

# **NGS analysis of rare *Campylobacter* isolates with ambiguous species differentiation**

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NRL for *Campylobacter* of Germany

# Species differentiation by real-time PCR

→ What do we find?

29 isolates with ambiguous *mapA/ceuE* detection  
out of 2059 *C. jejuni* and 775 *C. coli*

(Mayr et al. 2010 = Best et al. 2003 extended for *C. lari*  
detection; L06.32-1:2013, §64 German Feed and Food Law  
(LFGB))

→ around 1 % ambiguous results

→ Van Rensburg et al. 2016 J. Clin. Microbiol.:

out of 1713 isolates 6 *C. coli* (0.3 % of all isolates) were ambiguous  
in *mapA/ceuE* species differentiation by real-time PCR

# Species differentiation by real-time PCR

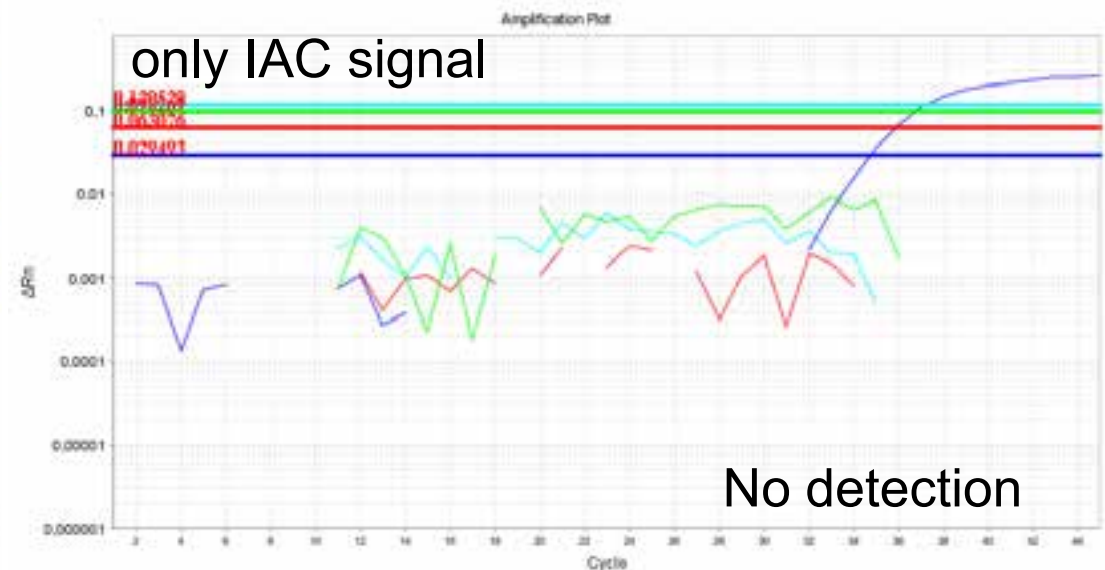
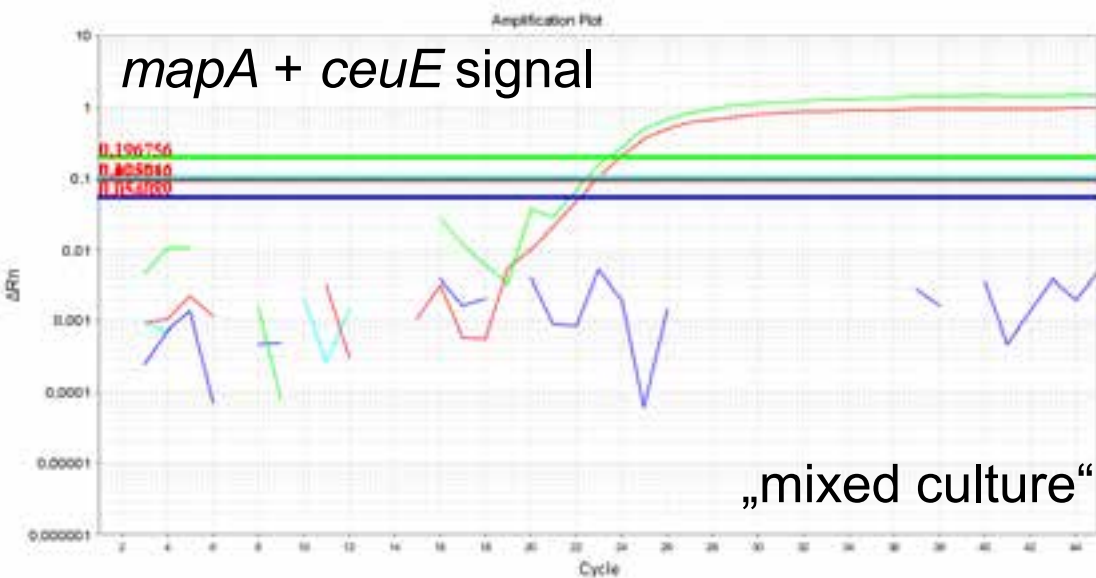
→ Where do these isolates come from?

Broiler meat, eggs, turkey meat/skin/cecum, duck meat

→ What is the real-time PCR phenomenon?

„mixed“ culture = both positive for *mapA* and *ceuE* (n=27)

no Cj, Cc, Cl = negative for both *mapA* and *ceuE* (n=2)



## MiSeq and PacBio sequencing

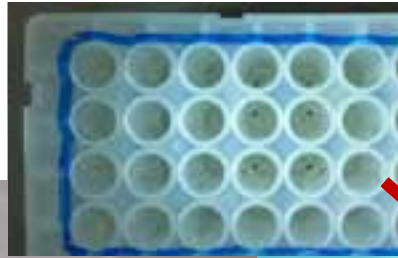
	MiSeq (BfR)	PacBio (GATC)
principle	Massively parallel sequencing (MPS)	Single molecule real-time sequencing (SMRT)
Read length	2x 300 bp	~10-20 kb
DNA required	20-100 ng	~5 µg
Instrument time	2 days	2 hours
price	80 Euro	2000 Euro

- At BfR a platform is established, providing hardware (the sequencers), optimized protocols and knowledge for the NRLs
- currently the platform is working on a common pipeline for data analysis

→ team of Burkhard Malorny

# NGS analysis of *Campylobacter*

Illumina MiSeq of 26 of the Cj/Cc hybrids, 21 *C. coli* and 2 *C. jejuni*  
Several other control strains, double sequencing for defining QC  
Nextera XT Kit





# NGS analysis of *Campylobacter*

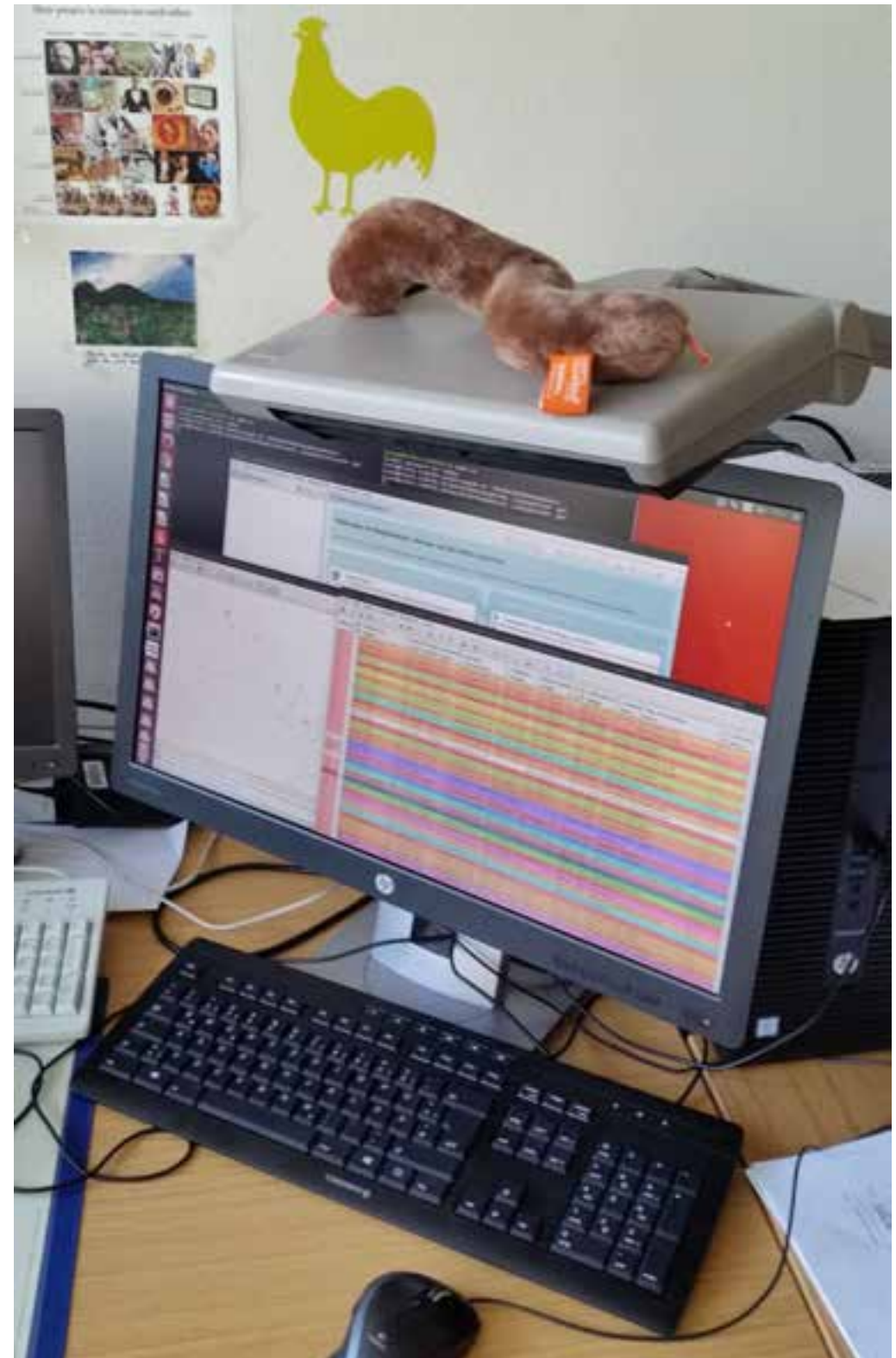
Wet lab results: fastq.gz files

Ridom Seqsphere+ 5.1.0 software  
run under Ubuntu 16.04

Trimming reads to Phred score  $\geq 30$   
Assembly via SPAdes 3.11.1

Ridom cgMLST (637 genes)  
Ridom accessory genes (958 genes)

Reference Sequence (default)  
is NC\_002163.1.gb (NCTC 11168)



# Quality control of the data

✓ Do reference sequences from NCBI match sequenced reference strains?

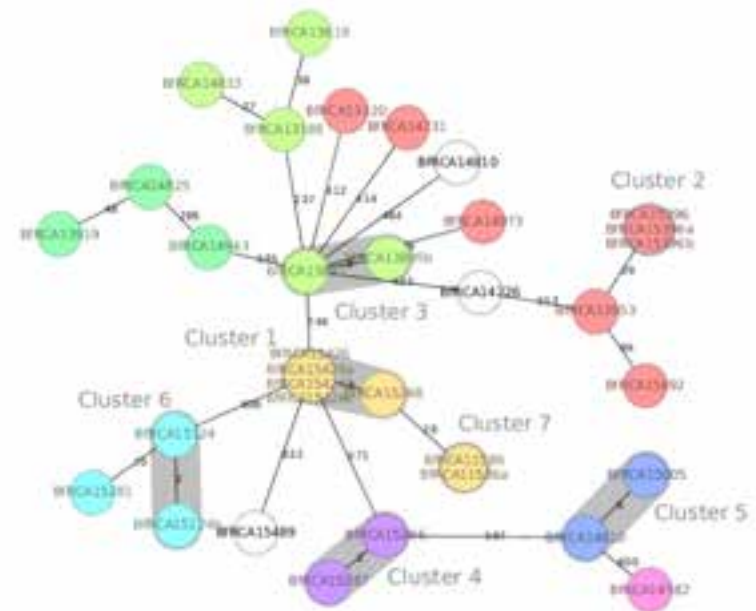
- NCTC11168
  - 81-176
  - RM1221
- } few allele differences

✓ Do PacBio sequences match MiSeq sequences?

- 7 strains were analysed by both techniques

✓ Do they match each other if sequenced twice?

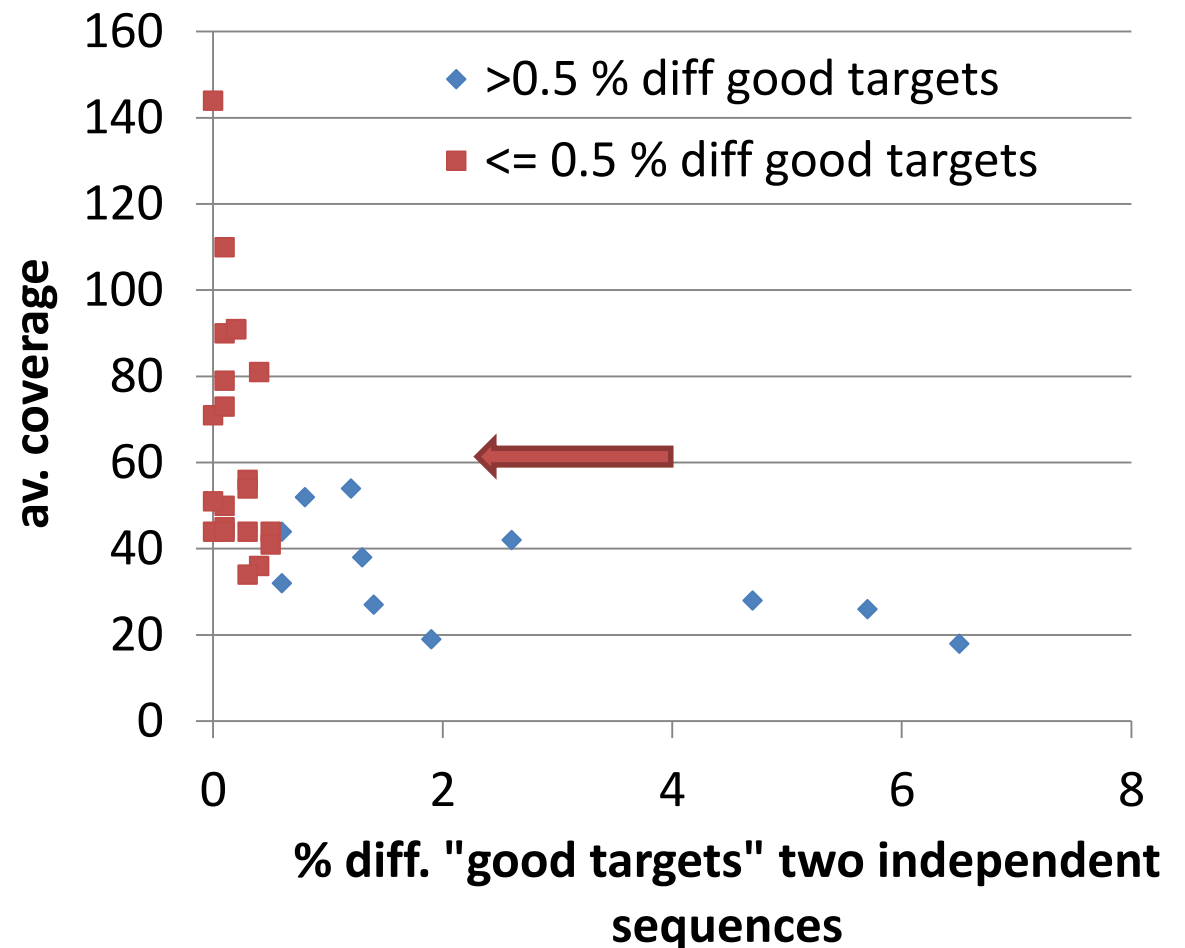
- 28 strains were sequenced twice



# Quality control of data

% good targets	diff. % good targets	Avg. Cov. (Proc., Unass.)	N50
97,8		50	178006
97,9	0,1	152	178006
97,8		131	231222
97,4	-0,4	36	84343
98,3		176	122381
97,7	-0,6	32	79334
98,5		180	154048
92	-6,5	18	16133
97,7		79	231120
97,8	0,1	180	231088

Examples of compared sequence results



→ data might indicate that an av. coverage of 60 is sufficient for cgMLST analysis by Ridom Seqsphere+ (with the additional pipeline QC parameters)



## Quality control of the data

	av. Cov. MiSeq	diff. % good targets
PacBio1	180	1,7
PacBio2	180	0,8
PacBio3	121	2,1
PacBio4	99	6,3
PacBio5	180	1
PacBio6	180	3,4
PacBio7	144	0,7

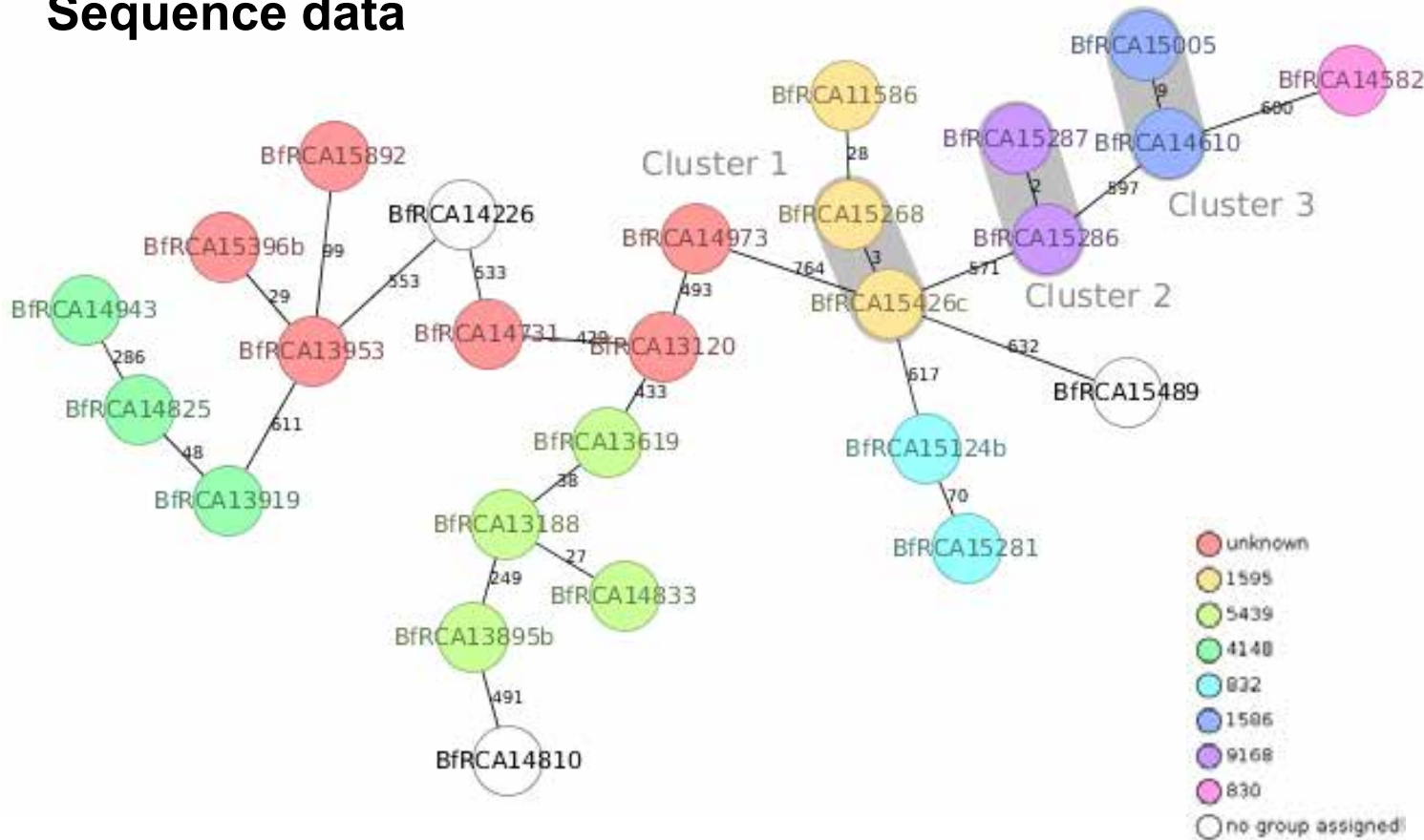
The screenshot shows a window titled "Multiple Alignment of target CAMP0124". The interface includes a toolbar with icons for file operations, navigation, editing (A, Q, M, G), search, and zoom. The main area displays a multiple sequence alignment. The top row is the "Consensus" sequence: GCTAAATGAATCTGAAAAAAAAAGAACCTAAAAAA. Below it are two sequences: "BfRCA13290:" and "BfRCA13290Pac..". The "BfRCA13290Pac.." sequence has a gap (represented by a dash) in the 14th position, which is highlighted by a red arrow. A red arrow also points to a 'G' in the consensus sequence at the 14th position.

- although PacBio is superior in terms of gene order and assembly of 1 whole chromosome plus epichromosomal elements, insertions and deletions are frequently found

→ hybrid assembly with PacBio and MiSeq data (future task)

# Are the Cj/Cc hybrids phylogenetically linked?

## Sequence data



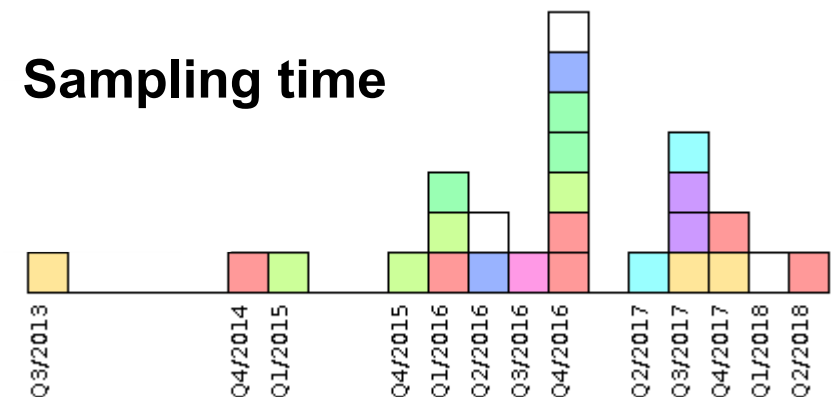
## Sampling location



- cgMLST + accessory genes
- pairwise ignore missing values → more differences possible!
- 3 “clusters“ (à 2 strains); rest of the strains is phylogenetically unlinked

→ Multiple events as cause for ambiguous species detection

## Sampling time

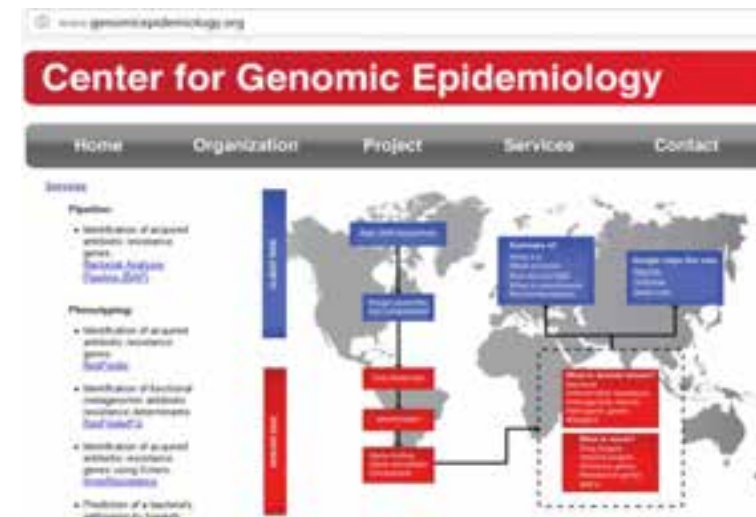


# What species do the isolates with ambiguous *mapA/ceuE* belong to?

Kmer Finder 3.0 by CGE genomics webpage (Kmer size 16)

**query\_coverage [%]:** is the percentage of input query Kmers that match the template

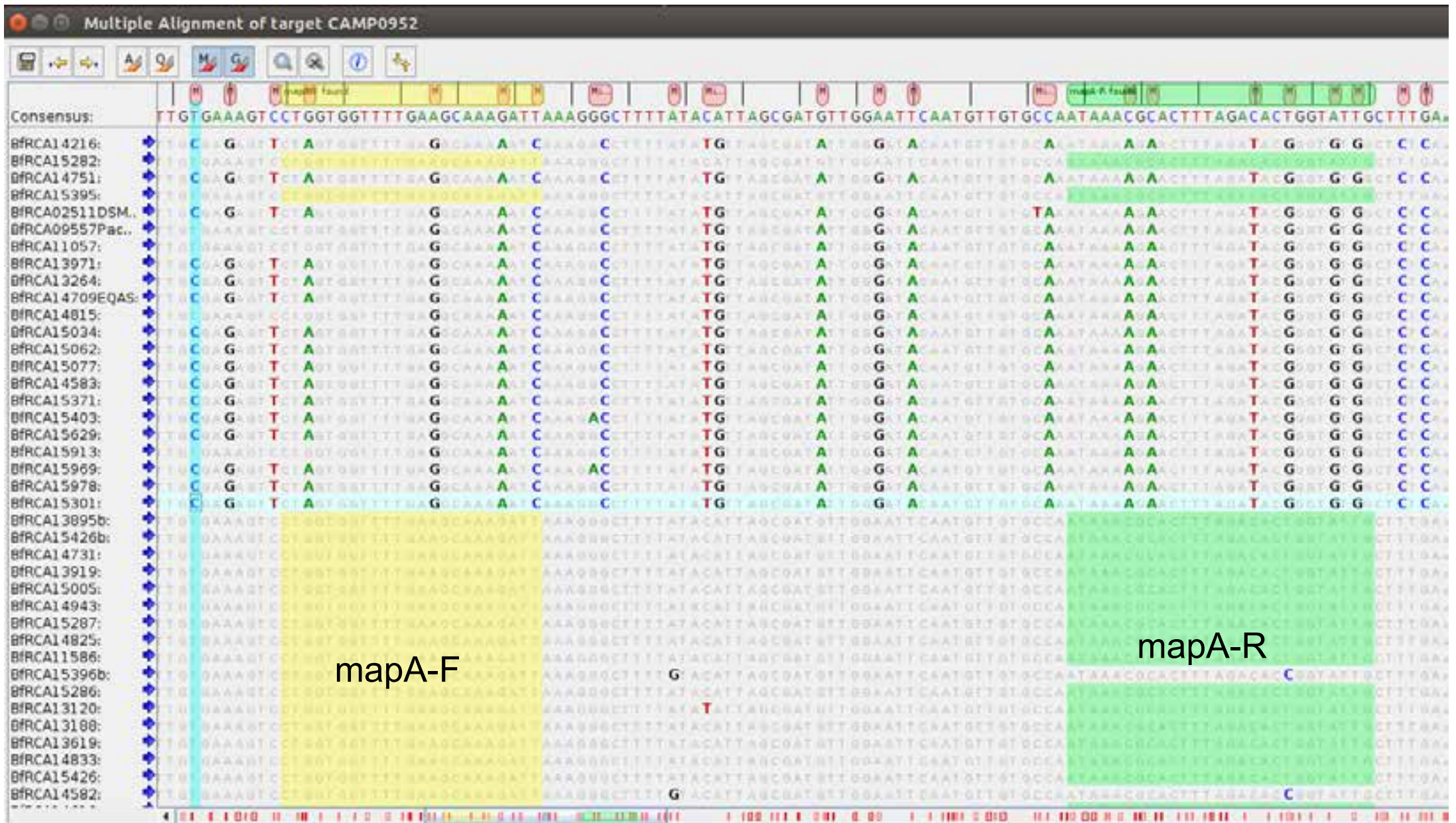
<i>C. jejuni</i> introgression	RT-PCR <i>C. coli</i>	RT-PCR Cj/Cc hybrid	
0%	8	1	 <i>C. coli</i>
< 3%	10	9	
3-6 %	2	1	
>6 %	1	15	



→ all isolates are *C. coli* with 0-14.4% *C. jejuni* introgression



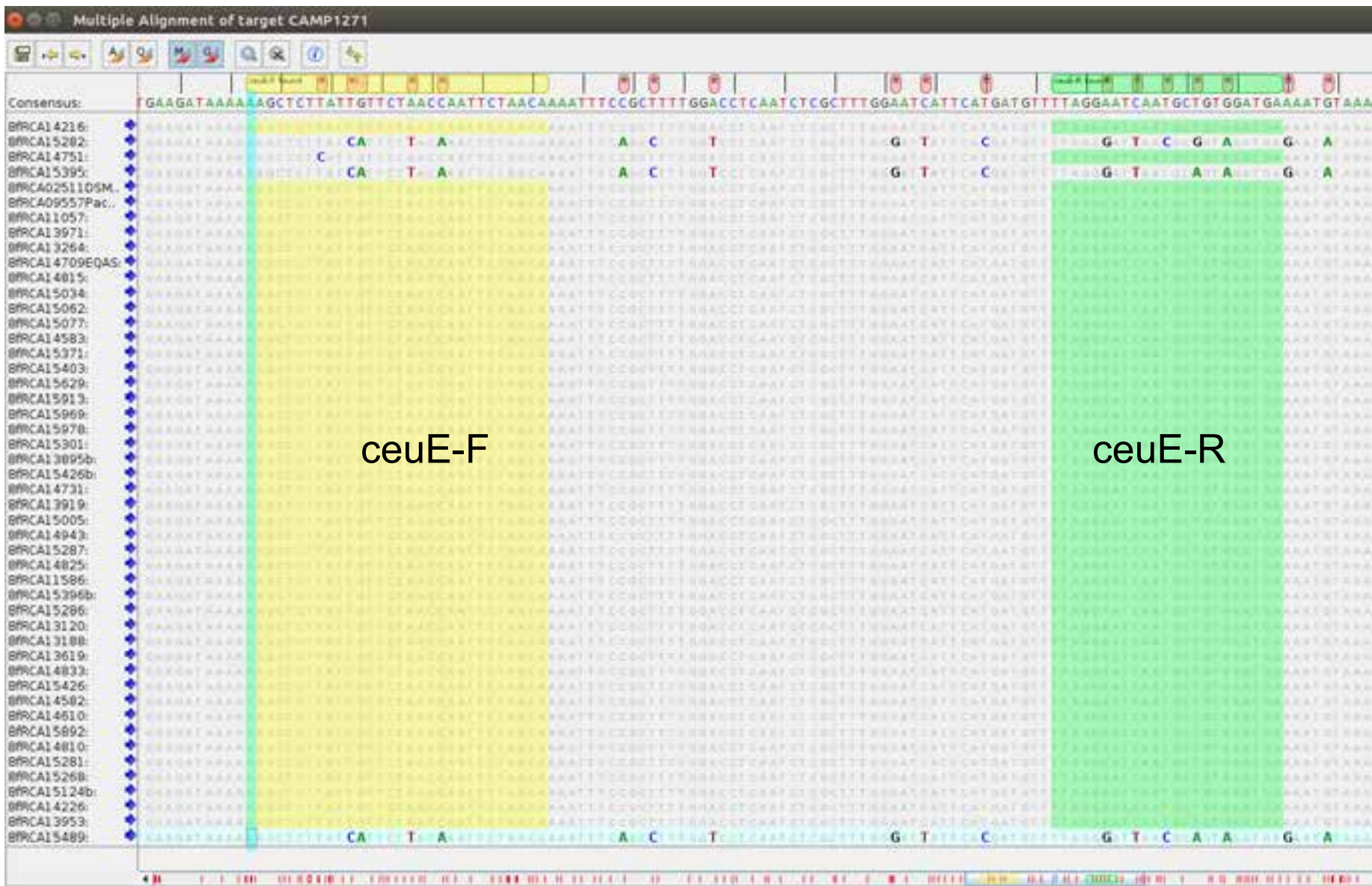
# What happened at *mapA*?



- Adjacent genes also implicated in recombination event – in some isolates Cj sequence spans over 4 genes



# What happened at *ceuE*?



- 15489 has *ceuE* form *C. jejuni*; the 14973 has a *ceuE* allele below the threshold of Ridom



## Could the Cj/Cc hybrids be correctly identified via other PCRs?

Gene target	function	Species	Ridom scheme	Discriminatory in “hybrids“	references
<i>glyA</i>	serine hydroxymethyl-transferase	<i>C. coli</i>	core	yes	Wang 2002; LaGier 2004
<i>hipO</i>	hippurate hydrolase	<i>C. jejuni</i>	accessory	yes	Wang 2002; LaGier 2004, Toplak 2012
<i>cpn60</i>	chaperone ( <i>groEL</i> )	<i>C. jejuni/ C. coli</i>	core	partial	Chaban 2009
<i>cadF</i>	Fibronectin-binding protein	<i>C. jejuni/ C. coli</i>	accessory	yes	Toplak 2012; Shams 2016
<i>lpxA</i>	N-actylglucosamine transferase	<i>C. jejuni/ C. coli</i>	accessory	yes	Klena 2004
<i>ccoN</i>	cytC subunit	<i>C. jejuni/ C. coli</i>	core	partial	Toplak 2012
<i>mapA</i>	Outer membrane protein (MOMP)	<i>C. jejuni</i>	accessory	no	Best 2003; Mayr 2010
<i>ceuE</i>	enterochelin transporter, substrate-binding	<i>C. coli</i>	accessory	no	Best 2003; Mayr 2010

- Results on phylogenetic tree based on gene sequence; oligo annealing sites have to be checked
- Wang et al. 2002 multiplex-PCR identifies *C. coli* (*glyA*) in wet lab



## Conclusions and perspective

- *mapA/ceuE* species differentiation is ambiguous for ~1 % of Cj/Cc isolates but does not provide false identification
- NGS analysis revealed them to be *C. coli*, which was confirmed by Wang et al. 2002 (*glyA*)  
→ Good decision to add both PCR options as Annex to ISO 10272
- QC analysis suggested that an average coverage of  $\geq 60$  might be suitable (Ridom pipeline)
- PacBio data should be „cured“ for insertion/deletions by MiSeq data (future task to use hybrid assembly such as Unicycler)
- Further characterization of the *C. coli* with huge amount of *C. jejuni* introgression
  - Are they special or just found by chance?
  - Do they have extended DNA uptake capacity?
  - Is there a trigger for DNA exchange by natural transformation?

Thanks to...

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BfR NGS platform

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NRL team:

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Britta Kraushaar

Maja Thieck

Petra Vogt

Imke Wulsten

**Thank you for  
your attention**

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