



Cairo University
Faculty of Veterinary Medicine



**Isolation, antigenic and molecular characterization
of Chicken Anemia virus in Egypt**

A Thesis Submitted by

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Abstract

Chicken Anemia Virus (CAV) is an important pathogen associated with immunosuppression in chicken. In this study, out of samples collected from 115 commercial poultry farms, 12 samples were CAV positive by PCR. Partial sequence and phylogenetic analysis of VP1 gene revealed that the detected viruses were clustered to genotype I (n=3) and genotype II (n=9). Motifs of both low (E144) and high pathogenic strains (T89, I125, Q141) were found in the three viruses of genotype I. Whereas genotype II viruses demonstrated the characteristic motifs of highly pathogenic strains (I75, T89, I125, Q141, and Q144). Three isolates represent the both genotypes (CAV/CA1, CAV/GZ1 and CAV/SK4) were selected for full genome sequencing and results revealed that the VP2 gene had two substitutions at V153 and E 175, while VP3 gene had only one substitution at C118. To evaluate virus pathogenicity, two isolates from each genotype (CAV/SK4 of genotype I and CAV/CA1 of genotype II) were intramuscularly inoculated in two groups of one-day-old specific pathogen free chicks (SPF). Eighteen days post inoculation, PCR detected CAV in 75% and 90% of chicks in group I and II; respectively. Mortalities in inoculated chicks were 5 % and 20 % and packed cell volume (PCV) values were 0.21 and 0.19; respectively. CAV/ CA1 and CAV/ SK4 isolates showed pathogenic evidences at the level of genome (Q141 and 394Q) with variable degree of virulence.

Keywords CAV; Full genome sequence; Genetic characterization; Pathogenicity evidence; Egypt.