Assignment of solute carrier family 2 (facilitated glucose transporter), members SLC2A2, SLC2A3, SLC2A5, SLC2A8 and SLC2A12 to porcine chromosomes by somatic cell and radiation hybrid panel mapping (Brief report)

Background: The transport of glucose plays an important role in cellular glucose homeostasis and metabolism [1]. Due to the hydrophilic character of glucose, the transport of glucose in and out of cells requires specific carrier proteins. The mammalian facilitative glucose transport family, which contains the energy-independent transporters (gene symbol SLC2A, protein symbol GLUT), catalyzes the entry of glucose into mammalian cells by facilitative diffusion down a concentration gradient. Thirteen members of mammalian GLUT family have been now characterized [1]. In swine, the chromosomal locations for the five genes (SLC2A2, SLC2A3, SLC2A5, SLC2A8 and SLC2A12) have not yet been determined. In this study, as the first step to better understand of the roles of these GLUTs in pigs which could subsequently be beneficial for pig production, we report the mapping of the five genes using both porcine somatic cell hybrid panel (INRA-SCHP) and radiation hybrid panel (IMpRH).

Procedure:
Prime sequences
SLC2A2F: 5'-TCT GAT GCT CTT CTT CTG TC-3'
SLC2A2R: 5'-TCT ATT TGT GCT TGT GTG AG-3'
SLC2A3-1F: 5'-CTT GGG CTT CAC CAT CAT TC-3'
SLC2A3-1R: 5'-GTG ACT TTC TTT TCC TGG GC-3'
SLC2A3-2F: 5'-GTC CTC GGT TCC TGC TCA TT-3'
SLC2A3-2R: 5'-CCT TCT CAC CCC ATT CTT CG-3'
SLC2A5F: 5'-TCT GAT GCT CTT CTT CTG TC-3'
SLC2A5R: 5'-TCT ATT TGT GCT TGT GTG AG-3'
SLC2A8F: 5'-AGT TCC CGC TGC TGC TCT GT-3'
SLC2A8R: 5'-AGT GCC TGG TGG TGC TCT GT-3'
SLC2A12F: 5'-ACA GTT GCC ACT CAT TCT AC-3'
SLC2A12R: 5'-CCA AAC TGT AAG CCT GTG AT-3'

Human SLC2A2, SLC2A5, SLC2A8 and SLC2A12 mRNA sequences were used to search the homologous pig genome sequences (http://www.animalgenome.org/blast/) or ESTs (http://www.tigr. org/tdb/tgi/ssgi). Pig specific primers were then designed based on the retrieved pig sequences for localization of the gene on pig chromosomes. For SLC2A3, the pig EST homologous to human SLC2A3 mRNA sequence was selected to design primers (named SLC2A3-1F and SLC2A3-1R) to obtain a genomic fragment. Subsequently, the pig specific primes (SLC2A3-2F, SLC2A3-2R) were used to map the gene. All the PCR products were cloned into a pMD-18T vector (Takara Biotechnology) and sequenced commercially. GenBank accession numbers, primer
locations, PCR sizes, human locations and mapping results are presented in the Table.

**Somatic cell hybrid and radiation hybrid mapping**

In this study, the primers used for mapping only amplified pig genomic DNA, and not hamster or mouse control. The PCR conditions were 95 °C for 5 min and 34 cycles of 94 °C for 30 s, 56–65 °C for 30 s and 72 °C for 20 s, and a final extension of 72 °C for 5 min. The PCR results for the five porcine SLC2A genes were analyzed by the tools provided at http://www.toulouse.inra.fr/lgc/pig/hybrid.htm for INRA-SCHP and http://imprh.toulouse.inra.fr/ for IMpRH mapping [2, 3].

**Results:** As shown in the Table, we assigned SLC2A2, SLC2A3, SLC2A5, SLC2A8 and SLC2A12 to SSC13q23-(1/2q41), SSC5q25, SSC6q22-q23, SSC1q28-q213, and SSC1p24-p25 using INRA-SCHP, respectively. We then confirmed and refined the chromosomal locations of the five genes by using IMpRH. In this study, the mapping results of the five genes are in agreement with previous comparative mapping results as human chromosomes 3, 12, 1, 9 and 6 share syntenic groups with porcine chromosomes 13, 5, 6, 1, 1 respectively [4].

**Table: Chromosomal assignments of the five porcine SLC2A genes**

<table>
<thead>
<tr>
<th>Gene symbol</th>
<th>Primer</th>
<th>PCR size in bp</th>
<th>Human Location</th>
<th>Porcine INRA-SCHP</th>
<th>Porcine RH</th>
</tr>
</thead>
<tbody>
<tr>
<td>SLC2A2</td>
<td>SLC2A2F, SLC2A2R</td>
<td>289</td>
<td>3q26-q26</td>
<td>13q23-(1/2 q41)</td>
<td>Retention (%)</td>
</tr>
<tr>
<td>SLC2A3</td>
<td>SLC2A3-2F, SLC2A3-2R</td>
<td>215</td>
<td>12p13</td>
<td>5q25</td>
<td>0.8173</td>
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<tr>
<td>SLC2A5</td>
<td>SLC2A5F, SLC2A5R</td>
<td>276</td>
<td>1p36</td>
<td>6q22-q23</td>
<td>0.7379</td>
</tr>
<tr>
<td>SLC2A8</td>
<td>SLC2A8F, SLC2A8R</td>
<td>195</td>
<td>9q33</td>
<td>1q28-q213</td>
<td>0.4444</td>
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<tr>
<td>SLC2A12</td>
<td>SLC2A12F, SLC2A12R</td>
<td>256</td>
<td>6q23</td>
<td>1p24-p25</td>
<td>0.8779</td>
</tr>
</tbody>
</table>

The locations of genes of the human map were collected from http://www.ncbi.nlm.nih.gov/Locuslink/

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**References**


