RESEARCH ABSTRACT
SWINE HEALTH

Title: Gene expression by PRRSV-infected macrophages – **NPB #98-056**

Investigator: Mark S. Rutherford

Institution: Department of Veterinary PathoBiology
University of Minnesota
1988 Fitch Ave., Room 295
St. Paul, MN 55108

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ABSTRACT:

The detailed mechanism(s) by which porcine reproductive and respiratory syndrome virus (PRRSV) impairs alveolar Mø homeostasis and function remains to be elucidated. We used differential display reverse-transcription PCR (DDRT-PCR) to identify molecular genetic changes within PRRSV-infected Mø over a 24 h post infection period. From over 4,000 DDRT-PCR amplicons examined, 19 porcine-derived DDRT-PCR products induced by PRRSV were identified and cloned. Northern blot analysis confirmed that four gene transcripts were induced during PRRSV infection. PRRSV attachment and penetration alone did not induce these gene transcripts. DNA sequence revealed that one PRRSV-induced expression sequence tag (EST) encoded porcine *Mx*1, while the remaining 3 clones represented novel ESTs. A full-length cDNA clone for EST G3V16 was obtained from a porcine blood cDNA library. Sequence data suggests that it encodes an ubiquitin-specific protease (UBP) that regulates protein trafficking and degradation. In pigs infected *in vivo*, upregulated transcript levels were observed for *Mx*1 and *Ubp* in lung and tonsils, and for *Mx*1 in tracheobronchial lymph node (TBLN). These tissues correspond to sites for PRRSV persistence, suggesting that the *Mx*1 and *Ubp* genes may play important roles in clinical disease during PRRSV infection.