

Title:

De novo Mutations of *KIAA2022* in Females Cause Epileptic Encephalopathy

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First Author:

Katherine Helbig

Division of Clinical Genomics, Ambry Genetics, Aliso Viejo, CA

Co-Author(s):

Iris de Lange

Department of Medical Genetics, University Medical Center Utrecht, The Netherlands

,
Sarah Weckhuysen

Inserm U 1127, CNRS UMR 7225, Sorbonne Universités, UPMC Univ Paris 06 UMR S 1127, Institut du Cerveau et de la Moelle épinière, ICM, AP-HP, Hôpital de la Pitié Salpêtrière, Service de Neurologie, Paris, France

,
Rikke Møller

Danish Epilepsy Center, Dianalund, Denmark; Institute for Regional Health Research, University of Southern Denmark, Odense, Denmark

,
Milen Velinov

NYS Institute for Basic Research in Developmental Disabilities
Staten Island, NY

Laura Farach

Division of Medical Genetics, Department of Pediatrics, The University of Texas Medical School at Houston, Houston, TX

,
Eric Marsh

Division of Neurology, The Children's Hospital of Philadelphia, Philadelphia, PA

,
Ingo Helbig

Division of Neurology, The Children's Hospital of Philadelphia, Philadelphia, PA;
Department of Neuropediatrics, Christian-Albrechts-University of Kiel and University Medical Center Schleswig-Holstein, Kiel, Germany

,
Sha Tang

Ambry Genetics

,
Heather Mefford

Department of Pediatrics, Division of Genetic Medicine, University of Washington, Seattle, WA

,
Candace Myers

Department of Pediatrics, Division of Genetic Medicine, University of Washington, Seattle, WA

,
Wim Van Paesschen

Laboratory for Epilepsy Research, KU Leuven, Leuven, Belgium

,
Pasquale Striano

Pediatric Neurology and Muscular Diseases Unit, Department of Neurosciences, Rehabilitation, Ophthalmology, Genetics, Maternal and Child Health, University of Genoa, G. Gaslini Institute, Genova, Italy

,
Koen van Gassen

Department of Medical Genetics, University Medical Center Utrecht, The Netherlands

,
Marjan van Kempen

Department of Medical Genetics, University Medical Center Utrecht, The Netherlands

,
Carolien de Kovel

Department of Medical Genetics, University Medical Center Utrecht, The Netherlands

,
Juliette Piard

Centre de génétique humaine, Université de Franche-Comté, Besançon, France

,
Berge Minassian

Division of Neurology, Department of Paediatrics, The Hospital for Sick Children, Toronto, Ontario, Canada

,
Marjan Nezarati

Prenatal Diagnosis and Medical Genetics Program, Mount Sinai Hospital, Toronto, Canada; Genetics, North York General Hospital, Toronto, Canada

,
André Pessoa

School of Medicine, University of Fortaleza, Fortaleza, Brazil

,
Aurelia Jacqueline

Service de génétique, GHU Pitié-Salpêtrière; Université Pierre et Marie Curie, Paris, France

,
Ruben van 't Slot

Department of Medical Genetics, University Medical Center Utrecht, The Netherlands

,
Lionel Van Maldergem

Centre de génétique humaine, Université de Franche-Comté, Besançon, France

,
Eva Brilstra

Department of Medical Genetics, University Medical Center Utrecht, The Netherlands

,
Bobby Koeleman

Department of Medical Genetics, University Medical Center Utrecht, The Netherlands

Description:

Introduction: The X-chromosome gene *KIAA2022* encodes a protein of unknown function, which is highly expressed in postmitotic neurons in the fetal and adult brain and has been suggested to play an important role in early brain development. Hemizygous loss-of-function mutations in *KIAA2022* have been previously reported in male patients with X-linked intellectual disability and other variable features including mild non-specific dysmorphic features, muscular hypotonia, autistic features, and epilepsy. Carrier females in these families are unaffected with random X-inactivation patterns and normal *KIAA2022* expression levels. While the male *KIAA2022* phenotype is well established, little is known about the phenotype of female patients. Here, we report 11 new female patients with heterozygous *de novo* loss-of-function mutations of *KIAA2022*.

Methods: We evaluated whole genome sequencing, whole exome sequencing, and NGS panel data of individuals with neurodevelopmental disorders and epilepsy to identify female patients with *de novo* mutations in *KIAA2022*. One patient was diagnosed after array CGH indicated a microdeletion disrupting *KIAA2022*. X chromosome inactivation and *KIAA2022* RNA expression studies were performed where possible.

Results: We identified 11 previously unreported female patients, all with *de novo* loss-of-function mutations in *KIAA2022*. Refractory generalized epilepsy with onset in infancy or early childhood was present in 9/11 (81.8%) patients. Myoclonic seizures were a predominant seizure type, seen in 8/9 (88.9%) patients. Other seizure types included absence (7/9; 77.8%), generalized tonic-clonic (6/9; 66.7%), atonic (4/9; 44.4%), and tonic seizures (4/9; 44.4%). Status epilepticus was reported in 3/9 (33.3%) patients with epilepsy. Cognitive outcomes ranged from mild to severe intellectual disability. All but one patient had limited speech and language skills. Autism or autistic features were noted in 6/11 (54.5%) patients. Behavioral problems including aggression, hyperactivity, and ADHD were identified in 8/11 patients (72.7%). X chromosome inactivation studies revealed a random inactivation pattern in 6/7 patients (85.7%), but a ratio of 0:100 in 1/7 (14.3%) *KIAA2022* RNA expression studies showed detectable but decreased expression in 4/5 patients (80.0%) and absent RNA expression in the patient with 100% skewed X-inactivation. The patient with 100% skewing and absent expression did not have seizures and had a phenotype more consistent with affected males, including severe generalized hypotonia, microcephaly, postnatal growth restriction, and mild dysmorphic facial features. In comparison to previously described affected males, females with *KIAA2022* encephalopathy do not show the distinct phenotype characterized by severe intellectual disability, microcephaly, growth restriction, and dysmorphic facial features as seen in most males. However, refractory generalized seizures consistent with epileptic encephalopathy were a prominent feature in affected females.

Conclusion: *De novo* loss-of-function mutations in *KIAA2022* in females cause a distinctive phenotype characterized by refractory myoclonic epilepsy, mild to severe intellectual disability, autistic features, and behavioral disturbances. This phenotype is in contrast to the male phenotype which is characterized by more severe intellectual disability and dysmorphic features. The mechanisms that may underlie the female phenotype may

be haploinsufficiency or cellular interference, due to a mosaic cell population expressing both mutant and wild type cells. Random X-chromosome inactivation patterns, both in affected and unaffected carrier females, suggest that other factors explain the strongly reduced expression in symptomatic females.

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Brain/Nervous System

Cognitive Disorders

Delineation of Diseases

Identification of Disease Genes

Intellectual disability

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Phenotypic delineation of disorders

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X-Inactivation/X-Linked Disease

Primary Topic Focus:

Clinical Genetics