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CASE REPORT

Coronavirus–associated enteritis in a quail farm

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ABSTRACT

An enteric syndrome observed in semi-intensively reared quails is described. The affected birds showed depression, severe diarrhoea and dehydration. The mortality occurred particularly in young birds. At necropsy, the prominent lesion was catarrhal enteritis. Laboratory investigations demonstrated the presence of coronavirus in the gut of dead animals. No additional pathogens were detected. To our knowledge, this is the first evidence for the presence of CoVs in quail with enteritis.

Key words: Coronavirus, Quail, Enteritis.

Introduction

Coronaviruses are classified into three major groups on the basis of antigenic and genetic differences (Cavanagh, 2005). A fourth group is formed by coronavirus associated with severe acute respiratory syndrome (SARS) (Kim et al., 2006). All avian coronaviruses (CoV) are classified in group III. Infection by CoV is of high relevance in poultry. CoV-induced diseases have been known since several years. Until recently, only a few species of birds, such as chicken, turkey and pheasant, were believed to be sensitive to CoVs. However, in the last years, CoVs have been detected in the gut of a number of avian species, including guinea fowl, graylag goose, mallard and...
investigations. All samples were examined by negative contrast electron microscopy. The samples were inoculated into the allantoic and amniotic cavities of 10-day embryonated hens' eggs after the addition of antibiotics and antifungicals. Eggs were candled daily to monitor embryo liveability. The fluids were harvested after 5 days. Three sequential passages in embryonated hen's egg were made. RNA extracts were prepared from 100 µl of each specimen (or eggs fluids) with the GeneAmp RNA PCR Core Kit (Applera Italia, Monza). The oligonucleotide primers IN-2 (sense) and IN-4 (antisense) were used for detection of coronavirus RNA by reverse transcription (RT) polymerase chain reaction (PCR) (Ksiasek et al., 2003). The primers target a highly conserved region (1b) of the coronavirus polymerase complex. RT and PCR were performed in a one-step procedure using Superscript III One step (Invitrogen, UK). RT-PCR products were analyzed on agarose gel electrophoresis and stained with ethidium bromide. The RT-PCR product bands were visualized by using UV light.

Results and discussion

The carcasses resulted dehydrated and under-weight. The feathers of the animals were rarefied. At necropsy, catarrhal enteritis was the prominent lesion in all the examined birds. The gut was distended and filled with watery clear content. No additional specific gross lesions were observed. Histopathological examination of the gut confirmed the presence of severe mucosal inflammatory reaction. No specific bacterial and parasitical pathogens were detected in all samples examined. Interestingly, by electron microscopy observation, coronavirus-like viral particles were detected in the gut samples of all the examined animals. The broadly-reactive primers, designed to detect all members within the Coronavirus genus, amplified a 405 bp fragment from the pooled samples and from 3 on 5 gut individual samples, thus confirming the electron microscopy observation. Further
investigations about sequence analysis are actually carrying out. To our knowledge, this could be the first evidence for the presence of CoVs in quail.

Virus growth on chicken embryos was not successful and this may have been due to host species barriers between chicken and quail. For instance, CoVs from graylag geese, mallards and feral pigeons were not cultivatable in chicken embryos (Jonassen et al., 2005). Turkey CoV was adapted to grow in chicken eggs, although with titres 10^4 lower than in turkey embryos (Adams and Hofstad, 1971). Against, CoVs from peafowl and teal were isolated in chicken embryos, replicating at high titres and inducing embryo lesions similar to those of infectious bronchitis virus (IBV), but the viruses were shown to be genetically highly related to IBV (Liu et al., 2005).

It is uncertain whether CoV played a role into the genesis of the enteric syndrome observed in the reared quails. In turkey, CoV is responsible for enteric diseases and may cause high mortality, notably in young birds. In chickens, IBV has a tropism to a broader spectrum of tissues/organs, but often affects the gastrointestinal tract. However, infections by CoV are not necessarily associated with specific clinical signs, as CoVs have been also detected in the gut of normal peafowls and teals (Jonassen et al., 2005; Liu et al., 2005). Similarly, Pasucci et al. (1983) did not necessarily correlate the coronavirus-like viral strains which they found in quails with the respiratory syndrome observed. Accordingly, it is not sure whether CoV was responsible for the enteric syndrome observed in the outbreak herewith described. However, except for CoV, no other specific pathogens were detected in our investigation. The description of CoV in quail rises several questions, as to whether the quail CoV could be a new members of the Coronavirus genus or a CoV from other avian hosts. Epidemiological investigations of the outbreak ruled out the introduction of CoVs in the farm by other avian flocks or farms. CoVs are usually not considered strictly species-specific, as they may replicate in heterologous hosts with or without symptoms. Experimental infections of chickens with turkey CoV may result in asymptomatic virus replication in the gut (Ismail et al., 2003). Likewise, IBV-induced disease usually is observed only in chickens. On the contrary, experimental infection of pigs with feline CoV may result in a syndrome similar to the disease induced by TGEV (Woods et al., 1981).

Conclusions

This is the first description of probable CoV enteric infection in quail. It will be interesting to characterize molecularly the quail CoV to assess whether this is a new CoV or from other avian species. Sequence analysis of viral genome will be useful to clear up this matter. Another important issue is the pathogenic attitude of the quail CoV. The clinical signs and lesions observed in the quails were very similar to those induced by CoVs in turkeys and chickens. Because no other specific pathogen was detected, a pathogenic role of CoV may strongly suggest, although other factors may have been involved in exacerbating the clinical signs. For example, the disease was more severe in the young birds after introduction in the external aviary than in cages. Stress factors such as handling and change of environment may have contributed to increase the severity of the syndrome. Experimental transmission with this pathogen is necessary also in order to address this hypothesis. In addition, it will be paramount to understand the ecology of this novel CoV and to investigate the potential impact in quail breeding.

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