

Table 2 (Continued)

ID	Age	Mutation allele 1/allele 2	Age of							Threshold (Rt) (dB) ^a	Threshold (Lt) (dB) ^a	Hearing level in the low frequencies ^b
			awareness	Progression	Fluctuation	Tinnitus	Vertigo	Goiter				
4486	20	p. [1707 + 5G>A]; [1707 + 5G>A]	4	+	+	+	+	+	72.5	95	78.1	
4490	25	p. [T410M];[T410M]	0	-	-	-	+	+	87.5	92.5	90.0	
4508	29	p. [H723R];[H723R]	5	+	+	-	-	-	85	110	91.9	
4518	26	p. [H723R];[919-2A>G]	0	+	+	+	+	-	105	97.5	98.1	
4530	5	p. [H723R];[919-2A>G]	0	+	+	-	+	-	67.5	86.25	71.9	
4545	12	p. [1707 + 5G>A];[H723R]	4	+	+	+	+	+	86.25	28.75	53.1	
4549	13	p. [V659L];[1219delCT]	NA	+	+	+	+	-	38.75	50	38.1	
4663	0	p. [1707 + 5G>A];[H723R]	0	-	+	NA	NA	-	68.75	68.75	99.2	
4696	0	p. [V659L];[H723R]	0	+	-	NA	NA	-	NA	NA	97.5	
4362	26	p. [H723R]; [=]	6	+	-	-	-	-	70	68.75	63.8	
4513	34	p. [H723R]; [=]	NA	+	+	+	NA	-	71.25	53.75	61.3	
4645	23	p. [919-2A>G]; [=]	14	+	-	+	-	-	96.25	105	93.8	
723	NA	p. [H723R]; [=]	NA	NA	NA	NA	NA	NA	NA	NA	NA	
724	NA	p. [2111ins5bp]; [=]	NA	NA	NA	NA	NA	NA	NA	NA	NA	
742	NA	p. [H723R]; [=]	NA	NA	NA	NA	NA	NA	NA	NA	NA	
1975	3	p. [H723R];[H723R]	0	NA	NA	NA	NA	NA	80	70	62.5	
2082	2	p. [H723R];[H723R]	0	-	-	-	-	-	NA	NA	NA	
4735	9	p. [H723R];[919-2A>G]	0	+	+	+	+	-	107.5	110	103.8	
195	20	p. [=];[=]	2	+	+	+	+	-	83.75	83.75	81.9	
670	8	p. [=];[=]	3	+	-	+	-	-	26.25	107.5	62.5	
1755	16	p. [=];[=]	NA	NA	NA	NA	NA	NA	NA	NA	NA	
2607	5	p. [=];[=]	0	-	+	-	-	-	97.5	105	98.8	
3851	33	p. [=];[=]	0	+	+	+	-	+	103.75	103.75	100.6	
4194	11	p. [=];[=]	NA	+	+	-	-	-	67.5	80	76.3	
4215	5	p. [=];[=]	0	+	+	-	-	-	98.75	93.75	93.8	
4216	55	p. [=];[=]	NA	+	+	+	+	NA	51.25	78.75	68.8	
4258	30	p. [=];[=]	28	NA	-	+	-	-	17.5	7.5	13.8	
4281	6	p. [=];[=]	2	-	-	-	-	-	57.5	61.25	63.1	
4324	37	p. [=];[=]	6	-	-	-	-	-	10	27.5	22.5	
4352	3	p. [=];[=]	0	+	+	-	-	-	86.25	88.75	88.1	
4357	6	p. [=];[=]	4	+	+	+	-	-	71.25	72.5	67.5	
4397	5	p. [=];[=]	0	-	-	-	-	-	102.5	105	100.6	
4402	8	p. [=];[=]	0	+	-	-	-	-	100	90	88.8	
4450	12	p. [=];[=]	NA	+	+	+	-	-	NA	NA	NA	
4462	8	p. [=];[=]	7	+	-	+	-	-	63.75	20	41.3	
4488	1	p. [=];[=]	0	-	-	NA	-	-	97.5	97.5	95.0	
4671	2	p. [H723R];[I600 + 1G>T]	0	+	-	-	+	-	NA	NA	NA	
3253	NA	p. [I529S];[H723R]	NA	NA	NA	NA	NA	NA	NA	NA	NA	
4949	0	p. [L727X];[H723R]	0	+	-	-	-	-	NA	NA	51.7	
J27	NA	p. [H723R];[S448L]	NA	NA	NA	NA	NA	NA	NA	NA	90.6	
3309	5	p. [919-2A>G];[P76S]	0	+	+	+	+	-	106.25	106.25	101.3	
J15	0	p. [P123S];[H723R]	0	NA	NA	NA	NA	NA	NA	NA	NA	
FUK2004	1	p. [H723R];[T94I]	0	NA	NA	NA	NA	NA	NA	NA	85.0	
1299	NA	p. [S610X];[S657N]	0	NA	NA	NA	NA	NA	NA	NA	NA	
SNS5500	42	p. [919-2A>G];[919-2A>G]	4	+	+	+	+	+	70	81.3	64	
SNS5503	37	p. [H723R];[1707 + 5G>A]	5	+	+	+	+	+	67.5	70	NA	

Abbreviation: EVA, enlarged vestibular aqueduct.

^aAverage of 500, 1000, 2000 and 4000 Hz.

^bAverage of 125, 250 and 500 Hz.

retention of improperly folded Pendrin mutants in the endoplasmic reticulum has been suggested as the major pathological mechanism for Pendred syndrome.^{19,20} In this study, we compared not only the difference between the T and NT mutations, but also compared the individual mutations and severity of hearing. However, there were no

correlations (data not shown). Indeed, there was great variation regarding hearing loss severity even with the same mutations. For example, in the patients homozygous for the most prevalent mutation, p.-H723R, hearing level at low frequency varied from 61 to 99 dB (Table 2). In addition, many reports have described intrafamilial

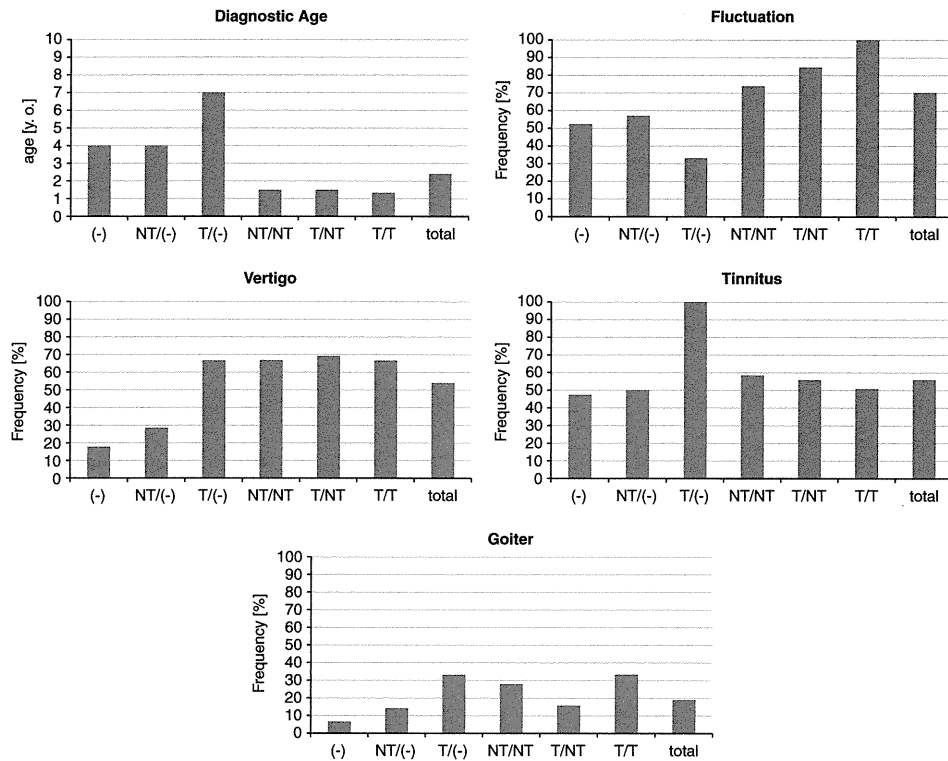


Figure 1 Genotypes and phenotypes (diagnostic age, fluctuation, vertigo, tinnitus and goiter) in the current study. NT/(-), heterozygote of nontruncating mutation; NT/NT, nontruncating/nontruncating; NT/T, nontruncating/truncating; T/(-), heterozygote of truncating mutation; T/T, truncating/truncating; (-), wild type.

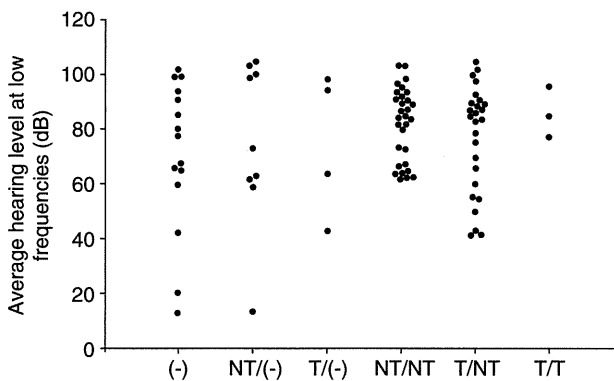


Figure 2 The relationship between hearing level at the lower frequencies and genotype. Hearing level was the average of 125, 250 and 500 Hz. NT/(-), heterozygote of nontruncating mutation; NT/NT, nontruncating/nontruncating; NT/T, nontruncating/truncating; T/(-), heterozygote of truncating mutation; T/T, truncating/truncating; (-), wild type.

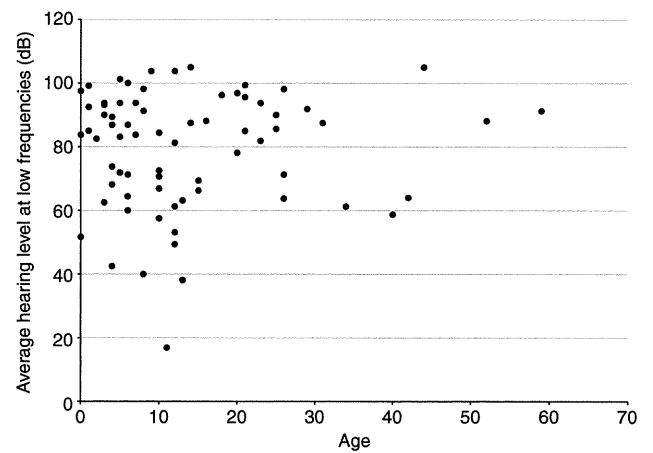


Figure 3 The relationship between hearing level and age in subjects with biallelic SLC26A4 mutations. Hearing level was calculated as the average of 250, 500, 1000 and 2000 Hz in both sides.

phenotypic variation.⁸⁻¹² Therefore, phenotype may be determined not only by SLC26A4 mutations but also other factors (genetic as well as environmental), contributing to such variability (Figure 2).

Unlike in the case of GJB2, phenotype cannot be predicted from the genotype;⁶ however, the clarification of clinical features will enable more appropriate genetic counseling and proper medical management for these patients.

The present study confirmed clinical characteristics of 66 patients with EVA caused by biallelic SLC26A4 mutations. These included

congenital (5/63, 7.9%), fluctuated (42/52, 80.8%) and progressive (49/56, 87.5%) hearing loss usually associated with vertigo (35/52, 67.3%) and/or goiter (12/53, 22.6%) during long-term follow-up, in accordance with our previous study.⁶ It is known that goiter sometimes becomes apparent between 10 and 20 years of age. The present cohort included young children, and therefore the frequency of goiter may be underestimated. As seen in Figure 3, in 66 patients with biallelic mutations for whom data were available, onset of hearing loss was likely to be early onset, and progressive with age.

CONCLUSIONS

Pendred syndrome and nonsyndromic hearing loss associated with EVA are a continuum of disease characterized as being associated with congenital, fluctuating and progressive hearing loss, and most patients have vertigo and/or goiter. However, in the present study, no genotype–phenotype correlation was found. The results obtained from the present study will facilitate accurate molecular diagnosis and better genetic counseling.

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- 1 Usami, S., Nishio, S., Nagano, M., Abe, S. & Yamaguchi, T. Deafness Gene Study Consortium. Simultaneous screening of multiple mutations by invader assay improves molecular diagnosis of hereditary hearing loss: a multicenter study. *PLoS One* **7**, e31276 (2012).
- 2 Tsukamoto, K., Suzuki, H., Harada, D., Namba, A., Abe, S. & Usami, S. Distribution and frequencies of PDS (*SLC26A4*) mutations in Pendred syndrome and nonsyndromic hearing loss associated with enlarged vestibular aqueduct: a unique spectrum of mutations in Japanese. *Eur. J. Hum. Genet.* **11**, 916–922 (2003).
- 3 Usami, S., Abe, S., Weston, M. D., Shinkawa, H., Van Camp, G. & Kimberling, W. J. Non-syndromic hearing loss associated with enlarged vestibular aqueduct is caused by PDS mutations. *Hum. Genet.* **104**, 188–192 (1999).

- 4 Namba, A., Abe, S., Shinkawa, H., Kimberling, W. J. & Usami, S. Genetic features of hearing loss associated with ear anomalies: PDS and *EYA1* mutation analysis. *J. Hum. Genet.* **46**, 518–521 (2001).
- 5 Iwasaki, S., Tsukamoto, K., Usami, S., Misawa, K., Mizuta, K. & Mineta, H. Association of *SLC26A4* mutations with clinical features and thyroid function in deaf infants with enlarged vestibular aqueduct. *J. Hum. Genet.* **51**, 805–810 (2006).
- 6 Suzuki, H., Oshima, A., Tsukamoto, K., Abe, S., Kumakawa, K., Nagai, K. et al. Clinical characteristics and genotype-phenotype correlation of hearing loss patients with *SLC26A4* mutations. *Acta Otolaryngol.* **127**, 1292–1297 (2007).
- 7 Tsukada, K., Nishio, S. & Usami, S. Deafness Gene Study Consortium. A large cohort study of *GJB2* mutations in Japanese hearing loss patients. *Clin. Genet.* **78**, 464–470 (2010).
- 8 Wang, Q. J., Zhao, Y. L., Rao, S. Q., Guo, Y. F., Yuan, H., Zong, L. et al. A distinct spectrum of *SLC26A4* mutations in patients with enlarged vestibular aqueduct in China. *Clin. Genet.* **72**, 245–254 (2007).
- 9 Park, H.-J., Lee, S.-J., Jin, H.-S., Lee, J. O., Go, S.-H., Jong, H. S. et al. Genetic basis of hearing loss associated with enlarged vestibular aqueducts in Koreans. *Clin. Genet.* **67**, 160–165 (2005).
- 10 Dai, P., Stewart, A. K., Chebib, F., Hsu, A., Rozenfeld, J., Huang, D. et al. Distinct and novel *SLC26A4*/Pendrin mutations in Chinese and U.S. patients with nonsyndromic hearing loss. *Physiol. Genomics* **38**, 281–290 (2009).
- 11 Albert, S., Blons, H., Jonard, L., Feldmann, D., Chauvin, P., Loundon, N. et al. *SLC26A4* gene is frequently involved in nonsyndromic hearing impairment with enlarged vestibular aqueduct in Caucasian populations. *Eur. J. Hum. Genet.* **14**, 773–779 (2006).
- 12 Pera, A., Villamar, M., Viñuela, A., Gandía, M., Medà, C., Moreno, F. et al. A mutational analysis of the *SLC26A4* gene in Spanish hearing-impaired families provides new insights into the genetic causes of Pendred syndrome and DFNB4 hearing loss. *Eur. J. Hum. Genet.* **16**, 888–896 (2008).
- 13 Yang, T., Vidarsson, H., Rodrigo-Blomqvist, S., Rosengren, S. S., Enerback, S., Smith, R. J. et al. Transcriptional control of *SLC26A4* is involved in Pendred syndrome and nonsyndromic enlargement of vestibular aqueduct (DFNB4). *Am. J. Hum. Genet.* **80**, 1055–1063 (2007).
- 14 Park, H. J., Shaikat, S., Liu, X. Z., Hahn, S. H., Naz, S., Ghosh, M. et al. Origins and frequencies of *SLC26A4* (PDS) mutations in east and south Asians: global implications for the epidemiology of deafness. *J. Med. Genet.* **40**, 242–248 (2003).
- 15 Pryor, S. P., Madoe, A. C., Reynolds, J. C., Sarlis, N. J., Arnos, K. S., Nance, W. E. et al. *SLC26A4*/PDS genotype-phenotype correlation in hearing loss with enlargement of the vestibular aqueduct (EVA): evidence that Pendred syndrome and nonsyndromic EVA are distinct clinical and genetic entities. *J. Med. Genet.* **42**, 159–165 (2005).
- 16 Pera, A., Dossena, S., Rodighiero, S., Gandía, M., Bottà, G., Meyer, G. et al. Functional assessment of allelic variants in the *SLC26A4* gene involved in Pendred syndrome and nonsyndromic EVA. *Proc. Natl Acad. Sci. USA* **105**, 18608–18613 (2008).
- 17 Yoon, J. S., Park, H. J., Yoo, S. Y., Namkung, W., Jo, M. J., Koo, S. K. et al. Heterogeneity in the processing defect of *SLC26A4* mutants. *J. Med. Genet.* **45**, 411–419 (2008).
- 18 Dossena, S., Rodighiero, S., Vezzoli, V., Nofziger, C., Salvioni, E., Boccazzi, M. et al. Functional characterization of wild-type and mutated pendrin (*SLC26A4*), the anion transporter involved in Pendred syndrome. *J. Mol. Endocrinol.* **43**, 93–103 (2009).
- 19 Taylor, J. P., Metcalfe, R. A., Watson, P. F., Weetman, A. P. & Trembath, R. C. Mutations of the PDS gene, encoding pendrin, are associated with protein mislocalization and loss of iodide efflux: implications for thyroid dysfunction in Pendred syndrome. *J. Clin. Endocrinol. Metab.* **87**, 1778–1784 (2002).
- 20 Rotman-Pikielny, P., Hirschberg, K., Maruvada, P., Suzuki, K., Royaux, I. E., Green, E. D. et al. Retention of pendrin in the endoplasmic reticulum is a major mechanism for Pendred syndrome. *Hum. Mol. Genet.* **11**, 2625–2633 (2002).



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