Prevalence of THAP1 sequence variants in German patients with primary dystonia.

Primary dystonias are a clinically and genetically heterogeneous group of movement disorders, but only for two of them, i.e., dystonia 1 and dystonia 6, the disease causing gene has been identified. Dystonia 1 is characterized by an early onset and is caused by a mutation in the TOR1A gene. Only recently, mutations in THAP1 have been shown to be the cause of DYT6 dystonia. We analyzed 610 patients with various forms of dystonia for sequence variants in the THAP1 gene by means of high resolution melting to delineate the prevalence of sequence variants and phenotypic variability. We identified seven sequence variants in patients and one sequence variant in a control. The sequence variants were not detected in 537 healthy controls. Four patients present with generalized dystonia with speech involvement of early onset, another three patients suffered exclusively from cervical dystonia of adult onset. These findings suggest that THAP1 sequence variations seem to be associated with different ages of onset and distribution of symptoms. Consequently, the phenotypic spectrum might be broader than previously assumed.