



IMMUNOLOGY & VACCINOLOGY

IMM-032

EVALUATION OF THE GENETIC DIVERSITY OF H1PDM INFLUENZA FIELD VIRUSES IN RESPECT TO RESPIPORC® FLUPAN H1N1

S. Pesch, V. Fachinger.

IDT Biologika GmbH, Dessau-Rosslau, Germany.

Introduction

Since the emergence of pandemic H1N1 Influenza virus in the swine population in 2009 this subtype has established itself as endemic in swine. In contrast to pandemic H1N1 variant isolates in humans, which hardly undergo any change genetically, the swine isolates frequently undergo genetic events of drift and shift characteristic for Influenza A viruses.

Material & Methods

Field isolates of pandemic H1Nx (n=27) and nucleotide sequences of hemagglutinin gene (n=74) derived from the Influenza Research Database IRD were pairwise compared, phylogenetically analysed, and aligned in respect to their antigenic sides. For proof of efficacy of Respiporc® FLUpan H1N1 against different H1pdm virus isolates, isolates from different phylogenetical positions were chosen for challenge trials.

Results

Compared to the vaccine strain, pairwise comparison of the 101 available full length nucleotide sequences from pandemic H1 gene revealed nucleotide homologies of 95.5 to 99.8 percent (average = 98.1 percent) and amino acid identities of 95.5 to 99.8 percent (average = 98.5 percent). Phylogenetic analyses indicated genetic diversity without strong tendency of creating clusters. This is new as cluster building is commonly seen in non-pandemic subtypes of swine influenza viruses. One challenge strain with 96.2 na homology and 97.7 aa identity to the vaccine strain was positioned separately from the vaccine strain in the phylogenetic tree. Respiporc® FLUpan H1N1 showed significant efficacy with regard to viral shedding and vial lung load in all challenge trials including challenges with the heterologous field virus isolate. Additional benefit was the reduction of dyspnoea. In the heterologous challenge the reduction of dyspnoea was highly significant ($p < 0.0001$) with a relative reduction of 99%.

Discussion

In spite of genetic diversity of pandemic H1 isolates indicating frequent events of genetic drift and shift, efficacy of Respiporc® FLUpan H1N1 could be demonstrated in homo- and heterologous challenge trials.