Deep-intronic variant of fukutin is the most prevalent point mutation of Fukuyama congenital muscular dystrophy in Japan.

Kobayashi K¹, Kato R¹, Kondo-Iida E², Taniguchi-Ikeda M¹,³, Osawa M⁴, Saito K², Toda T¹.

Abstract

Fukuyama congenital muscular dystrophy (FCMD), which is caused by mutations in the fukutin gene, is the second most common form of childhood muscular dystrophy in Japan. The founder haplotype is the most prevalent in the chromosomes of Japanese FCMD patients, and corresponds to an SVA retrotransposonal insertion in the 3'-untranslated region of fukutin. Although other mutations have been reported, the mutation corresponding to the second most prevalent haplotype in Japanese FCMD patients remained unknown. Recently a deep-intronic point mutation c.647+2084G>T was identified in Korean patients with congenital muscular dystrophy. Here, we performed mutational analysis of 10 patients with the second most prevalent haplotype and found that all of them were compound-heterozygous for the SVA insertion and this c.647+2084G>T mutation. The fukutin mRNA of these patients contained a pseudoexon between exon 5 and exon 6, which was consistent with the previous Korean study. As expected, the mutated fukutin protein was smaller than the normal protein, reflecting the truncation of fukutin due to a premature stop codon. Immunostaining analysis showed a decrease in the signal for the glycosylated form of α-dystroglycan. These findings indicated that this mutation is the second most prevalent loss-of-function mutation in Japanese FCMD patients. Journal of Human Genetics advance online publication, 6 July 2017; doi:10.1038/jhg.2017.71.

PMID: 28680109   DOI: 10.1038/jhg.2017.71
Deep-intronic variant of fukutin is the most prevalent point mutation of Fukuyama congenital muscular dystrophy in Japan.