Erratum

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This erratum is being published to correct the printing and nomenclature errors of the article entitled 'Heterogeneous Spectrum of *CFTR* Gene Mutations in Korean Patients with Cystic Fibrosis' by Haiyoung Jung, Chang-Seok Ki, Won-Jung Koh, Kang-Mo Ahn, Sang-Il Lee, Jeong-Ho Kim, Jae Sung Ko, Jeong Kee Seo, Seung-Ick Cha, Eun-Sil Lee, Jong-Won Kim in Korean J Lab Med 2011;31:219-224, DOI 10.3343/kjlm.2011.31.3.219 as follows. The GenBank accession number of the *CFTR* gene should be read NM_000492.3. In addition, nomenclatures of three mutations should be corrected as follows: p.K684NfsX38 rather than p.L728NfsX38 (case 1), c.2089dupA rather than c.2089_2090insA (case 8), and c.1322T>C rather than c.1454T>C (case 9). Therefore, all mutation nomenclatures in the text and Table 2 should be corrected accordingly.

Before correction

1. Page 220: NM_00492.3
2. Page 221: p.L728NfsX38
3. Page 222: 1 duplication with frameshift (c.3908dupA), 1 insertion with frameshift (c.2089-2090insA)
4. Page 222: Table 2 (see below)

Table 2. Frequency of *CFTR* mutations in Korean CF patients

Case No.	Amino acid change	Exon	Nucleotide number	Nucleotide change	Type of mutation	Method of detection	Familial targeted mutation study				Ref
							Father	Mother	Brother	Sister	
1	Q98R	Exon 4	293	A>G	Missense	Sequencing	ND	-	-	NA	This study
	L728NfsX38	Exon 13	2,052	delA	Frameshift	Sequencing	ND	+	+	NA	
2		IVS 4	579+5	G>A	Splicing	Sequencing	ND	ND	NA	NA	This study
3	Q98R	Exon 4	293	A>G	Missense	Sequencing	+	-	+	-	[15]
	Q220X	Exon 6a	658	C>T	Nonsense	Sequencing	-	+	-	-	
4	Q98R	Exon 4	293	A>G	Missense	Sequencing	+	-	NA	NA	[16]
	Q1352H	Exon 24	4,056	G>C	Missense	Sequencing	-	+	NA	NA	
5		IVS 12	1,766+2	T>C	Splicing	Sequencing	+	-	NA	NA	[18]
	N1303KfsX6	Exon 21	3,908	dupA	Frameshift	Sequencing	-	+	NA	NA	
6		IVS 17a	3,272-26	A>G	Splicing	Sequencing MLPA	ND	ND	NA	NA	[17]
		Exon14a	2,623-2,751+?	del	Deletion		+	-	NA	NA	
7	Q1291X	Exon 20	4,003	C>T	Nonsense	Sequencing	+	-	+	NA	[14]
		IVS8		T5	Splicing	Sequencing	-	+	-	NA	
8	L88X	Exon 3	263	T>G	Nonsense	Sequencing	+	-	NA	NA	[29]
	R697KfsX33	Exon 13	2,089-2,090	insA	Insertion	Sequencing	-	+	NA	NA	
9	L441P	Exon 9	1,454	T>C	Missense	Sequencing & DGGE	ND	-	ND	NA	[19]

Abbreviations: IVS, intervening sequence; MLPA, multiplex ligation-dependent probe amplification; ND, not done; NA, not applicable; DGGE, denaturing gradient gel electrophoresis.

After correction

1. Page 220: NM_000492.3
2. Page 221: p.K684NfsX38
3. Page 222: 2 duplications with frameshift (c.3908dupA and c.2089dupA)
4. Page 222: Table 2 (see below)

Table 2. Frequency of *CFTR* mutations in Korean CF patients

Case No.	Amino acidchange	Exon	Nucleotide number*	Nucleotide change	Type of mutation	Method of detection	Familial targeted mutation study				Ref
							Father	Mother	Brother	Sister	
1	Q98R	Exon 4	293	A>G	Missense	Sequencing	ND	-	-	NA	This study
	K684NfsX38	Exon 13	2,052	delA	Frameshift	Sequencing	ND	+	+	NA	
2		IVS 4	579+5	G>A	Splicing	Sequencing	ND	ND	NA	NA	This study
3	Q98R	Exon 4	293	A>G	Missense	Sequencing	+	-	+	-	[15]
	Q220X	Exon 6a	658	C>T	Nonsense	Sequencing	-	+	-	-	
4	Q98R	Exon 4	293	A>G	Missense	Sequencing	+	-	NA	NA	[16]
	Q1352H	Exon 24	4,056	G>C	Missense	Sequencing	-	+	NA	NA	
5		IVS 12	1,766+2	T>C	Splicing	Sequencing	+	-	NA	NA	[18]
	N1303KfsX6	Exon 21	3,908	dupA	Frameshift	Sequencing	-	+	NA	NA	
6		IVS 17a	3,272-26	A>G	Splicing	Sequencing	ND	ND	NA	NA	[17]
		Exon14a	2,623-2,751+?	del	Deletion	MLPA	+	-	NA	NA	
7	Q1291X	Exon 20	3,871	C>T	Nonsense	Sequencing	+	-	+	NA	[14]
		IVS8		T5	Splicing	Sequencing	-	+	-	NA	
8	L88X	Exon 3	263	T>G	Nonsense	Sequencing	+	-	NA	NA	[29]
	R697KfsX33	Exon 13	2,089	dupA	Insertion	Sequencing	-	+	NA	NA	
9	L441P	Exon 9	1,322	T>C	Missense	Sequencing & DGGE	ND	-	ND	NA	[19]

*Nucleotide numbers are based on the *CFTR* reference mRNA sequence, NM_000492.3.
Abbreviations: IVS, intervening sequence; MLPA, multiplex ligation-dependent probe amplification; ND, not done; NA, not applicable; DGGE, denaturing gradient gel electrophoresis.

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