CLINICS

READERS OPINION

Modified Hodge test as screening test for spreading Carbapenemase resistance has become more important

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Dear Editor,

We read the article by Cury et al. titled ''The modified Hodge test is a useful tool for ruling out *Klebsiella pneumoniae* carbapenemase'' with interest (1). The authors aimed to evaluate the modified Hodge test (MHT) as a phenotypic screening test for *Klebsiella pneumoniae* carbapenemase (KPC). They concluded that standardizing MHT interpretation may improve the specificity of KPC detection. Additionally, negative test results ruled out 100% of the isolates harboring *Klebsiella pneumoniae* carbapenemase-2. The test may therefore be regarded as a good epidemiological tool.

Carbapenemase resistance has become a major problem around the world. However, the prevalence of carbapenemase resistance genes may have epidemiological differences between different regions, such as BlaKPC in the American and European zones, NDM in India, and OXA-48 in Turkey (2). BlaKPC examination in these trials was used to identify the genotype. Other resistance genes have been neglected. Thus, we believe that if BlaKPC-negative isolates, as determined by PCR, were to be tested in the presence of BlaIMP, BlaNDM, and BlaOXA-48, the significance of the study would increase.

Molecular detection of the presence of carbapenemases is the gold standard for diagnosis, but testing performed on a routine basis is expensive and impractical (2). All carbapenemase resistance caused by the resistance genes is detectable using the MHT, for which the sensitivity and specificity of the screening is known to be very good (1,2). However, the weakest aspect of the MHT is specificity. In a recent study using *K. pneumoniae* ATCC 700603 as the indicator strain instead of *E. coli* ATCC 25922 in a test procedure, the MHT had 97% sensitivity and 100% specificity (3). Another study reported a problem with sensitivity in expressing NDM-1 strains and found that specificity increased with the addition of $ZnSO_4$ (4). Therefore, different resistance genes in different bacteria must be considered when designing a methodology to increase sensitivity and specificity. We believe that more studies are needed on this subject.

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