

Molecular basis of stiff patient syndrome caused by mutations in *ACTA1* and *TPM3*

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3 of the 4 documented patients with stiff patient syndrome have mutations at the interface of actin and tropomyosin and therefore could affect the equilibrium of the Ca²⁺-dependent switch of muscle. *ACTA1* gene (skeletal actin) K326N was previously reported, and we recently found stiff patients with $\Delta E218$ and $\Delta E224$ mutations in the *TPM3* gene (Tpm3.12 protein). The atomic resolution structure of tropomyosin bound to actin in the 'switched off' state shows that tropomyosin makes contact with actin at only two points, one of which is a cluster of basic amino acids actin K326, K328 and R147. Tropomyosin has a seven-fold repeated structure corresponding to seven actin-binding interactions. We have demonstrated that two Tpm2.2 mutations, $\Delta E139$ and E181K, and the actin K326N mutation destabilise the actin–tropomyosin interface. We predicted that equivalent charge loss mutations at EE 218–219, EE 224–224, or ED 257–258 would also destabilise the interaction with actin, leading to a partial switch-on of the muscle. This was investigated by determining the Ca²⁺-dependence of activation of motility in a single filament assay. Using the quantitative *in vitro* motility assay and skeletal muscle thin filaments containing recombinant mutant Tpm3.12, we found increased Ca²⁺-sensitivity in both $\Delta E224$ and $\Delta E218$ tropomyosin mutations. $\Delta E218$ led to a 2.5-fold increase in Ca²⁺-sensitivity (EC₅₀ ratio $\Delta E218$ /WT = 0.40 ± 0.07 , $p = 0.004$). $\Delta E224$ also showed an increase in Ca²⁺-sensitivity by 2.2-fold (EC₅₀ ratio $\Delta E224$ /WT for = 0.46 ± 0.09 , $p = 0.0$). It has been previously shown that there was a 2.5-fold increase in Ca²⁺-sensitivity for K326N actin (EC₅₀ ratio K326N/WT = 0.4 ± 0.05 , $p = 0.07$) in thin filaments reconstituted with wild type or mutant actin from biopsy and native tropomyosin and troponin. Increased Ca²⁺-sensitivity indicates that both mutations cause a gain of function that was predicted from the structural analysis and that can account for the stiff patient syndrome.