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Making sense of PRRS virus sequences and a new view for PRRS inactivated vaccine – MJPRRS™: old problem – new approach

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Since clinical outbreaks of Porcine Reproduction and Respiratory Syndrome (PRRS) were first reported in the United States in late 1980's, investigators have made significant progress in understanding the PRRS virus and have accumulated substantial amount of scientific information surrounding PRRS, which have been made available to the swine industry and its constituents. Control of PRRS through vaccination and/or various biosecurity measures has been somewhat improved based on such information. Nonetheless, PRRS still remains as the most devastating disease in the swine industry.

The MJPRRS™ Technology introduced by MJ Biologics, Inc. ("MJ") allows enhanced control and prevention of PRRS outbreaks and symptoms through its bio-technical advantages in the following two aspects: (i) verification and inclusion of the most relevant strains of PRRS virus in the vaccine production determined via ORF5 based PRRS strain classification algorithm and grouping method; and (ii) enhanced antigen quality and increased antigenicity in the vaccine by the adoption of PRRS virus subunit component reproduction technology. MJ has collected, reviewed and reevaluated data and experiences of producers and clinicians as to conventional PRRS control methods used in the past and results of such use. Those evaluated methods include attenuated live virus vaccines, use of farm-origin live virus exposure, and conventional killed autogenous vaccines. The main focus of MJ's evaluation was at PRRSV ORF5 sequence information combining with clinical observations made for each case. Under MJ's classification algorithm PRRS viruses are classified based on their immunological properties by looking at PRRS viruses "as a pig" instead of "as a virus". The evaluation based on MJ's classification algorithm was compared to other conventional understanding of PRRS virus strain variation such as RFLP and Dendogram information for such viruses. The results from and the conclusions made by applying MJ's algorithm to the on-farm PRRS outbreak cases provided reasonable explanation as to how and why so many PRRS outbreaks had repeatedly occurred at the same farms notwithstanding the use of conventional PRRS control methods. MJ's grouping method based on its proprietary classification algorism classifies several thousand currently identified North American PRRS isolates and European-like isolates into 16 groups (Group D-1 through D-8, and Group S-1 through S-8) and 8 groups (Group E-1 through E-8), respectively. In the process of making autogenous inactivated MJPRRS™ vaccines, MJ's PRRS virus grouping method allows selection of the most immunologically relevant viruses for a farm at a given time among the historical PRRS viruses previously introduced to the farm.

This presentation is composed of two parts; Part 1 will review published data based on MJPRRS™ grouping method to show how previous PRRSV challenge trial results fit with the grouping data, and Part 2 will review data from a small trial of selecting proper adjuvant for MJPRRS™ vaccine.