



Short communication

Foot-and-mouth disease virus strains and examination of exposure factors associated with seropositivity of cattle herds in Nigeria during 2007–2009

Folorunso O. Fasina^{a,*}, Dana R. Connell^b, Oladele A. Talabi^c, David D. Lazarus^{a,e}, Gabriel A. Adeleke^d, Taiwo P. Olusanya^d, Jorge A. Hernandez^b

^a Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Onderstepoort 0110, South Africa

^b Department of Large Animal Clinical Sciences, College of Veterinary Medicine, University of Florida, Gainesville, FL, USA

^c College of Veterinary Medicine, University of Agriculture, Abeokuta, Ogun State, Nigeria

^d Department of Animal Production, Olabisi Onabanjo University, Ogun State, Nigeria

^e National Veterinary Research Institute, Vom, Plateau State, Nigeria

ARTICLE INFO

Article history:

Received 7 June 2012

Received in revised form

25 September 2012

Accepted 9 October 2012

Keywords:

FMD

Case-control

Nigeria

Cattle

ABSTRACT

New outbreaks of foot-and-mouth disease (FMD) occurred in cattle herds in Nigeria during 2007–2009. The objectives of the study reported here were: (i) to identify current FMD virus strains circulating in cattle herds and (ii) to identify exposure factors associated with a seropositive diagnosis of FMD in cattle herds. This study provides evidence that FMD virus serotypes O, A and SAT-2 were co-circulating in cattle herds in Nigeria during 2007–2009. Cattle herds in a neighborhood affected with FMD had higher odds of being classified as seropositive to FMD, compared to herds that were in a neighborhood not affected with FMD (OR = 16.27; 95% CI = 3.61, 18.74; $P < 0.01$). Cattle herds that share water points along the trek routes with other cattle herds had higher odds of being classified as seropositive to FMD (adjusted OR = 4.15; 95% CI = 0.92, 18.74; $P < 0.06$). Results from this study can be used by veterinary services in Nigeria and neighboring countries to evaluate current or future FMD control and eradication programs.

© 2012 Elsevier B.V. All rights reserved.

1. Introduction

Foot and mouth disease virus (FMDV) is an RNA virus of the *Picornaviridae* family that naturally infects cattle and other livestock species, causing an acute illness characterized by lameness and vesicular lesions in the buccal cavity, interdigital space and teats. There are seven FMDV serotypes worldwide (O, A, C, Southern African Territories: SAT-1, SAT-2, and SAT-3, and Asia-1). The genome is over 8 kb in length and encode four structural proteins (SPs, VP1, VP2, VP3 and VP4) that form an icosahedral capsid, and a total of ten mature nonstructural proteins (NSPs) (L, 2A, 2B,

2C, 3A, 3B, 3C, 3D; or some complex, such as 3AB or 3ABC) (Mason et al., 2003; Ma et al., 2011).

Foot-and-mouth disease (FMD) is considered one of the most contagious diseases affecting economically important livestock species such as cattle, sheep, and pigs in the 2007 Terrestrial Animal Health Code by the World Organization for Animal Health (Office-International-des-Epizooties) (Orsel et al., 2009). Although FMD is reported worldwide, it is particularly endemic in sub-Saharan Africa, with widespread outbreaks of clinical disease occurring almost yearly (Sahle et al., 2004; Rweyemamu et al., 2008). In sub-Saharan Africa, two cycles of FMD occur: one where the virus circulates between wildlife and domestic animals and the other where the virus spreads among domestic animals (Vosloo et al., 2004). In southern Africa and eastern Africa, the cycle between wildlife and domestic

* Corresponding author. Tel.: +27 12 529 8069; fax: +27 12 529 8396.
E-mail address: daydupe2003@yahoo.co.uk (F.O. Fasina).

animals occurs, while in West Africa, due to the low numbers of wildlife, the disease is maintained mainly in domestic animals. Six serotypes (A, O, C, SAT-1, SAT-2, and SAT-3) have been identified in Africa and four in West Africa (A, O, SAT-1, and SAT-2) (Sangare et al., 2004). Disease control has become more complicated because of marked regional differences in the distribution and prevalence of various serotypes and topotypes (Knowles and Samuel, 2003; Vosloo et al., 2004; Sahle et al., 2004).

Foot-and-mouth disease was first reported in Nigeria in 1924 in sporadic outbreaks in cattle herds attributed to serotype O virus (Libeau, 1960). Subsequently, other serotypes (A, SAT-1 and SAT-2) were identified, and each of these introductions was associated with trade of cattle entering Nigeria from neighboring countries (Owolodun, 1971; Nawathe and Goni, 1976; Durojaiye, 1981). The disease remains endemic because other transboundary animal diseases (rinderpest, African swine fever, highly pathogenic avian influenza) have been assigned higher priorities by Nigeria's national veterinary services, movement of cattle is not controlled, and vaccination is not practiced except for a few established farms that have exotic animals. Control and eradication of FMD in Nigeria is important to meet a growing population's high demand for animal protein and to access regional and international markets of animals and animal products. During 2007–2009, new outbreaks of FMD occurred in cattle herds in Nigeria. The objectives of the study reported here were: (i) to identify current FMD virus strains circulating in cattle herds and (ii) to identify exposure factors associated with a seropositive diagnosis of FMD in cattle herds.

2. Materials and methods

2.1. Study site

Nigeria is a West African country that shares largely uncontrolled land borders with the Republic of Benin in the west, Chad and Cameroon in the east, and Niger in the north. Its coasts lie on the Gulf of Guinea in the south and it borders Lake Chad to the northeast. The country has a cattle population of ~16 million (FAO, 2012a,b) aside the countless heads of cattle that cross the various borders into the country daily. The country serves as a major meeting point for most of cattle arriving from certain West and Central African countries (Sumption et al., 2007) in view of the abundant feed resources, the enormous human population, geographic contiguity to many countries and the relative wealth/purchasing power of the country in the sub-region.

The majority of the Nigerian cattle move from the extreme north of the country down toward the south traversing the Sahel Savannah, Sudan Savannah, Guinea Savannah, the sub-humid and the humid belts of the country largely in search of available feed resources (Fadiga et al., 2011). The study cattle populations based on residency of the animals include the:

- (i) Sedentary (cattle population that are managed under a semi-intensive system, they are resident near human habitats and only rarely move within a few kilometers from human populations. Feedstuffs and water are

often provided for the animals but animals are supplemented by grazing).

- (ii) Pastoralist (the majority of Nigerian cattle which mainly traverses the national, state and other boundaries in search of food and water. These extensively raised animals and their owners move through the different ecoclimatic zones and sometimes come into contact with wildlife and human habitats on their ways. The owners are often involved in conflicts with arable farmers due to damage to the crops of the latter).
- (iii) Cattle market (animals that may originate from any two of the above but are resident in or around the livestock markets. Such markets are well established in major cities, main boundaries and certain points along the trek routes and operators of such markets often keep a few cows which they sell from time to time).
- (iv) Others (a not well defined system of cattle residency which may be a mix of the defined populations above).

2.2. Identification of FMD virus strains

Between 2007 and 2009, cattle herds affected with FMD-like clinical signs (vesicular lesions in the mouth, nares, muzzle, feet and teats, excessive salivation, lameness) or oral lesions (crusting of the muzzle and erosion or ulceration of the oral mucosa) were reported to the National Veterinary Research Institute (NVRI) in Vom, Nigeria. NVRI veterinarians were assigned to conduct a disease herd investigation. During the investigation, blood serum, epithelial and vesicular fluid samples were collected from 3 to 5 affected cattle for diagnosis of FMD. In the field, an attempt was made by the attending NVRI veterinarian to collect and transport epithelium and vesicular fluid for diagnosis of FMD following Office International des Epizooties guidelines (Kitching and Donaldson, 1987). Due to funding limitations, logistics, location accessibility and work load, it took 1–28 days from the time a farmer reported the presence of animals in his/her herd with FMD-like lesions or oral lesions until the field investigation was conducted.

At the NVRI, blood serum samples were processed for detection of FMDV non-structural protein (NSP) antibodies using an ELISA test (3-ABC ELISA; Prionics, Lelystad B.V., The Netherlands) and recommended procedures (Brocchi et al., 2006). The test detects antibodies to the FMD NSP 3-ABC antigens (expressed as a recombinant antigen using a Baculovirus) which are directly coated onto a microplate. The optical density (OD) of the ELISA results was measured at 450 nm on a Multiskan® spectrophotometer (Thermo Scientific, USA), and the results were expressed as Percentage Inhibition relative to the OD₄₅₀ max. Samples with PI ≥ 50% were considered positive, while PI < 50% negative using the formula: $PI = 100 - [OD_{450} \text{ test sample} / OD_{450} \text{ max}] \times 100$ (Sorensen et al., 1998).

The 3-ABC ELISA test is used to differentiate FMD-infected from FMD-vaccinated cattle. Foot-and-mouth disease virus infection in cattle induces antibodies against both structural proteins (SP) and NSP. Cattle vaccinated with a NSP-free vaccine produces antibodies against SP, but not against NSP. A seropositive result is an indication of previous exposure of cattle to FMDV. The

Download English Version:

<https://daneshyari.com/en/article/5793912>

Download Persian Version:

<https://daneshyari.com/article/5793912>

[Daneshyari.com](https://daneshyari.com)