

## BIALELIC PATHOGENIC (C.830G>A (P.R277Q)) VARIANT DISRUPTING THE GNE GENE FUNCTION AND CAUSES NONAKA MYOPATHY PHENOTYPE

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*Nonaka myopathy (MIM 605820) is caused by homozygous pathogenic variants in the GNE gene. It is a recessively inherited early adult-onset myopathy that usually preserves the quadriceps and presents with bilateral foot drop, usually caused by anterior tibialis weakness. In patients with Nonaka myopathy, serum creatine kinases are slightly elevated, muscle weakness progresses slowly, and ambulation loss develops after 15–20 years. The current study aims to raise awareness of Nonaka myopathy that occurs as a rare phenotype due to pathogenic variants in GNE gene. Detailed family histories and clinical data were recorded. Whole exome sequencing was performed and co-segregation analysis of the family were done by Sanger sequencing. Also the homology model of the mutant protein was created with the ProMod3 algorithm. We identified a biallelic pathogenic variant (c.830G>A) in GNE gene, which explain the patients' clinical status. We present the main findings of two siblings with Nonaka myopathy together with detailed clinical and genetic profiles of the patients together with a three-dimensional mutant GNE protein model. We think that the clinical characteristics and the effect of the (c.830G>A) variant will facilitate our understanding of GNE gene in Nonaka myopathy pathogenesis.*

**Key words:** GNE myopathy, distal myopathy, sialic acid, Nonaka disease, rare diseases.

**ДІАЛЕЛЬНИЙ ПАТОГЕННИЙ (C.830G>A(P.R277Q)) ВАРІАНТ, ЩО ПОРУШУЄ ФУНКЦІЮ ГЕНУ GNE І ВИКЛИКАЄ ФЕНОТИП МІОПАТІЇ НОНАКА**

Міопатію Нонака (MIM 605820) викликають гомозиготні патогенні варіанти в гені GNE. Це міопатія

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з раннім початком розвитку в дорослих, яка успадковується рецесивно та за якої зберігаються чотириголові м'язи і виникає двостороннє обвисання стіп, що зазвичай спричинено слабкістю переднього великомілкового м'язу. У пацієнтів із міопатією Нонака дещо вищий рівень креатин-кінази сироватки, повільне прогресування м'язової слабкості та втрата здатності самостійно переміщатися розвиваються через 15–20 років. Поточне дослідження спрямоване на підвищення обізнаності про міопатію Нонака, яка виникає як рідкісний фенотип через патогенні варіанти в гені GNE. Проводиться детальна реєстрація історії хвороби та клінічних даних. Було проведено повне секвенування екзому і косегрегаційний аналіз родин за допомогою секвенування Сенгера. Також було створено модель гомології мутантного білка за використання алгоритму ProMod3. Ми ідентифікували діалельний патогенний варіант (c.830G>A) у гені GNE, який пояснює клінічний стан пацієнтів. Ми представляємо основні результати двох дітей із однієї родини, які мають міопатію Нонака, а також детальні клінічні та генетичні профілі пацієнтів і тривимірну модель мутантного білку GNE. Ми вважаємо, що клінічні характеристики та вплив варіанта(c.830G>A) сприятимуть нашому розумінню ролі гена GNE у патогенезі міопатії Нонака.

**Ключові слова:** міопатія GNE, дистальна міопатія, сіалова кислота, хвороба Нонака, рідкісні захворювання.

### REFERENCES

- Argov Z (2014) GNE myopathy: a personal trip from bedside observation to therapeutic trials., Acta Myol 33(2):107–110.
- Awasthi K, Srivastava A, Bhattacharya S et al (2021) Tissue specific expression of sialic acid metabolic pathway: role in GNE myopathy, J Muscle Res Cell Motil 42(1):99–116. <https://doi.org/10.1007/s10974-020-09590-7>.
- Barp A, Mosca L, and Sansone VA (2021) Facilitations and Hurdles of Genetic Testing in Neuromuscular Disorders. Diagnostics (Basel) 11(4). <https://doi.org/10.3390/diagnostics11040701>
- Buchan DW, Minneci F, Nugent TC et al (2013) Scalable web services for the PSIPRED Protein Analysis Workbench. Nucleic Acids Res 41(W1):W349–357. <https://doi.org/10.1093/nar/gkt381>.
- Carrillo N, Malicdan MC, Huizing M (2018) GNE Myopathy: Etiology, Diagnosis, and Therapeutic Challenges. Neurotherapeutics 15(4):900–914. <https://doi.org/10.1007/s13311-018-0671-y>.
- Carrillo N, Malicdan MC, Gahl WA (2021) Safety and efficacy of N-acetylmannosamine (ManNAc) in pa-

- tients with GNE myopathy: an open-label phase 2 study. *Genet Med* 23(11):2067–2075. <https://doi.org/10.1038/s41436-021-01259-x>.

Celeste FV, Vilboux T, Ciccone C (2014) Mutation update for GNE gene variants associated with GNE myopathy. *Hum Mutat* 35(8):915–926. <https://doi.org/10.1002/humu.22583>.

Cerino M, Gorokhova S, Behin A et al (2015) Novel Pathogenic Variants in a French Cohort Widen the Mutational Spectrum of GNE Myopathy. *J Neuromuscul Dis* 2(2):131–136. <https://doi.org/10.3233/JND-150074>.

Chen VB, Arendall WB, Headd JJ et al (2010) MolProbity: all-atom structure validation for macromolecular crystallography. *Acta Crystallogr D Biol Crystallogr* 66(Pt 1):12–21. <https://doi.org/10.1107/S0907444909042073>.

Chen Y, Xi J, Zhu W et al (2019) Correction: GNE myopathy in Chinese population: hotspot and novel mutations. *J Hum Genet* 64(3):269. <https://doi.org/10.1038/s10038-018-0547-3>.

Crowe KE, Zygmunt DA, Martin PT (2022) Visualizing Muscle Sialic Acid Expression in the GNED-207VTgNge-/- Cmah-/- Model of GNE Myopathy: A Comparison of Dietary and Gene Therapy Approaches. *J Neuromuscul Dis* 9(1):53–71. <https://doi.org/10.3233/JND-200575>.

Effertz K, Hinderlich S, Reutter W (1999) Selective loss of either the epimerase or kinase activity of UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase due to site-directed mutagenesis based on sequence alignments. *J Biol Chem* 274(40):28771–28778. <https://doi.org/10.1074/jbc.274.40.28771>.

Eisenberg I, Avidan N, Potikha T et al (2001) The UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase gene is mutated in recessive hereditary inclusion body myopathy. *Nat Genet* 29(1):83–87. <https://doi.org/10.1038/ng718>.

Grecu N, Villa L, Cavalli M et al (2021) Motor axonal neuropathy associated with GNE mutations. *Muscle Nerve* 63(3):396–401. <https://doi.org/10.1002/mus.27102>.

Grover S, Arya R (2014) Role of UDP-N-acetylglucosamine2-epimerase/N-acetylmannosamine kinase (GNE) in beta1-integrin-mediated cell adhesion. *Mol Neurobiol* 50(2):257–273. <https://doi.org/10.1007/s12035-013-8604-6>.

Hanisch F, Weidemann W, Grossmann M et al (2013) Sialylation and muscle performance: sialic acid is a marker of muscle ageing. *PLoS One* 8(12):e80520. <https://doi.org/10.1371/journal.pone.0080520>.

Harazi A, Becker-Cohen M, Zer H et al (2017) The Interaction of UDP-N-Acetylglucosamine 2-Epi-

merase/N-Acetylmannosamine Kinase (GNE) and Alpha-Actinin 2 Is Altered in GNE Myopathy M743T Mutant. *Mol Neurobiol* 54(4):2928–2938. <https://doi.org/10.1007/s12035-016-9862-x>.

Kazamel M, Sorenson EJ, Milone M (2016) Clinical and Electrophysiological Findings in Hereditary Inclusion Body Myopathy Compared With Sporadic Inclusion Body Myositis. *J Clin Neuromuscul Dis* 17(4):190–196. <https://doi.org/10.1097/CND.0000000000000113>.

Koroglu C, Yilmaz R, Sorgun MH et al (2017) GNE missense mutation in recessive familial amyotrophic lateral sclerosis. *Neurogenetics* 18(4):237–243. <https://doi.org/10.1007/s10048-017-0527-3>.

Krause S, Hinderlich S, Amsili S et al (2005) Localization of UDP-GlcNAc 2-epimerase/ManAc kinase (GNE) in the Golgi complex and the nucleus of mammalian cells. *Exp Cell Res* 304(2):365–379. <https://doi.org/10.1016/j.yexcr.2004.11.010>.

Lv XQ, Xu L, Lin PF et al (2022) Clinical, genetic, and pathological characterization of GNE myopathy in China. *Neurol Sci*. <https://doi.org/10.1007/s10072-022-05938-8>.

Nishino I, Carrillo-Carrasco N, Argov Z (2015) GNE myopathy: current update and future therapy. *J Neurol Neurosurg Psychiatry* 86(4):385–392. <https://doi.org/10.1136/jnnp-2013-307051>.

Pandurangan AP, Ochoa-Montano B, Ascher DB et al (2017) SDM: a server for predicting effects of mutations on protein stability. *Nucleic Acids Res* 45(W1):W229–W235. <https://doi.org/10.1093/nar/gkx439>.

Pires DE, Ascher DB, Blundell TL (2014a) DUET: a server for predicting effects of mutations on protein stability using an integrated computational approach. *Nucleic Acids Res* 42:W314–319. <https://doi.org/10.1093/nar/gku411>.

Pires DE, Ascher DB, Blundell TL (2014b) mCSM: predicting the effects of mutations in proteins using graph-based signatures. *Bioinformatics* 30(3):335–342. <https://doi.org/10.1093/bioinformatics/btt691>.

Pogoryelova O, Cammish P, Mansbach H et al (2018) Phenotypic stratification and genotype-phenotype correlation in a heterogeneous, international cohort of GNE myopathy patients: First report from the GNE myopathy Disease Monitoring Program, registry portion. *Neuromuscul Disord* 28(2):158–168. <https://doi.org/10.1016/j.nmd.2017.11.001>.

Pogoryelova O, Gonzalez Coraspe JA, Nikolenko N et al (2018) GNE myopathy: from clinics and genetics to pathology and research strategies. *Orphanet J Rare Dis* 13(1):70. <https://doi.org/10.1186/s13023-018-0802-x>.

Pogoryelova O, Wilson IJ, Mansbach H et al (2019)

- GNE genotype explains 20 % of phenotypic variability in GNE myopathy. *Neurol Genet* 5(1):e308. <https://doi.org/10.1212/NXG.0000000000000308>.

Previtali SC, Zhao E, Lazarevic D et al (2019) Expanding the spectrum of genes responsible for hereditary motor neuropathies. *J Neurol Neurosurg Psychiatry* 90(10):1171–1179. <https://doi.org/10.1136/jnnp-2019-320717>.

Richards S, Aziz N, Bale S et al (2015) Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med* 17(5):405–424. <https://doi.org/10.1038/gim.2015.30>.

Rodrigues CHM, Myung Y, Pires DEV et al (2019) mCSM-PPI2: predicting the effects of mutations on protein-protein interactions. *Nucleic Acids Res* 47(W1):W338–W344. <https://doi.org/10.1093/nar/gkz383>.

Rodrigues CHM, Pires DEV, Ascher DB (2021) DynaMut2: Assessing changes in stability and flexibility upon single and multiple point missense mutations. *Protein Sci* 30(1):60–69. <https://doi.org/10.1002/pro.3942>.

Savarese M, Sarparanta J, Vihola A et al (2020) Panorama of the distal myopathies. *Acta Myol* 39(4):245–265. <https://doi.org/10.36185/2532-1900-028>.

Schauer R (2009) Sialic acids as regulators of molecular and cellular interactions. *Curr Opin Struct Biol* 19(5):507–514. <https://doi.org/10.1016/j.sbi.2009.06.003>.

Schwarzkopf M, Knobeloch KP, Rohde E et al (2002) Sialylation is essential for early development in mice. *Proc Natl Acad Sci* 99(8):5267–5270. <https://doi.org/10.1073/pnas.072066199>.

Sharma S, Chanana P, Bharadwaj R et al (2022) Functional characterization of GNE mutations prevalent in Asian subjects with GNE myopathy, an ultra-rare neuromuscular disorder. *Biochimie* 7(199):36–45. <https://doi.org/10.1016/j.biochi.2022.03.014>.

Stasche R, Hinderlich S, Weise C et al (1997) A bi-functional enzyme catalyzes the first two steps in N-acetyleneuraminic acid biosynthesis of rat liver. Molecular cloning and functional expression of UDP-N-acetyl-glucosamine 2-epimerase/N-acetylmannosamine kinase. *J Biol Chem* 272(39):24319–324. <https://doi.org/10.1074/jbc.272.39.24319>.

Waterhouse A, Bertoni M, Bienert S et al (2018) SWISS-MODEL: homology modelling of protein structures and complexes. *Nucleic Acids Res* 46(W1):W296–W303. <https://doi.org/10.1093/nar/gky427>.

Weidemann W, Klukas C, Klein A et al (2010) Lessons from GNE-deficient embryonic stem cells: sialic acid biosynthesis is involved in proliferation and gene expression. *Glycobiology* 20(1):107–117. <https://doi.org/10.1093/glycob/cwp153>.

Wiederstein M, Sippl MJ (2007) ProSA-web: interactive web service for the recognition of errors in three-dimensional structures of proteins. *Nucleic Acids Res* 35:W407–410. <https://doi.org/10.1093/nar/gkm290>.

Xu J, Zhang Y (2010) How significant is a protein structure similarity with TM-score = 0.5?. *Bioinformatics* 26(7):889–895. <https://doi.org/10.1093/bioinformatics/btq066>.

Yubero D, Natera-de Benito D, Pijuan J et al (2021) The Increasing Impact of Translational Research in the Molecular Diagnostics of Neuromuscular Diseases. *Int J Mol Sci* 22(8). <https://doi.org/10.3390/ijms22084274>.

Zhang KY, Duan HQ, Li QX et al (2021) Expanding the clinicopathological-genetic spectrum of GNE myopathy by a Chinese neuromuscular centre. *J Cell Mol Med* 25(22):10494–503. <https://doi.org/10.1111/jcmm.16978>.

Zhu W, Mitsuhashi S, Yonekawa T et al (2017) Missing genetic variations in GNE myopathy: rearrangement hotspots encompassing 5'UTR and founder allele. *J Hum Genet* 62(2):159–166. <https://doi.org/10.1038/jhg.2016.134>.

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