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Nucleotide and deduced sequence analysis of VP2 gene of chicken infectious anemia virus circulating in commercial broiler farms of Northeast Iran

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Objectives: Chicken infectious anemia virus (CIAV) is a ubiquitous resistant virus of chickens causing chicken infectious anemia disease and immunosuppression. It is a small DNA virus with a circular, covalently linked, negative-sense single-stranded genome. The genome has 3 open reading frames encoding 3 viral proteins (VP1, VP2, and VP3). In the present study, samples from commercial broiler chickens from liver, spleen and thymus from Northeast Iran, were screened by PCR and VP2 gene from 14 samples were sequenced and their phylogenetically analyzed.

Materials & Methods: 120 samples from commercial broiler chickens from liver, spleen and thymus in Northeast Iran, were screened by diagnostic primers and then in fourteen positive samples, VP2 gene were processed for nucleotide and deduced amino acid sequence analysis. The edited sequences, along with respected sequences deposited in genetic databases, were compared by multiple alignment and phylogenetic analysis tree, using Benedict software and clustal W program. For phylogenetic analysis blosum 30 matrix, neighbor-joining method with 1000 replicate for bootstrapping were employed.

Results & Conclusion: Similarity and identity between fourteen Iranian sequences and their VP2 counterparts in genetic databases were defined. Based on deduced amino acid sequences of VP2 in phylogenetic tree, fourteen Iranian strains were clustered in two groups. Despite differences detected in deduced amino acid sequence of VP2 and clustering of Iranian strains in at least two clusters, it appears that genotyping based on this gene may not be a great help. It is the first molecular study of VP2 gene of Northeast Iran strains of CIAV amplified from viruses circulating in commercial broiler farms.

Keywords: CIAV, Chicken Infectious Anemia (CIA), VP2, PCR, Phylogenetic Tree

Molecular detection of Avian Nephritis Virus (ANV) in broiler flocks in Iran

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Objectives: Avian nephritis virus has been associated with diarrhea, growth retardation, nephritis and runting-stunting syndrome in broiler chicken. The importance of the virus as causative agent of acute kidney disease has been documented. In this article, for the first time, molecular detection and partial characterization of ANV in broiler baby chickens suffering from kidney lesions is reported in Iran.

Materials & Methods: Forty-eight kidney and feces specimens from affected chickens in broiler flocks with enteritis, kidney lesion and nephritis were collected. RNA were isolated. The integrity of extracted RNA samples was tested. RT-PCR assay employed for ANV detection. RT-PCR assay also conducted for IBV detection on kidney samples. The flocks were inspected for water deprivation and mycotoxicosis. The Amplified products of ANV were sequenced. Nucleotide and deduced amino acid sequence of amplicons were analyzed and compared with counterpart sequences in genetic databases followed by phylogenetic analysis.

Results & Conclusion: No IBV assay was positive. No evidence for water deprivation and mycotoxicosis was found. RNA integrity of extracted RNA samples were confirmed. RT-PCR assay detected 21 positive samples out of 48 samples. Sequence analysis verified the identity of ANV. It showed the highest identity with the nucleotide sequence of ANV in BLAST search. Phylogenetic tree of the Iranian strain clustered with reference ANV strain. Isolation, phenotyping, pathotyping and pathogenecity studies are needed for full characterization of the virus. Significance and economical impact of disease is unknown and has to be assessed. To our knowledge it is a first report of Avian nephritis virus infection with the history of kidney lesions and nephritis, diarrhea, growth retardation in baby chicken in Iran, more specifically in Northeast of country.

Keywords: Avian Nephritis Virus, ANV, Broiler Kidney Lesion, Diarrhea