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A new serotyping method of *S. pneumoniae* using an automated microarray-based assay

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Introduction / objectives

Serotype replacement is a major concern following the introduction of polysaccharide-conjugated vaccine against *S. pneumoniae* and requires a close monitoring in the population. Antibody-based serotyping methods are expensive, semi quantitative, cross-reactions are common and a significant number of isolates cannot be typed. Multiplex PCR-based assays have been developed but quantification of PCR products remains problematic. To address these issues a novel PCR-based automated microarray assay was developed and tested on clinical samples.

Methods

Autolysin, pneumolysin and eight other genes located in the capsular operon were first amplified using multiplex PCR. This step was followed by a tagged primer extension step targeting serotype-specific polymorphisms. The tagged primers were then assigned to a specific spot on a microarray, and processed and scanned in an ISO-certified automated molecular diagnostic system, using a confocal laser microscope. Results from the assay were exported to the analysis software/expert system that transformed genetic typing data into capsular serotype identification.

Results

Using this new technology, 51 serotypes of *S. pneumoniae* can be precisely and uniquely identified, including the 13 types present in the new conjugate vaccine. The remaining 39 are assigned to a serogroup. Blood, CSF and nasopharyngeal samples from children with *S. pneumoniae* infection or carriage were tested and serotype was confirmed by sequence analysis. 26 different serotypes were detected and concordance between both methods was greater than 96%.

Conclusion

This automated microarray assay is robust and could identify precise serotypes of *S. pneumoniae* directly from clinical samples. It is easy to handle and will be most useful in clinical settings and for the evaluation of serotype prevalence changes.

Disclosure of interest

None declared.

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