

Whole-Exome Sequencing in a Movement Disorders Clinic

Chintan Shah¹, Laurie Robak², Emily J. Hill^{1,3}, Joseph Jankovic¹



¹Parkinson's Disease Center and Movement Disorders Clinic, Department of Neurology, Baylor College of Medicine, Houston, TX, USA

²Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA

³Gardner Family Center for Movement Disorders, University of Cincinnati, Cincinnati, OH, USA

Objective

 To evaluate the diagnostic utility of whole exome sequencing (WES) in patients from a movement disorder clinic.

Background

- · Many patients with suspected genetic movement disorders do not have a known molecular diagnosis.
- Molecular diagnosis can significantly impact patients and their families by guiding treatment, providing prognostic information and informing genetic counseling for at-risk family members.

Methods

- We performed a retrospective chart review of movement disorder patients evaluated in our clinic with WES analyzed between January 2013 and December 2020.
- Cases were ascertained through a search of the electronic medical records for presence of multiple movement disorder phenotypes, early age at onset, or positive family history.

Results

- WES was requested for 41 patients and 28 (68.3%) received WES results; the other 13 (31.7%) were denied approval by their insurance company.
- The median age at symptom onset was 20.5 years (range: birth-63 years).
- The median age at testing was 45.5 years (range: 4-69 years).
- A positive family history of a movement disorder in a 1st or 2nd degree relative was present in 57.1% of patients.
- 46% of the patients had undergone targeted genetic testing prior to WES.
- The molecular diagnostic yield in our WES cohort was 17.9% (5/28 patients).

Figure 1: Predominant movement disorder phenomenology for which WES was completed

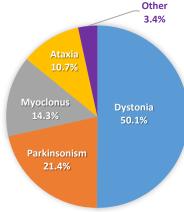


Table 1: Genes with pathogenic variants detected in our WES cohort

| GeneVariantMovement DisorderDiagnosisZygosityInheritancePANK2p.K478E: c.1432A>GDystoniaNeurodegeneration with brain iron accumulation (NBIA)HetARSPG11p.E1630X: c.4888G>TSpasticityHereditary spastic paraplegia (HSP)HetARPSEN1p.E120G: c.359A>GMyoclonusEarly-onset dementiaHetADTOR1Ap.E303del: c.907_909delGAGDystoniaTorsion dystoniaHetADGLRA1p.E403del: c.1207_1209delGAGDystoniaHereditary hyperkplexiaHetAD | | | | | | |
|--|-------|---------|------------|-------------------------|----------|-------------|
| c.1432A>G iron accumulation (NBIA) SPG11 p.E1630X: | Gene | Variant | | Diagnosis | Zygosity | Inheritance |
| c.4888G>T (HSP) PSEN1 p.E120G: Myoclonus Early-onset dementia Het AD C.359A>G TOR1A p.E303del: Dystonia Torsion dystonia Het AD C.907_909delGAG GLRA1 p.E403del: Dystonia Hereditary hyperkplexia Het AD | PANK2 | • | Dystonia | <u> </u> | Het | AR |
| c.359A>G TOR1A p.E303del: Dystonia Torsion dystonia Het AD c.907_909delGAG GLRA1 p.E403del: Dystonia Hereditary hyperkplexia Het AD | SPG11 | • | Spasticity | , , , , , | Het | AR |
| c.907_909delGAG GLRA1 p.E403del: Dystonia Hereditary hyperkplexia Het AD | PSEN1 | • | Myoclonus | Early-onset dementia | Het | AD |
| | TOR1A | • | Dystonia | Torsion dystonia | Het | AD |
| | GLRA1 | • | Dystonia | Hereditary hyperkplexia | Het | AD |

Conclusions

• WES has an important diagnostic value in movement disorder patients, particularly in those with atypical presentation and high index of suspicion for genetic etiology.