



Biopharming: A Biosecurity Measure to Combat Newcastle Disease for Household Food Security

Muhammad Sarwar Khan* and Iqar Ahmad Khan

Center of Agricultural Biochemistry and Biotechnology (CABB), University Road, University of Agriculture, Faisalabad, Pakistan

*Corresponding author: Muhammad Sarwar Khan, Center of Agricultural Biochemistry and Biotechnology (CABB), University Road, University of Agriculture, Faisalabad, Pakistan, Tel: 041-9201087; E-mail: sarwarkhan_40@hotmail.com

Rec date: Mar 04, 2015; Acc date: Mar 05, 2015; Pub date: Mar 09, 2015

Copyright: © 2015 Khan MS. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Editorial

Agricultural land is shrinking because of ever increasing population in the developing world. Shrinking farm land warrants alternative measures of food security, particularly of the rural community. One of the options on the list is rearing of poultry birds at both captive and commercial levels. Poultry provides food, energy, fertilizer and a renewable asset to over 80 percent of rural household [1]. Nevertheless, 100 percent potential is not harvested due to a number of factors; including, poor housing, insufficient quality nutrition and devastating diseases. Amongst diseases, Newcastle has become a pandemic disease. It not only affects domesticated but also wild poultry throughout the world [2-5].

Newcastle is a highly contagious viral disease caused by avian Paramyxovirus type-1, commonly known as Newcastle disease virus (NDV), which is a member of genus *Avulavirus* of the *Paramyxoviridae* family. NDV is an enveloped, non-segmented, single-stranded and negative-sense RNA virus [6-8]. Its genome encodes six structural proteins; namely, nucleocapsid (NP), phosphoprotein (P), matrix (M), fusion (F), hemagglutinin-neuraminidase (HN), and large RNA-dependent RNA polymerase (L). Based on the sequence of the pathogenic precursor protein (F) the NDV strains are grouped into three types; velogenic, mesogenic and lentogenic. NDV outbreaks are occurring not only in the domesticated poultry birds but also in wild birds [6-8]. During 2010-12, a number of outbreaks were recorded that heavily damaged commercial and wild poultry birds in Pakistan [5].

Poultry sector is one of the vibrant segments of agriculture industry of Pakistan. This sector generates employment (direct/indirect) and income for about 1.5 million people. Its contribution in agricultural and Livestock growth is 4.81% 9.84%, respectively. Poultry meat contributes 19% of the total meat production in the country. The success of the Pakistan poultry industry depends on the ability to maintain healthy birds. Current disease management approach of poultry industry in Pakistan is to immunize birds by using live or killed bugs-based vaccines. Despite extensive vaccination of commercial poultry birds using live lentogenic strains, for example Lasota, outbreaks are witnessed in Pakistan. Since disease continues to appear in both vaccinated flocks as well as unvaccinated commercial and wild poultry birds, therefore molecular characterization of evolving NDV strains from different countries is reported [9-14] that will help in developing vaccines.

One of the approaches is genotype-matched using reverse genetics approach [10] but development of a reverse genetics system for a circulating NDV strains is very costly and laborious. This necessitates exploring alternative approaches to develop genotype-matched vaccines. Of the alternative strategies, expressing engineered pathogenicity-causing genes in edible plants could be a cost effective

and clean-gene strategy to immunize wild captive, rural and commercial poultry flocks.

When we talk about plant system to express antigenic proteins there are a number of options; including, nuclear transformation, protein targeting to plastids after expression from nuclear genome and chloroplast genome engineering. Of these systems, chloroplast genome engineering is considered superior because it addresses biosafety issues by providing natural transgene containment since plastid DNA is lost during pollen maturation and hence is not transmitted to the next generation [15,16]. Additionally, biologically active proteins may accumulate to exceptionally high levels due to the polyploid nature of plastids and presence of chaperonin proteins in plastids [17-20].

References

1. Alexander DJ, Bell JG, Alders RG (2004) A technology review: Newcastle disease with special emphasis on its effect on village chickens. Animal Production and Health, Food and Agriculture Organization of the United Nations, Rome; pp. 1-22.
2. Miller PJ, Decanini EL, Afonso CL (2010) Newcastle disease: evolution of genotypes and the related diagnostic challenges. Infect Genet Evol 10: 26-35.
3. Xiao S, Paldurai A, Nayak B, Samuel A, Bharoto EE, et al. (2012) Complete genome sequences of Newcastle disease virus strains circulating in chicken populations of Indonesia. J Virol 86: 5969.
4. Umali DV, Ito H, Suzuki T, Shirota K, Katoh H, et al. (2013) Molecular epidemiology of Newcastle disease virus isolates from vaccinated commercial poultry farms in non-epidemic areas of Japan. Virol J 10: 330.
5. Shabbir MZ, Zohari S, Yaqub T, Nazir J, Shabbir MAB, et al. (2013) Genetic diversity of Newcastle disease virus in Pakistan: a countrywide perspective. Virol J 10: 170.
6. Abolnik C, Horner RF, Bisschop SP, Parker ME, Romito M, et al. (2004) A phylogenetic study of South African Newcastle disease virus strains isolated between 1990 and 2002 suggests epidemiological origins in the Far East. Arch Virol 149: 603-619.
7. Czegledi A, Ujvari D, Somogyi E, Wehmann E, Werner O, et al. (2006) Third genome size category of avian paramyxovirus serotype 1 (Newcastle disease virus) and evolutionary implications. Virus Res 120: 36-48.
8. Aldous EW, Mynn JK, Banks J, Alexander DJ (2003) A molecular epidemiological study of avian paramyxovirus type 1 (Newcastle disease virus) isolates by phylogenetic analysis of a partial nucleotide sequence of the fusion protein gene. Avian Pathol 32: 239-256.
9. Khan TA, Rue CA, Rehmani SF, Ahmed A, Wasilenko JL, et al. (2010) Phylogenetic and biological characterization of Newcastle disease virus isolates from Pakistan. J Clin Microbiol 48: 1892-1894.
10. Kim S-H, Wanasen N, Paldurai A, Xiao S, Collins PL, et al. (2013) Newcastle disease virus fusion protein is the major contributor to protective immunity of genotype-matched vaccine. PLoS ONE 8: e74022.
11. Miller PJ, King DJ, Afonso CL, Suarez DL (2007) Antigenic differences among Newcastle disease virus strains of different genotypes used in

- vaccine formulation affect viral shedding after a virulent challenge. *Vaccine* 25: 7238-7246.
12. Miller PJ, Estevez C, Yu Q, Suarez DL, King DK (2009) Comparison of viral shedding following vaccination with inactivated and live Newcastle disease vaccines formulated with wild-type and recombinant viruses. *Avian Dis* 53: 39-49.
 13. Xiao S, Nayak B, Samuel A, Paldurai A, Kanabagattebasavarajappa M, et al. (2012) Generation by reverse genetics of an effective, stable, liveattenuated Newcastle disease virus vaccine based on a currently circulating, highly virulent Indonesian strain. *PLOS ONE* 7: e527518.
 14. Herczeg J, Wehmann E, Bragg RR, Travassos Dias PM, Hadjiev G, et al. (1999) Two novel genetic groups (VIIb and VIII) responsible for recent Newcastle disease outbreaks in Southern Africa, one (VIIb) of which reached Southern Eur. *Arch Virol* 144: 2087-2099.
 15. Svab Z, Maliga P (1993) High-frequency plastid transformation in tobacco by selection for a chimeric aadA gene. *Proc Natl Acad Sci USA* 90: 913-917.
 16. Khan MS, Maliga P (1999) Fluorescent antibiotic resistance marker for tracking plastid transformation in higher plants. *Nat Biotechnol* 17: 910-915.
 17. Bock R (2001) Transgenic plastids in basic research and plant biotechnology. *J Mol Biol* 312: 425-438.
 18. Daniell H, Khan MS, Allison L (2002) Milestones in chloroplast genetic engineering: an environmentally friendly era in biotechnology. *Trends Plant Sci* 7: 84-91.
 19. Khan MS, Khalid AM, Malik KA (2005) Intein-mediated protein trans-splicing and transgene containment in plastids. *Trends Biotechnol* 23: 217-220.
 20. Khan MS (2012) Plastid Genome engineering in plants: Present status and future trends. *Mol Plant Breed* 3: 91-102.