

Detection of the VP6 gene of group F and G rotaviruses in broiler chicken fecal samples from the Amazon region of Brazil

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Abstract The aim of this study was to detect rotavirus F (RVF) and rotavirus G (RVG) in fecal specimens of broiler chickens in Brazil. During 2008 and 2011, a total of 85 fecal samples were collected. The viral genome was extracted, followed by polyacrylamide gel electrophoresis (PAGE), reverse transcription polymerase chain reaction (RT-PCR), and nucleotide sequencing. Samples were screened for rotaviruses by PAGE, and RVF and RVG genome banding patterns were not seen. Using RT-PCR, it was found that 9.4 % (8/85) of the pools contained RVF, whereas 10.6 % (9/85) contained RVG. The predicted amino acid sequences of RVF and RVG from Brazilian samples were 94.4–95.7 % and 96.8–96.9 % identical, respectively, to those of prototypes from Germany. The detection of RVF and RVG in this study provides important epidemiological data about the simultaneous circulation of rotaviruses affecting broiler flocks in the Amazon region of Brazil.

Keywords Rotavirus F · Rotavirus G · RT-PCR · Broiler

Rotaviruses (RVs) are important viral agents associated with acute gastroenteritis in young animals of various

species, including mammals and birds. They may be associated with other enteropathogens in the genesis of disease. In animals, RV infections are often associated with diarrhea outbreaks and can have a significant economic impact because of production losses due to poor weight gain [1–4].

RV infections in birds cause disorders such as enteritis, diarrhea, dehydration, weakness, anorexia, reduced feed conversion and weight gain rates, decreased growth rate, and lack of flock uniformity. They can also cause increased susceptibility to other diseases, increasing medication costs and mortality rates and decreasing egg production, causing serious economic losses to producers and the industries [5–8].

RVs belong to the genus *Rotavirus*, family *Reoviridae*, and possess a genome that is divided into 11 segments of double-stranded RNA (dsRNA) that encode twelve proteins, of which six are structural (VP1–VP4, VP6 and VP7) and six are non-structural (NSP1–NSP6) [9]. VP6 protein is excellent target for laboratory diagnosis, as well as a determinant of nine RV groups/species (A–I) [10, 11]. Birds can be infected by species A, which also infects humans and other mammals, and members of species D, F and G are exclusively associated with birds [12, 13]. Rotavirus F (RVF) and rotavirus G (RVG) are identified based on the migration profiles of their genomic segments in polyacrylamide gel electrophoresis (PAGE), where the RVF and RVG segments produce a 4-1-2-2-2 and a 4-2-2-3 pattern, respectively [14].

RVF and RVG were first described in 1984 by McNulty et al. [15], and although they are relatively common in birds, few studies have characterized these viruses. Until recently, they were described only based on their electrophoretic profiles; however, the complete genome sequences of RVF and RVG have provided new

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