# SUPPORTING INFORMATION

# Systematic quantification of the anion transport function of pendrin (SLC26A4) and its disease-associated variants

Koichiro Wasano, Satoe Takahashi, Samuel K. Rosenberg, Takashi Kojima, Hideki Mutai, Tatsuo Matsunaga, Kaoru Ogawa, and Kazuaki Homma

## Contents

- 1. Supplemental Figures (Pages: S1-S10)
  - Supp. Figure S1 (Page: S1)
  - Supp. Figure S2 (Page: S2)
  - Supp. Figure S3 (Pages: S3-S6)
  - Supp. Figure S4 (Page: S7)
  - Supp. Figure S5 (Pages: S8-S9)
  - Supp. Figure S6 (Page: S10)
- 2. The DNA sequences of portions of the pendrin gene cloned in a pET01 vector (Pages: S11-S15)
- 3. Supplemental Tables (Pages: S16-S18)

# 1. Supplemental Figures



**Supp. Figure S1**. The optical configuration of the plate reader (Synergy Neo2) with a list of excitation/emission filters and dichroic mirrors used in this study.



**Supp. Fig. S2**. HEK293T cells heterologously expressing WT-pendrin-mTq2. Fluorescence of mTq2 was imaged. The doxycycline dosage used are shown atop each image. The scale bars indicate 10 μm.







**Supp. Figure S3**. Representative examples of doxycycline dosage-dependent  $HCO_3^-/Cl^-$  antiport assay and fluorescence images of HEK293T cells expressing the mTq2-tagged pendrin constructs. Results of the transport assay are presented in the same way as in Figs. 2e and 2f. Scale bars indicate 10  $\mu$ m.



**Supp. Figure S4.**  $HCO_3^-/Cl^-$  antiport assay conducted under a high extracellular  $Cl^-$  condition. (a) An inward  $Cl^-$  gradient across the cell membrane drives pendrin-mediated efflux of  $HCO_3^-$ , which concomitantly decreases intracellular pH. (b and c) Examples of  $HCO_3^-/Cl^-$  antiport assay for WT- and V239D-pendrin-expressing cells, respectively. The broken lines indicate the initial rates. (d) Summaries of doxycycline dosage-dependent  $HCO_3^-/Cl^-$  antiport assay shown in panels b and c. The broken line indicates the basal transport rate determined for non-induced cells (negative control). (e) A comparison of  $HCO_3^-/Cl^-$  antiport rates measured by opposite  $Cl^-$  gradients (inward vs. outward) at 1 µg/mL doxycycline. The error bars indicate the standard deviations. The solid line indicates Deming linear regression. The broken lines indicate the basal transport rates determined for non-induced cells (n=5) and 0.34 ± 0.05 (n=9) nM/sec for "Efflux of  $HCO_3^-$ " antiport rates at 1 µg/mL doxycycline) and Supp. Table S3.



**Supp. Figure S5**. Representative examples of doxycycline dosage-dependent I<sup>-</sup>/Cl<sup>-</sup> antiport assay.



$$K_{CO2} = \frac{[H_2CO_3^*]}{pCO_2} \quad K_1 = \frac{[H^+][HCO_3^-]}{[H_2CO_3^*]} \quad K_2 = \frac{[H^+][CO_3^{2-}]}{[HCO_3^-]}$$
$$K_{water} = [H^+][OH^-] \quad K_{HEPES} = \frac{[H^+][HEPES^-]}{[HEPES]}$$

**Supp. Figure S6**. Change of pH during  $\Gamma/C\Gamma$  antiport assay. (a) Measurement of intracellular pH of WT-pendrinexpressing cells during  $\Gamma/C\Gamma$  antiport assay. (b) Estimation of  $HCO_3^-$  concentration in the solutions used for  $\Gamma/C\Gamma$  antiport assay under various atmospheric CO<sub>2</sub> conditions. The  $HCO_3^-$  concentration,  $[HCO_3^-]$ , was determined by numerically solving Eq. 1 shown in panel **c** using the equilibrium constants also shown in the panel. (c) A schematic representation of a solution containing carbonic acid, bicarbonate, and carbonate, which are in equilibrium with the atmospheric carbon dioxide.  $[H_2CO_3^*]$  denotes the equilibrium mixture of the aqueous carbon dioxide and carbonic acid. The solution also contains HEPES (20 mM) and NaOH (10 mM), which were added to adjust and maintain the solutions' pH at 7.5. This exercise shows that inclusion of pH buffer (20 mM HEPES-NaOH, pH 7.5) allows atmospheric CO<sub>2</sub>-equilibrated HCO<sub>3</sub><sup>-</sup> to reach ~170 µM, which would be sufficiently high to support the possibility raised in the main text that the small pH changes shown in panel **A** ( $\Delta[H^+] \approx 10 \ nM$ ) was due to efflux of endogenous HCO<sub>3</sub><sup>-</sup> during  $\Gamma/C\Gamma$  antiport assay.

# 2. The DNA sequences of portions of the pendrin gene cloned in a pET01 vector (splicing assay)

#### PCR primers used

5'-CCTGGCCTGCCCAGGCTTTTGTCAACA-3' 5'-CCACCTCCAGTGCCAAGGTCTGAAGGTCA-3'

Gray highlights indicate the annealing sites of the primers shown above. The region within the pET01 vector that is spliced out is shown by gray characters. Portions of the pendrin gene used for the splicing assay are indicated by pale blue (intron sequences) and bold blue with underlines (exon sequences).

#### Empty pET01 vector

#### (Expected size of the PCR product: 190-bp)

#### Exon2 of wild-type human pendrin

#### (Expected size of the PCR product: 190+167 = 357-bp)

# Exon3 of wild-type human pendrin

#### (Expected size of the PCR product: 190+140 = 330-bp)

#### > Exon4 of wild-type human pendrin

(Expected size of the PCR product: 190+111 = 301-bp)

#### Exon5 of wild-type human pendrin

#### (Expected size of the PCR product: 190+185 = 375-bp)

# Exon6 of wild-type human pendrin

(Expected size of the PCR product: 190+165 = 355-bp)

# > Exon7 and exon8 of wild-type human pendrin

(Expected size of the PCR product: 190+153+83 = 426-bp)

#### Exon9 of wild-type human pendrin

(Expected size of the PCR product: 190+148 = 338-bp)

#### Exon10 of wild-type human pendrin

(Expected size of the PCR product: 190+114 = 304-bp)

# Exon11 + exon12 of wild-type human pendrin (Expected size of the PCR product: 190+78+96 = 364-bp)

# Exon13 of wild-type human pendrin

(Expected size of the PCR product: 190+107 = 297-bp)

TGCCTCCTGTGCTGACTTAGCAGGGGATAAAGTGAGAGAAAGCCTGGGCTAATCAGGGGGGTCGCTCAGCTCCTCCTAACTG<u>GATTGTCCTATGTGTCTT</u> TGCTTCTGTGCTGCTGATGCTCTGCCCTGTGCTGACATGACCTCCCTGGCAC**TGGCACAACTGGAGCTGGGTGGAGGCCCG<mark>TGACCTTCAGACCTTGGC</mark> ACTGGAGGTGG** 

# Exon14 of wild-type human pendrin

(Expected size of the PCR product: 190+70 = 260-bp)

## > Exon15 of wild-type human pendrin

(Expected size of the PCR product: 190+93 = 283-bp)

# > Exon16 of wild-type human pendrin

(Expected size of the PCR product: 190+96 = 286-bp)

# > Exon17 of wild-type human pendrin

(Expected size of the PCR product: 190+231 = 421-bp)

# Exon18 of wild-type human pendrin (Expected size of the PCR product: 190+55 = 245-bp)

## > Exon19 of wild-type human pendrin

#### (Expected size of the PCR product: 190+146 = 336-bp)

Supp. Table S1. SLC26A4 genotype and clinical phenotype of subjects.

Pedigree individual		Age at genetic	c	Amino acid change	Amino acid change	Hearing	Onset age of	51/4			400	4.000		0.11	
No.	ID	test	Relationship	on Allele 1	on Allele 2	loss	hearing loss (y)	EVA	PIA	DP-OAE	ABR	ASSR	COR	Goiter	
867	1	16	Proband	Y214C	H723R	Yes	0	Yes	Moderate-to-severe	No response	-	-	-	No	
	2	-	Father	=	H723R	No	-	-	-	-	-	-	-	-	
	3	-	Mother	Y214C	=	No	-	-	-	-	-	-	-	-	
2467	4	24	Proband	Y214C	H723R	Yes	0	Yes	Profound	-	-	-	-	No	
	5	61	Father	=	H723R	No	-	-	-	-		-	-	-	
	6	57	Mother	Y214C	=	No	-	-	-	-	-	-	-	-	
2518	7	6	Proband	Y214C	H723R	Yes	0	Yes	Moderate	-	-	-	-	No	
1936	8	1	Poband	T410K	L703P	Yes	0	Yes	-	-	No response to 100dB click	-	Moderate to severe	No	
	9	-	Father	T410K	=	No	-	-	-	-		-	-	-	
	10	-	Mother	=	L703P	No	-	-	-	-	-	-	-	-	
1130	11	1	Proband	L703P	\$551Ffs*13	Yes	Ō	Yes	-		Mild~moderate	-	Moderate	No	
	12	4	Brother	L703P	H723R	Yes	0	Yes	Severe	-		-	-	No	
	13	-	Father	L703P	H723R	Yes	0	-	Profound	-		-	-	Yes, found at 25y.o.	
	14	-	Mother	H723R	S551Ffs*13	Yes	0	-	Profound	-		-	-	Yes, found at 12y.o.	
	15	36	Father's sister	L703P	H723R	Yes	0	Yes	Profound	-	-	-	-	Yes, found at 31y.o.	
	16	36	(11 and 12 are identical twins.)	L703P	H723R	Yes	0	Yes	Profound	-	-	-	-	Yes, found at 31y.o.	
2345	17	27	Proband	L703P	H723R	Yes	0	Yes	Profound	No response	No response to 90dB click	-	-	Yes, found at 22y.o.	
2208	18	41	Proband	L703P	H723R	Yes	0	Yes	Severe	-	-	-	-	No	
873	19	7	Proband	V483E	=	Yes	7	Borderline	Mild	Normal	Response to 30dB click	40~50dB	-	Yes (mild)	

EVA, Enlarged Vestibular Aqueduct PTA, Pure Tone Audiometry DP-OAE, Distortion Product Otoacoustic Emission ABR, Auditory Brainstem Response ASSR, Auditory Steady State Response COR, Conditioned Orientation Reflex audiometry =, not detected -, not available

Supp. Table S2. A summary of novel pendrin missense variants.

Genome position	Exon	Nucleotide change	Amino acid change	dbSNP150	1000genomes gnomAD_ex				CADD	DE\/EI
(hg19)		(NM_000441)	Annino acid change		_east_asia	ome_ALL	HOVD	110403.3K	CADD	REVEL
chr7: 107315430	Exon 6	c.641A>G	p.Y214C	none	none	none	0.000826	none	28.6	0.969
chr7: 107330648	Exon 10	c.1229C>A	p.T410K	none	none	none	none	none	27.1	0.901
chr7: 107336388	Exon 13	c.1448T>A	p.V483E	none	none	none	none	none	26.7	0.932
chr7: 107350517	Exon 19	c.2108T>C	p.L703P	none	none	none	none	none	31	0.925

dbSNP, The Single Nucleotide Polymorphism Database

1000genomes, The 1000 genomes project

gnomAD, The Genome Aggregation Database

HGVD, Human Genetic Variation Database

iJGVD, Integrative Japanese Genome Variation Database

CADD, Combined Annotation Dependent Depletion  $\ (v1.4)$ 

REVEL, Rare Exome Variant Ensemble Learner

Supp. Table S3. A summary of  $HCO_3^-/Cl^-$  antiport activities measured under a high  $Cl^-$  condition (1 µg/mL doxycycline).

	mean ± SD (n)		mean ± SD (n)		mean ± SD (n)		mean ± SD (n)
WT	2.58 ± 0.79 (15)	p.V163I	1.88 ± 0.21 (3)	p.S399P	2.08 ± 0.19 (3)	p.T527P	0.73 ± 0.26 (4)
p.S28G	0.89 ± 0.31 (4)	p.V186F	0.37 ± 0.11 (3)	p.S408F	0.31 ± 0.11 (3)	p.I529S	0.61 ± 0.26 (5)
p.S49R	2.46 ± 0.86 (4)	p.T193I	0.37 ± 0.08 (3)	p.R409H	0.34 ± 0.03 (3)	p.Y556C	0.40 ± 0.02 (3)
p.P76S	0.54 ± 0.16 (4)	p.Y214C	1.10 ± 0.38 (5)	p.T410K	0.26 ± 0.02 (3)	p.C565Y	1.68 ± 0.55 (5)
p.S90L	0.26 ± 0.05 (3)	p.V239D	0.36 ± 0.05 (4)	p.T410M	0.30 ± 0.04 (3)	p.S657N	0.80 ± 0.10 (4)
p.T99R	0.23 ± 0.03 (3)	p.D266N	2.49 ± 0.66 (3)	p.T416P	0.35 ±0.14 (3)	p.V659L	1.11 ± 0.07 (5)
p.L117F	2.08 ± 0.44 (8)	p.T307A	2.05 ± 0.08 (4)	p.Q421L	0.46 ± 0.02 (3)	p.S666F	0.56 ± 0.12 (4)
p.P123S	0.25 ± 0.01 (3)	p.N324Y	2.23 ± 0.16 (3)	p.1426N	1.10 ± 0.41 (3)	p.D669E	0.37 ± 0.02 (3)
p.G131V	0.26 ± 0.05 (3)	p.G334V	1.44 ± 0.14 (3)	p.L445W	0.30 ± 0.09 (3)	p.F683S	0.41 ± 0.06 (5)
p.S133T	0.22 ± 0.06 (3)	p.F354S	1.80 ± 0.11 (3)	p.N457K	0.94 ± 0.05 (3)	p.F692L	1.03 ± 0.24 (5)
p.G139A	0.31 ± 0.09 (3)	p.K369E	0.92 ± 0.34 (4)	p.R470H	1.95 ± 0.38 (4)	p.L703P	0.37 ± 0.02 (3)
p.M147T	0.41 ± 0.12 (4)	p.A372V	0.28 ± 0.04 (3)	p.V483E	1.16 ± 0.50 (5)	p.T721M	0.36 ± 0.02 (3)
p.M147V	0.48 ± 0.11 (3)	p.N392Y	0.21 ± 0.02 (3)	p.G497S	0.70 ± 0.23 (4)	p.H723R	0.58 ± 0.11 (4)

S18