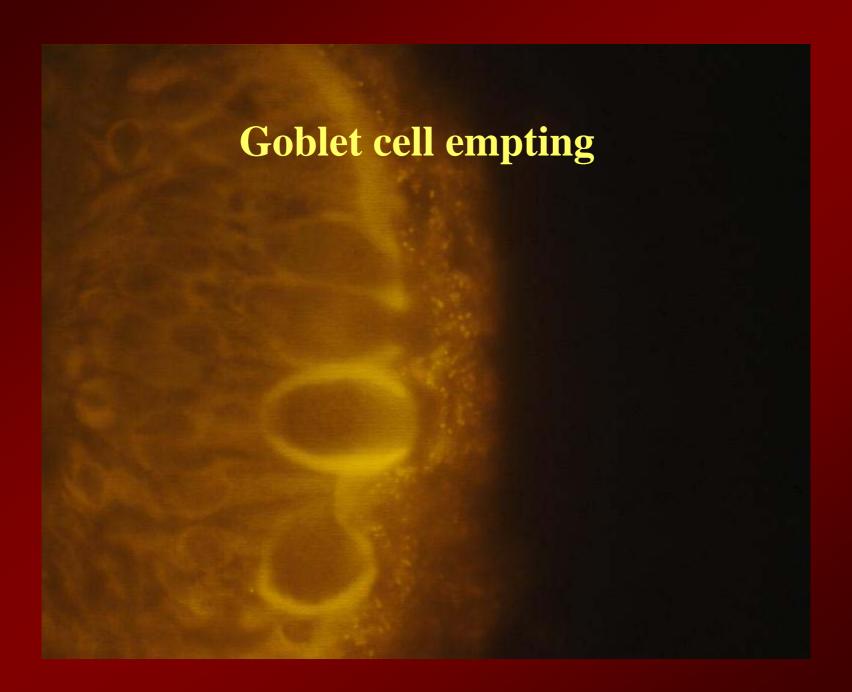


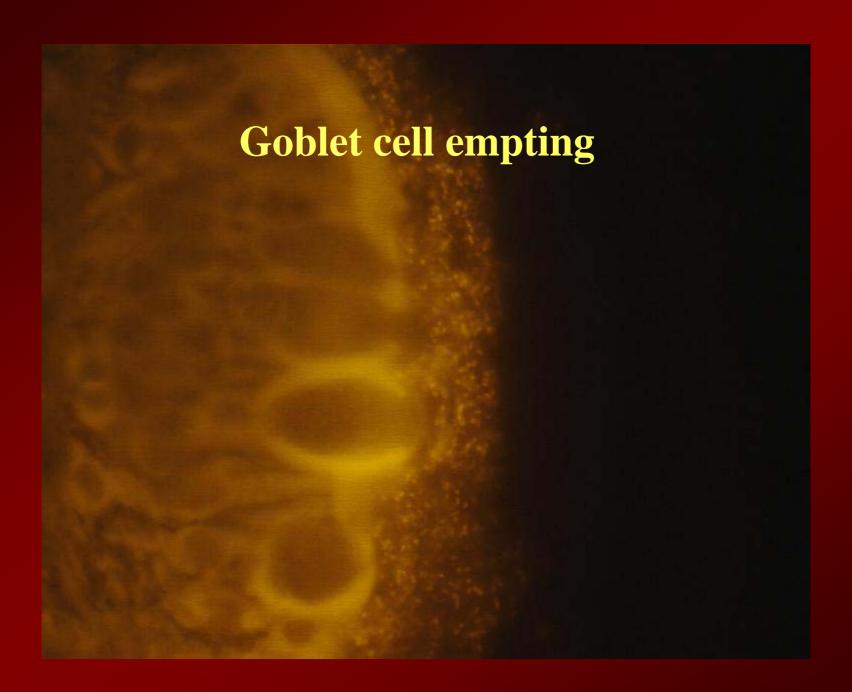


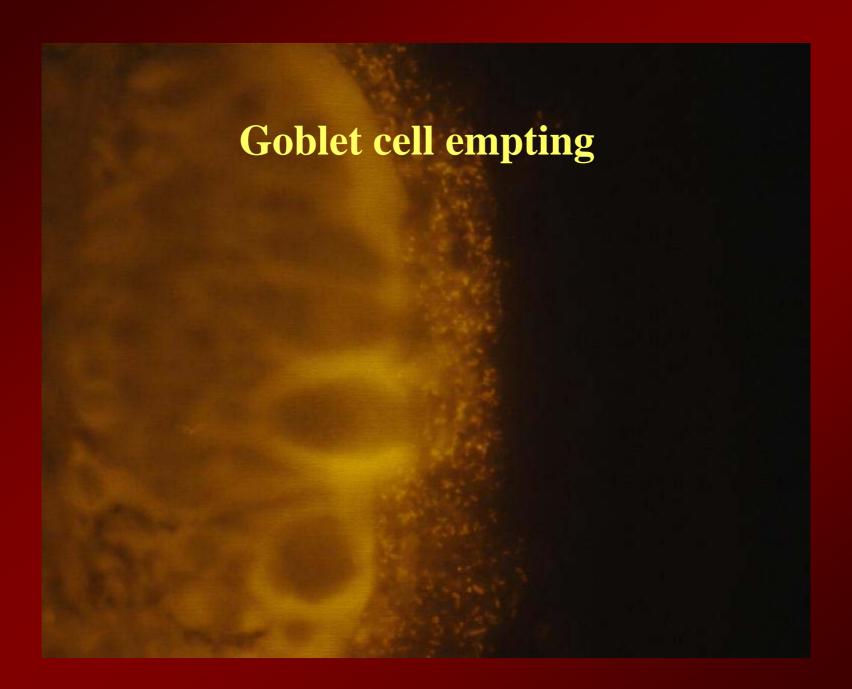


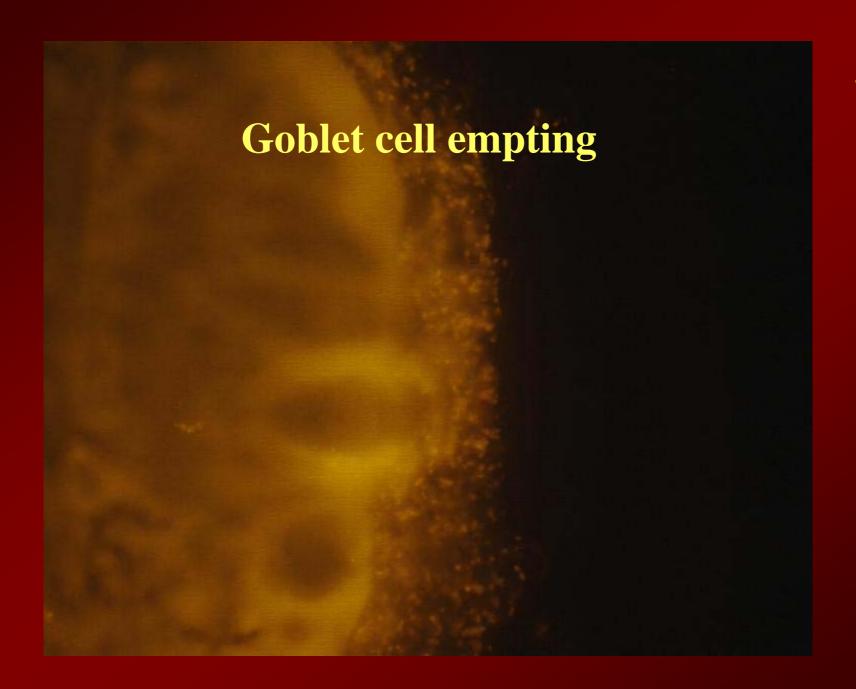














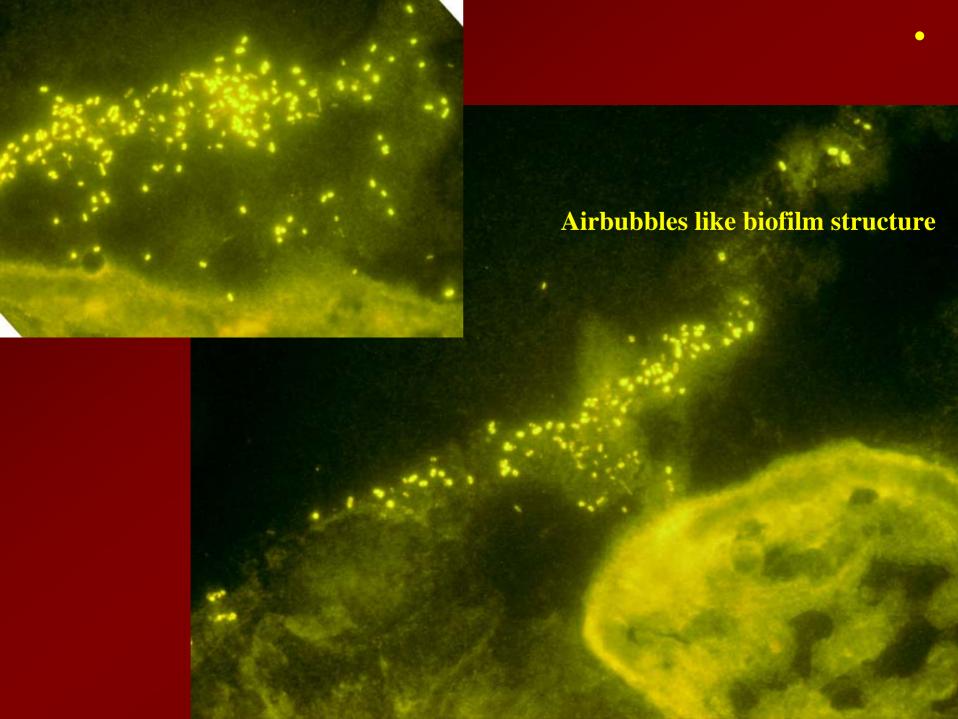


Table 1 FISH probes

Name Target

Eub338 virtually all *Bacteria*, Kingdom (Eu)Bacteria

Arch915 Archaea

Alf1b Alpha group of Proteobacteria: Rhodobacter, Acetobacter, Paracoccus, some Pseudomonas etc.

Beta 42a Beta subclass of Proteobacteria: Rhodocyclus, Bordetella, Neisseria, Thiobacillus, Alcaligenes and other

Gam42a gamma subclass of Proteobacteria: Enterobacteriaceae, Proteus, Legionella, Azotobacter

Ec1531 Escherichia coli

Srb385 sulfate reducing bacteria, the main component of the delta subclass of *Proteobacteria*

Hpy-1
Arc1430
Arcobacter ssp. epsilon subclass of Proteobacteria
HGC
Gram positive bacteria with high G+C content
Gram positive bacteria with low G+C content

Sfb Segmented filamentous bacteria

Erec482 Clostridium coccoides - Eubacterium rectale group

Chis150 Clostridium histolyticum group

Clit135 C. lituseburense group

Lab158 Lactobacillus and Enterococcus group

Strc493 Streptococcus

Ecyl Eubacterium biforme, Clostridium innocuum and other

Phasco Acidaminococcus fermentans and other

Veil Veillonella group

Rbvo,Rfla Ruminococcus flavefaciens, Clostridium leptum

Bif164 Bifidobacterium

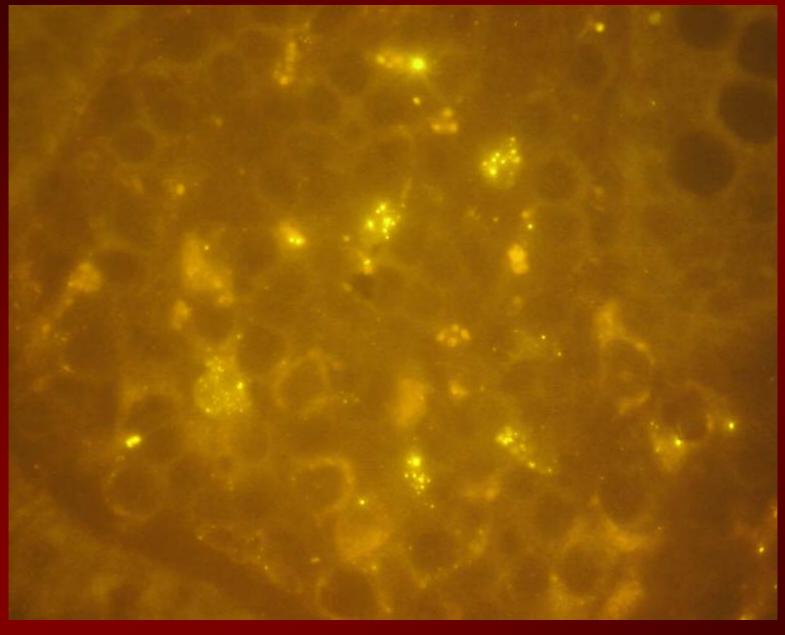
Ato291 Atopobium, Coriobacterium, Eggerthella and Collinsella spp

CF319a Cytophaga-Flavobacterium group
Bac303 Bacteroides/Prevotella group
Bfra602 Bacteroides fragilis group

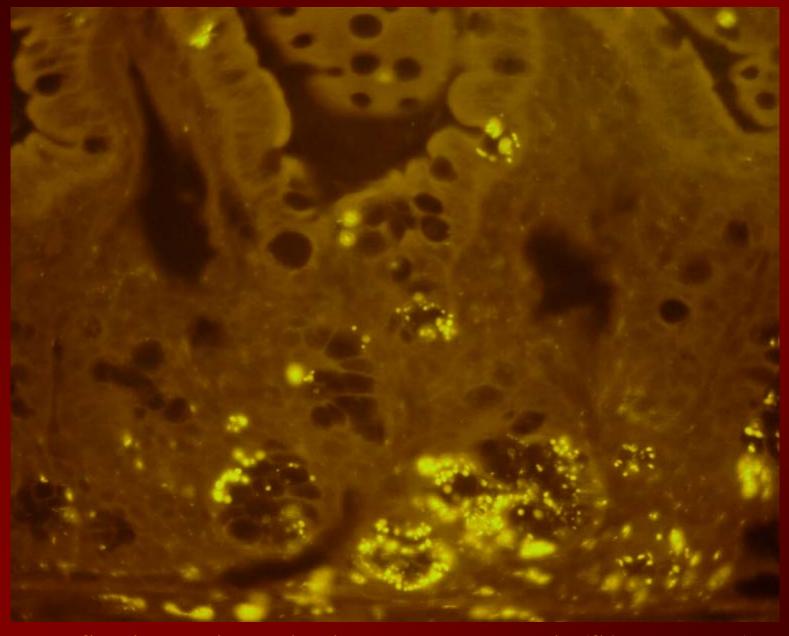
Bdis656 B. distasonis group



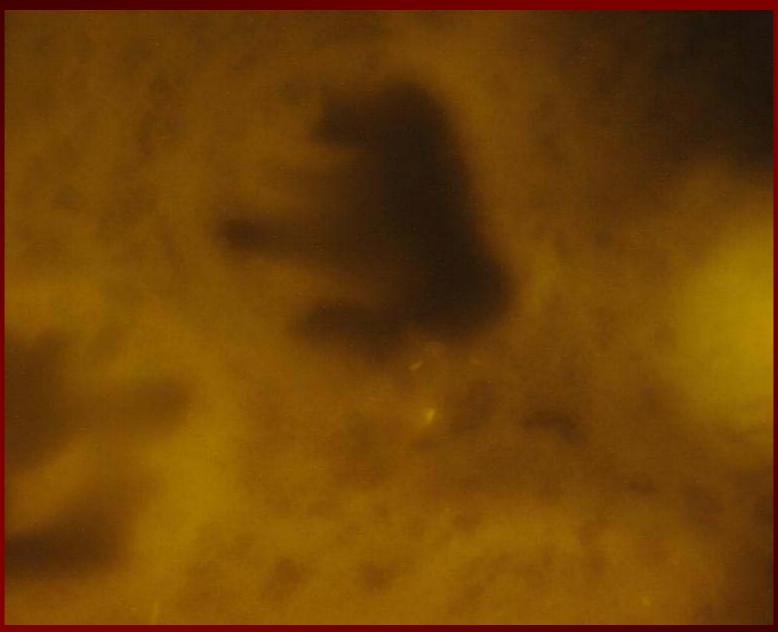
FISH signals simulating intracellular bacteria



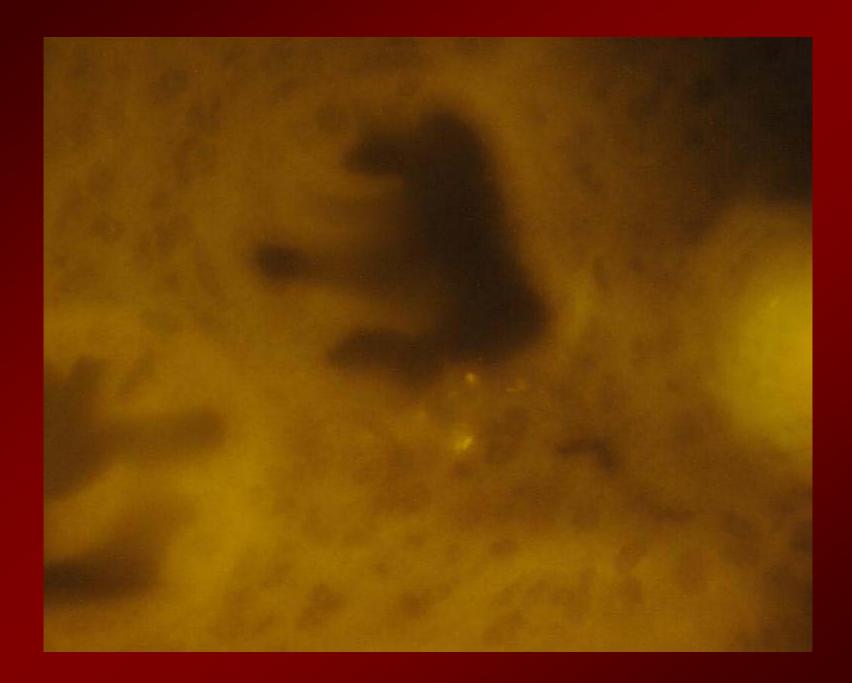
FISH signals simulating intracellular bacteria

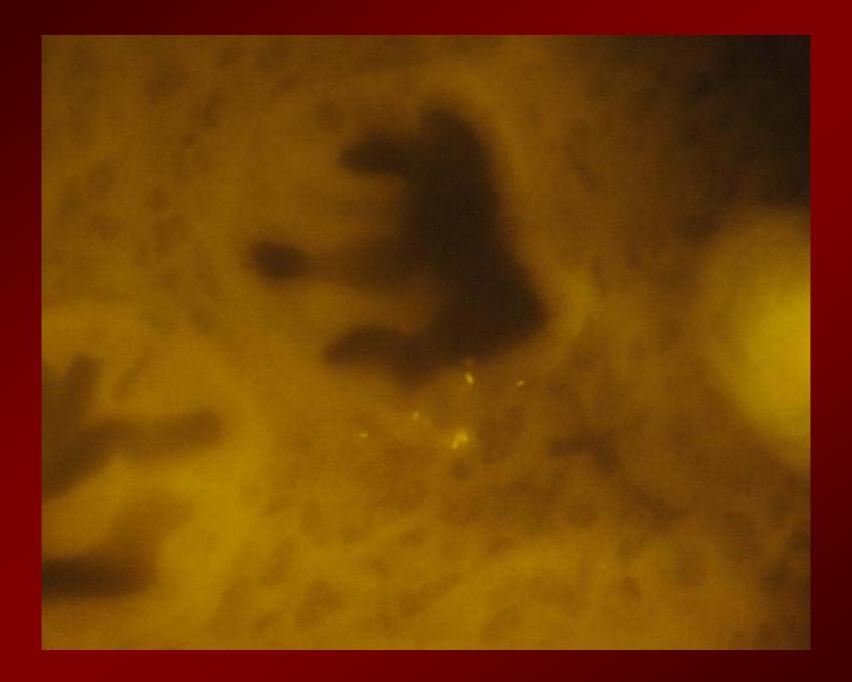


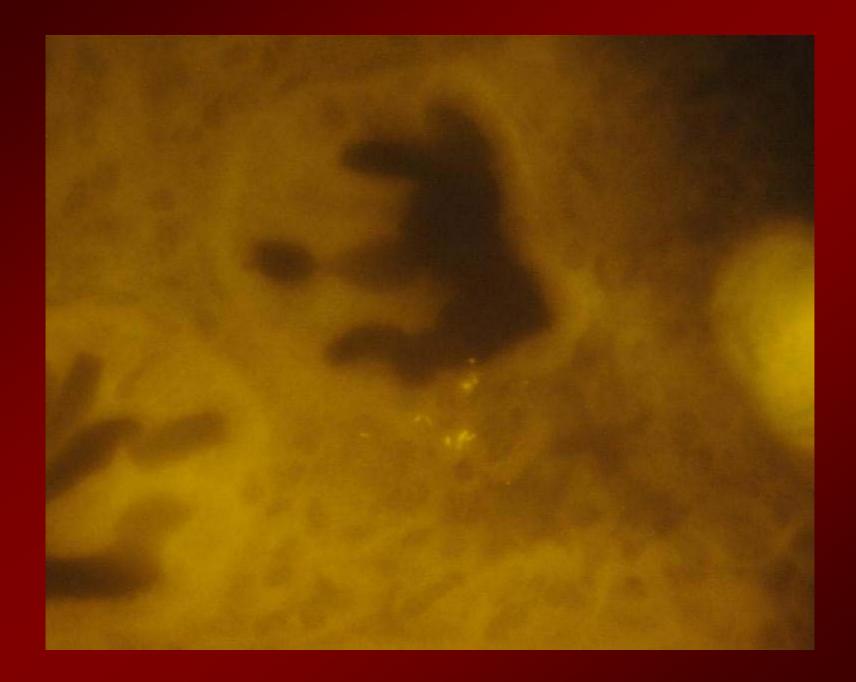
FISH signals simulating intracellular bacteria (SAMP mouse)



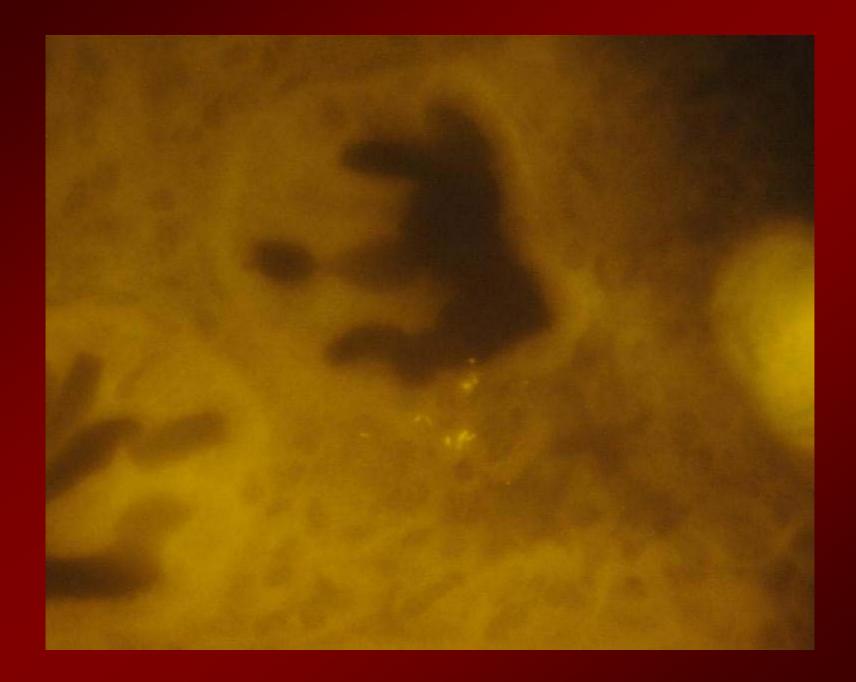
Intraepithelial bacteria located perinuclear at different levels

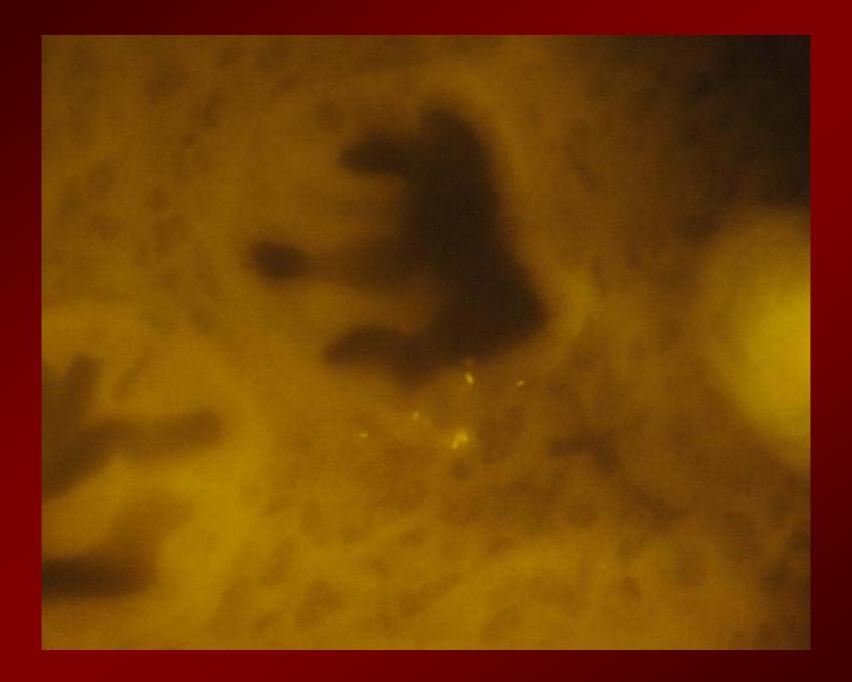


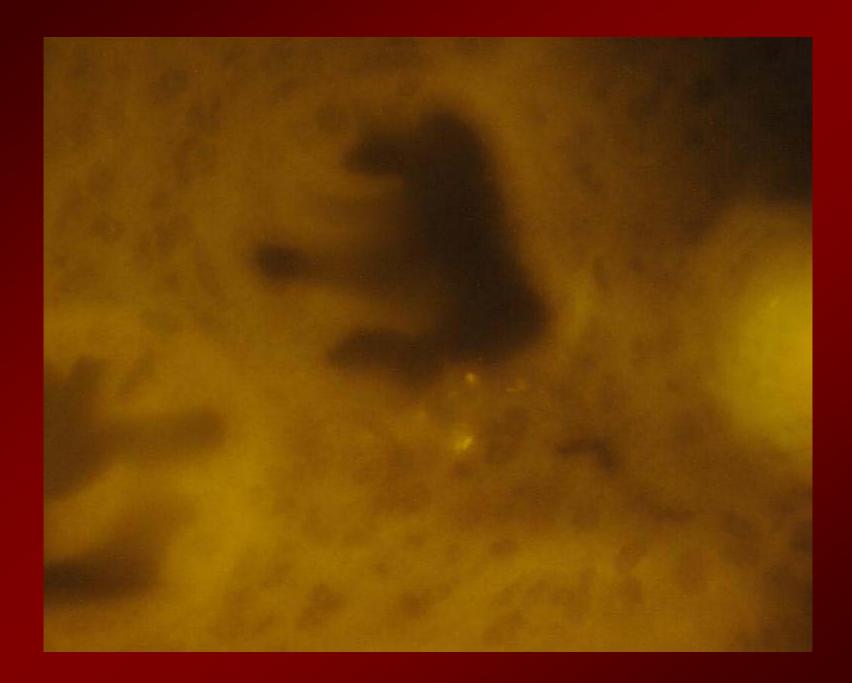


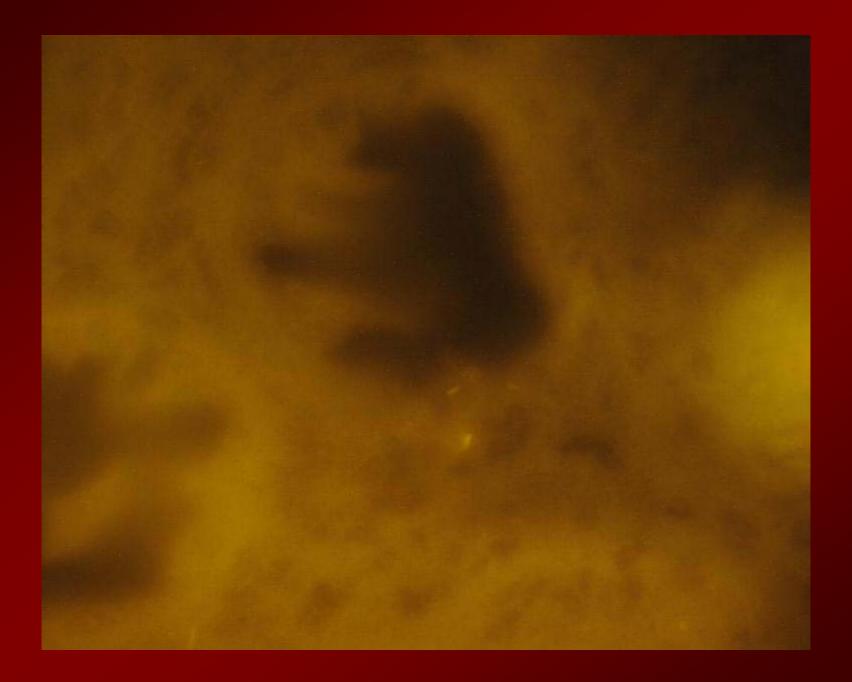


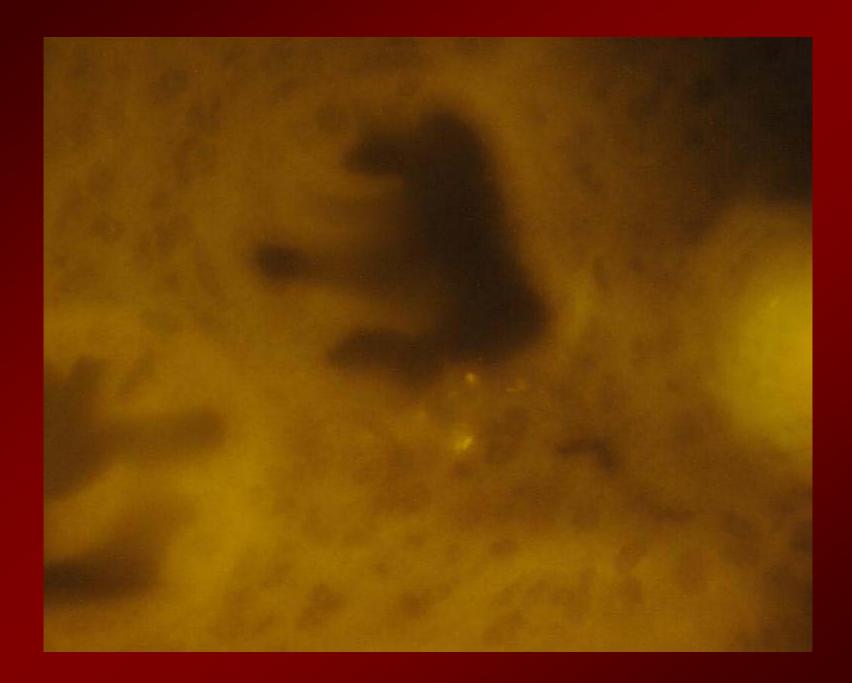


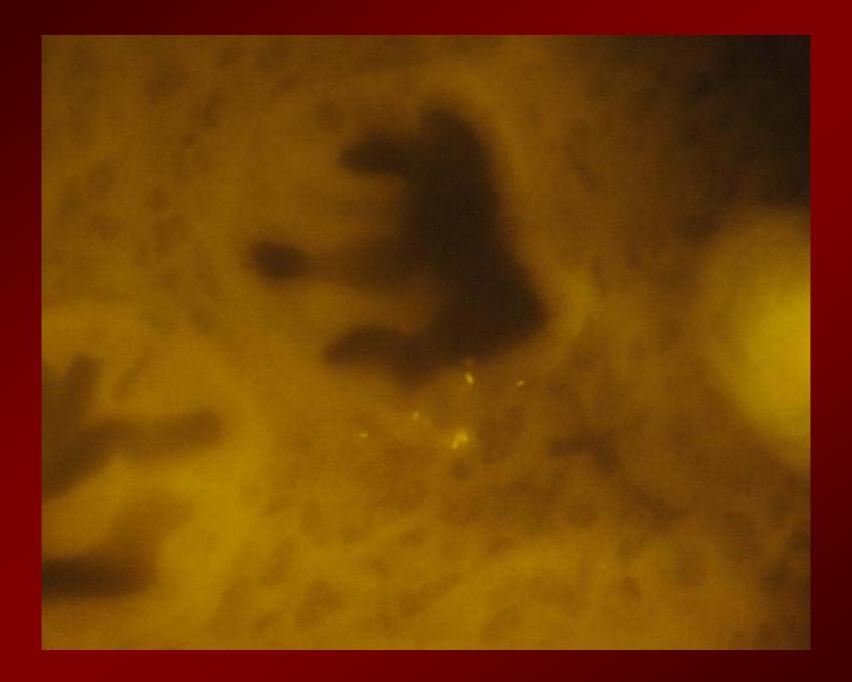


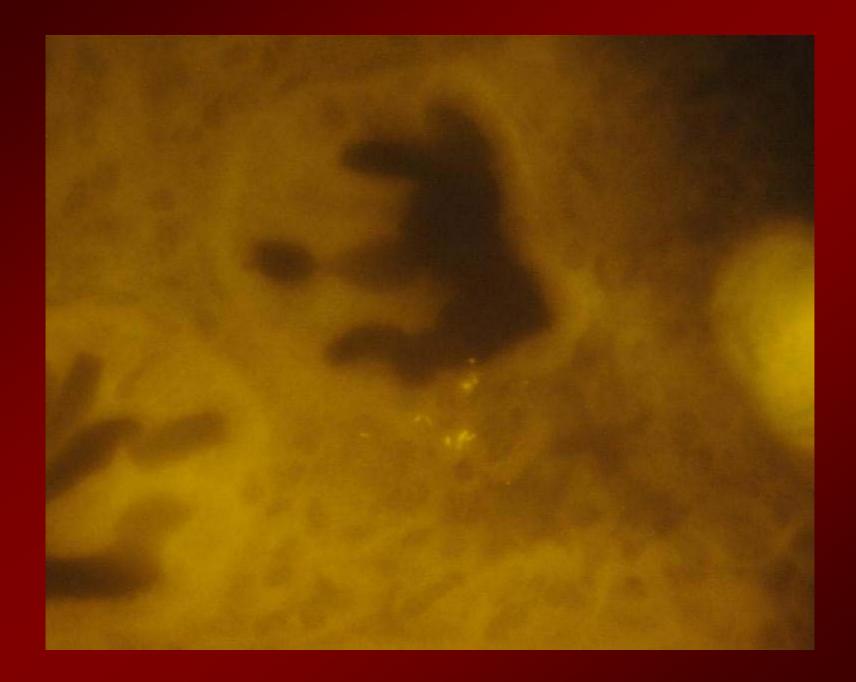


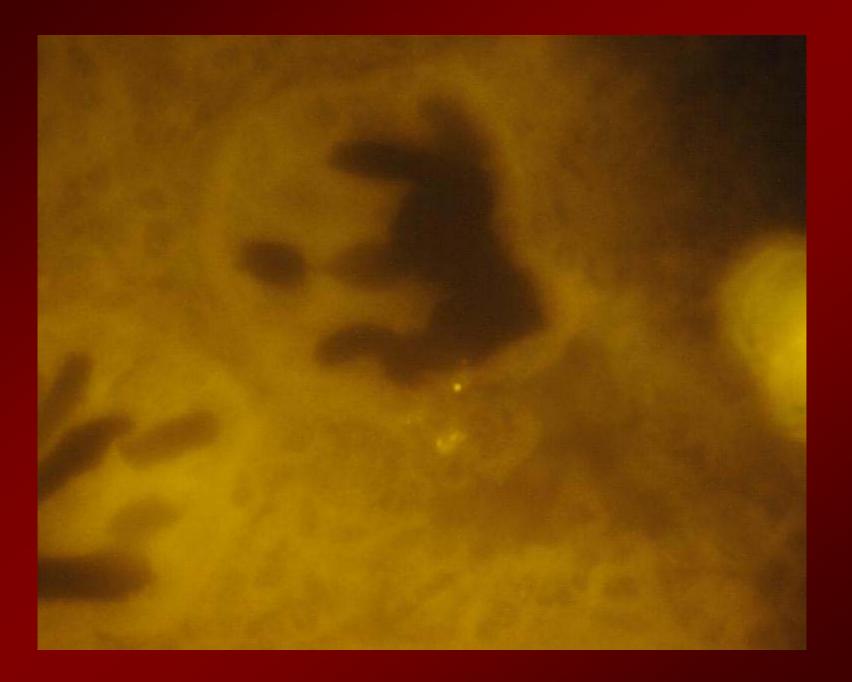












The mucosa of patients with IBD is covered with a complex spatially structured multispecies biofilm. This biofilm is organized in islands, patches and lawns of multispecies bacteria.

Biofilm patches and layers penetrate mucus leading to direct contact between fecal flora and epithelia. They are ideal for luminal antigens and toxins to reach the unshielded epithelial surface and to trigger cascades of host responses.

The peculiarities of individual immunity and genetic disposition may explain the rest.

We thank Broad Medical Research Program BMRP for supporting this project