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Published in:
epilepsia open
DOI:
10.1002/epi4.12009

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Document Version
Publisher's PDF, also known as Version of record

Publication date:
2016

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):
Zutt, R., Drost, G., Vos, Y., Elting, J. W., Miedema, I., tijsen, M. A., Brouwer, O., & de Jong, B. M. (2016). Unusual course of Lafora disease. epilepsia open, 1(3-4), 136-139. https://doi.org/10.1002/epi4.12009

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Download date: 29-10-2021
Unusual Course of Lafora Disease

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Epilepsia Open, 1(3-4):136–139, 2016
doi: 10.1002/epi4.12009

SUMMARY

A 42-year-old male was admitted for refractory status epilepticus. At the age of 25, he had been diagnosed with juvenile myoclonic epilepsy. He had a stable clinical course for over a decade until a recent deterioration of behavior and epilepsy. After exclusion of acquired disorders, diagnostic work-up included application of next-generation sequencing (NGS), with a gene panel targeting progressive myoclonic epilepsies. This resulted in the diagnosis Lafora disease resulting from compound heterozygous NHLRC1 pathogenic variants. Although these pathogenic variants may be associated with a variable phenotype, including both severe and mild clinical course, the clinical presentation of our patient at this age is very unusual for Lafora disease. Our case expands the phenotype spectrum of Lafora disease resulting from pathogenic NHLRC1 variants and illustrates the value of using NGS in clinical practice to lead to a rapid diagnosis and guide therapeutic options.

KEY WORDS: Myoclonus epilepsy, Refractory status epilepticus, Lafora disease, Next-generation sequencing.
male patient, initially diagnosed with JME, who appeared to have Lafora disease. Most remarkable was the unusual clinical course with very late adult onset and disease progression only after 17 years.

CASE REPORT

This 42-year-old male was admitted with a generalized convulsive status epilepticus. At age 25, he had had a single unprovoked GTCS, followed 2 years later by mild multifocal myoclonic jerks, mainly distally in his arms. Family history was negative for epilepsy. Electroencephalogram (EEG) at that time showed frequent generalized 2- to 3-Hz (poly)spike waves without photosensitivity, and a diagnosis of JME was made. With valproate treatment, myoclonic jerking persisted without seizures. Personal and social functioning appeared normal until a few weeks before admission, when friends noticed manic behavior.

Despite standard antiepileptic drug treatment, seizures persisted, requiring intubation and sedation with propofol and midazolam. After tapering sedation, tonic-clonic seizures and myoclonus of his feet reappeared. EEG showed continuous generalized spikes and high-voltage sharp waves with a bifrontocentral maximum. Sedation was restarted to induce electrographic burst suppression, and lacosamide was added. After 48 h of burst suppression, tapering of sedation again led to myoclonus of the feet and reappearance of epileptic paroxysms in the EEG. Subsequently, burst suppression with thiopental was maintained for another 48 h. After regaining consciousness 5 days later, the patient developed action-provoked and stimulus-sensitive multifocal myoclonus in his face (predominant left-sided) and distal limbs. Without an obvious EEG correlate, the cortical origin was substantiated with back averaging (Fig. 1A). Somatosensory evoked potentials (SEPs) showed no enlarged late potential complex (P27/N30), possibly owing to medication. The following days, still artificially ventilated, he responded adequately with normal facial and oculomotor functions while voluntary limb control was strongly impaired. This progressed into tetraparesis with continuously myoclonic limb jerking. A week later, convulsive status epilepticus reappeared with facial myoclonus and tonic-clonic seizures. EEG showed continuous generalized spikes and high-voltage sharp waves with a (right) frontocentral maximum. Under propofol, valproate was switched to gabapentin and phenytoin, clonazepam, levetiracetam, and lacosamide treatment was continued. His epilepsy finally became controlled and limbs and p.Gly121Ser 1/112232 alleles. The variants are part of one of the six NHL domains of the protein, a conserved domain probably involved in protein–protein interaction. Pro129 and Gly121 are both highly conserved amino acids.

The NHLRC1 gene variants detected in our patient are considered pathogenic based on a number of arguments. Both variants are found only once in the publicly available control population database (Exome Aggregation Consortium; http://exac.broadinstitute.org/): p.Pro129His 1/116492 alleles and p.Gly121Ser 1/112232 alleles. The variants are part of one of the six NHL domains of the protein, a conserved domain probably involved in protein–protein interaction. Pro129 and Gly121 are both highly conserved amino acids. Alamut (version 2.6) from Interactive Biosoftware (http://www.interactive-biosoftware.com) was used to predict pathogenicity. It includes Align GVGD, SIFT, PolyPhen-2, and Mutation Taster. All four programs predicted the variants damaging the protein structure and function. Finally, both variants were published previously in patients with Lafora disease.5,6,13 Because segregation analysis in the family of our patient was not possible, the diagnosis of Lafora disease was confirmed by immune histochemical testing.

Later age at onset and milder clinical course are described in patients with pathogenic NHLRC1 variants, resulting in lower neurologic disability scores and less severe seizure phenotype compared with patients with pathogenic EPM2A variants.5,14 However, to our knowledge, no patient with an initially mild disease presentation suddenly deteriorating toward refractory status epilepticus after more than 15 years has been described before.

Discussion

This case report describes a patient with Lafora disease following an atypical clinical course with late onset and long-lasting clinically stable course with sudden deterioration into refractory status epilepticus at the age of 42 years. The NHLRC1 gene variants detected in our patient are considered pathogenic based on a number of arguments. Both variants are found only once in the publicly available control population database (Exome Aggregation Consortium; http://exac.broadinstitute.org/): p.Pro129His 1/116492 alleles and p.Gly121Ser 1/112232 alleles. The variants are part of one of the six NHL domains of the protein, a conserved domain probably involved in protein–protein interaction. Pro129 and Gly121 are both highly conserved amino acids. Alamut (version 2.6) from Interactive Biosoftware (http://www.interactive-biosoftware.com) was used to predict pathogenicity. It includes Align GVGD, SIFT, PolyPhen-2, and Mutation Taster. All four programs predicted the variants damaging the protein structure and function. Finally, both variants were published previously in patients with Lafora disease.5,6,13 Because segregation analysis in the family of our patient was not possible, the diagnosis of Lafora disease was confirmed by immune histochemical testing.

Later age at onset and milder clinical course are described in patients with pathogenic NHLRC1 variants, resulting in lower neurologic disability scores and less severe seizure phenotype compared with patients with pathogenic EPM2A variants.5,14 However, to our knowledge, no patient with an initially mild disease presentation suddenly deteriorating toward refractory status epilepticus after more than 15 years has been described before.
The characteristic visual hallucinations were not present in our case, which, on the other hand, is in accord with the study of Ferlazzo et al.\textsuperscript{5}

Mild brain atrophy has been described in 35–40\% of patients with typical and mild Lafora disease with normal MRI in the remaining patients.\textsuperscript{5,14} The transient MRI

**Figure 1.**
Diagnostic investigations of patient with Lafora disease. (A) The left panel shows 8 s of raw EEG and electromyography (EMG) data of muscles of the right leg. Note the short duration of the EMG bursts. The EEG shows no epileptic abnormalities. The middle panel shows a clear positive-negative potential in the central electrode after back averaging, which starts approximately 40 ms before myoclonus onset. Right panel: Topographic mapping of the cortical potential. (B) Three consecutive brain MRIs (transversal sections). The left and middle slices show diffusion weighted images (DWIs); the right image is based on fluid attenuation inversion recovery (FLAIR) sequences. The first MRI shows hyperintensity of the gyrus cinguli corresponding to the maximum of seizure activity. The second MRI shows extension of the gray matter abnormalities likely associated with repeated periods of epileptic seizure activity. The third MRI shows complete disappearance of the abnormal T2 hyperintensity of the gray matter. (C) The left panel shows a hematoxylin and eosin (H&E) stain overview of the axillary biopsy. The right panel shows a detailed periodic acid Schiff staining with multiple Lafora bodies (arrows) in the myoepithelial cells surrounding the glands.

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abnormalities of our patient may well have been caused by the intensive seizure activity because they were localized in the area with the highest seizure activity registered on EEG and had normalized after 3-month follow-up. Transient MRI abnormalities with diffusion restriction have been described previously in patients with focal status epilepticus.15

Our case thus expands the phenotypic spectrum of Lafora disease due to pathogenic NHLRC1 variants and highlights the importance of NGS in epileptic myoclonus syndromes.

**Disclosure of Conflicts of Interest**

M.A.J. Tijssen has received educational grants from Actelion, Allergan, Ipsen, Medtronic, and Merz. O.F. Brouwer has received educational grants (UCB Pharma, Nutricia) and has presented lectures at sponsored meetings (UCB Pharma). The remaining authors have no conflicts of interest. We confirm that we have read the Journal’s position on issues involved in ethical publication and affirm that this report is consistent with those guidelines.

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