Comparative sequence analysis of six independent chicken and turkey parvovirus nonstructural (NS) genes revealed specific genomic regions with 100% nucleotide sequence identity. A polymerase chain reaction (PCR) assay with primers targeting these conserved genome sequences proved to be highly specific and sensitive to detecting parvoviruses in experimentally infected chickens. In a nationwide survey, a total of 138 field enteric samples from poultry flocks were tested by PCR for parvovirus presence. Of the tested chicken samples that were collected in 54 farms, 77% showed the presence of parvovirus, while 78% of the turkey samples that were received from 29 farms were parvovirus positive. For the first time, our data clearly demonstrate that parvoviruses are widely distributed in commercial poultry flocks in the United States. The high prevalence of parvovirus infection in birds from enteric disease-affected flocks suggests a potential role of these viruses in the etiology of enteric disease of poultry. Phylogenetic analyses comparing NS gene segments showed that most of the chicken and turkey parvovirus isolates formed separate phylogenetic groups. These findings suggest that the chicken and turkey parvoviruses might have diverged from a common ancestor and have subsequently undergone host-specific adaptation.

**Abstract**

Comparative sequence analysis of six independent chicken and turkey parvovirus nonstructural (NS) genes revealed specific genomic regions with 100% nucleotide sequence identity. A polymerase chain reaction (PCR) assay with primers targeting these conserved genome sequences proved to be highly specific and sensitive to detecting parvoviruses in experimentally infected chickens. In a nationwide survey, a total of 138 field enteric samples from poultry flocks were tested by PCR for parvovirus presence. Of the tested chicken samples that were collected in 54 farms, 77% showed the presence of parvovirus, while 78% of the turkey samples that were received from 29 farms were parvovirus positive. For the first time, our data clearly demonstrate that parvoviruses are widely distributed in commercial poultry flocks in the United States. The high prevalence of parvovirus infection in birds from enteric disease-affected flocks suggests a potential role of these viruses in the etiology of enteric disease of poultry. Phylogenetic analyses comparing NS gene segments showed that most of the chicken and turkey parvovirus isolates formed separate phylogenetic groups. These findings suggest that the chicken and turkey parvoviruses might have diverged from a common ancestor and have subsequently undergone host-specific adaptation.

**Resumen**

Desarrollo de un procedimiento de reacción en cadena por la polimerasa para la detección de parvovirus de pollo y pavo.

Mediante el análisis comparativo de los genes no estructurales de seis parvovirus de pollo y pavo independientes, se reveló la existencia de regiones genómicas específicas que compartían una identidad del 100% en sus secuencias. Mediante la utilización de iniciadores dirigidos para estas regiones conservadas, se demostró que un procedimiento de reacción en cadena por la polimerasa (de las siglas en inglés PCR) era altamente específico y sensible para detectar parvovirus en pollos infectados experimentalmente. En un muestreo realizado en los Estados Unidos con el fin de detectar la presencia del parvovirus, se analizaron mediante la PCR un total de 138 muestras de intestinos recolectadas en parvadas avícolas en el campo. De las muestras de pollo recolectadas de 54 granjas y que fueron analizadas, el 77% mostró la presencia del parvovirus, mientras que de las muestras recibidas de 29 granjas de pavos, el 78% de las muestras fueron positivas a la presencia de dicho virus. Nuestros datos muestran por primera vez, que los parvovirus están ampliamente distribuidos en las parvadas avícolas comerciales de los Estados Unidos. La alta prevalencia de la infección de parvovirus en aves con problemas entéricos sugiere el papel potencial de estos virus dentro de la etiología de enfermedades entéricas de las aves comerciales. El análisis filogenético que comparó los genes no estructurales mostró que la mayoría de los aislamientos de parvovirus de pollo y pavo se distribuyeron en grupos filogenéticos separados. Estas observaciones sugieren que los parvovirus de pollo y pavo pudieron haber evolucionado a partir de un ancestro común y posteriormente, desarrollaron una adaptación específica para cada huésped.

Abbreviations: bp = base pair; CEF = chicken embryo fibroblast; CEL = chicken embryo liver; DPI = days postinfection; ITR = inverted terminal repeat; LB = Luria Bertani; nm = nanometer; NS = nonstructural; nt = nucleotide; PEC = poult enteritis complex; PEMS = poult enteritis mortality syndrome; PCR = polymerase chain reaction; RSS = runting–stunting syndrome; SEPRL = Southeast Poultry Research Laboratory; SPF = specific-pathogen-free; VP = viral protein