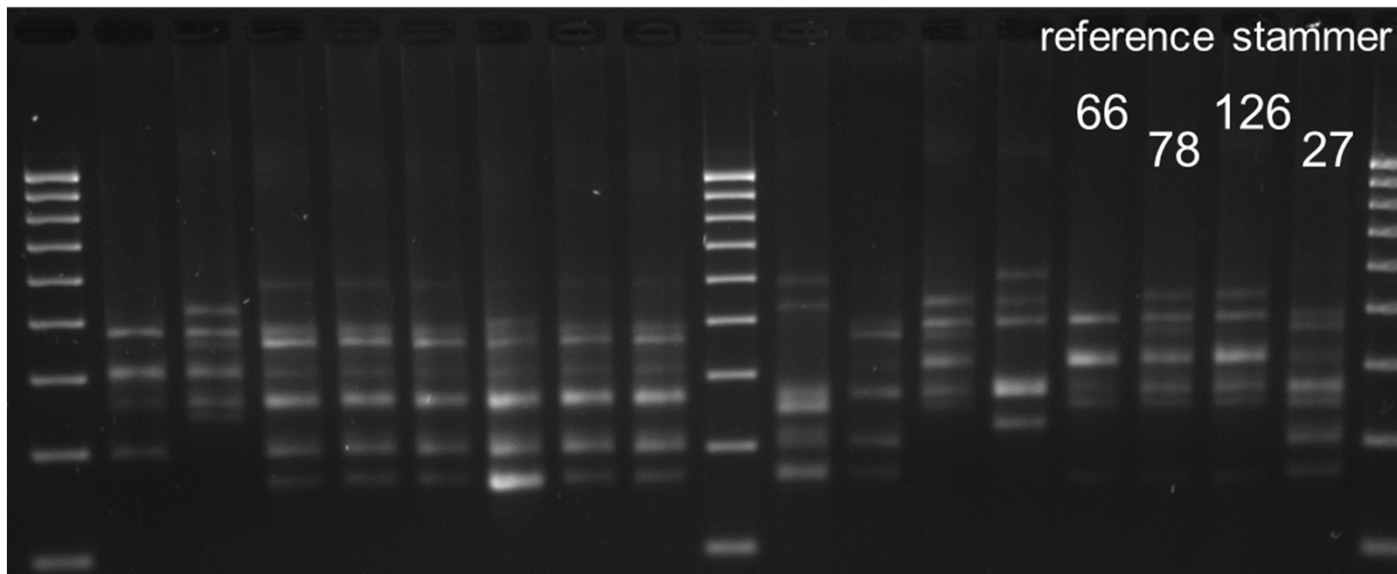


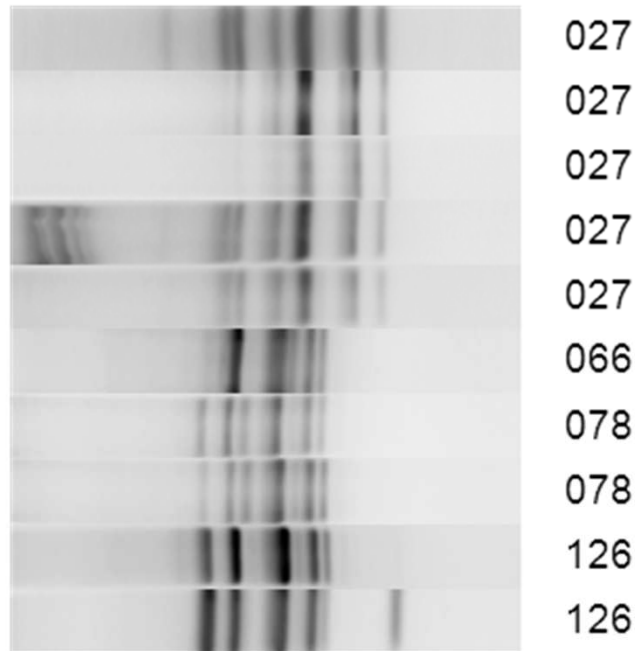
TANDEM REPEAT SEQUENCE TYPING
(TRST)
AF
CLOSTRIDIUM DIFFICILE

Mia Torpdahl (mtd@ssi.dk)
Fødevarebårne Infektioner
Mikrobiologi & Infektionskontrol

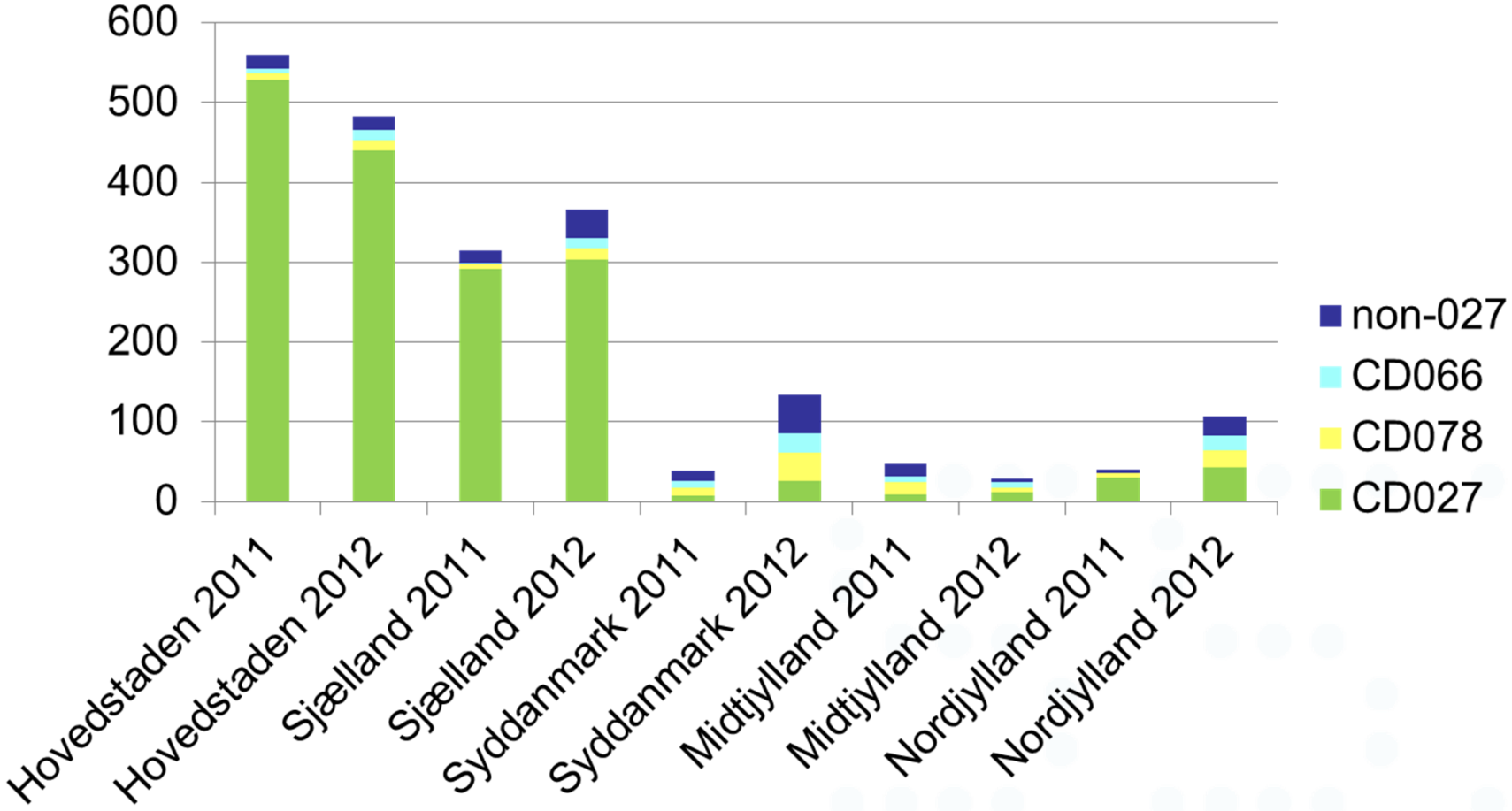
PCR Ribotypning



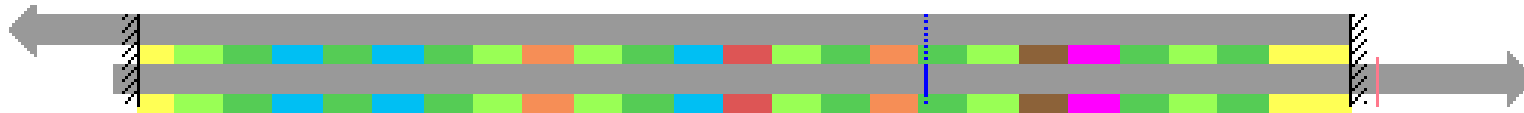
PCR RIBOTYPNING



HYPPIGE PCR RIBOTYPER

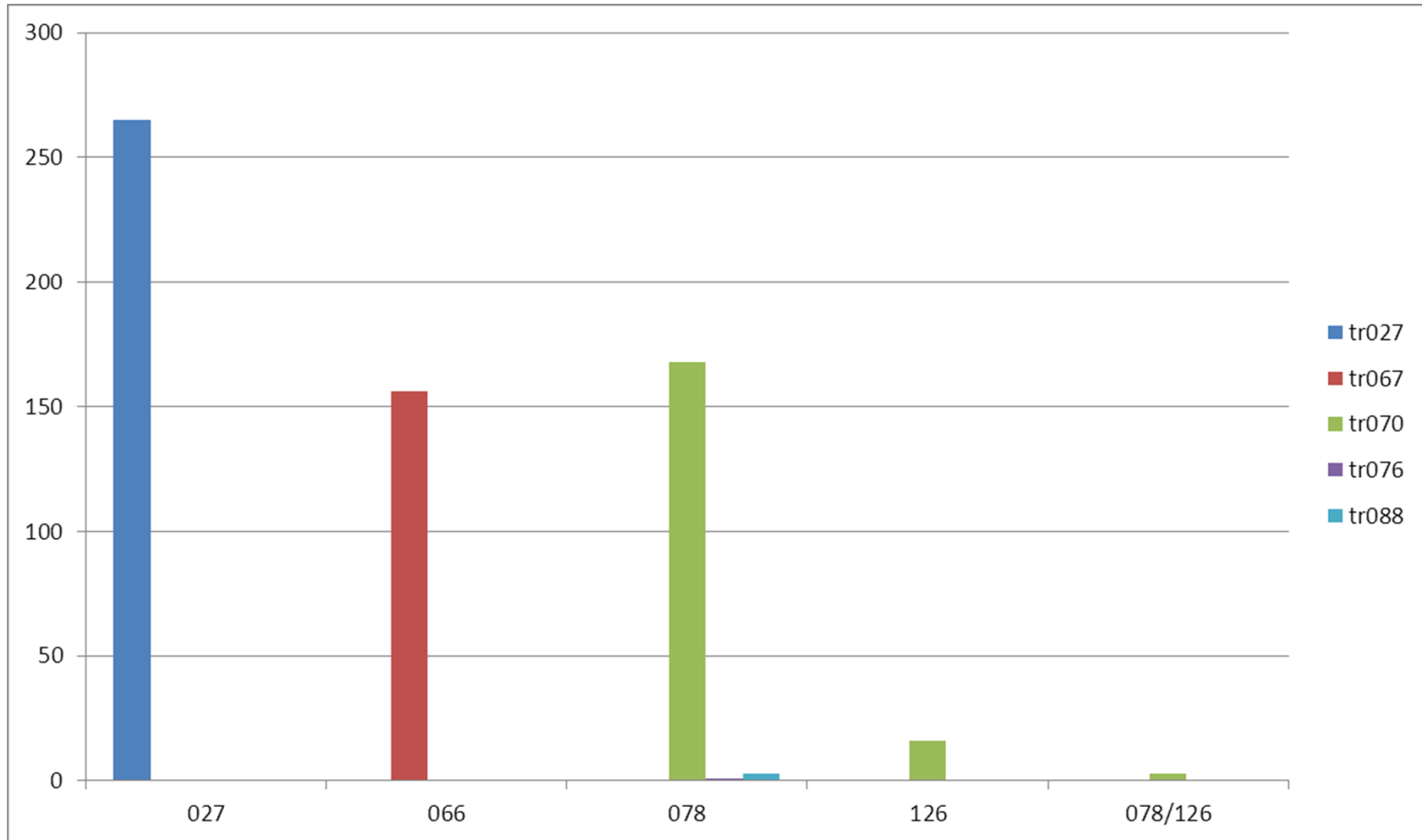


Tandem Repeat Sequence Typing, TRST (DNA-sekvenser)

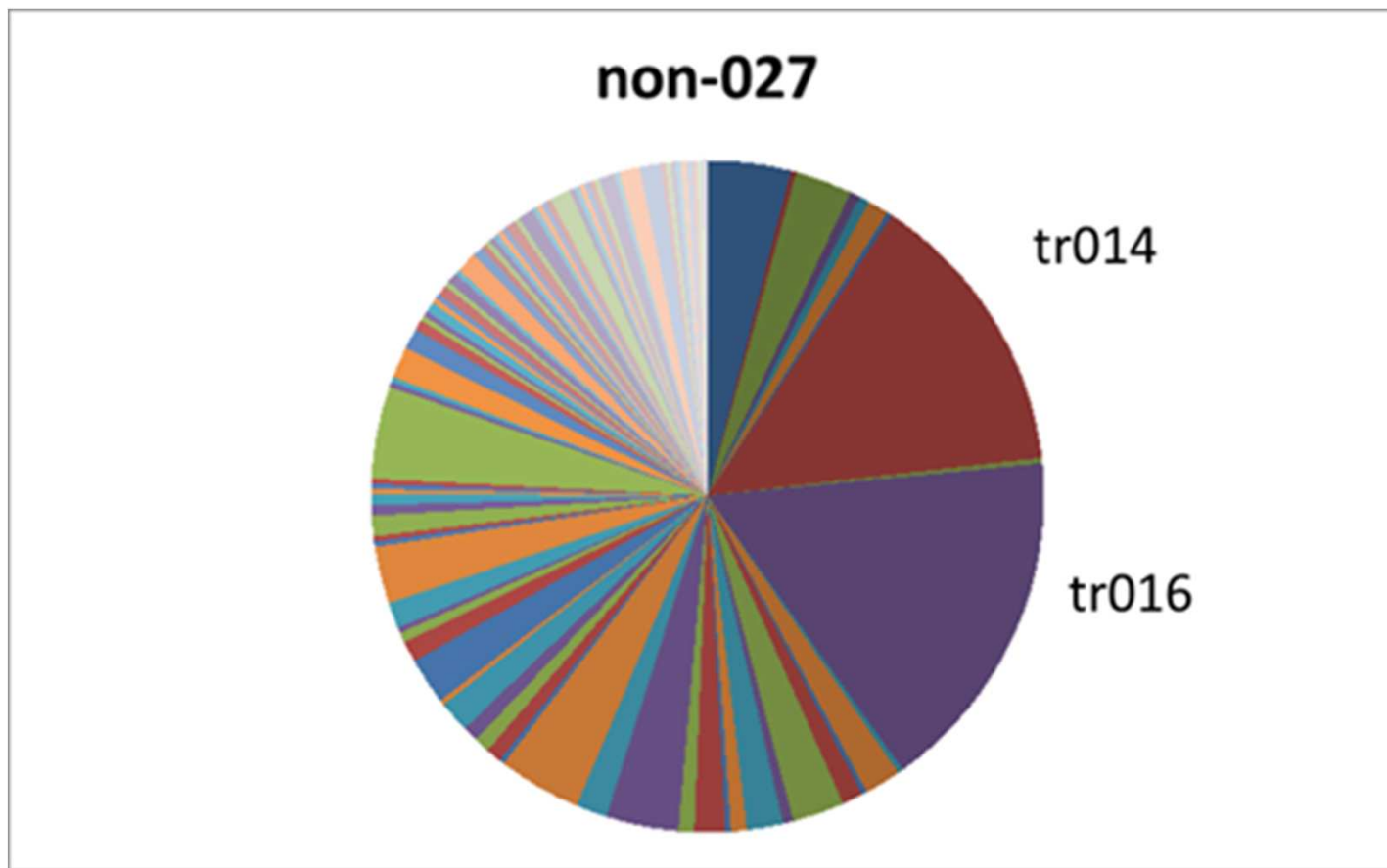


- Sekventering af to tandem repeat loci (TR6 og TR10)
- Stor sekvensvariation i disse loci
- Kombinationen af disse repeat units bruges derefter til at tildele en subtype

God sammenhæng mellem PCR-ribotype og TRST





Alle isolater kan nu tildeles en type



Og vi TRST-typer på alle toksinpositive isolater



PubTRST  Sitemap 

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pubtrst

Tandem Repeat Sequence Typing (TRST)

Methods involving variable number of tandem repeats (VNTR) has been found useful for the typing of several pathogens. For *Clostridium difficile*, the major typing method has so far been PCR ribotyping. A major disadvantage of PCR ribotyping and other band-based typing techniques is the poor portability and interlaboratory comparability of the generated data. Typing procedures based on DNA sequences overcome these limitations, since sequence data may easily be exchanged and stored in databases that are accessible via the internet. A new typing method for genotyping *C. difficile*, tandem repeat sequence typing (TRST), has been developed by Zaiss *et al*¹. Two tandem repeat loci (designated 'TR6' and 'TR10'), which display extensive sequence variation in the repeat units, are sequenced. The combination of repeat units in the two loci is then used for designation of sequence-based subtypes.

However, optimum use of this typing approach requires a convenient means where newly generated data can be catalogued and compared in an internationally shared database. Researchers are encouraged to submit new TRST repeat unit sequences and new TRST types to the curators for verification and inclusion into the database.

¹Zaiss NH, Rupnik M, Kuijper EJ, Harmanus C, Michielsen D, Janssens K, Nübel U. 2009. Typing *Clostridium difficile* strains based on tandem repeat sequences. *BMC Microbiol* Jan 8;9:6

The database currently contains

- 85 TR6 repeat sequences
- 70 TR6 repeat successions
- 54 TR10 repeat sequences
- 71 TR10 repeat successions
- 134 TRST types

2012-12-19
1 New TR6 sequences, 1 New TR6 repeat succession, 1 New TR10 repeat succession, 15 New TRST types

2012-12-07
3 new TR6 repeat succession, 2 new TR10 repeat succession, 5 new TRST type

Dataset update 2012-08-31
3 new TR6 repeat succession, 1 new TR10 repeat succession, 4 new TRST types

Dataset update 2012-07-24
1 new TR6 repeat, 1 new TR6 repeat succession, 1 new TR10 repeat succession, 3 new TRST types

Dataset update 2012-07-17
1 new TR6 repeat succession, 2 new TRST types.

Dataset update 2012-06-21
4 new TR6 repeat successions, 1 new TR10 repeat succession, 1 new TRST type. New TR10 Start trimming sequence

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