

# Molecular study of porcine transmissible gastroenteritis virus after serial animal passages revealed point mutations in S protein

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**Abstract** Porcine respiratory coronavirus is related genetically to porcine transmissible gastroenteritis virus with a large deletion in S protein. The respiratory virus is a mutated form that may be a consequence of the gastroenteritis virus's evolution. Intensive passages of the virus in its natural host may enhance the appearance of mutations and therefore may contribute to any attenuated form of the virus. The objective of this study was to characterize the porcine transmissible gastroenteritis virus TMK22 strain after passages in piglets from 1992 until 2007. A typical experimental infection, molecular characterization, and serological analysis were also carried out to further characterize and to evaluate any significant difference between strains. The sequence analysis showed two amino acid deletions and loss of an *N*-glycosylation site in

transmissible gastroenteritis virus S protein after passages in piglets. Although these deletions were positioned at the beginning of the antigenic site B of S protein, no clinical differences were observed in piglets infected experimentally either with the native virus or the mutated one. Serological tests did not show any antibody reactivity difference between the two strains. In this article, we report that the S protein deletion did not affect the virus's pathogenicity. The variety of the virus's evolutionary forms may be a result, not only of the multiple passages in natural hosts, but also of other factors, such as different pathogens co-infection, nutrition, immunity, and others. Further studies need to be carried out to characterize the mutated strain.

**Keywords** Gastroenteritis · Experimental infection · Porcine disease · RT-PCR · DNA sequencing

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## Introduction

Porcine transmissible gastroenteritis virus (TGEV) is an enteropathogenic coronavirus [26, 31]. It infects pigs of all ages; however, infection is most severe in newborn piglets, resulting in a fatal diarrhea [27, 33]. The disease outbreaks were observed in many countries such as Japan, Canada, Russia, and causing considerable economic damages in swine industries [15]. The mortality of the newborn piglets can reach 100% [5, 32].

TGEV has three major structural proteins: the spike (S), the nucleoprotein (N), and the membrane (M) [18, 39]. Protein S is the major inducer of TGEV neutralizing antibodies (Abs).

Studies of TGEV mutations were enhanced by the detection of porcine respiratory coronavirus (PRCV) in the