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Avian Infectious Bronchitis: Viral Control with MiRNAs

Resume :

The research focuses on the avian infectious bronchitis (IBV) virus, cases of which have been on the rise in Quebec since 2015. Indeed, although the virus mainly attacks broilers, it also affects laying hens causing an increase in mortality and the number of secondary infections. In addition, it leads to a reduction in egg production through false layer syndrome, causing heavy losses to the poultry industry, since Quebec supplies around 20% of Canadian production. Combining the nature of the virus, the emergence of new strains between 2015 and 2017 and the difficulty of achieving anything other than local immunity, this research proposes an alternative.

The aim of the proposed project is to explore antiviral strategies against IBV using small regulatory sequences known as microRNAs (miRNAs). The latter are small non-coding RNA sequences whose role is to regulate protein synthesis.

Our objectives are firstly to describe the antiviral responses induced and the miRNAs used by IBV-infected macrophages, and secondly to assess the functions of antigen-presenting cells during infection. Secondly, in silico analysis of the non-coding genes used during infection will help predict the miRNAs with a regulatory impact in order to assess their antiviral activities against several IBV strains. Finally, a possible extension of the research would be to study the regulatory dynamics of antiviral responses in the respiratory and reproductive systems of chickens infected with avian infectious bronchitis virus. The hypothesis of this project is that IBV will modify the expression profile of miRNAs causing an effect, positive or negative, on viral replication. For the relevance of the methodology, first, an avian cell culture will be established as well as the preparation of two IBV viral strains, Mass41 and DMV1639. Then, nitric oxide production and phagocytosis of antigen-presenting cells will be measured before and after infection. In addition, miRNA expression profiles will be assessed by high-throughput sequencing, using our MiSeq (Illumina). Subsequently, the miRNA sequences and their expression profiles will be analyzed via bioinformatics and 5 will be selected for future experiments.