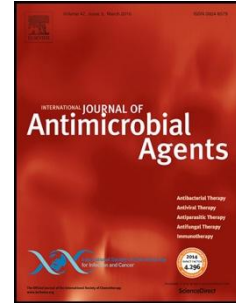


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- 1 Prediction of recurrent *Clostridium difficile* infection at the bedside: the GEIH-
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69

70 Running title: Prediction tool for recurrent CDI

71

72 Highlights:

73

74

75

76 • Based on data from a large cohort of patients, a clinical tool for prediction of
77 recurrent CDI has been developed.

78

79 • The tool makes it possible to identify a subgroup of patients with a high probability of
80 recurrence, thus enabling clinicians to select patients for new and expensive
81 therapies that reduce the risk of recurrence

82 Abstract

83 Recurrence of *Clostridium difficile* infection (CDI) has major consequences for both patients

84 and the health system. The ability to predict which patients are at an increased risk of

85 recurrent CDI makes it possible to select candidates for therapy with new drugs and

86 therapies (including fecal microbiota transplantation) that have proven to reduce the

87 incidence of recurrence of CDI. Our objective was to develop a clinical prediction tool, the

88 GEIH-CDI score, to determine the risk of recurrence of CDI. Predictors of recurrence of CDI

89 were investigated using logistic regression in a prospective cohort of 274 patients diagnosed

90 with CDI. The model was calibrated using the Hosmer-Lemeshow test. The tool comprises 4

91 factors: age (70-79 years and ≥ 80 years), history of CDI during the previous year, direct

92 detection of toxin in stool, and persistence of diarrhea on the fifth day of treatment. The

93 functioning of the GEIH-CDI score was validated in a prospective cohort of 183 patients. The

94 area under the ROC curve was 0.72 (0.65 – 0.79). Application of the tool makes it possible to

95 select patients at high risk ($>50\%$) of recurrence and patients with low risk ($<10\%$) of

96 recurrence. GEIH-CDI score may be useful for clinicians treating patients with CDI.

97

98 Keywords: *Clostridium difficile*, recurrence, clinical prediction tool

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106 Introduction

107 *Clostridium difficile* is the main cause of antibiotic-associated diarrhea and one of the main
108 causes of health care–associated infection.[1,2] Around 85% of the patients diagnosed with
109 *Clostridium difficile* infection (CDI) respond well to antibiotic therapy.[3] However, the
110 disease recurs in at least 20% of patients during the weeks immediately following
111 completion of treatment. [3,4] The impact of recurrence of CDI was recently reported after it
112 was shown to be associated with higher costs and increased mortality. [5-7] Recurrence is
113 associated with persistence of spores, an insufficient immune response, and loss of the
114 diversity of gut microbiota.[4] Many studies have identified risk factors for recurrence,[8]
115 although clinical decision making cannot be based merely on knowing whether or not a
116 patient is at a greater risk of an event. Rather, it would be interesting to predict the real risk
117 of the event by taking into account relevant factors and the interactions between them.
118 Such information could be obtained using clinical prediction tools.[9]

119

120 More clinical tools have been developed for prediction of death or complicated disease
121 course (colectomy, admission to intensive care) than for prediction of recurrence.[10]

122 However, interest in such tools is limited because of the lack of new drugs and strategies

123 that significantly reduce the risk of complications of CDI and death. In contrast, prediction of

124 recurrence would help physicians to better select candidates for new expensive treatments

125 and fecal microbiota transplantation that have been shown to significantly reduce the
126 frequency of recurrence of CDI.[11-13]. Furthermore, prediction tools would enable earlier
127 diagnosis and treatment of recurrence thanks to closer follow-up and increased access to
128 health care for patients at greater risk of recurrence. Finally, prediction tools could be used
129 to improve the design of future clinical trials in this disease.

130 Most studies on clinical tools for prediction of recurrence of CDI are methodologically
131 deficient or difficult to apply in clinical practice.[10] The objective of our study was to
132 develop a simple clinical prediction tool that is easy to apply in daily clinical practice and
133 could thus enable us to identify patients who are at a high risk of recurrence of CDI.

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136 Patients and methods

137 *Patient selection*

138 Patients were prospectively included in the derivation cohort between July 2014 and
139 February 2015 from 14 Spanish hospitals belonging to the Grupo de Estudio de Infección
140 Hospitalaria (GEIH [*Nosocomial Infection Study Group*]) of the Sociedad Española de
141 Enfermedades Infecciosas y Microbiología Clínica (SEIMC [*Spanish Society of Infectious*
142 *Diseases and Clinical Microbiology*]). In order to be included in the study, patients had to
143 have symptomatic CDI (defined as ≥ 3 loose stools in 24 hours), ileus, or pseudomembranous
144 colitis confirmed microbiologically using free toxin testing of stool (immunoassay), the
145 nucleic acid amplification test (NAAT), or culture of toxigenic *C. difficile*. Patients expected to
146 die (in opinion of the investigator) during the following days were excluded, as were patients
147 for whom follow-up and data collection were likely to be problematic, patients already
148 participating in clinical trials, and patients who had received fidaxomicin since the onset of
149 their disease.

150

151 *Data collection*

152 Patients were followed at 4 visits (baseline and 7-10 days after the initiation of treatment,
153 and at 1 and 2 months after completion of treatment). The data collected at the baseline
154 visit were demographic data, history, degree of dependence, clinical presentation, need for
155 hospitalization, severity of CDI, time since onset of symptoms, and method of diagnosis. At
156 the second visit, the data collected were treatment received, time until resolution of
157 diarrhea, place of treatment, and therapy with antibiotics and proton pump inhibitors. At
158 visits 3 and 4, we verified whether the disease had recurred and whether recurrence had
159 been documented using microbiological techniques. Patients were seen in the hospital or

160 interviewed by telephone if they were not hospitalized. When it was not possible to obtain
161 reliable data by telephoning the patient or his/her carers, we retrieved data from hospital
162 information systems and public health network. All the participating centers had access to
163 an online database.

164

165 *Measurement of outcome*

166 Recurrence was defined using the criteria applied in the case definition. Recurrence was also
167 defined as reappearance of symptoms suggestive of CDI that resolved with vancomycin,
168 metronidazole, or fidaxomicin if a new sample had not been sent to the laboratory. In
169 contrast, if a sample sent to the laboratory was negative for toxigenic *C. difficile* despite a
170 response to specific treatment for CDI, then reappearance of diarrhea was not considered a
171 recurrence. Patients whose disease recurred were not readmitted to the derivation cohort,
172 although clinical data on new episodes were collected. The importance of avoiding the
173 overdiagnosis of recurrence was emphasized to the investigators.

174

175 Data are expressed as mean (standard deviation) and absolute and relative frequencies as
176 appropriate. The *t* test and Mann-Whitney test were used to compare continuous variables
177 and the chi-square test was used for categorical variables.

178

179 *Derivation cohort*

180 We performed a logistic regression model to estimate a predictive model for recurrence.
181 Candidate predictors were selected from those that were significant in the univariate
182 analysis and those selected by investigators based on the medical literature and clinical
183 practice.

184 We used a parsimonious backward approach to investigate combinations of variables for
185 inclusion in our final model (with $p \leq 0.05$ as an initial criterion for statistical significance).
186 We then computed the points for each predictive variable's risk categories as the rounded
187 value of the quotient resulting from dividing the coefficient of each category by the lowest
188 coefficient. The simplicity of this scoring system allows a patient's risk to be estimated
189 without using a calculator. The GEIH-CDI score was calculated for each patient based on a
190 sum of individual points of each predictive variable included in the final model.

191
192 Discrimination for prediction of the event was estimated using the area under the ROC curve.
193 The model was calibrated using the Hosmer-Lemeshow test for logistic regression.

194
195 The sensitivity, specificity, and likelihood ratios of the model were calculated for different
196 cutoffs. The accuracy of the model was also calculated by dividing the sum of the true
197 positives and negatives by the total population.

198
199 *Validation cohort*

200 The GEIH-CDI score was tested using a validation cohort. A new prospective cohort was
201 recruited from 16 hospitals of the GEIH (12 of which had participated in the derivation
202 cohort) between September 2015 and February 2016. The researchers collected a set of
203 variables from the patients without knowing the results of the model from the derivation
204 cohort (although the coordinating center had full knowledge of the results). The same
205 inclusion criteria and definitions of CDI were applied.

206
207 All analyses were performed using Stata 14.1 for Windows.

208 Results

209 During the study period (July 2014 to February 2015), a total of 581 cases of CDI were
210 recorded in the derivation cohort. Of these, 263 were excluded for various reasons:
211 difficulties affecting the researchers (eg, vacations, workload) in 100 cases, refusal of
212 informed consent or impossibility of obtaining it in 58 cases, difficulties with follow-up in 55
213 cases, probable death during the following days in 25 patients, and other situations in 25
214 cases. Therefore, the final sample included 318 patients. Of these, patients were excluded
215 because they died before 30 days (22 cases), were participating in clinical trials (15 cases),
216 received fidaxomicin after inclusion (4 cases), and were lost to follow-up or had insufficient
217 data (3 cases). The remaining 274 patients were identified based on detection of toxin in
218 stool in 152 cases, NAAT in 116 cases, and culture in only 6 cases. Mean (SD) age was 67.1
219 (19.0) years, 55% of patients were women, and 29 (10.6%) had had at least 1 other episode
220 of CDI during the previous year. Recurrence of CDI during follow-up was recorded in 70 cases
221 (25.6%, 63 diagnosed using microbiological techniques and 7 by response to treatment)
222 (Figure 1). A single recurrence was recorded in 51 patients, 2 recurrences in 13 patients, 3
223 recurrences in 5 patients, and 4 recurrences in 1 patient.

224

225 *Predictive model*

226 We compared variables in patients who experienced recurrence with those who did not
227 (Table 1). We started with a maximum model comprising the variables age, sex, positive
228 toxin result, dependence according to the Katz index, previous episodes of CDI, underlying
229 disease (analyzed using a composite variable that included presence of heart failure, kidney
230 disease, diabetes, cancer, or immunosuppression), maximum temperature at the time of
231 diagnosis, and persistence of diarrhea after 5 days of antibiotic treatment for CDI. The final

232 model included the following variables: age (<70 years [0 points], 70-79 years [1 point], and
233 ≥80 years [2 points]), history of CDI during the previous year (2 points), persistence of
234 diarrhea on the fifth day of treatment (2 points), and positive result in direct detection of
235 toxin in stool (1 point) (table 2, Figure 2). The points for each variable were added, so that
236 the GEIH-CDI score ranged from 0 to 7 points, with higher scores indicating a greater risk of
237 recurrence

238

239 The score was calculated for each of the patients included in the cohort, and the scores were
240 compared with the risk of recurrence observed for each score level. A greater risk was
241 observed for the higher score ranges (Figure 3). The area under the ROC curve was 0.73
242 (0.66 – 0.80) for the original model and 0.72 (0.65 – 0.79) for simplified model and the
243 Hosmer-Lemeshow goodness-of-fit test p value was 0.704.

244

245 With a cutoff of 4 points, sensitivity was 48.6% and specificity was 84.2%. With a cutoff of 2
246 points, sensitivity reached 91.4%, although specificity fell to 34.5%. The positive and
247 negative likelihood ratio of the model was 3.08 and 0.61, respectively, and accuracy was
248 0.75.

249

250 Given that some patients in the derivation cohort died before recurrence and, therefore,
251 were excluded, we performed a sensitivity analysis including these cases. The results
252 obtained were identical, with an area under the ROC curve of 0.71 (0.64 – 0.78). Also,
253 because the free toxin test was not done in fifty-one patients of the derivation cohort we
254 performed a sensitive analysis excluding these patients. Again, the performance of the
255 model showed no changes: area under the ROC curve of 0.74 (0.67 - 0.81).

256

257 The validation cohort included 183 patients whose demographic characteristics were similar
258 to those of the derivation cohort. Mean age was 67.3 (19.0) years, 53% of patients were
259 women, and 9.8% had had an episode of CDI during the previous year. The number of
260 patients with recurrences was very similar to that in the derivation cohort (25.1%). The
261 results of applying the model in the validation cohort with the derivation cohort can be seen
262 in Figure 3. The accuracy of the model was similar (0.77). With the same cutoff of 4 points,
263 sensitivity reached 50% and specificity 86%, whereas the area under the ROC curve was 0.75
264 (0.67 – 0.83). Finally, Table 3 summarizes the functioning of the predictive model including
265 both cohorts. A composite score based on 3 ranges makes it possible to select a low-risk
266 group (0-1 points; 29.9% of patients; risk of recurrence, 8.8%), an intermediate-risk group (2-
267 3 points; 46.4% of patients; risk of recurrence, 22.3%), and a high-risk group (≥ 4 points;
268 23.9% of cases; risk of recurrence, 52.8%). The accuracy of the model applied to both
269 cohorts was 0.76.

270

271

272 Discussion

273 Our study confirms that one-quarter of patients diagnosed with CDI and treated in a hospital

274 experience a subsequent episode during the 2 months following completion of treatment.

275 Even after excluding patients who have had a previous episode, we found that this

276 proportion reached 21.2%. Our clinical prediction tool makes it possible to identify a high-

277 risk population that could benefit from recently marketed or forthcoming treatments that

278 have proven to reduce the risk of recurrence [11,12] but whose cost is very high and limits

279 widespread administration,[14,15], as well fecal microbiota transplantation.

280

281 Several models for prediction of recurrence of CDI have been investigated; however, these

282 have not been consolidated in clinical practice owing to their limitations. The accuracy

283 reported by D'Agostino et al.[16] was somewhat lower than that found in our study,

284 although this was not validated externally. In addition, the model was obtained from a

285 cohort comprising patients participating in pivotal clinical trials of fidaxomicin, thus likely

286 implying major biases. Hu et al.[17] reported details of their model, which included age,

287 severity (measured according to the Horn index), and creatinine. However, the number of

288 patients included in the validation cohort was small and the proportion of recurrences very

289 different from that observed in the derivation cohort, in which it seems reasonable to

290 suspect bias, given that the frequency of recurrence reached 50%. One recent study did not

291 specifically consider recurrence as an outcome measure but included it within a broader

292 category known as "complicated CDI". Furthermore, prediction depended on a specific

293 laboratory test.[18] Finally, other attempts were affected by poor accuracy or could not be

294 applied in clinical practice.[19-21]

295

296 The main strengths of our prediction tool are the size of the derivation cohort, the fact that
297 patients were recruited from several centers, the low probability of inclusion bias (since the
298 recurrence rate corresponds with that reported in the literature), the low number of losses
299 to follow-up, and confirmation of the model in a validation cohort. Furthermore, the tool
300 can be applied at the bedside without the need for laboratory tests other than routine
301 diagnostic tests. Advanced age,[8] a history of previous episodes, [22] and direct detection
302 of toxin in stool (compared with cases diagnosed using NAAT)[23] are known risk factors for
303 recurrence. This last fact supports the policy of including toxin immunoassay in the
304 diagnostic algorithm as it has been recently recommended.[24] Patients with negative toxin
305 detection diagnosed by NAAT could have fewer recurrences due to a lower toxin and a
306 bacterial burden but also due to an earlier detection and treatment of the disease.
307 [23]Persistence of diarrhea has not been reported to be a risk factor for recurrence,
308 probably because almost all studies on risk factors for recurrence of CDI have been
309 retrospective and this information was not available. This variable is not present at diagnosis.
310 However, in our opinion, it allows for more dynamic management that is compatible with
311 routine clinical practice. For example, new treatments with monoclonal antibodies against *C.*
312 *difficile* toxins are administered during the course of treatment with *C. difficile*-specific
313 antibiotics.[12]
314
315 Interestingly our predictive tool can identify some patients on first episode of CDI having
316 higher risk of CDI recurrence than some patients on the second episode.
317 Our study is subject to a series of limitations. The accuracy of the model is not very high;
318 therefore, with a high cutoff, sensitivity is low. Nevertheless, the cutoff can be modified
319 depending on how the model is to be applied. The laboratory methods were not

320 homogeneous due to the multicenter design of the study. In fact in some patients the free
321 toxin test in feces was not performed. However the model performed well after excluding
322 these patients. It could also be argued that patients diagnosed by positive NAAT but
323 negative direct toxin tests could be merely colonized. Nevertheless, only symptomatic
324 patients were accepted to have CDI or CDI recurrence and this was emphasized to
325 investigators. The study was restricted to Spain, and many of the centers that participated
326 in the derivation cohort also participated in the validation cohort. Finally, the variable time
327 to resolution of diarrhea may not always be fully consistent or objective, since the fact that
328 patients can experience changes in their intestinal rhythm can make it difficult to identify on
329 which day diarrhea resolved. Greater accuracy might be obtained by combining this model
330 with specific biomarkers of CDI.[25,26]

331

332 In summary, prediction of recurrence of CDI is increasingly important owing to its potential
333 role in the management of patients and in decisions on therapy.[27]The prediction tool we
334 propose may be useful for clinicians treating patients with CDI.

335

336 Declarations

337 Funding: This study was carried out by internal funding

338 Competing Interests: JC has received consultancy and speaking fees from Astellas Pharma
339 and MSD.

340 CHC has received speaking fees from Astellas Pharma.

341 JGA has received consultancy and speaking fees from MSD.

342 MS has received consultancy and speaking fees from Astellas Pharma and MSD

343 Ethical Approval: Local ethics committees approved the study

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Fig 1. Flow chart of cases (derivation cohort)

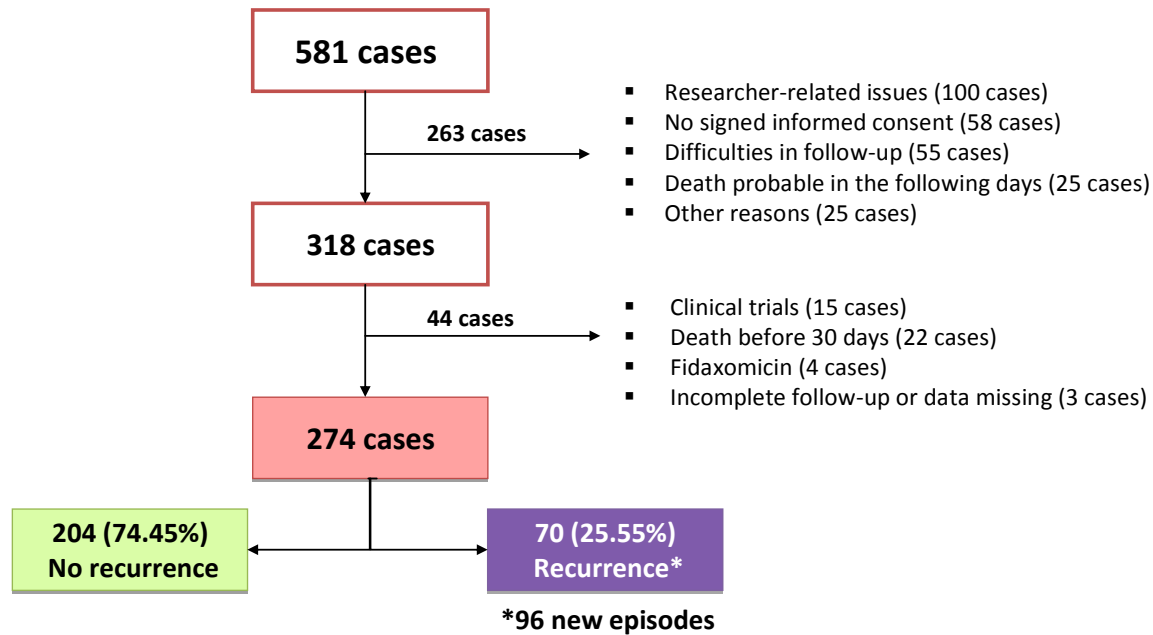


Fig 2. GEIH-CDI score

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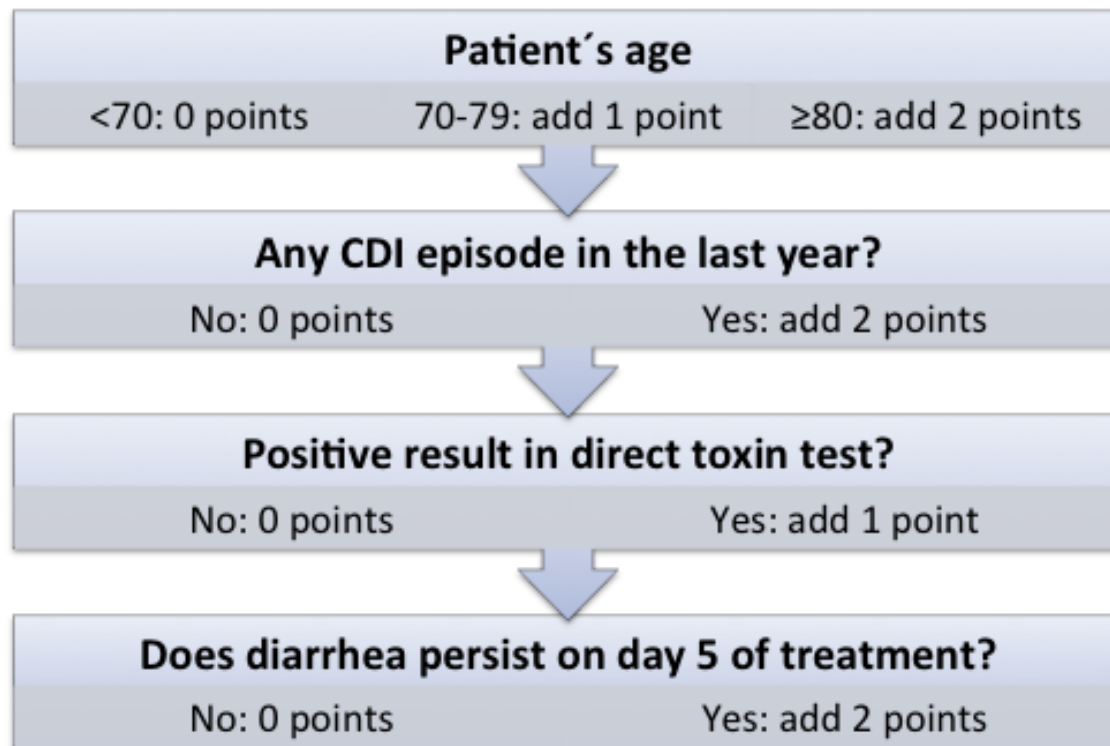
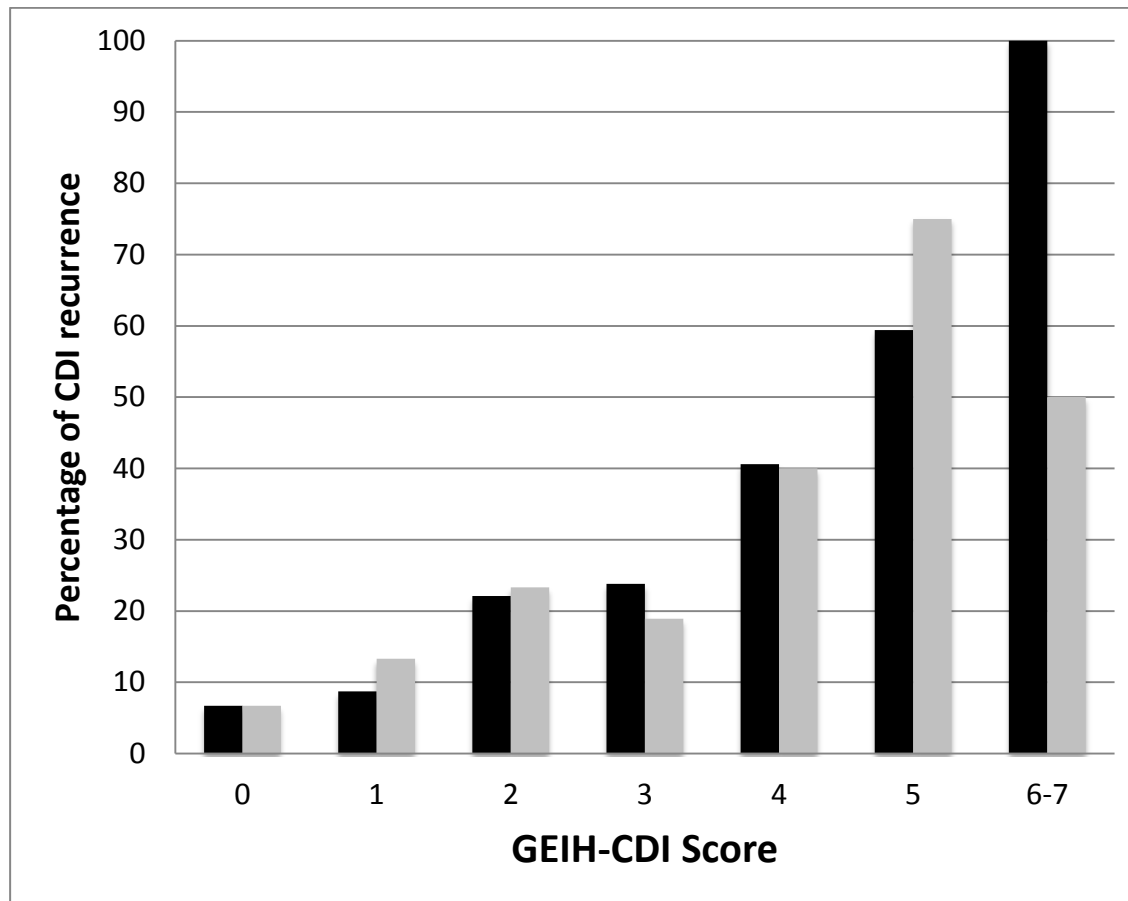


Fig 3. Risk of recurrence and GEIH-CDI score. Black bars: derivation cohort; grey bars: validation cohort



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Table 1. Derivation cohort: comparison between patients with and without recurrence

Variable		No recurrence (204)	Recurrence (70)	p
Sex	Male (123)	98 (79.7)	25 (20.3)	0.074
	Female (151)	106 (70.2)	45 (29.8)	
Age	<70 (128)	104 (81.3)	24 (18.8)	0.015
	70-79 (51)	39 (76.5)	12 (23.5)	
	≥80 (95)	61 (64.2)	34 (35.8)	
Time to diagnosis since the onset of symptoms	<7 days (190)	148 (77.9)	42 (22.1)	0.037
	≥7 days (82)	54 (65.9)	28 (34.1)	
Previous episode	No (245)	189 (77.1)	56 (22.9)	0.003
	Yes (29)	15 (51.7)	14 (48.3)	
Type of episode ¹	Nosocomial (138)	102 (73.9)	36 (26.1)	0.979
	Health care–acquired (68)	51 (75.0)	17 (25.0)	
	Community-acquired (68)	51 (75.0)	17 (25.0)	
Temperature (maximum in the first 24 h)	<38 (203)	155 (76.4)	48 (23.6)	0.156
	≥38 (67)	45 (67.6)	22 (32.4)	
No. of bowel movements	Ileus (2)	2 (100)	0	0.408
	3 (56)	43 (76.8)	13 (23.2)	
	4-6 (127)	93 (73.2)	34 (26.8)	
	7-10 (52)	35 (67.3)	17 (32.7)	
	>10 (32)	27 (84.4)	5 (15.6)	

Direct detection of toxin in feces	Positive (152)	105 (69.1)	47 (30.9)	0.023
	Negative/not performed (122)	99 (81.1)	23 (18.9)	
Severity	Mild-moderate (201)	154 (76.6)	47 (23.4)	0.206
	Severe or complicated (71)	49 (69.0)	22 (31.0)	
Incontinence (fecal)	No (163)	131 (80.4)	32 (19.6)	0.005
	Yes (109)	71 (65.1)	38 (34.9)	
Comorbidities	Inflammatory bowel disease (15)	13 (86.7)	2 (13.3)	0.274
	Cancer (71)	53 (74.6)	18 (25.4)	0.915
	Immunosuppression ² (64)	51 (79.7)	13 (20.3)	0.256
	Heart failure (48)	33 (68.1)	15 (31.9)	0.271
	Kidney disease (49)	34 (69.4)	15 (30.6)	0.398
	Diabetes (56)	44 (78.6)	12 (21.4)	0.370
	Dementia (32)	21 (65.6)	11 (34.4)	0.223
Laboratory	Leukocyte count (264)	11,299.8 (8603.5)	12,960.1 (8476.9)	0.172
	Creatinine (mg/L) (264)	1.2 (1.1)	1.2 (1.4)	0.874
	Proteins (g/L) (175)	5.7 (0.9)	5.5 (1.0)	0.096
	Albumin (g/L) (156)	3.0 (0.7)	3.0 (0.7)	0.840
	C-reactive protein (mg/L) (187)	60.8 (78.3)	82.8 (76.2)	0.094
Able to dress	Yes (186)	147 (79.0)	39 (21.1)	0.012
	No (88)	57 (64.8)	31 (35.2)	
Able to walk several blocks	Yes (179)	142 (79.3)	37 (20.7)	0.011
	No (95)	62 (65.3)	33 (34.7)	
Time until resolution of diarrhea	<5 days (159)	131 (82.4)	28 (17.6)	0.000
	≥5 days (124)	72 (63.2)	42 (36.8)	
Treatment	Metronidazole (152)	119 (78.3)	33 (22.7)	0.556

	Vancomycin (76)	52 (68.4)	24 (31.6)	
	Metronidazole plus vancomycin (31)	22 (71.0)	9 (29.0)	
	Metronidazole followed by vancomycin (10)	7 (70.0)	3 (30.0)	
Continue on antibiotics (on day 7)	Yes (128)	96 (75.0)	32 (25.0)	0.955
	No (144)	107 (74.3)	37 (25.7)	
Continue on proton pump inhibitors (on day 7)	Yes (163)	131 (80.4)	32 (19.6)	0.017
	No (110)	67 (67.3)	33 (32.7)	

1. Nosocomial: CDI symptoms that were not present on the day of admission appear during hospitalization (at least 48 hours after admission) or within 3 days after discharge. Health care-associated: hospitalization in the last 3 months or living in a residence or periodic dialysis or IV ambulatory treatment or outpatient treatment. Community-acquired: all other cases
2. HIV infections with less than 200 CD4 cell count/mm³ or treatment with immunosuppressive drugs

Table 2. Logistic model. Derivation cohort

	Coefficient	95% Confi.interval	Score
Constant	-2.7	-3.6 to -1.9	-
Age 70-79	0.49	0.35 - 1.33	1
Age ≥80	1.17	0.50 - 1.83	2
Toxin-positive	0.65	0.09 - 1.40	1
Previous episode	1.30	0.45 - 2.14	2
Diarrhea on day 5	1.18	0.58 - 1.78	2

Table 3. Risk of recurrence in the study population (derivation and validation cohorts) for different score values.

Score	Derivation cohort (273) ¹				Validation cohort (182) ¹				Both cohorts (455)				Composite score	Cases (%)	Recurrence (%)
	No recurrence	Recurrence	Cases (%)	Recurrence (%)	No recurrence	Recurrence	Cases (%)	Recurrence (%)	No recurrence	Recurrence	Cases (%)	Recurrence (%)			
6-7	0	2	0.7	100	3	3	3.3	50	3	5	1.8	62.5			
5	13	19	11.7	59.4	4	12	8.8	75	17	31	10.5	64.6	4-7 (high risk)	23.7	52.8
4	19	13	11.7	40.6	12	8	11.0	40	31	21	11.4	40.4			
3	53	15	24.9	22.1	30	7	20.3	18.9	83	22	23.1	21.0	2-3 (intermediate risk)	46.4	22.3
2	48	15	23.1	23.8	33	10	23.6	23.3	81	25	23.3	23.6			
1	42	4	16.8	8.7	26	4	16.5	13.3	68	8	16.7	10.5	0-1 (low risk)	29.4	8.8
0	28	2	11.0	6.7	28	2	16.5	6.7	56	4	13.2	6.7			

1. One case in both the derivation cohort and the validation cohort was not included in the model because of lack of data for one of the variables included in the score.

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