



# Genetic features of a translation initiation system composed of IRES element, nucleotide context surrounding the initiation codon, and translation initiation region of classical swine fever virus RNA

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**ABSTRACT.** Nucleotide and codon usage are typically examined to investigate viral evolution. In this study, we analyzed the genetic information of 46 strains of classical swine fever virus (CSFV) RNA, nucleotide usage in the internal ribosome entry site (IRES), the nucleotide context surrounding the initiation codon, and synonymous codon usage in the translation initiation region. Phylogenetic analysis of the IRES element indicated that the genetic diversity of this element is generally similar to the phylogenetic clusters of CSFV genotypes. Nucleotides surrounding the initiation codon of CSFV RNA were generally more stable (ACAUGGCACAAUGGAGUUG) compared to the internal AUG in the CSFV coding sequence. The second codon position after the initiation codon was generally selected to be GAG, which has

lower tRNA abundance in pigs than its synonymous member (GAA). Regarding the synonymous codon usage bias in the CSFV translation initiation region, some codons showing low tRNA abundance in pigs are more frequently located in the translation initiation region than in the open reading frame of CSFV. Although CSFV, similarly to other RNA viruses, has a high mutation rate in nature, the regulatory features of nucleotide and synonymous codon usage of the IRES element, the nucleotide context surrounding the initiation codon and the translation initiation region in CSFV RNA have been 'branded' in the system of translation initiation to accommodate gene expression mediated by the cap-independent translation mechanism.

**Key words:** Cap-independent translation mechanism; tRNA abundance; Classical swine fever virus; Internal ribosome entry site; Synonymous codon usage; Translation initiation region;