Research gaps identified
3. Research gaps identified

As mentioned in the review of literature the well-established epidemiological success of influenza viruses is primarily due to antigenic variation in the HA and NA surface glycoproteins. Antigenic variations result in the emergence of new strains that cause infections in a vast number of individuals despite prior immunity by previous infection or vaccination (Cox & Subbarao, 2000). However, genetic analysis of HA gene is well-documented, but limited information is available about the genetic and antigenic variation of the other surface protein, NA, especially from the Indian subcontinent. Such studies may serve as an appropriate platform to gain insights into the evolution of influenza virus, thereby facilitating drugs/vaccines design and development.

The influenza NA protein was recognized as a potential target for anti-influenza drugs during the 1970’s (Air, 2012). Although many studies have reported the usefulness of NA as a vaccine antigen, NA is mostly ignored in the context of influenza vaccine development (Wohlbold et al., 2015). Standardization of the NA content in vaccines is difficult because the ratio of HA: NA is strain-specific (Getie-Kebtie et al., 2013).

Next generation vaccines such as the VLP are reported to incorporate consistent amounts of NA (Eichelberger & Wan, 2014). Although a number of influenza VLPs have been developed to date, VLP containing N1 and N2 proteins along with HA and M have not been reported. N1 and N2 based immunity might be beneficial to protect against influenza viruses that possess homologous N1 or N2 and also during the emergence of new pandemic influenza virus that may carry a heterologous N2 or N1 NA, such as H2N2 or H5N1 (Wohlbold et al., 2015).