Avian infectious bronchitis virus in Africa: a review

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ABSTRACT
Infectious bronchitis virus (IBV) is worldwide in distribution, highly infectious, and extremely difficult to control because it has extensive genetic diversity, a short generation time, and a high mutation rate. IBV is a Gammacoronavirus, single-stranded, and positive-sense RNA virus. Avian infectious bronchitis is well studied in European countries with identification of a large number of IBV variants, whereas in African countries epidemiological and scientific data are poor and not updated. However, previous studies reported that an IBV variant continues to appear regularly in Africa, as currently described in Morocco. No cross-protection between IBV strains was reported, some being unique to a particular country, others having a more general distribution. This review aims to provide a general overview on IB disease distribution in African countries and an update on the available studies of IBV variants in each country.

KEYWORDS
Poultry; chicken; avian; infectious bronchitis virus; IBV; Africa; review

1. Introduction
Avian infectious bronchitis (IB) is an acute, highly contagious disease with severe economic consequences in poultry industry worldwide (Cavanagh 2007). The causative viral agent of IB is a member of the Gammacoronavirus genus, formerly Group 3, within the Coronaviridae family, and it is the type species of the avian Coronavirus of the domestic chicken (Gallus gallus) (Eterradossi & Britton 2013).

Chickens of all ages may be infected with the infectious bronchitis virus (IBV), and infected chickens show signs of depression, coughing, sneezing, nasal discharge, and death. The virus negatively affects egg production and quality in laying flocks, and deep pectoral myopathy may occur in the broiler breeder (Cavanagh & Naqi 1997). IBV was first reported in the USA for replicating in the respiratory tract and some other epithelial cells of gut, kidney, and oviduct (Cavanagh 2007). Thereafter, IB was reported in other parts of the world (De Wit et al. 2011). Subsequently, some strains of IBV caused pathology in non-respiratory organs (such as kidney and gonads) (Cavanagh 2003; Balestrin et al. 2014).

The transmission of the IBV is horizontal by direct contact with chickens (between sick birds to susceptible birds) or indirect (through wild birds, water, materials, etc) (Cavanagh et al. 2002). In addition, it may persist in small amounts in the cecal tonsils of the intestinal tract in an asymptomatic way during a long time (Alexander et al. 1978). Even if vaccination has been used for several years, protection might not be effective (Jeong et al. 2010).

IBV is an enveloped virus with a single-stranded positive-sense linear RNA molecule (approximately 27.6 kb in size). Its genome consists of five genes encoding the structural proteins, in the following order: 5′-ORF1a / b - S - E - M - N -3′. Two-thirds of the genome consists of two overlapping regions (ORF1a and ORF1b) that encode into the large polyproteins 1a and 1ab, and contribute to the formation of the replication and transcription complex. The structural protein genes are also interspaced by two small genes 3 and 5, which both express two accessory proteins of unknown function numbered 3a, 3b and 5a, 5b, respectively.

The remaining part of the genome consists of regions coding for the four structural proteins: the membrane (M), small membrane (E), nucleoprotein (N), and spike (S). The multimeric coiled-coil S protein is post-translationally cleaved into the amino-terminal S1 (92 kDa) and the carboxyl-terminal S2 (84 kDa) subunits (Lai & Cavanagh 1997).

The S1 subunit protein, which is anchored to the membrane by association with S2, is responsible for the infection of the host cells, is involved in virus entry, and also contains epitopes for virus-neutralizing antibodies and protective immunity (Lai & Cavanagh 1997; Casais et al. 2003). Mutations in S1 gene result in the emergence of new genotypes and serotypes that can be partially or poorly neutralized by existing vaccine serotypes. The sequencing of this gene is the most
useful strategy for the molecular characterization of IBV strains, because it correlates closely with the serotype and permits the selection of the appropriate vaccinal serotypes for IB control in each geographic region (Liu et al. 2003).

Since IBV was first described, several serotypes in addition to the originally identified Massachusetts (MA) type of IBV have been found (Fabricant 1998; Jackwood 2012). The majority of the previously unknown serotypes or variants, identified in the past (two decades) around the world, have either disappeared or become endemic in certain geographical areas (Bochkov et al. 2006), while some of them have become widespread and predominant in the majority of the countries with a significant poultry industry over a period of time (Terregino et al. 2008).

IBV has a wide geographical distribution and it was found in regions of Africa, Asia, Australia, Europe, and the Americas (Cavanagh 2007; Cook et al. 2012; Jackwood 2012). In Africa, IBV is one of the most common viral respiratory diseases of chickens and it is considered an epidemic virus and widely spread both in vaccinated and in unvaccinated poultry farms (Casais et al. 2003; Liu et al. 2003; Jeong et al. 2010). Jones et al. (2004) suggested that North Africa, where variants have been less studied, might be a reservoir of the most important IBV variants (793B, 4/91, CR88) and as such these might be found in European countries as well.

Indeed, the 793B variant has been found to have been present in France since 1985, originating from North Africa (Cavanagh et al. 1992). In line, it has been demonstrated that the 793B genotype was isolated in Morocco for the first time in 1983 (El-Houadfi et al. 1986; Jones et al. 2004). In this review, we report a retrospective overview and an update on the IBV variants found in African countries.

2. Infectious bronchitis in North Africa

IB was described and recognized for the first time in North Africa, especially in Egypt, in the 1950s by Ahmed (1954) from birds showing respiratory signs and confirmed by Eissa et al. (1963) and in Morocco in 1983 by El Houadfi & Jones (1985).

In Egypt, IB was associated with various diseases, including respiratory, and renal and egg production declines, and has continued to be an economically important disease in Egyptian poultry industry. It has been shown serologically that IBV isolates from different poultry farms were closely related to the Massachusetts, Dutch D3128, D274, D-08880, and 4/91 variants (Ahmed 1964; Amin and Moustaggar 1977; Sheble et al. 1986; Bastami et al. 1987; El-Kady 1989; Eid 1998).

This seemed also the case for Morocco where IBV isolates (D, E, F, H, and M) were serologically identified as Massachusetts serotype and were held responsible for the respiratory form of the disease (El-Houadfi & Jones 1985). In addition, El-Houadfi et al. (1986) determined a new genotype, the so-called Moroccan ‘G’ type, which differed serologically from the Massachusetts type. Interestingly, S1 sequence data have shown that IBV ‘G’ is very closely related to 4/91 possibly with a common origin (Jones et al. 2004). The suggestion was made that parts of Africa, where variants were not thoroughly studied, might be a reservoir for such viruses, although the increasing number of variants being reported in other countries indicate that several such reservoirs might exist.

Between 1996 and 2005, researchers in Morocco were promoting molecular genotyping of IBV field strains in order to better understand the pathogenesis of various isolates in circulation. They have demonstrated the circulation of nephropathogenic IBV strains in the country. Thus, Al arabi (2004) conducted a study underlining the relationship between IBV and outbreaks in broiler flocks in Morocco. Three different groups of IBV strains were identified using reverse transcriptase-polymerase chain reaction (RT-PCR) coupled to restriction fragment length polymorphism (RFLP). The isolates were classified into three groups. Group I identified the Massachusetts genotype, and group II and group III contained serotypes that differed from the Massachusetts one. The isolate 12/97 in group III was found to cause severe kidney lesions and a higher mortality level than the isolate 7/97 strain in group II did. Cross-protection studies demonstrated that dual vaccinations using the Massachusetts H120 and 4/91 vaccine strains administered on the first day of coming into existence and then after 14 days, respectively, provided better protection against 12/97 compared with a single vaccination with one vaccine strain. In addition, the 12/97 strain was very similar to the Moroccan G strain previously isolated in 1986 (El-Houadfi et al. 1986).

Continuous research identified five different field IBV nephropathogenic genotypes of which three differed from Massachusetts-type vaccine strains, regarded as three new IBV genotypes, the fourth genotype was similar to the vaccine strain MAS (Massachusetts type), and the fifth genotype was similar to vaccine strain 4/91 (El Bouqdaoui et al. 2005). Subsequently, in 1998, the Egyptian variant ‘Egypt/Beni-Seuf/01’ isolated from broiler flocks vaccinated with H120 and the Israeli variant ‘Israel/720 /99’ were regarded as new IBV genotypes that are suggested to be assigned to as Egypt/Beni-Seuf (Abdel-Moneim et al. 2002). One year later, results of serological identification and characterization by RT-PCR, and genotyping using S1 gene sequence analysis revealed that the Egyptian strain of IB ‘Egypt/F/03’ is closely related to the Massachusetts serotype Beaudette-US, H120, and M41, with high nucleotide sequence identity (Abdel-moneim et al. 2006).
Between 2009 and 2013, a recent study of IB variants in Tunisia was conducted by Bourougaa et al. (2009) using cross-neutralization and molecular tools based on the hypervariable region (HVR) of the S1 gene. The results of this study showed that the Tunisian isolates are closely related to Massachusetts types found in Europe, such as D274 and 793/8.

Susan et al. (2010) showed by isolation in the specific pathogen free (SPF) embryonic egg and characterization by amplification of the S1 gene that the Egyptian nephropathogenic strain of IB was closely related to the IS/1494/06 variant strain.

Around the year 2012, five isolates isolated from Egyptian broiler chickens were characterized by RT-PCR and sequence analysis of HVR 3 of the S1 gene, indicating that three out of the five isolates formed a distinct phylogenetic group with the Egypt/Beni-Suef/01 variant (Var1), suggesting that CK/Eg/BU-2/2011 and CK/Eg/BSU-3/2011 can be considered new IBV variants (Abdel-moneim et al. 2012). The same tools as described previously were used to reveal that IB circulating in Egypt during 2012 was classified into two variant groups. The first group comprised variants from IS/885 and the second group was related to variant vaccine strain viruses such as 4/91 and CR/88121 (Selim et al. 2013). One year later, two emerging variants IBV-CU-2-sp1 and Eg/12120s/2012 were isolated from different Egyptian poultry farms by Afifi et al. (2013) and Arafa et al. (2013), respectively.

IBV was first detected in Libya in 2012, and the phylogenetic data of the gene S1 show a co-circulation of IBV variants in broiler flocks, a part of which have a strong relationship with the Egyptian strains CK/Eg/BSU-2/2011, CK/Eg/BSU-3/2011, and Eg/1212B, whereas the rest are closely related to the Eg/CLEVB-2/IBV/012 and IS/1494/06 strains (Awad et al. 2014).

Recently, Sarah et al. (2014) showed by molecular tools and sequence analysis of HVR3 of the S1 gene, that the Egyptian isolates obtained from broiler chickens suffering from severe renal and respiratory distresses can be considered a variant 2, as described previously (Abdel-moneim et al. 2012). Another phylogenetic analysis of novel IBV isolates by Ashraf et al. (2014) demonstrated that Egyptian IBV field strains isolated from vaccinated chicken farms showed high nucleotide similarities to the IBV-CU-2-SP1 and Eg/12120s/2012 strains. The sequences of these isolates were regarded as similar to IBV-CU-2-SP1 (Afifi et al. 2013) and Eg/12120s/2012-SP1 (Arafa et al. 2013), and are in agreement with the concept that IBV mutates commonly and that the endemic variants (Var1 and 2) are co-circulating in Egypt (Abdel-moneim et al. 2012, Sarah et al. 2014).

Continuous monitoring of the spread of IB in Morocco has shown the emergence of a novel strain of Italy 02 genotype with 32%, detected for the first time in Africa between 2010 and 2014, co-circulating with both serotypes: Massachusetts with 66% and 4/91 with 2% from vaccinated and unvaccinated chicken flocks (Fellahi et al. 2015). In addition, epidemiological analysis of 360 poultry farms surveyed in, by real-time RT-PCR, revealed that IB is considered endemic in most regions of Morocco with 51.7% of the flocks suspected of being infected by IB found IBV-positive (Fellahi et al. 2015).

So far, data concerning IB disease in other North African countries are not available.

3. Infectious bronchitis virus in West Africa

Between 1994 and 2004, Owode et al. (2006) first reported serological evidence of the avian viruses in Nigerian poultry farms, including avian IBV. Results showed that the prevalence was very high for IBV (84%).

Between 2002 and 2007, Ducatez et al. (2009) reported of IBV infection in Nigeria and Niger, using the phylogenetic analysis of full-length sequences of the spike 1 (S1) gene. The report revealed the presence of a new genotype of IBV named ‘Ibadan’, with its referenced genome being (NGA/A1167E/2006), which is antigenically and genetically different from other known IBVs. However, no association with disease has been demonstrated, and no information on the effectiveness of vaccines currently available against these strains of Ibadan is available.

Two years later, in Burkina Faso, Tarnagda et al. (2011) confirmed during a study on avian diseases [avian influenza virus (AIV), IBV and Newcastle disease (NCDV)] in domestic and wild birds in highly pathogenic avian influenza outbreaks areas that the prevalence of IBV was 3.9% and no co-infection by AIV, IBV, and/or NCDV was found.

4. Infectious bronchitis virus in South Africa

In Southern Africa, IBV was isolated in 1980 by Morley and Thomson 1984, and was associated with swollen head syndrome causing severe problems. It was confirmed as a variant that showed to be poorly protected by Massachusetts vaccines (Cook et al. 1999).

Kelly et al. (1994) based their research on serological techniques (enzyme-linked immunosorbent assay, ELISA) to show the potential existence of IB in all bird flocks of Chitungwiza, Zimbabwe, with a prevalence of 86%. In addition, other serological studies in 2000 showed 43% of IB prevalence in villages in QwaQwa, a province of South Africa (Thekisoa et al. 2003).

The same was true for Botswana, where the circulation of IBV through serological analysis revealed the presence of antibodies to IBV in unvaccinated poultry farms (Mushi et al. 2006).

Another study revealed that the genotype designated as QX-like IBV associated with respiratory signs,
nephritis, and with the so-called ‘false layer syndrome’ was reported for the first time in industrial chickens in the Southern part of the African continent (Zimbabwe) as well (Toffan et al. 2011).

Between 2011 and 2012, Knoetze et al. (2014) used molecular and serological tools such as RT-PCR and virus neutralization tests followed by S1 gene sequencing to compare the antigenic relationships between the different strains isolated from KwaZulu-Natal with those emerged in other provinces of South Africa. Results of phylogenetic analysis showed that two groups of IBV genotypes were circulating in provinces of South Africa. The first group of isolates was of the Massachusetts genotype, resulting from S1 gene variation and mutation of the vaccine Massachusetts strain (H120) used in poultry flocks, and the second group was of IBV strains of the QX-like genotype.

5. Conclusion

This review compares different IBV strain studies in African countries, mainly those isolated from vaccinated chickens showing symptoms of IB and being identified as variants generated from S1 region mutation of the S gene, which could explain the absence of efficiency regarding vaccination aimed to stop the spread of IBV disease.

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