**Author's response to reviews**

**Title:** Dystrophin deficiency in canine X-linked muscular dystrophy in Japan (CXMDJ) alters myosin heavy chain expression profiles in the diaphragm more markedly than in the tibialis cranialis muscle.

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**Author's response to reviews:** see over
Dear Dr. Melissa Norton

Thank you for your e-mail of November 28, 2007.

The comment of the reviewer has been helpful in allowing us to revise our manuscript (MS: 6682191301619432) “Dystrophin deficiency in canine X-linked muscular dystrophy in Japan (CXMD) alters myosin heavy chain expression profiles in the diaphragm more markedly than in the tibialis cranialis muscle” by Yuasa K et al. for publication as an article in *BMC Musculoskeletal Disorders*.

We have attempted to address the question raised by the reviewer. We have prepared the reply letter to the reviewer and attached. The corrected parts in the manuscript have been indicated by red color.

Thank you for your consideration of the revised version in advance.

Sincerely yours,

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Minor Essential Revisions

1. The only point that was not addressed by the authors in the revision is how the wild type and dystrophic littermates were distinguished from each other, especially at the youngest age (one month) studied.

>CXMD1 has a point mutation at the border of intron 6 and exon 7 of the dystrophin gene, which leads to an abnormal splicing and creates a pre-mature stop codon. To distinguish the phenotypes of dogs (wild-type, carrier, or dystrophy), we have determined the genotypes of the normal and/or mutated alleles in the dystrophin gene by a snapback method of single-strand conformation polymorphism (SSCP) analysis [16]. Furthermore, we have confirmed the phenotypes by measuring serum CK level [5]. These analyses were carried out within a few days after birth. Therefore, we could examine normal and affected dogs at the youngest age.

According to the reviewer’s suggestion, we added a following sentence and a reference number 16 into the methods and references.

Methods (Page 9, lines 5-8)
Within a few days after birth, the genotypes (wild-type, carrier, or dystrophy) of the littermates were determined by a snapback method of single-strand conformation polymorphism (SSCP) analysis [16], and the phenotypes were also confirmed by measuring serum CK level [5].

References (Pages 29-30)