The 7th International Symposium on Emerging and Re-emerging Pig Diseases

Proceedings

June 21-24, 2015

Kyoto International Conference Center

Kyoto, Japan

ORGANIZERS

The 7th International Symposium on Emerging and Re-emerging Pig Diseases Organizing Committee

Science Council of Japan

CO-ORGANIZERS

The Japanese Society of Veterinary Science

Japan Pig Veterinary Society

Japanese Association of Swine Veterinarians (JASV)

P096

GENETIC MARKERS ASSOCIATED WITH INFLUENZA VACCINATION EFFICACY IN SWINE

Ricardo Zanella[1], Danielle Gava[2], Jane O. Peixoto[2], Rejane Schaefer[2], Janice R.C. Zanella[2], Natalha Biondo[3], Marcos V.G. da Silva[4], Mauricio E. Cantão[2] & Mônica C. Ledur[2]

[1] University of Passo Fundo, Passo Fundo, Brazil, [2] Embrapa Swine and Poultry National Research Center, Brazil, [3] Santa Catarina State University, Brazil, [4] Embrapa Dairy Cattle National Research Center, Brazil.

Introduction

Influenza A virus (IAV) is one of the the most important pathogen of the porcine respiratory disease complex and genetically diverse IAV subtypes (H1N1pdm, H1N2 and H3N2) are circulating in pig farms in most of the Brazilian states [1]. Infection of pigs with IAV cause considerable economic losses to the producers due to the high morbidity among infected pigs and it is also considered a global health concern [2]. To reduce those losses, several management strategies have been used. Currently, vaccination is considered the most efficient method to control and to diminish the disease burden, reducing the clinical signs and the transmission of the disease [3]. However, the immune response to vaccination can be variable between individuals [4]. It has been proposed that immune response to vaccination is a complex trait with variation resulting from environmental and genetic factors [5]. Therefore, the objective of this research was to identify genetic mechanisms involved in host immune response to IAV vaccination.

Materials and methods

One hundred and three piglets were vaccinated with an inactivated pandemic H1N1 IAV, A/swine/Brazil/107/2010 (KF683611-KF683618), with a titer of $10^{4.38}$ 50% tissue culture infectious dose (TCID50) per mL. The virus was inactivated with 2-bromoethylamine hydrobromide and an adjuvant (Emulsigen D) was added to the vaccine preparation. Piglets were vaccinated with 1.5mL via intramuscular route at 34 days-old and boosted at 55 days-old. Blood samples were collected from piglets at 21, 34, 55 and 76 days-old and tested for the presence of antibodies for the nucleoprotein (NP) of IAVs using IDEXX Influenza A- Ab test® (IDEXX Laboratories Inc). DNA was extracted from piglets' lungs and was genotyped using the Illumina PorcineSNP60V2 BeadChip which contains 61,565 SNPs evenly spaced across the swine genome. The active immunity was considered based on the presence or absence of NP antibody related to the vaccination (day 76). A standard chi-square test and the odds ratio was used to test association of SNP and immune response using PLINK [6]. Significance was considered if an unadjusted P-value was $<5.0x10^{-5}$ [7].

Results

At day 34 none of the piglets had antibodies to IAV, indicating that any titer post-vaccination were due to immunization. On day 76, seventy-five piglets (n=75) did not respond to vaccination and twenty-eight piglets (n=28) had antibodies to IAV vaccination. When we tested the association of SNPs with immune response, two markers on *SSC12*, located at 27,241,826bp and 31,875,247bp of the pig genome, were moderated associated ($P<5x10^{-5}$) with immune response IAV vaccination. The LD between these two markers *rs81433411* and *rs81341245* was D'= 0.861. The frequency of the "A" allele of *rs81433411* was 0.58 in control and 0.25 in case animals. For the SNP *rs81341245*, the frequency of the "G" allele was 0.31 in control and 0.62 in case animals. Testing the combined effect of the associated markers did not improve the significance of the test.

Discussion

The efficacy of the *in house* vaccine was 28%, indicating a moderate level of protection. This moderate protection was possibly caused by the final amount of antigen delivered by the vaccine. The region on *SSC12* associated with immune response to IAV vaccination harbor four annotated genes in the swine genome: *TOB1, NME1, NME2* and *STAT2*. All the genes located in the associated region were previously described as involved with immunity, more specifically with influenza vaccination in human, therefore they are good positional and functional candidate genes that could be used to explain the efficacy of vaccination to IAV in swine[3,8,9,10] . The identification of genetic markers and the understanding of the genetic mechanisms involved in the immune response to vaccination would be useful to select pigs that better respond to IAV challenge. It could contribute to reduce the losses caused by IAV infection in swine.

Acknowledgements

Zanella, R. is an early investigator fellow (BJT) from CNPq at Embrapa Swine and Poultry. The authors sincerely appreciate the technical assistance of Marisete F. Schiochet on ELISA tests, Vanessa Haach in sampling collection and Dr. Jack Dekkers for the experimental design discussion.

References

1. Schaefer et al.(2014). Arch Virol.
2. Olsen et al.(2002). Emerg Infect Dis 8:814-819.
3. Poland e al.(2014). C.O Imm. 29:62-68.
4. Rajao et al.(2014). C.T.M.Imm. 385: 307-326.
5. Newport et al.(2004). Genes Imm.5: 122-129.
6. Purcell et al.(2007). Am J H. Gen. 81: 559-575.
7. WTCCC (2007). Nature 447: 661-678.8.
8. Salerno et al.(2014) Eur J Im 44: 646-649.
9. Hasan et al. (2013) Inf Im 81: 2499-2506.
10. Nakaya et al. (2011) Nat Im 12: 786-795.