
Sponsors

University of Minnesota

College of Veterinary Medicine

College of Agricultural, Food and Environmental Sciences

Extension Service

Swine Center

Editors

W. Christopher Scruton

Stephen Claas

Layout

David Brown

Logo Design

Ruth Cronje, and Jan Swanson;

based on the original design by Dr. Robert Dunlop

Cover Design

Shawn Welch

The University of Minnesota is committed to the policy that all persons shall have equal access to its programs, facilities, and employment without regard to race, color, creed, religion, national origin, sex, age, marital status, disability, public assistance status, or sexual orientation.

GENETIC AND SEROLOGIC CLASSIFICATION OF SWINE INFLUENZA VIRUS H3N2 ISOLATES

J. H. Lee¹, Y.K. Choi² and Han S. Joo¹

¹University of Minnesota, St. Paul; ² St. Jude Children Research Hospital, Memphis

Introduction

Three predominant subtypes of swine influenza virus (SIV) are prevalent in swine. In North America, only one subtype of H1N1 had been identified in pigs. However, since 1998, isolation of H3N2 from clinically affected pigs has been reported from different farms. Triple reassortant H3N2 viruses containing genes originated from human influenza virus, classical SIV and avian influenza virus have been most common in pigs. Wholly human and double reassortant H3N2 viruses were also reported from pigs. The purpose of this study was to investigate if triple reassortant H3N2 viruses can be classified genetically and serologically into different groups.

Materials and methods

Field isolates of triple reassortant H3N2 viruses were obtained from the Minnesota Veterinary Diagnostic Laboratory. For each isolate, viral RNA was extracted, and RT-PCR was performed. Nucleotide sequencing of the amplified hemagglutinin (HA) gene was carried out. Phylogenetic analyses using the sequence were performed. These methods were described in a previous study¹. Five H3N2 virus isolates were selected by phylogenetic analyses, and antiserum to each isolate was produced by repeated inoculation of each virus in SIV free pigs. Sera were tested for SIV antibodies by hemagglutinin inhibition (HI) technique by a routine method.

Results and Discussion

In a phylogenetic analysis with 5 selected H3N2 isolates, at least 3 different clusters were identified. Isolates A (A/SW/NC/39615/01) and D (A/SW/MN/23062/02) were classified into cluster II, B (A/SW/MO/22582/02) and C (A/SW/NC/5854/02) into cluster I, and E (A/SW/46710-35) into cluster III. By cross-HI tests, the antibody titers were 4-256 times higher with homologous virus than those with heterologous isolates (Table 1).

The present results show wide ranges of HI antibody titers by different H3N2 viruses. It is not known how effective cross protection can be expected in pigs by cross-challenge experiments with different H3N2 viruses.

Table 1. Cross HI antibody titers of swine immune sera to homologous and heterologous H3N2 viruses

H3N2	Antiserum to H3N2 virus isolate				
	A	B	C	D	E
A	320*	20	20	20	20
B	80	1280	20	160	320
C	80	160	2560	320	80
D	10	10	80	2560	20
E	10	160	10	20	1280

* Reciprocals of HI antibody titers to homologous (bold) and heterologous H3N2 viruses

References

1. Choi YK, Goyal SM, Joo HS (2002) Arch Virol 147:1209-1220