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Molecular characteristics of the *spike* gene of porcine epidemic diarrhoea virus strains in Eastern China in 2016

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Highlights

- The positive rate of PEDV in diarrhea samples collected from Chinese porcine farms in 2016 is 28.93%.
- The detected prevalent Eastern China PEDVs clustered into a new subgroup, G2-b (Chinese non S-INDEL).
- G2-b only included strains circulating in China after 2014.
- Eastern China PEDVs were genetically distinct and had various amino acid differences in the neutralizing epitope domain of the S protein, as well as different patterns of predicted high-specificity N-glycosylation sites compared with the CV777 vaccine strain.

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