First Report of Hepatitis E Virus Circulation in Domestic Pigs in Nigeria

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Abstract. Hepatitis E virus (HEV) is an important cause of acute hepatitis in humans. Zoonotic transmission between pigs and humans has been confirmed. Human HEV infection is common in Nigeria; however, characterization of HEV infection in other species was lacking. The objective of this study was to investigate HEV infection in Nigerian pigs. A total of 286 serum samples from six states in Nigeria were tested for presence of anti-HEV IgG. Ninety fecal samples from one of these states (Plateau State) were tested for presence of HEV RNA. The overall prevalence of anti-HEV IgG-positive or suspect-positive pigs was 55.6% (159 of 286) with regional prevalence rates ranging from 36% (9 of 25; Delta State) to 88% (22 of 25; Taraba State). The overall HEV RNA prevalence rate was 76.7% (69 of 90). All polymerase chain reaction-positive samples belonged to HEV genotype 3 based on sequencing. The results indicate that HEV genotype 3 infection is widespread in Nigerian pigs.

INTRODUCTION

Hepatitis E, a usually self-limiting but occasionally fulminant hepatitis is an important public health concern in low- and middle-income countries worldwide. Hepatitis E is the single most important cause of acute clinical hepatitis among adults throughout Central and Southeast Asia and the second most important cause throughout the Middle East and North Africa following hepatitis B. Models derived from epidemiologic and clinical studies project a conservative estimate of the annual impact of hepatitis E to include ~3.4 million symptomatic and clinical cases. The etiologic agent of hepatitis E is hepatitis E virus (HEV), classified as a member of the genus Hepevirus, family Hepeviridae. The virus is a non-enveloped, single-stranded positive-sense RNA virus that contains three open reading frames (ORFs). ORF1 encodes proteins for non-structural proteins, ORF2 encodes for the capsid protein, and ORF3 encodes for a multi-functional small protein.

Currently, HEV has at least four recognized genotypes capable of infecting humans. The HEV genotypes 1 and 2 are restricted to humans and related to waterborne large outbreaks of hepatitis E in developing countries with poor sanitation conditions. Genotype 1 is primarily found in North Africa and Central and South Asia. Genotype 2 circulates in Mexico and West Africa. Genotype 3 circulates worldwide and contains strains from sporadic, cluster, and chronic cases of hepatitis E in humans and strains from pigs and wild boars, which are considered the most important reservoirs for HEV. Genotype 4 circulates mainly in Asia; however, it has been reported recently in Europe and includes strains from sporadic and cluster cases of hepatitis E in humans and strains from pigs.

In Africa, HEV is still an emerging pathogen. The very low rate of reporting is the result of suboptimal investigations and neglect of the disease and its public health problem. The majority of available reports describe human HEV outbreaks in North Africa and there are few reports from Uganda.

Central African Republic, the Democratic Republic of the Congo, Sudan, South Sudan and Kenya. Available information on HEV infection in animals in Africa is very limited. Two reports describe detection of HEV in pigs in the Democratic Republic of the Congo and in Cameroon, indicating increased awareness, surveillance, and widespread nature of the virus in the environment. The only available characterized isolate of a human HEV case in Nigeria belongs to genotype 2. This particular genotype is commonly linked to human outbreaks. As in other African countries, the HEV infectious status of pigs in Nigeria is largely unknown. The objective of this study was to characterize HEV infection in pigs of various ages from the main pig farming regions in Nigeria.

MATERIALS AND METHODS

Samples. Samples used in this study included 176 blood samples from apparently healthy pigs collected at slaughter at the Jos main abattoir, located in the Plateau State, from January 2011 to January 2012. The samples were obtained from pigs that were 4 months to 3 years of age. The pigs came from different farming systems including intensively raised pigs and alternative free ranging pigs. All blood samples were stored on ice before being transported to the laboratory. Serum was decanted after centrifugation and stored at -80°C until use. In addition, archived serum samples (N = 112) collected in 2009 for an African swine fever virus survey were also used. The archived serum samples were from 6 months to 3-year-old pigs from the following five states: Delta (N = 25), Oyo (N = 24), Ogun (N = 19), Lagos (N = 17), and Taraba (N = 25) (Figure 1A). Serum samples were unrelated to fecal samples.

Nine fecal samples from each of 10 different regions within the Plateau State including Barkin Ladi, Bassa, Bokkos, Jos North, Jos South, Langtag North, Langtag South, Mangu, Pankshin, and Shendam were also included (Figure 1B) resulting in a total number of 90 samples tested. Sampled pigs ranged from 1 to 6 months of age (average ± SD, 3.35 ± 1.25) (Table 1). Each sample within a given area corresponded to a different farm.

Anti-HEV immunoglobulin G (IgG) enzyme-linked immunosorbent assay (ELISA). All serum samples were tested for anti-HEV IgG using an ELISA protocol previously described. In brief, a commercially available Escherichia coli-derived
Figure 1. Geographic origin of the samples tested in this study. (A) Map of Nigeria indicating the states where samples were obtained for serology. (B) Map of the Plateau State indicating the regions where samples were obtained for detection of HEV RNA.
recombinant protein of the HEV ORF2 (Genway, San Diego, CA) was used to coat the plates. Each well of a microtiter plate (Nunc, Thermo Fischer Scientific, Inc., Rochester, NY) was coated with 100 µL of the antigen at a concentration of 0.6 µg/mL in phosphate buffered saline (PBS). The plates were incubated at room temperature overnight. The microtiter plate was washed three consecutive times with PBS containing 0.05% Tween-20 and subsequently blocked with 1% fetal bovine serum (FBS) (Gibco, Grand Island, NY). Serum samples at a dilution of 1:100 with PBS containing FBS were added into each well and incubated for 30 min at 37°C. The plates were washed three times and 100 µL of a 1:25,000 dilution of horse radish peroxidase goat anti-swine IgG conjugate (Jackson ImmunoResearch, Inc., Groove, PA) was added into each well and incubated at 37°C for 30 min. Plates were again washed and the reaction was visualized by using tetramethylbenzidine-hydrogen peroxidase as substrate (KPL, Gaithersburg, MD). The reaction was terminated after 15 min by adding 2.5 M sulphuric acid to each well and the plates were read at 450 nm using a spectrophotometer. Three internal controls, a positive control, a negative control, and a cut-off control, originating from pigs negative for HEV and pigs infected experimentally with HEV genotype 3 as described were included on each plate. Cut-off controls were determined by means of a detailed receiver operating characteristic (ROC) curve analysis as described elsewhere. When the internal cut-off control value was within the expected range (0.50–0.54), the run was considered valid and the sample results were used. The results were calculated as “antibody index” (sample optical density [OD]/cut-off serum mean OD) with results < 0.9, 0.9–1.0, and ≥1.1 defined as negative, inconclusive, and positive, respectively.

RNA extraction. Total nucleic acid extraction was carried out on 50 µL fecal supernatant using the MagMAX 96 Viral Isolation kit (Ambion, Foster City, CA) according to the manufacturer’s instructions on an automated extraction platform (KingFisher Flex; Thermo Scientific, Waltham, MA). A negative control (nuclease-free water) and a positive control (fecal suspension from pigs experimentally infected with HEV genotype 3, GenBank accession no. AF082843) kindly provided by Dr. Xiang-Jin Meng, Virginia Polytechnic Institute and State University, Blacksburg, VA were added to each extraction plate. The extracted RNA was stored at −80°C until use.

Real-time reverse transcriptase (RT)-PCR assay. The real-time RT-PCR targeting the HEV ORF3 region was carried out in a 96-well plate using the TaqMan One-Step RT-PCR Master Mix Reagent (Applied Biosystems, Foster City, CA) in a 25 µL volume comprising 5 µL of extracted RNA and 20 µL of master mix according to the manufacturers’ recommendation using the following primers and probe: JVHEV-F (5’-GTTGGTTTTCGAGGTTGGAC-3’); JVHEV-R (5’-AGGGGGTTGGATGAA-3’); JVHEV-P (5’-FAM-TGATTTCAGGGCTTGC-G-HQ-3’). One-step RT-PCR amplification was performed on an ABI 7500 real-time PCR instrument (Applied Biosystems) under the following conditions: 30 min at 50°C for the RT reaction, 15 min at 95°C followed by 45 cycles at 95°C for 15 s for denaturation and 60°C for 45 s for annealing and extension. A sample was considered negative if the cycle threshold (Ct) was ≥41 amplification cycles. A no template control (nuclease-free water) and a positive HEV RNA control were added to each PCR plate. The positive control had an expected Ct value of 28.

Conventional nested RT-PCR assay. At least one sample per geographic region and all samples with real-time RT-PCR Ct values lower than 35 were selected for amplification by a conventional nested RT-PCR using primers targeting an ORF2 fragment as described. Briefly, 6 µM each of primers 3156N (5’-AATTATTGCGATYCGRGTGGT-3’) and 3157N (5’-CCCTTTRCTGCTGMCATCTCTC-3’) and OneStep RT-PCR kit (Qiagen, Valencia, CA) were used. The thermalycler conditions for the first reaction were as follows: 50°C for 30 min, 95°C for 15 min, 35 cycles of 94°C for 30 s, 55°C for 30 s, and 72°C for 1 min, and a final elongation step at 72°C for 10 min. The second reaction was performed with 0.2 µM each of primers 3158N (5’-GWTATCGTCTGCA TWCATGCTGCT-3’) and 3159N (5’-AGGGCAGAAATCA ATTTGCTGCT-3’) and ReadyMix Taq PCR Reaction Mix (Sigma-Aldrich, St. Louis, MO). The thermal cycler conditions for the second PCR reaction were as follows: 95°C for 5 min, 35 cycles at 94°C for 30 s, 55°C for 30 s, and 72°C for 30 s, and a final elongation step at 72°C for 7 min. The 348 nucleotides (nt) second round PCR products were visualized after electrophoresis on a 1% agarose gel. To avoid contamination, the following precautions were taken: each step of the experimental procedure, reaction mixture preparation, RNA preparation and extraction from the samples, first reaction of the RT-PCR amplification, pipetting of the first reaction template to the second PCR reaction, and analysis of the PCR products, was performed in separate rooms. Separate disposable filter tips, which were changed for each step and sample, were used throughout the entire experimental procedure. In addition, all procedures with the exception of the gel analysis were performed inside a biosafety cabinet level 2. To exclude carryover contamination, at least three negative controls, including a no RNA template control, were tested together with the actual samples in each RT-PCR run.

Sequencing and phylogenetic analysis. Sequencing of HEV RNA positive samples was performed directly on both strands at the Iowa State University DNA Facility, Ames, IA. Sequences were aligned with published data using the basic local alignment search tool (BLAST) at the National Center for Biotechnology Information (NCBI, http://www.ncbi.nlm.nih.gov/). Sequences were compiled using Lasergene software and the Clustal W alignment algorithm (DNASTar, Madison, WI). For sequence analysis, the 310 nt sequences of the 5’ end of the ORF2 gene were compared with each other and to sequences of genotype 3 HEV isolates from Cameroon.

Table 1
Prevalence of HEV RNA positive samples in fecal samples collected in different regions of the Plateau State. Each sample in a given region was collected from different farms within the specified region. Data presented as percentage (total number of positive samples).

<table>
<thead>
<tr>
<th>Region</th>
<th>Number tested</th>
<th>Age (months)</th>
<th>Positive</th>
</tr>
</thead>
<tbody>
<tr>
<td>Barkin Ladi</td>
<td>9</td>
<td>2–4</td>
<td>88.9% (8)</td>
</tr>
<tr>
<td>Bassa</td>
<td>9</td>
<td>1–6</td>
<td>88.9% (8)</td>
</tr>
<tr>
<td>Bokkos</td>
<td>9</td>
<td>2–6</td>
<td>88.9% (8)</td>
</tr>
<tr>
<td>Jos North</td>
<td>9</td>
<td>2–4</td>
<td>77.8% (7)</td>
</tr>
<tr>
<td>Jos South</td>
<td>9</td>
<td>2–4</td>
<td>66.7% (6)</td>
</tr>
<tr>
<td>Langtang North</td>
<td>9</td>
<td>2–4</td>
<td>77.8% (7)</td>
</tr>
<tr>
<td>Langtang South</td>
<td>9</td>
<td>2–5</td>
<td>77.8% (7)*</td>
</tr>
<tr>
<td>Mangu</td>
<td>9</td>
<td>2–6</td>
<td>66.7% (6)*</td>
</tr>
<tr>
<td>Pankshin</td>
<td>9</td>
<td>2–5</td>
<td>77.8% (7)</td>
</tr>
<tr>
<td>Shendam</td>
<td>9</td>
<td>2–3</td>
<td>55.5% (5)*</td>
</tr>
<tr>
<td>TOTAL</td>
<td>90</td>
<td></td>
<td>76.7% (69)</td>
</tr>
</tbody>
</table>

*The presence of HEV was confirmed by sequencing of one reverse transcription-polymerase chain reaction (RT-PCR) positive sample from the Langtang South region, three from the Mangu region, and one from the Shendam region.
HEV RNA was identified in Nigerian pigs and belongs to genotype 3. The PCR results are summarized in Table 1. Samples positive for HEV RNA were identified in all regions and pig populations tested. A total of 15 samples were selected for follow-up sequencing. Among these, eight samples could be amplified using the nested RT-PCR and five yielded a sequence. Sequencing confirmed that all of the positive samples belonged to HEV genotype 3 (Figure 2). Sequencing results on one sample from the Langtang South region, three from the Mangu region, and one from the Shendam region indicated that the strains in this study had 99.3% to 92.5% nucleotide identities for the 310 nt fragment of the 5’ end ORF2. Specifically, the MG25 and MG18 samples shared 99.3% of nucleotide identity with each other, 97.2% with LS13, 94.8% with SHD50, and 92.5% with the MG7 sample. Between sequences described here and other available African pig HEV sequences, there was 85.2–89.6% nucleotide identity (GenBank accession nos. KC012634 and FJ600536). The HEV sequences reported herein were closely related to strains from Japan (GenBank accession no. AB094231) and from the Netherlands (GenBank accession no. AF332620) with 90.5–94% and 88–92.2% nucleotide identity, respectively.

**RESULTS**

Evidence of seroconversion to HEV in Nigerian pigs. The HEV ELISA results are summarized in Table 2. The overall prevalence of anti-HEV IgG was 47.2% (135 of 286) among the samples. Although anti-HEV antibodies were detected in pigs in all states tested, there were regional differences. Particularly in the Ogun and Taraba States the prevalence of HEV positive pigs was 73.7% (14 of 19) and 88% (22 of 25), although it was only 36% (9 of 25) in the Delta State. An association between the type of husbandry and HEV infection detection could not be established (data not shown).

**Table 2**

<table>
<thead>
<tr>
<th>State</th>
<th>Number tested</th>
<th>Sample source</th>
<th>Age (months)</th>
<th>Positive</th>
<th>Suspect</th>
<th>Negative</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plateau</td>
<td>176</td>
<td>Abattoir</td>
<td>&lt;5</td>
<td>66.7% (10)</td>
<td>0</td>
<td>33.5% (5)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>5–8</td>
<td>37.5% (18)</td>
<td>8.3% (4)</td>
<td>54.2 (26)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>8–12</td>
<td>41.2% (21)</td>
<td>3.9% (2)</td>
<td>54.9% (28)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>&lt; 12</td>
<td>56.5% (35)</td>
<td>4.8% (3)</td>
<td>38.7% (24)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Total</td>
<td>50.6% (89)</td>
<td>4% (7)</td>
<td>45.5% (80)</td>
</tr>
<tr>
<td>Delta</td>
<td>25</td>
<td>Farms</td>
<td>Unknown</td>
<td>20% (5)</td>
<td>16% (4)</td>
<td>64% (16)</td>
</tr>
<tr>
<td>Lagos</td>
<td>17</td>
<td>Farms</td>
<td>Unknown</td>
<td>29.4% (5)</td>
<td>23.5% (4)</td>
<td>47.1% (8)</td>
</tr>
<tr>
<td>Ogun</td>
<td>19</td>
<td>Farms</td>
<td>Unknown</td>
<td>63.2% (12)</td>
<td>10.5% (2)</td>
<td>26.3% (5)</td>
</tr>
<tr>
<td>Oyo</td>
<td>24</td>
<td>Farms</td>
<td>Unknown</td>
<td>20.8% (5)</td>
<td>16.7% (4)</td>
<td>62.5% (15)</td>
</tr>
<tr>
<td>Taraba</td>
<td>25</td>
<td>Farms</td>
<td>Unknown</td>
<td>76% (19)</td>
<td>12% (3)</td>
<td>12% (3)</td>
</tr>
<tr>
<td>TOTAL</td>
<td>286</td>
<td></td>
<td></td>
<td>47.2% (135)</td>
<td>8.4% (24)</td>
<td>44.4% (127)</td>
</tr>
</tbody>
</table>

*Data presented as percentage (total number of positive samples).*

In Nigeria, although hepatitis of other viral origin is widely recognized,19–21 the HEV situation is still largely unknown.

**Figure 2.** Phylogenetic tree based on a 310 nucleotide region in the 5’ end ORF2 of the HEV genome. Sequences that were obtained in this study are underlined. The phylogenetic tree was constructed by the NJ method. Significant bootstrap P values are indicated as a percentage for 1,000 replicates.
because incidence of the disease and its etiologic agent are likely underreported. Human HEV genotype 2 infection in Nigeria has been documented\(^1\) and the prevalence of anti-HEV antibodies in humans is \(-13.4\%\).\(^2\) The HEV transmission occurs mainly through the fecal–oral route, and pigs have been established to be reservoirs. The objective of this study was to characterize HEV infection by determining the presence of anti-HEV antibodies and RNA in Nigerian pigs.

Pig husbandry systems in Nigeria are similar to what is currently used in Asia and South American countries where HEV has been identified in pig populations.\(^1,2\) In Nigeria, the husbandry systems practiced include intensive, semi-intensive, and extensive or free range farming\(^2\) where pigs are either housed or allowed to roam freely to scavenge for food. In the free range system, pigs travel far in search of food and water. They visit waste heaps and stagnant or flowing water bodies thereby contaminating such areas with feces and urine. These husbandry systems predispose pigs to diverse infections including HEV and thus facilitate subsequent transmission to humans, especially in environments where there is close association of pigs and people. However, an association between the type of husbandry and HEV infection detection could not be established herein.

Presence of HEV antibodies and HEV RNA was demonstrated in varying proportions of pigs in several important pig rearing regions in Nigeria. There was a high detection rate of HEV RNA in fecal samples from 2 to 6 months old pigs; however, pigs in Nigeria are usually slaughtered at 9 months of age. Further studies testing samples of pigs at different ages need to be done to verify the shedding of HEV RNA, especially in pigs at slaughter age.

Similar to other reports in Africa, HEV genotype 3 was identified.\(^12,13\) Interestingly, strains characterized in this study presented a higher nucleotide identity with Japanese and European HEV strains than with published African strains. Indeed, HEV transmission from one country to another through international trading has been previously discussed in Asia, South America, and Africa.\(^12,25\) The majority of the pigs raised in Nigeria belong to the pure Nigerian local pig breed, although crossbreeds between the local breed and Large White, Hampshire, or Landrace\(^2\) imported from North America and Europe are common. The HEV genotype 3 recovered in this study could potentially be traced back to European pigs but more information is needed to confirm this.

Both HEV genotype 3 and 4 circulate in pigs and are also associated with sporadic HEV infections in humans, whereas genotypes 1 and 2 are mainly linked to human epidemics.\(^6,8\) In addition to reports of large hepatitis E outbreaks in Africa, sporadic hepatitis E in Africa has been reported in Nigeria, Kenya, and Egypt. In these cases, routes of HEV transmission were not documented, and the extent of sporadic hepatitis E in Africa remains largely unknown. Food-borne transmission of HEV through consumption of raw or undercooked pork meat and entrails in high-income countries has been extensively documented.\(^8\) In contrast to countries in which pork is traditionally consumed raw, in Nigeria meat products are usually well-cooked and served in the form of stew and very often are conserved in salt for preservation. Cooking of the meat thoroughly is the most efficient method to inactivate HEV and to prevent food-borne HEV infection in humans.\(^5\) However, foodborne transmission cannot be ruled out as a possible transmission route in Nigeria.

To the authors’ knowledge this is the first report of characterization of HEV infection in pigs in Nigeria.

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