Abstract Preview

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- Do not use all caps
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De novo missense variants in the alternative exon 5 of *SCN2A* are a rare cause of neurodevelopmental disorders with or without seizures

D.N. Shinde¹, L. Rohena^{2,3}, S. Weatherspoon⁴, K.L. Helbig⁵, C. Antolik¹, D.R. Hamlin², J.M. Berg², C. Schultz¹, Z. Powis¹, S. Tang¹, K. Radtke¹. 1) Ambry Genetics, Aliso Viejo, CA; 2) Department of Pediatrics, Division of Medical Genetics, San Antonio Military Medical Center, San Antonio, TX; 3) Department of Pediatrics, Division of Medical Genetics, University of Texas Health Science Center at San Antonio, San Antonio, TX; 4) Department of Pediatric Neurology, Le Bonheur Children's Hospital, University of Tennessee Health Science Center, Memphis, TN; 5) Division of Neurology, Children's Hospital of Philadelphia, Philadelphia, PA. *SCN2A* encodes Na_v1.2, the alpha subunit of the neuronal voltage-gated sodium channel that is responsible for

generation and propagation of action potentials. Heterozygous mutations in SCN2A cause a spectrum of neurodevelopmental disorders including benign familial infantile seizures and early infantile epileptic encephalopathy, with or without autism spectrum disorders and intellectual disability. Na_v1.2 has two

developmentally regulated isoforms (neonatal [N] and adult [A]) that use alternatively spliced coding exons 5N and 5A, respectively. During early brain development, the N isoform is more abundantly expressed than the A isoform, but its relative proportion decreases as it is replaced by the A isoform during postnatal development. N channels are less excitable than A channels, and mutations in SCN2A that increase neuronal excitability of the N channels to the level of the A channels, are thought to increase susceptibility to seizures in the neonatal period. Although most mutations in SCN2A are found in both the isoforms, to date, there is only one report of a likely pathogenic variant, c.634A>G (p.N212D), found exclusively in the N isoform in an infant with Ohtahara syndrome. Here, we report two additional unrelated affected individuals with de novo missense variants in exon 5N of SCN2A, c.647T>A (p.L216H) and c.668G>T (p.R223I), that were identified using trio-based whole exome sequencing. Both the affected individuals presented with global developmental delay and abnormal brain MRI findings. Additionally, infantile spasms were observed in one of the affected individuals, while the other presented with intellectual disability and autistic behaviors. Both altered amino acids are located in the voltagesensor S4 transmembrane helix of Na_v1.2, and structural analysis indicates that the alterations impact channel function by disrupting charge gating. Functional studies to determine impact on channel activity are ongoing, and identification of additional affected individuals may help to elucidate the phenotypic spectrum of variants in exon 5N of SCN2A. Our results highlight the clinical utility of reporting variants in alternative isoforms of genes with clinically well-characterized primary isoforms.

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