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Phenotypic and Molecular Methods for the Detection of Antibiotic Resistance Mechanisms in Gram Negative Nosocomial Pathogens

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Additional information is available at the end of the chapter

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1. Introduction

Antibiotic resistance among clinical isolates of *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, *Escherichia coli*, *Enterobacter* spp and *Proteus* spp is causing worldwide concern [1-5] especially when mediated by transferable genetic elements.

The role of the Clinical Microbiology Department in this regard is crucial for the isolation of non-susceptible bacteria and the detection of the underlying mechanisms leading to their resistant phenotype. Rapid and reliable results are of the utmost importance in order to apply the appropriate treatment and to contain the spread of resistance determinants within hospital settings.

In the present chapter, laboratory procedures for the detection of antibiotic resistance mechanisms will be discussed focusing mainly on those more frequently used for Gram negative clinical isolates around the world.

2. Antibiotic resistance mechanisms among Gram negative nosocomial pathogens

Antibiotic resistance may be intrinsic (the microorganism is by definition resistant against a certain antibiotic) or acquired. Acquired refers to resistance that is a consequence of mutational events or gene acquisition via horizontal gene transfer.

Four general mechanisms leading to acquired antibiotic resistance have been described: (1) decreased entrance of the antibiotic into the bacterial cell; (2) increased extrusion of the antibiotic by bacterial efflux systems; (3) mutational modification of the antibiotic's target and; (4) production of antibiotic-inactivating enzymes. Characteristic examples for each mechanism are presented in Table 1.

Mechanism	Examples
Decreased permeability	Diminished expression or loss of the OprD porin in <i>Pseudomonas aeruginosa</i> and OmpK35, OmpK36 porins in <i>Klebsiella pneumoniae</i> [6-9]
Efflux	Overexpression of MexAB-OprM and MexXY-OprM in <i>Pseudomonas aeruginosa</i> and OqxAB in <i>Klebsiella pneumoniae</i> [10-13]
Target modification	Mutations of gyrases and topoisomerases leading to fluoroquinolone resistance [14-16]
Inactivating enzymes	Production of beta-lactamases and aminoglycoside modifying enzymes [17-19]

Table 1. Examples of antibiotic resistance mechanisms.

Among the aforementioned mechanisms, the production of beta-lactamases is considered of major importance because these enzymes are commonly transferable and inactivate multiple beta-lactam antibiotics. Within this large enzymatic family, carbapenemases (class B metallo-beta-lactamases (MBLs) [20] that contain zinc in their active center and class A KPC [21]) hydrolyze in vitro all or almost all beta-lactams, including carbapenems [22]. Class A extended spectrum beta-lactamases (ESBLs) hydrolyze penicillins, monobactams and cephalosporins whereas are inhibited by the beta-lactamase inhibitors [23,24]. Class C cephalosporinases (AmpC) present various spectrums of cephalosporin hydrolysis but are not inhibited by the beta-lactamase inhibitors [25]. Additionally, AmpC enzymes may be inducible in *Serratia* spp, *Pseudomonas* spp, Indole-positive *Proteus*, *Citrobacter* spp and *Enterobacter* spp (SPICE group of bacteria) complicating the treatment of infections caused by these pathogens. Finally, molecular class D beta-lactamases (OXA) comprise numerous enzymes with variable spectrums of beta-lactam hydrolysis [26].

3. Phenotypic tests

Phenotypic tests may be used in the everyday laboratory practice in order to identify the presence of acquired resistance mechanisms among frequently isolated nosocomial pathogens. In the present chapter, the procedure and the interpretation of seven useful phenotypic tests are described. Special attention has been given to the phenotypic detection of beta-lactamases and especially those hydrolyzing carbapenems together with other beta-lactams (carbapenemases).

3.1. Double Disc Synergy Test (DDST)

The DDST is used for the detection of beta-lactamases that are inhibited by beta-lactamase inhibitors such as clavulanic acid (Ambler class A beta-lactamases and especially ESBLs). For SPICE organisms, cloxacillin should be incorporated in Mueller-Hinton agar during its preparation in order to prevent any AmpC interference [27].

3.1.1. Procedure

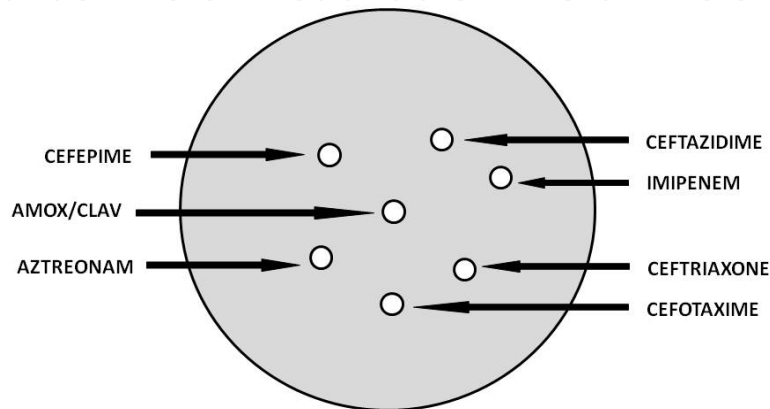


Figure 1. Double Disc Synergy Test preparation.

Step 1: Prepare agar plates containing 200µg/ml cloxacillin (by adding 1ml solution containing 80 mg cloxacillin in 399 ml Mueller-Hinton agar at the liquid phase). Omit this step when testing non-SPICE bacteria.

Step 2: Make a 0.5 McFarland bacterial suspension.

Step 3: Inoculate with a sterile cotton swab and place an amoxicillin/clavulanic acid disc at the center of the plate (20 µg amoxicillin+10 µg clavulanic acid).

Step 4: Place ceftazidime, imipenem, ceftriaxone, cefotaxime, aztreonam and cefepime discs around the central amoxicillin/clavulanic acid disc (Figure 1).

Step 5: Incubate at 37°C for 18-24h.

3.1.2. Interpretation

The DDST is considered positive when the inhibition zone of any of the antibiotics is larger towards the clavulanic acid disc (Figure 2-lower left plate) or a ghost inhibition zone appears between the central disc and any of the other antibiotics (Figure 2-lower right plate). This is happening because of the ESBL's inhibition by the clavulanic acid. In proximity to the central disc the enzyme's activity is blocked. Thus, the growth inhibition zone appears only towards the clavulanic acid disc. If resistance to cephalosporins is not due to ESBL production, the test results negative (Figure 2-upper plates).

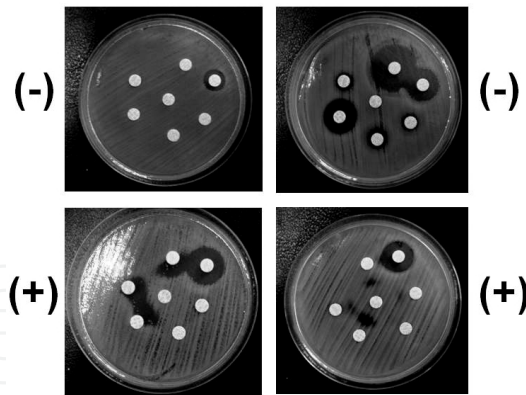


Figure 2. Interpretation of the DDST. (-): Negative; (+): Positive.

3.2. Imipenem-EDTA synergy test

EDTA (ethylene-diamine-tetraacetic acid) is a polyamino carboxylic acid that binds metal ions like zinc and can inactivate the metallo-beta-lactamases. Therefore, it is used for the phenotypic detection of MBL production in clinical isolates [28].

3.2.1. Procedure

Step 1: Soak paper discs within a 0.1 M EDTA solution.

Step 2: Make a 0.5 McFarland bacterial suspension.

Step 3: Inoculate with a sterile cotton swab and place an imipenem and a ceftazidime disc at the center of the plate.

Step 4: Place the EDTA discs at both sides in respect to the antibiotics as shown in Figure 3.

Step 5: Incubate at 37°C for 18-24h.

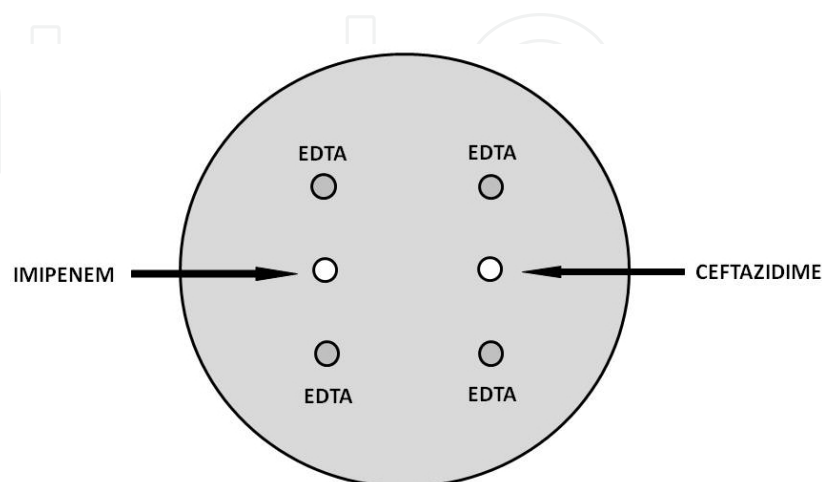


Figure 3. Preparation of the imipenem-EDTA synergy test.

3.2.2. Interpretation

The imipenem-EDTA synergy test is positive when the inhibition zone takes a characteristic keyhole shape because of the MBL inactivation by the EDTA (Figure 4). In proximity to the EDTA discs, the hydrolytic activity of MBLs is blocked. Consequently, imipenem and ceftazidime inhibition zones may appear larger towards the EDTA discs.

3.3. Boronic acid test

Phenylboronic acid acts as an inhibitor for KPC carbapenemases and class A and C beta-lactamases. The boronic acid test has been proposed for the phenotypic detection of KPC-producers because it is easier to perform than the DDST and also presents less false positive results because of the presence of ESBLs or AmpC beta-lactamases [29-31].

3.3.1. Procedure

Step 1: Make a 0.5 McFarland bacterial suspension.

Step 2: Inoculate with a sterile cotton swab and place two meropenem discs (Figure 5).

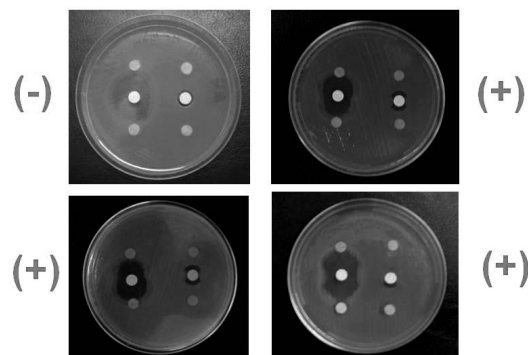


Figure 4. Interpretation of the imipenem-EDTA synergy test. (-): Negative; (+): Positive. Note that the upper left isolate is negative for MBL production but shows positive D-test between imipenem and ceftazidime indicating for the presence of inducible AmpC beta-lactamases (The D-test is described in paragraph 3.6).

Step 3: Add 20 µl of phenylboronic acid 20 g/L on one of the two meropenem discs.

Step 4: Incubate at 37°C for 18-24h.

3.3.2. Interpretation

In case of KPC production, the phenylboronic acid that has been added to the second meropenem disc will block the hydrolytic activity of the enzyme. As a consequence, the second disc will have a larger inhibition halo. The test is considered positive when the inhibition zone of the meropenem+phenylboronic acid is ≥ 5 mm larger than the inhibition zone of meropenem alone (Figure 6).

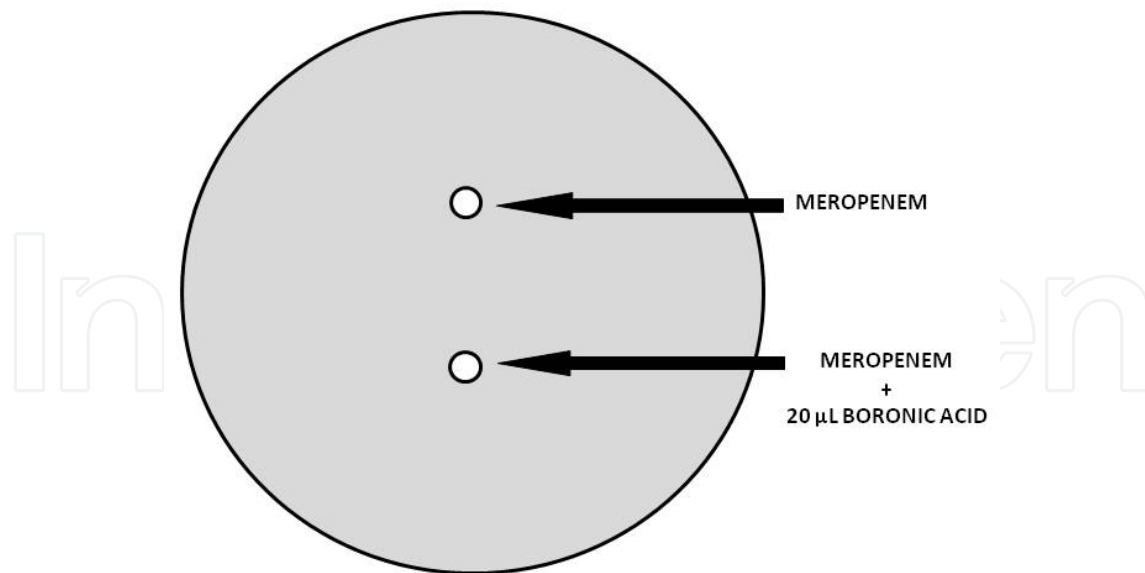


Figure 5. Preparation of the boronic acid test.

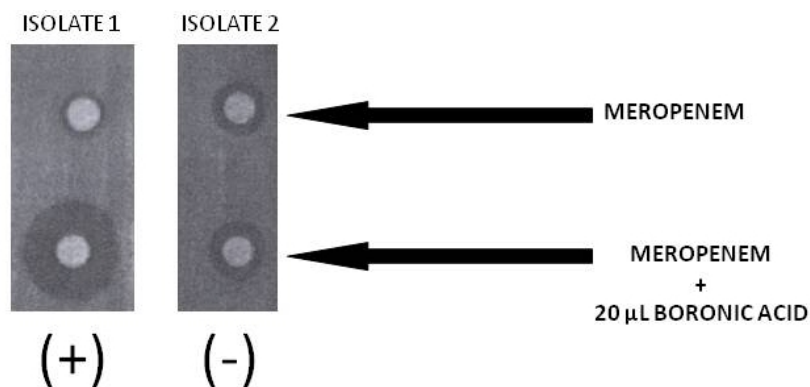


Figure 6. Interpretation of the boronic acid test. (+): Positive; (-): Negative.

3.4. Hodge test

The Hodge test is used to reveal carbapenemase production [32]. This is achieved by inoculating the study isolate together with a carbapenem-susceptible indicator strain and evaluating the distortion of the indicator strain's inhibition zone because of carbapenemase production by the study isolate. Despite its usefulness, this test presents a disadvantage: it detects the presence of carbapenemases only, without being able to discriminate between different carbapenemase types (KPC or MBLs).

3.4.1. Procedure

Step 1: Make a 0.5 McFarland suspension of the indicator strain (for example *E. coli* ATCC 25922).

Step 2: Inoculate with a sterile cotton swab and place a carbapenem disc at the center of the plate.

Step 3: Streak 3-5 colonies of the test isolate from the center to the periphery of the plate (Figure 7).

Step 4: Incubate at 37°C for 18-24h.

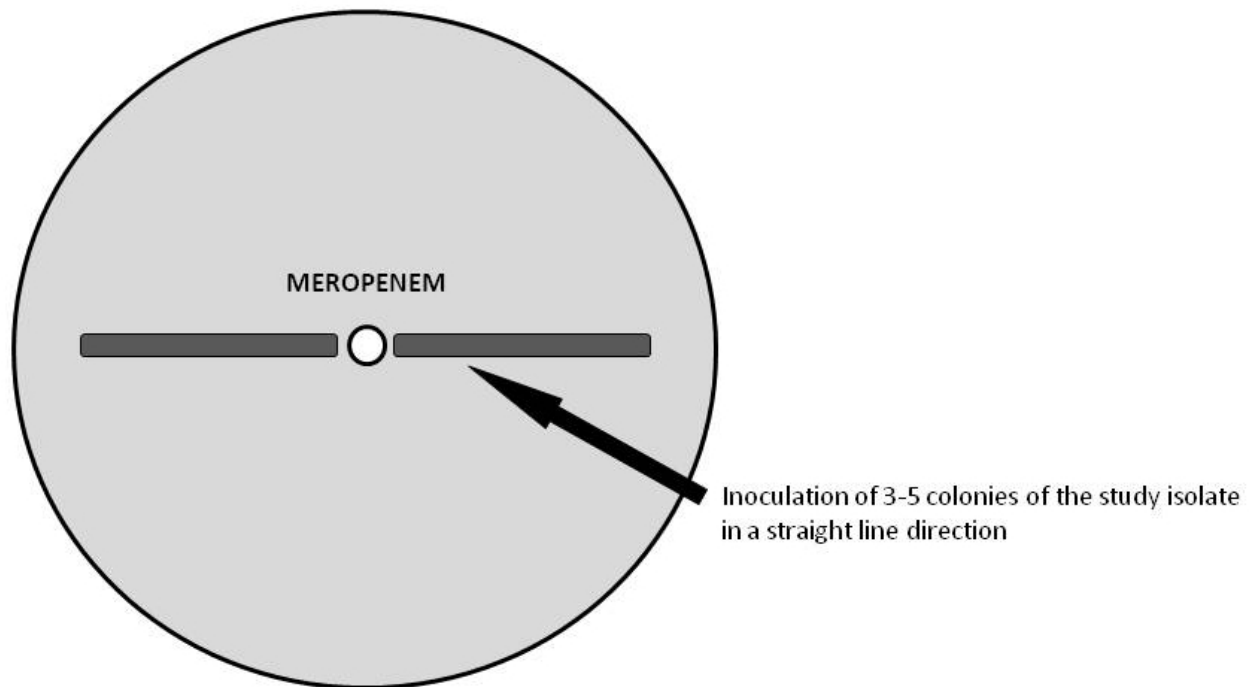


Figure 7. Preparation of the Hodge test.

3.4.2. Interpretation

The presence of a distorted inhibition zone due to growth of the indicator strain toward the carbapenem disc is interpreted as a positive result (Figure 8). This occurs due to carbapenemase production by the study isolate. Uncertain results need to be confirmed by other tests or molecular methods.

3.5. Combination meropenem disc test

This test is a combination of the EDTA and the boronic acid test in a single plate and has been introduced in Greece after the emergence of Gram negative isolates co-producing KPC and MBL carbapenemases [33-37]. The advantage of the test is that it discriminates between carbapenem-susceptible, KPC-producing, MBL-producing and double-carbapenemase-producing bacteria.

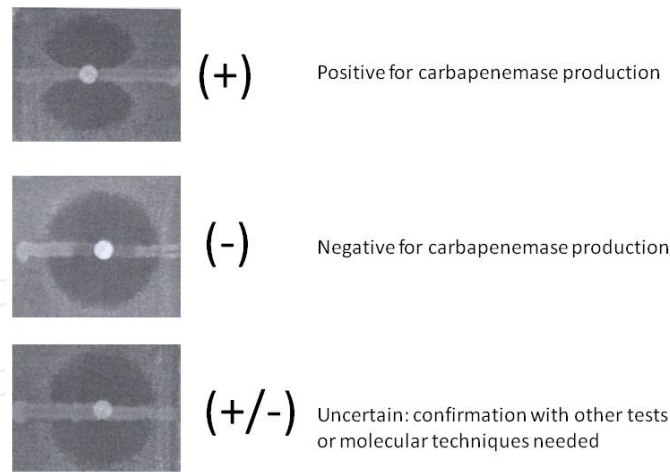


Figure 8. Interpretation of the Hodge test.

3.5.1. Procedure

Step 1: Make a 0.5 McFarland bacterial suspension.

Step 2: Inoculate with a sterile cotton swab and place four meropenem discs (Figure 9).

Step 3: Add 10 µl EDTA 0.1 M on the second disc, 20 µl of phenylboronic acid 20 g/L on the third disc and 20 µl of phenylboronic acid 20 g/L+10 µl EDTA 0.1 M on the fourth disc.

Step 4: Incubate at 37°C for 18-24h.

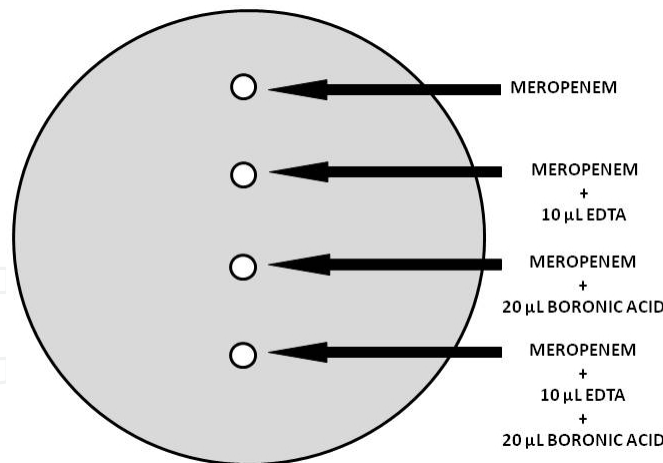


Figure 9. Preparation of the combination meropenem disc test.

3.5.2. Interpretation

The interpretation of the combination meropenem disc test is based on the comparison between the inhibition zones of the four meropenem discs as presented in Figure 10. If no carbapenemase is present, the zone diameters of the discs where inhibitors have been added

will not present significant differences ($\geq 5\text{mm}$) from the meropenem disc alone. In case of KPC production, an increase of $\geq 5\text{mm}$ in the discs that are supplemented with boronic acid will be observed. MBL production will become evident by an increase of $\geq 5\text{mm}$ in the discs that are supplemented with EDTA. In case of a KPC+MBL-producer, the fourth disc will present the larger zone diameter of all. The EDTA-supplemented and boronic acid-supplemented discs may or may not have a $\geq 5\text{mm}$ larger zone diameter than that of the meropenem disc alone.

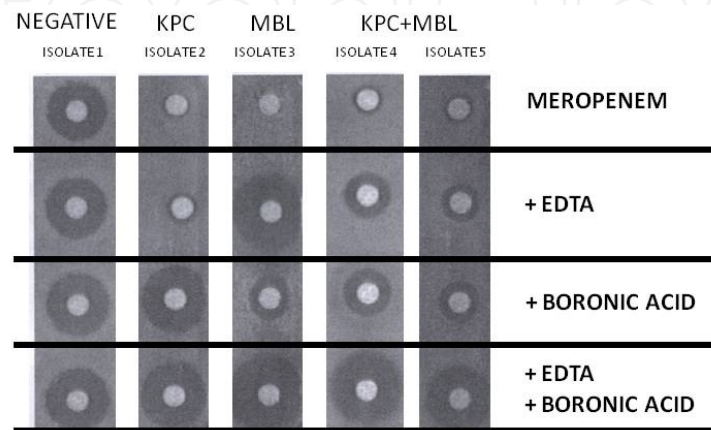


Figure 10. Interpretation of the combination meropenem disc test.

Recently, a novel variation of this test has been proposed [38] for surveillance cultures from rectal swabs. The same principle is generally followed, except that each swab is initially suspended in 1 ml sterile saline by rotating and agitating it to release the microorganisms. Afterwards, the suspension is cultured onto McConkey agar using a different swab. This method allows the identification and differentiation of carbapenemase-producing *Enterobacteriaceae* (Figure 11) directly at patient admission.

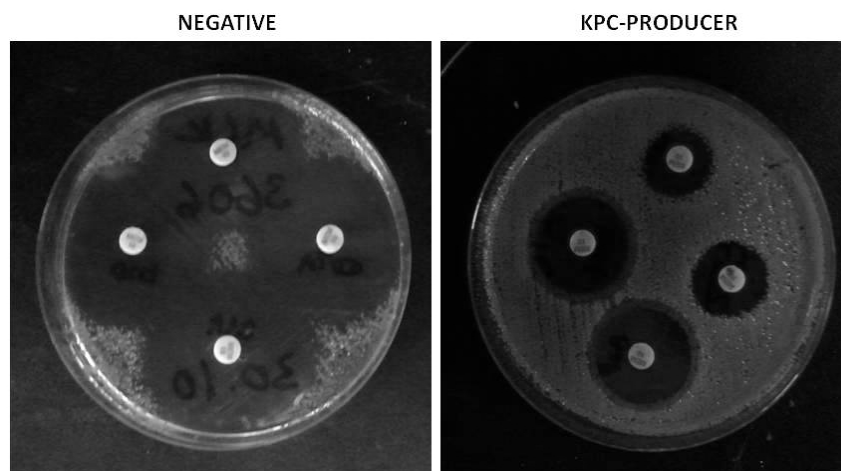


Figure 11. Application of the combination meropenem disc test for the direct differentiation of carbapenemase-producing *Enterobacteriaceae* in rectal swabs.

3.6. D-test

The D-test is used for the detection of inducible AmpC beta-lactamases [39]. An antibiotic is used as an inducer for AmpC production (imipenem or ceftoxitin) whereas others are used as substrates (ceftazidime, cefotaxime, piperacillin/tazobactam).

3.6.1. Procedure

Step 1: Make a 0.5 McFarland bacterial suspension.

Step 2: Inoculate with a sterile cotton swab and place an imipenem disc.

Step 3: Place substrate discs (for example ceftazidime and piperacillin/tazobactam) near the imipenem disc as shown in Figure 12.

Step 4: Incubate at 37°C for 18-24h.

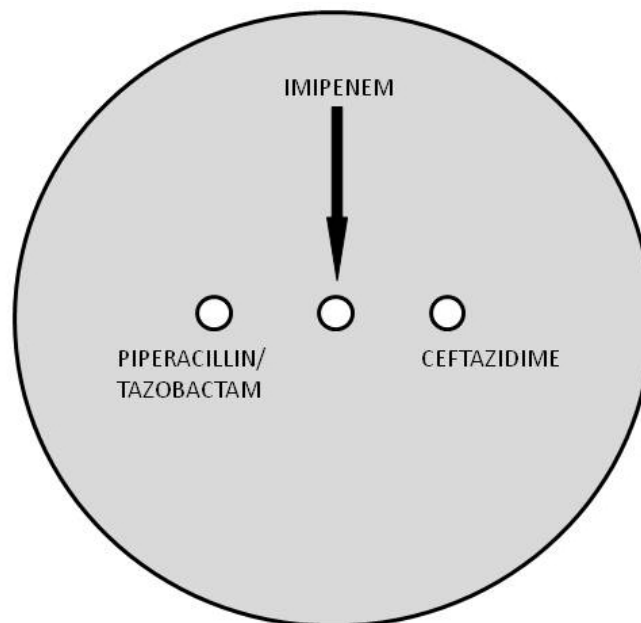


Figure 12. Preparation of a D-test.

3.6.2. Interpretation

The test is positive when a D-shaped inhibition zone is observed for one of the substrate discs (Figure 13) because of the imipenem-mediated induction of the AmpC production and the subsequent inactivation of the substrate antibiotic by the beta-lactamase. An important advantage of the test is that it can be easily incorporated within any routine antibiogram as shown in Figure 14.

3.7. CCCP test

CCCP (Carbonyl cyanide m-chlorophenyl hydrazone) is an efflux pump inhibitor that can be added in Mueller-Hinton agar during its preparation. The test is used to detect efflux pump overexpression that contributes to or determines carbapenem resistance in the study isolate [40].

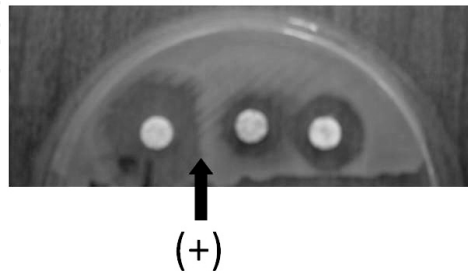


Figure 13. Interpretation of the D-test.

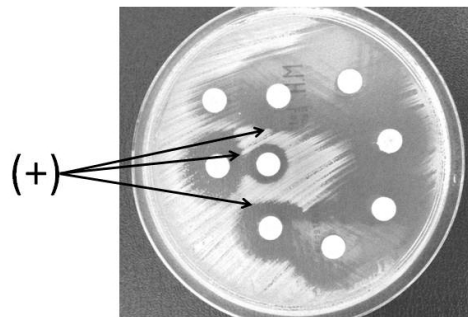


Figure 14. Incorporation of the D-test in a common antibiogram.

3.7.1. Procedure

Step 1: Prepare agar plates containing CCCP at a concentration of 12.5 μM .

Step 2: Make a 0.5 McFarland bacterial suspension.

Step 3: Inoculate with a sterile cotton swab on a CCCP-supplemented plate and in parallel on a CCCP-free plate. For economy reasons, two isolates may be inoculated on the same plate as shown in Figure 15.

Step 4: Place a meropenem disc on both plates for each inoculation.

Step 5: Incubate at 37°C for 18-24h.

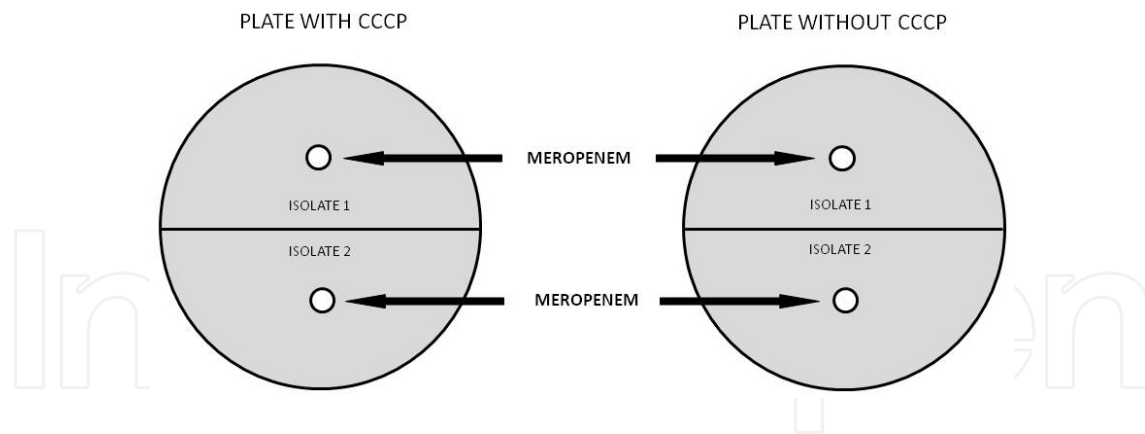


Figure 15. Preparation of the CCCP test.

3.7.2. Interpretation

The test is considered positive when synergy between meropenem and CCCP is observed on the CCCP-supplemented plate (Figure 16).

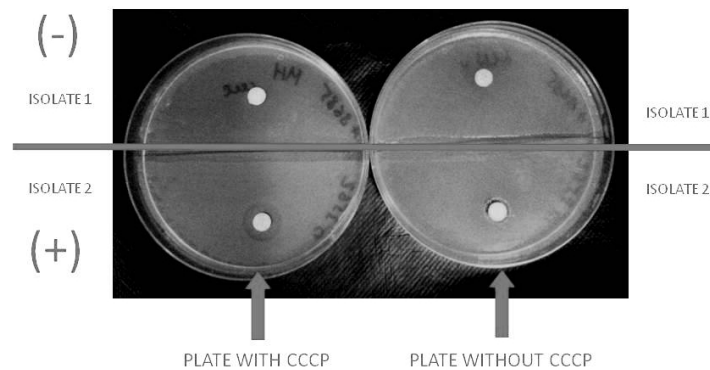


Figure 16. Interpretation of the CCCP test. Isolate 1 is inoculated on the upper side and isolate 2 is inoculated on the lower side of the plates. (+): Positive; (-): Negative.

4. Molecular methods

Genetic methods for the detection of resistance genes are based on nucleic acid hybridization and amplification. Therefore, the knowledge of specific primers (amplification nucleotides) and probes (labeled single-stranded oligonucleotides) is necessary in order to detect the genetic target of interest. The technique used depends on the type of resistance that is suspected. A simple polymerase chain reaction (PCR) may be applied searching for a gene that confers a certain level of resistance when it is expressed. This is the case for example, of genes encoding for antibiotic-inactivating enzymes. In Tables 2 and 3, primers for the detection of aminoglycoside or fluorquinolone resistance-conferring enzymes and beta-lactamases are shown, respectively.

Gene	Primers (5' - 3')	Product size	Reference
aac(6')-Ia	ATGAATTATCAAATTGTG	558 bp	[41]
	TTACTCTTGATTAAGT		
aac(6')-Ic	CTACGATTACGTCAACGGCTGC	130 bp	[42]
	TTGCTTCGCCACTCCTGCACC		
aac(3)-Ia	ACCTACTCCCAACATCAGCC	169 bp	[43]
	ATATAGATCTCACTACGCGC		
aac(3)-Ic	GATGATCTCTACTCAAACC	472 bp	[44]
	TTAGGCAGCAGGTTGAGG		
aac(3)-IV	GTTACACCGACCTTGGGA	675 bp	[45]
	AACGGCATTGAGCGTCAG		
aphA-3	GGGACCACCTATGATGTGGAACG	595 bp	[46]
	CAGGCTTGATCCCCAGTAAGTC		
aph(3')-Via	ATACAGAGACCACATACAGT	235 bp	[47]
	GGACAATCAATAATAGCAAT		
aad(2'')-Ia	ATGTTACGCAGCAGGGCAGTCG	188 bp	[48]
	CGTCAGATCAATATCATCGTGC		
aph(3')-IIIa	GGCTAAAATGAGAATATCACCGG	523 bp	[49,50]
	CTTTAAAAATCATAAGCTCGCG		
ant(4')-Ia	CAAAGTCTAAATCGGTAGAAGCC	294 bp	[49,50]
	GGAAAGTTGACCAGACATTACGAAT		
strA-strB	TATCTGCGATTGGACCCTCTG	519 bp	[51]
	CATTGCTCATCATTTGATCGGCT		
armA	AGGTTGTTCCATTCTGAG	590 bp	[52]
	TCTCTCCATTCCCTTCTCC		
rmtA	CTAGCGTCCATCCTTCTCTC	635 bp	[53]
	TTTGCTTCCATGCCCTTGCC		
rmtB	ATGAACATCAACGATGCCCT	769 bp	[54]
	CCTTCTGATTGGCTTATCCA		
gyrA (<i>A. baumannii</i>)	AAATCTGCCCGTGCATTGGT	343 bp	[55]
	GCCATACCTACGGCGATACC		
gyrA (E. coli)	ACGTAAGGCAATGACTGG	190 bp	[56]
	AGAAGTCGCCGTCGATAGAAC		
qnrA	TCAGCAAGAGGATTTCTCA	627 bp	[57]
	GGCAGCACTATTACTCCA		
Qnr	CCGTATGGATATTATTGATAAAG	661 bp	[58]
	CTAATCCGGCAGCACTATTA		

Table 2. Primers used for the detection of aminoglycoside and quinolone resistance determinants.

Gene	Primers (5'-3')	Product size	Reference
bla_{SHV}	GGTTATGCGTTATATTCGCC	867 bp	[59]
	TTAGCGTTGCCAGTGCTC		
bla_{TEM}	ATGAGTATTCAACATTTCCG	867 bp	[59]
	CTGACAGTTACCAATGCTTA		
bla_{CTX-M}	CGCTTTGCGATGTGCAG	550 bp	[60]
	ACCGCGATATCGTTGGT		
bla_{CTX-M-2}	ATGATGACTCAGAGCATTCCG	884 bp	[61]
	TTATTGCATCAGAAACCGTG		
bla_{CTX-M-9}	GTGACAAAGAGAGTGCAACGG	857 bp	[62]
	ATGATTCTCGCCGCTGAAGCC		
bla_{CTX-M-10}	GCTGATGAGCGCTTTGCG	684 bp	[63]
	TTACAAACCGTTGGTGACG		
bla_{GES/IBC}	GTTTTGCAATGTGCTCAACG	371 bp	[64]
	TGCCATAGCAATAGGCGTAG		
bla_{PER-1}	ATGAATGTCATTATAAAAGC	926 bp	[65]
	AATTTGGGCTTAGGGCAAGAAA		
bla_{PER-2}	CGCTTCTGCTCTGCTGAT	469 bp	[66]
	GGCAGCTTCTTTAACGCC		
bla_{PSE}	ACCGTATTGAGCCTGATTTA	321 bp	[67]
	ATTGAAGCCTGTGTTTGAGC		
bla_{TLA-1}	TCTCAGCGCAAATCCGCG	974 bp	[68]
	CTATTTCCCATCCTTAAGTAG		
bla_{VEB-1}	CGACTTCCATTTCCCGATGC	643 bp	[69]
	GGACTCTGCAACAAATACGC		
bla_{KPC}	TGTCACTGTATCGCCGTC	331 bp	[70]
	TATTTTCCGAGATGGGTGAC		
bla_{SME-1}	AACGGCTTCATTTTGTTAG	830 bp	[71]
	GCTCCGCAATAGTTTTATCA		
bla_{IMP}	CTACCGCAGCAGAGTCTTTG	587 bp	[72]
	AACGATTTTGCTTACCAT		
bla_{IMP-1}	ATGAGCAAGTTATCTGTATTC	741 bp	[73]
	TTAGTTGCTTGGTTTTGATGG		
bla_{IMP-2}	ATGAAGAAATTATTTGTTTTATG	741 bp	[73]
	TTAGTTACTTGGCTGTGATG		

Gene	Primers (5'- 3')	Product size	Reference
bla_{VIM}	TCTACATGACCGGTCTGTC	748 bp	[74]
	TGTGCTTTGACAACGTTGCG		
bla_{VIM-1}	GTAAAAAGTTATTAGTAGTTTATTG	799 bp	[73]
	CTACTCGGCGACTGAGC		
bla_{VIM-2}	ATGTTCAAACCTTTGAGTAAG	801 bp	[73]
	CTACTCAACGACTGAGCG		
bla_{SPM-1}	CCTACAATCTAACGGCGACC	649 bp	[75]
	TCGCCGTGTCCAGGTATAAC		
bla_{NDM-1}	GGTTTGCGATCTGGTTTTC	621 bp	[76]
	CGGAATGGCTCATCACGATC		
bla_{OXA-1}	CCAAAGACGTGGATG	540 bp	[77]
	GTAAATTCGACCCCAAGTT		
bla_{OXA-10}	CGTGCTTTGAAAAGTAGCAG	652 bp	[78]
	CATGATTTTGGTGGGAATGG		
bla_{OXA-23}	CCTCAGGTGTGCTGGTTATTC	513 bp	[79]
	CCCAACCAGTCTTTCCAAAA		
bla_{OXA-24}	TCCCCTAACATGAATTTGT	1020 bp	[80]
	GTACTAATCAAAGTTGTGAA		

Table 3. Primers used for the detection of beta-lactamases frequently encountered among Gram negative pathogens.

In cases in which resistance depends upon the expression level (overexpression or downregulation) of the gene, real time Reverse Transcriptase-PCR (rt RT-PCR) is used to detect not only the presence, but also the mRNA expression of the gene. The results are consequently confronted with the expression level of the same gene in a control strain. This technique is useful for the study of the expression of specific porins and efflux pumps (primers and probes for such resistance determinants in *P. aeruginosa* are shown in Table 4).

Gene	Primers (5'- 3')	Reference
ampC	CGCCGTACAACCGGTGAT	[81]
	CGGCCGTCTCTTTTGA	
probe	[DFAM]TCAGCCTGAAAGGAGAACCGCATTACTTC[DTAM]	
OprD	CTACGGCTACGGCGAGGAT	[81]
	GACCGGACTGGACCACGTACT	
probe	[DFAM]CACCACGAAACCAACCTCGAAGCC[DTAM]	
mexA	AACCCGAACAACGAGCTG	[81]

Gene	Primers (5'-3')	Reference
	ATGGCCTTCTGCTTGACG	
probe	[DFAM]CATGTTTCGTTACGCGCAGTTG[DTAM]	
mexC	GGAAGAGCGACAGGAGGC	[81]
	CTGCACCGTCAGGCCCTC	
probe	[DFAM]CCGAAATGGTGTGCCGGTG[DTAM]	
mexE	TACTGGTCTGAGCGCCT	[81]
	TCAGCGTTGTTTCGATGA	
probe	[DFAM]CGGAAACCACCCAAGGCATG[DTAM]	
mexX	GGCTTGGTGAAGACGTG	[81]
	GGCTGATGATCCAGTCGC	
probe	[DFAM]CCGACACCCTGCAGGGCC[DTAM]	

Table 4. Primers and probes used in real-time RT PCR for the determination of the expression levels for specific resistance mechanisms in *P. aeruginosa*.

Finally, sequencing [82-84] of the PCR product allows its confrontation with the already known gene sequences that are available in genetic databases. This can lead to the detection of mutations or to the characterization and classification of the gene within a genetic family.

5. Conclusion

There are several benefits and limitations using either phenotypic or molecular methods for the detection of resistance mechanisms in Gram negative pathogens. Phenotypic tests require bacteria in pure culture from a clinical sample thus needing 24-48h to obtain a final result. Molecular techniques on the other hand, can be performed directly with clinical specimens reducing significantly the procedure time.

The detection of low-level resistance is by definition problematic using phenotypic tests thus interpretation problems may appear. In such cases, molecular techniques are an option for clarifying the possible involvement of any known resistance mechanism.

Moreover, genetic detection gives a definite answer for the presence or not of specific resistance determinants within a study isolate (a specific beta-lactamase for example) whereas this is not possible with the phenotypic tests which provide only general information about the resistance mechanisms involved.

Genetic assays however, present also some major limitations: (i) It is possible to screen exclusively for known mechanisms and for one gene at the time (unless a multiplex PCR assay [85-88] can be applied) and; (ii) their cost is high and becomes higher when screening for multiple resistance determinants.

Consequently, the combined and rational use of the available methodologies seems to be the optimal solution for the cost-effective detection of resistance mechanisms in Gram negative pathogens by the Clinical Microbiology laboratory.

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References

- [1] Meletis G. Editorial: war against multi-drug-resistant pathogens: what is new in the armory? *Recent Pat Antiinfect Drug Discov* 2012;7. 173-174.
- [2] Hanson ND. Editorial: Resistance in gram-negative pathogens: a threat to global health. *Curr Pharm Des* 2013;19. 163.
- [3] Savard P, Perl TM. A call for action: managing the emergence of multidrug-resistant Enterobacteriaceae in the acute care settings. *Curr Opin Infect Dis* 2012;25. 371-377.
- [4] Grundmann H, Klugman KP, Walsh T, et al. A framework for global surveillance of antibiotic resistance. *Drug Resist Updat* 2011;14. 79-87.
- [5] Campbell S. The need for a global response to antimicrobial resistance. *Nurs Stand* 2007;21. 35-40.

- [6] Meletis G, Vavatsi N, Exindari M, et al. Accumulation of carbapenem resistance mechanisms in VIM-2-producing *Pseudomonas aeruginosa* under selective pressure. *Eur J Clin Microbiol Infect Dis* 2014;33. 253-258.
- [7] Li H, Luo YF, Williams BJ, et al. Structure and function of OprD protein in *Pseudomonas aeruginosa*: from antibiotic resistance to novel therapies. *Int J Med Microbiol* 2012;302. 63-68.
- [8] Zhang Y, Jiang X, Wang Y, et al. Contribution of β -lactamases and the porin proteins OmpK35 and OmpK36 to carbapenem resistance in clinical isolates of KPC-2-producing *Klebsiella pneumoniae*. *Antimicrob Agents Chemother* 2014;58. 1214-1217.
- [9] Hong JH, Clancy CJ, Cheng S, et al. Characterization of porin expression in *Klebsiella pneumoniae* Carbapenemase (KPC)-producing *K. pneumoniae* identifies isolates most susceptible to the combination of colistin and carbapenems. *Antimicrob Agents Chemother* 2013;57. 2147-2153.
- [10] Zeng ZR, Wang WP, Huang M, et al. Mechanisms of carbapenem resistance in cephalosporin-susceptible *Pseudomonas aeruginosa* in China. *Diagn Microbiol Infect Dis* 2014;78. 268-270.
- [11] Perez F, Rudin SD, Marshall SH, et al. OqxAB, a quinolone and olaquinox efflux pump, is widely distributed among multidrug-resistant *Klebsiella pneumoniae* isolates of human origin. *Antimicrob Agents Chemother* 2013;57. 4602-4603.
- [12] Rodríguez-Martínez JM, Díaz de Alba P, Briaies A, et al. Contribution of OqxAB efflux pumps to quinolone resistance in extended-spectrum- β -lactamase-producing *Klebsiella pneumoniae*. *J Antimicrob Chemother* 2013;68. 68-73.
- [13] Skiada A, Markogiannakis A, Plachouras D, et al. Adaptive resistance to cationic compounds in *Pseudomonas aeruginosa*. *Int J Antimicrob Agents* 2011;37. 187-193.
- [14] Fu Y, Zhang W, Wang H, et al. Specific patterns of *gyrA* mutations determine the resistance difference to ciprofloxacin and levofloxacin in *Klebsiella pneumoniae* and *Escherichia coli*. *BMC Infect Dis* 2013;13. 8.
- [15] Aldred KJ, McPherson SA, Turnbough CL Jr, et al. Topoisomerase IV-quinolone interactions are mediated through a water-metal ion bridge: mechanistic basis of quinolone resistance. *Nucleic Acids Res* 2013;41. 4628-4639.
- [16] Drlica K, Hiasa H, Kerns R, et al. Quinolones: action and resistance updated. *Curr Top Med Chem* 2009;9. 981-998.
- [17] Gutkind GO, Di Conza J, Power P, et al. β -lactamase-mediated resistance: a biochemical, epidemiological and genetic overview. *Curr Pharm Des* 2013;19. 164-208.
- [18] Ramirez MS, Tolmasky ME. Aminoglycoside modifying enzymes. *Drug Resist Updat* 2010;13. 151-171.

- [19] Labby KJ, Garneau-Tsodikova S. Strategies to overcome the action of aminoglycoside-modifying enzymes for treating resistant bacterial infections. *Future Med Chem* 2013;5. 1285-1309.
- [20] Cornaglia G, Giamarellou H, Rossolini GM. Metallo- β -lactamases: a last frontier for β -lactams? *Lancet Infect Dis* 2011;11. 381-393.
- [21] Munoz-Price LS, Poirel L, Bonomo RA, et al. Clinical epidemiology of the global expansion of *Klebsiella pneumoniae* carbapenemases. *Lancet Infect Dis* 2013;13. 785-796.
- [22] Queenan AM, Bush K. Carbapenemases: the versatile beta-lactamases. *Clin Microbiol Rev.* 2007;20. 440-458.
- [23] Falagas ME, Karageorgopoulos DE. Extended-spectrum beta-lactamase-producing organisms. *J Hosp Infect.* 2009;73. 345-354.
- [24] Bradford P. Extended-Spectrum- β -Lactamases in the 21st century: Characterization, epidemiology, and detection of this important resistance threat. *Clin Microbiol Rev* 2001;14. 933-951.
- [25] Jacoby GA. AmpC beta-lactamases. *Clin Microbiol Rev.* 2009;22. 161-182.
- [26] Brown S, Amyes S. OXA (beta)-lactamases in *Acinetobacter*: the story so far. *J Antimicrob Chemother.* 2006;57. 1-3.
- [27] Jiang X, Zhang Z, Li M, et al. Detection of extended-spectrum beta-lactamases in clinical isolates of *Pseudomonas aeruginosa*. *Antimicrob Agents Chemother* 2006;50. 2990-2995.
- [28] Lee K, Lim YS, Yong D, et al. Evaluation of the Hodge test and the imipenem-EDTA double-disk synergy test for differentiating metallo-beta-lactamase-producing isolates of *Pseudomonas* spp. and *Acinetobacter* spp. *J Clin Microbiol* 2003;41. 4623-4629.
- [29] Pournaras S, Poulou A, Tsakris A. Inhibitor-based methods for the detection of KPC carbapenemase-producing Enterobacteriaceae in clinical practice by using boronic acid compounds. *J Antimicrob Chemother* 2010;65. 1319-1321.
- [30] Tsakris A, Kristo I, Poulou A, et al. Evaluation of boronic acid disc tests for differentiating KPC-possessing *Klebsiella pneumoniae* isolates in the clinical laboratory. *J Clin Microbiol* 2009;47. 362-367.
- [31] Tsakris A, Poulou A, Themeli-Digalaki K, et al. Use of boronic acid disc tests to detect extended-spectrum b-lactamases in clinical isolates of KPC carbapenemase-possessing Enterobacteriaceae. *J Clin Microbiol* 2009;47. 3420-3426.
- [32] Pasteran F, Veliz O, Rapoport M, et al. Sensitive and specific modified Hodge test for KPC and metallo-beta-lactamase detection in *Pseudomonas aeruginosa* by use of a

- novel indicator strain, *Klebsiella pneumoniae* ATCC 700603. *J Clin Microbiol* 2011;49: 4301-4303.
- [33] Giakkoupi P, Pappa O, Polemis M, et al. Emerging *Klebsiella pneumoniae* isolates coproducing KPC-2 and VIM-1 carbapenemases. *Antimicrob Agents Chemother* 2009;53: 4048–4050.
- [34] Meletis G, Tzampaz E, Protonotariou E, et al. Emergence of *Klebsiella pneumoniae* carrying bla(VIM) and bla(KPC) genes. *Hippokratia* 2010;14: 139–140.
- [35] Papagiannitsis CC, Giakkoupi P, Vatopoulos AC, et al. Emergence of *Klebsiella pneumoniae* of a novel sequence type (ST383) producing VIM-4, KPC-2 and CMY-4 beta-lactamases. *Int J Antimicrob Agents* 2010;36: 573–574.
- [36] Pournaras S, Poulou A, Voulgari E, et al. Detection of the new metallo-beta-lactamase VIM-19 along with KPC-2, CMY-2 and CTX-M-15 in *Klebsiella pneumoniae*. *J Antimicrob. Chemother* 2010;65: 1604–1607.
- [37] Zioga A, Miriagou V, Tzelepi E, et al. The ongoing challenge of acquired carbapenemases: a hospital outbreak of *Klebsiella pneumoniae* simultaneously producing VIM-1 and KPC-2. *Int J Antimicrob Agents* 2010;36: 190–191.
- [38] Pournaras S, Zarkotou O, Poulou A, et al. A combined disk test for direct differentiation of carbapenemase-producing enterobacteriaceae in surveillance rectal swabs. *J Clin Microbiol* 2013;51: 2986-2990.
- [39] Dunne WM Jr, Hardin DJ. Use of several inducer and substrate antibiotic combinations in a disk approximation assay format to screen for AmpC induction in patient isolates of *Pseudomonas aeruginosa*, *Enterobacter* spp., *Citrobacter* spp., and *Serratia* spp. *J Clin Microbiol* 2005;43: 5945-5949.
- [40] Pournaras S, Maniati M, Spanakis N, et al. Spread of efflux pump-overexpressing, non-metallo-beta-lactamase-producing, meropenem-resistant but ceftazidime-susceptible *Pseudomonas aeruginosa* in a region with blaVIM endemicity. *J Antimicrob Chemother* 2005;56: 761-764.
- [41] Ploy MC, Giamarellou H, Bourlioux P, et al. Detection of aac(6')-I genes in amikacin-resistant *Acinetobacter* spp. by PCR. *Antimicrob Agents Chemother* 1994;38: 2925-2928.
- [42] Hannecart-Pokorni E, Depuydt F, de wit L, et al. Characterization of the 6'-N-aminoglycoside acetyltransferase gene aac(6')-Im [corrected] associated with a *sulI*-type integron. *Antimicrob Agents Chemother* 1997;41: 314-318.
- [43] Van de Klundert JM, Vliegenthart JS. PCR detection of genes coding for aminoglycoside-modifying enzymes, p. 547-552. In: *Diagnostic Molecular Microbiology: Principles and Applications*. American Society for Microbiology, Washington, D.C.

- [44] Riccio ML, Docquier JD, Dell'Amico E, et al. Novel 3-N-aminoglycoside acetyltransferase gene, *aac(3)-Ic*, from a *Pseudomonas aeruginosa* integron. *Antimicrob Agents Chemother* 2003;47. 1746-1748.
- [45] Guerra B, Soto SM, Argüelles JM, et al. Multidrug resistance is mediated by large plasmids carrying a class 1 integron in the emergent *Salmonella enterica* serotype [4,5,12:i:-]. *Antimicrob Agents Chemother* 2001;45. 1305-1308.
- [46] Gibreel A, Sköld O, Taylor DE. Characterization of plasmid-mediated *aphA-3* kanamycin resistance in *Campylobacter jejuni*. *Microb Drug Resist* 2004;10. 98-105.
- [47] Vila J, Ruiz J, Navia M, et al. Spread of amikacin resistance in *Acinetobacter baumannii* strains isolated in Spain due to an epidemic strain. *J Clin Microbiol* 1999;37. 758-761.
- [48] Vanhoof R, Content J, Van Bossuyt E, et al. Identification of the *aadB* gene coding for the aminoglycoside-2"-O-nucleotidyltransferase, ANT(2''), by means of the polymerase chain reaction. *J Antimicrob Chemother* 1992;29. 365-374.
- [49] Sundsfjord A, Simonsen GS, Haldorsen BC, et al. Genetic methods for detection of antimicrobial resistance. *APMIS* 2004;112. 815-837.
- [50] Vakulenko SB, Donabedian SM, Voskresenskiy AM, et al. Multiplex PCR for detection of aminoglycoside resistance genes in enterococci. *Antimicrob Agents Chemother* 2003;47. 1423-1426.
- [51] Sunde M, Norström M. The genetic background for streptomycin resistance in *Escherichia coli* influences the distribution of MICs. *J Antimicrob Chemother* 2005;56. 87-90.
- [52] Yamane K, Wachino J, Doi Y, et al. Global spread of multiple aminoglycoside resistance genes. *Emerg Infect Dis* 2005;11. 951-953.
- [53] Yokoyama K, Doi Y, Yamane K, et al. Acquisition of 16S rRNA methylase gene in *Pseudomonas aeruginosa*. *Lancet* 2003;362. 1888-1893.
- [54] Yan JJ, Wu JJ, Ko WC, et al. Plasmid-mediated 16S rRNA methylases conferring high-level aminoglycoside resistance in *Escherichia coli* and *Klebsiella pneumoniae* isolates from two Taiwanese hospitals. *J Antimicrob Chemother* 2004;54. 1007-1012.
- [55] Vila J, Ruiz J, Goñi P, et al. Mutation in the *gyrA* gene of quinolone-resistant clinical isolates of *Acinetobacter baumannii*. *Antimicrob Agents Chemother* 1995;39. 1201-1203.
- [56] Everett MJ, Jin YF, Ricci V, et al. Contributions of individual mechanisms to fluoroquinolone resistance in 36 *Escherichia coli* strains isolated from humans and animals. *Antimicrob Agents Chemother* 1996;40. 2380-2386.

- [57] Robicsek A, Sahm DF, Strahilevitz J, et al. Broader distribution of plasmid-mediated quinolone resistance in the United States. *Antimicrob Agents Chemother* 2005;49: 3001-3003.
- [58] Mammeri H, Van De Loo M, Poirel L, et al. Emergence of plasmid-mediated quinolone resistance in *Escherichia coli* in Europe. *Antimicrob Agents Chemother* 2005;49: 71-76.
- [59] Rasheed JK, Jay C, Metchock B, et al. Evolution of extended-spectrum beta-lactam resistance (SHV-8) in a strain of *Escherichia coli* during multiple episodes of bacteremia. *Antimicrob Agents Chemother* 1997;41: 647-653.
- [60] Bonnet R, Dutour C, Sampaio JL, et al. Novel cefotaximase (CTX-M-16) with increased catalytic efficiency due to substitution Asp-240-->Gly. *Antimicrob Agents Chemother* 2001;45: 2269-2275.
- [61] Petroni A, Corso A, Melano R, et al. Plasmidic extended-spectrum beta-lactamases in *Vibrio cholerae* O1 El Tor isolates in Argentina. *Antimicrob Agents Chemother* 2002;46: 1462-1468.
- [62] Sabaté M, Tarragó R, Navarro F, et al. Cloning and sequence of the gene encoding a novel cefotaxime-hydrolyzing beta-lactamase (CTX-M-9) from *Escherichia coli* in Spain. *Antimicrob Agents Chemother* 2000;44: 1970-1973.
- [63] Oliver A, Pérez-Díaz JC, Coque TM, et al. Nucleotide sequence and characterization of a novel cefotaxime-hydrolyzing beta-lactamase (CTX-M-10) isolated in Spain. *Antimicrob Agents Chemother* 2001;45: 616-620.
- [64] Weldhagen GF, Prinsloo A. Molecular detection of GES-2 extended spectrum Beta-lactamase producing *Pseudomonas aeruginosa* in Pretoria, South Africa. *Int J Antimicrob Agents* 2004;24: 35-38.
- [65] Vahaboglu H, Hall LM, Mulazimoglu L, et al. Resistance to extended-spectrum cephalosporins, caused by PER-1 beta-lactamase, in *Salmonella typhimurium* from Istanbul, Turkey. *J Med Microbiol* 1995;43: 294-299.
- [66] Bauernfeind A, Stemplinger I, Jungwirth R, et al. Characterization of beta-lactamase gene blaPER-2, which encodes an extended-spectrum class A beta-lactamase. *Antimicrob Agents Chemother* 1996;40: 616-620.
- [67] Bert F, Branger C, Lambert-Zechovsky N. Identification of PSE and OXA beta-lactamase genes in *Pseudomonas aeruginosa* using PCR-restriction fragment length polymorphism. *J Antimicrob Chemother* 2002;50: 11-18.
- [68] Alcantar-Curiel D, Tinoco JC, Gayosso C, et al. Nosocomial bacteremia and urinary tract infections caused by extended-spectrum beta-lactamase-producing *Klebsiella pneumoniae* with plasmids carrying both SHV-5 and TLA-1 genes. *Clin Infect Dis* 2004;38: 1067-1074.

- [69] Naas T, Poirel L, Karim A, et al. Molecular characterization of In50, a class 1 integron encoding the gene for the extended-spectrum beta-lactamase VEB-1 in *Pseudomonas aeruginosa*. *FEMS Microbiol Lett* 1999;176. 411-419.
- [70] Yigit H, Queenan AM, Anderson GJ, et al. Novel carbapenem-hydrolyzing beta-lactamase, KPC-1, from a carbapenem-resistant strain of *Klebsiella pneumoniae*. *Antimicrob Agents Chemother* 2001;45. 1151-1161.
- [71] Queenan AM, Torres-Viera C, Gold HS, et al. SME-type carbapenem-hydrolyzing class A beta-lactamases from geographically diverse *Serratia marcescens* strains. *Antimicrob Agents Chemother* 2000;44. 3035-3039.
- [72] Senda K, Arakawa Y, Ichiyama S, et al. PCR detection of metallo-beta-lactamase gene (blaIMP) in gram-negative rods resistant to broad-spectrum beta-lactams. *J Clin Microbiol* 1996;34. 2909-2913.
- [73] Gutiérrez O, Juan C, Cercenado E, et al. Molecular epidemiology and mechanisms of carbapenem resistance in *Pseudomonas aeruginosa* isolates from Spanish hospitals. *Antimicrob Agents Chemother* 2007;51. 4329-4335.
- [74] Poirel L, Naas T, Nicolas D, et al. Characterization of VIM-2, a carbapenem-hydrolyzing metallo-beta-lactamase and its plasmid-and integron-borne gene from a *Pseudomonas aeruginosa* clinical isolate in France. *Antimicrob Agents Chemother* 2000;44. 891-897.
- [75] Sader HS, Reis AO, Silbert S, et al. IMPs, VIMs and SPMs: the diversity of metallo-beta-lactamases produced by carbapenem-resistant *Pseudomonas aeruginosa* in a Brazilian hospital. *Clin Microbiol Infect* 2005;11. 73-76.
- [76] Nordmann P, Poirel L, Carrër A, et al. How to detect NDM-1 producers. *J Clin Microbiol* 2011;49. 718-721.
- [77] Siu LK, Lo JY, Yuen KY, et al. beta-lactamases in *Shigella flexneri* isolates from Hong Kong and Shanghai and a novel OXA-1-like beta-lactamase, OXA-30. *Antimicrob Agents Chemother* 2000;44. 2034-2038.
- [78] Steward CD, Rasheed JK, Hubert SK, et al. Characterization of clinical isolates of *Klebsiella pneumoniae* from 19 laboratories using the National Committee for Clinical Laboratory Standards extended-spectrum beta-lactamase detection methods. *J Clin Microbiol* 2001;39. 2864-2872.
- [79] Brown S, Young HK, Amyes SG. Characterisation of OXA-51, a novel class D carbapenemase found in genetically unrelated clinical strains of *Acinetobacter baumannii* from Argentina. *Clin Microbiol Infect* 2005;11. 15-23.
- [80] Bou G, Oliver A, Martínez-Beltrán J. OXA-24, a novel class D beta-lactamase with carbapenemase activity in an *Acinetobacter baumannii* clinical strain. *Antimicrob Agents Chemother* 2000;44. 1556-1561.

- [81] Quale J, Bratu S, Gupta J, et al. Interplay of efflux system, ampC, and oprD expression in carbapenem resistance of *Pseudomonas aeruginosa* clinical isolates. *Antimicrob Agents Chemother* 2006;50. 1633-1641.
- [82] Franca LT, Carrilho E, Kist TB. A review of DNA sequencing techniques. *Q Rev Biophys* 2002;35. 169-200.
- [83] Diene SM, Rolain JM. Investigation of antibiotic resistance in the genomic era of multidrug-resistant Gram-negative bacilli, especially Enterobacteriaceae, *Pseudomonas* and *Acinetobacter*. *Expert Rev Anti Infect Ther* 2013;11. 277-296.
- [84] Fournier PE, Drancourt M, Raoult D. Bacterial genome sequencing and its use in infectious diseases. *Lancet Infect Dis* 2007;7. 711-723.
- [85] Woodford N. Rapid characterization of beta-lactamases by multiplex PCR. *Methods Mol Biol* 2010;642. 181-192.
- [86] Bisiklis A, Papageorgiou F, Frantzidou F, et al. Specific detection of blaVIM and blaIMP metallo-beta-lactamase genes in a single real-time PCR. *Clin Microbiol Infect* 2007;13. 1201-1203.
- [87] Poirel L, Walsh TR, Cuvillier V, et al. Multiplex PCR for detection of acquired carbapenemase genes. *Diagn Microbiol Infect Dis* 2011;70. 119-123.
- [88] Huang XZ, Cash DM, Chahine MA, et al. Development and validation of a multiplex TaqMan real-time PCR for rapid detection of genes encoding four types of class D carbapenemase in *Acinetobacter baumannii*. *J Med Microbiol* 2012;61. 1532-1537.