Corrigenda

Characterization of translational frame exception patients in Duchenne/Becker muscular dystrophy


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The authors wish to note a typographical error in table 2, the last line in the column, ‘Junction sequence 5’bp/3’bp’. The base pair was reported as 1684/7307. The correct base pair numbers should read 1690/7307. All other information regarding the junction sequence and exon numbering is correct.

A 2 base pair deletion in the RDS gene associated with butterfly-shaped pigment dystrophy of the fovea


The authors wish to note that an incorrect version of figure 1 was published with this paper. The correct version of figure 1 is published with its legend below.

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**Figure 1.** SSCP analysis from the family with butterfly-shaped pigment dystrophy of the fovea. Oligonucleotide primers were chosen from the human RDS gene (13, 16). The primers for exon 3 were as follows: 5'-AGATTGCTCTAATCTCCT-3' and 5'-AGGGGAGGGGCCCCAGGGCC-3'. The polymerase chain reaction (PCR) with α-35S-dATP incorporation was carried out as previously described (4), with the exception that the annealing temperature used was 60°C. Samples were denatured and electrophoresed on fan-cooled nondenaturing 5% polyacrylamide gels containing 5% glycerol at 20 watts for approximately 4 hours at room temperature. Autoradiograms were created by exposing Kodak Xomat AR film to the dried gels for 24–36 hours. Closed symbols in the pedigree above the gel indicate patients clinically affected with the disorder. Unaffected patients or spouses are indicated by open symbols. Blood samples were unavailable from the three deceased patients indicated with a diagonal line through each symbol. The allele corresponding to the mutation is indicated with arrows and the polymorphism is indicated with asterisks.
Alternative splicing in the fragile X gene FMR1


The authors wish to note a mistake which was incorporated in figure 3 where both Asp and Asn were given the letter FMR1 to the prior published sequence (3) and the numbering starts at the first ATG 3' from the CGG repeat.

Figure 3. FMR1 cDNA sequence. Additional (exon) sequences are integrated in the sequence of the original BC22/BC72 cDNA clones (3). Sequences that undergo alternative splicing are indicated in grey and are indicated A, B, C and D in the left margin. Additional sequences (underlined) have been added at the 5' and 3' end of the FMR1 cDNA. The location of the primers is given and the sequences are contained in boxes. The sequence has been renumbered as compared to the prior published sequence (3) and the numbering starts at the first ATG 3' from the CGG repeat.