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Authors: Helena Eriksson, Robert Söderlund, Linda Ernholm, Lennart Melin, Désirée S. Jansson

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

Helena Eriksson[a,*], Robert Söderlund[b], Linda Ernholm[c], Lennart Melin[b] and Désirée S. Jansson[a]

[a]*Department of Animal Health and Antimicrobial Strategies, National Veterinary Institute, SE-751 89 Uppsala, Sweden*

[b]*Department of Microbiology, National Veterinary Institute, SE-751 89 Uppsala, Sweden*

[c]*Department of Disease Control and Epidemiology, National Veterinary Institute, SE-751 89 Uppsala, Sweden*

[*]Corresponding author. Telephone: +46 18 67 40 00. Fax: +46 18 30 91 62. E-mail address: helena.eriksson@sva.se

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