The stored bacteria were sub-cultured and DNA was isolated. The subpopulations were identified by PCR amplification and sequencing of the rpoB gene.

For isolates identified as AB through sequencing of the rpoB gene, multi-locus sequence typing (MLST) using the Oxford database (https://pubmlst.org/baumannii) was carried out.

Clinical data were retrospectively reviewed.

RESULTS

During the 12-year study period, 121 AB isolates were obtained from patients treated for invasive infections.

Duplicate isolates (n=11), isolates that did not subculture for DNA isolation (n=4), and isolates without any clinical data (n=3) were eliminated.

A total 103 isolates underwent further subpopulation identification, which were cultured from the blood (n=87), pleural fluid (n=11), pleural fluid (n=2), cerebrospinal fluid (n=2), and bronchoalveolar fluid (n=1).

The median age of the patients was 2 (IQR 0-7) years old and 47 (45.6%) were male.

The misidentification rate was 45.6%.

The most frequently identified non-AB subspecies was A. nosocomialis (n=26, 25.2%), followed by A. pittii (n=11, 10.7%), both of which belong to the ACB complex.

Isolates identified as AB underwent MLST.

SUMMARY AND CONCLUSION

There was a high rate of misidentification of the Acinetobacter subspecies causing invasive infections in children.

CC92 is the dominant strain causing invasive AB infections in children in South Korea after 2010.

Correct identification and effective measures to prevent the spread of AB are urgent, especially as they are a threat to the most vulnerable patients in healthcare settings.

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Misidentification Rate of Acinetobacter baumannii Isolated from Invasive Infections in Children
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OBJECTIVES

The primary objective of this study was to examine the rate of misidentification of AB isolated from invasive infections in children.

The secondary objective was to observe the clinical types and relationships of AB strains isolated from these patients.

MATERIALS AND METHODS

From January 2001 to December 2017, patients 18 years old and below who were treated for invasive AB infections at Seoul National University Hospital were included.

All isolates identified as AB by commercial identification systems, cultured from sterile body fluids of the study participants, were prospectively collected and stored at -70°C.

The stored bacteria were sub-cultured and DNA was isolated. The subpopulations were identified by PCR amplification and sequencing of the rpoB gene.

For isolates identified as AB through sequencing of the rpoB gene, multi-locus sequence typing (MLST) using the Oxford database (https://pubmlst.org/baumannii) was carried out.

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REFERENCES


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