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The Diabetes Susceptibility Gene *SLC30A8* that Encodes the Zinc Transporter ZnT8 is a Pseudogene in Guinea Pigs Potentially Contributing to Low Guinea Pig Islet Zinc Content

Kristen E. Syring, Karin J. Bosma, James K. Oeser, Masakazu Shiota, and Richard M. O'Brien $^{\$}$

Department of Molecular Physiology and Biophysics, Vanderbilt University School of Medicine, Nashville, TN 37232

Abstract

In most mammals pancreatic islet beta cells have very high zinc levels that promote the crystallization and storage of insulin. Guinea pigs are unusual amongst mammals in that their islets have very low zinc content. The selectionist theory of insulin evolution proposes that low environmental zinc led to the selection of a mutation in Guinea pig insulin that negated the requirement for zinc binding. In mice deletion of the *Slc30a8* gene, that encodes the zinc transporter ZnT8, markedly reduces islet zinc content. We show here that *SLC30A8* is a pseudogene in Guinea pigs. We hypothesize that inactivation of the *SLC30A8* gene led to low islet zinc content that allowed for the evolution of insulin that no longer bound zinc.

Keywords

Islet; Zinc; Diabetes; Insulin; Evolution

High islet zinc levels have been reported to be important for multiple aspects of pancreatic islet beta cell function including paracrine signaling from beta to alpha cells (Hardy et al. 2011; Robertson et al. 2011), proinsulin processing (Dunn 2005), crystallization of insulin hexamers (Chausmer 1998; Dunn 2005) and promotion of insulin aggregation (Xu et al. 2012), which may be protective against proteolysis (Zimmerman and Yip 1974). However, the importance of islet zinc appears at odds with the observation that in some mammalian species, for example Guinea pigs (*Cavia porcellus*), islet zinc content is very low (Havu et al. 1977; Zimmerman and Yip 1974). This is thought to be because in these species insulin does not bind zinc due to the absence of a histidine residue in the B10 position of the insulin molecule (Beintema and Campagne 1987; Blundell et al. 1972; Smith 1966). The observation that deletion of *Slc30a8* in mice markedly lowers islet zinc, with little effect on

[§]To whom correspondence should be addressed: Department of Molecular Physiology and Biophysics, 8415 MRB IV, 2213 Garland Ave, Vanderbilt University Medical School, Nashville, TN 37232-0615, richard.obrien@vanderbilt.edu. Author Contributions

K.E.S, K.J.B, J.K.O all contributed to gene expression analyses and wrote parts of the manuscript. M.S. and R.O'B. designed experiments and wrote parts of the manuscript.

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As a first step towards determining whether Guinea pig islets still maintain high *SLC30A8* expression, despite low zinc content, we attempted to isolate a Guinea pig *SLC30A8* cDNA. A BLAST search of the NCBI nr and refseq_rna databases using the human *SLC30A8* cDNA sequence (NM_173851) as the query failed to identify any clones. We therefore searched for the Guinea pig *SLC30A8* gene by performing a BLAST search of the NCBI refseq_genomic database using the human *SLC30A8* cDNA sequence as the query. This identified a genomic scaffold that contains the entire Guinea pig *SLC30A8* gene as a contiguous sequence (NT_176419).

in Guinea pigs islets despite the low zinc content.

Potential exon/intron splice junctions in the putative Guinea pig SLC30A8 gene were determined by comparison with the human SLC30A8 (Chimienti et al. 2004) and mouse Slc30a8 (Pound et al. 2009) genes and the consensus sequence for RNA splicing (Jackson 1991) (Table I). As with the human SLC30A8 (Chimienti et al. 2004) and mouse Slc30a8 (Pound et al. 2009) genes, the Guinea pig SLC30A8 gene appeared to contain 8 exons, 7/8 of which matched the sizes of the human and/or mouse exons (Table I). However, closer inspection of the sequence while attempting to re-construct a putative Guinea pig SLC30A8 cDNA revealed that the Guinea pig SLC30A8 gene is a pseudogene (Fig. 1). Notable differences with the human SLC30A8 open reading frame include a switch from a starting methionine to a value, the presence of two in-frame stop codons and the deletion of 11 base pairs in exon 7 (Table I) that would result in a frame-shift (Fig. 1). In addition, comparison with the splice junctions identified in the human SLC30A8 (Chimienti et al. 2004) and mouse Slc30a8 (Pound et al. 2009) genes reveals changes away from the consensus at three junctions that would be predicted to impair splicing (Table I). Since sequencing of the Guinea pig genome is complete, the possibility that the SLC30A8 gene underwent duplication in Guinea pigs and that we have failed to identify an intact SLC30A8 variant appears remote. In addition, this pseudogene is flanked on one side by Guinea pig homologs of EIF3H, UTP23 and RAD21 and on the other by homologs of MED30 and EXT1, a relationship and orientation that are consistent with other known mammalian SLC30A8 genes. The discovery that SLC30A8 is a pseudogene in Guinea pigs suggests that the inability of Guinea pig insulin to bind zinc and the absence of ZnT8 may both contribute to low islet zinc content.

Evolutionary studies suggest that Guinea pigs are closely related to chinchillas (*Chinchilla lanigera*) and naked mole rats (*Heterocephalus glaber*) (Gorbunova and Seluanov 2009). A BLAST search of the NCBI nr database using the human *SLC30A8* cDNA sequence (NM_173851) identified *SLC30A8* homologs of both chinchillas (XM_013512711) and naked mole rats (XM_013074097) that were derived by computer prediction from genomic scaffolds that contain the entire putative chinchilla (NW_004955417) and naked mole rat (NW_004624763) *SLC30A8* genes as contiguous sequences. A BLAST search of the NCBI

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refseq_genomic database using the human *SLC30A8* cDNA sequence as the query showed that, even if expressed, chinchilla and naked mole rat *SLC30A8* mRNAs would contain frameshift mutations. This suggests that *SLC30A8* is also a pseudogene not only in Guinea pigs but also in evolutionarily-related chinchillas and naked mole rats. However, this conclusion will only be proven once the complete sequencing of the chinchilla and naked mole rat genomes have ruled out the existence of gene duplication events.

The demonstration that *SLC30A8* is a pseudogene in Guinea pigs has interesting implications for the neutralist and selectionist theories of insulin evolution (Chan et al. 1984). The selectionist theory is based on the idea that a local environmental deficit in zinc availability drove adaptations in the Guinea pig insulin molecule that removed the requirement to bind zinc (Chan et al. 1984). This theory appears weak since zinc is required for the activity of multiple enzymes such that the effects of zinc deprivation would be predicted to be broad and severe. In addition, zinc has a ubiquitous environmental distribution making deprivation unlikely. The demonstration that deletion of Slc30a8 in mice markedly lowers islet zinc levels (Davidson et al. 2014; Rutter and Chimienti 2015) implies that inactivation of the Guinea pig SLC30A8 gene could have created a local cellular deficit in zinc that allowed for the evolution of a Guinea pig insulin that no longer bound zinc, consistent with the selectionist theory. On the other hand, if sequencing of the chinchilla and naked mole rat genomes confirm that SLC30A8 is a pseudogene in those species, and if biochemical studies demonstrate the predicted low islet zinc levels, it would be hard to reconcile this low zinc environmental selectionist theory of insulin evolution with the fact that both chinchilla (XP 005384246) and naked mole rat (XP 004852149) insulin have retained the B10 histidine that is critical for zinc binding.

In mice individual deletion of *Slc30a8* or *Slc30a7*, which encodes ZnT7, markedly reduces islet zinc content but has little effect on glucose-stimulated insulin secretion (GSIS) (Syring et al. 2016). However, deletion of Slc30a8 in combination with Slc30a7 abolishes GSIS (Syring et al. 2016). This further suggests that high islet zinc levels are not important for GSIS and that ZnT7 can compensate for the absence of ZnT8 in islets. We therefore next explored the possibility that ZnT7 may be able to compensate for the absence of ZnT8 in Guinea pigs as it can in mice. A BLAST search of the NCBI nr database using the human SLC30A7cDNA sequence (NM_133496) as the query identified a computer predicted Guinea pig SLC30A7 cDNA (XM_003479176). The computer predicted sequence generates a peptide that differs at 4 amino acids that are highly conserved in other species leading us to suspect that the computer prediction was incorrect. We therefore cloned a Guinea pig SLC30A7cDNA (KY847522). An alignment of human and Guinea pig ZnT7 shows 96.5% amino acid identity, including conservation of all 4 ambiguous amino acids (data not shown). Similar BLAST searches identified predicted chinchilla (XM 005388805) and naked mole rat (XM_004869139) SLC30A7 cDNAs that encode proteins showing 95% and 97% amino acid identity with human ZnT7, respectively. Guinea pig SLC30A7 is expressed in multiple tissues, namely brain, liver, pancreas and testis (data not shown). Mouse SIc30a7 is expressed in the same tissues (data not shown) whereas mouse *Slc30a8* is predominantly expressed in pancreas (data not shown). No signal was detected using primers to Guinea pig SLC30A8 as predicted (data not shown). These results suggest that ZnT7 may be able to compensate for the absence of ZnT8 in Guinea pigs as it can in mice.

Flannick *et al.* (Flannick et al. 2014) have strikingly shown that *SLC30A8* haploinsufficiency is protective against the development of type 2 diabetes (T2D) in humans. Because *SLC30A8* is expressed most highly in islets it has been assumed that this protection against T2D is mediated through an effect on islet function. However, multiple groups have shown that deletion of *Slc30a8* in mice has little or no effect on GSIS (Davidson et al. 2014; Rutter and Chimienti 2015) leading to the hypothesis that ZnT8 is not essential for islet function and that *SLC30A8* haploinsufficiency may affect T2D susceptibility through actions in other tissues where it is expressed at low levels rather than through effects on pancreatic islet function (Syring et al. 2016). The observation that *SLC30A8* is a pseudogene in Guinea pigs (Table I; Fig. 1), naked mole rats and chinchillas supports the hypothesis that ZnT8 is not essential for islet function.

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Abbreviations:

GSIS	glucose-stimulated insulin secretion
T2D	type 2 diabetes
SNP	single nucleotide polymorphism
GWAS	genome-wide association studies

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Guinea Pig	1	VESLERTYLVTDKDIRMYDCTLESMELQRNTANKDRGPGKRSEQ-EPGGIYHCHSSSKAT +E LERTYLV DK +MY TLES+ELO+ NKD+ P +R E+ E GG+YHCHS SK T	59
Human	1	MEFLERTYLVNDKAAKMYAFTLESVELQQKPVNKDQCPRERPEELESGGMYHCHSGSKPT	60
Guinea Pig	60	ENRTKEQVGGRWKLGVAWAICLLLVIAEVVVGHIAGSLAIITGAAHLLVDLTNFLLCLFS	119
Human	61	EKGANEYAYAKWKLCSASAICFIFMIAEVVGGHIAGSLAVVTDAAHLLIDLTSFLLSLFS	120
Guinea Pig	120	LWLSTRSSSKKLTFGWYQAEIFGALLSILCICVMTRLLMDLVSGHLLCPDWXIQAILLII	179
Human	121	LWLSSKPPSKRLTFGWHRAEILGALLSILCIWVVTGVLVYLACERLLYPDYQIQATVMII	180
Guinea Pig	180	ISGCAVVADVVINVLLHQRCLGHNHKKVXVNASVRAAFMHTLGDVLDSISVLTSTLVTYF	239
Human	181	VSSCAVAANIVLTVVLHQRCLGHNHKEVQANASVRAAFTH LGDT SISVL S LT IF	240
Guinea Pig	240	KTDYRIADLICMFVFTILVLGSTITIVKNFTIVLMEGVAKGLSYSYVKTLILAINGVZZZ	299
Human	241	KPEYKIADPICTFIFSILVLASTITILKDFSILLMEGVPKSLNYSGVKELILAVDGVLSV	300
Guinea Pig	300	KGLNLCSLTMNQVMLLVKVTAVASWDSQIVWRGVTRALSKSFTIYLLTIQMESLADQNPK	359
Human	301	HET SLIMMQVEL V AS DSQEV K E FALSKSFIFF LIIQMES DQEP HSLHIWSLTMNQVILSAHVATAASRDSQVVRREIAKALSKSFTMHSLTIQMESPVDQDPD	360
Guinea Pig	360	CFLCEDPKD 368	

C CEDP D Human 361 CLFCEDPCD 369

Figure 1. Alignment of the Human and Non-Functional Guinea Pig ZnT8 Peptide Sequences. The alignment of the peptide sequence of human ZnT8 (Accession Number NM_173851) with the non-functional Guinea pig ZnT8 is shown. Identities are indicated by matching letters and similarities by the '+' symbol. The two stop codons (X) in the Guinea pig peptide sequence are shown in red. An 11 bp deletion in the putative Guinea pig exon 7 deletes 3 amino acids (indicated by ZZZ in blue) and creates a frameshift mutation. If translated, the open reading frame would be maintained 3 ' of this frameshift as shown. Putative transmembrane domains predicted using TOPCONS web server (Tsirigos et al. 2015) are shaded in gray. The locations of the 6 transmembrane domains are somewhat different to those previously predicted (Chimienti et al. 2004).

Table I.

Comparison of the Exon/Intron Boundaries of the Human and Guinea Pig SLC30A8 Genes.

			EXOII	(da) azte uova
	CACTAGAAAG/gtaatagatg	tcatccatag/TGTGGAACTCCAA	1/2	71/200
	CTCTAGACAG/gtaagaagat	tcctcaacag/AGAACTTCGA		71/197
a Pig	CCCTGGAGAG/gtaagagaca	tcatccacag/TATGGAACTC		71/197
	GAGGTCGTGG/gtgagtcttt	cattctctag/GTGGGCACAT	2/3	200/147
a	GAGGTGG/gtgagtactg	catctcacag/GTGGACACGT		197/147
ea Pig	GAAGTCGTGG/gtaagtacgg	accctgtag/TTGGGCACAT		197/147
я	CACCGAGCAG/gtacggttca	gaattcctag/AGATCCTTGG	3/4	147/154
e	TATCGAGCAG/gtaacattct	tgactcccag/AGATCCTCGG		147/154
lea Pig	TACCAAGCAG/gtacagttct	gaattctcac/AGATTTTTGG		147/154
an	CCAACATTGT/gtaagtcatc	tctctttcag/ACTAACTGTG	4/5	154/151
se	CCAACATTGT/gtaagtcata	tctctttcag/ACTAACTATG		154/151
nea Pig	CCGACGTTGT/tgtgtaagta	tctttttcag/AATAAATGTG		154/151
an	CTACTTTAAG/gtgagtttga	ttttttctag/CCAGAGTATA	5/6	151/106
se	CTACTTTAAG/gtgagtgtgt	tgttttccag/CCTGACTACA		151/106
nea Pig	CTACTTTAAG/gtgaatgtga	tgttttccag/ACAGATTACA		151/106
an	CTCATGGAAG/gtaggagtga	cttttgtcag/GTGTGCCAAA	6/7	106/135
se	CTCATGGAAG/gtaggactgc	cctttgtcag/GTGTTCCAAA		106/135
nea Pig	CTCATGGAAG/ataggaggga	ccttcatcag/GTGTAGCCAA		106/124
an	GTTGCTACAG/gtcagtgagt	ttatcaacag/CAGCCAGCCG	7/8	135/146
e	GTTGCTACAG/gtcagtgagt	ttatcaacag/CTGCCAGCCA		135/143
lea Pig	GTCACTGCAG/gtcactgagc	ctaccatcag/TGGCCAGCTG		124/146
onono	(A OK H/C/2400	0/200		

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Exon and intron sequences are shown in uppercase and lowercase letters, respectively. The 5' and 3' consensus splice sequences are from Jackson et al. (Jackson 1991). The sizes of exons 1 and 8 represent just the coding sequence within these exons and do not include untranslated regions. Differences between human and mouse are shown in red, differences between human and Guinea pig are shown in blue. Both mouse and Guinea pig exon 2 encode one less amino acid than human exon 2 but the changes occur in different locations.