

**Molecular epidemiology of coronavirus in quails raised near to laying hens**

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Although coronavirus has already been detected in quails in Brazil and other countries, knowledge on molecular characterization and epidemiology of this virus in the referred host is poorly known. In Brazil, quails flocks are frequently raised in laying hens properties. Thus, the aim of the present study was to detect coronavirus occurrence in quails raised in laying hens properties, and perform molecular characterization of the detected virus. To this end, pools of lungs, trachea, female reproductive tracts, kidneys and enteric contents were collected from quails flocks co-housed with laying hens, showing IB-like symptoms. Samples were screened for IBV with a RT-PCR to the 3'UTR and positive samples were also submitted to a RT-PCR targeting RNA-dependent RNA-polymerase (RdRp) and a typing-multiplex one. Amplicons of 3'UTR and RdRp genes were sequenced and submitted to distance analysis, with homologous sequences obtained from GeneBank. All avian coronavirus found were classified as variants by multiplex RT-PCR. Based on the DNA sequences for RdRp and 3'UTR regions its possible to conclude that avian coronavirus detected in quails are closely related to avian infectious bronchitis virus. Therefore, it is possible to speculate that quails co-housed with laying hens may be important in avian coronaviruses epidemiology and might interfere on gammacoronaviruses evolution.