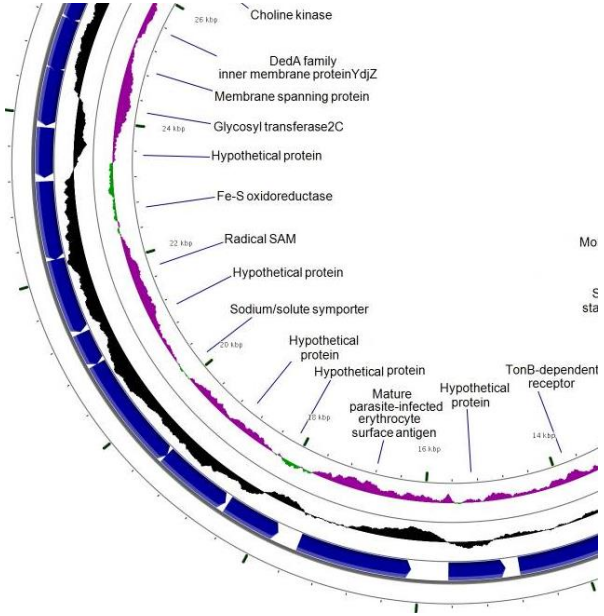
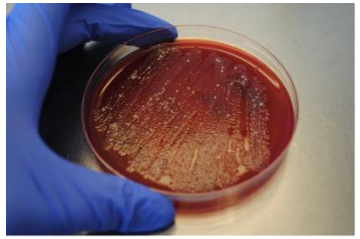


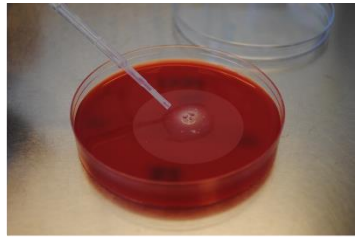
Campylobacter concisus og inflammatorisk tarmsygdom

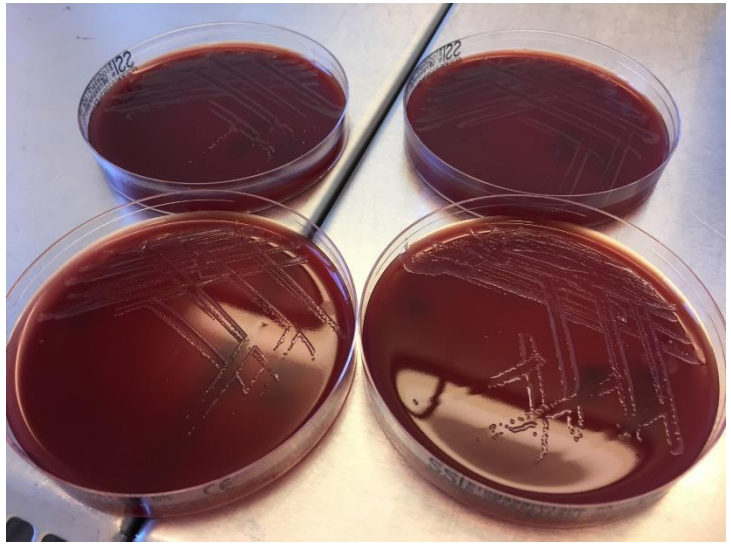
Karina Frahm Kirk, læge, ph.d.
Infektionsmedicinsk Afdeling
Aalborg Universitetshospital

DSKM tarmbakteriologisk møde, Slagelse juni 2017

Program



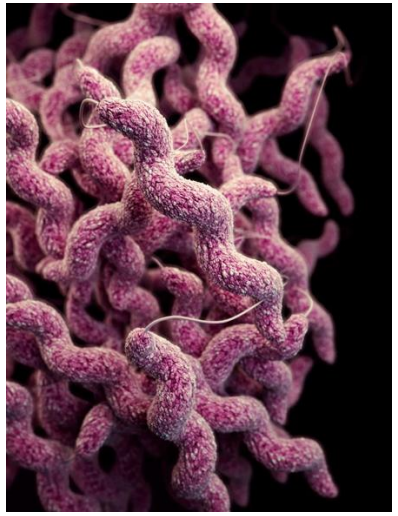


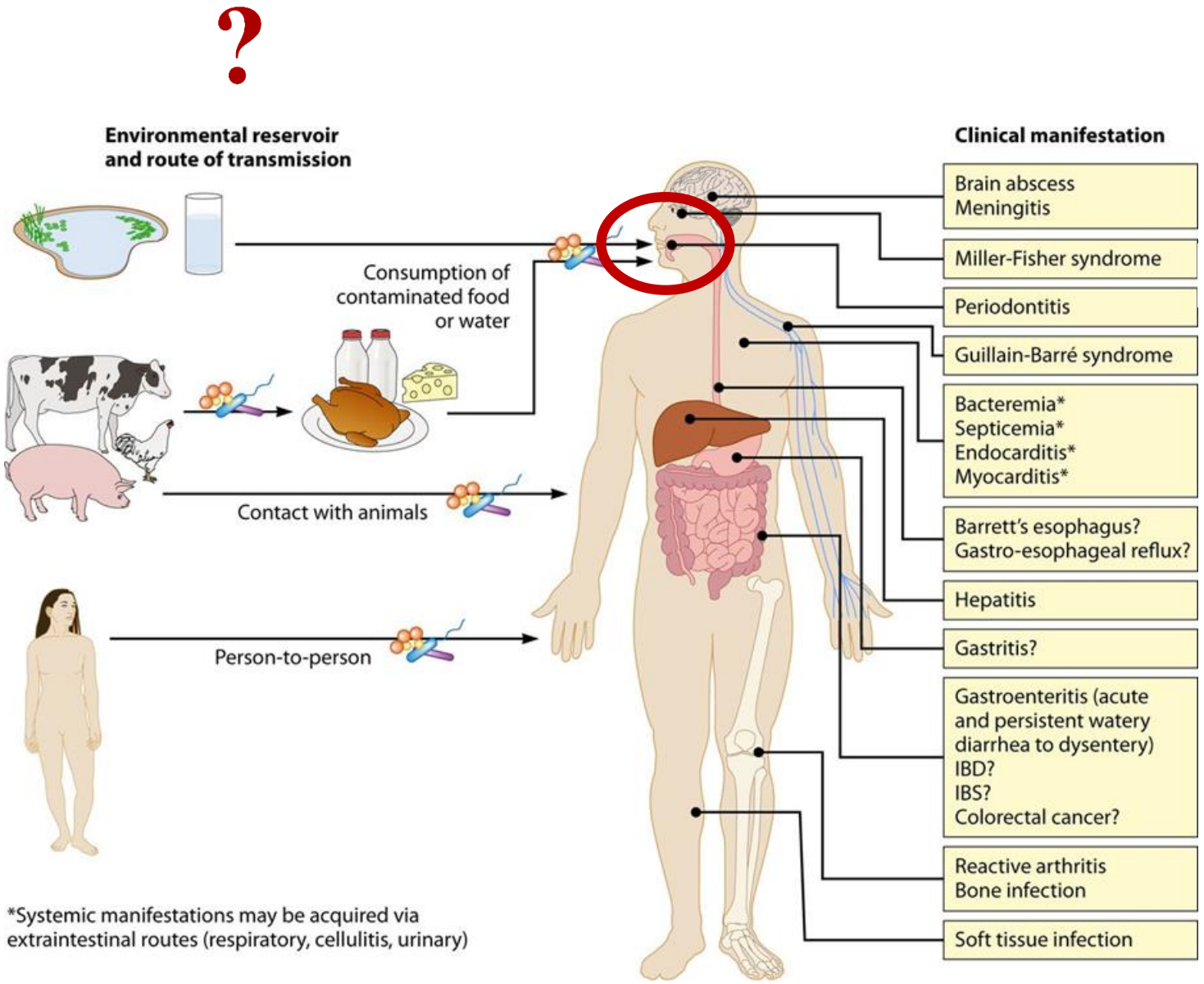


- Baggrund
  - *Campylobacter concisus*
  - Inflammatorisk tarmsygdom (IBD)

- Dyrkning af *C. concisus* fra kliniske prøver
- WGS af *C. concisus*

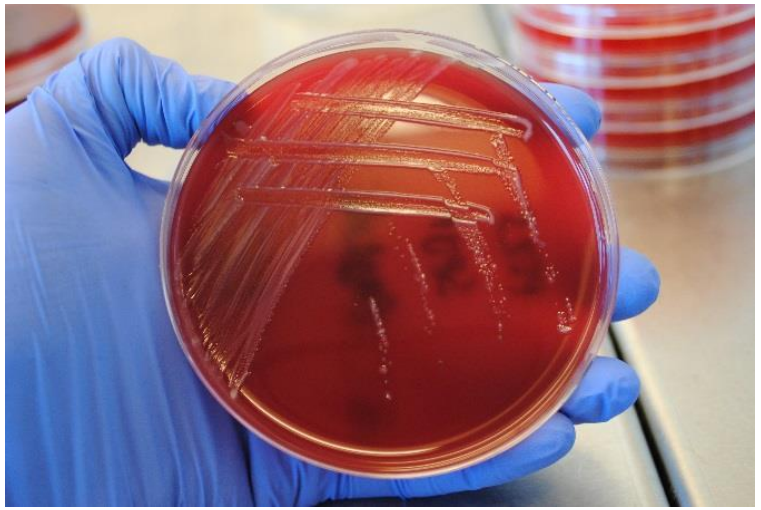
- Konklusion og perspektiver





Kaakoush et al. *Clin Microbiol Rev* 2015

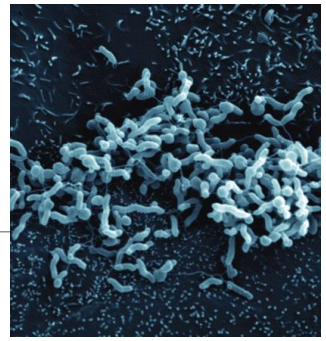
Campylobacter concisus

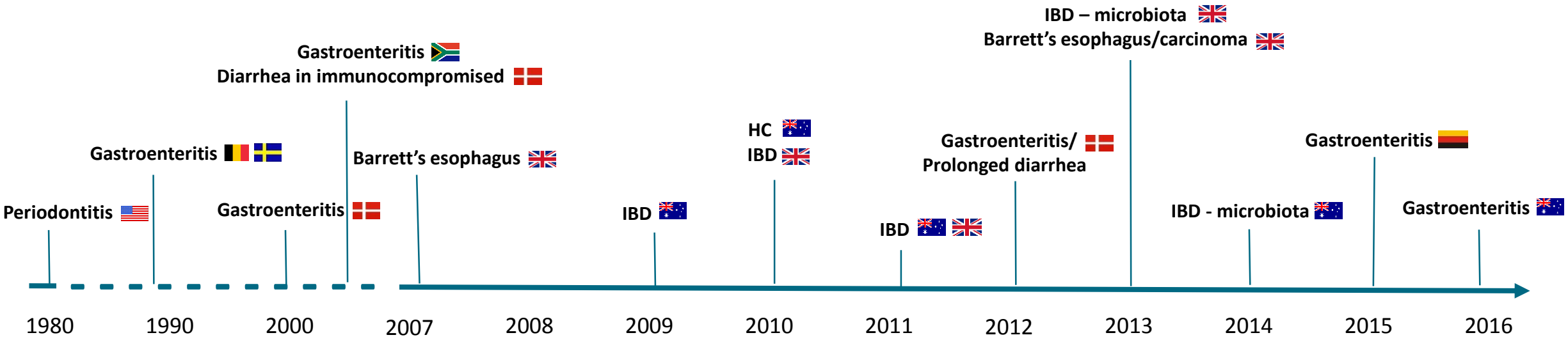


- Første beskrivelse i 1980erne hos patienter med periodontitis[1]
- Del af den normale mundhuleflora[2]
- Følsomme for cefoperazone (i mCCDA)
- Dyrkning ved filter-metode[3]
- H_2 bedrer væksten

1. Tanner et al. *Int J Syst Bacteriol* 1981
2. Zhang et al. *J Clin Microbiol* 2010
3. Engberg et al. *J Clin Microbiol* 2000

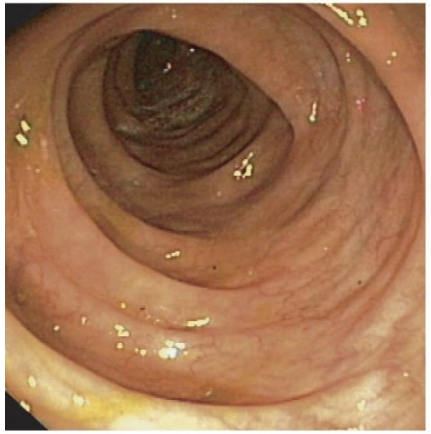
Campylobacter concisus tidslinie

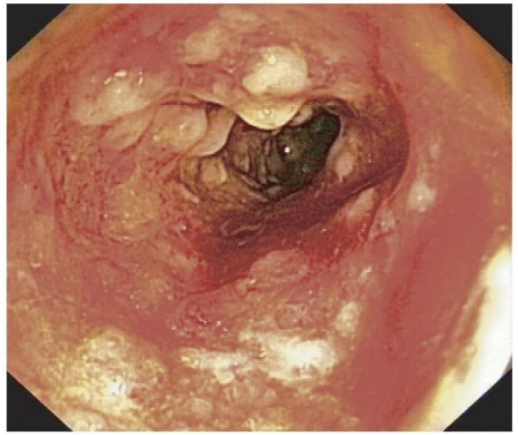


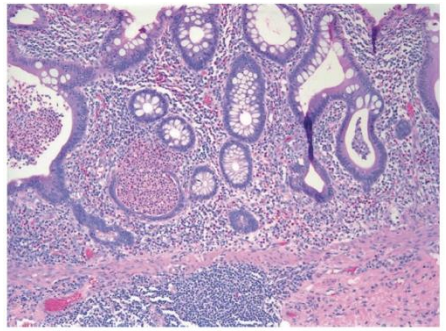


Inflammatorisk tarmsygdom (IBD)

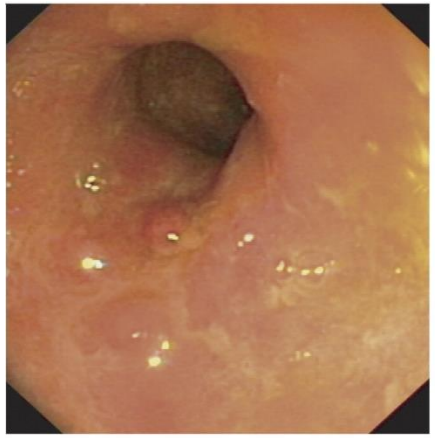
Colitis Ulcerosa (UC)

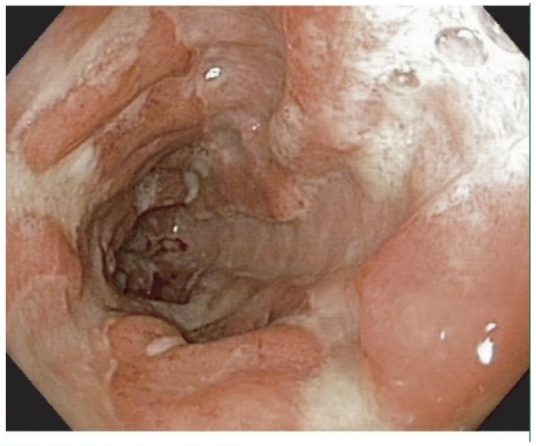


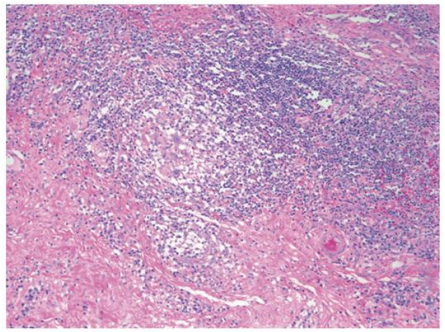




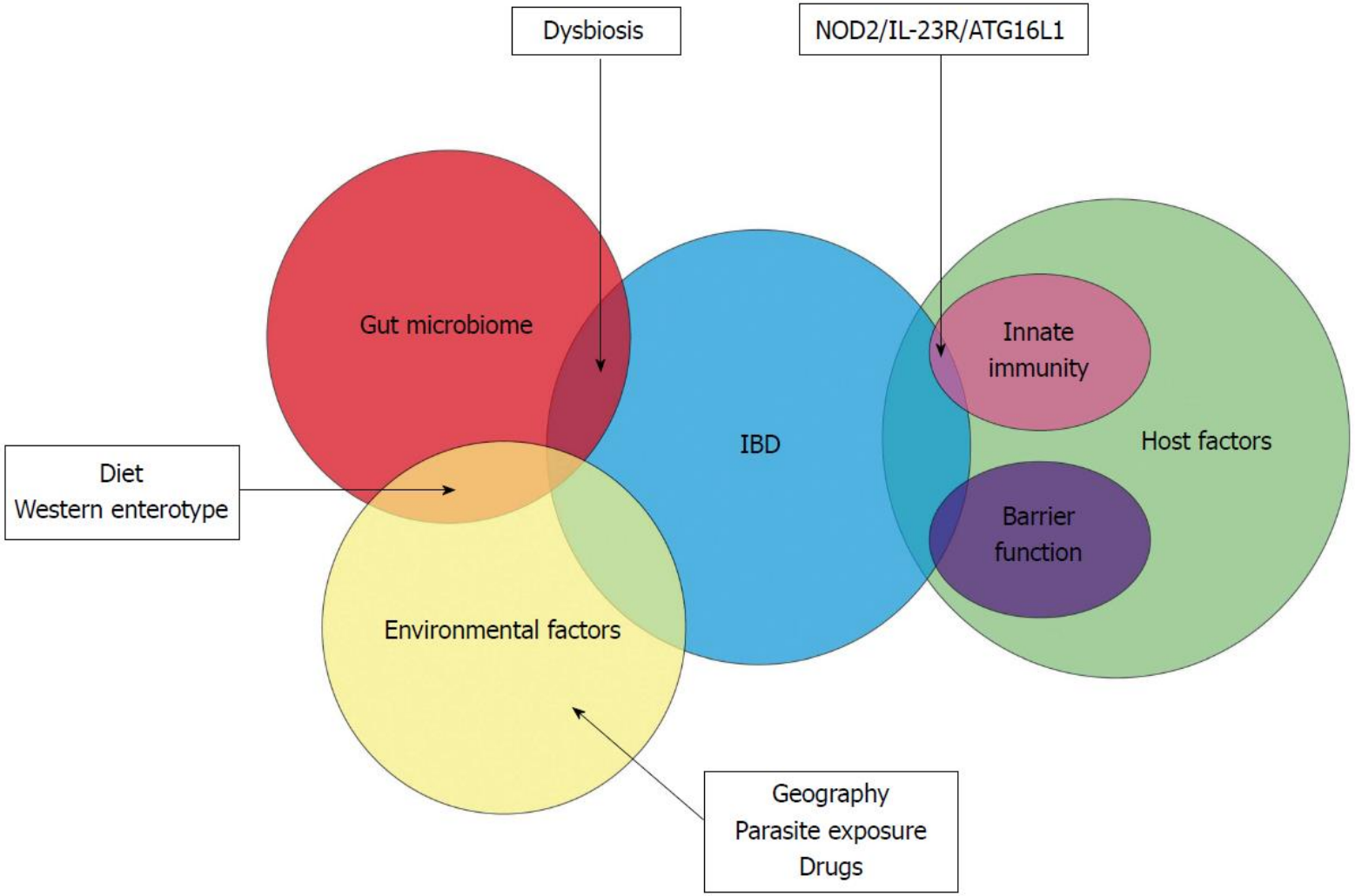
Morbus Crohn (CD)





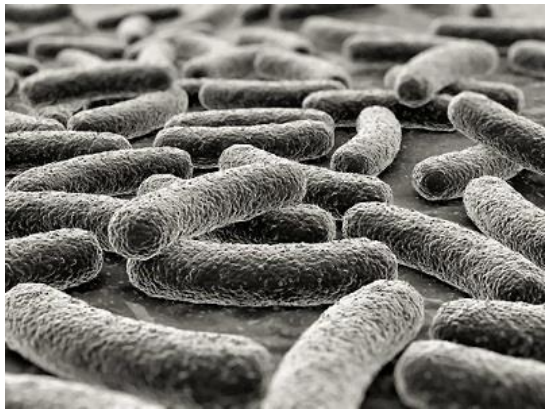


Baumgart et al. *Lancet* 2007



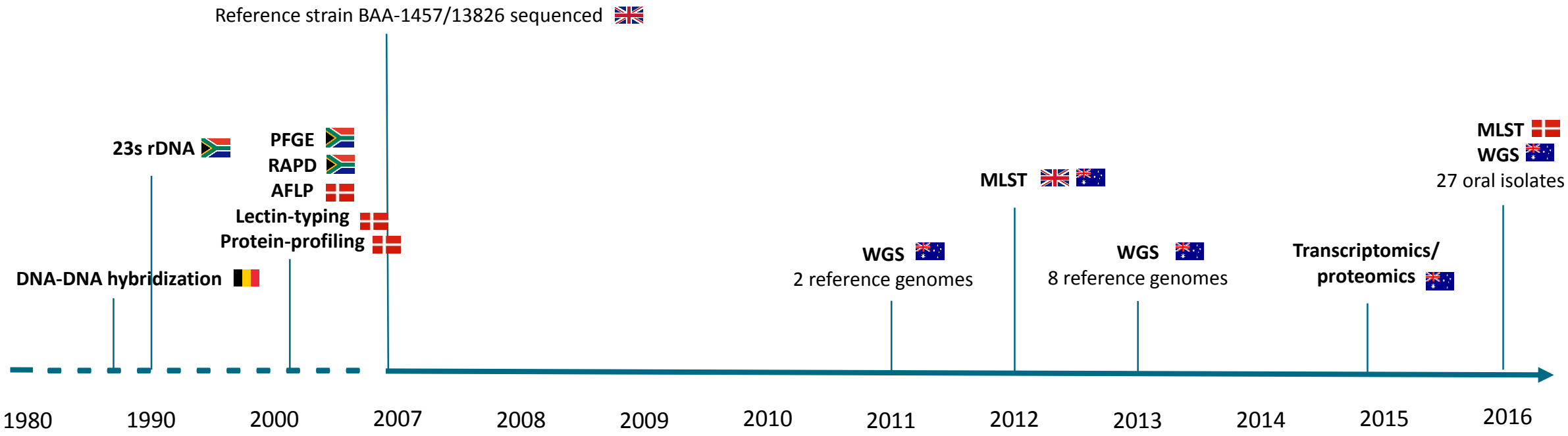
Hold et al. *W J Gastroenterology* 2014

Mikroorganismer i IBD



- *Mycobacterium avium* subsp. *paratuberculosis*
- *E. coli*
- *Campylobacter*
- *Salmonella*
- *Clostridium difficile*
- Cytomegalovirus
- Epstein-Barr virus

Genetisk diversitet – typning

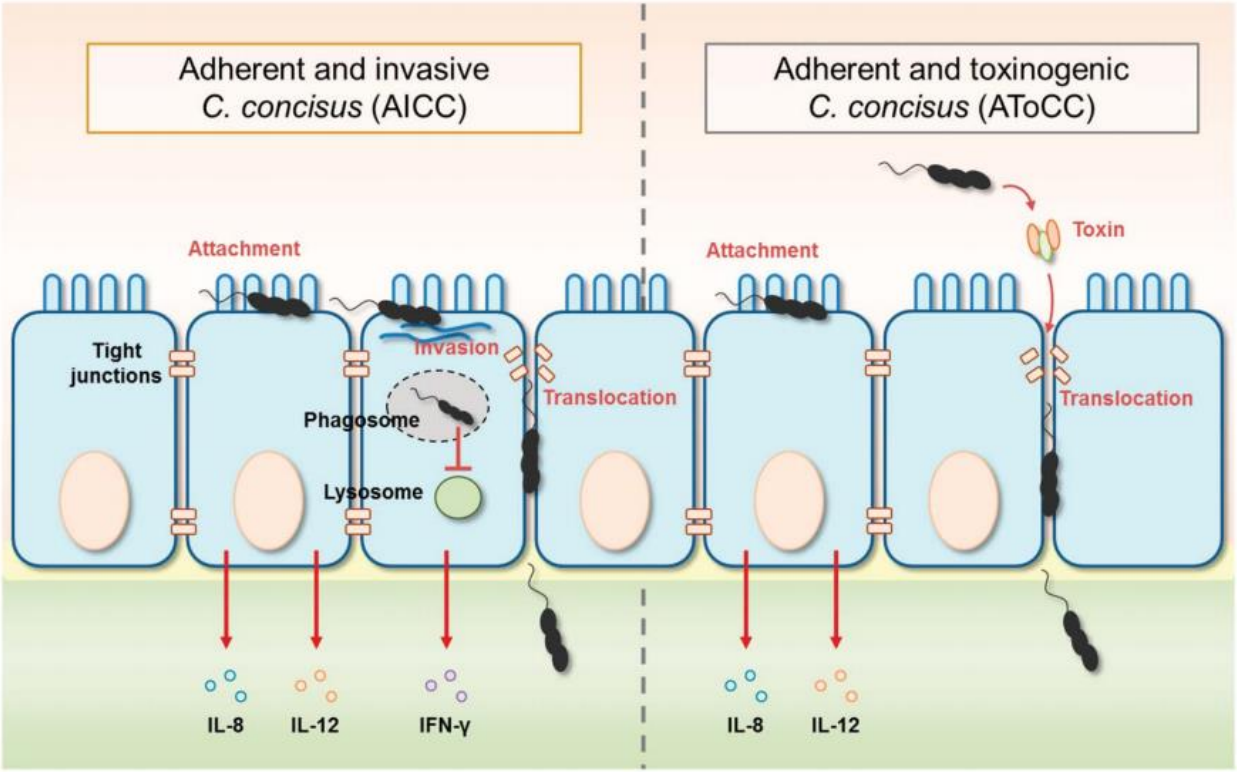


Patogene potentiale

TABLE 2. Classification of *C. concisus* Subtypes (Pathotypes) Based on Genetic and Functional Characteristics

	C. concisus Subtypes		
	AICC	AToCC	Commensals
Motility	✓	✓	✓
Attachment	✓	✓	✓
Intracellular survival	✓ (high)	✓ (low or none)	✗
Paracellular invasion	✓	✓	✗
Restriction–modification system[a]	✓	✗	✗
Toxin production	✗	✓	✗
Pathogenic	✓	✓	✗

[a]Restriction–modification systems are protective mechanisms used by bacteria to defend against foreign DNA.



Kaakoush et al. *Inflamm Bowel Dis* 2014

Formål

- At optimere dyrkning fra tarmbiopsier og evaluere forekomsten af levedygtige *C. concisus* hos tarm-syge og –raske
- At undersøge om individer kan være koloniseret med forskellige *C. concisus* isolater
- At undersøge om specifikke *C. concisus* virulente subtyper er associeret til tarmsygdom

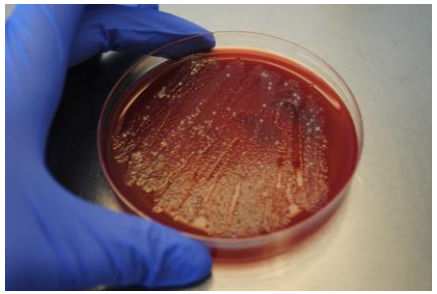
Prøveindsamling

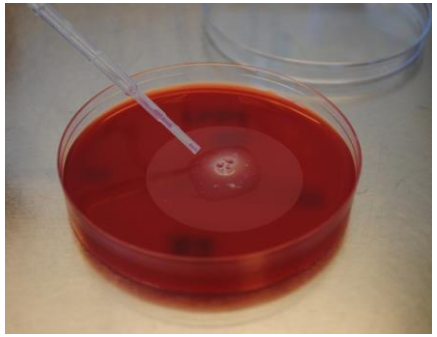
IBD n=57
HC n=28
GE n=2

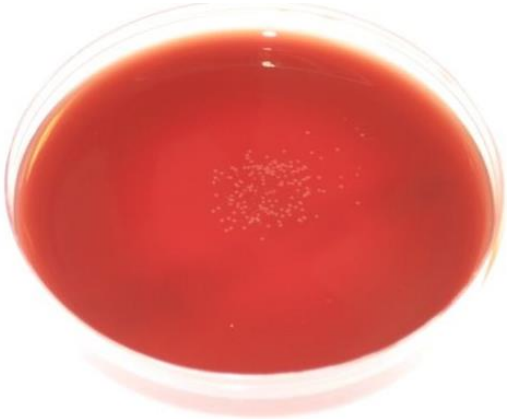
Koloskopi – biopsier
spytprøve

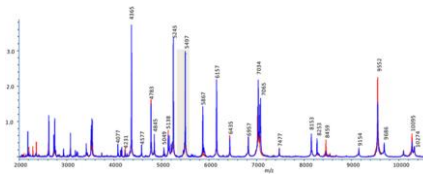
Afføringsprøve

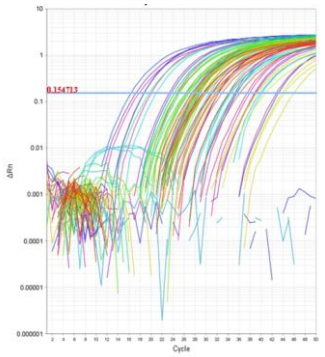
Dyrkning fra biopsier

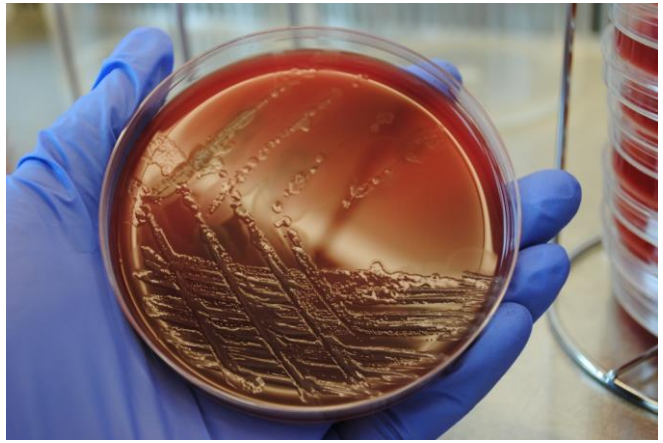






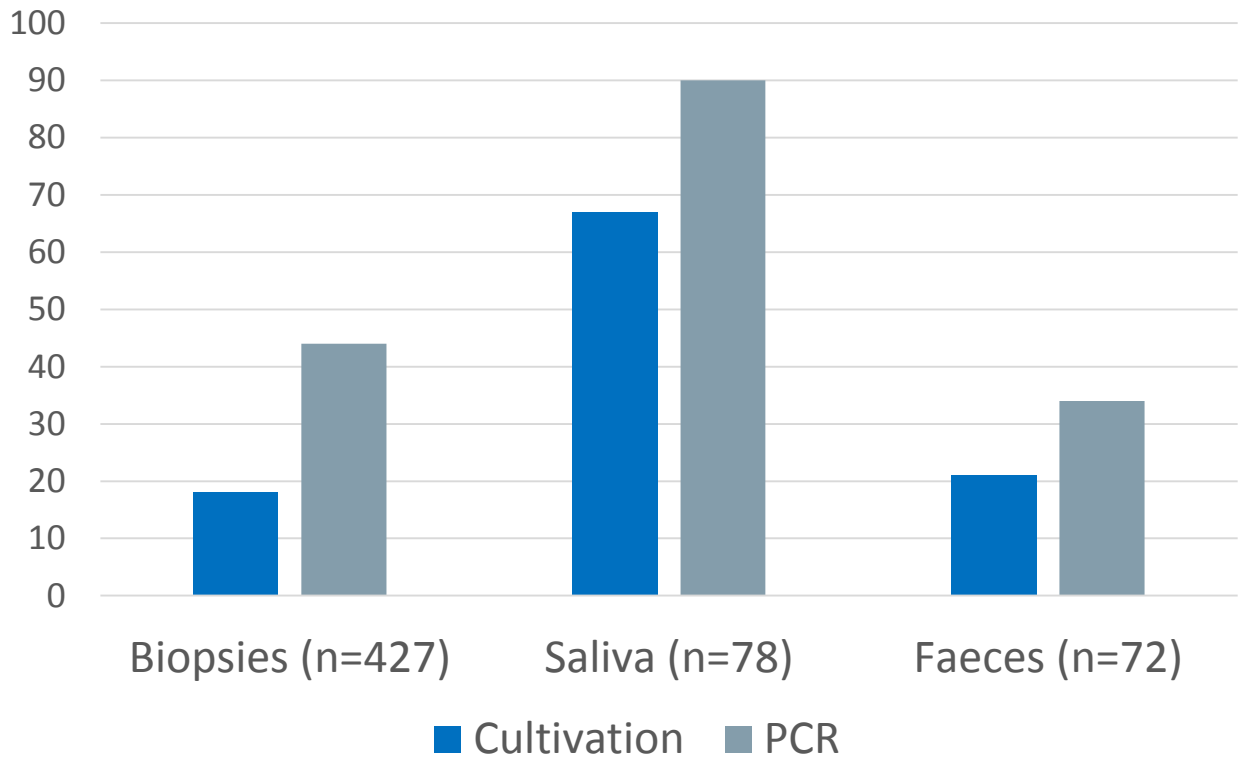




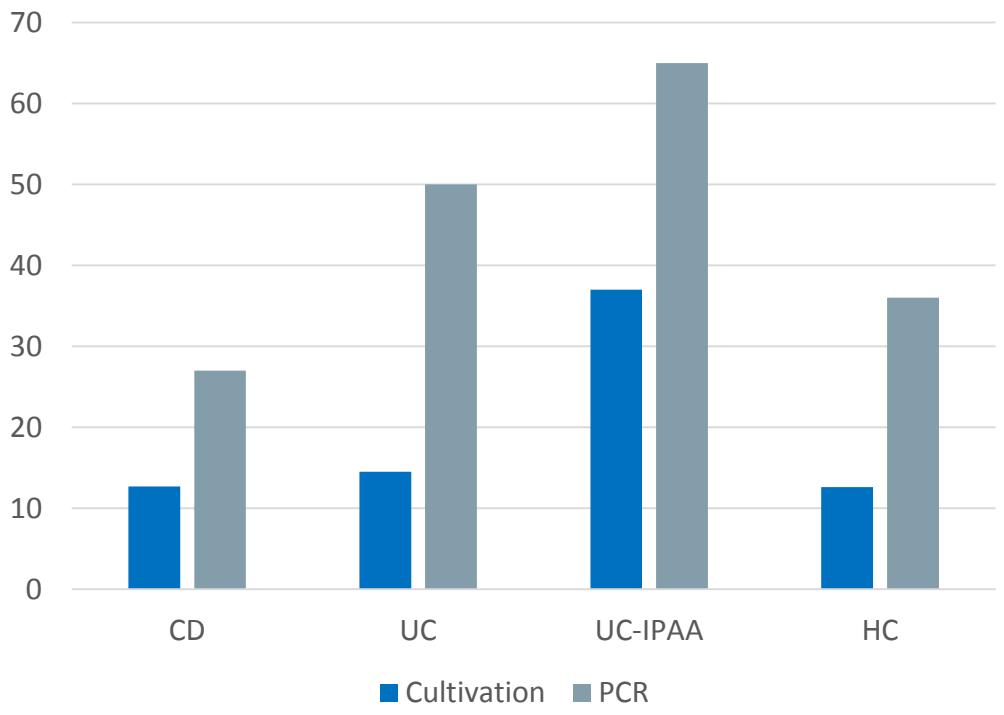


0 2 4 6 8 10

Resultater


100
90
80
70
60
50
40
30
20
10
0
Biopsies (n=427)
Saliva (n=78)
Faeces (n=72)
Cultivation
PCR

Resultater - biopsier



	CD	UC	IPAA	HC	P-value
Age, mean (SD)	42 (13)	54 (13)	43 (11)	56 (12)	0.95
Sex, male (%)	4 (44)	7 (44)	13 (50)	15 (58)	0.80
Inf. symptoms (%)*	5/9 (56)	7/16 (44)	22/27 (82)	-	0.03
Endoscopic inf. (%)	4/9 (44)	7/16 (44)	18/27 (67)	-	0.26
Microscopic inf. (%)	5/9 (56)	7/16 (44)	21/27 (78)	-	0.07

Bacterial Isolate Sequence Database (BIGSdb)

Search or browse Maiden Group Campylobacter BIGSdb database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance/phenotype fields: id = Enter value...

Attribute values list: Field: id

5686
5680
5685
5700
5682
5696

Display/sort options: Order by: id ascending; Display: 25 records per page

Action: Reset Submit

Modify form options

19 records returned. Click the hyperlinks for detailed information.

Isolate fields								Seqbin size (bp)	Contigs	MLST									Loci		
id	isolate	country	year	disease	source	epidemiology	penner			faspA	fglnA	fgltA	fglyA	fpgm	ftkt	funcA	ST	clonal complex	flaA	flaB	porA
5599	AAUH-10UCil-a	Denmark	2016		human unspecified			2034805	29												
5613	AAUH-12CDdes3	Denmark	2016		human unspecified			1800193	73												
5618	AAUH-10UCf2	Denmark	2016		human stool			2004950	56												
5629	AAUH-11UCsig-a	Denmark	2016		human unspecified			2003896	47												
5649	AAUH-12CDrec-a	Denmark	2016		human unspecified			1927419	83												
5650	AAUH-11UCdes-a	Denmark	2016		human unspecified			1917437	65												
5651	AAUH-11UCo	Denmark	2016		human unspecified			1913684	153												
5659	AAUH-12CDce	Denmark	2016		human unspecified			1871198	47												
5660	AAUH-12CDdes4	Denmark	2016		human unspecified			1858196	40												
5661	AAUH-12CDdes2	Denmark	2016		human unspecified			1856131	64												
5670	AAUH-12CDo	Denmark	2016		human unspecified			1814912	44												
5680	AAUH-10HCdes4	Denmark	2016	carrier	human unspecified			1902852	100												
5682	AAUH-10HCdes7	Denmark	2016	carrier	human unspecified			1906753	79												
5685	AAUH-10HCdes5	Denmark	2016	carrier	human unspecified			1910057	88												
5686	AAUH-10HCdes3	Denmark	2016	carrier	human unspecified			1910929	66												
5688	AAUH-11HCf	Denmark	2016	carrier	human stool			1924722	235												
5692	AAUH-11HCo-a	Denmark	2016	carrier	human unspecified			1940932	238												
5696	AAUH-10HCtra	Denmark	2016	carrier	human unspecified			1948506	76												
5700	AAUH-10HCdes6	Denmark	2016	carrier	human unspecified			1980280	111												

Analysis tools:

Breakdown: Fields | Two Field | Polymorphic sites | Combinations | Schemes/alleles | Publications | Sequence bin | Tag status

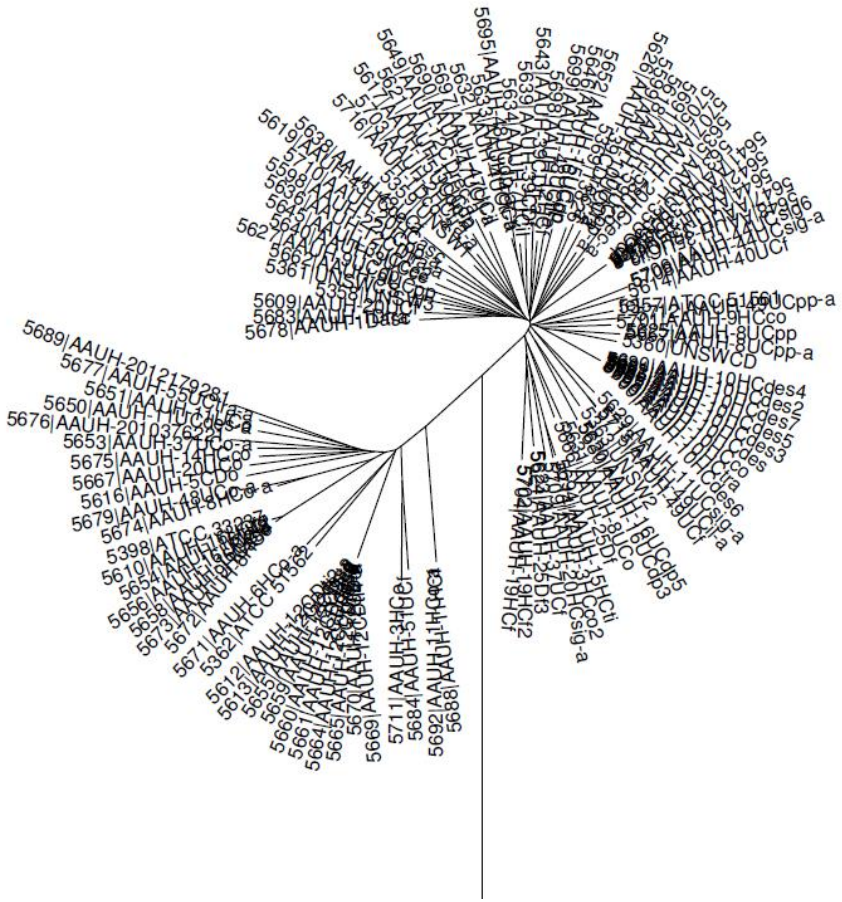
Analysis: BURST | Codons | Presence/Absence | Genome Comparator | BLAST | PhyloTree | PhyloViz

Export: Dataset | Contigs | Sequences

- 104 isolater (42 patienter)
  - spyt n=14
  - biopsier n=71
  - fæces n=19
- 9 reference genomer

UNIVERSITY OF BATH

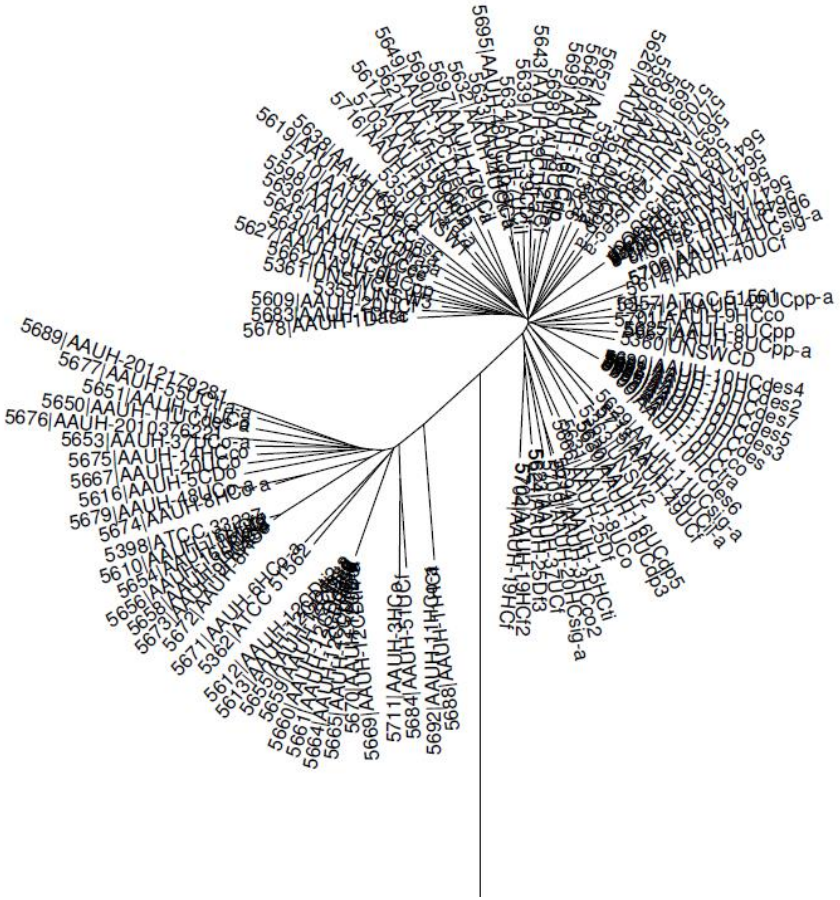
MLST – *C. concisus* husholdningsgener

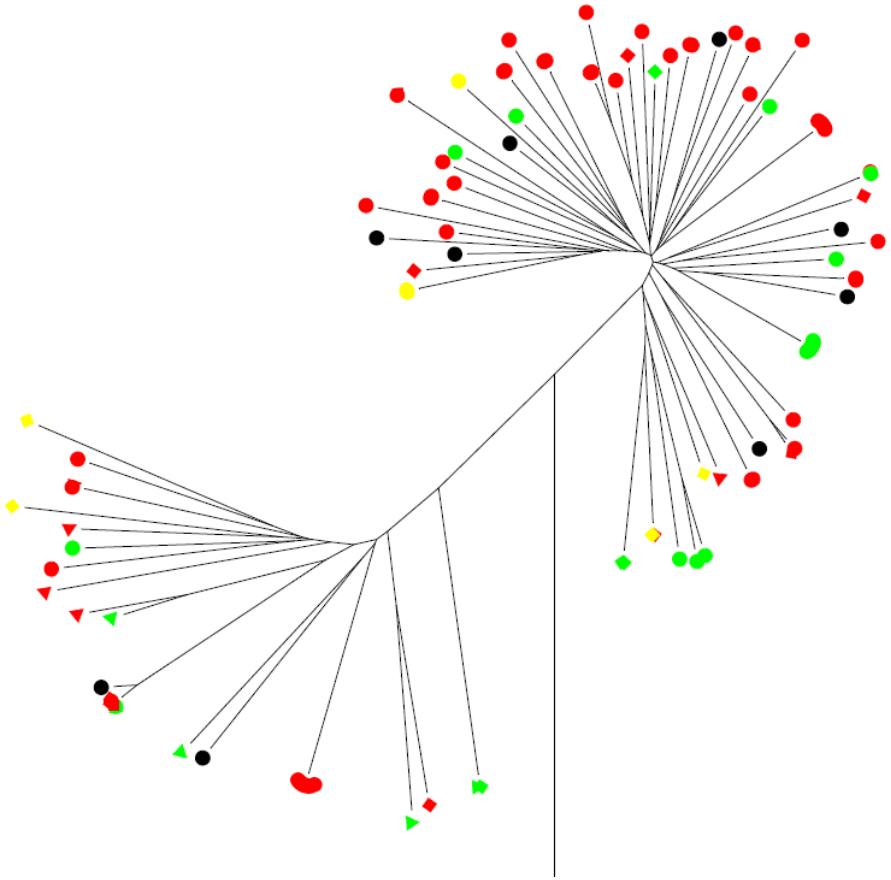


- aspatase (*aspA*)
- ATP synthase subunit alpha (*atpA*)
- glutamine synthetase (*glnA*)
- citrate synthase (*gltA*)
- serine hydroxyl methyl transferase (*glyA*)
- dihydroxy-acid dehydratase (*ilvD*)
- phosphor glucomutase (*pgm*)

- 71 ST typer

MLST – kliniske grupper





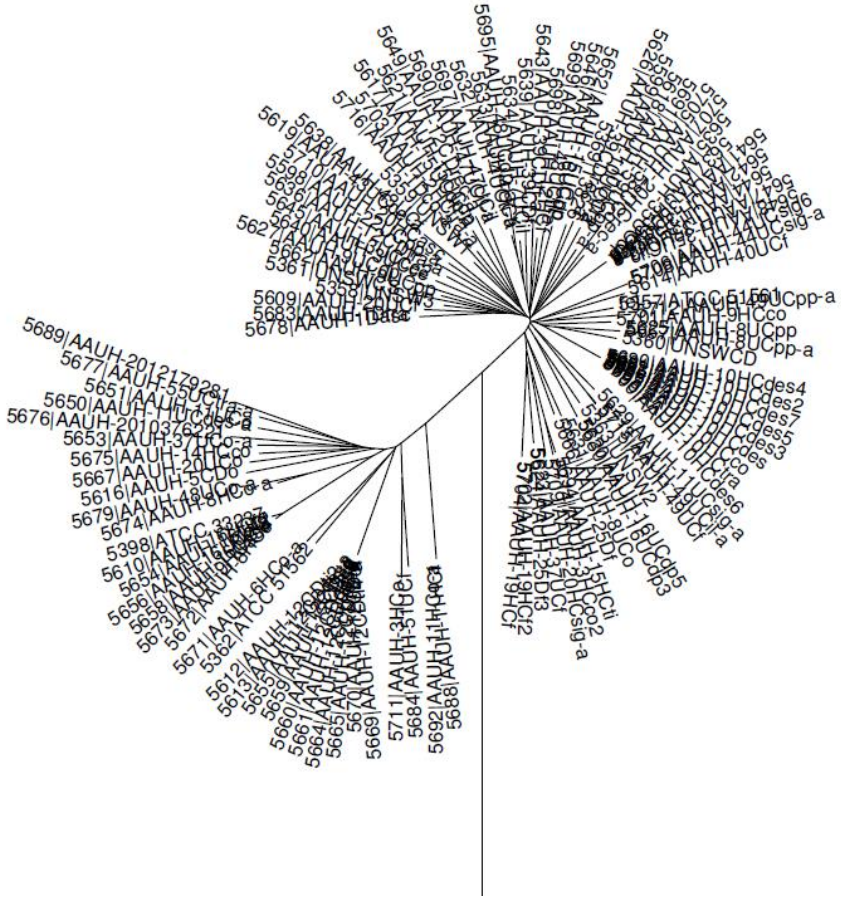
IBD

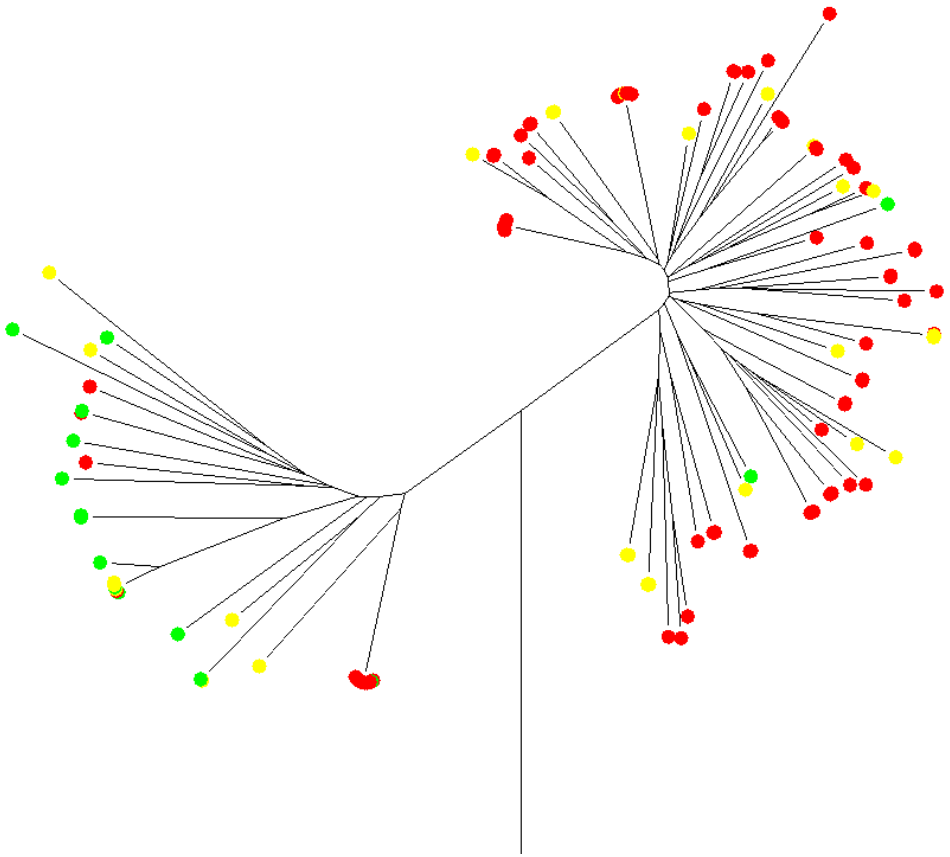
GE

HC

p=1.0

MLST – prøvetagningsted





Biopsies

Faeces

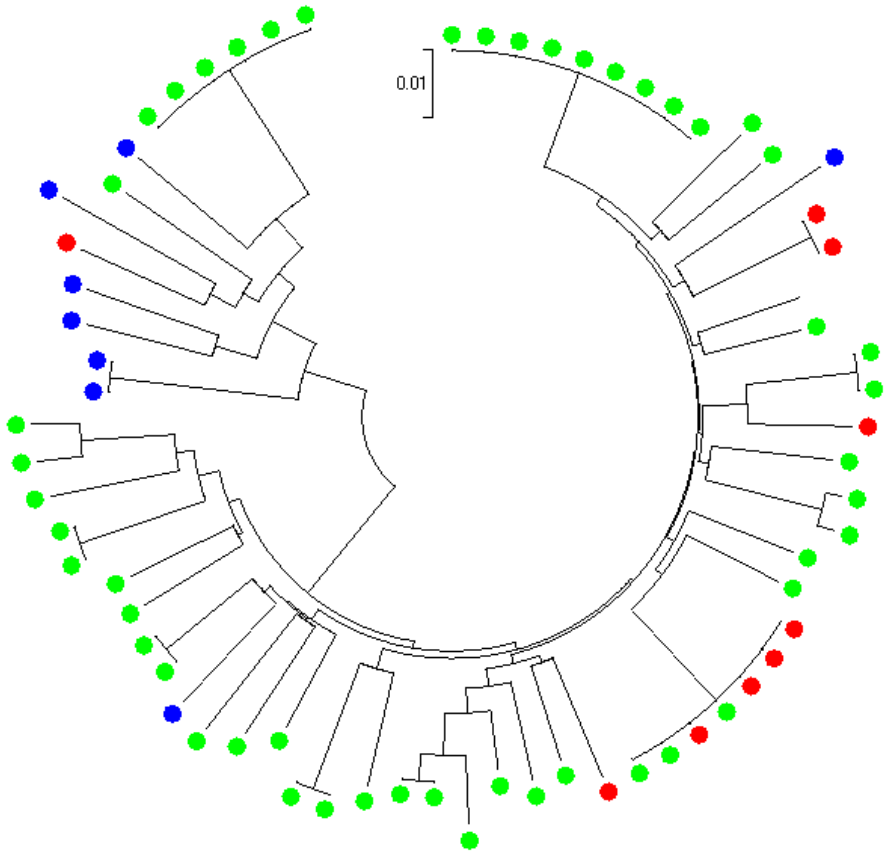
Saliva

p<0.0001

Virulens-associerede gener

- ***zot*** – producerer Zot (zonula occludens toxin) – ødelægger tights junctions imellem epithel cellerne i tarmen (AToCC)

- **Exotoxin 9**: Proxy for et plasmid der bl.a. koder for et restriction/modification enzym (AICC)



Konklusioner

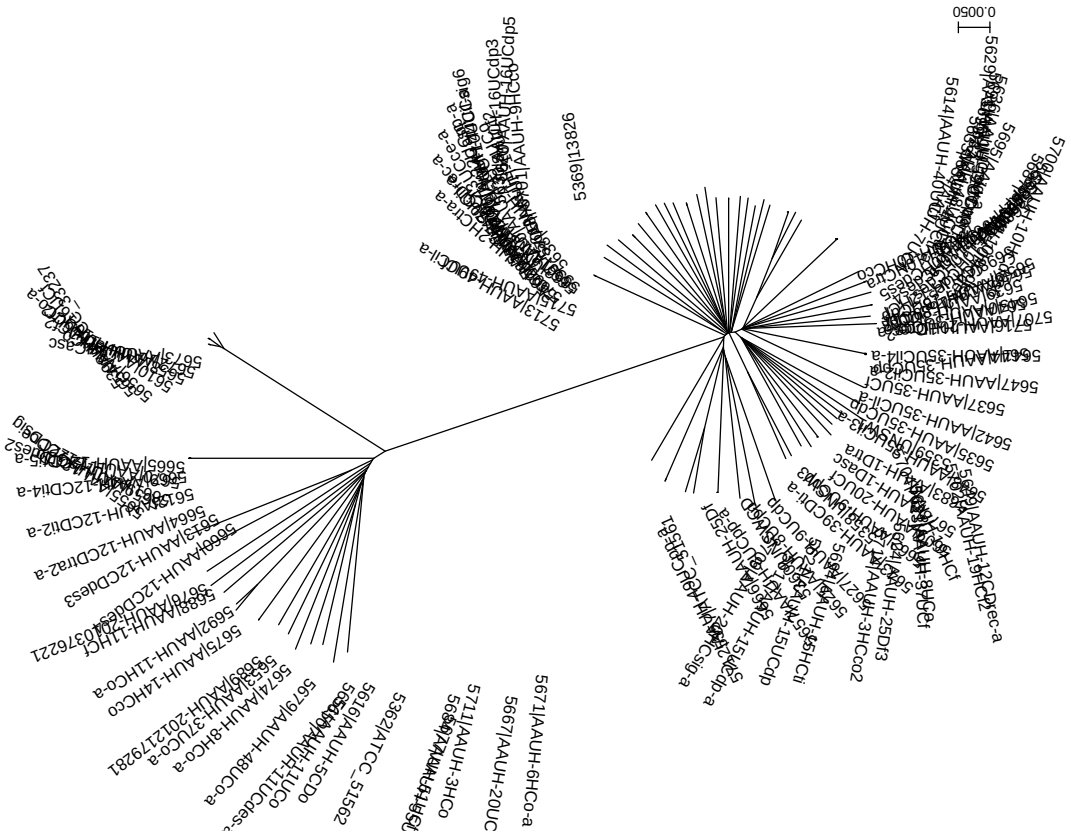
- *Campylobacter concisus* kan dyrkes i tarmprøver fra IBD patienter og raske kontroller
- Udtalt species diversitet
- MLST kan ikke skelne isolater fra forskellige kliniske grupper men muligt prøvelokalisationer
- Der er ingen forskel i forekomsten af virulens faktorerne *zot* eller Exotoxin 9 hos IBD patienter sammenlignet med raske

Formellinje

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN
1				**BIGs ID**	5678	5710	5673	5619	5659	5693	5640	5675	5714	5645	5701	5716	5650	5687	5661	5681	5613	5686	5660	5680	5685	5700	5682	5635	5646	5621	5627	5695	5617	5630	5620	5634	5697	5599	5641	5642	5647
2				**Isolate ID**	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-	AAUH-
3				**PT ID**	1D	20HC	9HC	43UC	12CD	10HC	3UC	14HC	3HC		9HC		11UC											35UC	16UC	15UC	9UC	48UC				7UC	47UC				
4				**Disease**	Diarrhe	Healthy	healthy	Ulcerat	Crohn's	Healthy	Ulcerat	Healthy	Healthy control				Ulcerative colitis											Ulcerat	Ulcerat	Ulcerat	Ulcerat	Ulcerative colitis -IPAA				Ulcerat	Ulcerative colitis -IPAA				
5				**Sample**	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy	Biopsy
6				**Location (biopsies)**	ascend	ascend	ascend	cecum	cecum	cecum	cecum	cecum	cecum	cecum	cecum	cecum	descer	descer	descer	descer	descer	descer	descer	descer	descer	descer	descer	distal p	distal p	distal p	distal p	distal p	distal p	distal p	distal p	ileum	ileum	ileum	ileum	ileum	ileum
7				**Age**	57	49	57	67	63	63	44	69	66				63											23	48	28	45	21				51	38				
8				**Sex**	F	F	M	F	F	F	M	M	M				F											F	F	M	M	M				F	F				
9				**Colo (macroscopic inf 1=yes, 0=no)**	0	0	0	0	0	0	1	0	0				1											0	1	0	1	0				1	0				
10				**micro (microscopic inflammation 1=yes, 0=no)**	0	0	0	0	0	0	1	0	0				1											0	1	1	1	1				1	1				
11				**Clinical (Symptoms 1=yes, 0=no)**	1	0	0	0	1	0	1	0	0				1											1	1	1	1	1				1	0				
12	**Locus**	**Product**	**Sequence length**	**Genome position**	**5678 (AAUH-1Dasc)**	**5710 (AAUH-20HCasc)**	**5673 (AAUH-9HCasc)**	**5619 (AAUH-43UCce-)**	**5659 (AAUH-12CDce)**	**5693 (AAUH-10HCco)**	**5640 (AAUH-3UCce)**	**5675 (AAUH-14HCco)**	**5714 (AAUH-3HCco2)**	**5645 (AAUH-3UCce2)**	**5701 (AAUH-9HCco)**	**5716 (AAUH-1Dco-a)**	**5650 (AAUH-11UCdes-)**	**5687 (AAUH-10HCdes)**	**5661 (AAUH-12CDdes2**	**5681 (AAUH-10HCdes2**	**5613 (AAUH-12CDdes3**	**5686 (AAUH-10HCdes3**	**5660 (AAUH-12CDdes4**	**5680 (AAUH-10HCdes4**	**5685 (AAUH-10HCdes5**	**5700 (AAUH-10HCdes6**	**5682 (AAUH-10HCdes7**	**5635 (AAUH-35UCdp)**	**5646 (AAUH-16UCdp)**	**5621 (AAUH-15UCdp)**	**5627 (AAUH-9UCdp)**	**5695 (AAUH-48UCdp-**	**5617 (AAUH-15UCdp-**	**5630 (AAUH-16UCdp3)**	**5620 (AAUH-16UCdp5)**	**5634 (AAUH-7UCil)**	**5697 (AAUH-47UCil)**	**5599 (AAUH-10UCil-a)**	**5641 (AAUH-35UCil4-**	**5642 (AAUH-35UCil-**	**5647 (AAUH-35UCil2-**
13	CCC13826_RS00005	chromosomal replic	1311	1	31	46	X	14	11	X	X	X	I	X	40	X	25	X	11	X	11	X	11	X	X	X	X	X	X	13	19	X	13	15	15	X	35	9	X	X	X
14	CCC13826_RS00010	DNA polymerase III s	1068	1312	42	I	9	17	36	44	31	40	63	31	53	64	34	44	13	44	13	44	13	44	44	44	I	27	4	16	22	25	16	18	18	26	48	11	29	27	27
15	CCC13826_RS00015	DNA topoisomerase	2310	2380	45	64	8	17	13	52	31	42	68	31	57	69	35	46	13	46	13	46	13	46	46	46	46	28	33	16	22	54	16	24	18	27	50	10	28	28	28
16	CCC13826_RS00020	7-cyano-7-deazag	585	4690	43	60	34	16	12	50	28	40	64	28	15	65	32	44	12	44	12	44	12	44	44	44	44	25	30	15	21	52	15	17	17	24	48	10	25	25	25
17	CCC13826_RS00025	hydrolase	1236	5275	45	64	40	17	13	53	30	42	67	30	57	68	34	47	13	47	13	47	13	47	47	47	47	27	32	16	22	26	16	18	18	26	51	11	27	27	27
18	CCC13826_RS00035	hypothetical protein	435	6511	32	47	X	13	X	36	23	X	49	23	40	50	27	33	X	33	X	33	X	33	33	33	33	21	25	12	16	20	12	14	14	20	34	9	21	21	21
19	CCC13826_RS00040	RDD family protein	420	6946	42	57	9	16	13	43	28	39	61	28	51	62	32	43	13	43	13	43	13	43	43	43	43	25	30	15	21	19	15	17	17	24	46	11	25	25	25
20	CCC13826_RS00045	phosphoribosylform	984	7366	42	59	9	17	13	43	29	40	49	29	52	63	33	43	13	43	13	43	13	43	43	43	43	26	31	16	22	25	16	18	18	25	47	11	26	26	26
21	CCC13826_RS00050	dephospho-CoA kir	603	8350	35	50	X	14	11	36	27	X	40	27	43	54	X	36	11	36	11	36	11	36	36	36	36	24	29	13	19	22	13	15	15	23	38	9	24	24	24
22	CCC13826_RS00055	phosphomethylpyrir	621	8953	32	48	X	13	X	33	26	X	36	26	40	50	X	33	X	33	X	33	X	33	33	33	33	23	28	12	18	21	12	14	14	22	34	9	23	23	23
23	CCC13826_RS00060	diaminopimelate epi	744	9574	44	60	9	17	13	45	30	41	51	30	54	63	34	45	13	45	13	45	13	45	45	45	45	27	32	16	22	25	16	18	18	26	49	11	27	27	27
24	CCC13826_RS00065	50S ribosomal prote	357	10318	35	47	9	11	13	36	26	33	49	26	42	50	27	36	13	36	13	36	13	36	36	36	36	24	5	16	21	5	16	17	17	23	39	11	24	24	24
25	CCC13826_RS00070	50S ribosomal prote	192	10675	3	20	6	1	7	3	11	16	8	11	9	3	12	3	7	3	7	3	7	3	3	3	3	5	3	8	3	I	8	9	9	5	11	3	5	5	5
26	CCC13826_RS00075	peptidase	1497	10867	44	63	9	18	13	45	30	41	66	30	55	68	34	45	13	45	13	45	13	45	45	45	45	28	32	16	23	52	16	19	19	27	49	11	28	28	28
27	CCC13826_RS00080	5-methyltetrahydrop	2274	12364	46	65	13	19	14	48	32	43	54	32	58	69	36	48	14	48	14	48	14	48	48	48	48	29	34	17	24	55	17	20	20	28	52	11	29	29	29
28	CCC13826_RS00085	hypothetical protein	459	14638	20	32	X	X	6	21	18	X	25	18	27	34	X	21	6	21	6	21	6	21	21	21	21	16	3	8	X	14	8	9	9	15	23	5	16	16	16
29	CCC13826_RS00090	DNA-binding protein	885	15097	27	42	X	10	7	28	22	X	32	22	35	45	X	28	7	28	7	28	7	28	28	28	28	20	23	9	15	18	9	11	11	19	30	6	20	20	20
30	CCC13826_RS00095	response regulator	647	15982	26	40	X	11	23	27	19	X	10	19	33	43	X	27	9	27	9	27	9	27	27	27	27	X	21	10	14	16	10	12	12	17	31	7	X	X	X
31	CCC13826_RS00100	cytochrome c	705	16629	32	46	X	14	11	33	27	X	13	27	39	49	X	33	11	33	11	33	11	33	33	33	33	24	29	13	19	22	13	15	15	23	34	9	24	24	24
32	CCC13826_RS00105	cytochrome c	435	17334	32	45	X	14	11	33	27	X	48	27	39	49	X	33	11	33	11	33	11	33	33	33	33	24	29	13	19	22	13	15	15	23	34	9	24	24	24
33	CCC13826_RS00115	hypothetical protein	1317	17769	25	42	X	11	X	27	22	X	10	22	34	45	X	26	X	26	X	27	X	26	27	26	26	19	24	10	X	31	10	12	12	18	28	7	19	19	19
34	CCC13826_RS00120	alanine glycine pern	1419	19086	I	61	9	17	13	44	30	41	16	30	54	65	34	44	13	44	13	47	13	44	44	44	44	27	32	16	22	52	16	18	18	26	50	11	27	27	27
35	CCC13826_RS00125	hypothetical protein	516	20505	31	46	X	13	X	32	26	X	36	26	39	49	X	32	X	32	X	33	X	32	32	32	32	23	27	12	18	37	12	14	14	22	35	9	23	23	23
36	CCC13826_RS00130	ATPase AAA	1185	21021	42	61	9	17	13	44	30	39	65	30	54	66	33	44	13	44	13	44	13	44	44	44	44	27	31	16	22	51	16	18	18	26	48	11	27	27	27
37	CCC13826_RS00135	5-nitroimidazole ant	531	22206	42	58	9	17	13	43	30	39	62	30	52	63	34	43	13	43	13	43	13	43	43	43	43	27	32	16	22	25	16	18	18	26	47	11	27	27	27
38	CCC13826_RS00140	hypothetical protein	294	22737	37	49	X	15	X	17	26	34	53	26	44	54	X	17	X	17	X	17	X	17	17	17	17	24	28	14	20	23	14	16	16	17	40	10	24	24	24
39	CCC13826_RS00145	uracil-DNA glycosyl	693	23031	44	59	9	17	13	26	30	41	63	30	52	64	34	26	13	26	13	26	13	26	26	26	26	27	32	16	22	25	16	18	18	26	48	11	27	27	27
40	CCC13826_RS00150	hypothetical protein	576	23724	I	56	9	17	13	26	30	41	63	30	53	64	34	26	13	26	13	26	13	26	26	26	26	27	32	16	22	25	16	18	18	26	48	11	27	27	27
41	CCC13826_RS00155	threonine--tRNA lig	1821	24300	44	63	9	17	13	46	30	41	67	30	56	68	34	46	13	46	13	46	13	46	46	46	46	27	32	16	22	25	16	18	18	26	51	11	27	27	27
42	CCC13826_RS00160	translation initiation	519	26121	44	58	9	17	13	10	30	41	49	30	52	59	34	10	13	10	13	10	13	10	10	10	10	27	32	16	22	25	16	18	18	26	26	11	27	27	27
43	CCC13826_RS00165	hypothetical protein	186	26640	X	10	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	6	6	X	X	3	X	X	X
44	CCC13826_RS00170	glutamate dehydrog	1359	26826	43	58	9	17	13	44	30	40	48	30	52	62	9	44	13	44	13	44	13	44	44	44	44	27	32	16	22	25	16	18	18	26	48	11	27	27	27
45	CCC13826_RS00175	endonuclease	573	28185	41	59	8	16	12	42	29	38	62	29	52	63	8	42	12	42	12	42	12	42	42	42	42	26	31	15	21	24	15	17	17	25	46	10	26	26	26
46	CCC13826_RS00180	dehydrogenase	930	28758	39	55	37	15	X	40	27	38	59	27	48	60	31	40	X	40	X	40	X	40	40	40	40	24	29	14	19	22	14	16	16	23	43	10	24	24	24
47	CCC13826_RS00185	acetyl-CoA carboxy	1440	29688	43	60	9	17	13	44	29	40	64	29	54	65	33	44	13	44	13	44	13	44	44	44	44	26	31	16	22	51	16	18	18	25	48	11	26	26	26
48	CCC13826_RS00190	hypothetical protein	546	31128	29	53	9	17	13	12	29	39	59	29	50	60	9	12	13	12	13	12	13	12	12	12	12	26	31	16	22	47	16	18	18	25	45	11	26	26	26
49	CCC13826_RS00195	membrane protein	435	31674	29	58	9	17	13	12	29	40	61	29	51	62	33	12	13	12	13	12	13	12	12	12	12	26	31	16	22	48	16	18	18	25	46	11	26	26	26
50	CCC13826_RS00200	hypothetical protein	363	32109	29	55	13	18	14	43	29	40	61	29	52	62	33	43	14	43	14	43	14	43	43	43	43	26	31	17	22	49	17	19	19	25	47	11	26	26	26
51	CCC13826_RS00205	signal peptidase II	453	32472	29	56	9	17	13	43	29	40	63	29	53	64	33	43	13	43	13	43	13	43	43	43	43	26	31	16	22	50	16	18	18	25	47	11	26	26	26
52	CCC13826_RS00210	phosphoglucosamir	1341	32925	43	61	9	17	13	44	29	40	65	29	54	I	33	44	13	44	13	44	13	44	44	44	44	26	31	16	22	51	16	18	18	25	48	11	26	26	26
53	CCC13826_RS00215	30S ribosomal prote	270	34266	36	20	8	15	12	20	25	33	45	25	41	14	28	20	12	20	12	20	12	20	20	20	20	22	27	14	20	40	14	16	16	20	9	10	22	22	22
54	CCC13826_RS00220	peptide chain releas	1068	34536	45	62	I	17	13	47	30	42	66	30	56	67	34	47	13	47	13	47	13	47	47	47	47	27	32	16	22	27	16	18	18	26	50	11	27	27	27
55	CCC13826_RS00225	ModE family transcri	420	35604	44	57	9	17	13	45	30	41	60	30	52	61	34	45	13	45	13	45	13	45	45	45	45	27	32	16	22	27	16	18	18	26	11	11	27	27	27
56	CCC13826_RS00230	flavocytochrome c	1566	36024	32	46	X	14	11	36	26	X	49	26	40	50	X	33	11	33	11	33	11	33	33	33	33	23	28	13	19	23	13	15	15	22	34	9	23	23	23

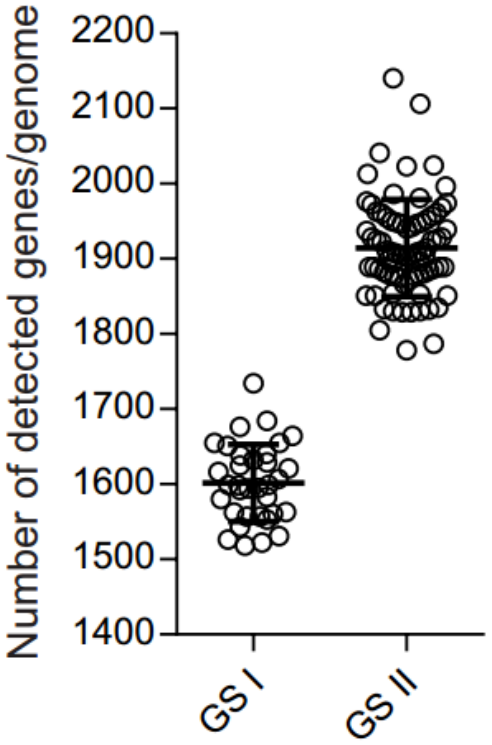
METADATA | all | increasing freq | decreasing freq

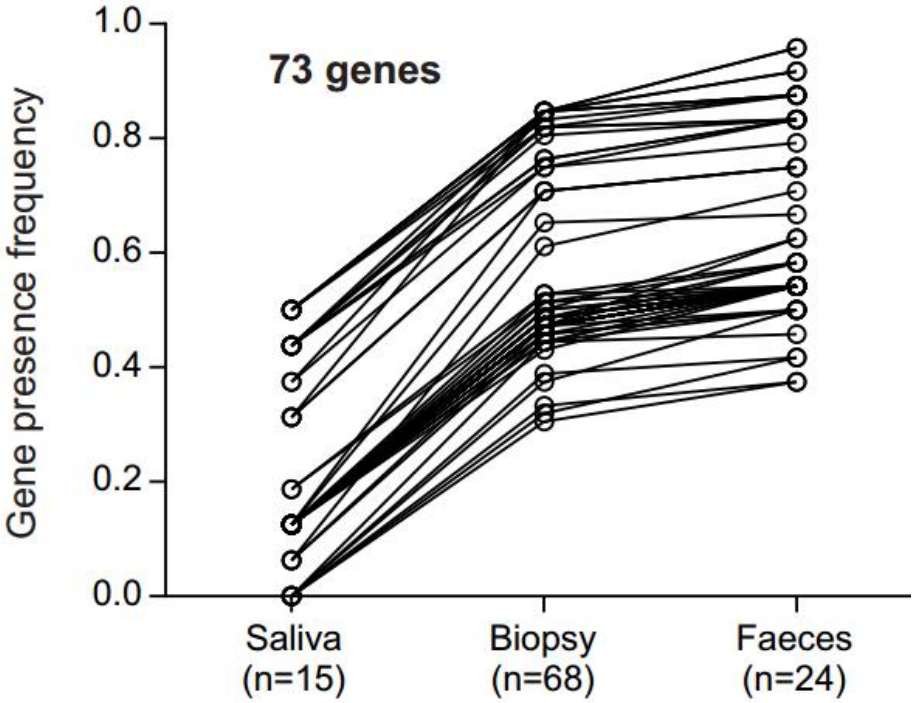
C. concisus genomet

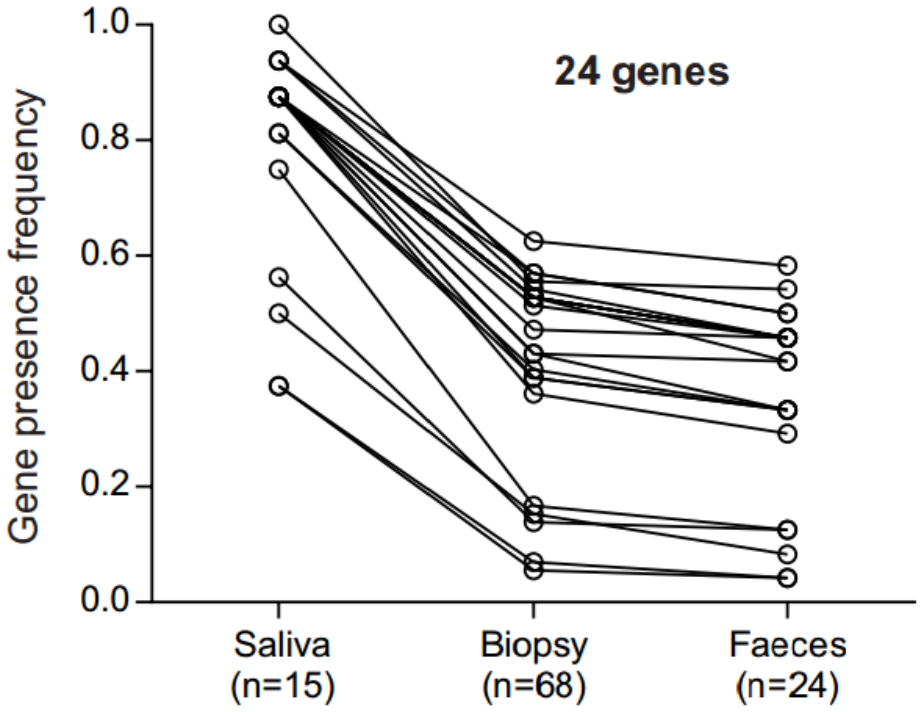


Pan-genom: 4833 gener
Core-genom: 864 gener

WGS analyse


Number of detected genes/genome
2200
2100
2000
1900
1800
1700
1600
1500
1400
GS I
GS II

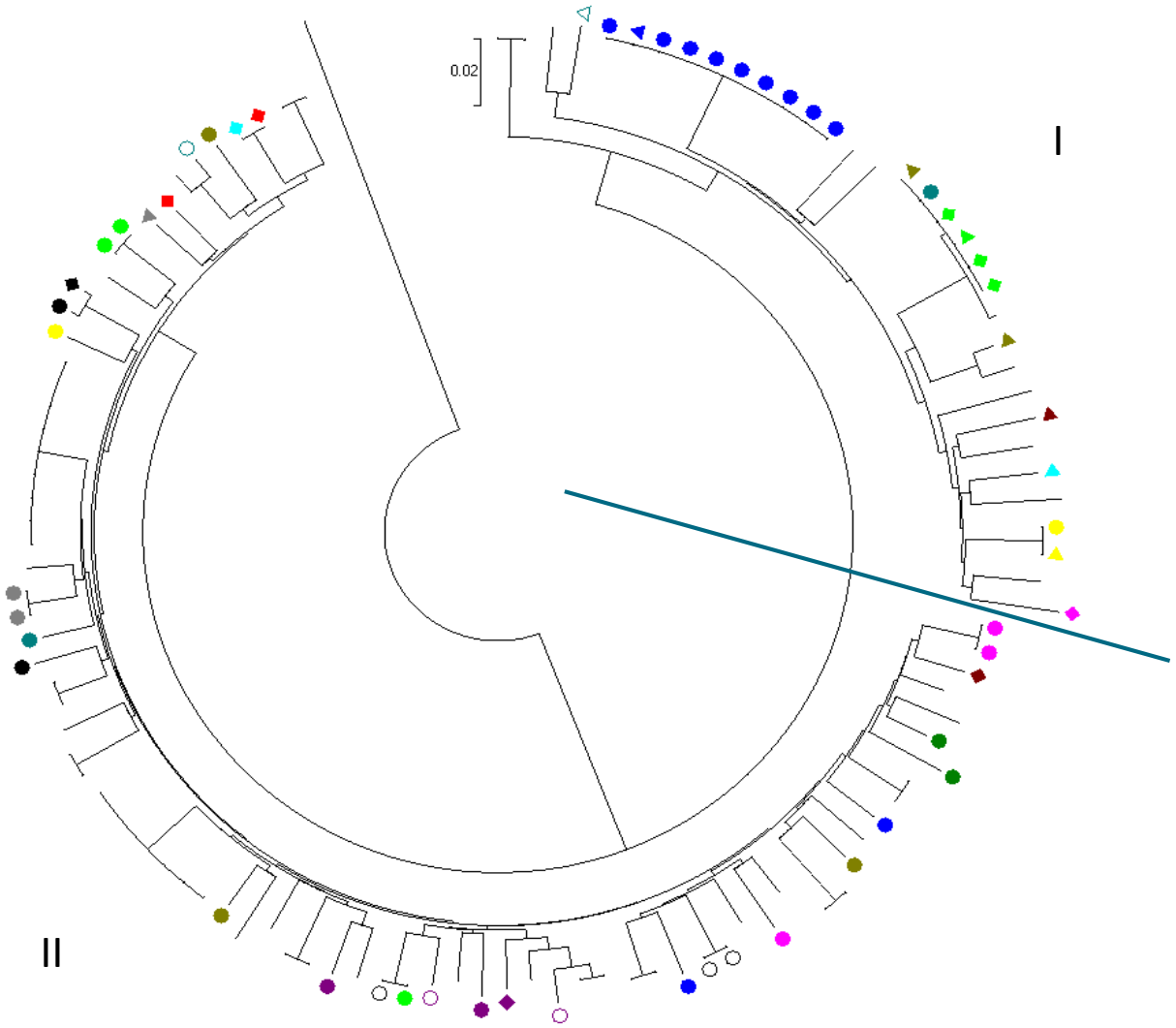

73 genes
Gene presence frequency
1.0
0.8
0.6
0.4
0.2
0.0
Saliva (n=15)
Biopsy (n=68)
Faeces (n=24)


24 genes
Gene presence frequency
1.0
0.8
0.6
0.4
0.2
0.0
Saliva (n=15)
Biopsy (n=68)
Faeces (n=24)

Tak for opmærksomheden

MLST – individuals

- 27 individuals had > 1 isolate sequenced (18 IBD, 7 HC, 2 GE)
- 17/27 had isolates from different ST
- 7 had isolates in different clusters



Preliminary genomic analysis

Genomic variety:

- Preliminary analysis of whole genome MLST indicates that the extensive heterogeneity of *C. concisus* (in our isolates) could be explained by:
  - Under-sampling
  - Extensive hypermutation and microevolution
- Horizontal gene transfer uncommon (unlike *C. jejuni*)

  - Pan-genome: 4833 genes
  - Core-genome: 864 genes

COG class description	Number of corresponding genes in the GS I core genome	Number of corresponding genes in the GS II core genome	Difference in proportion of respective core genomes (%)
Amino acid transport and metabolism	75	127	2,323%
Carbohydrate transport and metabolism	43	82	2,130%
Cell cycle control, cell division, chromosome partitioning	13	27	0,836%
Cell motility	38	56	0,452%
Cell wall/membrane/envelope biogenesis	46	65	0,305%
Coenzyme transport and metabolism	18	27	0,255%
Defense mechanisms	12	18	0,170%
Energy production and conversion	21	30	0,167%
Function unknown	10	15	0,142%
General function prediction only	6	9	0,085%
Inorganic ion transport and metabolism	66	88	-0,020%
Intracellular trafficking, secretion, and vesicular transport	31	39	-0,212%
Lipid transport and metabolism	14	16	-0,236%
Multiple classes	76	98	-0,313%
Nucleotide transport and metabolism	44	55	-0,332%
Posttranslational modification, protein turnover, chaperones	17	18	-0,411%
Replication, recombination and repair	80	102	-0,430%
Secondary metabolites biosynthesis, transport and catabolism	24	25	-0,615%
Signal transduction mechanisms	74	84	-1,297%
Transcription	49	50	-1,347%
Translation, ribosomal structure and biogenesis	104	120	-1,653%
Total number of genes assigned to COG	861	1151	
Total number of genes in respective core genomes	975	1367	

WGS data

- Average number of contigs per genome: 92 (3-356)
- Average genome size: 1.94 Mb (1.78-2.22)
- Average N50: 97693 (13858-934037)
- Average GC content: 98.94 % (37.26-39.88)

Other emerging *Campylobacter* species

- *Campylobacter ureolyticus* (8 isolates from 6 IBD patients and 2 HC)
- *Campylobacter curvus* (3 isolates from 1 IBD patient)
- *Campylobacter showae* (2 isolates from 1 IBD patient and 1 HC)

- The majority also positive for *C. concisus*

- No thermophilic *Campylobacter* species