Scientific Abstract: Porcine epidemic diarrhea virus (PEDV) is a major cause of severe diarrhea and dehydration in pigs. Belonging to the *Coronaviridae* family, PEDV is an enveloped, positive-sense, single-stranded RNA virus with a genome size of approximately 28kb. The first detection of PEDV was reported in 1971 from England while Japan, China, South Korea, and Thailand also have reported PEDV infections. The United States first detected PEDV in May 2013 (1-5). The veterinary diagnostic laboratories quickly developed sensitive and specific real-time RT-PCR (RRT-PCR) assays to detect PEDV in a variety of porcine and environmental samples. In this study, we compared the PEDV-TGEV multiplex RRT-PCR assay developed at the University of Minnesota (UMN) to a commercial TGEV-PEDV multiplex RRT-PCR assay. In addition, 13 United States PEDV complete genomes were generated to understand the genetic diversity of PEDV, and the phylogenetic relationship to the worldwide PEDV strains.