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Diagnostics, epidemiological observations and genomic subtyping in an outbreak of pullorum disease in non-commercial chickens

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Highlights

- High-throughput sequencing outperforms both PFGE and MLVA for *S. Pullorum* subtyping
- High-throughput sequencing rapidly differentiates *S. Pullorum* and *S. Gallinarum*
- Multiple types discovered suggests persistence of *S. Pullorum* among hobby flocks
- More than one, or a common genetically mixed source for the outbreak is suggested

Abstract

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