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Different orientation of myosin crossbridges around the thick filament between non- and full-overlapped skeletal muscles obtained by X-ray fiber diffraction

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Introduction

The intensity analysis of the X-ray diffraction patterns from the full- and non-overlapped skeletal muscles allows us to reveal the orientation of resting myosin crossbridges around the thick filaments [1, 2]. In the analysis we used the cylindrically averaged difference Patterson function $(\triangle Q(\mathbf{r}, \mathbf{z}))$ to correct the sampling effects due to the irregular hexagonal arrays of thick filaments on the layer lines by cutting off the outer peaks (r > 32 nm) on the $\triangle Q(\mathbf{r}, \mathbf{z})$ map [3]. However, it was difficult to remove completely the sampling effect. Recently, we found that the inter-crossbridge vectors between thick filaments, which are facing with each other, contribute to the intermediate region (r = 20 ~ 32 nm) in the $\triangle Q(r,z)$ map (see Fig. 1A, yellow arrows). In this report we examined the effect of the facing inter-crossbridge vectors on the corrected intensities, and investigated whether they affect the finding that the orientations of myosin heads on the thick filament are significantly different between the nonand full-overlapped muscles.

Experimental and modeling calculation

X-ray diffraction experiments were performed at BL15A1 as reported previously [1, 2]. In modeling we used the single filament model and the hexagonal-filament-array model to qualify the differences in the corrected intensities caused by the facing intercrossbridge vectors in the unit cell using the *RMSDI* as described previously [3].

Results and discussion

To examine the effect of the facing inter-crossbridge vectors on the corrected intensities, we calculated the number of these inter-crossbridge vectors in the intermediate region on the Q(r,z) map. The ratio of the number of the facing inter-crossbridge vectors to that of the total vectors was about 0.52. These inter-vectors are responsible for the fact that the RMSDI in the corrected layer line intensities between the single and hexagonal filament-array models was 0.133 as reported previously [3]. To observe how the facing inter-crossbridge vectors affect the layer-line intensities, we used some hexagonalfilament array models to estimate the maximum difference in the RMSDI of the layer line intensities caused by these inter-crossbridge vectors and calculated the layer-line intensities by rotating the whole structure of each thick filament around its filament axis every 1° in a range of 0 to 60°, assuming that the lattice structure is a simple lattice. We derived the RMSDIs in the corrected layer line intensities between the rotated hexagonalfilament array models and the single filament model (Fig. 1B). The maximum value of the RMSDI was 0.137,

which is smaller than the value of the *RMSDI* (0.171) between the corrected intensities from the full- and nonoverlapped muscles as reported previously [2]. Our examination reveals that the effect of the facing intercrossbridge vectors cannot reproduce such a large difference in the corrected intensities observed between the full- and non-overlapped muscles. Thus the structure of a thick filament is significantly different between the full- and non-overlapped muscles.

In our best-fit models [1, 2], the configuration of myosin crossbridges in the regular region of a crossbridge repeat is similar in the non- and full-overlapped models, but is somewhat different in the perturbed region. In their end-on views (Fig. 2), the two heads of a crossbridge form a horse' hoof structure in both models but they cross at the outer end in the full-overlapped model (Fig. 2B).

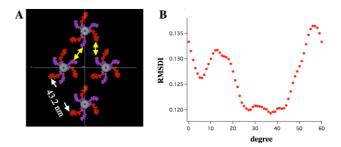


Figure 1. A, the end-on view of the hexagonal filamentarray model. Myosin two heads are denoted by red and purple spheres, respectively. B, the *RMSDIs* in the layerline intensities between the rotated hexagonal filamentarray models and the single filament model.

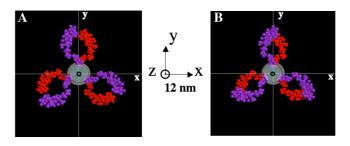


Figure 2. Orientations of two heads of a myosin crossbridge. A, non-overlap model, B, full-overlap model.

References

- [1] Oshima et al., PF Activity Rep. #23, 234. (2006).
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