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Review Article

A Complex Genetic Diversity of Newcastle Disease Virus (Ndv) In Africa Continent: An Updated Review

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Abstract | Newcastle disease (ND) is a highly contagious viral disease of domestic and wild birds with worldwide distributions that listed A by OIE as it causes severe economic losses in the poultry industry. In developing country, it considers a major limiting factor for poultry production which represent an important source for income and food security. In Africa, Newcastle disease virus (NDV) outbreaks is rampant for decades, however the information about the genetic characteristics of the virulent strains circulating Africa is still scarce. Based on the full genome length and F gene sequence, NDV strains are classified into class I (9 genotypes) and II (18 genotypes) within a single serotype. Outbreak in North African countries (like Egypt) caused by genotypes II, VI and VII. In the Eastern African countries such as Tanzania, genotypes V, VII and XIII are the circulating strains. In the central (Nigeria, Niger, Cameroon and Uganda) and western African countries (Mali, Mauritania, Côte d'Ivoire and Burkina Faso), newly circulating genotypes (XIV,XVII and XVIII) are isolated and restricted to this area in addition to other genotypes such as II, VII and V. In Southern African countries, (namely South Africa, Madagascar and Mozambique) genotypes II, VII, VIII, XI and XIII are prevalent. The variable NDV genotypes are been introduced to the different African countries via variable ways, wild and exotic birds, illegal poultry trading through neighboring borders or live bird market. The complex genetic diversity among circulating genotypes, sub optimal prevention afforded by the genotype II vaccine may be major factors that complicate the control of NDV in Africa.

Keywords | Newcastle disease virus, Genotypes, Africa, Genetic diversity, ND

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INTRODUCTION

Poultry industry is a crucial component of animal production industry, with a huge number of backyard flocks, particularly in the developing countries. They depend on poultry production in the backyard system, to meet household food requirements and as extra-added amount of money source (Maqbool, 2002). Unfortunately, the backyard production system involves a low standard of biosecurity measures and high risk of contagious disease transmission, such as Newcastle disease (ND) (Canan et al., 2012). ND is a highly contagious disease with great negative impact to the poultry industry. Therefore, it is classified as one of the "notifiable diseases" on the World Organization for Animal Health (OIE). Recurrent outbreaks of ND occur across the globe, particularly in the low-income countries.

Newcastle disease virus (NDV), avian paramyxovirus serotype 1 (APMV-1), belongs to the family *Paramyxoviridae;* genus *Avulavirus* (Lamb and park, 2007; Samal. 2011; Kuhn et al., 2019). It is an enveloped virus with a non-segmented, single-stranded, negative sense RNA. The virus genome encodes eight proteins, fusion (F) protein, hemagglutinin-neuraminidase protein (HN), nucleocapsid protein (N), phosphoprotein (P), matrix protein (M), large polymerase protein (L), and two additional non-structural proteins, V and W, that is expressed by RNA editing of P mRNA (Lamb and park, 2007). Relying on their pathogenicity in chickens, there are three main pathotypes for NDV isolates, lentogenic (low virulence), mesogenic (intermediate virulence) and velogenic (high virulence) (Beard and Hanson, 1984; Alexander, 1991). The disease in chickens is associated with respiratory distress with often nervous system disorder as well as gastrointestinal and reproductive troubles (Alexander, 1997; Nanthakumar et al., 2000; Tiwari et al., 2004).

Despite the intense vaccination program is being exercised by the poultry breeders across the world, ND has challenged all the rationality and continues to evolve to create new genotypes and sub genotypes that continue to spread across the globe. The current commercially available ND vaccines do not completely induce sterilized immunity as there is still virus shedding and disease can spread in to non-immunized bird (Xiao et al., 2012). Furthermore, most of the commercially available ND vaccines belong to genotype II and are not entirely compatible and deliver complete protection against the newly emerged ND virus species, particularly VII (Kapczynski and King, 2005; Miller et al., 2007; Perozo et al., 2008; Kilany et al., 2015). NDV has a high impact in large and smallholder African poultry breeders, where it results in negative socioeconomic impact (Alders and Pyme, 2009). They regularly regarded ND as the most significant disease of chickens in Africa. As a disease reportable to OIE, it also affects international trade and national movement of poultry (Alders, 2001). In a 12 year study (January 2000–December 2011) conducted to examine the frequency of recurrent ND outbreaks in 54 African countries, only 40.7 % was discovered to have always reported to OIE (Gardner and Alders, 2014).

In this review, we decided to state the history and the complex situation of NDV genotyping in Africa. Hence, we focused of the endemic genotypes in each region and their transmissibility across the continent. We presented different reference NDV strains of different genotypes from the Africans continent in Table 1 and Figure 1.

History

The first outbreaks of ND occurred in Indonesia (Java) during 1926 (Kraneveld, 1926) and the same outbreak occurred at a different geographical location on the map of the world, Newcastle-upon Tyne, the UK (Doyle, 1927). However, closely related disease outbreaks in Central Europe have been reported earlier than these dates (Halasz, 1912). One example, Macpherson (Macpherson, 1956) explains the reason of chicken death in the Western Isles of Scotland during 1896 because of NDV infection. Therefore, ND may exist earlier than 1926, but its identification as a specific disease with viral etiology dates back to the outbreaks during this year in Newcastle-upon-Tyne (Alexander et al., 2004).

Figure 1: Map for African countries illustrate distribution of variable NDV genotypes.

In the African continents, they were initially diagnosed NDV for the first time during 1944 in South Africa, after chicken's affections with severe respiratory, nervous and intestinal troubles with high mortalities in the province of Natal (Kaschula et al., 1945). They used in diagnosis serum neutralization test where it was performed at Weybridge laboratory, England. In fact, Kashscula and colleagues believed that the symptoms and post-mortem findings in Natal were so closely to those described by Hudson in Mombasa, Kenya in 1935. Therefore, they suggested that the disease may introduced via ship arrived to Mombasa harbor on the East Coast of Africa. Hudson considered that the infection had spread south to Lindi and the entire African East Coast may be affected (Kaschula et al., 1945). In Madagascar, ND was detected in 1946 (Rajaonarison, 1991), and is now responsible for the mortality rate in the backyard farms, which represent a large sector of Madagascar avian production. In Egypt, ND was identified for the first time in 1948 (Daubney and Mansy, 1948) and since then, Egypt has been regarded as an endemic country by ND. Two years later, they detected the virus in the middle of Congo and the Gambia on the West Coast of Africa (Hamilton, 1950; Lindley, 1951). One year later, it appeared on the Gold Coast (Sudan) and the southern Cameroons (Anon, 1951). In Zambia, they firstly reported the disease in 1952 as the infection spreads along the line of rail with the largest concentration of birds occurred. There was a definite correlation between the number of outbreaks and the amount of vaccine used in any one year (Sharma et al., 1986). Interestingly, due to the presence of the disease

Table 1: NDV reference strains genotypes on Genbank that isolated from different parts in Africa.

References	Genotype	Accession number	Strain
Snoeck et al; 2013	I	HF969159	chicken/Cameroon/CAE11-855/2011
Snoeck et al; 2009	I	HF969159	chicken/Cameroon/CAE11-855/2011
Snoeck et al; 2009	I	FM200800	chicken/Nigeria/SH11/2005
Snoeck et al; 2009	I	M24693	fowl/Australia/Queensland-V4/1966
Snoeck et al ;2009	I	HQ702462	chicken/Mozambique/ndv42_564/2005
Snoeck et al; 2009	I	AY175774	pigeon/South Africa/PZAPI99091/1999
Aldous et al., 2003	I	AY 175774	AV 888/99 MZ-5-99South Africa
Mohamed et al., 2011	II	FJ969395	NDV/chicken/Egypt/4/2006
Mohamed et al., 2011	II	FJ969393	NDV/chicken/Egypt/2/2006
Radwan et al ,2013	II	JX193769	NDV/chicken/Egypt/MR2-1998
Aldous et al .2003	II	AY 175708	AV 72/95 B/K) Zambia
Aldous et al .2003	II	AY 175661	AV 1141/98 10603 South Africa
Aldous et al .2003	II	AY 135740	AV 1433/95 D1702-95 South Africa
Aldous et al .2003	II	AY 175710	AV 862/95 5249Zimbabwe
Aldous et al .2003	II	AY 135755	AV 992/94 0915/94South Africa
Fenti et al 2013	II	KC851842	12RS1402-13/APMV1/CK/ Ethiopia
Fenti et al 2013	II	KC851853	12RS1402-83/APMV1/CK/ Ethiopia
Aldous et al .2003	V	AY 175654	AV 1300/95 MG-10-05-CTanzania
Aldous et al .2003	V	AY 175656	AV 1300/95 TB-02-24-DTanzania
Aldous et al .2003	V	AY 175728	AV 1300/95 MG-04-08CTanzania
Da Silva et al 2020	V	Mt33577389261	Chicken/Tanzania /2016
Da Silva et al 2020	V	Mt335727	Chicken/ Tanzania /2011
Snoeck et al ;2009	VI	AJ880277	Pigeon paramyxovirus-1/IT-227/82
Aldous et al .2003	VI	AY 175720	Panvac (2/P2 UQ vet path AuEthiopia
Snoeck et al ;2013	VIg	JQ039395	pigeon/Nigeria/VRD07-173/2007
Snoeck et al ;2013	VIg	JQ039385	dove/Nigeria/VRD07-163/2007
Snoeck et al ;2013	VII	KC205475	chicken/Ethiopia/Dhera/2011
Snoeck et al ;2013	VIb	AY288997	chicken/Kenya/139/90
Snoeck et al ;2013	VIh	JQ039391	pigeon/Nigeria/VRD07-231/2007
Snoeck et al ;2013	VIh	JQ039387	pigeon/Nigeria/VRD08-37BRpe(7-9)/2008
Snoeck et al ;2013	VIa	EF030963	chicken/Cameroon/CAE11-855/2011
Snoeck et al ;2013	VIa	EF030951	pigeon/South Africa/PIZA05N277/2005
Snoeck et al ;2013	VIa	EF030953	chicken/South Africa/CKZA06N606/2006
Snoeck et al ;2013	VIa	AY445669	dove/South Africa/DOZA05N240/2005
Snoeck et al ;2013	VIa	EF030958	chicken/South Africa/469/2002
Snoeck et al ;2013	VIa	EF030962	dove/South Africa/DOZA06N589/2006
Snoeck et al ;2013	VIa	EF030950	pigeon/South Africa/PIZA04N230/2004
Snoeck et al ;2009	VIa	EF030957	pigeon/South Africa/PIZA06N642/2006
Snoeck et al ;2009	VIb	AY288997	dove/South Africa/DOZA06N549/2006
Chake et al 2013	VIf	Kc205476	NDV/ Ethiopia/ 2011
Chake et al 2013	VIf	Kc205475	NDV/ Ethiopia/ 2011
Megahed et al 2018	VII	KX231853	NDV/Chicken/Egypt/2/2015
Megahed et al 2018	VII	KX231854	NDV/Chicken/Egypt/4/2015
Megahed et al 2018	VII	KX231852	NDV/Chicken/Egypt/1/2015

Megahed et al 2018	VII	KX231851	NDV/Chicken/Egypt/3/2015
Fenti et al 2013	VII	KC851841	12RS1402-39/APMV1/CK/ Ethiopia
Fenti et al 2013	VII	KC851848	12RS1402-67/APMV1/CK/ Ethiopia
Radwan et al ,2013	VIId	JX173098	NDV/Chicken/Giza/Egypt/MR0/2012
Abolink et al.,2017	VIIh	HQ697256	Chicken/Makassar/003/09
Abolink et al.,2017	VIIh	HQ697255	Chicken/Sukorejo/019/10
Abolink et al.,2017	VIIh	KR074405	IBS005/11
Abolink et al.,2017	VIIh	KX231366	NDV/chicken/ Mozambique/1205/2011
Abolink et al.,2017	VIIh	KT760568	Chicken/Guizhou/1032/ 2012
Abolink et al.,2017	VIIh	KU523524	NDV/chicken/ Mozambique/466/2012
Abolink et al.,2017	VIIh	JX870619	KH-cmb08-2/12
Abolink et al.,2017	VIIh	KU523528	NDV/chicken/ Mozambique/658/2012
Abolink et al.,2017	VIIh	KU523529	NDV/chicken/ Mozambique/584/2013a
Abolink et al.,2017	VIIh	KR815908	Turkey/South Africa/ N2057/2013a
Abolink et al.,2017	VIIh	MF622045	Chicken/South Africa/ RBNW-1/2013a
Abolink et al.,2017	VIIh	MF622047	Chicken/South Africa/ RBNW-3/2013a
Abolink et al.,2017	VIIh	MF622037	Chicken/South Africa/ 239391/2013a
Abolink et al.,2017	VIIh	KU523533	NDV/chicken/ Mozambique/622/2014
Abolink et al.,2017	VIIh	MF622034	Chicken/South Africa/ 32995/2015a
Abolink et al.,2017	VIIh	MF622044	Chicken/South Africa/ N2683/2015a
Abolink et al.,2017	VIIh	MF622042	Chicken/Zambia/ Mbeweka/2015
Abolink et al.,2017	VIIh	KX231368	NDV/chicken/ Mozambique/192A/2016
Hertzeg et al. (1998	VIIb	AF136767	ZA 20/93/ South Africa
Hertzeg et al. (1998	VIIb	AF136768	ZA 25/93/ South Africa
Hertzeg et al. (1998	VIIb	AF136769	ZA 26/93/ South Africa
Hertzeg et al. (1998	VIIb	AF136772	ZA 33/94/ South Africa
Hertzeg et al. (1998	VIIb	AF136774	ZA 35/95/ South Africa
Hertzeg et al. (1998	VIIb	AF109876	ZA 360/95/ South Africa
Hertzeg et al. (1998	VIIb	AF136775	MZ 13/94 Mozambique
Hertzeg et al. (1998	VIIb	AF136776	MZ 35/94 Mozambique
Aldous et al .2003	VIIb	AY 175640	AV 990/99 -1145 South Africa
Aldous et al .2003	VIIb	AY 175650	AV 1111/92 X 988Sweden
Aldous et al .2003	VIId	Y 175641	AV 990/99 96-0842South Africa
Ahmed et al 2011	VIId	(MF418017	(NDV/Chicken/EG-MN/NRC/2015
Ahmed et al 2011	VIId	MF418018	NDV/Chicken/EGQU/NRC/2015
Ahmed et al 2011	VIId	MF418019	NDV/Chicken/EG-SH/NRC/2015
Ahmed et al 2011	VIId	(MF418020	NDV/Chicken/EG -SH2/ NR/2015
Orabi et al 2016	VIId	KY075880	NDV/chicken/Egypt/Sharkia7/2016
Orabi et al 2016	VIId	KY075882	NDV/chicken/Egypt/Damietta9/2016
Hertzeg et al. (1998	VIII	AF136764	ZA 16/90/ South Africa
Hertzeg et al. (1998	VIII	AF136765	ZA 17/90/ South Africa
Hertzeg et al. (1998	VIII	AF136766	ZA 18/90/ South Africa
Hertzeg et al. (1998	VIII	AF136773	ZA34/94/ South Africa
Hertzeg et al. (1998	VIII	AF136762	ZA 5/68/ South Africa
Da Silva et al 2020	XIII	Mt335739	Chicken/ Tanzania /2016
Da Silva et al 2020	XIII	Mt335748	Chicken/ Tanzania /2017

Snoeck et al ;2013	XIVa	JQ039386	chicken/Nigeria/VRD08-36/2008
Snoeck et al ;2013	XIVa	JN872165	Chicken/Niger/VIR 1377-7/2006
Snoeck et al ;2013	XIVa	FJ772452	chicken/Niger/1377-8/2006
Snoeck et al ;2013	XIVb	JQ039390	chicken/Nigeria/VRD07-233/2007
Snoeck et al ;2013	XIVb	JX546245	chicken/Benin/463MT/2009
Snoeck et al ;2013	XIVb	JF966386	chicken/Mali/ML029_07/2007
Snoeck et al ;2013	XVIIb	FJ772446	avian/Nigeria/913-1/2006
Snoeck et al ;2013	XVIIa	JX546243	chicken/Benin/373GC/2009
Snoeck et al ;2013	XVIIa	JX546244	chicken/Benin/376GT/2009
Snoeck et al ;2013	XVIIa	FJ772486	avian/Nigeria/3724-6/2008
Snoeck et al ;2013	XVIIa	FJ772469	chicken/Niger/2602-348/2008
Snoeck et al ;2013	XVIIa	FJ772472	chicken/Niger/2602-468/2008
Snoeck et al ;2013	XVIIa	JF966385	chicken/Mali/ML007_08/2008
Snoeck et al ;2013	XVIIa	FJ772463	chicken/Burkina Faso/2415-580/2008
Snoeck et al ;2013	XVIIa	FJ772458	chicken/Burkina Faso/2415-361/2008
Snoeck et al ;2013	XVIIa	JX546247	chicken/Benin/488MT/2009
Snoeck et al ;2013	XVIIa	FJ772449	avian/Nigeria/913-33/2006
Snoeck et al ;2013	XVIIa	JQ039392	avian/Nigeria/VRD07-733/2007
Snoeck et al ;2013	XVIIa	JQ039394	chicken/Nigeria/VRD07-410/2007
Snoeck et al ;2013	XVIIa	FJ772478	chicken/Cameroon/3490-149/2008
Snoeck et al ;2013	XVIIa	FJ772484	chicken/Cameroon/3490-147/2008
Snoeck et al ;2013	XVIIa	JQ039393	chicken/Nigeria/VRD07-141/2007
Snoeck et al ;2013	XVIIa	FJ772475	chicken/Niger/2602-605/2008
Snoeck et al ;2013	XVIIa	FJ772481	chicken/Niger/2602-625/2008
Da Silva et al 2020	XVIII	Mt335753	2018Chicken/Ghana/
Snoeck et al ;2013	XVIIIa	JF966388	chicken/Mali/ML225_08/2008
Snoeck et al ;2013	XVIIIa	JF966389	guinea fowl/Mali/ML038_07/2007
Snoeck et al ;2013	XVIIIb	JN942101	Finch/Eastern Hemisphere/1409-12/2008
Snoeck et al ;2013	XVIIIb	FJ772466	chicken/Ivory Coast/2601/2008
Snoeck et al ;2013	XVIIIb	JX390609	chicken/Togo/AKO18/2009
Snoeck et al ;2013	XVIIIa	JN872157	chicken/Mali/ML008_09/2009
Snoeck et al ;2013	XVIIIa	JN872157	GWH/Eastern Hemisphere/5801-22/10
Snoeck et al ;2013	XVIIIa	FJ772455	avian/Mauritania/1532-14/2006
Snoeck et al ;2013	XVIIIb	HF969127	chicken/Ivory Coast/CIV08-069/2007
Snoeck et al ;2013	XVIIIb	HF969126	duck/Ivory Coast/CIV08-062/2006
Snoeck et al ;2013	XVIIIb	JX390609	chicken/Togo/AKO18/2009
Snoeck et al ;2013	XVIIIb	HF969216	chicken/Nigeria/NIE11-1286/2011
Snoeck et al ;2013	XVIIIa	HF969179	chicken Ivory Coast/CIV08-026/2007
Snoeck et al ;2013	XVIIIa	FJ772455	avian/Mauritania/1532-14/2006

in neighboring territories, Nigeria applied the prophylactic vaccination against NDV, using the Komarov strain of Newcastle disease vaccine obtained from the Onderstepoort Laboratories, Pretoria, South Africa. However, they confirmed the first outbreak of NDV in Nigeria at Ibadan province during December 1952, which they confirmed by laboratory diagnosis in February 1953 (Hill et al., 1953).

The first documented evidence of ND in Chad occurred in 1954 since then, it occurs so epizootic and endemic (Provost et al., 1968). The first documented evidence of ND in Uganda occurred in 1955 (Mukabii, 1992). In July 1960, for the first time they diagnosed mild lento genic type of NDV in South Africa, known as the 'American type', was. The strain of the virus induced mild clinical signs that the careful observer can see only (Kluge, 1964). Up to our knowledge, the first documented evidence of NDV in Ethiopia dates back to 1978 when an outbreak occurred in Eritrea then spread to the Northern part of the country. Epidemiological and virological studies on intensively reared commercial chicken revealed that the velogenic strains are widely distributed through Ethiopia (Nasser, 1998). In the Sahara desert region, they characterized virulent isolates NDV of in Morocco during 1982 (Bell, 1985).

Nowadays, all African countries reported ND as being the most serious problem in live backyard rural poultry (Bell, 1991, 1992). Hence, it has been reported in the traditionally managed village poultry from Morocco (Bell and Moulodi, 1988), Mauritania (Bell et al., 1990a), Ethiopia (Bawke et al., 1991), Nigeria (Olabode et al., 1991), Sudan (Fadol, 1991), the Ivory Coast (Couacy-Hymann et al., 1991), Mozambique (Fringe and Dias, 1991) and Uganda (George, 1991).

Genotypes of NDV in Africa

The NDV phylogenetic analysis is an effective technique for evaluating the epidemiological relationships among the NDV isolates present in different parts of the world (Mase et al., 2002).

Currently two nomenclatures systems are in use for the classification of NDV, based on the phylogenetic analysis, a system that divides NDV into six lineages with several sub-lineages. As example, lineages 3 and 4 were further classified into four sub-lineages (a- d) whereas lineage 5 was divided into five sub-lineages (a -e). This system had several limitations as they focused on the restriction enzyme analysis and partial sequence of the F-gene (Ballagi-Pordany et al., 1996; Aldous et al., 2003).

The used second system based on full F or full genome sequences (Czegledi et al., 2006). It therefore categorized NDV into two main classes; I- II into one serotype, in which class II further split up to 18 genotypes they (Diel et al., 2012; Courtney et al., 2013; Snoeck et al., 2013). The comparison between the two systems revealed that sub-lineages 3a, 3b, 3c and 3d correlated to genotypes III, IV,V and VIII and sub-lineages 5a to 5d correlated to genotypes VII a to d (Aldous et al., 2003). However, novel subgenotypes VIIk are recently characterized (Molini et al., 2017).

Recurrent outbreaks of NDV attack the different regions of the Africa continent for years, despite of the previous the information about the genetic characteristics of the virulent strains circulating in that region is still limited. Until now, twelve NDV genotypes, I, II, IV, V, VI, VII, VIII, XI, XIII, XIV, XVII and XVIII, isolated from various African countries in different periods (Da Silva et al., 2020).

Genotype II

It belongs to class II NDVs and is a mixture of lentogenic and velogenic strains (Kim et al., 2008), which were firstly identified in North America. Genotype II virulent, Beaudette C/1945 and Texas/GB/1948, and lentogenic, Hitchner/B1/47 and LaSota/1946, strains were isolated during 1940 in the United States. The lentogenic strains commercialized and they used as vaccines in poultry (Ballagi-Pordany et al., 1996; Millar et al., 2010).

They isolated NDV strains from South Africa in a period from 1999 identified as genotype II lentogenic strains and suggested that its source the commercial vaccine. Thus, no true lentogenic wild type NDV strains they identified in this study (Abolink et al., 2004). A few years later, molecular characterization of 11 NDV strains isolated from Egypt during the period 1996 -2005 revealed that they belong to genotype II and VI, suggesting that these genotypes are the most abundant NDV genotypes circulating in the Egyptian poultry flocks (Saad et al., 2010). In Egypt, sequences analysis of the F genes from virulent NDV 2006 Egyptian isolates revealed that they belong to genotype II. Further, they are closely related to other strains isolated in Egypt in 2005 (Mohamed et al., 2009) and the North American strain, which strength the suggestion that those strains are probably the most abundant genotype in the bird population in Egypt (Mohamed et al., 2011). Furthermore, NDV strains of genotype II which were similar or variant from LaSota strain were identified in Nigeria and Burkina Faso in 2006 /2007 (Snoeck et al., 2009) an in northwest Ethiopia (Fentie et al., 2013). In northwest Ethiopia, recent study concluded that live chicken market plays important role in spreading and dissemination of NDV in chicken. They isolated NDV from apparently healthy appearing birds in all seasons of the year with high percent in prerainy dry season, showing evidence for climatic and socioeconomic aspects as risk factor in the occurrence of ND in chicken (Haile and Fentie, 2020).

Genotype V

Genotype V had started to emerge in the Americas for the first time around the 1970s and disseminate to the European continent in 1980s, scientists have recently reported its introduction to Africa in Eastern region (Aldous et al., 2003; Yongolo et al., 2011). The previous suggesting the increase of the genotype geographic distribution (Sabra et al., 2017). It possesses mainly pathogenic strains which sub classified in to several genotypes (a- d). In Tanzania, the analysis of NDV strains isolated between 1994 and 1995 revealed that they belong to genotype V and it may spread through migration of wild birds or live birds markets (Yongolo et al., 2011). Consistently, healthy live birds in live poultry markets act as reservoir for virulent NDV (Byarugaba et al., 2014). A recent study suggested possible cross border spread of velogenic NDV between Kenya and neighboring Uganda through live bird trade (Ogali et al., 2018). The Ugandan NDV strains has low genetic diversity suggesting low evolution rate with amino acid mutations in the HN protein that differ from the Kenyan strains, suggesting independent evolution. The first complete genome sequence analysis of subgenotype Vd was performed on single NDV strain isolated also from live poultry market in the Mbeya region, Tanzania (Goraichuk et al., 2019). Later on, similar study reports the first complete genome sequence of NDV from backyard chicken in Kenya. The three isolates characterized to be velogenic by MDT and ICPI. Those were phylogenetically related to genotype V strains, and form a distinct cluster together with NDV strains from the East African countries of Uganda and Tanzania to form the newly characterized subgenotype Vd (Ogali et al., 2020). Another recent study utilized the third-generation portable sequencing device in identification of nine Tanzanian NDV strains belonging to genotype V. The NDV strains of this study were collected from Morogoo, Tanzania in a period between 2011and 2017 and were closely related to other isolates from Mbeya, Kenya and Uganda (Da Silva et al., 2020). Circulation of closely related NDV strains of genotype V appeared within these three East African countries and the unrestricted movement of cross-border trade of live birds might be the main reason for endemic situation of this genotype in this region (Byarugaba et al., 2014; Msoffe et al., 2019).

Genotype VI

Genotype VI viruses, pigeon paramyxoviruses 1, is usually isolated from Columbidae and sub classified in to subgenotypes VIa to k. Isolates of NDV belonging to the genotype VIb were mainly restricted to the western African region. In 2007, two sequences of genotype VI with two nucleotides mismatching obtained from a parrot and pigeon in Nigeria (Snoeck et al., 2009). Further investigation confirmed the circulation of genotype VIb in pigeons and rural poultry samples from six Nigerian states during 2007-2008 (Vam Borm et al., 2012). Introduction of putative subgenotypes derived from genotype VI, VIh and VIi, was reported in 2013 from pigeon samples (Snoeck, 2013). The existence of genotype VIh from Pigeon samples and their clustering with foreign strains such as Pigeon/Argentina/Capital_3/97 indicated strong evidence for the responsibility of the wild birds in the introduction of genotype VI to the Western region of the African continents. The Nigerian subgenotype VIg isolates were highly correlated to other NDV strains from Egypt, Russia and Ukraine while the subgenotype VIh isolates have high homology with wild bird isolates from Kenya. Further, the Nigerian subgenotypes VIi were closely related with Italian strains from outbreak in doves. These close genetic relationships among the isolates could be of epidemiological significance and strongly recommend a previous common origin during their natural selection (Snoeck et al., 2013).

Not only restricted to the western part of the African continent, as the free birds-specificity of genotype VI, led to dissemination of the genotype to other countries such as Egypt (VIg) and central Ethiopia (VIf) (Sabra et al., 2017; Chaka et al., 2013).

Genotype VII

It represents NDV strains isolated during the epizootics of Mozambique and South Africa (1990-1995), hence they classified as subgenotype VIIb (Herczeg et al., 1999). The authors suggested that the genotype might be emerged to the country from the Far East and western European countries.

Subgenotype VIId was initially isolated during 1999 from shanghai goose flocks which were suffered from moderate mortality rates in goslings. The causative virus strain, SF02, was initially termed as Goose paramyxovirus thereafter it was identified as genotype VIId. NDV strains belong to subgenotype VIId are highly pathogenic to different domesticated birds with intra-cerebral pathogenicity indexes (ICPIs) ranged from 1.80 to 1.94 (Jinding et al., 2005; Liu et al., 2003; Zou et al., 2002; Zou and Gong 2003). The phylogenetic analysis of NDV strains isolated from Egypt between 2011 and 2012 revealed that they belong to genotypeVII subgenotype d and closely related to the Middle East isolates (Radwan et al., 2013). Since 2011, NDV outbreaks caused by genotype VII occur in several vaccinated and non-vaccinated poultry in different governorates of Egypt, there is a strong probability that the Egyptian VIId strains are introduced from China or Middle Eastern countries such as Israel and enter Egypt through infected poultry products or wild birds (Hussein et al., 2014; Megahed et al., 2018).

Two virulent NDV isolates was clustered with genotype VIId (lineage 5) and were similar to those NDV isolates from northeastern African countries (Sudan and Egypt), which were reported to GenBank between 2004 and 2012. The close genetic similarity of the northern Ethiopian virulent isolates with that of the Sudanese and Egyptian isolates provides evidence for potential epidemiologic links between outbreaks of NDV in these countries, likely due to the geographical proximity and movement of poultry among borders (Fentie et al., 2013). Recent study includes molecular and phylogenetic characterization of 116 tissue / organ collected from NDV outbreak in Egypt and reveals that they are velogenic strains with high identity to velogenic strains from Jordan, Israel and Turkey. Phylogenetic analysis showed that they belong to genotypes (VIId,VIIa and II) and VIId is predominant genotype circulating in

Egypt (Mouhamed et al., 2020).

In the period between 2002 and 2007, different virulent NDV strains isolated from backyard farms and live bird markets in four Sub-Saharan countries in the West Africa, Nigeria, Niger, Burkina Faso and Cameroon. The strains were clustered within subgenotype VIIf and g which represent NDV variants indigenous to West Africa (Snoeck et al., 2009).

Subgenotype VIIh has introduced to South-East Asia and caused serious outbreaks for the poultry flocks in Malaysia, Indonesia, southern China, Vietnam and Cambodia. It was recorded in the African continent in 2011 during outbreaks in poultry flocks. Thereafter, the virus spread north through Mozambique (Mapaco et al., 2016) into the north-eastern provinces of Zimbabwe and then south towards Botswana and South Africa causing serious outbreak in 2013 (Abolnik et al., 2017). Further, the virus transmitted from Mozambique toward neighboring countries such as Malawi and Zambia. Recent study determines the NDV genotype circulating in Botswana. Phylogenetic analysis of fourteen samples that collected from NDV outbreak in 2014, 2018 and 2019 reveals that they clustered in genotype VII. They closely related to viruses from South Africa and Mozambique than other southern African countries (Nambia, Zambia and Zimbabwe) (Kgotlele et al., 2020). In Fact, Abolnik and his colleagues suggested that the absence of genotype VIIh outside of South-East Asia and Southern Africa is strong evidence that wild migratory birds are not responsible for disease dissemination. Hence, there are strong evidences that illegal live bird trade or infected wastes from ships are the source of the virus emergence to Mozambique in 2011.

Genotype VIII

Genotype VIII NDV strains are geographically restricted viruses which were originated from Southeast Asia between 1979 and 1985 (Aldous et al., 2003; Liang et al., 2002), this genotype has emerged in South Africa since decades (Herczeg et al., 1999). Hence, it was characterized in South African strains that were detected in the 1960 and in the period from 1990 to 1995. However, no record for the isolation of this genotype has been available since June 2000 (Abolnik, 2007).

Genotype XI

NDV strains belong to genotype XI are mainly virulent. It is geographically restricted in Africa. Hence, reporting only in Madagascar, where it circulated between the wild birds and domestic chicken (De Almeida et al., 2013).

Genotype XIII

Virulent genotype, which subclassified in to three subgenotypes, namely, XIIIa, XIIIb, and XIIIc. Subgenotype XIIIa strains have been isolated during poultry outbreaks in Europe, Africa, and the Middle East, but subgenotypes XIIIb and XIIIc remain localized to India and Pakistan (Dimitrov et al., 2016). In Africa, genotype XIII strains have been recovered from an ostrich in South Africa (1995), chickens in Burundi (2008), and passerines in Tanzania (2010) (Cattoli et al., 2010; Benson et al., 2015). Recently, this genotype has been isolated from Zambia, Burundi, South Africa and Tanzania (Msoffe et al., 2019; Da Silva et al., 2020).

Genotypes XIV, XVII and XVIII

These moderately recent discovered regional genotypes found endogenous in West and Central Africa.

Genotypes XIV: It is NDV variant that endogenous in West African countries such as Nigeria, Niger, Cameroon and Burkina Faso. It was initially isolated from live poultry market and backyard flocks in the period from 2002 to 2008 and was initially termed as lineage 5f (Snoeck et al., 2008; Solomon et al., 2012) or 7d (Cattoli et al., 2010). Thereafter it was renamed as genotype XIV according to the new classification (Snoeck et al., 2013) with two subgenotypes, a and b or 1 and 2 (Dimitrov et al., 2019). Fourteen and 33 strains of subgenotype XIVa and XIVb, respectively, were detected in different Nigerian cities in the period from 2007 to 2011 (Snoeck et al., 2013). Interestingly, all the sequenced strains possess the cleavage site specific for NDV virulent pathotype. Accordingly, pathogenicity study trial revealed that genotype XIV isolated from West Africa is velogenic viscerotropic pathotype that caused severe clinical signs or mortality by the day 4-post infection (Susta et al., 2014). Further, it led to systemic infection and necrosis in the lymphoid tissue and gastrointestinal tract. The first complete genomic sequence of genotype XIVb NDV strain (duck/Nigeria/NG-695/KG.LOM.11-16/2009) that isolated from healthy duck in live poultry market in Nigeria was reported in (Shittu et al., 2016).

Genotype XVII: Snoeck and his colleagues defined it together with genotype XVIII (Snoeck et al., 2013) according to criteria described by (Diel et al., 2012). They isolated it from domestic birds from different countries in West Africa plus Central African Republic (Snoeck et al., 2013) that may suggest the genotype ability to spread across the continent. The virus classified into two subgenotypes with virulent characteristics.

Genotype XVIII: Viruses of class II genotype XVIII, previously identified as lineage 7a (Cattoli et al., 2010) with a high correlation with genotypes XIV and XVII. In fact, both genotypes XVII and XVIII have been suggested to be the same genotype (Desingu et al., 2016). However, this conclusion was not accepted by Snoeck and Muller (2016) as they stated that Desingu and colleagues used incorrect bioinformatics parameters to analyze NDV genotyping. However, until now it has still been classified as distinctive genotype divided in to two subgenotypes XVIIIa and XVIIIb by (Snoeck et al., 2013) or the more updated XVIII.1 and XVIII.2 by (Dimitrov et al., 2019). West African countries seem to have the most complex situation in terms of genetic diversity of NDV genotypes and subgenotypes. The two subgenotypes, XVIII.1, and XVIII.2 have been found independently circulated or either co-circulated together or with other genotypes, such as subgenotype XVIIa, in Côte d'Ivoire, Mauritania, Mali, Togo and Nigeria since 2006 or may be earlier (Cattoli et al., 2010; Snoeck et al., 2013). In 2018, four sequences obtained from two distant cities in Ghana, Wa and Pokoasi, found to be belong to subgenotype XVIII.2 and were highly correlated to an isolate from Mali (JX518886) (Da Silva et al., 2020). With the fact that it is geographically restricted or regional genotype in the Western Africa, the international trade of exotic birds can play a role in its worldwide dissemination.

NDV Challenges in Africa

Based on the available information, it is obvious that there is broaden ecological distribution of various NDV genotype across the continent. The continuous genetic modification in NDV with mutation in the cleavage site and the neutralizing epitopes could lead to what is called vaccination failure phenomena. Accordingly, all the previous together with the existence of wild birds and the unrestricted movement between neighbor countries border will obscure the problem of recurrent NDV outbreak in Africa.

CONCLUSION

ND is considering a major threat for poultry production in Africa. Several genotypes are isolated and their distribution in most of African countries was recorded. Genotype VII which is responsible for the fourth panzootic ND outbreak is also found in the region. Genetic diversity between NDV strains continue to grow mainly in central and West Africa where the recent discovered genotypes XIV, XVII, XVIII are geographically restricted. Africa is considering a reservoir for new virulent strains, the efficacy of the classical vaccinal strains against these recent strains need to be further studied. Wild, exotic birds, live bird market and illegal trading play important role in entrance and spreading of NDV strains and their control is necessary.

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CONFLICT OF INTEREST

There is no conflict of interest.

AUTHORS CONTRIBUTION

Wala Mohamed and Ola Hassanin collected and analyzed the previously published scientific articles as well as designed and wrote the first draft of the review. Mohamed Megahed reviewed and approved the final version of the review.

REFERENCES

- Abolnik C (2007). Molecular epidemiology of Newcastle disease and avian influenza in South Africa', PhD thesis, Dept. of Zoology, University of Pretoria, viewed 01 July 2016.
- Abolnik C, Horner RF, Bisschop SP, Parker ME, Romito M, Viljoen GJ (2004). A phylogenetic study of South African Newcastle disease virus strains isolated between 1990 and 2002 suggests epidemiological origins in the Far East. Arch. Virol. 149: 603 - 619. https://doi.org/10.1007/s00705-003-0218-2
- Abolnik C, Mubamba C, Wandrag DR, Horner RB, Dautu G, Bisschop SPR (2017). Tracing the origins of genotype VIIh Newcastle disease in southern Africa. 15 August 2017. https://doi.org/10.1111/tbed.12771
- Ahmed HM, Amer MM, Elbayoumi KM, Kutkat MA (2017). Isolation and identification of Genotype VII of Newcastle disease virus from chicken flocks in six Egyptian Governorates. J Med. Res. Health Sci. 2(1). https://doi.org/10.21608/ejvs.2017.1236.1015
- Alders RG (2001). SADC planning workshop on Newcastle disease control in village chickens. Proceedings of an International Workshop, Maputo, Mozambique, 6-9 March, 2000. (ACIAR Proceedings No.103), 158pp.
- Alders RG, Pym RAE (2009). Village poultry: still important to millions, eight thousand years after domestication. World's Poul. Sci. J. 65: 181 - 190. https://doi.org/10.1017/S0043933909000117
- Aldous EW, Mynn JK, Banks J, Alexander DJ (2003). A molecular epidemiological study of avian paramyxovirus type 1 (Newcastle disease virus) isolates by phylogenetic analysis of a partial nucleotide sequence of the fusion protein gene. Avian Pathol. 32: 239 - 256. https://doi.org/10.1080/030794503100009783
- Aldous EW, Seekings JM, McNally A, Nili H, Fuller CM, Irvine RM, Alexander DJ, Brown IH (2010). Infection dynamics of highly pathogenic avian influenza and virulent avian paramyxovirus type 1 virus in chickens, turkeys and ducks. Avian Pathol. 39: 265 – 273. https://doi.org/10.1080/03079457.2010.492825
- Alexander DJ (1991). Newcastle disease. In: Rweyemamu MM, Palya V, Win T, Sylla D. Newcastle Disease Vaccines for Rural Africa. Proceedings of a Workshop held at Pan African Veterinary Vaccine Centre (PANVAC), DebreZeit, Addis Ababa, Ethiopia. 1 - 45.

- Alexander DJ (1997). Newcastle disease, other Avian Paramyxoviruses and Pneumoviridae. In: Calnek BW, Barnes HJ, Beard CW, McDougals LR, Saif YM (1997). Disease of Poultry. Chapter 20. Iowa State University Press, Ames, Iowa, USA. 541 - 569. https://doi.org/10.2307/1592156
- Alexander DJ, Bell JG, Alders RG (2004). A Technology Review: Newcastle Disease. With Special Emphasis on its Effect on Village Chickens. FAO Anim. Prod. Health. 161.
- Alexander DJ, Manvell RJ, Lowings JP, Frost KM, Collins MS, Russell PH, Smith JE (1997). Antigenic diversity and similarities detected in avian paramyxovirus type 1 (Newcastle disease virus) isolates using monoclonal antibodies. Avian Pathol. 26: 399 – 418. https://doi.org/10.1080/03079459708419222
- Anon I (1951). Annual report of of the Sudan Veterinary services.
- Ballagi-Pordany A, Wehmann E, Herczeg J, Belák S, Lomniczi B (1996). Identification and grouping of Newcastle disease virus strains by restriction site analysis of a region from the F gene. Arch. Virol. 141(2): 243 - 261. https://doi.org/10.1007/BF01718397
- Bawke L, Naser M, Berhanu A, Mengistu A (1991). Newcastle disease in Ethiopia. In: Rweyemamu MM, Palya V, Win T, Sylla D (Eds) Newcastle Disease Vaccines for Rural Africa. Proceedings, of a Workshop held at Pan African Veterinary Vaccine Centre (PANVAC), DebreZeit, Addis Ababa, Ethiopia. 49 – 51.
- Beard CW, Hanson RP (1984). Newcastle disease. In: Hofstad MS, Barnes HJ, Calnek BW, Reid WM, Yoder JR (Eds). Diseases of Poultry, 8th edn. 452 - 470. (Ames, Iowa State University Press).
- Bebay CE (2006). Première évaluation de la structure et de l'importance du secteuravicole commercial et familial en Afrique de l'Ouest. Synthèse des rapports nationaux. FAO, Rome, Italy.
- Bell JG (1985). Velogenic Viscerotropic Newcastle Disease Virus Strains in Morocco: Avian Dis. 30(1): 231 - 233
- Bell JG (1991). Vaccination of African village poultry against Newcastle disease. In: Demey F, Pandey VS (Eds). Newcastle Disease Vaccination of Village poultry in Africa and Asia. Proceedings of the Seminar held on 13 and 14 February 1991, Antwerp. 3 - 8.
- Bell JG (1992). Newcastle disease in village chickens in North, West and Central Africa. In: Spradbrow PB (Ed.) Newcastle Disease in Village Chickens, Control with Thermostable Oral Vaccines. Proceedings, International Workshop held in Kuala Lumpur, Malaysia, 6-10 October 1991. Centre for International Agricultural Research (ACIAR), Canberra. 142 -143.
- Bell JG, AitBelarbi D, Amara A. (1990). A controlled vaccination trial for Newcastle disease under village conditions. Preventive Vet. Med. 9: 295 - 300. https://doi.org/10.1016/0167-5877(90)90075-S
- Bell JG, Moulodi S (1988). A reservoir of virulent Newcastle disease virus in village chicken flocks. Preventive Vet. Med. 6: 37 - 42. https://doi.org/10.1016/0167-5877(88)90024-4
- Benson DA, Clark K, Karsch-Mizrachi I, Lipman DJ, Ostell J, Sayers EW (2015). GenBank. Nucleic Acids Res 43:D30 –D35. https://doi.org/10.1093/ nar/gku1216.
- Byarugaba DK, Mugimba KK, Omony JB, Okitwi M, Wanyana A, Otim MO, Kirunda H, Nakavuma JL, Teillaud A, Paul, MC (2014). High pathogenicity and low genetic evolution of avian paramyxovirus type I (Newcastle disease virus) isolated from live bird markets in Uganda. Virol. J. 11: 173. https://doi.org/10.1186/1743-422X-11-173
- Cattoli G, Fusaro A, Monne I, Molia S, Le Menach A, Maregeya B, Nchare A, Bangana I, Maina AG, Koffi JN, Thiam H, Bezeid OE, Salviato A, Nisi R, Terregino C, Capua I (2010). Emergence of a new genetic lineage of Newcastle disease virus in West and Central Africa—implications for diagnosis and control. Vet. Microbiol. 142: 168–176. https://doi.org/10.1016/j.vetmic.2009.09.063
- Chaka H, Goutard F, Gil P, Abolnik C, Servan de Almeida R, Bisschop S, Thompson PN (2013). Serological and molecular Trop Anim Health Prod investigation of Newcastle disease in household chicken flocks and associated markets in Eastern Shewa zone, Ethiopia.Trop. Anim. Health and Produc. 45(3): 705 - 714.
- Chantal J, Snoeck Claude P, Muller A. (2016). Reply to "May Newly Defined Genotypes XVII and XVIII of Newcastle Disease Virus in Poultry from West and Central Africa Be Considered a Single Genotype XVII. J. Clin. Microbiol. 54: 9.
- Conan A, Goutard FL, Sorn S, Vong S (2012). Biosecurity measures for backyard poultry in developing countries: a systematic review. BMC. Vet. Res. 8: 240. https://doi.org/10.1186/1746-6148-8-240
- Couacy-Hymann E, Sanogo B, Domanech J (1991). Epidemiologie de la Maladie de Newcastle en Cote D'Ivoire. In: Rweyemamu MM, Palya V, Win T, Sylla D (Eds). Newcastle Disease Vaccines for Rural Africa. Proceedings of a Workshop held at Pan African Veterinary Vaccine Centre (PANVAC), DebreZeit, Addis Ababa, Ethiopia. 65 - 68.
- Courtney SC, Susta L, Gomez D, Hines NL, Pedersen JC, Brown CC, Miller PJ, Afonso CL (2013). Highly divergent virulent isolates of Newcastle disease virus from the Dominican Republic are members of a new genotype that may have evolved unnoticed for over 2 decades. J. Clin. Microbiol. 51: 508 –517.
- Czegledi A, Ujvari D, Somogyi E, Wehmann E, Werner O, Lomniczi B (2006). Third genome size category of avian paramyxovirus serotype 1 (Newcastle dis-ease virus) and evolutionary implications. Virus Res., 120(1-2): 36 - 48.
- Da Almeida S, Hammoumi P. Gil L (2013). New avian paramyxoviruses type I strains identified in Africa provide new outcomes for phylogeny reconstruction and genotype classification. PLoS One. 8(10): 76413. https://doi.org/10.1371/journal.pone.0076413
- Da Silva AP, Emily JA, Gaspar HC, Ashley B, Amandus PM, Boniface BK, Terra K, Huaijun Z, Rodrigo AG (2020). Molecular characterization of Newcastle disease viruses isolated from chickens in Tanzania and Ghana. Viruses J. 12: 916. https://doi.org/10.3390/v12090916
- Daubney R, Mansy W (1948). The occurrence of Newcastle disease in Egypt. J. Compar. Pathol. 58: 189 - 196. https://doi.org/10.1016/S0368-1742(48)80019-6
- De Almeida RS, Hammoumi S, Gil P, Briand F-X, Molia S, Gaidet N (2013). New Avian paramyxoviruses type I strains identified in Africa provide new outcomes for phylogeny reconstruction and genotype classification. PLoS One. 8: 76413. https://doi.org/10.1371/journal.pone.0076413
- Desingu PA, Dhama K, Malik YS, Singh RK (2016). May newly defined genotypes XVII and XVIII of newcastle disease virus in poultry from west and central Africa be considered a single genotype (XVII)?. J. Clin. Microbiol. 54 (9): 2399, 2016. https://doi.org/10.1128/JCM.00667-16

- Diel DG, da Silva LH, Liu H, Wang Z, Miller PJ, Afonso CL (2012). Genetic diversity of avian paramyxovirus type 1: proposal for a unified nomenclature and classification system of Newcastle disease virus genotypes. Infec. Genetics Evol., 12(8): 1770 - 1779. https://doi.org/10.1016/j.meegid.2012.07.012
- Diel DG, Susta L, Cardenas GS, Killian ML, Brown CC, Miller PJ, Afonso CL (2012b). Complete genome and clinicopathological characterization of a virulent Newcastle disease virus isolate from South America. J. Clin. Microbiol. 50: 378 - 387. https://doi.org/10.1128/JCM.06018-11
- Dimitrov KM, Ramey AM, Qiu X, Bahl J, Afonso CL (2016). Temporal, geographic, and host distribution of avian paramyxovirus 1 (Newcastle disease virus). Infect. Genet. Evol. 39: 22 - 34. https://doi.org/10.1016/j.meegid.2016.01.008
- Dimitrov KM, Abolnik C, Afonso CL, Albina E, Bahl J, Berg M, Briand F, Brown IH, Choi K, Chvala I, Diel DG, Durr PA, Ferreira HL, Fusaro A, Gil P, Goujgoulova GV, Grund C, Hicks JT, Joannis TM, Torchetti MK, Kolosov S, Lambrecht B, Lewis NS, Liu H, McCullough S, Miller PJ, Monne I, Muller CP, Munir M, Reischak D, Sabra M, Samal SK, de Almeida RS, Shittu I, Snoeck CJ, Suarez DL, Van Borm S, Wang Z, Wong FYK (2019). Updated unified phylogenetic classification system and revised nomenclature for Newcastle disease virus. Infec. Genet. Evol. 74:103917. https://doi.org/10.1016/j.meegid.2019.103917
- Doyle T (1927). A hitherto unrecorded disease of fowls due to a filter passing virus. J. Comp. Pathol.Ther. 40: 144 - 69.
- Fadol MA (1991). Newcastle disease in Sudan, Type of the Virus and its Control. In: Rweyemamu MM, Palya V, Win T, Sylla D (Eds) Newcastle Disease Vaccines for Rural Africa. Proceedings of a Workshop held at Pan African Veterinary Vaccine Centre (PANVAC), DebreZeit, Addis Ababa, Ethiopia. 61 - 64.
- Fentie T, Heidari A, Aiello R, Kassa T, Capua I, Cattoli G (2014). Molecular characterization of Newcastle disease viruses isolated from rural chicken in northwest Ethiopia reveals the circulation of three distinct genotypes in the country. Trop. Anim. Health Prod. 46: 299 – 304. https://doi.org/10.1007/s11250-013-0487-z
- Fringe R, Dias PT (1991). Newcastle disease in Mozambique. In: Rweyemamu MM, Palya V, Win T, Sylla D (Eds). Newcastle Disease Vaccines for Rural Africa. Proceedings of a Workshop held at Pan African Veterinary Vaccine Centre (PANVAC), DebreZeit, Addis Ababa, Ethiopia. 73 – 74.
- Gardner E, Alders R (2014). Livestock risks and opportunities: Newcastle disease and Avian influenza in Africa. Davos: Global Risk Forum GRF Davos. 208 - 211.
- George MM (1991). Epidemiology of Newcastle disease in rural Uganda. In: Rweyemamu MM, Palya V, Win T, Sylla D (Eds). Newcastle Disease Vaccines for Rural Africa. Proceedings of a Workshop held at Pan African Veterinary Vaccine Centre (PANVAC), DebreZeit, Addis Ababa, Ethiopia. 75 - 76
- Goraichuk IV, Msoffe PLM, Chiwanga GH, Dimitrov KM, Afonso CL, Suarez DL (2019). First complete genome Sequence of a subgenotypeVd Newcastle disease virus isolate. Microbiol. Resour. Announc. 8: e00436-19. https://doi.org/10.1128/MRA.00436-19
- Haile B, Fentie T (2020). The role of live chicken markets as a source of replication and dissemination of Newcastle disease virus in chickens, northwest Ethiopia. Poul Sci. 99(11): 5415-5421. https://doi.org/10.1016/j.psj.2020.08.025
- Halasz F (1912). Contributions to the knowledge of fowl pest. Veterinary Doctoral Dissertation, Communications of the Hungarian Royal Veterinary School. Patria Budapest. 1 - 36.
- Hamilton DF (1950). Vet. Rec. 63: 525. https://doi.org/10.1088/0370-1298/63/9/311
- Herczeg J, Wehmann E, Bragg RR, Travassos Dias PM, Hadjiev G, Werner O, Lomniczi B (1999). Two novel genetic groups (VIIb and VIII) responsible for recent Newcastle disease outbreaks in Southern Africa, one (VIIb) of which reached Southern Europe. Arch. Virol. 144: 2087 – 2099. https://doi.org/10.1007/s007050050624
- Hill HD, Davis OS, Wilde JE (1953). Newcastle disease in Nigeria. British Vet. J. 109: 381–385. https://doi.org/10.1016/S0007-1935(17)50788-5
- Hussein HA, Emara MM, Rohaim MA (2014). Molecular characterization of Newcastle disease virus genotype VIId in Avian influenza H5N1 infected broiler flock in Egypt. Int. J. Virol. 10(1): 46 - 54. https://doi.org/10.3923/ijv.2014.46.54
- Jinding C, Ming L, Tao R, Chaoan X (2005). A goose-sourced paramyxovirus isolated from southern China. Avian Dis. 49: 170–173.
- Kapczynski DR, King DJ (2005). Protection of chickens against overt clinical disease and determination of viral shedding following vaccination with commercially available Newcastle disease virus vaccines upon challenge with highly virulent virus from the California 2002 exotic Newcastle disease outbreak. Vaccine. 23: 3424 - 3433. https://doi.org/10.1016/j.vaccine.2005.01.140
- Kaschula VR, Canham AS, Diesel AM, Coles JDWA (1945). Newcastle disease in Natal. J. South African Vet. Med. Assoc. 17: 1 - 14.
- Kgotlele T, Modise B, Nyange JF (2020). First molecular characterization of avian paramyxovirus-1 (Newcastle disease virus) in Botswana. Virus Genes. 56(1–2). https://doi.org/10.1007/s11262-020-01770-4
- Kilany WH, Ali A, Bazid AI, Zain El-Abideen MA, El Sayed M (2015). Evaluation of two inactivated Newcastle disease virus vaccines (genotype II and VII) against challenge of Newcastle disease genotype vii infection in chicken. J. Anim. Vet. Adv. 14(7): 211 - 218.
- Kim LM, King DJ, Guzman H. (2008). Biological and phylogenetic characterization of pigeon paramyxovirus serotype 1 circulating in wild North American pigeons and doves. J. Clin. Microbiol. 46(10): 3303 - 3310. https://doi.org/10.1128/JCM.00644-08
- Kim LM, Suarez DL, Afonso CL (2008). Detection of a broad range of class I and II Newcastle disease viruses using multiplex real-time reverse transcription polymerase chain reaction assay. J. Vet. Diag. Invest. 20(4): 414 – 425. https://doi.org/10.1177/104063870802000402
- Kluge EB (1964). Newcastle disease and its control in South Africa. Bull. Office Int. des Epizs. 62: 897 - 902.
- Kraneveld FC (1926). A poultry disease in the Dutch East Indies. Ned. Indisch. Blvoor. Diergeneeskd. 38: 448 - 450.
- Kuhn JH, Wolf YI, Krupovic M, Zhang YZ, Maes P, Dolja VV, Koonin EV (2019). Classify viruses — the gain is worth the pain. Nature. 566(7744): 318 - 320.
- Lamb RA, Parks GD (2007). Paramyxoviridae: the viruses and their replication, p 1449–1496 In Knipe DM, Howley PM (eds), Fields virology. Lippincott Williams and Wilkins, Philadelphia, PA.
- Liang R, Cao DJ, Li JQ, Chen J, Guo X, Zhuang FF, Duan MX

(2002). Newcastle disease outbreaks in western China were caused by the genotypes VIIa and VIII. Vet. Microbiol. 87: 193 – 203. https://doi.org/10.1016/S0378-1135(02)00050-0
- Lindley EP (1951). Paper submitted at the Fifth Veterinary Conference, Vom, Nigeria.
- Liu XF, Wan HQ, Ni XX, Wu YT, Liu WB (2003). Pathotypical and genotypical characterization of strains of Newcastle disease virus isolated from outbreaks in chicken and goose flocks in some regions of China during 1985–2001. Arch. Virol. 148: 1387–1403.
- Macpherson LW (1956). Some observations on the epizootiology of Newcastle disease. Can. J. Comp. Med. Vet. Sci. 20: 155 - 68.
- Maminiaina OF, Koko M, Ravaomanana J, Rakotonindrina SJ (2007). Epidemiology of Newcastle disease in village poultry farming in Madagascar. Rev. Sci.Technol. 26(3): 691 - 700. https://doi.org/10.20506/rst.26.3.1776
- Mapaco LP, Monjane IV, Nhamusso AE, Viljoen GJ, Dundon WG, Achá SJ (2016). Phylogenetic analysis of Newcastle disease viruses isolated from commercial poultry in Mozambique (2011-2016). Virus Genes. 52(5): 748 - 753. https://doi.org/10.1007/s11262-016-1362-6
- Maqbool A (2002). Marketing of commercial poultry, poultry meat and eggs in Faisalabad City. MSc Thesis University of Agriculture, Pakistan.
- Mase M, Imai K, Sanada Y, Sanada N, Yuasa N, Imada T (2002). Phylogenetic analysis of Newcastle disease virus genotypes isolated in Japan. J. Clin. Microbiol. 40(10): 3826 - 3830. https://doi.org/10.1128/JCM.40.10.3826-3830.2002
- Megahed MM, Eid AM, Mohamed W, Hassanin O (2018). Characterization of Egyptian Newcastle disease virus strains isolated from flocks vaccinated against Newcastle disease virus. Slov. Vet. Res. 55 (20): 17 – 29.
- Miller PJ, King DJ, Afonso CL, Suarez DL (2007). Antigenic differences among Newcastle disease virus strains of different genotypes used in vaccine formulation affect viral shedding after a virulent challenge. Vaccine, 25: 7238 - 7246. https://doi.org/10.1016/j.vaccine.2007.07.017
- Molini U, Aikukutu G, Khaiseb S, Cattoli G, Dundon WG (2017). First genetic characterization of Newcastle disease viruses from Namibia: Identification of novel VIIk subgenotype. Arch Virol. 162(8): 2427–2431. https://doi.org/10.1007/s00705-017-3389-y
- Miller PJ, Decanini EL, Afonso CL (2010). Newcastle disease: Evolution of genotypes and the related diagnostic challenges. Infect. Genet. Evol. 10: 26 - 35.
- Mohamed MH, Kumar S, Paldurai A, Megahed MM, Ghanem IA, Lebdah MA, Samal SK (2009). Complete genome sequence of a virulent Newcastle disease virus isolated from an outbreak in chickens in Egypt. Virus Genes. 39: 234 – 237.
- Mohamed MH, Kumar S, Paldurai A, Samal SK (2011). Sequence analysis of fusion protein gene of Newcastle disease virus isolated from outbreaks in Egypt during 2006. Virol. J. 8: 237.
- Mouhamed AA, Mohamed MA, Bakheet BM, Aziz El-Din KA, Song CS (2020). Molecular studies on Newcastle Disease virus isolates in relation to field vaccine strains in Egypt (2012-2015). Int. J. Poul. Sci. 19: 193-209. https://doi.org/10.3923/ijps.2020.193.209
- Msoffe PLM, Chiwanga GH, Cardona CJ, Miller PJ, Suarez DL (2019). Isolation and characterization of Newcastle disease virus from live bird markets in Tanzania. Avian Dis. 63: 634 - 640. https://doi.org/10.1637/aviandiseases-D-19-00089
- Mukiibi MG (1992). Epidemiology of Newcastle disease and the need to vaccinated local chickens in Uganda in:sparadbrow P.B(Ed.),Newcastle disease in village chickens control with thermostable oral vaccines proceeding NO 93of international workshop held in Kuala Lumpur, malasyia, Australia center for international agricultural research. 155 - 158.
- Nanthakumar T, Kataria RS, Tiwari AK, Butchaiah G, Kataria JM (2000). Pathotyping of Newcastle disease viruses by RT-PCR and restriction enzyme analysis. J. Vet. Res. Commun. 24: 275 - 286. https://doi.org/10.1023/A:1006403017578
- Nasser M, Lohr JB, Mebratu Y, Zesin KH, Ademe Z (1998). Oral feed-based Newcastle disease vaccination trials in Ethiopia with the Australia V4 vaccine strain .Scientific proceedings of the 4th Asia Pacific poultry health conference, November 22-26, Melbourne, Australia.129.
- Ogali IN, Okumu PO, Mungube EO, Lichoti JK, Ogada S, Moraa GK, Agwanda PR, Ommeh SC (2020). Genomic and pathogenic characteristics of virulent Newcastle Disease virus isolated from chicken in live bird markets and backyard flocks in Kenya. Int. J. Microbiol. ID 4705768, 11 pages. https://doi.org/10.1155/2020/4705768
- Ogali IN, Wamuyu LW, Lichoti JK, Mungube EO, Agwanda B, Ommeh SC (2018). Molecular characterization of Newcastle Disease virus from backyard poultry farms and live bird markets in Kenya. Int. J. Microbiol. ID 2368597, 11 pages. https://doi.org/10.1155/2018/2368597
- OIE (2009). Manual of diagnostic tests and vaccines for terrestrial animals: mammals, birds and bees. Biol. Standards Comm. 1(2): 576 - 589.
- OIE (2011). Newcastle Disease, In: Manual of diagnostic tests and vaccines for Lippincott Williams and Wilkins Inc, Philadelphia. 41: 1449 - 1496.
- OIE (2012). Newcastle disease. Chapter 2.3.14. OIE Manual of Standards for Diagnostic Tests and Vaccines, NB: Version adopted by the World Assembly of Delegates of the OIE in May 2012 http://www.oie.int/fileadmin/Home/eng/Health standards/tahm/2.03.14.
- Olabode AO, Shidali NN, Lamorde AG (1991). Epidemiology of Newcastle disease in Nigeria. In: Rweyemamu MM, Palya V, Win T, Sylla D (Eds) Newcastle Disease Vaccines for Rural Africa. Proceedings of a Workshop held at Pan African Veterinary Vaccine Centre (PANVAC), DebreZeit, Addis Ababa, Ethiopia. 53 – 59.
- Orabi A, Hussein A, Saleh AA, Abu ElMagd M, Munir M (2017). Evolutionary insights into the fusion protein of Newcastle disease virus isolated from vaccinated chickens 2016in Egypt. Arch. Virol. https://doi.org/10.1007/s00705-017-3483-1
- Perozo F, Villega P, Dol R, Afonso CL, Purvis LB (2008). The VG/GA strain of Newcastle disease virus: mucosal immunity, protection against lethal challenge and molecular analysis. Avian Patho. 37(3): 237 - 245. https://doi.org/10.1080/03079450802043734
- Provost C, Boredon C (1968). Revue Elev. Med. Vét. Pays Trop. 21: 165-179. https://doi.org/10.19182/remvt.7581
- Qin Z, Sun L, Ma B, Cui Z, Zhu Y, Kitamura Y, Liu W (2008). F gene recombination between genotype II and VII Newcastle disease virus. Virus Res. 131: 299 -303. https://doi.org/10.1016/j.virusres.2007.10.001
- Radwan MM, Darwish SF, El-Sabagh IM, El-Sanousi AA,

Shalaby MA (2013). Isolation and molecular characterization of Newcastle disease virus genotypes II and VIId in Egypt between 2011 and 2012. Virus Genes. 47(2): 311 - 316. https://doi.org/10.1007/s11262-013-0950-y
- Rajaonarison JJ (1991). Production de vaccincontre la maladie de Newcastle à Madagascar.Workshop on Newcastle disease vaccines for rural Africa. DebreZeit, Addis Ababa: Pan-African Veterinary Vaccine Centre.
- Saad AM, Hussein HA, Arafa A, Sultan H, Hassan MK, Aly MM (2010): Phylogenetic analysis and pathogenicity study of field Newcastle disease virus (NDV) strains isolated from chicken in Egypt. Proceeding of the third International Conference of Virology, Cairo University Conference Center. 53
- Sabra MKM, Dimitrov IV, Goraichuk L (2017). Phylogenetic assessment reveals continuous evolution and circulation of pigeon-derived virulent avian avulaviruses 1 in Eastern Europe, Asia, and Africa. BMC Vet. Res. 13: 1. https://doi.org/10.1186/s12917-017-1211-4
- Samal SK (2011). Newcastle disease and related avian paramyxoviruses, p 69 –114. In Samal SK (ed), The biology of paramyxoviruses. Caister Academic Press, Norfolk, United Kingdom.
- Samuel A, Nayak B, Paldurai A, Xiao S, Aplogan GL, Awoume KA, Webby RJ, Ducatez MF, Collins PL, Samal SK (2013). Phylogenetic and pathotypic characterization of Newcastle disease viruses circulating in West Africa and the efficacy of a current vaccine. J. Clin. Microbiol. 51: 771 – 781. https://doi.org/10.1128/JCM.02750-12
- Seal BS, King DJ, Locke DP, Senne DA, Jackwood MW (1998). Phylogenetic relationships among highly virulent Newcastle disease virus isolates obtained from exotic birds and poultry from 1989 to 1996. J. Clin. Microbiol. 36: 1141 - 1145. https://doi.org/10.1128/JCM.36.4.1141-1145.1998
- Seal BS, Wise MG, Pedersen JC (2005). Genomic sequences of low-virulence avian paramyxovirus-1 (Newcastle disease virus) isolates obtained from live-bird markets in North America not related to commonly utilized commercial vaccine strains. Vet. Microbiol. 106(1-2): 7 - 16. https://doi.org/10.1016/j.vetmic.2004.11.013
- Sharma RN, Hussein NA, Padney GS, Shandomo MN (1986). A study of Newcastle disease outbreaks in Zambia, 1975-1984. Rev. Sci. Tech. OIE. 5: 5 - 14. https://doi.org/10.20506/rst.5.1.233
- Shittu I, Sharma P, Volkening JD, Solomon P, Sulaiman LK, Joannis TM, Williams-Coplin D, Miller PJ, Dimitrov KM, Afonso CL (2016). Identification and Complete Genome Sequence Analysis of a Genotype XIV Newcastle Disease Virus from Nigeria. Gen. Announ. 4(1). https://doi.org/10.1128/genomeA.01581-15
- Snoeck CJ, Ducatez MF, Owoade AA, Faleke OO, Alkali BR, Tahita MC, Tarnagda Z, Ouedraogo JB, Maikano I, Mbah PO, Kremer JR, Muller CP (2008). Newcastle disease virus in West Africa: new virulent strains identified in non-commercial farms. Arch Virol. 154(1):47-54. https://doi.org/10.1007/s00705-008-0269-5
- Snoeck CJ, Ducatez MF, Owoade AA, Faleke OO, Alkali BR, Tahita MC, Tarnagda Z, Ouedraogo JB, Maikano I, Mbah PO, Kremer JR, Muller CP (2009). Newcastle disease virus in West Africa: new virulent strains identified in non-commercial farms. Arch. Virol. 154: 47–54.
- Snoeck CJ, Owoade AA, Couacy-Hymann E (2013). High genetic diversity of newcastle disease virus in poultry in west and central Africa: Cocirculation of genotype XIV and newly defned genotypes XVII and XVIII. J. Clin. Microbiol. 51(7): 2250 - 2260. https://doi.org/10.1128/JCM.00684-13
- Solomon P, Abolnik C, Joannis TM, Bisschop S. Virulent Newcastle disease virus in Nigeria (2012). identification of a new clade of sub-lineage 5f from livebird markets. Virus Genes. 44(1):98-103. https://doi.org/10.1007/s11262-011-0678-5
- Susta L, Jones ME, Cattoli G, CardenasGarcia S, Miller PJ, Brown CC, Afonso CL (2014). Pathologic Characterization of Genotypes XIV and XVII Newcastle Disease Viruses and Efficacy of Classical Vaccination on Specific PathogenFree Birds. Vet. Pathol.
- Tiwari AK, Katari RS, Nanthakumar T, Dash BB, Desai G (2004). Differential detection of Newcastle disease virus strains by degenerate primers based RT-PCR. J. Comp. Immunol. Microbiol. Infectious Dis. 27:163 - 169. https://doi.org/10.1016/j.cimid.2003.09.002
- Van Borm S, Obishakin E, Joannis T, Lambrecht B, van den Berg T (2012). Further evidence for the widespread co-circulation of lineages 4b and 7 velogenic Newcastle disease viruses in rural Nigeria. Avian Pathol. 41: 377 - 382. https://doi.org/10.1080/03079457.2012.696311
- Xiao S, Nayak B, Samuel A, Paldurai A, Kanabagattebasavarajappa M, Prajitno TY, Bharoto E.E, Collins PL, Samal SK (2012). Generation by reverse genetics of an effective, stable, live-attenuated Newcastle Disease virus vaccine based on a currently circulating, highly virulent Indonesian strain. PLoS One. 7(12): 52751. https://doi.org/10.1371/journal.pone.0052751
- Yongolo MG, Christensen H, Handberg K, Minga U, Olsen JE (2011). On the origin and diversity of Newcastle disease virus in Tanzania. Onderstepoort J. Vet. Res. 78: 312. https://doi.org/10.4102/ojvr.v78i1.312
- Zhang S, Wang X, Zhao C, Liu D, Hu Y, Zhao J, Zhang G (2011). Phylogenetic and pathotypical analysis of two virulent Newcastle disease viruses isolated from domestic ducks in China. PLoS One 6:e25000. https://doi.org/10.1371/journal.pone.0025000
- Zou J, Shan SH, Yao NT, Gong ZX (2002). Acta Bioch Bioph Sin. 34: 439 – 444.
- Zou J, Gong ZX (2003). Inhibition of replication of goose paramyxovirus SF02 by hammerhead ribozyme targeting to the SF02 F mRNA in chicken embryo fibroblasts', Sheng Wu Hua Xue Yu Sheng Wu Wu Li Xue Bao (Shanghai). 35(9): 801 – 805.