New tool for Genomic Sequencing of *Bordetella pertussis*

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The spread of antigen-deficient strains may threaten acellular vaccine efficacy. Dynamics of strain transmission are poorly defined because of shortcomings in current strain genotyping methods. The objective of this study was to develop a whole-genome genotyping strategy with sufficient resolution for local epidemiologic questions and sufficient reproducibility to enable international comparisons of clinical isolates.

We defined a core genome multilocus sequence typing scheme comprising 2,038 loci and demonstrated its congruence with whole-genome single-nucleotide polymorphism variation. Most cases of intrafamilial groups of isolates or of multiple isolates recovered from the same patient were distinguished from temporally and geographically cocirculating isolates. However, epidemiologically unrelated isolates were sometimes nearly indistinguishable.

The increasing incidence of pertussis and large outbreaks have been reported recently in many countries (Winter et al. 2014; Crespo et al. 2015; Sealey et al. 2015; Safarchi et al. 2016). The resurgence of whooping cough underlines the need for reinforced surveillance of strain evolution, local spread, and global transmission.

Whole-genome sequencing (WGS) provides the highest possible resolution of genetic differences among individual isolates. A study using WGS of an international collection of *B. pertussis* isolates (Bart et al. 2014) provided a global phylogenetic structure of *B. Pertussis*. This pioneering study found genotype mixing across countries at shallow phylogenetic depth, revealing frequent long-distance spread of *B. pertussis* isolates.

In the present study it was found that temporally or geographically unrelated isolates can be nearly indistinguishable, illustrating the rapid diffusion of isolates through hidden chains of transmission.

We made the cgMLST strategy for *B. pertussis* isolate characterization publicly available through a Web-accessible genotyping platform (http://bigsdb.pasteur.fr/bordetella), providing a novel tool for tracking the international spread of *B. pertussis* variants. (http://bigsdb.pasteur.fr/bordetella), providing a novel tool for tracking the international spread of *B. pertussis* variants.

References


**Comment**

Pertussis is increasingly reported world wide and the discussion of the celler versus the acellular vaccine is still ongoing. There is an urgent need to a international, standardized typing method which can be used to map the spread of the disease and link this to the immunization status of the infected individuals.

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