

Typing of *Riemerella anatipestifer* by Fourier-transform infrared spectroscopy

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BACKGROUND

- ***Riemerella anatipestifer*** (RA) is an important avian pathogen, causing epizootic septicemic diseases, especially in ducks and responsible for significant economic losses
- Autogenous vaccines have become one of the most effective preventive strategies, and strain serotyping during outbreaks is essential for selecting the most appropriate strains to include
- RA displays considerable serotype diversity, which complicates disease control and contributes to recurrent outbreaks
- Currently serotyping is performed by using polyclonal rabbit serum and by molecular methods (e.g. Multi-Locus Sequence Type (MLST)).

AIM

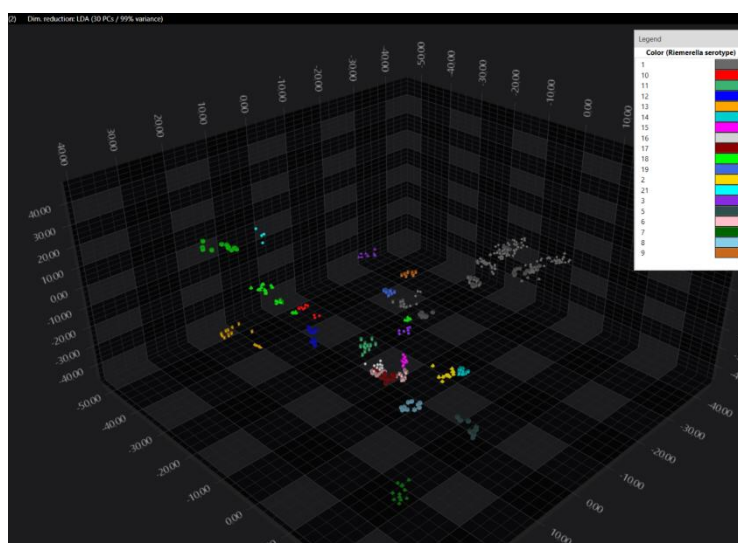
This study aimed to evaluate the potential of Fourier-transform infrared spectroscopy (FTIRS) as a reliable tool for the differentiation of RA at both serotype and sequence type levels.

METHODS

- **STRAINS:** 56 RA, including reference and field strains from outbreaks in avian hosts (turkeys, chickens, ducks and geese) were included in this study .
- **CULTIVATION:** 37 °C for 48 h on blood agar plates in microaerophilic atmosphere.
- **TYPING:** serotyping by rapid agglutination with in house rabbit polyclonal sera (Bisgaard M., 1982) and by MLST (Zhou et al., 2015).
- **FTIR:** spectra acquisition, processing, and analysis were performed using the IR Biotyper® system (IRBT; Bruker Daltonics, Germany). Four spectra from each one of three independent biological replicates were acquired. Similarity analysis was performed by hierarchical cluster analysis (HCA), principal component analysis (PCA) and linear discriminant analysis (LDA).

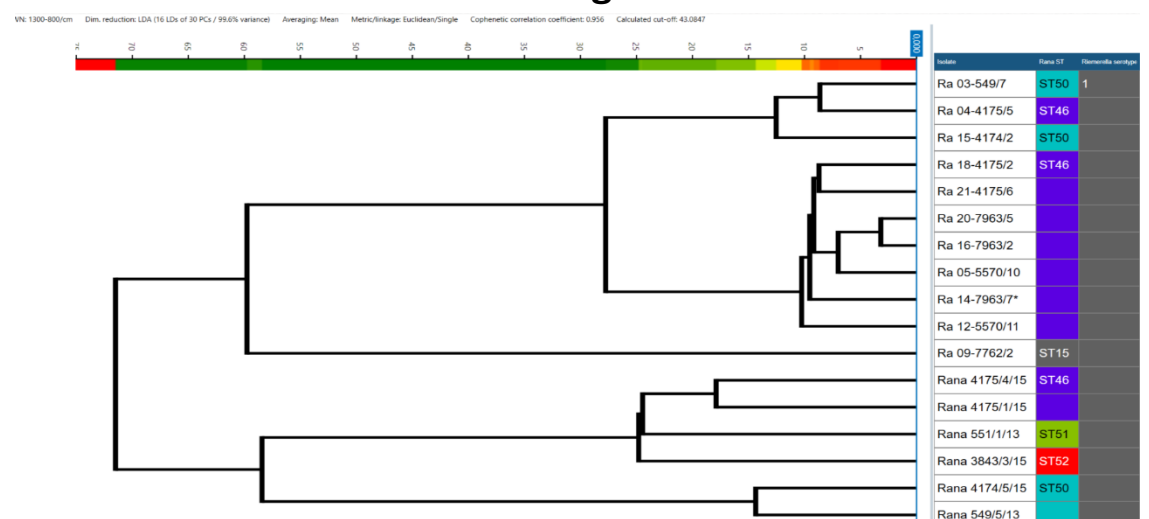
RESULTS

3D scatterplot



IRBT analysis showed the clear separation of all 19 RA serotypes in the multidimensional space.

Subclustering of ST1 isolates



Within serotype 1, the most prevalent and virulent serotype, encompassing multiple sequence types (46, 15, 50, 51, and 52), further sub-clustering was observed, correlating with the different sequence types.

CONCLUSIONS

IRBT proved to be a highly promising tool for the rapid and reliable detection and tracking of RA outbreaks, demonstrating high discriminatory power, with differentiation observed even within sequence types. However, these preliminary findings require validation using a larger number of strains, and the integration of automated machine learning-based approaches could enable FTIR to become a routine typing method.