Key Lab of Agricultural Animal Genetics, Breeding, and Reproduction of Ministry of Education & Department of Animal Genetics and Breeding, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, 430070, PR China

KE LIU, SHUHONG ZHAO, BANG LIU, BIN FAN, CHANGCHUN LI, and MEI YU

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)
(Kartierung von porcinen solute carrier family 2 Genen)

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'-CGT GAG AGG AGA AAC CGT GG-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

Gene symbol (GenBank Acc. No.)	Primer	PCR size in bp	Human Location[1]	Porcine INRA-SCHP			Porcine RH		
				Porcine location	Regional probability	Correlation coefficient	Retention (%)	Nearest marker (Distance in cR)	LOD score
SLC2A2 (EF011104)	SLC2A2F SLC2A2R	289	3q26-q26	13q23-(1/2 q41)	0.8003	0.8478	13	S0084 (76)	4.29
SLC2A3 (EF012367)	SLC2A3-2F SLC2A3-2R	215	12p13	5q25	0.8173	1.0000	32	Sw963 (27)	14.46
SLC2A5 (EF012368)	SLC2A5F SLC2A5R	276	1p36	6q22-q23	0.7379	1.0000	24	Sw1355 (60)	6.65
SLC2A8 (EF012369)	SLC2A8F SLC2A8R	195	9q33	1q28-q213	0.4444	1.0000	28	Sw705 (80)	4.32
SLC2A12 (EF012370)	SLC2A12F SLC2A12R	256	6q23	1p24-p25	0.8779	1.0000	23	Sw1851 (64)	6.22

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

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Correspondence to MEI YU, E-mail: yumei@mail.hzau.edu.cn