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Newcastle Disease Virus in Egypt

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Review Article

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Abstract

Newcastle disease virus (NDV) poses a significant risk to the poultry industry, which is an important sector in the global financial system since it provides inexpensive protein and supports economic growth. NDV is extremely infectious, affecting a wide range of bird species and resulting in high mortality rates, substantial decreases in egg production, and huge economic losses, particularly in chicken flocks. To combat this virus, strict biosecurity precautions and well-structured immunization programs are required, including live attenuated, inactivated, and recombinant vaccines. Despite these efforts, outbreaks continue worldwide, including in Egypt, where poultry density and vaccination delivery issues make control more challenging. To avoid NDV transmission, successful management necessitates continuous monitoring, strict vaccination and confinement procedures, and culling infected flocks during outbreaks. Given NDV economic importance, a thorough study of its history, morphology, and management measures is critical to protecting the poultry industry.

Keywords: *Newcastle, Egypt, poultry, Paramyxoviridae*

Introduction

Newcastle disease (ND) is a very deadly avian illness that affects the global chicken industry, with the Newcastle disease virus (NDV) causing major mortality, morbidity, and economic loss. This illness costs millions of dollars each year because to mortality, veterinary bills, treatment, vaccination, and trade restrictions **(Alexander and Senne 2003, Clemmons Alfson *et al.* 2021).** The World Organization for Animal Health (OIE) recognizes ND as a notifiable disease, which must be reported as soon as it is discovered **(Caceres Awada *et al.* 2017).** ND is the second most common endemic viral sickness infecting poultry, after avian influenza viruses, and is regarded as one of the most serious poultry illnesses, alongside highly and low pathogenic avian influenza and infectious bronchitis viruses **(Dimitrov, Afonso *et al.* 2017).** NDV, an avian orthoavulavirus-1 from the Paramyxoviridae family, affects about 236 wild bird species from 27 of the 50 bird orders, with animals frequently functioning as virus reservoirs **(Ferreira, Reilley *et al.* 2020).** Unvaccinated birds are the most vulnerable to ND outbreaks **(Kim 1965, Brown and Bevins 2017),** and NDV strains are classified according to pathogenicity as lentogenic, mesogenic, or velogenic. As a zoonotic virus, NDV may infect people, producing mild con-

junctivitis and flu-like symptoms, with severe instances potentially leading to long-term vision loss **(Saikia, Yadav *et al.* 2019).** To effectively manage ND, strong biosecurity policies and country-specific immunization programs are required **(Absalón, Cortés-Espinosa *et al.* 2019).**

Morphology of the virus

Newcastle disease virus (NDV) with a negative polarity and a linear, non-segmented, single-stranded RNA genome of around 15.2 kb, Newcastle disease virus (NDV) is an enveloped virus **(Samal, 2021).** A lipid bilayer envelope with spike glycoproteins, including 17-nanometer-long projections of Fusion (F) and Hemagglutinin-Neuraminidase (HN) proteins, is present in the spherical virions of NDV, which are created by budding from the host cell membrane **(Dey *et al.* 2019; Hanson & Brandly, 1955).**

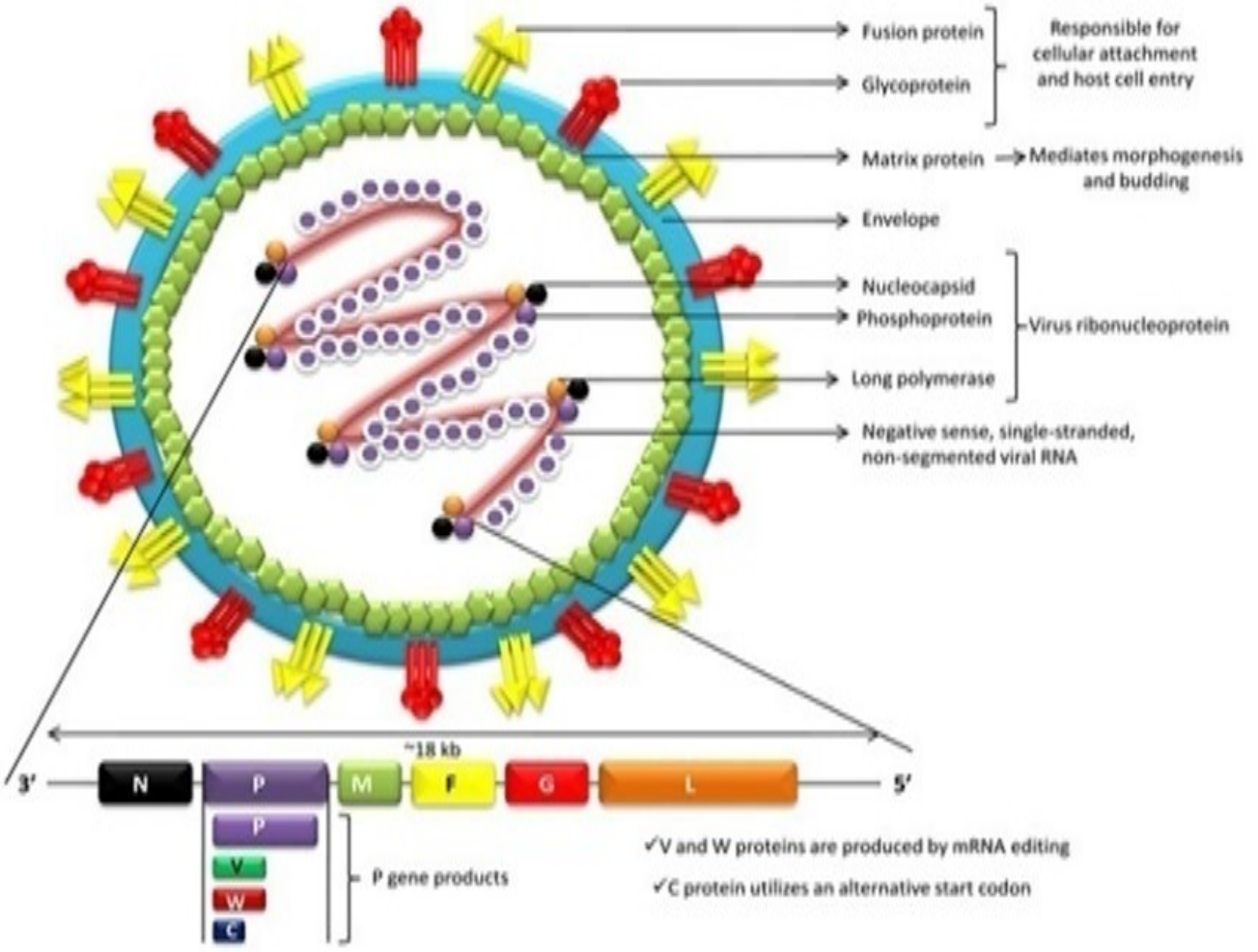

Figure (1). NDV virus morphology (A) and the genomic structure (B)

Three envelope-associated proteins (Fusion, Hemagglutinin-Neuraminidase, and Matrix) and three RNA-associated proteins (nucleoprotein, phosphoprotein, and RNA polymerase) are among the six structural proteins encoded by the genome of NDV **(Seal, 2004; Nath *et al.* 2020).** Both the F and HN proteins are necessary for efficient viral cell entrance in the Paramyxoviridae family, with F facilitating membrane fusion and HN mediating attachment **(Aguilar *et al.* 2016).** The conserved complementary nucleotides at the ends of the NDV genome imply that transcription and replication depend on these areas **(Marcos *et al.* 2005).** The fusion protein plays a crucial role in determining the pathogenicity of NDV **(Samal, 2012),** and in vitro studies suggest that the hemagglutinin-neuraminidase protein has a significant impact on viral replication within the host **(Yuan *et al.*, 2012).**

Taxonomy and Classification of NDV

The International Committee on Virus Taxonomy (ICTV) has designated Newcastle disease virus (NDV) as Orthoavulavirus 1, putting it in the order Mononegavirales, family Paramyxoviridae, subfamily Avulavirinae, and genus Orthoavulavirus **(Alexander, 1987).** NDV is classified into two classes based on phylogenetic study of the F gene: class I, which largely comprises avirulent strains that use aquatic wild birds as their natural reservoir, and class II, which includes both avirulent and virulent strains from at least 20 genotypes (I-XXI) **(Kim *et al.*, 2007).** NDV strains are further classified into three pathotypes based on their pathogenicity in poultry. (i) Apathogenic strains are non-virulent and enterotropic; (ii) Lentogenic strains are low-virulent, causing mild respiratory disease; and (iii) Mesogenic and velogenic strains cause severe infections—velogenic strains include viscerotropic variants that cause gastrointestinal hemorrhages and neurotropic variants that cause encephalitis **(Alexander & Senne, 2003; Beard, 1984; Cattoli *et al.*, 2011).**

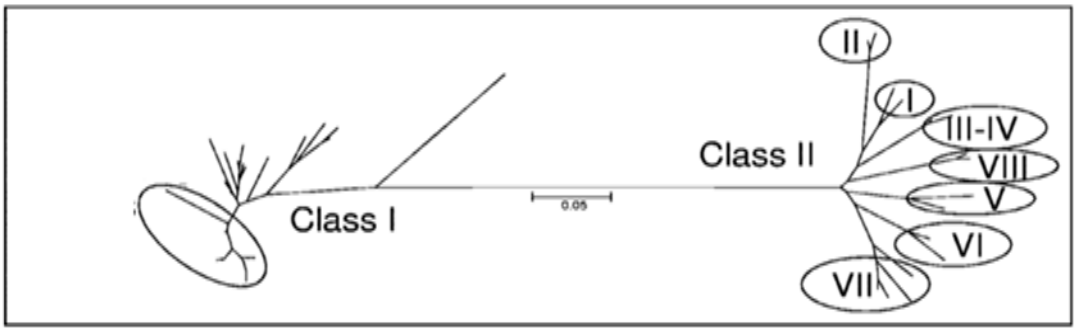

Figure (2). Taxonomy and Classification of NDV

NDV pathotypes are defined using pathogenicity indicators such as mean death time (MDT), intracerebral pathogenicity index (ICPI), and intravenous pathogenicity index (IVPI). Virulent strains have a particular F protein cleavage site sequence (112R/K-R-Q-R/K-RF117), whereas avirulent strains have 112G/E-K/R-Q-G/E-RL117 (Collins et al., 1993). NDV genotyping is mostly based on F gene sequences, with help from HN gene analysis.

Class I has one genotype and three subgenotypes (1.1.1, 1.1.2, and 1.2).While class II is split into multiple genotypes (I-XXI) and sub-genotypes, the most common genotype in Egypt is VII.1.1, which causes major health risks to poultry due to its high pathogenicity and widespread occurrence in both commercial and backyard flocks. While VII.1.1 typically affects chickens, it has also been found in pigeons, teal, quail, and infrequently in wild species such as cattle egrets, indicating the possibility of cross-species transmission. Along with VII.1.1, additional genotypes such as VII.2 and VI.2.1.1.2.2 are mostly detected in

pigeons, emphasizing the importance of these species as potential reservoirs and contributors to the virus's transmission throughout bird populations. The identification of genotypes II and XXI.1.1, particularly in chickens and pigeons, demonstrates the complexity of NDV's genetic landscape in Egypt. This variation and the virulent strains' tenacity highlight the necessity of strict biosecurity protocols, focused vaccination campaigns, and improved surveillance to limit the effects of NDV on Egyptian poultry and lower the likelihood of future outbreaks. **(Naguib *et al.*, 2022; Mansour *et al.*, 2021).**

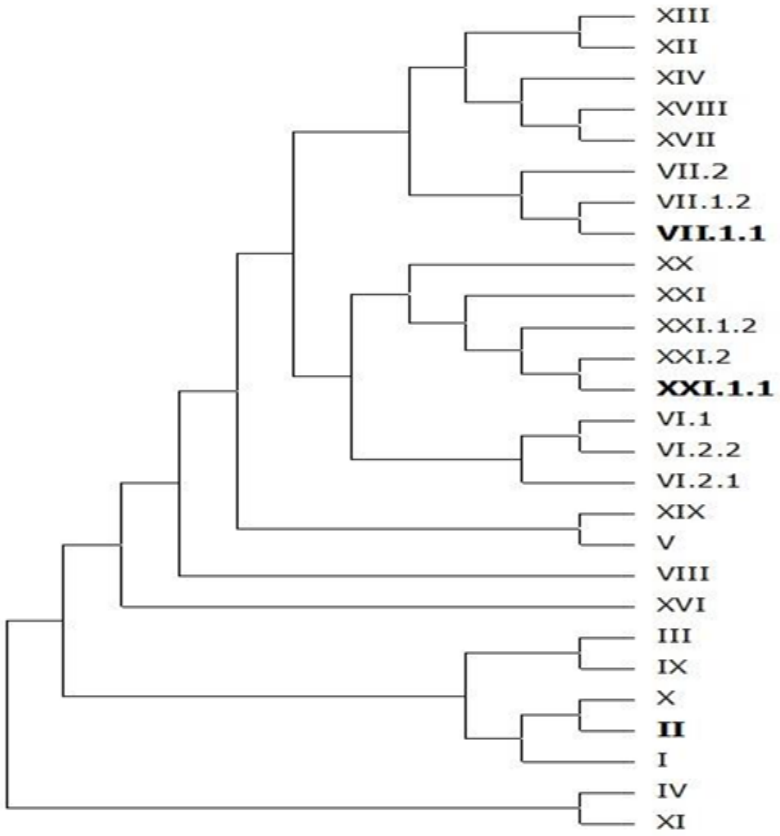

Figure (3). Genotyping of NDV class II viruses based on **Dimitrov *et al.*, (2017).** The most common genotypes in Egypt are indicated in bold font **(Ali, Abdallah *et al.* 2022)**

History and epidemiology of NDV

In 1926, the first known cases of ND were documented in Newcastle upon Tyne, England, and Java, Indonesia **(Doyle 1927).** The first panzootic was caused by viruses of genotypes II, III, and IV, and it began to spread gradually from the Far East (Asia) in the 1920s **(Ballagi-Pordany, Wehmann *et al.* 1996).** Most likely, genotype V viruses were the cause of the second panzootic, which started in Europe in the early 1970s **(Czegledi, Herczeg *et al.* 2002, Wehmann, Ujvári *et al.* 2003).** Nonetheless, these viruses remain the most common cause of epidemics in the United States **(Pedersen, Senne *et al.* 2004).** The third panzootic, produced by genotype VI viruses, mostly affected pigeons **(Czegledi, Herczeg *et al.* 2002).** It first appeared in the Middle East in the late 1970s and swiftly spread to Europe **(Biancifiori and Fioroni 1983),** where it had a devastating influence on the poultry sector, producing epidemics **(Alexander, Wilson *et al.* 1985).**

According to genomic research, these pigeon viruses most likely originated from many chicken-to-pigeon transmission episodes **(Aldous, Fuller *et al.* 2004).** Outbreaks of the fourth panzootic of ND, which started in

Southeast Asia in the early 1990s, have been caused by the common genotype VII viruses **(Lien, Lee *et al.* 2007).** In the late 1980s, genotype VII strains were genetically closest to NDV isolates from Indonesia, but they had first been isolated in Italy, Spain, the Netherlands, Belgium, and Germany **(Lomniczi, Wehmann *et al.* 1998).** In Asia, Europe, Africa, the Middle East, and South America, genotype VII has been implicated in the most recent epidemics **(Zhang, Wang *et al.* 2011).**

Newcastle disease virus (NDV) outbreaks in both vaccinated and unprotected chicken flocks have been documented in Egypt since the beginning of 2011. NDV strains were shown to belong to genotype VII, which is linked to the China genotype, based on phylogenetic and F protein sequence analysis **(Ahmed *et al.,* 2017; Radwan *et al.,* 2013).** According to Radwan et al. (2013), VII.1.1 is the most common sub-genotype in Egypt and has been implicated in many NDV outbreaks in poultry. NDV still has a major effect on chicken populations across the world, even with improvements in illness detection and immunization since the virus's discovery **(D. J. Alexander, Aldous, & Fuller, 2012).** Since 1948, when the virus first became prevalent in Egypt, the government has been keeping an eye on NDV **(Daubney & Mansy, 1948).** According to **Ahmed *et al*. (2017),** NDV has resulted in significant financial losses for the poultry business thus far. Genotype VII may spread further in Egypt as a result of trade in chickens and poultry products with China and the Middle East **(Radwan *et al.,* 2013; Sedeik *et al.,* 2019).**

Host range susceptibility to NDV and Mode of transmission

NDV infections have been found in over 236 bird species **(Kaleta and Baldauf 1988)**. Apart from lentogenic strains of NDV **(Kim, King *et al.* 2007),** velogenic NDV has also been found to infect shorebirds, chickens, pigeons, cormorants, and wild ducks **(Pearson and McCann 1975, Diel, da Silva *et al.* 2012).** Ducks seldom exhibit clinical symptoms, and turkeys are somewhat less susceptible to NDV infection than chickens. Depending on the strains of the virus that attack, geese are much more susceptible to NDV infection **(Ali, Abdelaziz *et al.* 2021).** Due to poor feed conversion, reduced hatchability, and increased mortality, NDV has a significant negative impact on quails and causes significant financial losses **(Dimitrov, Afonso *et al.* 2017).** Direct contact between healthy and sick birds is the most typical way that the virus is spread **(Kaleta and Baldauf 1988).** The NDV is spread via the droppings of infected birds and by secretions from the eyes, mouth, and nose. Additionally, eating, inhalation, or contact with the conjunctiva can all result in infection **(Ali, Abdelaziz *et al.* 2021).**

Clinical signs of NDV

It is crucial to screen out other serious avian illnesses, such as chicken cholera and highly pathogenic avian influenza (HPAI), before diagnosing Newcastle disease (ND) (D. Alexander, 2000; D. J. Alexander & Senne, 2003). The virulence of the strain and host-related variables, such as the host's species, immunological state, and the existence of co-infecting pathogens, influence how Newcastle disease virus (NDV) manifests clinically **(D. Alexander, 2000; D. J. Alexander & Senne, 2003; Cattoli *et al.,* 2011).** Several pathogenicity categories are used to categorize NDV strains based on the clinical symptoms they produce in birds: Velogenic strains are very virulent, causing up to 100% mortality in susceptible birds as well as hemorrhagic lesions in the viscera. Avirulent isolates, which do not cause any clinical symptoms in infected birds; lentogenic strains, which mostly cause mild respiratory signs, especially in young birds and when other pathogens are present, with a very low mortality rate; and mesogenic strains, which have intermediate virulence and frequently cause respiratory problems and lower mortality rates **(Cattoli *et al.,* 2011).**

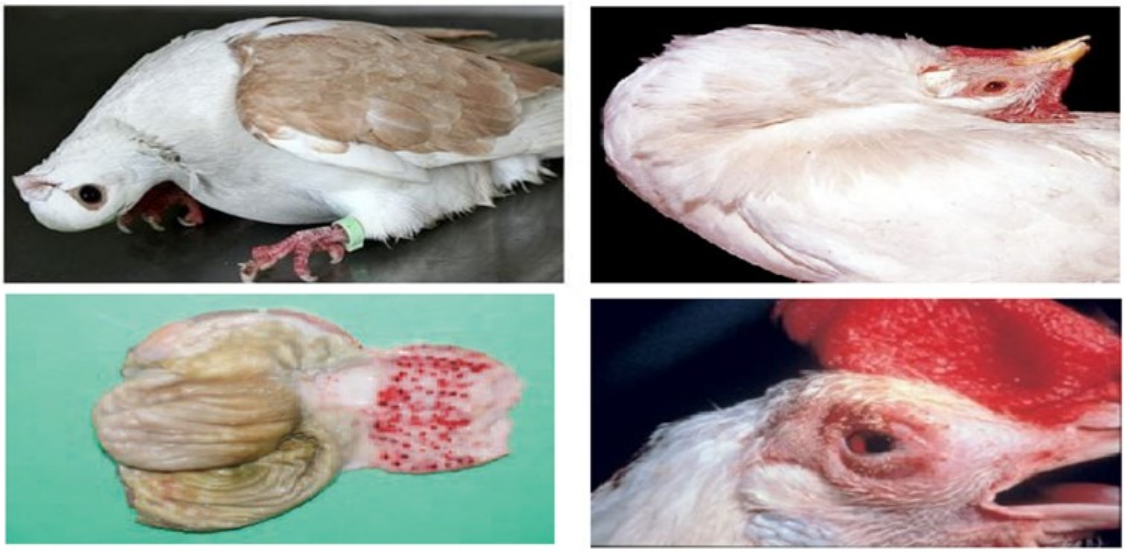

Figure (4). Common Clinical signs of NDV.

Vaccination and Biosecurity Measures Against NDV in Poultry Farms.

The prevention and control of Newcastle disease virus (NDV) depend on biosecurity measures and strict vaccination schedules (D. Alexander, 2000). According to Kapczynski, Afonso, and Miller (2013), vaccination programs are intended to accomplish three main goals: (a) reduce clinical symptoms, egg production declines, and mortality rates; (b) lessen NDV shedding via the intestinal and respiratory routes; and (c) lower the viral load or infection pressure within poultry populations. Strong biosecurity measures are essential for controlling many illnesses on poultry farms, but for NDV, pre-infection vaccination is the main way to reduce disease losses, especially in endemic areas.

Effective vaccination plans must take into account a number of variables, including as the vaccine type, the birds' health, and the degree of protection against strains that are locally circulating. Generally speaking, vaccination programs need at least 85% of the flock to get the right dosage of the vaccine and react well in order to create herd immunity **(van Boven *et al.,* 2008).** The effectiveness of NDV vaccination campaigns can also be greatly impacted by variables including maternal immunity, the virulence of endemic NDV strains in a particular geographic region, the time between vaccinations, and the lifespan of the birds (D. Alexander, 1987). These factors are essential for maximizing NDV control strategies and guaranteeing the wellbeing and efficiency of chicken farms.

The forms of Newcastle disease virus (NDV) vaccinations that are often utilized both globally and in Egypt will be briefly described in this section, beginning with conventional vaccines. Among the earliest and most well-established choices are conventional NDV vaccines, which were initially described in the early 1950s **(SB, Reising, & Van Roekel, 1951)**. Live attenuated and inactivated vaccines are the two primary varieties that fall under this category. To boost avian immunity against real NDV infections, live attenuated NDV vaccines use low or medium pathogenicity strains, particularly mesogenic strains like Komorov and Mukteswar and lentogenic strains like B1, F, LaSota, V4, and I2 **(Stear, 2005).** Recombinant NDV vaccines have been made possible by advances in DNA technology, which allow for the selective alteration of desired qualities (genes connected to immunogenicity) while removing unwanted ones (genes linked to pathogenicity). Reverse genetics vaccines, DNA vaccines, virus-vectored vaccinations, and viral -like particles that elicit immune responses are

the four types of recombinant NDV vaccines **(McGinnes *et al.*, 2010; Park *et al.*, 2014).** These DNA vaccines are not commonly accessible in Egypt, despite efforts to modify them to fit circulating NDV genotypes.

Conclusion

In Egypt, Newcastle disease virus (NDV) genotypes and sub-genotypes are highly prevalent, especially virulent strains like VII.1.1 and VII.2. This highlights the urgent need for ongoing research and monitoring in order to effectively address and mitigate this serious viral threat. In order to assist many players in the Egyptian poultry business, we are concentrating on the crucial significance that vaccination and control measures play. We hope to increase the sector's sustainability and resilience as it negotiates the continuous difficulties presented by this powerful virus by promoting efficient vaccination and management techniques.

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