LETTERS TO THE EDITOR

The Significance of Genome-based Diagnosis for the Bacillus Cereus Species

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The Authors Reply We are grateful to Savini and colleagues for providing this additional information. They have quite rightly identified the problem of heterogeneity in the Bacillus cereus group. In this report, we have included a postscript stating that detection of B. cereus was routinely performed when the presence of the Bacillus species was suspected by estimating the hemolytic activity on blood agar, thus confirming surface motility, and by performing fermentation tests with glucose, arabinose, mannitol and xylose. Among the six species of the Bacillus group, B. cereus and Bacillus anthracis are the most common mammalian pathogens that also affect humans (1). Tests for hemolytic activity and motility are useful for differentiating between these pathogens (2). Nevertheless, our case series may be subject to selection bias because the number of clinical tests available for detection of rare species is limited, thus making it difficult to characterize a member of the Bacillus species. We agree that the source of bacteremia should have been identified as being of Bacillus species origin and not specified as being of Bacillus cereus origin.

On the other hand, the prevalence of this pathogen is currently underestimated since most clinical observations of the Bacillus species are reported without performing genome-based bacterial typing. We previously emphasized that delays in the detection of these microorganisms and the presence of resistant B. cereus strains are serious issues (3). Physicians always need to choose the most effective treatment agent while simultaneously attempting to detect the cause of the complications. However, more cases need to be studied, and these pathogens need to be classified accurately to enable physicians to make an accurate diagnosis. Furthermore, another issue has been addressed.

It is very important to identify which Bacillus species is resistant to carbapenems and/or clindamycin. Even though B. cereus is considered to be susceptible to carbapenem and clindamycin, we encountered some cases of resistance towards these antimicrobial agents (3). Importantly, antibiotic susceptibility may differ for each species. Previous studies have demonstrated that only a few species, such as B. cereus and Bacillus mycoides, are resistant to meropenem, whereas Bacillus mycoides and Bacillus pseudomycoides are frequently found to be resistant to clindamycin (4). These findings imply that if genome-based examinations of the Bacillus species were routinely performed in clinical practice, they would yield significant information not only to accurately classify these pathogens, but also to appropriately select antibiotic therapy. That is, the frequent performance of genome-based studies would contribute to physicians’ decision-making, thus leading to the administration of sufficient and appropriate treatment.

We hope that basic researchers will explore and develop rapid methods for detecting microorganisms such as the Bacillus cereus species. Such methods would aid the accumulation of more reliable clinical data and thus have a significant impact on patient prognosis.

The authors state that they have no Conflict of Interest (COI).

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References


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