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1 **Detection of AmpC beta-lactamase in *Escherichia coli*: comparison of three phenotypic**
2 **confirmation assays and genetic analysis**
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14 **Running title: Detection of AmpC beta-lactamases in *Escherichia coli***

15 **Keywords:** AmpC beta-lactamase , *ampC* promoter, *Escherichia coli*

16 **Abstract**

17 Two mechanisms account for AmpC activity in *E. coli*: mutations in the *ampC* promoter and
18 attenuator regions resulting in *ampC* overexpression and/or acquisition of plasmid-encoded
19 *ampC* genes. In this study we analyzed 51 clinical *E. coli* isolates with reduced susceptibility to
20 amoxicillin/clavulanic acid, piperacillin/tazobactam or third generation cephalosporins for the
21 presence of AmpC production. Three phenotypic AmpC confirmation assays (cefoxitin/cloxacillin
22 disk diffusion test, cefoxitin/EDTA disk diffusion test, AmpC ETest) were compared for the
23 detection of AmpC activity. All 51 isolates were genetically characterized by mutation analysis of
24 the chromosomal *ampC* promoter/attenuator region and by PCR detection of plasmid-encoded
25 *ampC* genes. Altogether, 21/51 (41 %) *E. coli* isolates were considered true AmpC producers.
26 AmpC activity due to chromosomal *ampC* promoter/attenuator mutations was found in 12/21
27 strains, plasmid-encoded *ampC* genes were detected in 8/21 isolates. 1/21 strains contained
28 both, *ampC* promoter mutations and a plasmid-encoded *ampC* gene. All three phenotypic tests
29 were able to detect the majority (>90%) of AmpC positive strains correctly. Cefoxitin resistance
30 was found to be a discriminative parameter, detecting 20/21 AmpC producing strains.
31 Susceptibility to third generation cephalosporines, e.g. ceftriaxone, cetazidime and cefotaxime,
32 was found in 9 of the 21 AmpC positive strains. When considering the elevated zone diameter
33 breakpoints of the 2010 CLSI guidelines 2/21 AmpC positive strains were categorized susceptible
34 to third generation cephalosporines.

35 **Introduction**

36 The prevalence of multidrug resistant Gram negative bacteria has continuously increased over
37 the past years and bacterial strains producing AmpC beta-lactamases and/or extended spectrum
38 beta-lactamases (ESBLs) are of particular concern. AmpC beta-lactamases can confer resistance
39 to aminopenicillins, cephalosporins, oxyimino-cephalosporins (e.g. ceftriaxone, cefotaxime,
40 ceftazidime), cephamycins (e.g. cofexitin, cefotetan) and monobactams (15). Cloxacillin and 3-
41 aminophenylboronic acid inhibit AmpC beta-lactamases (2, 15, 36), while AmpC beta-lactamase
42 activity is not affected by the ESBL inhibitor clavulanic acid. In Gram negative bacteria AmpC
43 beta-lactamase production is chromosomally- or plasmid-mediated. Chromosomal *ampC* genes
44 are constitutively expressed at a low level. Some *Enterobacteriaceae* such as *Enterobacter* spp.,
45 *Citrobacter* spp. and *Serratia* spp., encode an inducible *ampC*. In these cases, the gene is strongly
46 induced by β -lactams such as cefoxitin and imipenem with expression mediated by the regulator
47 AmpR. Mutations in the repressor gene *ampD* may lead to overproduction of AmpC beta-
48 lactamases (15). The regulation of chromosomal *ampC* expression in *E. coli* differs considerably
49 from that in other *Enterobacteriaceae*. *E. coli* lacks *ampR* and thus *ampC* expression is not
50 inducible (14). In *E. coli*, *ampC* is constitutively expressed at a low level (16). Various mutations
51 in the *ampC* promoter/attenuator region of *E. coli* have been identified that result in
52 constitutive overexpression (7, 8, 18, 22, 24, 34, 39, 40). In addition to chromosomal *ampC*, *E.*
53 *coli* may carry plasmids encoding *ampC* (pAmpC), transferred via horizontal gene transfer and
54 derived from the chromosomal *ampC*'s of other *Enterobacteriaceae* spp. (15). Plasmid based
55 *ampC* genes are in most of the cases constitutively expressed. However, some plasmid-encoded
56 *ampCs*, such as DHA-1, are inducible by β -lactams, with expression similarly regulated as inducible
57 chromosomal *ampCs*. All plasmid-encoded *ampC* s are considered to be of significant clinical

58 relevance (23, 27). AmpC overproduction in addition to porin mutations of the outer membrane
59 can reduce susceptibility to carbapenems, in particular in plasmid-mediated AmpC producers
60 (19, 26).

61 AmpC producers may appear susceptible to third generation cephalosporins when initially
62 tested (27, 38, 40) and standardized procedures for the detection and identification of AmpC
63 beta-lactamase producing strains have not been established thus far. However, proper
64 recognition of AmpC overproducing *E. coli* strains is important for clinical management, as
65 administration of beta-lactam antibiotics frequently results in therapeutic failure. For example,
66 a recent study described the isolation of AmpC overproducing *E. coli* strains from patients who
67 did not respond to oxyimino-cephalosporin therapy (34). Another study analyzed the clinical
68 outcome of patients with bloodstream infection caused by plasmid-mediated AmpC producing
69 *Klebsiella pneumoniae* and show high rates of treatment failure when cephalosporins were
70 administered (27).

71 Different phenotypic AmpC confirmation tests have been reported in literature (15). A recently
72 described disk diffusion test is based on the comparison of the zone diameters around a
73 ceftioxin disk with a ceftioxin disk supplemented with the inhibitor cloxacillin. The test was
74 shown to have a sensitivity and a specificity of 95 % for the detection of plasmidic AmpC when
75 investigating 127 strains of *E. coli*, *Klebsiella* spp. and *Proteus* spp. (36). Another AmpC
76 confirmation test is based on antagonism phenomena using a ceftioxin susceptible indicator
77 strain. This test was evaluated for the detection of plasmid AmpC production in species lacking
78 chromosomal *ampC* (4). Reportedly, the test had a sensitivity of 100% and specificity of 98%
79 when testing 140 isolates of *Klebsiella* spp., *Proteus mirabilis* and *Salmonella* sp. (4). In this

80 study we aimed to evaluate and compare the diagnostic performance of the two disk diffusion
81 tests and a commercially available assay (Etest AB bioMérieux, Sweden) as a confirmation test
82 for the detection of AmpC activity in clinical *E. coli* isolates with a suspicion of AmpC production.
83 Molecular analyses were used to assess the specificity of the phenotypic assays and to
84 characterize the genetic basis for AmpC (over)production in these strains.

85 **Methods**

86 **Clinical isolates.**

87 51 *E. coli* clinical strains with reduced susceptibility to amoxicillin/clavulanic acid,
88 piperacillin/tazobactam or oxyimino-cephalosporins (ceftazidime, cefotaxime or ceftriaxone)
89 were collected at the Institute of Medical Microbiology, Zurich over a period of two years from
90 July 2006 until July 2008. The strains were isolated from urine (n=12), blood culture (n=12),
91 respiratory specimens (n=8), perianal swabs (n=4), wound swabs (n=4), inguinal swabs (n=3),
92 abscesses (n=2), tissue (n=2), vaginal swab (n=1), gastric aspirate (n=1), cerebrospinal fluid (CSF)
93 (n=1) and unknown origin (n=1).

94 **Antibiotic susceptibility testing.**

95 Antibiotic susceptibility testing was performed using susceptibility test disks (Becton Dickinson,
96 Germany), interpretation was done according to CLSI guidelines 2009 and 2010 (9, 10). For
97 cefotetan susceptibility testing the AmpC Etest strip (AB bioMérieux, Sweden) was used, as
98 described below. Susceptibility testing was performed on Müller-Hinton agar (bioMérieux,
99 France) using McFarland 0.5 from overnight cultures followed by incubation at 35° C for 16-18 h.

100 **Phenotypic AmpC and ESBL activity testings**

101 The AmpC ETest (AB bioMérieux, Sweden) for cefotetan susceptibility was performed according
102 the manufacturer's instructions. The AmpC ETest consists of a strip, containing cefotetan on one
103 end and cefotetan/cloxacillin on the other end. Ratios of the MICs of cefotetan and
104 cefotetan/cloxacillin which are ≥ 8 are considered positive for AmpC beta-lactamase production.
105 The ceftioxin/cloxacillin disk diffusion test was performed as described by Tan et al (36). The
106 test is based on the inhibitory effect of cloxacillin on AmpC. In brief, 30 μg ceftioxin disks

107 (Becton Dickinson, Germany) were supplemented with 200 µg cloxacillin. The test strain was
108 inoculated on Müller-Hinton agar. The diameters of the ceftazidime inhibition zones with and
109 without cloxacillin were compared; if the difference in inhibition was ≥ 4 mm for the
110 ceftazidime/cloxacillin disk the strain was considered positive for AmpC production.

111 The ceftazidime /EDTA disk test was performed as described by Black et al (4). In brief, a lawn of
112 the ceftazidime susceptible *E. coli* strain ATCC 25922 was inoculated on a Müller-Hinton agar plate.
113 A 30 µg ceftazidime disk (Becton Dickinson, Germany) was placed on the bacterial lawn and flanked
114 by two disks (A and B) containing each 20 µl of a 1:1 mixture of saline and 100X Tris-EDTA
115 solution. Colonies of the test strain were applied to disk A, colonies of the ceftazidime susceptible
116 *E. coli* strain ATCC 25922 (as negative control) were applied to disk B. Flattening or indentation
117 of the growth inhibition zone of the ceftazidime disk at the side of disk A containing the test strain
118 indicated the release of AmpC beta-lactamase.

119 To analyze induction of the DHA plasmid-encoded AmpC, a disk approximation assay using
120 imipenem as an inducer and ceftazidime, ceftazidime, ceftriaxone and piperacillin/tazobactam as
121 substrate antibiotics was used (12).

122 For phenotypic detection of ESBL activity and according to CLSI guidelines, the DDS test using
123 ceftazidime, and cefotaxime (30 µg) disks with and without clavulanic acid (10 µg) (Liofilchem,
124 Roseto degli Abruzzi, Italy). were used The bacterial test strains were inoculated on Muller-
125 Hinton agar using McFarland 0.5 followed by incubation at 35° C for 16-18 h. Diameters of
126 inhibition zones were measured with a standard caliper. A difference in the inhibition zone of \geq
127 5 mm for at least one third generation cephalosporin/clavulanic acid combination versus the

128 corresponding third generation cephalosporin alone was considered indicative for ESBL
129 production.

130 **Beta-lactamase hydrolysis assays**

131 For phenotypic detection of beta-lactamase activity the chromogenic nitrocefin (Calbiochem,
132 San Diego, USA) was used (35). 3-aminophenylboronic acid (Sigma-Aldrich Chemie, GmbH, Zug,
133 Switzerland) was used as specific AmpC inhibitor (2) and clavulanic acid (Sigma-Aldrich Chemie,
134 GmbH, Zug, Switzerland) was used as inhibitor of Ambler class A β -lactamases (e.g. ESBL, TEM-1)
135 (5). A bacterial suspension McFarland standard 0.5 in 0.45% NaCl was prepared from overnight
136 cultures. *E. coli* strain DH5 α was used as negative control strain. Reaction mixtures consisted of
137 50 μ l bacterial cell suspension, 25 μ l nitrocefin (0.5 mg/ml 10 mM phosphate buffer pH 6.8), 25
138 μ l 3-aminophenylboronic acid (3.6 mg/ml 10 mM phosphate buffer pH 6.8) and/or 25 μ l
139 potassium clavulanate (2.2 mg/ml 10 mM phosphate buffer pH 6.8). In case 3-
140 aminophenylboronic acid and/or clavulanic acid were not added, the end volume of 125 μ l was
141 reached by adding 10 mM phosphate buffer pH 6.8. Reaction mixtures were incubated in micro
142 titerplates at 37 °C. The nitrocefin hydrolysis product was detected by quantifying the absorption
143 after 8 hours at OD_{492nm} using a titerplate photospectrometer (Biochrom Asys Expert Plus
144 Microplate Reader, Biochrom Ltd, Cambridge, UK)

145

146 ***ampC* promoter/attenuator sequencing.** DNA was extracted from colonies grown on agar
147 medium using the InstaGene Matrix (Bio-Rad, Switzerland) following the manufacturer's
148 instructions. For the *ampC* promoter/attenuator mutation analysis a 271-bp fragment was
149 amplified using primers AB1(5'-GATCGTTCTGCCGCTGTG-3') and ampC2 (5'-

150 GGGCAGCAAATGTGGAGCAA-3') (11). PCR amplicons were purified with the QIAquick PCR
151 purification kit (Qiagen, Switzerland) followed by cycle sequencing using the BigDye reagent kit
152 (Applied Biosystems, Switzerland). Sequence analysis was performed on an ABI Prisma 3100
153 DNA sequencer (Applied Biosystems, Switzerland) following standard protocols. Sequences
154 were analyzed and edited using Lasergene 7 MegAlign software (DNASTAR Inc., USA). The *ampC*
155 promoter/attenuator sequences were compared to the *ampC* wild-type sequence of *E.coli* strain
156 ATCC 25922.

157 **Molecular detection of plasmid-encoded *ampC* beta-lactamase genes.**

158 A multiplex PCR was used for the detection of plasmid-encoded *ampC* beta-lactamase genes
159 (29). This assay is able to detect the six plasmid-encoded *ampC* genes families. Resulting PCR
160 amplicons were sequenced with the amplification primers following the protocol described
161 above. The sequences were compared to reference sequences in the NCBI Genbank (National
162 Center for Biotechnology Information (GenBank),<http://www.ncbi.nlm.nih.gov/>).

163 **Detection of ESBL and *Klebsiella* carbapenamase (KPC) genes**

164 For detection of TEM and SHV beta lactamase genes a multiplex PCR was performed as
165 described previously (21). Sequences were analyzed and edited using Lasergene 7 MegAlign
166 software (DNASTAR Inc., USA). The TEM beta-lactamases sequences were compared to wt *E. coli*
167 AF427133.1 TEM-1 using the publicly available database at <http://www.lahey.org/studies>. For
168 the detection of CTX-M beta-lactamase genes a multiplex PCR was performed as described by
169 Pitout *et al.*, 2004. For detection of a *Klebsiella* carbapenamase (KPC) gene a PCR was used as
170 described previously (33).

171

172 **Interpretation.**

173 *E. coli* strains positive for AmpC activity in at least one phenotypic test (AmpC ETest, AmpC
174 ceftioxin/EDTA disk test, AmpC ceftioxin/cloxacillin disk test) validated by genetic analysis
175 (presence of plasmid-encoded *ampC* genes, *ampC* promoter/attenuator mutations associated
176 with chromosomal *ampC* overexpression) were considered to be true AmpC producers. Strains
177 with discrepant test results were analyzed in further detail for β -lactamase production using
178 nitrocefin hydrolysis assays, phenotypic ESBL assays, molecular assays for ESBL and KPC
179 detection and sequence analysis of detected TEM and SHV genes.

180

181 **Results**

182 **Phenotypic screening for AmpC production.**

183 For 18/51 (35 %) of the *E. coli* isolates all three phenotypic tests gave a positive result for AmpC
184 production (Table 1). The ratios of the AmpC ETest ranged from 8 to 64. In the AmpC
185 ceftioxin/cloxacillin disk test the differences in zone diameters ranged from 4 mm to 14 mm
186 (Table 1). For 28/51 (55 %) of the *E. coli* strains negative results were obtained in all three
187 phenotypic assays (Table 2). In these strains the ratio of the AmpC ETest ranged from 1 to 4 and
188 the differences in zone diameters of the ceftioxin/cloxacillin disk test measured were 0 mm
189 (n=22), 1 mm (n=4), 2 mm (n=1) and 3 mm (n=1) (Table 2). Molecular testing confirmed the
190 results of the concordant phenotypic testing (18/18 positives and 28/28 negatives).

191 Discrepant test results were obtained for 5/51 (10 %) of the isolates, i.e. strains 19, 20, 21, 22
192 and 23. The analysis of the discrepant test results and their resolution is given in detail below.

193 Strain no. 19 was positive in the AmpC ETest (ratio=32), negative in the AmpC
194 ceftioxin/cloxacillin disk diffusion test (difference in zone diameter 0 mm) and positive in the
195 AmpC ceftioxin /EDTA disk diffusion test. In this strain, the *ampC* promoter/attenuator
196 sequence showed mutations associated with upregulation of the chromosomal *ampC* gene
197 expression (sequence variant 3; Table 3). Strain no. 20 was negative in the AmpC ETest (ratio=1)
198 and positive in both AmpC disk diffusion tests, the difference in zone diameter for the AmpC
199 ceftioxin/cloxacillin disk diffusion test was 6 mm. Genetic analysis showed promoter/attenuator
200 mutations associated with chromosomal *ampC* overexpression (variant 4; Table 3) (7, 16, 40).

201 Strain no. 21 was negative in the AmpC ETest (ratio=1.5), negative in the AmpC ceftioxin /EDTA
202 disk diffusion test, but positive in the AmpC ceftioxin/cloxacillin disk diffusion test (diameter

203 difference 4 mm). The *ampC* promoter and attenuator region of strain no. 21 resembles that of
204 the wildtype *E. coli* K12 strain. The multiplex PCR for plasmid-mediated *ampC* genes was
205 positive for DHA. Induction of the DHA gene in strain no. 21 was revealed by a disk
206 approximation assay (12) using imipenem as inducer and ceftazidime, cefoxitin, ceftriaxone and
207 piperacillin/tazobactam as substrate antibiotics. Nitrocefin hydrolysis assays showed that β -
208 lactamase activity of strains no. 19, 20 and 21 was inhibited by the AmpC inhibitor 3-
209 aminophenylboronic acid (Table 4). Phenotypic assays for ESBL detection (DDS assay) revealed
210 that strains no. 19 and 20 were ESBL negative and strain 21 was ESBL positive, which was
211 confirmed by the identification of a CTXM-1 gene in strain 21. A non-ESBL TEM-1 β -lactamase
212 was detected in strain no. 19 and 21. A corresponding inhibitory effect of the TEM-1 inhibitor
213 clavulanic acid on hydrolysis of nitrocefin was detected in strains no. 19 and 21, whereas strain
214 20 did not show such an inhibitory effect. A KPC PCR was negative for strains no. 19, 20 and 21.
215 (for a summary of the results see Table 4). Based on our interpretation criteria and the
216 additional β -lactamase analyses strains no. 19, 20 and 21 were considered true AmpC producers
217 (Table 1).

218 Two strains (no. 22 and 23) were positive in the AmpC cefoxitin /EDTA disk diffusion test and
219 negative in AmpC cefoxitin/cloxacillin disk diffusion test and the AmpC ETest. Both strains were
220 negative for plasmid-encoded *ampC* genes and genetic analysis of the *ampC*
221 promoter/attenuator region did not reveal mutations typically associated with chromosomal
222 *ampC* up regulation. Additional β -lactamase analysis for strains no. 22 and 23 showed that
223 nitrocefin hydrolysis was not inhibited by the AmpC inhibitor 3-aminophenylboronic acid (Table
224 4). Phenotypic ESBL testing (DDS assay) revealed that strains no. 22 was ESBL positive and no. 23

225 was ESBL negative, which was confirmed by the identification of a CTXM-1 gene in strain 22. A
226 TEM-1 β -lactamase was detected in strain no. 23. A corresponding inhibitory effect of clavulanic
227 acid on hydrolysis of nitrocefin was detected in both strains. KPC PCR was negative for strains
228 no. 22 and 23 (see Table 4). Based on our interpretation criteria and the additional β -lactamase
229 analyses, strains no. 22 and 23 were considered AmpC negative (Table 2).

230 In total, 21/51 (41 %) of the *E. coli* strains investigated in this study were considered AmpC
231 producers and 30/51 (59 %) were negative for AmpC production (Table 1 and Table 2). The
232 AmpC ETest detected 19/21 (90.5 %) correctly positive and showed no false positive results. The
233 AmpC ceftoxitin/cloxacillin disk test was correctly positive in 20/21 (95.2%) AmpC positive strains
234 and did not result in false positive results. The AmpC ceftoxitin /EDTA disk test was correctly
235 positive in 20/21 (95.2%) strains and gave two false positive results.

236 ***ampC* promoter/attenuator mutations and plasmid-encoded *ampC* beta-lactamases.**

237 In the 51 *E. coli* strains 15 different *ampC* promoter/attenuator sequence variants were
238 detected (Figure 1). For the 21 AmpC positive strains 10 different promoter/attenuator
239 sequence variants 1, 2, 3, 4, 5, 6, 11, 12, 14 and 15 were found (Table 3). Promoter/attenuator
240 sequence variants 1, 2, 3, 5, 6 were found in 11 strains with a positive AmpC production
241 phenotype and negative for plasmid-encoded *ampC*. Sequence variant 5 comprises two AmpC
242 positive strains, one positive for plasmid-encoded *ampC* genes and one negative strain for
243 plasmid-encoded *ampC*. Mutations detected in sequence variants 1, 2, 3, 4, 5 and 6 included (i)
244 mutations that created an alternate displaced promoter (variants 1 and 2), (ii) mutations in the
245 wildtype promoter/attenuator (variants 3 and 4) and (iii) mutations that increased the spacer
246 length between the -35 and -10 box (variants 5 and 6) by insertion of 1 or 2 basepairs. The

247 mutations found in these sequence variants are associated with an increase of *ampC* expression
248 (11). Sequence variants 11, 12, 14, and 15 were found in phenotypic AmpC positive strains,
249 which were all positive for the presence of plasmid-encoded *ampC* genes. Mutations in these
250 sequence variants were located in the attenuator region, the coding region of AmpC or resulted
251 in an alternate displaced -10 box. None of these changes has been reported to be associated
252 with significant chromosomal AmpC overproduction (see below). Variant no. 14 resembles the
253 wildtype *E. coli* K12 *ampC* promoter/attenuator (Table 3). In total, 13/21 AmpC positive strains
254 harbored changes in the promoter/attenuator region typically associated with chromosomal
255 AmpC overproduction (32).

256 Plasmid-encoded *ampC* genes were detected in 9 of the 21 strains. In 1 strain both
257 chromosomal and plasmid-mediated mechanisms responsible for AmpC production were
258 found., e.g. a two bp insertion in the spacer of the *ampC* chromosomal promoter/attenuator
259 region and a plasmid encoded *ampC* gene (Table 3). The plasmid-encoded *ampC* genes found in
260 the isolates belonged to the CIT family (n=8) and the DHA family (n=1). Sequences of the PCR
261 product showed 100% homology to the *bla*_{CMY-2} gene for the CIT family isolates and 100%
262 homology to the *bla*_{DHA-1} gene for the DHA family isolate (data not shown).

263

264 **Susceptibility to amoxicillin/clavulanic acid, piperacillin/tazobactam, cefoxitin and third-**
265 **generation cephalosporins.**

266 All 21 AmpC positive strains showed reduced susceptibility to amoxicillin/clavulanic acid. 20 of
267 21 strains were tested resistant, one strain was intermediate. In contrast, only 1/21 strains was

268 resistant to piperacillin/tazobactam, 6/21 isolates showed an intermediate level and 14/21
269 strains were tested susceptible.

270 For third-generation cephalosporins the following test results were obtained for the 21 AmpC
271 positive strains applying the 2009 CLSI guideline (9) zone diameter breakpoints: ceftazidime (11
272 strains susceptible, 3 strains intermediate and 7 strains resistant), cefotaxime (9 strains
273 susceptible, 7 strains intermediate and 5 strains resistant) and ceftriaxone (12 strains
274 susceptible, 4 strains intermediate and 5 strains resistant). All AmpC positive strains were
275 susceptible to cefepime (Table 1). Resistance patterns for AmpC negative strains are
276 summarized in Table 2. In 2010 the CLSI zone diameter breakpoints for ceftazidime, cefotaxime
277 and ceftriaxone were elevated (10). Applying these breakpoints resulted in the following
278 interpretation of susceptibility testing for AmpC positive strains: ceftazidime (susceptible 5
279 strains, intermediate 6 strains and resistant 10 strains), cefotaxime (susceptible 2 strains,
280 intermediate 7 strains and resistant 12 strains) and ceftriaxone (susceptible 9 strains,
281 intermediate 3 strains and resistant 9 strains) (supplemental material Table 1A). Results for the
282 AmpC negative strains are summarized in supplemental material Table 1B.

283 By disk diffusion susceptibility testing and according to CLSI guidelines 2009, 17/21 AmpC
284 producing strains (81 %) were resistant to cefoxitin, 3/21 strains were intermediate and 1/21
285 strain was susceptible (inhibition zone diameter 18 mm) (Table 1). 28/30 AmpC negative strains
286 (93 %) were susceptible to cefoxitin, for 1/30 strains an intermediate result was obtained and
287 1/30 strains was resistant (Table 2).

288 **Discussion**

289 Detection of AmpC beta-lactamases in *E. coli* poses a challenge to microbiological laboratories.
290 For practical reasons it is not feasible to routinely test all *E. coli* isolates for AmpC production in
291 detail. In our study we selected 51 *E. coli* clinical isolates collected during a two-year period for
292 putative AmpC production based on reduced susceptibility to amoxicillin/clavulanic acid,
293 piperacillin/tazobactam or oxyimino-cephalosporins (ceftriaxone, ceftazidime, cefotaxime).
294 Several AmpC confirmation tests have recently been evaluated (4, 36) or became commercially
295 available (AmpC Etest, AB bioMérieux). In this study we compared the performance of three of
296 these tests for accurate identification of AmpC producing *E. coli* strains, i.e. AmpC ETest (AB
297 bioMérieux, Sweden), AmpC ceftioxin /cloxacillin disk test (36), and AmpC ceftioxin /EDTA disk
298 test (4). AmpC producing *E. coli* strains were validated by genetic analyses. In addition, strains
299 with discrepant AmpC screening results were further analyzed for β -lactamase production by
300 nitrocefin hydrolysis assays, ESBL phenotypic testing, genetic testing for the presence of SHV,
301 TEM, CTX-M β -lactamases and KPC (Table 4). The additional test results confirmed the accuracy
302 of our interpretation criteria for AmpC production. In total, 21 of the selected 51 *E. coli* isolates
303 were identified as true AmpC producing strains (plasmidic *ampC* n=8, overexpression of
304 chromosomal *ampC* n=12, combination of plasmidic *ampC* and overexpression of chromosomal
305 *ampC* n=1). We found that the ceftioxin /cloxacillin disk test detected 20/21 AmpC positive *E.*
306 *coli* strains (Table 1) and gave 1 false negative result. The ceftioxin /EDTA disk test (4) detected
307 20/21 AmpC positive strains and gave 1 false negative result and 2 false positive results. A
308 drawback of the ceftioxin /EDTA disk assay is that carbapenemases may give rise to false
309 positive results as carbapenemases are able to inactivate ceftioxin (4), although KPC was not

310 detected in the 2 false positive strains. The AmpC Etest strip uses cefotetan for AmpC screening.
311 While cefotetan resistance ($R > 64$ mg/l) was not consistently present in the AmpC positive
312 strains (Table 1), the AmpC Etest was able to detect 19/21 strains correctly positive, 2 strains
313 gave a false negative test result.

314 The *ampC* promoter/attenuator mutations detected in the 51 *E. coli* isolates (Table 3) included
315 6 previously described variants associated with *ampC* overexpression (references 7, 16, 17, 24,
316 34, 40). Overall, 13/21 (61.9%) positive AmpC strains were associated with chromosomal *ampC*
317 promoter mutations resulting in hyperproduction of AmpC and 9/21 strains (42.9%) were AmpC
318 positive due to the presence of plasmid-encoded *ampC* genes. One strain had a two basepair
319 insertion in the *ampC* promoter spacer region (variant 5) and a plasmid-encoded *ampC* gene;
320 both mechanisms may have contributed to AmpC activity in this strain. The observed ratio of
321 AmpC production due to chromosomal *ampC* upregulation versus plasmid-mediated AmpC is in
322 accordance with the distribution observed in studies conducted in France, Spain and Norway (6,
323 13, 20). We did not detect any strain that was positive in the genetic analysis and negative in all
324 three phenotypic confirmation tests.

325 As the cefoxitin and cefotetan based AmpC disk assays effectively identify AmpC producers we
326 decided to evaluate whether cefoxitin and cefotetan susceptibility testing can be used as a
327 screening test for AmpC production. In the group of AmpC positive strains 20 of 21 (95%)
328 isolates were resistant or intermediate in the cefoxitin disk test. One strain showed an inhibition
329 zone of 18 mm which is just within the susceptible range (Table 1). For the AmpC negative
330 strains 26 of 30 (87%) strains were susceptible to cefoxitin with inhibition zones > 18 mm. Two
331 strains scored within the susceptible range with inhibition zones of 18 mm, one strain was

332 intermediate and one strain was resistant to ceftazidime (Table 2). Applying a screening criterium
333 of ceftazidime inhibition zone ≤ 18 mm, all AmpC positive strains would have been detected plus
334 an additional 4 false positives. However, the use of ceftazidime as screening marker is
335 compromised by isolates producing plasmid-encoded AmpC beta-lactamases of the ACC family.
336 ACC-1 itself is inhibited by ceftazidime and thus may appear ceftazidime susceptible (1, 15, 32). ACC-1
337 has first been isolated in Germany and in several other European countries. (1, 25, 31, 32).
338 Recently, AmpC betalactamase ACC-4 was identified in *E. coli*, conferring increased MICs for
339 oxyimino-cephalosporins with low MICs for ceftazidime and ceftazidime (28). In our study, strains
340 with a plasmid ACC beta-lactamases gene were not detected.

341 Analyzing ceftazidime MICs in the AmpC ETest revealed that 2 of the 21 (10%) AmpC positive
342 strains were resistant to ceftazidime. 10 of 21 (48%) of the AmpC positive strains were susceptible
343 to ceftazidime and intermediate results were obtained for 9 (42%) isolates (Table 1). On the basis
344 of these results we can not recommend ceftazidime susceptibility for initial AmpC screening.

345 We also evaluated whether reduced sensitivity to third generation cephalosporins can be used
346 as screening parameter for AmpC testing. Several studies showed that cephalosporine
347 susceptibility screening of *E. coli* isolates with the initial purpose of ESBL identification resulted
348 in selection for AmpC producing strains (3, 23). Nine of the 21 (43%) AmpC positive strains were
349 susceptible to ceftazidime, ceftazidime and ceftazidime in *vitro* according to the CLSI 2009
350 guidelines. Another two strains were susceptible to ceftazidime and ceftazidime and one strain
351 was susceptible to ceftazidime only (Table 1). Applying the elevated CLSI 2010 zone diameter
352 breakpoints two strains were susceptible to ceftazidime, ceftazidime and ceftazidime; another
353 two strains were susceptible to ceftazidime and ceftazidime, one strain was susceptible to

354 ceftazidime only and five strains were susceptible to ceftriaxone only (supplemental material
355 Table 1A). On the basis of our results we cannot recommend third generation cephalosporins as
356 screening parameters for AmpC .

357 In summary, we demonstrate that after a first screening procedure each of the three
358 phenotypic AmpC tests used in this study was capable to confirm the majority of AmpC beta-
359 lactamase producing *E. coli* strains (>90 %) including plasmid-mediated AmpC beta-lactamases
360 and chromosomal AmpC hyperproduction strains. Each of the three tests is an acceptable
361 phenotypic confirmation tool when AmpC production is suspected in *E. coli*.

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strain no.	AmpC ETest		AmpC disk test cefotetan/cefotaxim/ceftriaxone		AmpC disk test cefotaxim/EDTA		ampC plasmid PCR ^c (class)	ampC chrom ^d (promoter variant)	final AmpC assignment ^e	Antibiotic resistance disk testing (mm) ^f						
	cefotetan MIC (µg/ml)	Ratio ^a	AmpC	difference (mm) ^b	AmpC	AmpC				CAZ	CTX	GRO	FEP	AMC	TZP	FOX
1	S (12)	24	positive	8	positive	positive	negative	positive (1)	positive	S (18)	S (23)	S (23)	S (29)	R (7)	S (21)	R (7)
2	S (4)	8	positive	8	positive	positive	negative	positive (1)	positive	S (21)	I (22)	S (21)	S (27)	R (10)	S (23)	R (12)
3	I (32)	43	positive	8	positive	positive	negative	positive (1)	positive	R (12)	I (19)	S (21)	S (28)	R (7)	I (20)	R (7)
4	I (32)	64	positive	11	positive	positive	negative	positive (1)	positive	S (21)	S (24)	S (26)	S (30)	R (7)	I (20)	R (13)
5	I (32)	21	positive	5	positive	positive	negative	positive (1)	positive	S (20)	I (19)	S (21)	S (26)	I (16)	S (22)	R (7)
6	S (12)	24	positive	5	positive	positive	negative	positive (1)	positive	S (18)	S (25)	S (26)	S (28)	R (7)	I (18)	I (15)
7	S (4)	8	positive	8	positive	positive	negative	positive (3)	positive	S (28)	S (27)	S (28)	S (32)	R (11)	S (26)	I (17)
8	S (24)	48	positive	5	positive	positive	negative	positive (2)	positive	S (19)	S (23)	S (23)	S (30)	R (7)	I (19)	S (18)
9	S (16)	32	positive	10	positive	positive	negative	positive (5)	positive	S (20)	S (23)	S (25)	S (32)	R (10)	S (23)	R (13)
10	S (12)	24	positive	6	positive	positive	negative	positive (6)	positive	S (19)	S (25)	S (28)	S (29)	R (12)	S (21)	R (14)
11	R (>32)	8	positive	5	positive	positive	positive (CIT ^b)	negative (12)	positive	R (7)	R (7)	R (7)	S (24)	R (7)	I (18)	R (7)
12	R (>32)	8	positive	4	positive	positive	positive (CIT)	negative (12)	positive	R (7)	R (7)	R (7)	S (20)	R (7)	R (14)	R (7)
13	I (32)	8	positive	9	positive	positive	positive (CIT)	negative (12)	positive	R (7)	R (10)	R (7)	S (25)	R (7)	I (20)	R (7)
14	I (32)	64	positive	13	positive	positive	positive (CIT)	negative (15)	positive	I (15)	I (15)	I (16)	S (29)	R (7)	S (21)	R (7)
15	I (32)	64	positive	14	positive	positive	positive (CIT)	negative (15)	positive	I (16)	I (17)	I (16)	S (25)	R (10)	S (25)	R (7)
16	I (32)	64	positive	10	positive	positive	positive (CIT)	negative (11)	positive	R (7)	R (14)	R (12)	S (28)	R (10)	S (21)	R (7)
17	S (8)	16	positive	10	positive	positive	positive (CIT)	negative (11)	positive	I (17)	I (20)	I (18)	S (26)	R (11)	S (24)	R (9)
18	I (32)	43	positive	10	positive	positive	positive (CIT)	positive (5)	positive	R (7)	I (18)	I (15)	S (28)	R (7)	S (22)	R (7)
19	I (32)	32	positive	0	negative	positive	negative	positive (3)	positive	S (23)	S (25)	S (26)	S (31)	R (10)	S (24)	R (14)
20	S (0.5)	1	negative	6	positive	positive	negative	positive (4)	positive	S (26)	S (28)	S (37)	S (28)	R (12)	S (25)	I (17)
21	S (0.75)	2	negative	4	positive	negative	positive (DHA ^b)	negative (14)	positive	R (11)	R (13)	R (7)	S (18)	R (9)	S (23)	R (7)

535

536 **Table 1.** Characterization of 21 *E. coli* strains positive for AmpC activity.

537 Strains were analyzed for AmpC production using three phenotypic confirmation AmpC assays. Genetic analysis for AmpC
538 production was done by multiplex PCR for plasmid *ampC* detection and sequence analysis of the chromosomal *ampC*
539 promoter/attenuator region. In addition, for each strain antimicrobial susceptibility data were generated. Strains with
540 discrepant results in the three phenotypic confirmation AmpC assays are assays are highlighted in grey.

- 541 Abbreviations: S, susceptible; R, resistant; I, intermediate; AMC, amoxicillin-clavulanic acid; CAZ, ceftazidime; CRO,
542 ceftriaxone; CTT, cefotetan; CTX, cefotaxime; FEP, cefepime; FOX, cefoxitin; TZP, piperacillin-tazobactam;
- 543 a. Ratio of MIC cefotetan to cefotetan/cloxacillin is determined in the AmpC ETest (ratios ≥ 8 are considered AmpC positive).
544 b. Difference between diameters in the cefoxitin inhibition zones with and without cloxacillin were determined (increase ≥ 4
545 mm for the cefoxitin/cloxacillin disk is considered AmpC positive).
546 c. Plasmid-mediated *ampC* was detected by multiplex PCR (29).
547 d. For *ampC* promoter /attenuator sequence variants see Figure 1.
548 e. A final assignment for AmpC activity combining phenotypic and genetic results was made according to the definition
549 specified in the 'Materials and Methods'. A strain was scored positive when at least one phenotypic test was positive, which
550 was validated by genetic analysis (plasmid-encoded *ampC*, *ampC* promoter mutations associated with *ampC*
551 overexpression).
552 f. Diameter of growth inhibition zone in mm. The zone diameter breakpoints of the 2009 CLSI guidelines were applied (9).
553 g. CIT: plasmid-encoded *ampC* originating from *Citrobacter freundii*.
554 h. DHA: plasmid-encoded *ampC* originating from *Morganella morganii*.

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strain no.	AmpC ETest		AmpC disk test cefotetan/cefotaxime		AmpC disk test cefotaxime/EDTA	plasmid ampC PCR ^c	AmpC chrom ^d	final AmpC assignment ^e	Antibiotic resistance disk testing (mm) ^f						
	cefotetan MIC (µg/ml)	Ratio ^a	AmpC	difference ^b (mm)	AmpC	AmpC	Promoter variant		CAZ	CTX	CRO	FEP	AMC	TZP	FOX
22	S (2)	1	negative	0	negative	positive	negative	negative (10)	negative	R (14)	R (7)	I (15)	R (13)	S (23)	I (16)
23	S (3)	2	negative	0	negative	positive	negative	negative (8)	negative	S (30)	S (26)	S (25)	S (29)	I (16)	S (22) R (12)
24	S (0.5)	1	negative	0	negative	negative	negative	negative (12)	negative	S (28)	S (25)	S (29)	S (28)	I (16)	S (22) S (25)
25	S (0.75)	1	negative	0	negative	negative	negative	negative (15)	negative	S (23)	S (28)	S (23)	S (24)	R (10)	R (9) S (24)
26	S (0.5)	1	negative	0	negative	negative	negative	negative (15)	negative	S (20)	S (28)	S (27)	S (28)	R (10)	I (18) S (20)
27	S (2)	1	negative	0	negative	negative	negative	negative (15)	negative	S (22)	S (29)	S (26)	S (27)	R (7)	R (7) S (20)
28	S (1)	1	negative	3	negative	negative	negative	negative (15)	negative	S (22)	S (25)	S (26)	S (25)	I (17)	S (23) S (27)
29	S (0.5)	1	negative	0	negative	negative	negative	negative (15)	negative	S (29)	S (28)	S (28)	S (33)	I (14)	S (21) S (24)
30	S (0.5)	1	negative	0	negative	negative	negative	negative (11)	negative	S (26)	S (28)	S (26)	S (26)	R (10)	I (18) S (23)
31	S (0.5)	1	negative	0	negative	negative	negative	negative (11)	negative	S (28)	S (25)	S (25)	S (24)	R (7)	R (14) S (25)
32	S (0.5)	1	negative	0	negative	negative	negative	negative (11)	negative	S (26)	S (32)	S (28)	S (30)	R (12)	R (14) S (30)
33	S (0.5)	1	negative	0	negative	negative	negative	negative (10)	negative	S (27)	S (23)	S (25)	S (26)	R (10)	R (15) S (21)
34	S (0.5)	1	negative	0	negative	negative	negative	negative (10)	negative	S (28)	S (25)	S (28)	S (28)	I (15)	S (23) S (21)
35	S (0.5)	1	negative	0	negative	negative	negative	negative (8)	negative	S (26)	R (7)	R (7)	S (23)	S (19)	R (7) S (24)
36	S (0.5)	1	negative	0	negative	negative	negative	negative (7)	negative	S (20)	R (7)	R (7)	I (17)	R (10)	R (14) S (23)
37	S (0.5)	1	negative	0	negative	negative	negative	negative (7)	negative	S (25)	I (19)	I (14)	S (25)	I (15)	I (20) S (24)
38	I (32)	1	negative	0	negative	negative	negative	negative (7)	negative	R (7)	R (7)	R (7)	R (7)	R (7)	R (7) S (18)
39	S (0.5)	1	negative	0	negative	negative	negative	negative (7)	negative	S (24)	I (19)	R (7)	S (25)	R (11)	I (18) S (23)
40	S (0.75)	1	negative	0	negative	negative	negative	negative (7)	negative	S (26)	I (20)	R (7)	S (26)	R (13)	S (22) S (25)
41	S (0.5)	1	negative	0	negative	negative	negative	negative (7)	negative	S (25)	R (7)	R (7)	R (13)	I (14)	R (7) S (28)
42	S (0.5)	1	negative	0	negative	negative	negative	negative (14)	negative	S (25)	S (25)	S (28)	S (25)	I (15)	S (23) S (22)
43	S (0.5)	1	negative	0	negative	negative	negative	negative (14)	negative	S (27)	S (28)	S (28)	S (26)	I (14)	S (23) S (25)
44	S (0.5)	1	negative	1	negative	negative	negative	negative (15)	negative	S (29)	S (33)	S (26)	S (31)	R (13)	S (22) S (28)
45	S (0.5)	1	negative	1	negative	negative	negative	negative (14)	negative	S (26)	S (28)	S (27)	S (28)	I (17)	S (21) S (21)
46	S (1.5)	1	negative	1	negative	negative	negative	negative (9)	negative	S (21)	S (27)	S (25)	S (25)	R (10)	R (10) S (19)
47	S (0.5)	1	negative	2	negative	negative	negative	negative (13)	negative	S (26)	I (15)	I (15)	S (22)	I (17)	S (25) S (30)
48	S (0.75)	2	negative	0	negative	negative	negative	negative (7)	negative	S (26)	I (18)	I (16)	S (24)	I (16)	I (18) S (25)
49	S (0.75)	2	negative	0	negative	negative	negative	negative (7)	negative	S (25)	I (20)	S (25)	I (15)	R (7)	R (10) S (24)
50	S (0.75)	2	negative	0	negative	negative	negative	negative (14)	negative	S (25)	S (28)	S (26)	S (25)	I (17)	I (20) S (18)
51	S (8)	4	negative	1	negative	negative	negative	negative (14)	negative	S (26)	S (27)	S (26)	S (25)	R (13)	I (18) S (21)

556 **Table 2.** Characterization of the 30 *E. coli* strains negative for AmpC activity. Interpretation of susceptibility results according

557 to the CLSI guideline 2009.

558 Strains were analyzed for AmpC production using three phenotypic AmpC assays. Genetic analysis for AmpC production
559 was done by multiplex PCR for plasmid *ampC* detection and sequence analysis of the chromosomal *ampC*
560 promoter/attenuator region. In addition, for each strain antimicrobial susceptibility data were generated. Strains with
561 discrepant results in the three phenotypic confirmation AmpC assays are highlighted in grey.

562 For abbreviations see legend Table 1.

563 Footnotes a. to f. see Table 1.

564

promoter sequence variant ^a	<i>E.coli</i> strain no.	number of strains (n=51)	number of AmpC positive strains (%)	number of strains carrying plasmid-mediated <i>ampC</i>	a) b) position(s) of mutations in <i>ampC</i> promoter/attenuator region	b) localization and function of mutations
1	1, 2, 3, 4, 5, 6	6	6 (100%)	-	-42, -18, (-1), (+58), +81	alternate displaced promoter (-35 box and -10 box) and mutations in the AmpC coding region
2	8	1	1 (100%)	-	-42, -18, -15, (-1), (+58), +81	alternate displaced promoter (-35 box and -10 box) and mutations in the AmpC coding region
3	7, 19	2	2 (100%)	-	-32, +81	promoter mutation and mutation in the AmpC coding region
4	20	1	1 (100%)	-	-32, -28, +17	promoter mutation, mutations in the spacer region and in the AmpC coding region
5	9, 18	2	2 (100%)	1	INS (-13.1), INS (-13.2)	Increased distance between -35 and -10 box
6	10, 16	1	1 (100%)	-	-14, INS (-13.1), +81	Increased distance between -35 and -10 box, promoter mutation and mutation in the <i>ampC</i> coding region
7	36, 37, 38, 39, 40, 41, 48	8	none	-	-28	mutation in the spacer region
8	23, 35	2	none	-	-28, (+58)	mutation in the spacer region
9	46	1	none	-	-28, +17	mutation in the spacer region and mutation in the attenuator
10	22, 33, 34	3	none	-	-28, +34, (+58)	mutation in the spacer, attenuator mutation and mutation in the coding region <i>ampC</i>
11	16, 17, 30, 31, 32	5	2 (40%)	2	-18, (-1), (+58), +81	alternate displaced promoter (-10 box only) and mutation in the coding region <i>ampC</i>
12	11, 12, 13, 24	4	3 (75%)	3	+22, +26, +27, +32, +70, +81	attenuator mutations and mutations in the coding region <i>ampC</i>
13	47	1	none	-	(+58), +63	mutation in the coding region <i>ampC</i>
14	21, 42, 43, 45, 50, 51, 14, 15, 25, 26, 27, 28, 29, 44	6	1 (17%)	1	+81	mutation in the coding region <i>ampC</i>
15		8	2 (25%)	2	+70, +81	mutations in the coding region <i>ampC</i>

565

566 **Table 3** Genetic characterization of the 51 *E.coli* isolates by *ampC* promoter region sequence analysis and multiplex PCR for
567 detection of plasmid-mediated *ampC*. All isolates with promoter sequence variants 1, 2, 3, 4, 5 and 6 are considered positive
568 for AmpC activity due to chromosomal overexpression of *ampC*. Promoter variants 11, 12, 14 and 15 are found in
569 phenotypically AmpC positive and AmpC negative strains; the AmpC positive strains all harboured plasmid-encoded AmpC.
570 Promoter sequence variants 7, 8, 10 and 13 were not associated with increased phenotypic AmpC activity.

- 571 a. Analysis of *ampC* promoter/attenuator mutations (for detailed sequence analysis see Figure 1).
- 572 b. Mutations and mechanisms resulting in overexpression leading to *ampC* upregulation are typed in bold and highlighted in
- 573 grey. Insertion of nucleotides is marked with INS. Mutations outside functional promoter elements are displayed in brackets
- 574 (4).

575 **Table 4.** Characterization of β -lactamase activity in *E. coli* strains (n=5) considered false positive or false negative in phenotypic
 576 screening for AmpC overproduction.

<i>E. coli</i> strain ^a	Nitrocefim hydrolysis (OD _{nm=492}) ^b							ESBL ^c		KPC ^d
	Without inhibitor	aminophenylboronic acid		clavulanic acid		boronic acid and clavulanic acid		phenotypic	genetic	
		Inhibition		Inhibition		Inhibition				
19	0.309 ± 0.006	0.106 ±0.008	+	0.080 ±0.010	+	0.041 ±0.004	+	-	(TEM-1)	-
20	0.151 ± 0.014	0.006 ±0.005	+	0.120 ±0.008	-	0.015 ±0.006	+	-	-	-
21	0.344 ± 0.020	0.225 ±0.002	+	0.083 ±0.0	+	0.051 ±0.006	+	+	(TEM-1)/ CTXM-1	-
22	0.777 ±0.007	0.847 ±0.015	-	0.332 ±0.006	+	0.395 ±0.009	+	+	CTXM-1	-
23	0.366 ±0.005	0.314 ±0.005	-	0.074 ±0.001	+	0.066 ±0.007	+	-	(TEM-1)	-

577 a. Strain numbers correspond to Tables 1 and 2.

578 b. Nitrocefim hydrolysis was tested in absence and presence of boronic acid (as specific AmpC inhibitor) and/or clavulanic acid (as
 579 specific ESBL and TEM-1 inhibitor). Presented values are the average of duplicate reactions.

- 580 c. ESBL were phenotypically detected by the DDS test as described in Material and Methods. PCR detection of TEM, SHV and CTX-
581 M genes were done as described previously (21, 30). **Note:** TEM-1 is **not** an ESBL β -lactamase, but is able to hydrolyse nitrocefin.
582 Therefore the detection of TEM-1 is shown in brackets
583 d. PCR detection of KPC genes was performed as described previously (33).

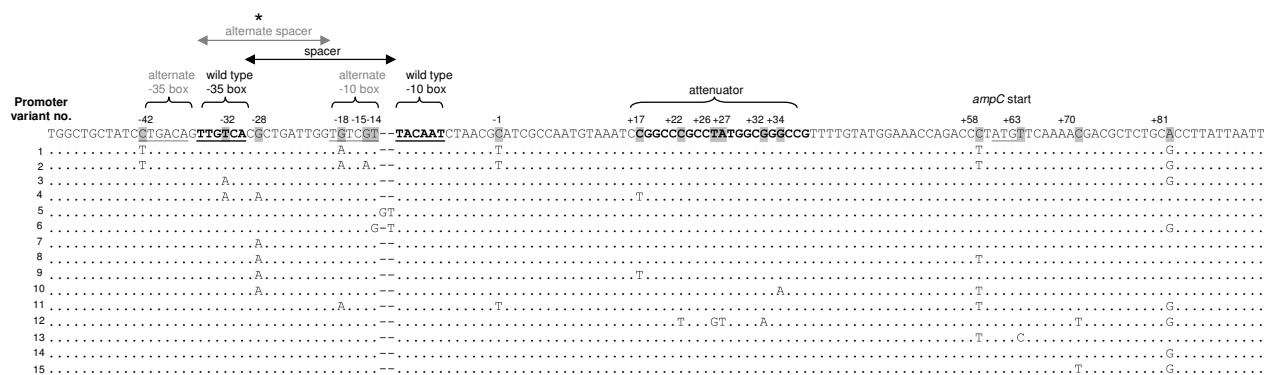


Figure 1 Alignment of the chromosomal *ampC* promoter, attenuator and 5'-end regions. For the 51 *E. coli* isolates, 15 different sequence variants were identified. * The chromosomal *ampC* sequence variant classification and description of functional elements was used according Tracz et al. (40).