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### Development of a Recombinant Newcastle Disease Virus Vaccine and its Efficacy in a Broiler Farm.

Morales, J.A.<sup>1</sup>, Merino, E.<sup>1</sup>, García, D.<sup>1</sup>, Ortega, R.<sup>1</sup>, Christy, N.<sup>1</sup>, Marrufo, D.<sup>1</sup>, Lucio, E.<sup>1</sup>, Cruz, M.<sup>1</sup>, Absalón, A.E.<sup>2</sup>, Aortés, D. V.<sup>2</sup>, Mariano, A.<sup>2</sup>, Vazques, A.<sup>2</sup>,

<sup>1</sup>*Investigación Aplicada S.A. de C.V., 7 Norte 416 Col. Centro, C. P. 75700 Tehuacan, Puebla, Mexico.* <sup>2</sup>*Instituto Politécnico Nacional, Av. Luis Enrique Erro S/N, Unidad Profesional Adolfo López Mateos, Zacatenco, Delegación Gustavo A. Madero, C.P. 07738, Distrito Federal, Mexico.*

#### Abstract

Studies by different authors have determined through DNA sequencing that viruses isolated in Mexico, Central America and some regions in The United States belong to the genotype V. With the object of achieving a more effective control of the problems caused by the Newcastle Disease Virus (NDV) in those regions, a recombinant live NDV vaccine that expresses the gene of the highly antigenic hemagglutinin-neuraminidase protein (HN) of a Genotype V strain was developed. This was done through the use of reverse genetics. This velogenic virus was genetically modified at the cleavage site of its Fusion protein (F) in order to change its highly pathogenic genome to one similar to that of La Sota strain, with the purpose of ensuring its low pathogenicity. The resulting homology of the recombinant vaccine to the circulating NDV Genotype V strains present in regions above mentioned has shown clear advantages over the use of heterologous vaccines, in both challenge controlled and field trials in Mexico. Here we present results of a trial where advantages show in reduced viral excretion, less severe post vaccinal reactions as well as improved productive parameters such as low mortality rate and better feed conversion. Moreover, the application of this vaccine has shown adequate control on egg production drop in field challenged birds.

#### Introduction

Newcastle Disease remains one of the most dynamic and impacting diseases in poultry all worldwide, representing an unavoidable concern for producers and researchers. The causative pathogen is the Newcastle disease virus (NDV) is a single-stranded, negative-sense RNA virus that belongs to the genus *Avulavirus* of the family *Paramyxoviridae* in the order *Mononegavirales* (Alexander, 1997). Its genomic organization consists of the transcriptional units: nucleocapsid protein (NP), phosphoprotein (P), matrix (M) protein, fusion (F) protein, hemagglutinin neuraminidase (HN), and large polymerase (L) protein (Chambers et al., 1986,16). The F glycoprotein of NDV mediates fusion of the viral and cellular membranes and is synthesized as an inactive precursor F0 (Chambers 1986, Salih 2000) until it is cleaved by cellular proteases in the body at the peptide bond of residues 116 and 117 generating two polypeptides, F1 and F2. The molecular basis for the different levels of pathogenicity has been found to be mainly determined by the amino acid sequence of the fusion protein cleavage site (Chambers, 1986, Nagai, 1976).

Current NDV classifications and phylogenetic trees developed by different authors have helped visualize how antigenic and genetic diversity have distanced currently isolated viruses such as genotype V strains found in Central America and South America, (Miller 2010) and in North America (Pedersen 2004), including Mexico (Perozo et al, 2008), from current vaccinal strains such as La Sota and B1 which belong to genotype II of Class II. Current vaccines prevent disease but cannot stop viral shedding which may cause infection of other susceptible birds (Kaczynski and King, 2005). There is recent evidence that using genotype-matched vaccines can significantly reduce viral shedding. Miller et al, (2007) showed that a vaccine homologous to the challenge virus (CA02 of genotype V) reduced oral shedding significantly more than heterologous inactivated vaccines containing strains such as B1 and Ulster (Genotype II and I respectively). Also in 2008, Miller et al., demonstrated increased capacity to prevent viral shedding of genotype V virus with an antigenically matched live vaccine compared with La Sota, B1 and Ulster strain live vaccines. More over, studies performed by Miller and Lucio, (2010) showed that after vaccination of a group of birds with La Sota strain and another group with CA/2002, which caused the most recent outbreak in the USA, both groups of birds were protected against disease and lesions. However the group vaccinated with La Sota showed a