

# Validation of three prediction tools for a complicated course of *C. difficile* infection

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## Aim

- To test **prediction tools** for a complicated course of *C. difficile* infection (CDI) for **clinical use**
- To provide **external validation**

## Methods

- Validation cohort:** all patients diagnosed with CDI between May 2013 – March 2014. In this period endemic CDI cases occurred (n=70), but also an outbreak due to ribotype 027 (n=78).
- Complicated course:** colectomy, death, ICU admission due to CDI.
- Model **calibration** and **discrimination** for selected prediction tools.

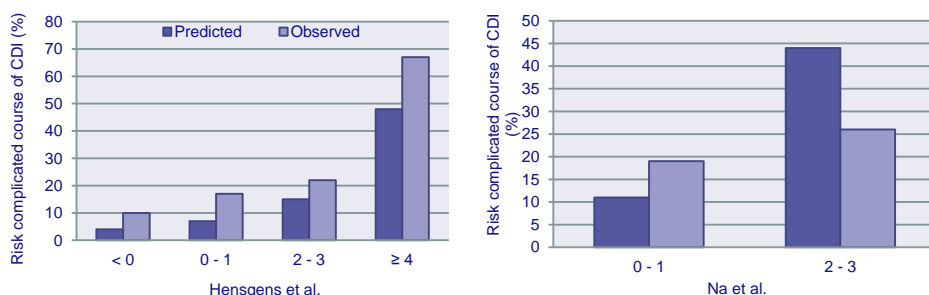
## Results

- 3 prediction tools selected** based on patient population, objective scoring parameters, and availability of variables

Reference	Predictors
Hensgens et al. 2014	Age, department of diagnosis, recent abdominal surgery, hypotension, diarrhea reason for admission
Na et al. 2015	Age, peak white blood cells, peak creatinine
Welfare et al. 2011	Age, renal disease, cancer

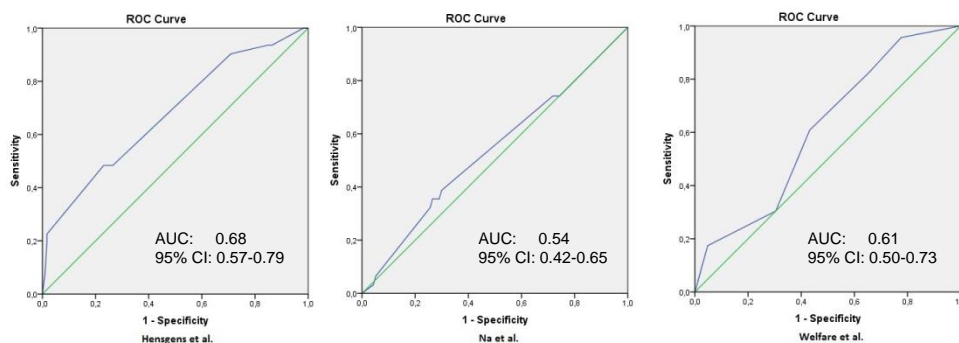
## Calibration

Observed vs predicted complicated course per risk group, following original prediction scores

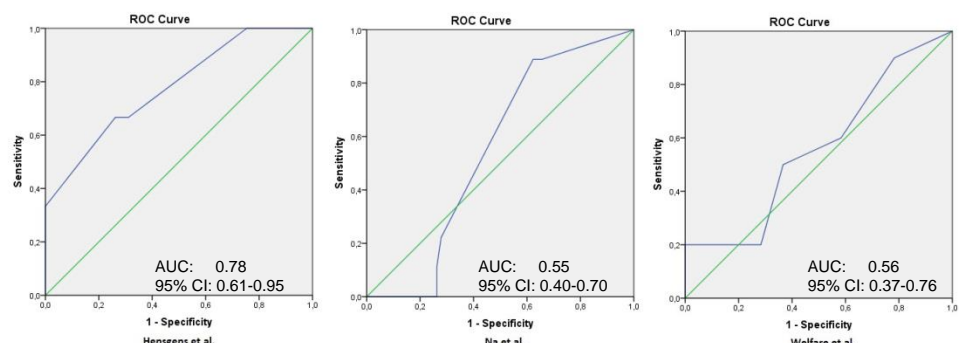


## Discrimination

Pooled ROC curve **total validation cohort**



Pooled ROC curve **when patients diagnosed with outbreak strain 027 were excluded**



## Conclusion

- All 3 prediction tools performed **poorly when applied to our total cohort**, that included patients from an outbreak, and endemic cases.
- Prediction score of **Hensgens et al.** performed relatively well (AUC 0.78; 95% CI 0.61-0.95) when patients diagnosed with CDI due to the outbreak strain 027 were excluded. This model **may be useful in endemic settings.**
- Prediction rules **should only be applied in a cohort that is comparable with the derivation cohort.**