**P7 Variation of the NSP2 Gene of PRRSV in Thailand**

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**Introduction and Objectives**

Porcine reproductive and respiratory syndrome virus (PRRSV) is the cause of porcine reproductive and respiratory syndrome (PRRS), an economically important swine disease. The genetics of PRRSV are heterogeneous, especially in the nonstructural protein (nsp) 2-coding regions. PRRSV isolates with deletions in the nsp2 regions have been reported in some countries and some have been reported to be highly pathogenic, such as MN184 (USA) (1) and SY0608 (China) (20. However, the significance of the nsp2 genetic variation has not yet been elucidated. In this study, we determined full and partial nsp2 nucleotide sequences of Thai isolates of PRRSV and we demonstrate that some of these had nucleotide deletions in the nsp2-coding region.

**Materials and Methods**

The Thai PRRSV isolates in this study were provided by Chulalongkorn Veterinary Diagnostic Laboratory. Viral RNA was extracted using NucleoSpin® RNA Virus (Macherey-Nagel) and reverse transcribed using OmniScript RT kit (Qiagen). PCR was done using GoTaq® Green Master Mix (Promega) and nsp2-specific primers. PCR products were cloned into pGEM-T Easy vectors (Promega). Recombinant clones were sequenced using Automated DNA Sequencer. Sequences were analyzed using the Clustal W program in MEGA 4.0 (3).

**Results and Discussion**

One complete nsp2 sequence of the Thai isolates (08RB1) and two partial sequences (07NP4 and L119) were compared with that of VR2332, the prototypic strain, MN184 and SY0608, which have been shown to contain nucleotide deletions in the nsp2 regions and are reported to be highly pathogenic. In this study, these three Thai isolates were shown to contain deletion in the nsp2 region, compared to the VR2332 strain. The sequence analysis revealed that none of these deletion patterns were exactly the same as the previous reported isolates but more or less similar to the MN184 and HB-2 (china) isolates (Table 1 and data not shown).

In this study, we investigated the variation of the nsp2 gene of PRRSV in Thailand. We demonstrated that some of the Thai isolates also had nucleotide deletions in the nsp2 regions. The complete nsp2 sequence analysis of the 08RB1 isolate demonstrated the 08RB1 isolate had a 294-base (98-aa) discontinuous deletion, compared to the VR2332 strain, becoming the shortest nsp2 among Thai isolates that have been previously reported. It is interesting that whether or not these Thai isolates, with deletion patterns were similar to that of the MN184, they were also highly pathogenic.

<table>
<thead>
<tr>
<th>Isolates</th>
<th>Deletion aa size</th>
<th>Possible aa position in nsp2 of VR2332</th>
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<tbody>
<tr>
<td>MN184</td>
<td>131</td>
<td>323-433, 482, 495-513</td>
</tr>
<tr>
<td>08RB1</td>
<td>98</td>
<td>332-428, 469</td>
</tr>
<tr>
<td>07NP4</td>
<td>47</td>
<td>328-366, 466-474</td>
</tr>
<tr>
<td>L119</td>
<td>97</td>
<td>332-428</td>
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</tbody>
</table>

**References**