

Comparison of four different molecular methods for Clostridium difficile outbreak investigations

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Background

Clostridium difficile infection is an urgent public threat and outbreaks increased markedly in hospitals in recent years. Ribotyping of strains has been the most widely used molecular tool to distinguish an outbreak from a coincidental accumulation. As ribotyping is time-consuming we investigated alternative methods for outbreak analysis.

Methods

14 *Clostridium difficile* bacterial isolates from different patients were collected in a cardiac surgery clinic within one month. The number of CDI in the hospital was much higher than the average of the previous month suggesting a *C. difficile* outbreak. Capillary gel electrophoresis-based PCR ribotyping was performed and resulting peak patterns were assigned to PCR ribotypes using the Webribo database. The results were compared to a subtyping dendrogram generated by MALDI-TOF mass spectrometry using Biotyper software. Random amplified polymorphic DNA (RAPD)-PCR was also performed. As RAPD-PCR is often used for subtyping Gram-negative bacteria, while the more recent method of Fourier transformation-Infrared Spectroscopy (FTIR) was published for different Gram-positive isolates (e.g. *Corynebacterium ulcerans*), we added this to the investigative panel.

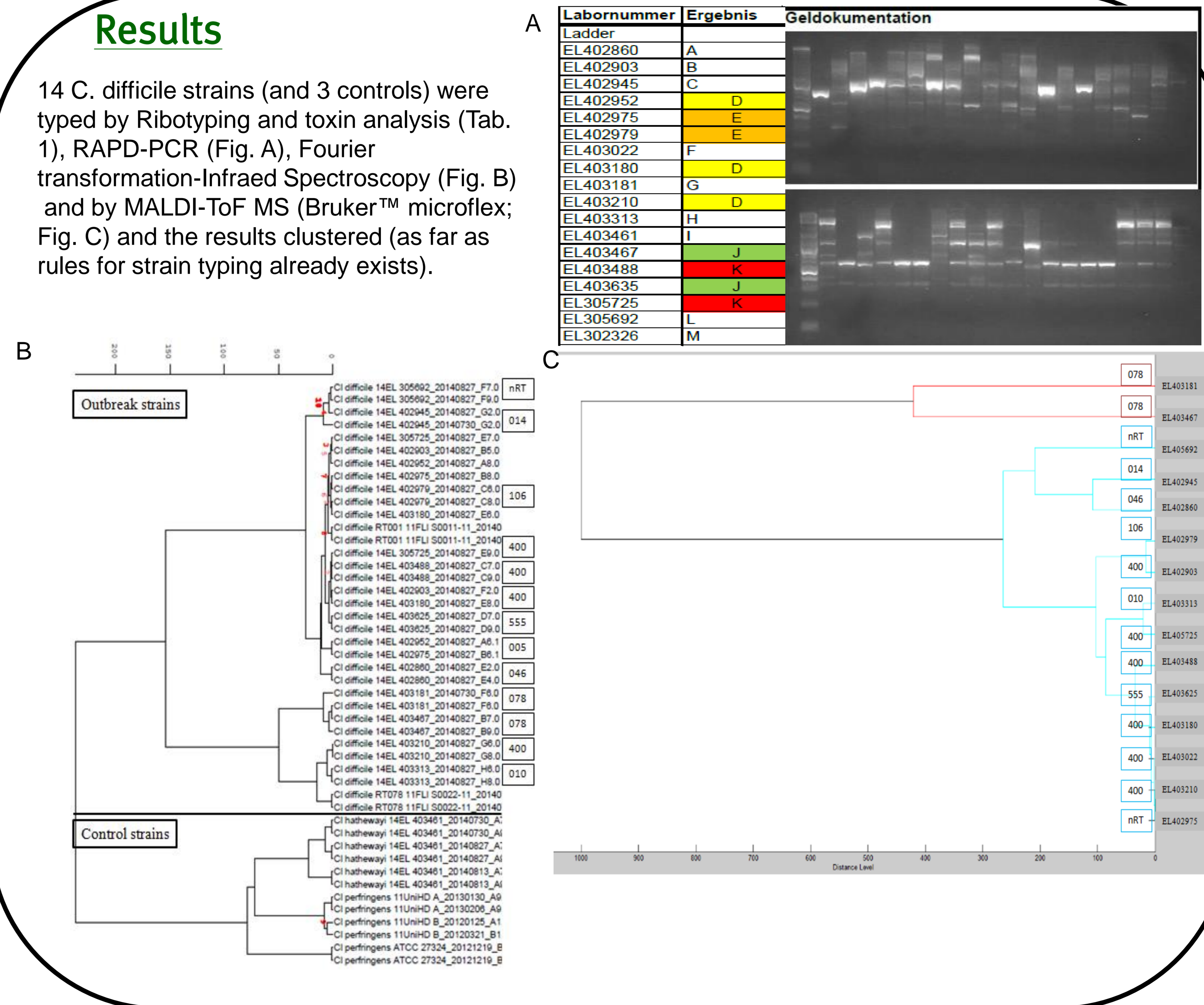
Tab.1

Strain	Age	Gender	Species	tcdA	tcdB	Ribotype	RAPD-PCR	FT-IR	MALDI
EL402860	62	m	<i>Clostridium difficile</i>	pos	pos	046	A		
EL402903	84	m	<i>Clostridium difficile</i>	pos	pos	400	B		
EL402945	72	m	<i>Clostridium difficile</i>	pos	pos	014	C		
EL402952	33	w	<i>Clostridium difficile</i>	pos	pos	005	D		
EL402975	71	w	<i>Clostridium difficile</i>	pos	pos	n RT	E		
EL402979	59	m	<i>Clostridium difficile</i>	pos	pos	106	E		
EL403022	80	w	<i>Clostridium difficile</i>	pos	pos	400	F		
EL403180	74	w	<i>Clostridium difficile</i>	pos	pos	400	D		
EL403181	84	m	<i>Clostridium difficile</i>	pos	pos	078	G		
EL403210	73	w	<i>Clostridium difficile</i>	pos	pos	400	D		
EL403313	43	w	<i>Clostridium difficile</i>	neg	neg	010	H		
EL403461	48	w	<i>Clostridium hathawayi</i>	nd	nd	nd	I		
EL403467	29	m	<i>Clostridium difficile</i>	pos	pos	078	J		
EL403488	74	w	<i>Clostridium difficile</i>	pos	pos	400*	K		
EL403625	81	m	<i>Clostridium difficile</i>	pos	pos	555	J		
EL305725	co	-	<i>Clostridium difficile</i>	pos	pos	400	K		
EL305692	co	-	<i>Clostridium difficile</i>	neg	neg	n RT	M		

[co: control; nd: not done; n RT: new Ribotype]

Results

14 *C. difficile* strains (and 3 controls) were typed by Ribotyping and toxin analysis (Tab. 1), RAPD-PCR (Fig. A), Fourier transformation-Infrared Spectroscopy (Fig. B) and by MALDI-ToF MS (Bruker™ microflex; Fig. C) and the results clustered (as far as rules for strain typing already exists).



Conclusions

The subsuned evaluation of the four methods clearly showed that CDI threat on the ward was more likely a coincidental accumulation than a confirmed outbreak, although single transmission (e.g. 078 strains) might have occurred. Even if the data for the alternative methods RAPD-PCR, mass spectrometry and FT-IR might be preliminary, it showed promising strength in differentiating the strains on a molecular level. Ribotyping seems to be the standard methods as comparison, for the other methods agreed interpretation rules are necessary.