

MALDI-TOF mass spectrometry applied to sanity in the poultry industry

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Gallibacterium anatis can cause respiratory, reproductive, and systemic diseases in poultry, especially under conditions such as immunosuppression or co-infection. Controlling such infections primarily relies on biosecurity measures and vaccination strategies. The production of autogenous vaccines depends on the accurate selection of the disease-causing isolate. Matrix-Assisted Laser Desorption/Ionization-Time of Flight Mass Spectrometry (MALDI-TOF-MS) proteomic phenotyping is an emerging technology for identifying and exploring the diversity of bacterial isolates, and it has wide applications in the veterinary pharmaceutical industry. In this study, a total of 23 samples from poultry showing clinical signs suggestive of G. anatis infection were collected from six different farms located in two Brazilian states, Minas Gerais and São Paulo. Of these, two samples were isolated from breeding birds, four from pre-breeding birds, and 17 from production birds. The isolated colonies were analyzed using MALDI-TOF-MS with a Microflex device to determine the protein profiles of the strains. To create a dendrogram of G. anatis, three isolated colonies were analyzed, and the Main Spectra Projections (MSPs) were compared across the samples using the Biotyper algorithm. The results revealed high protein diversity among the strains, and no complete clustering of samples from the same farm was observed, suggesting significant diversity within strains from the same location. Previous studies highlight how the indiscriminate use of antimicrobials can exert selective pressure on bacterial populations, promoting differentiation among strains. Additionally, biosecurity plays a crucial role in managing this issue. These findings demonstrate the complexity within the G. anatis species and suggest that MALDI-TOF-MS can be a valuable tool for selecting strains for autogenous vaccination. This approach may help mitigate economic losses in the poultry production chain.

References

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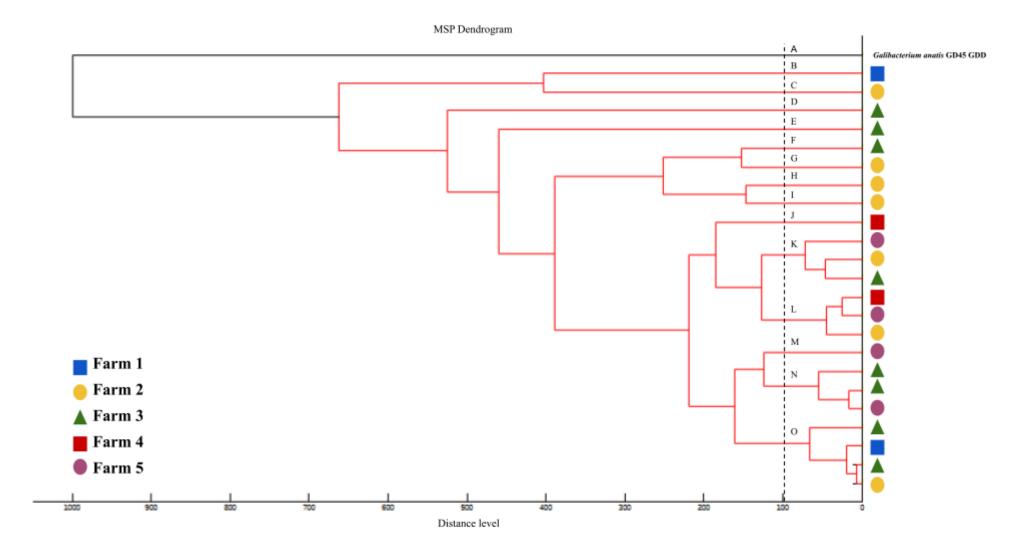




Figure 1: Dendrogram of protein profiles generated using MALDI Biotyper with *G. anatis* sample. The distance measure was defined as mean and the link was defined as distance measure by normality and link by average, which is distance 0 (total agreement in agreement). Dendrogram of the profiles was constructed using MATLAB 7.1 (The MathWorks, Inc.), integrated with MALDI Biotyper 3.1 software.