Erratum

The authors of an article in the August 1998 issue of the *Journal,* "Identification of a New Splice Form of the *EDA1* Gene Permits Detection of Nearly All X-Linked Hypohidrotic Ectodermal Dysplasia Mutations," by Monreal et al. (63:380–389), wish to make corrections to tables 1, 2, and 3. The corrections are underlined in the following tables:

Table 1

DNA Primers Used in This Study

Amplification Type and Exon(s)	Forward Primer (5′→3′)	Reverse Primer (5′→3′)	Sequencing Primer(s) (5′→3′)[a]	Method[b]
cDNA:				
1–3	ACCTCTGGCACCCTAAGCAGC	GCCATCTGCTCCTTCAT	…	…
1–5	Same as for exons 1–3	CCAGGGGGTCCTTGAGG	…	…
1–7	Same as for exons 1–3	TTGAATTGCTGACCCTTGGC	…	…
1–9	Same as for exons 1–3	CTGGGAAGTCACATAGGCC	…	…
Interexon, for genomic structure:				
3–4[c]	TTGTAATTTTTACAGATGGCCC	ACAGACAGACAATGCTGAAAG	…	…
4–5	GCCCAGTTAAAAACAAGAAAAAG	GGTCCTGGAGGGCCATTG	…	…
5–6	GACCACCTGGTCCTCCA	TGGTTTTCTCGAGTTCCAGC	…	…
6–7	GCTGGAACTCGAGAAAACCA	TTGAATTGCTGACCCTTGGC	…	…
7–8	GCCAAGGGTCAGCAATTCAA	CACCTTGGGGTTCATAGTGA	…	…
8–9	TCACTATGAACCCCAAGGTG	GGCAAAGTCAGTGAAGTTGATG	…	…
Exon, for mutation screening:				
1[d]	GTCGGCCGGGACCTCCTC	GCCGCCGCCCCTACTAGG	F: GGTGACTGGTGATGGGGCTGTC R: AGTTGCGCTCGGAGTTG	S
2[e]	TGGCTTCTCTAGTTAGGTTGGG	CATCTCAAATTTTCCTTCTGGG	F: TGGCTTCTCTAGTTAGGTTGGG R: CATCTCAAATTTTCCTTCTGGG	S
3	GGGCTCAGGGTTTAGACACA	GAGATGAGGCCCTTATAGAG	F: TTGTAATTTTTACAGATGGCCC R: TAGGATTACAGGCGTGAGC	S
4	GTGGCCTCAGGAGTCAGAAG	GAAAGAGGTGAATCATCACTGAA	R: ACAGACAGACAATGCTGAAAG	S
5[f]	CGGGAGGTGGAGGTTTCA AGTGAACCGAGATTGTGCCA	CACCTTGGGGTTCATAGTGA TGGTTTTCTCGAGTTCCAGC	F: GAACTCCAGCCTGGGCAA R: CTCTCAGGATCACCCACTC	XL
6[g]	AGAAAGCAGGACCTCCTGG GACCACCTGGTCCTCCA	CACCTTAGGGTTCATAGTGA CACCTTAGGGTTCATAGTGA	F: GGGGTGCACTCTGACTCTTC R: GAAAACCGTCAGAATCTCCG	XL
7[g]	Same as for exon 6	Same as for exon 6	F: CAGGGGAGAGGGATCAGAAT R: GGGGAGAAGCTCCTCTTTG	XL
8	GCCAAGGGTCAGCAATTCAA	GCACCGGATCTGCATTCTGG	F: GGGTTGTGAACTCCTTGGTA R: GAAGAGTTAGGCCTAAGACC	XL
9	TCACGTGTCCTTTCCTGTTG	TTGTCACCCTGGAGTCACT	F: TCACGTGTCCTTTCCTGTTG R: CACAGCAGCACTTAGAGG	S

[a] F = forward; R = reverse.
[b] S = standard PCR amplification using *Taq* DNA Polymerase or *rTth* DNA Polymerase; XL = extra-long amplification.
[c] The primers are located in the intronic sequence 5′ of exon 3 (forward) and in the intronic sequence 3′ of exon 4 (reverse).
[d] Primers previously published by Kere et al. (1996).
[e] Primers previously published by Ferguson et al. (1997).
[f] Product was obtained by nested PCR amplification.
[g] Product was obtained by hemi-nested PCR amplification.

Table 2

Intron-Exon Boundaries of Human *EDA1* Splice Form II

Exon	Exon Size (bp)	cDNA (nt)	5′ Intron/Exon…Exon/Intron 3′	Intron	Intron Size (kb)
1	637	1–637	ATTCCC…CACCAG/gtgagt	1b	>300
3	106	638–743	ttacag/ATGGCC…CAGATG/gtaagt	2	ND[a]
4	24	744–767	ttatag/GCCCAG…AAAAGG/gtaagt	3	5.0
5	180	768–947	tttcag/GAAAGA…CTTCTG/gtgagt	4	1.6
6	35	948–982	ttgcag/GTGCTG…AACCAG/gttggc	5	1.0
7	52	983–1034	tgccag/CCAGCT…AGAATG/gtaaga	6	2.8
8	131	1035–1165	actgag/ATCTTT…GTAGAA/gtgagt	7	2.0
9	252	1166–?	ttcgag/GTATAC…	…	…

[a] ND = not determined.

Table 3

***EDA1* Mutations in XLHED Patients**

Family	Sequence Change	Exon	Predicted Effect[a]
ED1081	C704T	3	R155C
ED1095[b]	C707T	3	R156C
ED1039	G708A	3	R156H
ED1011	C867T	5	P209L
ED1019	G912C	5	G224A
ED1050	Del794–829	5	Del185–196
ED1204[b]	Del794–829	5	Del185–196
ED1018[b]	Del803–830	5	Del188–197, FS 198, Ter 280
ED1097[b]	Del904–938	5	Del221–233, FS 234, Ter 240
ED1197	A996T	7	H252L
ED1007	G1136A	8	G299S
ED1002	G1136A	8	G299S
ED1001	G1202T	9	E321Ter
ED1021	G1285A	9	A349T
ED1126[b]	G1285A	9	A349T
ED1073	C1308A	9	A356D
ED1022	G1311C	9	R357P

[a] FS = frameshift; Ter = termination.
[b] De novo mutation.