Ryr1 and cacna1s genetic variants identified with statin-associated muscle symptoms.


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Abstract

AIM: To examine the genetic differences between subjects with statin-associated muscle symptoms and statin-tolerant controls.

MATERIALS & METHODS: Next-generation sequencing was used to characterize the exomes of 76 subjects with severe statin-associated muscle symptoms and 50 statin-tolerant controls.

RESULTS: 12 probably pathogenic variants were found within the Ryr1 and Cacna1s genes in 16% of cases with severe statin-induced myopathy representing a fourfold increase over variants found in statin-tolerant controls. Subjects with probably pathogenic Ryr1 or Cacna1s variants had plasma CK 5X to more than 400X the upper limit of normal in addition to having muscle symptoms.

CONCLUSIONS: Genetic variants within the Ryr1 and Cacna1s genes are likely to be a major contributor to the susceptibility to statin-associated muscle symptoms.

KEYWORDS: Ryr1; exome sequencing; malignant hyperthermia; myopathy; statin