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How the genetics of dystonia may bring big results

Christine Klein, MD
Schilling Professor of Neurogenetics
Institute of Neurogenetics
University of Lübeck
Lübeck, Germany
christine.klein@neuro.uni-luebeck.de
www.neurogenetics-luebeck.org

While all forms of dystonia share the core clinical features of involuntary dystonic movements, there is not only marked phenotypic but also etiologic heterogeneity. An important cause of dystonia is mutations in dystonia-related genes. With the advent of next generation sequencing, an unprecedented number of new dystonia genes have recently been described. Whereas it took 15 years to discover 10 dystonia genes, five novel ones have now been found in less than two years. These genes are grouped among the currently 25 'DYTs'. At present, genes have been reported for 14 different types of monogenic isolated and combined dystonia, in which dystonia is associated with another movement disorder, such as parkinsonism or myoclonus. Isolated dystonia can be caused by mutations in *TOR1A* (DYT1), *TUBB4* (DYT4), *THAP1* (DYT6), *PRKRA* (DYT16), *CIZ1* (DYT23), *ANO3* (DYT24), *and GNAL (DYT25).* Combined dystonias are further subdivided based on their temporal pattern into persistent (*TAF1* [DYT3], *GCHI* [DYT5], *SGCE* [DYT11], *ATP1A3* [DYT12]) and paroxysmal (*MR-1* [DYT8], *PRRT2* [DYT10], *SLC2A1* [DYT18]. Despite the need for independent confirmation, these recent findings raise two important questions regarding the role of i) genetics in dystonia overall and ii) different molecular mechanisms in dystonia pathogenesis. In the next decade of dystonia research, we expect to see the discovery of additional dystonia genes and susceptibility factors and to improve our understanding of the underlying and at least partially interconnected pathways involved in dystonia. Most importantly, however, we hope that these findings and research efforts will also translate into new treatment options for patients suffering from dystonia.