Candidate peptide-vaccine induced potent protection against CSFV and identified a principal sequential neutralizing determinant on E2

Classical swine fever virus (CSFV), the pathogen of classical swine fever (CSF), is a small (40–60 nm in diameter) enveloped positive-stranded RNA virus belonging to the genus *Pestivirus* of the *Flaviviridae* family. Three envelope-associated glycoproteins are derived from glycoprotein precursor E012 via post-translational processing. Envelope glycoprotein E2 (formerly termed E1 or gp51–54) and E0 (also termed E’ms) reside on the outer surface of the virion (2). Immunogenic response against glycoprotein E2 alone was proved sufficient for complete protection. Four distinct antigenic domains (A, B, C and D) were successfully mapped to the N-terminal of E2, and E2 containing either of the two structural antigenic units, domain B/C or domain A, was able to separately protect pigs from lethal challenge of CSFV (3). Five overlapping peptides (BC1–BC5) (aa693–777) and multi-peptide-vaccines (MPVs) based on antigenic domain A (aa773-865) covering the N-terminal part of glycoprotein E2 exhibited better protective activity than C-strain. They successfully induced peptide-specific neutralizing antibodies and could provide pigs with complete protection from the lethal challenge of CSFV. Scanning with a panel of sequential peptide-immunogens is an effective method to locate sequential neutralizing epitopes (1).

References