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External validation of three prediction tools for patients at risk of a complicated course of Clostridium difficile infection: disappointing in outbreak setting

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Background: Estimating the risk of a complicated course of *Clostridium difficile* infection (CDI) might help doctors to guide antibiotic treatment. We aimed to validate three published prediction models (Hensgens 2014; Na 2015; Welfare 2011).

Material/methods: The validation cohort comprised all patients diagnosed with CDI during a one year lasting outbreak at a university hospital (n = 148). Both patients diagnosed with CDI due to the outbreak strain ribotype 027 (n = 78), and patients with CDI due to other ribotypes (n = 70) were included (typed by Amplified Fragment Length Polymorphism). Model calibration and discrimination were assessed for the three prediction rules.

Results: A complicated course (death, colectomy, or ICU admission due to CDI) was observed in 31 patients (21%). Twenty-three patients (16%) died within 30 days after CDI diagnosis. The performance of all three prediction models was poor when applied to the total validation cohort. For those patients been diagnosed with CDI due to non-outbreak strains, the risk score of Hensgens *et al*. performed much better, with a Receiver Operating Characteristic area of 0.78. In contrast, the models of Na *et al*., and Welfare *et al.* retained very poor predictive value, with poor discrimination and calibration also when applied to patients with CDI due to the non-outbreak strains.

Conclusions: All three prediction models performed poorly when validated on our total outbreak cohort. The prediction score of Hensgens *et al*. performed relatively well for patients diagnosed with CDI due to non-outbreak strains, and may therefore be useful in endemic settings.