Genome-wide CRISPR/Cas9 Screen for Porcine Epidemic Diarrhea Virus Resistance in Pig Intestinal Epithelial Cells

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Porcine epidemic diarrhea which is caused by porcine epidemic diarrhea virus (PEDV) resulted in large economic losses in the pig industry because of the high morbidity and mortality approaching 100% in neonatal piglets. Recently, PEDV is still identified as the main pathogen causing severe diarrhea in pig farms, highlighting the urgency to genetically improve the ability of pigs to resist PEDV infections. Genome-wide CRISPR screen has been proven to be an effective technology to identify functional genes resistant to viral infections. Here, we designed >90 thousand sgRNAs targeting porcine protein coding genes and cloned them into CRISPR knockout vectors. After transfection and puromycin resistance selection in IPEC-J2 cell, cell libraries with gene knockout were obtained. PEDV was added to the cell library and cultured for 14 days with consistent infection. Finally, survival cells were collected, amplified by PCR, and sequenced by high-throughput sequencing platform. The MAGeCK software was used to compare the enrichment differences of sgRNA between the survival cells and control cells. A subset of genes including ERN1, THEM19, KDM2B, and SULT2A1 with high potential resistance to PEDV infection was screened out. These findings will be helpful for identifying genes with resistance to PEDV infection and further contribute to genetic resistance breeding for porcine epidemic diarrhea.

Research Biography

Haifei Wang received his PhD degree on animal genetics and breeding from China Agriculture University in 2016. Since September of 2016, he has served College of Animal Science and Technology of Yangzhou University as a lecturer. His research interests focus on identifying genes and genetic markers involved in regulating porcine pathogen infections and clarifying the underlying molecular mechanisms.