



## REVIEW ARTICLE

# Adaptation of Newcastle Disease Virus (NDV) in Feral Birds and their Potential Role in Interspecies Transmission

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### Abstract:

#### Introduction:

Newcastle Disease (ND), caused by Avian avulavirus 1 (AAvV 1, avulaviruses), is a notifiable disease throughout the world due to the economic impact on trading restrictions and its embargoes placed in endemic regions. The feral birds including aquatic/migratory birds and other wild birds may act as natural reservoir hosts of ND Viruses (NDVs) and may play a remarkable role in the spread of the virus in environment. In addition, other 19 avulaviruses namely: AAvV 2 to 20, have been potentially recognized from feral avian species.

#### Explantation:

Many previous studies have investigated the field prevailing NDVs to adapt a wide range of susceptible host. Still the available data is not enough to declare the potential role of feral birds in transmission of the virus to poultry and/or other avian birds. In view of the latest evidence related to incidences of AAvVs in susceptible avian species, it is increasingly important to understand the potential of viruses to transmit within the domestic poultry and other avian hosts. Genomic and phylogenomic analysis of several investigations has shown the same (RK/RQRR↓F) motif cleavage site among NDV isolates with same genotypes from domestic poultry and other wild hosts. So, the insight of this, various semi-captive/free-ranging wild avian species could play a vital role in the dissemination of the virus, which is an important consideration to control the disease outbreaks. Insufficient data on AAvV 1 transmission from wild birds to poultry and vice versa is the main constraint to understand about its molecular biology and genomic potential to cause infection in all susceptible hosts.

#### Conclusion:

The current review details the pertinent features of several historical and contemporary aspects of NDVs and the vital role of feral birds in its molecular epidemiology and ecology.

**Keywords:** Avian avulavirus 1 (AAvV 1), Wild and Migratory birds, Epidemiology, Phylogeny, Newcastle Disease (ND), Fusion gene.

## 1. INTRODUCTION

Newcastle Disease Virus (NDV) causes wide-spread mortality in poultry but clinical and subclinical presentations have also been observed in other avian species. Its causative agent belongs to *Avulavirus* genus under *Paramyxoviridae* family [1]. This family has the varied type of members which have been responsible to cause infections in several avian species including, domestic, captive/free-ranging wild, terrestrial, and aquatic birds globally [2 - 6]. Genus *Avulavirus* contains all the *Avian avulaviruses* (AAvVs) specie-types, causing clinical and subclinical infection in all avian species including poultry with interspecies transmission except for avian metapneumovirus. Based on Hemagglutination

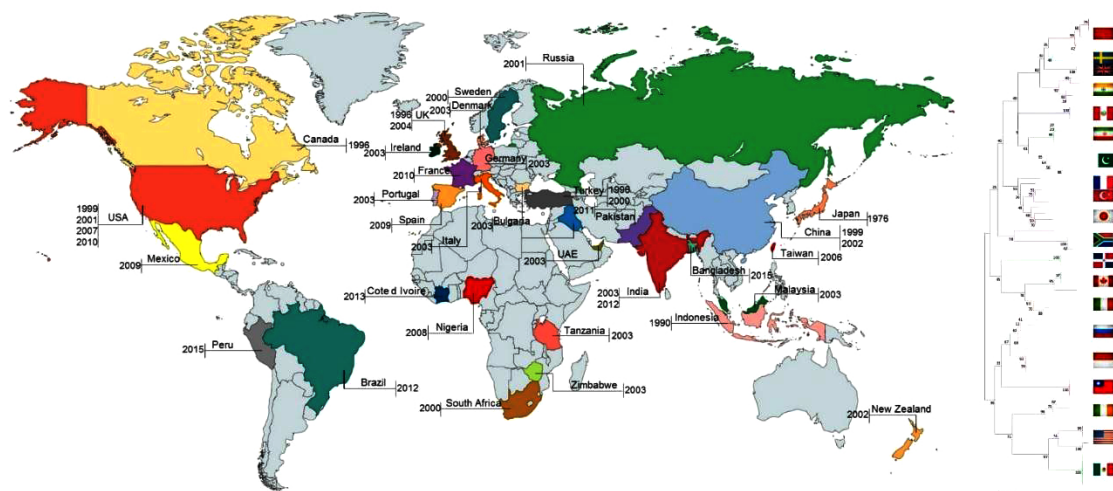
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Inhibition (HI) and Neuraminidase Inhibition (NI) tests [7], NDVs have been identified and classified into two different subgroups, AAvV 2 and 6 among 20 specie-types (AAvV 1 to 20) [8]. Of these, one antigenic variant of AAvV 1, causes severe infection and is responsible for epidemics in pigeon termed as Pigeon Paramyxovirus type 1 (PPMV-1) [9]. Since NDV (AAvV 1) is a highly contagious disease of poultry and other birds, it can create an alarming situation in developing countries.

So, to elucidate the interspecies transmission, attention on molecular epidemiology of AAvV 1 is the need of time. Alongside to this, the data about the molecular biology and pathogenesis of different avulaviruses 2-20 [Rahman *et al.*, 2018] is not enough to evaluate the virus mutation rate. AAvV 1 (or ND) is an OIE (Office International Epizootics; world organization for animal health) notifiable avian infection implicated with significant economic losses as well as natural genetic depletion of diverse hosts [5]. In the above context, the intention of this review is to provide a summary of overall pertinent evidence related to geographical distribution and susceptible host density of AAvV 1 with its temporal, terrestrial, and host density. However, up to date and comprehensive overview of the genetic diversity is the main consideration to assess the evolutionary analysis of NDVs among avian species. This review summarises, compares and discusses the available literature on NDVs genetic diversity and may be helpful to investigate the mutable aspects of NDVs in all genes particularly fusion (*F*) gene.

### 1.1. Geographical Distribution

Several avian species can spread the numerous microbes across the globe, which are harmful to captive and free-ranging birds including poultry [10, 11]. During the last few years, NDV and influenza virus have been found to be transmitted by migratory birds across the globe [12, 13]. It provided the strong evidence that wild avian species have been implicated in the transferring of NDV to domestic and wild bird population as biological carriers/ natural reservoir [14]. ND was first described in 1926 in Newcastle-on-Tyne, England (from where it got its name) and on the island of Java, now part of Indonesia, although there have been some suggestions that there may have been earlier outbreaks. It appears that initially the disease spreads rapidly in Asia [15] but slowly reported a series of devastating outbreaks around the globe including Africa, Central America and parts of South America [16 - 18]. A lot of outbreaks in different avian species associated with virulent NDV were reported from North America (USA, Canada and Costa Rica), Europe (France, Italy, England, Scotland, Spain and Russia), Africa (Kenya) and Asia (China, Japan, India, Israel, Saudi Arabia and Kazakhstan) [19] (Fig. 1).



**Fig. (1).** NDV from wild bird origin isolated in different regions/countries, also showed the geographical evolutionary relationship among these countries where it is endemic. For example, NDV from Pakistan, Iran, China and India grouped in same cluster.

Alongside poultry, NDV has been isolated from wild birds with incidences of virus transmission from wild psittacine/ cormorants to chickens in the United State during the 1970s and 1990s [20, 21]. The findings from these studies warrant the consistent monitoring of wild birds in a pause of virus dissemination. In India, many bird's species including chicken, turkey, quail, emu, duck, peacock, pigeon, duck and guinea fowl have been found as potential

susceptible host for NDV infection [22 - 29]. The current NDV epidemics in feral birds in Asian countries especially neighbours of India like Pakistan [17, 30] and Bangladesh [31] pose the threats to disease dissemination by sharing countries boundaries and the movement of migratory birds from one to another country. Regards to epidemiological context, different NDV strains are circulating in the field to infect the domestic and wild birds [32] that highlight the importance of the characterization of current prevailing NDV isolates from indigenous captive/semi-captive bird and from clinical or subclinical infection in free-ranging feral birds [33]. However, the interspecies transmission propensity of field circulating viruses may raise concerns about the efficacy of vaccine, used in the field. Various outbreaks have revealed the existence of vaccine strains of domestic poultry in wild birds from Mexico [34]. Moreover, vaccine NDV strain was confirmed in Australian wild bird [35] including feral birds in Japan [36], Finland [37], China [38], America [39] and in central Nigeria [40].

Except for Asian countries, zoo birds in Israel and Mexico have become infected with virulent NDV strains similar to those causing infection in domestic birds, which indicated the spill-over of virus in the environment [41]. In this account, the similar findings have been observed in Africa [42] and other continents [43, 44] which raised the concerns regarding the potential role of wild birds in shedding of NDVs in environment and transmission to poultry. Moreover, the existence of anti-NDV antibodies in feral birds of South Africa [45], Burkina Faso [46], and Nigeria [47] has also exposed the susceptibility of a wide range of avian hosts. The molecular detection, evolutionary dynamics and viral genetic manipulation will be helpful to control the epidemics and thus, we need to focus on the molecular and geographically epidemiology of NDV strains and should be perceived as an epidemiological alert to re-assess the control and quarantine measures against NDV [48, 49].

## 1.2. Genetic Variability of Newcastle Disease Virus

Avian avulaviruses are RNA viruses, having non-segmented, a single-stranded negative-sense genome with helical capsid symmetry. It has a molecular weight of about  $5 \times 10^6$  Da, with approximately 15.2 kb in length and encodes six structural and two non-structural proteins in the order 3'-NP-V/W/P-M-F-HN-L-'5 [50]. The surface projections on envelope are approximately 8 nm long, present on the HN molecule, whilst F molecules form smaller projections. The F protein has significance as a type-I integral membrane protein with the trans-membrane domain located in the carboxyl-terminal region followed by a short cytoplasmic domain [51], responsible for virulence. During the infection, the first HN protein of virus attaches to a cell and then fusion protein makes linkage for the invasion of viral genetic material into the host cell [52]. The virulence of NDV depends on the primary molecular determinant which is known as F protein cleavage site having specific amino acid sequence pattern and position [53]. The susceptible host got an infection when the cellular proteases cleave an inactive F0 precursor protein into F1 and F2 subunits [51]. The NDV pathotype totally depends on the F protein cleavage site having dibasic amino acids in velogenic and mesogenic strains, while the F protein of lentogenic NDV isolates lack this motif [51, 54]. The NDV isolates from migratory birds have shared the similar specific dibasic amino acid at the cleavage site of F gene which has been detected in chickens from the same area during an outbreak [55]. Usually, the virulent strain has RQK/RRF residue pattern whereas K/RQG/ERL residues [53] have been observed at specific position 112-117 in the NDV strain of low virulence [56] (Table 1). In comparison, a mutative NDV isolate has also been detected from a dove having a K for Q substitution at residue 114; evidence of adaptation of NDV to the environment [57, 58].

**Table 1. NDV susceptible host range with geographical distribution.**

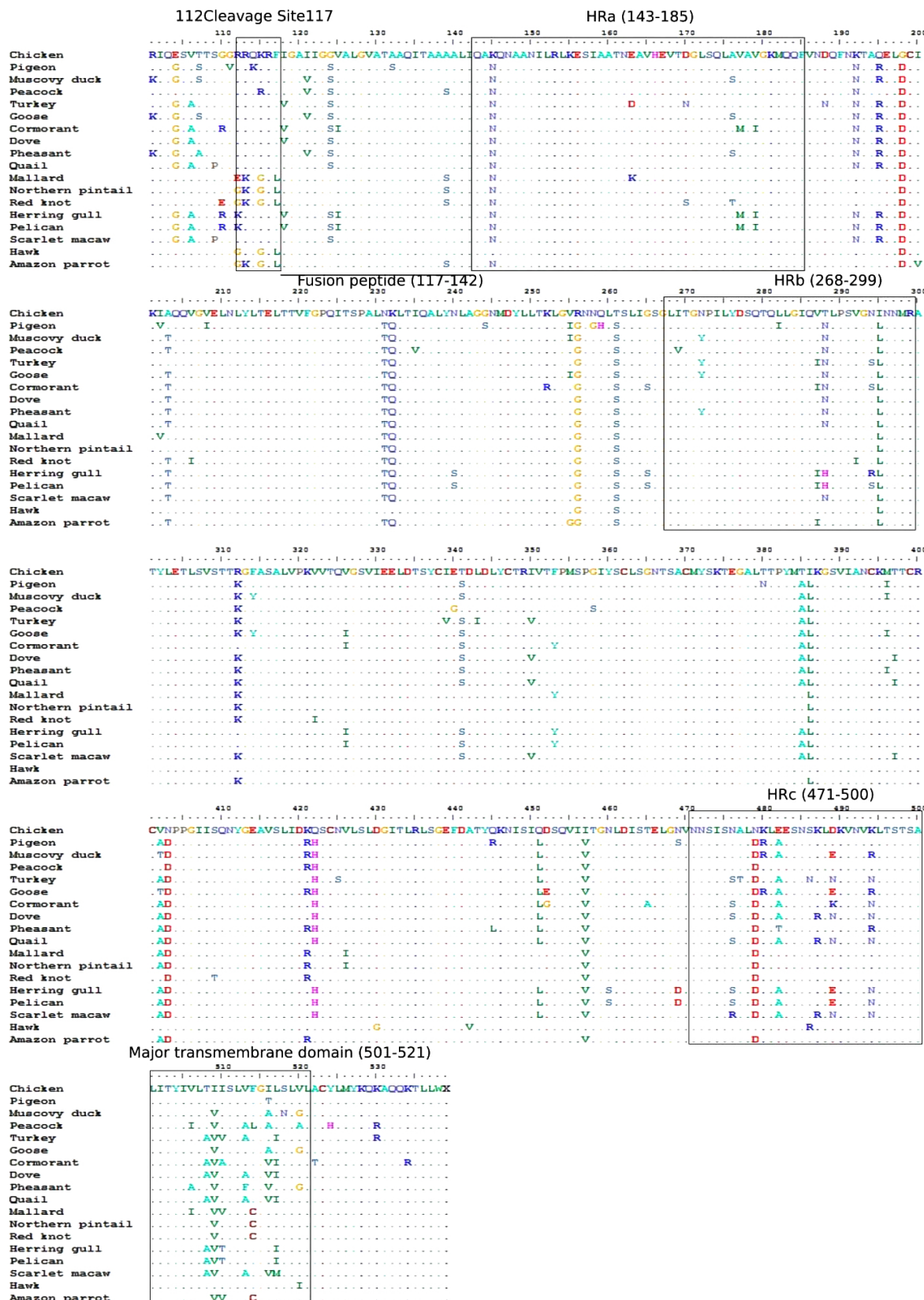
Accession No.	Host	Scientific Names	Year	Country	Genotype	CSP*	Virulence	References
FJ436303	Chicken	<i>Gallus gallus domesticus</i>	1986	China	IX	RRQRRF	virulence	[123]
FJ872531	Muscovy duck	<i>Cairina moschata</i>	2002	China	VII	RRQKRF	virulence	[124]
GQ288389	Mallard	<i>Anas platyrhynchos</i>	1999	USA	IIa	EKQGRL	avirulence	[48]
AY865652	Sterna	<i>S. hirundo</i>	2001	Russia	Vb	RRQRRF	virulence	[125]
JQ013039	Teal	<i>Anas crecca</i>	2010	France	Class I	ERQERL	avirulence	[126]
KJ627773	Crane	<i>Gruidae</i>	1992	India	-	GKQGRL	avirulence	[127]
KJ398400	Peafowl	<i>Pavo cristatus</i>	2012	India	VII	RRQRRF	virulence	[127]
AY581302	Guinea fowl	<i>Numididae</i>	2000	India	-	RRQRRF	virulence	[128]
GQ288391	Mottled duck	<i>Anas fulvigula</i>	2001	USA	IIa	GKQGRL	avirulence	[48]
GQ288378	Northern pintail	<i>Anas acuta</i>	1987	USA	IIa	GKQGRL	avirulence	[48]
EF564816	Red knot	<i>Calidris canutus</i>	2001	USA	Ia	GKQGRL	avirulence	[13]
AY289194	Turkey	<i>Meleagris gallopavo</i>	2003	Canada	-	GKQGRL	avirulence	[129]

(Table 1) contd.....

Accession No.	Host	Scientific Names	Year	Country	Genotype	CSP*	Virulence	References
JX854452	Pheasant	<i>Phasianus colchicus</i>	2011	Pakistan	VII	RRQKRF	virulence	[67]
KC934169	Blackbird	<i>Turdus merula</i>	2008	China	IX	RRQRRF	virulence	[130]
KC934170	Spotted dove	<i>Spilopelia chinensis</i>	2008	China	IX	RRQRRF	virulence	[130]
KC424431	White-checked starling	<i>Sturnus cineraceus</i>	2008	China	IX	RRQRRF	virulence	[131]
JN255774	Double-crested cormorant	<i>Phalacrocorax auritus</i>	2010	USA	VII	KRQKRF	virulence	[62]
JN255778	Black-backed gull	<i>Larus marinus</i>	2010	USA	VII	KRQKRF	virulence	[62]
JN255779	Herring gull	<i>Larus argentatus</i>	2010	USA	VII	KRQKRF	virulence	[62]
JN941993	Pelican	<i>Pelecanus</i>	2008	USA	-	KRQKRF	virulence	[132]
KC808510	Scarlet macaw	<i>Ara macao</i>	2009	Mexico	Vb	RRQKRF	virulence	[34]
KC503422	Spectacled eider	<i>Somateria fischeri</i>	2007	USA	Ib	GKQGRL	avirulence	[133]
KC503482	Slaty-backed gull	<i>Larus schistisagus</i>	2007	USA	Class I	GKQGRL	avirulence	[133]
AY562985	Cockatoo	<i>Cacatuidae</i>	1990	Indonesia	VIIId	RRQKRF	virulence	[134]
KF740478	Japanese quail	<i>Coturnix japonica</i>	2003	India	VII	RRQKRF	virulence	[135]
JN599167	Penguin	<i>Spheniscidae</i>	1999	China	VII	RRQKRF	virulence	[136]
AY471773	Budgerigar	<i>Melopsittacus undulatus</i>	1995	Turkey	VIIId	RRQKRF	virulence	[137]
HG326606	Spur-winged goose	<i>Plectropterus gambensis</i>	2008	Nigeria	I	GKQGRL	avirulence	[42]
HM063424	Water rail	<i>Rallus aquaticus</i>	2005	China	I	GKQGRL	avirulence	[138]
HM063425	Wild pigeon	<i>Columba livia</i>	2003	China	VI	RRQKRF	virulence	[138]
AF109886	Finches	<i>Fringillidae</i>	1997	UK	Ve	RRQKRF	virulence	[139]
AF091623	Goosander	<i>Mergus merganser</i>	1996	UK	Vb	RRQRRF	virulence	[139]
AY471818	Fantail	<i>Rhipidura</i>	1996	Turkey	VIIc	GRQKRF	avirulence	[137]
AY471721	Falcon	<i>Falconiforme</i>	2000	Turkey	VIIIf	RRQKRF	virulence	[137]
AY471785	Kestrel	<i>Falco tinnunculus</i>	1999	Turkey	VIIId	RRQKRF	virulence	[137]
AY471843	Turtle dove	<i>Streptopelia turtur</i>	1996	Turkey	VIIb	GRQKRF	avirulence	[137]
KC808497	Egret	<i>Ardea alba</i>	2009	Mexico	II	GRQGRL	avirulence	[34]
KC808491	Robin	<i>Turdus grayi</i>	2009	Mexico	II	GRQGRL	avirulence	[34]
KC808490	Yellow-napped parrot	<i>Amazona auropalliata</i>	2009	Mexico	II	GRQGRL	avirulence	[34]
KC808489	Hawk	<i>Buteo brachyurus</i>	2009	Mexico	II	GRQGRL	avirulence	[34]
KC808487	Oropendola	<i>Zacua spp.</i>	2009	Mexico	II	GRQGRL	avirulence	[34]
KC808493	Amazon parrot	<i>Amazona autumnalis</i>	2009	Mexico	Ia	GRQGRL	avirulence	[34]
KC808494	Chachalaca	<i>Ortalis vetula</i>	2009	Mexico	Ia	GRQGRL	avirulence	[34]
KC808498	Guan	<i>Penelopina nigra</i>	2009	Mexico	Ia	GRQGRL	avirulence	[34]
FJ938175	Sparrow	<i>Passer domesticus</i>	2005–2007	China	VII	RRQKRF	virulence	[140]
EF564817	Ruddy turnstone	<i>Arenaria interpres</i>	2002	USA	Ia	GKQGRL	avirulence	[13]
JX855036	Crested Ibis	<i>Nipponia nippon</i>	2013	China	VIIId	RRQKRF	virulence	116
JF820295	Ostrich	<i>Struthio camelus</i>	2011	Iran	VII	RRQKRF	virulence	141

Although, F protein is highly conserved among all isolates consisting of a series of Heptad Repeat (HR) regions [51], some sort of mutations have also been observed in it such as the mutation of the L at position 154 in the HR1 region from residues 130 to 170 interferes in cell fusion [59]. In addition, substitutions in the other conserved regions like HR2 region from N-terminal to the TM domain, a helical region HR3 domain from residues 263 to 289 and another helical domain HR4 from residues 81 to 102 [60, 61] have been observed (Fig. 2). Based on the evolutionary estimation, the F gene divergences of 1-18% between NDVs isolates from chicken-origin and wild-origin [62], and it was highly similar to the hawk origin NDV strain with 2% divergence. Although, NDVs from wild bird origin had nucleotide homologies of up to 99.8% and low homologies of 82% with chicken origin NDVs [63].

In addition, NDVs originated from quail and dove showed a minor nucleotide difference (15%) when compared to isolates from chicken, but these did not exhibit any significant antigenic differences (1%) between them. Similarly, duck and goose shared only 1% nucleotide dissimilarity (Table 2). To date, the complete genome sequences of a number of strains of AA<sub>v</sub>V 1-20 [64, 65] have been published. The genetic information was available only from Nigeria [66], Pakistan [17, 67], India [29, 33, 68, 69], China [70] and South Africa [71], but still, a wide range of birds remains uncovered to investigate the potential of NDV to transmit and infect diverse host range.



**Fig. (2).** Alignment of deduced amino acid sequence of complete F gene of NDV isolate from different wild birds with reference of chicken isolate with accession numbers AY562991, JX901111, FJ872531, HQ011508, JN942045, HG326605, GQ288385, GQ429293, JX854452, KC808512, KJ920203, EF612277, EF564816, JN255779, JN941993, KC808510, KC808489, KC808493 from chicken to amazon parrot, respectively. Structurally and functionally important residues are boxed and highlighted based on residue profile to explore similarities among them.

Table 2. The nucleotide based genome homology of different NDVs isolated from a wide range of wild/feral birds

	% Nucleotide Divergence and Homology Between Each Pair of Isolates																		
	Chicken	Pigeon	Muscovy duck	Peacock	Turkey	Goose	Cormorant	Dove	Pheasant	Quail	Mallard	Sterna	Northern pintail	Red knot	Herring gull	Pelican	Scarlet macaw	Hawk	Amazon parrot
Chicken		0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.01
Pigeon	0.17		0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Muscovy duck	0.17	0.11		0.01	0.01	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Peacock	0.14	0.14	0.13		0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Turkey	0.18	0.15	0.14	0.15		0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Goose	0.17	0.12	0.01	0.14	0.15		0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Cormorant	0.18	0.15	0.13	0.16	0.10	0.14		0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.01	0.01	0.01
Dove	0.15	0.12	0.11	0.12	0.06	0.11	0.07		0.01	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.01	0.01
Pheasant	0.18	0.13	0.08	0.15	0.15	0.08	0.16	0.13		0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Quail	0.15	0.13	0.11	0.13	0.07	0.11	0.08	0.01	0.14		0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.01	0.01
Mallard	0.11	0.16	0.16	0.13	0.18	0.16	0.18	0.15	0.17	0.16		0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Sterna	0.18	0.12	0.09	0.14	0.14	0.09	0.15	0.12	0.11	0.12	0.17		0.01	0.01	0.01	0.01	0.01	0.01	0.01
Northern pintail	0.10	0.16	0.15	0.14	0.17	0.15	0.17	0.15	0.16	0.15	0.04	0.16		0.01	0.01	0.01	0.01	0.01	0.01
Red knot	0.14	0.17	0.16	0.15	0.17	0.17	0.19	0.16	0.17	0.16	0.12	0.16	0.12		0.01	0.01	0.01	0.01	0.01
Herring gull	0.18	0.15	0.14	0.16	0.11	0.14	0.04	0.08	0.16	0.09	0.18	0.15	0.18	0.19		0.00	0.01	0.01	0.01
Pelican	0.18	0.15	0.14	0.16	0.10	0.14	0.04	0.08	0.16	0.08	0.18	0.15	0.17	0.18	0.01		0.01	0.01	0.01
Scarlet macaw	0.16	0.13	0.11	0.13	0.07	0.12	0.08	0.02	0.14	0.01	0.16	0.13	0.16	0.17	0.09	0.08		0.01	0.01
Hawk	0.02	0.17	0.17	0.14	0.18	0.17	0.19	0.15	0.18	0.15	0.11	0.17	0.10	0.14	0.18	0.18	0.16		0.01
Amazon parrot	0.11	0.15	0.14	0.13	0.16	0.15	0.17	0.13	0.14	0.14	0.10	0.14	0.09	0.08	0.17	0.16	0.15	0.11	

### 1.3. Host Range

According to the world organization for animal health (WHO), ND is a contagious disease affecting more than 250 avian species around the globe [72]. In this context, a lot of free-ranging aquatic fowls are considered as a potential carrier of AAvV 1 [7, 73]. In 1946, after the first evidence of virulent strain of NDV in United States of America and Mexico, wild migratory avian and white storks were found to be susceptible for virulent NDV strain [74, 75]. Such kind of circumstantial evidence revealed the potential of virus and mode of transmission AAvV 1 by implicating wild birds to poultry [14]. It is not only about migratory birds, some recreational birds and captive wild birds also seemed to be as a natural reservoir/ carrier and susceptible hosts of NDVs [76]. Previously, the incidences of NDVs in wild and migratory aquatic birds [37], pigeons [36, 40], Peacock [17, 29, 33, 68], pheasant [67], duck and geese [70] have been reported.

NDV as a mutable RNA virus has the ability to cross interspecies barrier by mutating itself. Related evidence has been observed in Luxembourg, where lentogenic viruses highly similar to the LaSota strain were isolated from waterfowl subsequent to spill over and interspecies adaptation [42]. In another previous study related to Turkey, the causative virus was identified in genotype Ia along with several cases of NDVs in wild birds which were kept in live bird's market [77]. Taken together, it was suggested that viruses from wild birds may spill over into poultry. Based on AAvVs genetic diversity analysis, the viral transmission between wild birds and poultry was proved, previously [13, 42, 78, 79]. Furthermore, the NDV strains isolated from wild birds could cause outbreaks in chickens. For example, NDV isolates from migrating cormorants were identified as the likely source of epidemic in poultry. The interaction between wild birds and poultry happens frequently; the wild birds possibly play a pivotal role in the evolution of NDV for the adaptation of environment [78, 80].

Interestingly, it has been shown that double-crested cormorant is an important reservoir of NDVs among all feral bird population [81]. Similarly, pigeons and mallards have been suggested to be the reservoir of NDVs [82, 83]. In New Zealand, NDV has been isolated from a red-breasted musk parrot following its seizure after illegal importation forms Fiji [84]. Specifically, waterfowls are considered important reservoirs of NDVs and may act as a carrier for NDV transfer to poultry, causing outbreaks of different pathogenicity [12, 85, 86]. In recent years, a disease resembling those of ND has been reported in ducks and geese in the regions of China [87]. Thus, it could be inferred that feral birds are carriers of virulent strains but transmission pattern of virulent NDV strains is not yet fully understood.

Small wild birds mainly Passeriformes can also transmit NDVs due to their peri-domestic habits and some avian



species are playing a significant role in epizootiology of NDVs [4]. NDV had also been recovered from domestic duck farms [88] and wild birds [89], which raise concerns regarding NDV transmission among several avian species. So, few reports on mortality in free-living birds other than feral pigeons (*Columba livia*), recently captured teal (*Anas crecca*) [90], double-crested cormorants (*Phalacrocorax auritus*), white pelicans (*Pelecanus erythrorhynchos*), and gulls (*Larus spp.*), raised the concerns about apparent epizootic nature of the virus [91]. In North America, during ND outbreaks, virulent strains of NDV of non-poultry origin have been reported from cormorants, gulls and pelicans [62, 92], and NDV strain of low virulence has been isolated from gulls, shorebirds, and waterfowl as part of avian influenza surveillance [12, 93]. NDV strains of variable virulence have also been isolated from wild pigeons and doves [94, 95]. In view of host susceptibility, NDVs have been reported from a quite wide range of various feral birds, including wild, aquatic and recreational birds (Table 1). Although a variety of wild birds are susceptible to ND, the information available is limited due to the non-availability of clinical/necropsy samples and poor disease surveillance in feral avian population. Thus, there is a need for NDV surveillance in all susceptible wild birds to insight the evolution and adaptation of virus for controlling ND outbreaks worldwide.

#### 1.4. Clinico-pathological Presentation of NDV

Based on pathogenicity, NDVs are classified into different four stains [19]. First, the Velogenic Viscerotrophic NDV (VVNDV) formerly Dolye form, responsible for acute and lethal infections causing hemorrhagic lesions in visceral organs. Second, the Velogenic neurotrophic NDV (VNNDV) formerly Beach form, responsible for high mortality involve in respiratory and neurologic signs (gut lesions are absent). Third, the Mesogenic NDV formerly Beaudette form causes low mortality with acute respiratory disease and nervous signs. At four, the Lentogenic or asymptomatic enteric NDV formerly Hitchner form is a virulent virus that appears to replicate primarily in the gut with mild or inapparent respiratory infections [96].

Wild and migratory birds were considered the natural reservoirs of NDV and harboured mainly Lentogenic strains but occasionally Velogenic strains have potential to shed in the environment [42, 89, 97]. Mortality in wild birds such as pigeon, juvenile double-crested cormorants (*Phalacrocorax auritus*) and teal (*Anas crecca*) has also been reported due to the infection caused by Velogenic strains [25, 29, 62, 74, 92]. Highly virulent viruses from psittacines and in a variety of zoo and live market birds have also been isolated [42, 98 - 100]. Depend on infection, strain, dose rate, route of exposure, hostage, immunological status and environmental conditions, signs can range from no clinical presentation to neurologic signs, paralysis, and/or acute death [19]. However, few pathotypes are responsible for peracute infection with almost 100% mortality to subclinical disease with no lesions [93].

##### 1.4.1 Galliformes, Anseriformes and Columbiformes Birds

Turkey is a susceptible host to vNDV with clinical signs of depression, nasal discharge, blood-tinged diarrhea and nervous incoordination [101]. Partridges and pheasants are considered to be extremely sensitive to vNDV [102] with similar clinical signs as observed in chickens from the acute onset with high mortality, severe nervous signs to inapparent infection [7]. In a study, neurological signs in experimentally infected ducks with a mesogenic NDV strain were also observed [103]. Similarly, the goose was also reported as a susceptible host for NDV [104, 105] with moderate to severe depression, anorexia, diarrhea, ocular and nasal discharges, and swelling of the eyelids [87]. Histopathologically, the susceptibility of birds was characterized by multifocal areas of ulceration and hemorrhages in the esophagus, gizzard, and multifocal necrosis of the intestinal mucosa [106]. Ulceration and fibrin deposition in the intestinal mucosa and over the cecal tonsils, severe atrophy of lymphoid organs, and lymphoid depletion, multifocal areas of necrosis in the pancreas and less frequently in the liver were also observed. In a few cases, the brain was affected by neuronal degeneration present [106]. These types of investigation have clear evidence about the interspecies transmission prosperity of NDV.

In pigeons, ND is caused by pigeon specific variant of ND virus known as pigeon paramyxovirus-1 (PPMV-1) [58]. The outbreak in pigeon was reported first time in the Middle East during 1970 and spread to Europe during 1980 and now become endemic around the globe [81]. Neurological signs and diarrhea are major clinical signs seen mainly in young birds [107]. Gross lesions in pigeons infected with PPMV-1 from natural outbreaks consist of pancreatic necrosis, enteritis, and proventricular hemorrhages [108]. Histologically, lesions consist of non-suppurative encephalitis, multifocal necrosis in spleen, bursa, liver, larynx, and pancreas, and multifocal accumulation of lymphocytes in several organs [108] with spleen enlargement and perivascular cuffing in the cerebellum and brainstem [101].

#### 1.4.2 Psittaciformes, Passeriformes and Suliformes Birds

NDVs were also isolated from non-domesticated species of *Psittaciformes* and *Passeriformes* [4] with neurological signs in psittacine and *Passeriformes* birds [109]. Different cases of ND were also reported in six different states of the United States in 1991 [110]. Clinical signs included tremors, lateral recumbency, respiratory distress, greenish diarrhea, ruffled plumage, and head drawn back between the shoulders, and eventual death. The VVND viruses were isolated from affected birds, including yellow-headed Amazon parrots (*Amazona ochrocephala oratrix*), yellow-naped Amazon parrots (*Amazona ochrocephala auropalliata*), cockatiels (*Nymphicus hollandicus*), and Canaries (*Serinus canarius*). In another study, VVNDV was isolated from experimentally infected birds including budgerigars (*Melopsittacus undulates*), Amazon parrots (*Amazona ochrocephala auropalliata*), and Canaries (*Serinus canaries*) with neurological signs consisting of tremors, ataxia, wing droop, and uni or bilateral leg paralysis [111].

Histopathology following exposure to VVNDV results in haemorrhages and necrosis of the intestinal mucosa, haemorrhages on the skullcap and around the orbit, fibrinous peritonitis, hepatosplenomegaly, focal hepatic necrosis, airsacculitis, and hemorrhagic tracheitis in the Canaries, Amazon parrots, and budgerigars. These birds were also able to spread the virus and infect cage-mates. Shedding of VVNDV has been observed for more than 1 year in Amazon parrots and for more than 80 days in budgerigars, both enabled in the spread of virus in the environment [111]. NDV outbreaks in double-crested cormorant (*Phalacrocorax auritus*) populations [112] were also reported with neurological signs including prominent gross lesions of enlarged and mottled spleen associated with bursal atrophy and multifocal hemorrhagic foci in the meninges [112]. Histologically, lesions having multifocal nonsuppurative encephalitis with areas of gliosis appeared more prominent in the cerebellar white matter, interstitial nephritis and multifocal myocarditis [113]. Isolation of NDVs from commercial or feral birds reported no associated clinical signs [114, 115]. So, based on previous studies, existence and transmission of NDVs among different avian species including domesticated and wild birds with a variable clinical infection impose the continuous surveillance of wild and migratory birds.

#### 1.5. Phylogenetic Analysis of Wild Originated NDVs

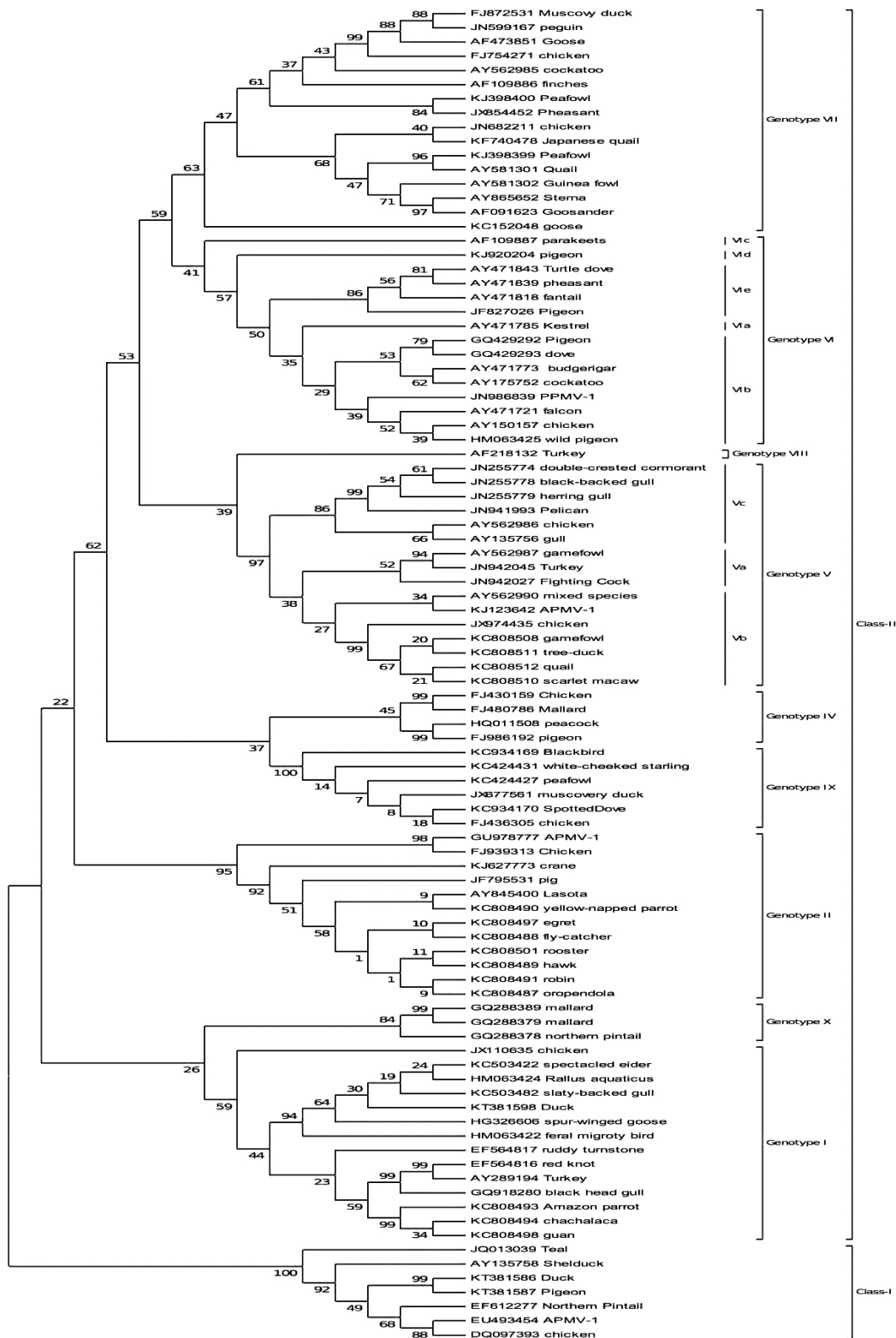
Two major classes (class I and II) of NDVs were premeditated according to genome length-based phylogenetic analysis [74]. In class I, there are atleast nine different genotypes, while in class II comprised of eighteen genotypes (I–XVIII) (Maminiaina *et al.*, 2010; Meng *et al.*, 2012). In class II, the genotypes VI and VII were further divided into nine (a-i) and five (a-e) sub-genotypes, respectively [116]. Noteworthy, Munir *et al.* [17] concluded that the isolates can be divided into six broadly distinct lineages (1 to 6). Of these, lineage 3 and 4 further subdivided into four (a-d) and five (a-e) sub-lineages, respectively. According to the phylogenetic analysis, most of NDV strains from pigeon or dove were classified into genotype VI [117] often considered as mesogenic strains, and a little information about other genotypes NDV from *Columbidae* was recorded [32, 92]. The diversity was found in amino acid sequences of *F* genes of NDVs, all publicly available isolates at GenBank®, indicating the evolutionary and mutative potential of NDVs. Dissimilarities among vaccine strain and field isolates from genotype V of class II have also been reported [74, 118], that aid in viral shedding, further, the persistence of NDVs in backyard poultry and free-living wild birds, explaining why vNDV caused sporadic outbreaks in the poultry industry until recently [119].

Similarly, phylogenetic relationships of non-virulent NDV strains in shorebirds and waterfowl provide support for the spread of viruses among different avian species and geography (12, 94). Virulent NDVs of identical genetic make-up were isolated from wild pigeons and doves in the United States, providing the evidence of virus spread from the different origin within different avian species and geography of North America [95, 96]. However, intercontinental transport of viruses may be attributed to the trade of racing pigeons. Thus, dissemination of NDVs within North America is supported, but evidence for intercontinental virus spread by migratory birds is limited. Thus, previous studies on genetic diversity among strains of NDVs revealed that some strains from wild birds were phylogenetically related with NDVs isolated from live-bird markets (12, 42). One previous study from Africa revealed the different host adaptation of NDVs where, the domestic pigeons originated NDVs of genotype VI have been found responsible for causing infection in different birds, such as feral pigeons and doves [57]. Such type of transmission has also been reported with high mortality rates in other studies [96, 120] This actually points out the viral evolution for adaptation of hosts leads to constrain in its eradication.

So far, among wild birds, virulent NDVs seem enzootic not only in cormorants in North America [62] but also in pigeons worldwide [87, 95]. Additionally, viruses from genotype XVIII have been reported from wild birds in the United States. Phylogenetically, the viruses originated from wild birds showed a close relationship to strains isolated from live birds markets [121], raise the questions about interspecies transmission of NDVs for the conservation of



endangered wild birds. Such findings highlight the potential of NDVs to transmit *via* migration of wild birds, which are natural reservoirs of NDVs [55]. Furthermore, isolation of virulent NDVs from wild aquatic birds raise the concern that wild and migratory waterfowls could play a role as a long-distance vector of virulent NDV, highlighting the need for increased NDV surveillance in aquatic fowls [89].



**Fig. (3).** Molecular phylogenetic analysis of fusion (F) gene by a maximum likelihood method conducted in MEGA6. All NDV isolates showed an evolutionary relationship with chicken origin NDVs and also with other wild or captive bird's origin NDVs.

To estimate the evolutionary distances between wild birds originated NDV strains, complete *F* gene-based phylogenetic analysis was performed by the maximum composite likelihood method in MEGA6 software [122]. The evolutionary analysis of already reported wild bird originated NDVs revealed the strong relationship among all NDVs originated from wild birds, domestic birds and poultry (Fig. 3).

In this figure, NDVs from different feral birds showed a strong evolutionary relationship with the poultry originated strains as mentioned in class I and II and also clustered within different genotypes. Generally, the velogenic NDV strains from poultry origin have been clustered in genotype VII but NDVs from wild bird's origin are also found in genotype IX, V and class I beyond its pathotype properties. Such type of grouping of NDV strain in different genotype points out the continuous evolution of field circulating viruses, which may be due to the vaccine failure because, in many countries, NDV epidemics have been observed in vaccinated birds. Therefore, the active surveillance and monitoring of wild birds can help us prevent the disease transmission in all susceptible host and evolution of NDVs.

## CONCLUDING REMARKS

Based on the previous molecular investigations, it can be concluded that poultry and non-poultry host cohabiting raise NDV epidemics around the globe particularly in endemic countries. Phylogenetic analysis of wild and domestic originated NDVs provided such evidence, which supports that wild birds are contributing to the global redistribution of NDVs alongside the regular vaccination but only in poultry. The cleavage site in F protein of the NDVs has been found to be an important factor contributing to the pathogenesis in hosts. However, few mutations have been observed in different isolates originated from different bird's species, result in variability of virulence. So, the investigation of genetic variation and isolate's evolutionary analysis can provide valuable data on characterization, epidemiology among different avian species and diagnosis of NDVs circulating in the environment. In future, the attention of the global scientific community towards these aspects would help to elucidate the complete epidemiology trends of NDVs and to validate the robustness of diagnostic screening, particularly in endemic countries. In addition, a continuous surveillance of wild and migratory/aquatic fowls will share the information to design the appropriate control strategies.

## CONSENT FOR PUBLICATION

Not applicable.

## CONFLICT OF INTEREST

The author declares no conflict of interest, financial or otherwise.

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## REFERENCES

- [1] ICTV. International Committee on Taxonomy of Viruses Virus Taxonomy. [https:// talk.ictvonline.org/ ictv-reports/](https://talk.ictvonline.org/ictv-reports/) [https:// talk.ictvonline.org/ taxonomy/ p/ taxonomy- history?taxnode\\_id=20161031](https://talk.ictvonline.org/taxonomy/p/taxonomy-history?taxnode_id=20161031). 2017. Accessed July 2017
- [2] Wang LF, Eaton BT. Emerging paramyxoviruses. *Infect Dis Rep* 2001; 3: 52-69.
- [3] Lamb RA, Parks GD. *Paramyxoviridae: The viruses and their replication*. In: Knipe, D.M., Howley, P.M. (Eds.), *Fields Virology*, 5<sup>th</sup> ed. Lippincott Williams and Wilkins, Philadelphia, 2007; 1449-96.
- [4] Alexander DJ, Aldous EW, Fuller CM. The long view: A selective review of 40 years of Newcastle disease research. *Avian Pathol* 2012; 41(4): 329-35. [<http://dx.doi.org/10.1080/03079457.2012.697991>] [PMID: 22834545]
- [5] OIE. Newcastle disease. In *Manual of diagnostic tests and vaccines for terrestrial animals*. OIE, Paris, France. 2012.[http:// www.oie.int/ fileadmin / Home/eng/ Health\\_standards/ tahm/2.03.14\\_NEWCASTLE\\_DIS.pdf](http://www.oie.int/fileadmin/Home/eng/Health_standards/tahm/2.03.14_NEWCASTLE_DIS.pdf)
- [6] Dimitrov KM, Ramey AM, Qiu X, Bahl J, Afonso CL. Temporal, geographic, and host distribution of avian paramyxovirus 1 (Newcastle disease virus). *Infect Genet Evol* 2016; 39: 22-34. [<http://dx.doi.org/10.1016/j.meegid.2016.01.008>] [PMID: 26792710]
- [7] Alexander DJ. Newcastle disease, other avian paramyxoviruses, and pneumovirus infection. In: *Disease of poultry*, ed. Shaif YM, Barnes HJ, Glisson JR, et al., 12<sup>th</sup> ed., pp. 75-100. Blackwell, Oxford, UK. 2003.
- [8] Munir M, Shabbir MZ. Comparative evolutionary and phylogenomic analysis of *Avian avulaviruses* 1 to 20. *Mol Phylogenet Evol* In press
- [9] Lipkind M, Shihmanter E. Antigenic relationships between avian paramyxoviruses. I. Quantitative characteristics based on hemagglutination and neuraminidase inhibition tests. *Arch Virol* 1986; 89(1-4): 89-111.

- [http://dx.doi.org/10.1007/BF01309882] [PMID: 2424406]
- [10] Hubalek Z. Pathogenic microorganisms associated with free-living birds (a review). *Acta Scientiarum Naturalium Brno* 1994; 28: 174.
- [11] Hubálek Z. An annotated checklist of pathogenic microorganisms associated with migratory birds. *J Wildl Dis* 2004; 40(4): 639-59. [http://dx.doi.org/10.7589/0090-3558-40.4.639] [PMID: 15650082]
- [12] Stroud DA, Davidson NC, West R, *et al.* Status of migratory wader population in Africa and Western Eurasia in the 1990s. *Int water studies* 2004; 15: 1-259.
- [13] Dhama K, Mahendran M, Tomar S. Pathogens transmitted by migratory birds: Threat perceptions to poultry health and production. *Int J Poultry Sci* 2008; 7: 516-25. [http://dx.doi.org/10.3923/ijps.2008.516.525]
- [14] Kim LM, King DJ, Suarez DL, Wong CW, Afonso CL. Characterization of class I Newcastle disease virus isolates from Hong Kong live bird markets and detection using real-time reverse transcription-PCR. *J Clin Microbiol* 2007; 45(4): 1310-4. [http://dx.doi.org/10.1128/JCM.02594-06] [PMID: 17287322]
- [15] Doyle TM. A hitherto unrecorded disease of fowls due to a filter-passing virus. *J Comp Pathol Ther* 1927; 40: 144-69.
- [16] Alexander DJ. Orthomyxoviridae—avian influenza. *Poultry diseases* 2008; 317. [http://dx.doi.org/10.1016/B978-0-7020-2862-5.50031-3]
- [17] Munir M, Abbas M, Khan MT, Zohari S, Berg M. Genomic and biological characterization of a velogenic Newcastle disease virus isolated from a healthy backyard poultry flock in 2010. *Virology* 2012; 9: 46. [http://dx.doi.org/10.1186/1743-422X-9-46] [PMID: 22340092]
- [18] Pedersen K, Marks DR, Arsnoe DM, *et al.* Avian paramyxovirus serotype 1 (Newcastle disease virus), avian influenza virus, and *Salmonella* spp. in mute swans (*Cygnus olor*) in the Great Lakes region and Atlantic Coast of the United States. *Avian Dis* 2014; 58(1): 129-36. [http://dx.doi.org/10.1637/10638-081413-Reg.1] [PMID: 24758125]
- [19] Alexander DJ, Senne DA. Newcastle disease, other avian paramyxoviruses and pneumovirus infections, p 75-100. In Saif YM, Fadly AM, Glisson JR, McDougald LR, Nolan LK, Swayne DE (ed), *Diseases of poultry*, 12<sup>th</sup> ed. Blackwell Publishing, Ames, IA. 2008.
- [20] Walker JW, Heron BR, Mixson MA. Exotic Newcastle disease eradication program in the United States. *Avian Dis* 1973; 17(3): 486-503. [http://dx.doi.org/10.2307/1589147] [PMID: 4748340]
- [21] Wobeser G, Leighton FA, Norman R, *et al.* Newcastle disease in wild water birds in western Canada, 1990. *Can Vet J* 1993; 34(6): 353-9. [PMID: 17424240]
- [22] Roy P, Venugopalan AT, Manvell R. Characterization of Newcastle disease viruses isolated from chickens and ducks in Tamilnadu, India. *Vet Res Commun* 2000; 24(2): 135-42. [http://dx.doi.org/10.1023/A:1006416724050] [PMID: 10720099]
- [24] Chang PC, Hsieh ML, Shien JH, Graham DA, Lee MS, Shieh HK. Complete nucleotide sequence of avian paramyxovirus type 6 isolated from ducks. *J Gen Virol* 2001; 82(Pt 9): 2157-68. [http://dx.doi.org/10.1099/0022-1317-82-9-2157] [PMID: 11514725]
- [25] Kataria JM, Dhama K. Sohini Dey, Madhan Mohan C. Ranikhet Disease in Pigeon. *Poultry World* 2006; 1(6): 16-8.
- [26] Naveen KA, Singh SD, Kataria JM, Barathidasan R, Dhama K. Detection and differentiation of pigeon paramyxovirus serotype-1 (PPMV-1) isolates by RT-PCR and restriction enzyme analysis. *Trop Anim Health Prod* 2013; 45(5): 1231-6. [http://dx.doi.org/10.1007/s11250-013-0352-0] [PMID: 23334380]
- [27] Gowthaman V, Singh SD, Barathidasan R, Ayanur A, Dhama K. Natural Outbreak of Newcastle Disease in Turkeys and Japanese Quails Housed Along with Chicken in a Multi-Species Poultry Farm in Northern India. *Adv Anim Vet Sci* 2013; 1(3S): 17-20.
- [28] Gowthaman V, Singh SD, Dhama K, *et al.* Isolation and characterization of genotype XIII Newcastle disease virus from Emu in India. *Virusdisease* 2016; 27(3): 315-8. [http://dx.doi.org/10.1007/s13337-016-0324-x] [PMID: 28466046]
- [29] Desingu PA, Singh SD, Dhama K, *et al.* Molecular characterization, isolation, pathology and pathotyping of peafowl (*Pavo cristatus*) origin Newcastle disease virus isolates recovered from disease outbreaks in three states of India. *Avian Pathol* 2016; 45(6): 674-82. a [http://dx.doi.org/10.1080/03079457.2016.1198005] [PMID: 27724072]
- [30] Shabbir MZ, Zohari S, Yaqub T, *et al.* Genetic diversity of Newcastle disease virus in Pakistan: A countrywide perspective. *Virology* 2013; 45(1): 170. [http://dx.doi.org/10.1186/1743-422X-10-170] [PMID: 23721461]
- [31] Nooruzzaman M, Mazumder AC, Khatun S, Chowdhury EH, Das PM, Islam MR. Pathotypic and genotypic characterization of two Bangladeshi isolates of Newcastle disease virus of chicken and pigeon origin. *Transbound Emerg Dis* 2015; 62(1): 102-7. [http://dx.doi.org/10.1111/tbed.12086] [PMID: 23601048]
- [32] Tirumurugaan KG, Vinupriya MK, Vijayarani K, Kumanan K. Analysis of the fusion protein cleavage site of Newcastle disease virus isolates from India reveals preliminary evidence for the existence of II, VI and VII genotypes. *Indian J Virol* 2011; 22(2): 131-7. [http://dx.doi.org/10.1007/s13337-011-0044-1] [PMID: 23637515]
- [33] Kumar A, Maan S, Mahajan NK, *et al.* Detection and molecular characterization of Newcastle disease virus in peafowl (*Pavo cristatus*) in Haryana State, India. *Indian J Virol* 2013; 24(3): 380-5.

- [http://dx.doi.org/10.1007/s13337-013-0169-5] [PMID: 24426301]
- [34] Cardenas Garcia S, Navarro Lopez R, Morales R, *et al.* Molecular epidemiology of Newcastle disease in Mexico and the potential spillover of viruses from poultry into wild bird species. *Appl Environ Microbiol* 2013; 79(16): 4985-92. [http://dx.doi.org/10.1128/AEM.00993-13] [PMID: 23770910]
- [35] Mackenzie J, Britten D, Hinshaw V, Wood J. Isolation of avian influenza and paramyxoviruses from wild birds in Western Australia, in *Veterinary Viral Diseases: Their significance in South-east Asia and the Western Pacific*. *Veterinary Viral Diseases*. 1985; pp. 336-9.
- [36] Jahangir A, Ruenphet S, Ueda S, *et al.* Avian influenza and Newcastle disease viruses from northern pintail in Japan: Isolation, characterization and inter-annual comparisons during 2006-2008. *Virus Res* 2009; 143(1): 44-52. [http://dx.doi.org/10.1016/j.virusres.2009.02.018] [PMID: 19463720]
- [37] Lindh E, Huovilainen A, Rätti O, *et al.* Orthomyxo-, paramyxo- and flavivirus infections in wild waterfowl in Finland. *Virol J* 2008; 5: 35. [http://dx.doi.org/10.1186/1743-422X-5-35] [PMID: 18307758]
- [38] Zeng X, Hua Y, Li X, Zhang Z. Monitoring influenza A virus and Newcastle disease virus in migratory waterfowls in Sanjiang natural reserve of Heilongjiang Province. *Wei Sheng Wu Xue Bao* 2008; 48(10): 1403-7. [PMID: 19160826]
- [39] Krauss S, Walker D, Pryor SP, *et al.* Influenza A viruses of migrating wild aquatic birds in North America. *Vector Borne Zoonotic Dis* 2004; 4(3): 177-89. [http://dx.doi.org/10.1089/vbz.2004.4.177] [PMID: 15631061]
- [40] Ibu OJ, Okoye JOA, Adulugba EP, *et al.* Prevalence of Newcastle disease viruses in wild and captive birds in central Nigeria. *Int J Poult Sci* 2009; 8: 574-8. [http://dx.doi.org/10.3923/ijps.2009.574.578]
- [41] Haddas R, Meir R, Perk S, *et al.* Newcastle disease virus in little owls (*Athene noctua*) and African penguins (*Spheniscus demersus*) in an Israeli zoo. *Transbound Emerg Dis* 2014; 61(6): e79-82. [http://dx.doi.org/10.1111/tbed.12064] [PMID: 23406442]
- [42] Snoeck CJ, Marinelli M, Charpentier E, *et al.* Characterization of newcastle disease viruses in wild and domestic birds in Luxembourg from 2006 to 2008. *Appl Environ Microbiol* 2013; 79(2): 639-45. [http://dx.doi.org/10.1128/AEM.02437-12] [PMID: 23160119]
- [43] Kaleta EF. Avian paramyxovirus infections. *Infect dis of Wild Mammal Bird Eur* 2012; pp. 59-66.
- [44] Yuan X, Wang Y, Li J, *et al.* Surveillance and molecular characterization of Newcastle disease virus in seafoal from coastal areas of China in 2011. *Virus Genes* 2013; 46(2): 377-82. [http://dx.doi.org/10.1007/s11262-012-0863-1] [PMID: 23247914]
- [45] Pfitzer S, Verwoerd DJ, Gerdes GH, *et al.* Newcastle disease and avian influenza A virus in wild waterfowl in South Africa. *Avian Dis* 2000; 44(3): 655-60. [http://dx.doi.org/10.2307/1593107] [PMID: 11007015]
- [46] Tarnagda Z, Yougbaré I, Kam A, Tahita MC, Ouedraogo JB. Prevalence of infectious bronchitis and Newcastle disease virus among domestic and wild birds in H5N1 outbreaks areas. *J Infect Dev Ctries* 2011; 5(8): 565-70. [http://dx.doi.org/10.3855/jidc.1441] [PMID: 21841299]
- [47] Oladele SB, Enam SJ, Okubanjo OO. Pathogenic haemoparasites and antibody to Newcastle disease virus from apparently healthy wild birds in Zaria, Nigeria. *Vet World* 2012; 5(1): 13-8. [http://dx.doi.org/10.5455/vetworld.2012.13-18]
- [48] Zhang GZ, Zhao JX, Wang M. Serological survey on prevalence of antibodies to avian paramyxovirus serotype 2 in China. *Avian Dis* 2007; 51(1): 137-9. [http://dx.doi.org/10.1637/0005-2086(2007)051[0137:SSOPOA]2.0.CO;2] [PMID: 17461281]
- [49] Desingu PA, Singh SD, Dhama K, Karthik K, Vinodh Kumar OR, Malik YS. Phylogenetic analysis of Newcastle disease virus isolates occurring in India during 1989-2013. *Virusdisease* 2016; 27(2): 203-6. [http://dx.doi.org/10.1007/s13337-016-0320-1] [PMID: 27366774]
- [50] Yan Y, Samal SK. Role of intergenic sequences in newcastle disease virus RNA transcription and pathogenesis. *J Virol* 2008; 82(3): 1323-31. [http://dx.doi.org/10.1128/JVI.01989-07] [PMID: 18032502]
- [51] Morrison TG. Structure and function of a paramyxovirus fusion protein. *Biochim Biophys Acta* 2003; 1614(1): 73-84. [http://dx.doi.org/10.1016/S0005-2736(03)00164-0] [PMID: 12873767]
- [52] Swanson K, Wen X, Leser GP, Paterson RG, Lamb RA, Jardetzky TS. Structure of the Newcastle disease virus F protein in the post-fusion conformation. *Virology* 2010; 402(2): 372-9. [http://dx.doi.org/10.1016/j.virol.2010.03.050] [PMID: 20439109]
- [53] Glickman RL, Syddall RJ, Iorio RM, Sheehan JP, Bratt MA. Quantitative basic residue requirements in the cleavage-activation site of the fusion glycoprotein as a determinant of virulence for Newcastle disease virus. *J Virol* 1988; 62(1): 354-6. [PMID: 3275436]
- [54] Nagai Y, Klenk HD, Rott R. Proteolytic cleavage of the viral glycoproteins and its significance for the virulence of Newcastle disease virus. *Virology* 1976; 72(2): 494-508.

- [http://dx.doi.org/10.1016/0042-6822(76)90178-1] [PMID: 948870]
- [55] Takakuwa H, Ito T, Takada A, Okazaki K, Kida H. Potentially virulent Newcastle disease viruses are maintained in migratory waterfowl populations. *Jpn J Vet Res* 1998; 45(4): 207-15. [PMID: 9553325]
- [56] Wei D, Yang B, Li YL, Xue CF, Chen ZN, Bian H. Characterization of the genome sequence of an oncolytic Newcastle disease virus strain Italien. *Virus Res* 2008; 135(2): 312-9. [http://dx.doi.org/10.1016/j.virusres.2008.03.003] [PMID: 18420299]
- [57] Terregino C, Cattoli G, Grossele B, Bertoli E, Tisato E, Capua I. Characterization of Newcastle disease virus isolates obtained from Eurasian collared doves (*Streptopelia decaocto*) in Italy. *Avian Pathol* 2003; 32(1): 63-8. [http://dx.doi.org/10.1080/0307945021000070732] [PMID: 12745382]
- [58] Ujvári D, Wehmann E, Kaleta EF, et al. Phylogenetic analysis reveals extensive evolution of avian paramyxovirus type 1 strains of pigeons (*Columba livia*) and suggests multiple species transmission. *Virus Res* 2003; 96(1-2): 63-73. [http://dx.doi.org/10.1016/S0168-1702(03)00173-4] [PMID: 12951266]
- [59] Sergel TA, McGinnes LW, Morrison TG. A single amino acid change in the Newcastle disease virus fusion protein alters the requirement for HN protein in fusion. *J Virol* 2000; 74(11): 5101-7. [http://dx.doi.org/10.1128/JVI.74.11.5101-5107.2000] [PMID: 10799584]
- [60] Chen L, Colman PM, Cosgrove LJ, et al. Cloning, expression, and crystallization of the fusion protein of Newcastle disease virus. *Virology* 2001; 290(2): 290-9. [http://dx.doi.org/10.1006/viro.2001.1172] [PMID: 11883193]
- [61] Chen L, Gorman JJ, McKimm-Breschkin J, et al. The structure of the fusion glycoprotein of Newcastle disease virus suggests a novel paradigm for the molecular mechanism of membrane fusion. *Structure* 2001; 9(3): 255-66. [http://dx.doi.org/10.1016/S0969-2126(01)00581-0] [PMID: 11286892]
- [62] Diel DG, da Silva LH, Liu H, Wang Z, Miller PJ, Afonso CL. Genetic diversity of avian paramyxovirus type 1: Proposal for a unified nomenclature and classification system of Newcastle disease virus genotypes. *Infect Genet Evol* 2012; 12(8): 1770-9. [http://dx.doi.org/10.1016/j.meegid.2012.07.012] [PMID: 22892200]
- [63] Courtney SC, Susta L, Gomez D, et al. 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* 2013; 51(2): 508-17. [http://dx.doi.org/10.1128/JCM.02393-12] [PMID: 23196361]
- [64] Krishnamurthy S, Samal SK. Nucleotide sequences of the trailer, nucleocapsid protein gene and intergenic regions of Newcastle disease virus strain Beaudette C and completion of the entire genome sequence. *J Gen Virol* 1998; 79(Pt 10): 2419-24. [http://dx.doi.org/10.1099/0022-1317-79-10-2419] [PMID: 9780047]
- [65] de Leeuw O, Peeters B. Complete nucleotide sequence of Newcastle disease virus: Evidence for the existence of a new genus within the subfamily Paramyxovirinae. *J Gen Virol* 1999; 80(Pt 1): 131-6. [http://dx.doi.org/10.1099/0022-1317-80-1-131] [PMID: 9934695]
- [66] Van Borm S, Obishakin E, Joannis T, Lambrecht B, van den Berg T. Further evidence for the widespread co-circulation of lineages 4b and 7 velogenic Newcastle disease viruses in rural Nigeria. *Avian Pathol* 2012; 41: 377-82.
- [67] Shabbir MZ, Goraya MU, Abbas M, et al. Complete genome sequencing of a velogenic viscerotropic avian paramyxovirus 1 isolated from pheasants (*Pucrasia macrolopha*) in Lahore, Pakistan. *J Virol* 2012; 86(24): 13828-9. [http://dx.doi.org/10.1128/JVI.02626-12] [PMID: 23166241]
- [68] Vijayarani K, Muthusamy S, Tirumurugaan KG, Sakthivelan SM, Kumanan K. Pathotyping of a Newcastle disease virus isolated from peacock (*Pavo cristatus*). *Trop Anim Health Prod* 2010; 42(3): 415-9. [http://dx.doi.org/10.1007/s11250-009-9436-2] [PMID: 19763869]
- [69] Khulape SA, Gaikwad SS, Chellappa MM, Mishra BP, Dey S. Complete genome sequence of a Newcastle disease virus isolated from wild peacock (*Pavo cristatus*) in India. *Genome Announc* 2014; 2(3): e00495-14. [http://dx.doi.org/10.1128/genomeA.00495-14] [PMID: 24903868]
- [70] Zhang X, Wang J, Li S, et al. Pathohistological studies on ducks infected with NDV of duck origin. *Chin J Prev Vet Med* 2010; 32: 27-31.
- [71] Abolnik C. Molecular epidemiology of Newcastle disease and avian influenza in South Africa. Ph.D. thesis, University of Pretoria, Pretoria, South Africa. 2007.
- [72] Kaleta EF, Baldauf C. Newcastle disease in free-living and pet birds. In: Alexander DJ, ed. *Newcastle Disease*. Boston: Kluwer Academic Publishers 1988: 197-246. [http://dx.doi.org/10.1007/978-1-4613-1759-3\_12]
- [73] Zanetti F, Berinstein A, Pereda A, Taboga O, Carrillo E. Molecular characterization and phylogenetic analysis of Newcastle disease virus isolates from healthy wild birds. *Avian Dis* 2005; 49(4): 546-50. [http://dx.doi.org/10.1637/7381-051605R.1] [PMID: 16404997]
- [74] Merino R, Villegas H, Quintana JA, Calderon N. Characterization of Newcastle disease viruses isolated from chicken, gamefowl, pigeon and quail in Mexico. *Vet Res Commun* 2009; 33(8): 1023-30. [http://dx.doi.org/10.1007/s11259-009-9321-5] [PMID: 19784791]

- [75] Perozo F, Merino R, Afonso CL, Villegas P, Calderon N. Biological and phylogenetic characterization of virulent Newcastle disease virus circulating in Mexico. *Avian Dis* 2008; 52(3): 472-9. [<http://dx.doi.org/10.1637/8276-022908-Reg.1>] [PMID: 18939638]
- [76] Senthuran S, Vijayarani K, Kumanan K, Nainar AM. Pathotyping of Newcastle disease virus isolates from pet birds. *Acta Virol* 2005; 49(3): 177-82. [PMID: 16178515]
- [77] Kim SH, Wanasen N, Paldurai A, Xiao S, Collins PL, Samal SK. Newcastle disease virus fusion protein is the major contributor to protective immunity of genotype-matched vaccine. *PLoS One* 2013; 8(8): e74022. [<http://dx.doi.org/10.1371/journal.pone.0074022>] [PMID: 24015313]
- [78] Bankowski RA, Conrad RD, Reynolde B. Avian influenza A and paramyxoviruses complicating respiratory disease diagnosis in poultry. *Avian Dis* 1968; 12(2): 259-78. [<http://dx.doi.org/10.2307/1588226>] [PMID: 4297592]
- [79] Susta L, Cornax I, Diel DG, *et al.* Expression of interferon gamma by a highly virulent strain of Newcastle disease virus decreases its pathogenicity in chickens. *Microb Pathog* 2013; 61-62: 73-83. [<http://dx.doi.org/10.1016/j.micpath.2013.05.009>] [PMID: 23711962]
- [80] Capua I, Marangon S. The use of vaccination as an option for the control of avian influenza. *Avian Pathol* 2003; 32(4): 335-43. [<http://dx.doi.org/10.1080/0307945031000121077>] [PMID: 17585456]
- [81] Cross TA, Arsnoe DM, Minnis RB, *et al.* Prevalence of avian paramyxovirus 1 and avian influenza virus in double-crested Cormorants (*Phalacrocorax auritus*) in eastern North America. *J Wildl Dis* 2013; 49(4): 965-77. [<http://dx.doi.org/10.7589/2012-06-164>] [PMID: 24502724]
- [82] Teske L, Ryll M, Rautenschlein S. Epidemiological investigations on the role of clinically healthy racing pigeons as a reservoir for avian paramyxovirus-1 and avian influenza virus. *Avian Pathol* 2013; 42(6): 557-65. [<http://dx.doi.org/10.1080/03079457.2013.852157>] [PMID: 24188518]
- [83] Tolf C, Wille M, Haidar AK, Avril A, Zohari S, Waldenström J. Prevalence of avian paramyxovirus type 1 in Mallards during autumn migration in the western Baltic Sea region. *Virol J* 2013; 10(1): 285. [<http://dx.doi.org/10.1186/1743-422X-10-285>] [PMID: 24028398]
- [84] Durham PJK, Poole WSH, Gow A, Watters CB. Characteristics of lentogenic strains of Newcastle disease virus isolated in New Zealand. *N Z Vet J* 1980; 28(6): 108-12. [<http://dx.doi.org/10.1080/00480169.1980.34713>] [PMID: 6933376]
- [85] Alexander DJ. Newcastle disease in countries of the European Union. *Avian Pathol* 1995; 24(1): 3-10. [<http://dx.doi.org/10.1080/03079459508419045>] [PMID: 18645762]
- [86] Stanislawek WL, Wilks CR, Meers J, *et al.* Avian paramyxoviruses and influenza viruses isolated from mallard ducks (*Anas platyrhynchos*) in New Zealand. *Arch Virol* 2002; 147(7): 1287-302. [<http://dx.doi.org/10.1007/s00705-002-0818-2>] [PMID: 12111409]
- [87] Liu H, Wang Z, Wang Y, Sun C, Zheng D, Wu Y. Characterization of Newcastle disease virus isolated from waterfowl in China. *Avian Dis* 2008; 52(1): 150-5. [<http://dx.doi.org/10.1637/8030-061507-Reg>] [PMID: 18459314]
- [88] Lee EK, Jeon WJ, Kwon JH, Yang CB, Choi KS. Molecular epidemiological investigation of Newcastle disease virus from domestic ducks in Korea. *Vet Microbiol* 2009; 134(3-4): 241-8. [<http://dx.doi.org/10.1016/j.vetmic.2008.08.020>] [PMID: 18829185]
- [89] Vidanović D, Sekler M, Asanin R, *et al.* Characterization of velogenic Newcastle disease viruses isolated from dead wild birds in Serbia during 2007. *J Wildl Dis* 2011; 47(2): 433-41. [<http://dx.doi.org/10.7589/0090-3558-47.2.433>] [PMID: 21441197]
- [90] Bozorgmehri-Fard MH, Keyvanfar H. Isolation of Newcastle disease virus from teals (*Anas crecca*) in Iran. *J Wildl Dis* 1979; 15(2): 335-7. [<http://dx.doi.org/10.7589/0090-3558-15.2.335>] [PMID: 480525]
- [91] Macpherson I, Watt RG, Alexander DJ. Isolation of avian paramyxovirus other than Newcastle disease virus from commercial poultry in Great Britain. *Vet Rec* 1983; 112(20): 479-80. [<http://dx.doi.org/10.1136/vr.112.20.479>] [PMID: 6868324]
- [92] Rue CA, Susta L, Brown CC, *et al.* Evolutionary changes affecting rapid identification of 2008 Newcastle disease viruses isolated from double-crested cormorants. *J Clin Microbiol* 2010; 48(7): 2440-8. [<http://dx.doi.org/10.1128/JCM.02213-09>] [PMID: 20107098]
- [93] Jindal N, Chander Y, Chockalingam AK, de Abin M, Redig PT, Goyal SM. Phylogenetic analysis of Newcastle disease viruses isolated from waterfowl in the upper midwest region of the United States. *Virol J* 2009; 6: 191. [<http://dx.doi.org/10.1186/1743-422X-6-191>] [PMID: 19891788]
- [94] Kim LM, King DJ, Guzman H, *et al.* Biological and phylogenetic characterization of pigeon paramyxovirus serotype 1 circulating in wild North American pigeons and doves. *J Clin Microbiol* 2008; 46(10): 3303-10. [<http://dx.doi.org/10.1128/JCM.00644-08>] [PMID: 18716227]



- [95] Schuler KL, Green DE, Justice-Allen AE, *et al.* Expansion of an exotic species and concomitant disease outbreaks: Pigeon paramyxovirus in free-ranging Eurasian collared doves. *EcoHealth* 2012; 9(2): 163-70. [<http://dx.doi.org/10.1007/s10393-012-0758-6>] [PMID: 22476688]
- [96] Alexander DJ, Pattison M, Macpherson I. Avian paramyxoviruses of PMV-3 serotype in British turkeys. *Avian Pathol* 1983; 12(4): 469-82. [<http://dx.doi.org/10.1080/03079458308436192>] [PMID: 18766806]
- [97] Xie Z, Xie L, Chen A, *et al.* Complete genome sequence analysis of a Newcastle disease virus isolated from a wild egret. *J Virol* 2012; 86(24): 13854-5. [<http://dx.doi.org/10.1128/JVI.02669-12>] [PMID: 23166257]
- [98] Alexander DJ. Newcastle disease in the European Union 2000 to 2009. *Avian Pathol* 2011; 40(6): 547-58. [<http://dx.doi.org/10.1080/03079457.2011.618823>] [PMID: 22107088]
- [99] Byarugaba DK, Mugimba KK, Omony JB, *et al.* High pathogenicity and low genetic evolution of avian paramyxovirus type I (Newcastle disease virus) isolated from live bird markets in Uganda. *Virology* 2014; 11: 173. [<http://dx.doi.org/10.1186/1743-422X-11-173>] [PMID: 25273689]
- [100] Mulisa DD, Alemu RB, Keno MS, *et al.* Characterization of Newcastle disease virus and poultry-handling practices in live poultry markets, Ethiopia. *Springerplus* 2014; 3: 459. [<http://dx.doi.org/10.1186/2193-1801-3-459>] [PMID: 25279281]
- [101] Wakamatsu N, King DJ, Kapczynski DR, Seal BS, Brown CC. Experimental pathogenesis for chickens, turkeys, and pigeons of exotic Newcastle disease virus from an outbreak in California during 2002-2003. *Vet Pathol* 2006; 43(6): 925-33. [<http://dx.doi.org/10.1354/vp.43-6-925>] [PMID: 17099149]
- [102] Aldous EW, Alexander DJ. Newcastle disease in pheasants (*Phasianus colchicus*): A review. *Vet J* 2008; 175(2): 181-5. [<http://dx.doi.org/10.1016/j.tvjl.2006.12.012>] [PMID: 17383205]
- [103] Higgins DA. Nine disease outbreaks associated with myxoviruses among ducks in Hong Kong. *Trop Anim Health Prod* 1971; 3(4): 232-40. [<http://dx.doi.org/10.1007/BF02359585>] [PMID: 4367727]
- [104] Jinding C, Ming L, Tao R, Chaoan X. A goose-sourced paramyxovirus isolated from southern China. *Avian Dis* 2005; 49(1): 170-3. [<http://dx.doi.org/10.1637/7270-090101R1>] [PMID: 15839435]
- [105] Zou J, Shan S, Yao N, Gong Z. Complete genome sequence and biological characterizations of a novel goose paramyxovirus-SF02 isolated in China. *Virus Genes* 2005; 30(1): 13-21. [<http://dx.doi.org/10.1007/s11262-004-4577-x>] [PMID: 15744558]
- [106] Wan H, Chen L, Wu L, Liu X. Newcastle disease in geese: Natural occurrence and experimental infection. *Avian Pathol* 2004; 33(2): 216-21. [<http://dx.doi.org/10.1080/0307945042000195803>] [PMID: 15276991]
- [107] Alexander DJ, Ed. Vindevogel H aJPD. *Panzootic Newcastle disease virus in pigeon. Newcastle disease*. Boston, MA: Kluwer Academic 1988; pp. 184-96.
- [108] Zanetti F, Mattiello R, Garbino C, *et al.* Biological and molecular characterization of a pigeon paramyxovirus type-1 isolate found in Argentina. *Avian Dis* 2001; 45(3): 567-71. [<http://dx.doi.org/10.2307/1592896>] [PMID: 11569728]
- [109] Beck I, Gerlach H, Burkhardt E, Kaleta EF. Investigation of several selected adjuvants regarding their efficacy and side effects for the production of a vaccine for parakeets to prevent a disease caused by a paramyxovirus type 3. *Vaccine* 2003; 21(9-10): 1006-22. [[http://dx.doi.org/10.1016/S0264-410X\(02\)00552-2](http://dx.doi.org/10.1016/S0264-410X(02)00552-2)] [PMID: 12547615]
- [110] Panigrahy B, Senne DA, Pearson JE, Mixson MA, Cassidy DR. Occurrence of velogenic viscerotropic Newcastle disease in pet and exotic birds in 1991. *Avian Dis* 1993; 37(1): 254-8. [<http://dx.doi.org/10.2307/1591484>] [PMID: 8452504]
- [111] Erickson GA, Maré CJ, Gustafson GA, Miller LD, Proctor SJ, Carbrey EA. Interactions between viscerotropic velogenic Newcastle diseases virus and pet birds of six species. I. Clinical and serologic responses, and viral excretion. *Avian Dis* 1977; 21(4): 642-54. [<http://dx.doi.org/10.2307/1589424>] [PMID: 606222]
- [112] Allison AB, Gottdenker NL, Stallknecht DE. Wintering of neurotropic velogenic Newcastle disease virus and West Nile virus in double-crested cormorants (*Phalacrocorax auritus*) from the Florida Keys. *Avian Dis* 2005; 49(2): 292-7. [<http://dx.doi.org/10.1637/7278-091304R>] [PMID: 16094838]
- [113] Kuiken T, Heckert RA, Riva J, Leighton FA, Wobeser G. Excretion of pathogenic Newcastle disease virus by double-crested cormorants (*Phalacrocorax auritus*) in absence of mortality or clinical signs of disease. *Avian Pathol* 1998; 27(6): 541-6. [<http://dx.doi.org/10.1080/03079459808419381>] [PMID: 18484041]
- [114] Alexander DJ, Collins MS. Pathogenicity of PMV-3/parakeet/Netherlands/449/75 for chickens. *Avian Pathol* 1982; 11(1): 179-85. [<http://dx.doi.org/10.1080/03079458208436091>] [PMID: 18770182]
- [115] Tumova B, Robinson JH, Easterday BC. A hitherto unreported paramyxovirus of turkeys. *Res Vet Sci* 1979; 27(2): 135-40. [PMID: 523797]
- [116] Chen S, Hao H, Liu Q, *et al.* Phylogenetic and pathogenic analyses of two virulent Newcastle disease viruses isolated from Crested Ibis (*Nipponia nippon*) in China. *Virus Genes* 2013; 46(3): 447-53.

- [http://dx.doi.org/10.1007/s11262-013-0881-7] [PMID: 23344613]
- [117] Pchelkina IP, Manin TB, Kolosov SN, *et al.* Characteristics of Pigeon Paramyxovirus serotype-1 isolates (PPMV-1) from the Russian Federation from 2001 to 2009. *Avian Dis* 2013; 57(1): 2-7.  
[http://dx.doi.org/10.1637/10246-051112-Reg.1] [PMID: 23678722]
- [118] Absalón AE, Mariano-Matías A, Vásquez-Márquez A, *et al.* Complete genome sequence of a velogenic Newcastle disease virus isolated in Mexico. *Virus Genes* 2012; 45(2): 304-10.  
[http://dx.doi.org/10.1007/s11262-012-0782-1] [PMID: 22821201]
- [119] Miller PJ, King DJ, Afonso CL, Suarez DL. Antigenic differences among Newcastle disease virus strains of different genotypes used in vaccine formulation affect viral shedding after a virulent challenge. *Vaccine* 2007; 25(41): 7238-46.  
[http://dx.doi.org/10.1016/j.vaccine.2007.07.017] [PMID: 17719150]
- [120] Bonfante F, Terregino C, Heidari A, *et al.* Identification of APMV-1 associated with high mortality of collared doves (*Streptopelia decaocto*) in Italy. *Vet Rec* 2012; 171(13): 327.  
[http://dx.doi.org/10.1136/vr.100448] [PMID: 22915679]
- [121] Liu X, Wang X, Wu S, *et al.* Surveillance for avirulent Newcastle disease viruses in domestic ducks (*Anas platyrhynchos* and *Cairina moschata*) at live bird markets in Eastern China and characterization of the viruses isolated. *Avian Pathol* 2009; 38(5): 377-91.  
[http://dx.doi.org/10.1080/03079450903183637] [PMID: 19937525]
- [122] Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol Biol Evol* 2011; 28(10): 2731-9.  
[http://dx.doi.org/10.1093/molbev/msr121] [PMID: 21546353]
- [123] Qiu X, Sun Q, Wu S, *et al.* Entire genome sequence analysis of genotype IX Newcastle disease viruses reveals their early-genotype phylogenetic position and recent-genotype genome size. *Viro J* 2011; 8: 117.  
[http://dx.doi.org/10.1186/1743-422X-8-117] [PMID: 21396134]
- [124] Shi SH, Huang Y, Cui SJ, *et al.* Genomic sequence of an avian paramyxovirus type 1 strain isolated from Muscovy duck (*Cairina moschata*) in China. *Arch Virol* 2011; 156(3): 405-12.  
[http://dx.doi.org/10.1007/s00705-010-0866-y] [PMID: 21152939]
- [125] Usachev EV, Fediakina IT, Shchelkanov MIu, L'vov DN, Prilipov AG, Iamnikova SS. Molecular genetic characteristics of the Newcastle Sterna/Astrakhan/Z275/2001 virus isolated in Russia. *Mol Gen Mikrobiol Virusol* 2006; 1(1): 14-20.  
[PMID: 16512605]
- [126] Briand FX, Henry A, Massin P, Jestin V. Complete genome sequence of a novel avian paramyxovirus. *J Virol* 2012; 86(14): 7710.  
[http://dx.doi.org/10.1128/JVI.00946-12] [PMID: 22733876]
- [127] Desingu PA, Singh SD, Dhama K, Kumar OR, Singh R, Singh RK. A rapid method of accurate detection and differentiation of Newcastle disease virus pathotypes by demonstrating multiple bands in degenerate primer based nested RT-PCR. *J Virol Methods* 2015; 212: 47-52.  
[http://dx.doi.org/10.1016/j.jviromet.2014.11.005] [PMID: 25449112]
- [128] Kumar S, Samal SK. Pathogenicity of avian paramyxovirus serotype-3 in Chickens and Turkeys. In: Perez- Marin, C. C. (ed.), *A Bird's-Eye View of Veterinary Medicine*, pp. 587-596. In Tech, Croatia 2012.  
[http://dx.doi.org/10.5772/30975]
- [129] Handel KA, Pasick J. 2016. Newcastle Disease Virus NDV/Turkey/Ontario/CN36/2003 matrix protein (M) and fusion protein (F) genes partial cds: Direct submitted by Virology, CFIA-NCFAD, 1015 Arlington Street, Winnipeg, Manitoba R3E 3M4, Canada. 2016.  
.https://www.ncbi.nlm.nih.gov/nucleotide/289194
- [130] Liu H, Zhang P, Wu P, *et al.* Phylogenetic characterization and virulence of two Newcastle disease viruses isolated from wild birds in China. *Infect Genet Evol* 2013; 20: 215-24.  
[http://dx.doi.org/10.1016/j.meegid.2013.08.021] [PMID: 23999544]
- [131] Duan X, Zhang P, Ma J, *et al.* Characterization of genotype IX Newcastle disease virus strains isolated from wild birds in the northern Qinling Mountains, China. *Virus Genes* 2014; 48(1): 48-55.  
[http://dx.doi.org/10.1007/s11262-013-0987-y] [PMID: 24085475]
- [132] Hines NL, Killian ML, Pedersen JC, *et al.* An rRT-PCR assay to detect the matrix gene of a broad range of avian paramyxovirus serotype-1 strains. *Avian Dis* 2012; 56(2): 387-95.  
[http://dx.doi.org/10.1637/10035-120811-Reg.1] [PMID: 22856199]
- [133] Ramey AM, Reeves AB, Ogawa H, *et al.* Genetic diversity and mutation of avian paramyxovirus serotype 1 (Newcastle disease virus) in wild birds and evidence for intercontinental spread. *Arch Virol* 2013; 158(12): 2495-503.  
[http://dx.doi.org/10.1007/s00705-013-1761-0] [PMID: 23807743]
- [134] Wise MG, Suarez DL, Seal BS, *et al.* Development of a real-time reverse-transcription PCR for detection of newcastle disease virus RNA in clinical samples. *J Clin Microbiol* 2004; 42(1): 329-38.  
[http://dx.doi.org/10.1128/JCM.42.1.329-338.2004] [PMID: 14715773]
- [135] Bhuvanewari S, Tirumurugaan KG, Jones JC, Kumanan K. Complete genome sequence of a Newcastle disease virus from a Coturnix coturnix japonica (Japanese Quail) covey in India. *Genome Announc* 2014; 2(3): e00374-14.  
[http://dx.doi.org/10.1128/genomeA.00374-14] [PMID: 24831141]

- [136] Shi SH, Huang Y, Cui SJ, *et al.* Genomic sequence of an avian paramyxovirus type 1 strain isolated from Muscovy duck (*Cairina moschata*) in China. *Arch Virol* 2011; 156(3): 405-12. [<http://dx.doi.org/10.1007/s00705-010-0866-y>] [PMID: 21152939]
- [137] Aldous EW, Fuller CM, Mynn JK, Alexander DJ. A molecular epidemiological investigation of isolates of the variant avian paramyxovirus type 1 virus (PPMV-1) responsible for the 1978 to present panzootic in pigeons. *Avian Pathol* 2004; 33(2): 258-69. [<http://dx.doi.org/10.1080/0307945042000195768>] [PMID: 15276997]
- [138] Cai S, Li J, Wong MT, *et al.* Genetic characterization and evolutionary analysis of 4 Newcastle disease virus isolate full genomes from waterbirds in South China during 2003-2007. *Vet Microbiol* 2011; 152(1-2): 46-54. [<http://dx.doi.org/10.1016/j.vetmic.2011.04.014>] [PMID: 21565454]
- [139] Alexander DJ. Newcastle disease in the European Union 2000 to 2009. *Avian Pathol* 2011; 40(6): 547-58. [<http://dx.doi.org/10.1080/03079457.2011.618823>] [PMID: 22107088]
- [140] Zhu W, Dong J, Xie Z, Liu Q, Khan MI. Phylogenetic and pathogenic analysis of Newcastle disease virus isolated from house sparrow (*Passer domesticus*) living around poultry farm in southern China. *Virus Genes* 2010; 40(2): 231-5. [<http://dx.doi.org/10.1007/s11262-009-0436-0>] [PMID: 20043198]
- [141] Ghalyanchi-Langeroudi A, Hosseini H, Madadgar O, Karimi V, Shahraini A, Ghafari MM. Sequence Analysis of Fusion Gene of Newcastle Disease Viruses Isolated from Ostrich (*Struthio camelus*) in Iran. *Indian J Virol* 2011; 5(3): 12-7.

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