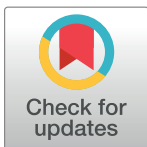CORRECTION

# Correction: Comprehensive target capture/next-generation sequencing as a second-tier diagnostic approach for congenital muscular dystrophy in Taiwan

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In Table 1, the COL6A2 mutation in Patient 14 is listed incorrectly. The mutation should be: c.1043_1051delCTGGAAACC, (p.Pro348_Asn350del). Please see the corrected Table 1 here.

**Table 1. Summary of the patients with UCMD.**

| | Sex | Age (Y) | Proximal joint contracture | Distal hyperlaxity | Keloid | Scoliosis | DDH | Torticollis | Walk independently | Loss of ambulation (Y) | Pathogenic variants in the COL6A genes (all heterozygous unless otherwise indicated) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| P1 | M | 17# | p | p | ? | p | n | n | Yes (>2y) | 7y | COL6A1: c.850 G>A (p.Gly284Arg) |
| P2 | M | 22 | p | p | n | p | p | n | Yes (1y6-7m) | 12y | COL6A1: c.815 G>T (p.Gly272Val) |
| P3 | F | 22 | p | p | n | p | n | n | Yes (1y1-2m) | not yet | COL6A1: c.868 G>A (p.Gly290Arg) |
| P4 | F | 15 | p | p | p | p | n | n | Yes (<2y) | not yet | COL6A1: c.868 G>A (p.Gly290Arg) |
| P5^ | F | 14 | n | p | p | p | p | p | Yes (1y2m) | not yet | COL6A3: c.1676_1677insT (p.Lys560*) (homo) |
| P6^ | M | 13 | n | p | n | p | n | n | Yes (1y2m) | not yet | COL6A3: c.1676_1677insT (p.Lys560*) (homo) |
| P7 | M | 10 | p | p | p | n | n | n | Yes (1y6-7m) | 8y | COL6A1: c.815 G>T (p.Gly272Val) |
| P8 | M | 17 | p | p | n | p | n | n | Yes (1y6m) | 10y | COL6A2: c.955-2A>G |
| P9 | F | 14 | p | p | p | p | n | n | Yes (1y2m) | not yet | COL6A1: c.868 G>A (p.Gly290Arg) |
| P10 | M | 6 | n | p | Equivocal | n | n | n | Yes (1y2m) | not yet | Not found |
| P11 | M | 14# | p | p | ? | p | n | n | Yes (<2y) | 12y | COL6A3: c.6309+2 T>A |
| P12 | M | 7 | n | p | p | n | n | n | Yes (1y6m) | not yet | COL6A3: c.6157G>T (p.Gly2053Cys) |
| P13 | M | 6 | p | p | p | n | p | p | Yes (2y) | not yet | COL6A1: c.886G>A (p.Gly296Arg) |
| P14 | M | 1y11m | n | p | Equivocal | p | p | n | no | no | COL6A2: c.1043_1051delCTGGAAACC, (p.Pro348_Asn350del) |
| P15 | M | 5y1m | p | p | p | n | n | n | no | no | COL6A2: exon5 deletion |

#: the age of death;

^: siblings;

?: no record;

p: present; n: nil

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In Table 2, the LAMA2 mutation in Patient 20 is listed incorrectly. The mutation should be: c.2451-6 A>G. Please see the corrected Table 2 here.

**Table 2. Summary of the patients with MDCMD.**

|  | Sex | Current age/ Age of onset | Hypotonia in infancy | Walk independently | Epilepsy | Intelligence | Brain MRI (abnormal white matter signal) | Pathogenic variants in *LAMA2* |
|---|---|---|---|---|---|---|---|---|
| P16 | F | 31y/6m | p | n | p | mild MR | p | c.624 delC (p.Leu209*) (m) |
|  |  |  |  |  |  |  |  | c.2209-3_2209–2 delCA (f) |
| P17^ | M | 27y/6m | p | n | p | moderate MR | p | c.8654 T>C (p.Leu2885Pro) (m) |
|  |  |  |  |  |  |  |  | c.2945 insG (p.Ser982Arg fs*16) (f) |
| P18^ | M | #12y/4m | p | n | p | mild MR | p | c.8654 T>C (p.Leu2885Pro) (m) |
|  |  |  |  |  |  |  |  | c.2945 insG (p.Ser982Arg fs*16) (f) |
| P19 | M | 18y/4m | P | n | n | borderline | p | c.6513_6515 delTGT (p. Val2172del) (m) |
|  |  |  |  |  |  |  |  | c.4311 G>A (p.Gln437Gln) (f) |
| P20 | F | 16y/4m | P | p | n | normal | p | c.8989-12 C>G (m) |
|  |  |  |  |  |  |  |  | c.2451-6 A>G (f) |
| P21 | F | 18y/5m | p | n | n | normal | p | c.2049_2050 delAG (p. Arg683Ser fs*21) (m) |
|  |  |  |  |  |  |  |  | c.1303 C>T (p.Arg435*) |

#: the age of death;

^: siblings;

p: present; n: nil; f: father; m: mother

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The LAMA2 mutation in Patient 20 is also listed incorrectly in the fourth sentence of the second paragraph of the MDCMD subsection of the Results section. The correct sentence is: Three frameshift deletions or insertions (c.624 delC, c.2049_2050delAG, c.2945insG), four splice site variants (c.2209-3_2209-2delCA, c.2451-6A>G, c.4311G>A, c.8989-12 C>G), and one nonsense mutation (c.1303C>T, p.Arg435) were expected to produce truncated proteins.

## Reference

1. Liang W-C, Tian X, Yuo C-Y, Chen W-Z, Kan T-M, Su Y-N, et al. (2017) Comprehensive target capture/ next-generation sequencing as a second-tier diagnostic approach for congenital muscular dystrophy in Taiwan. PLoS ONE 12(2): e0170517. https://doi.org/10.1371/journal.pone.0170517 PMID: 28182637