

Bölüm 41

NÖROGENETİK HASTALIKLAR

Bülent YAPRAK¹

Sibel ÇIPLAK²

Serhat SEYHAN³

GİRİŞ

Nörogenetik son yıllarda hızla gelişmekte olan bir alandır. Genel popülasyonun %1'inden fazlasında çeşitli kromozom varyantları bulunmaktadır. Bu genetik varyantlar pek çok nörolojik hastalığın gelişiminden sorumlu tutulmaktadır. Genetik alanında yeni gelişmeler sonucu tespit edilen birçok spesifik genlerin nörolojik hastalıkların %80'inden fazlasında etiyolojide sorumlu tutulduğu bilinmektedir. Genetik alanındaki son gelişmeler bireyin genetik dizisini belirleyip buna uygun tedavi stratejileri ortaya çıkarmak ve tedavisi zor olan nadir hastalıkların tedavisinde ilerleme sağlamayı amaçlamaktadır. Bu çalışmada amacımız nörogenetik hastalıkların sınıflandırılması ve genetik varyasyonlarının ortaya konulması ile ilgili bilgileri yeniden gözden geçirmektir.

FDA (Food and Drug Administration) tarafından tanımlanan verilere göre ABD (Amerika Birleşik Devletleri) 'inde 200.000'den az, Avrupa'da ise 5/10000 sayıda insanı etkileyen ve sıklıkla genetik geçişli olan nadir hastalıklar tespit edilmiştir. Bu hastalıkların sayısı yaklaşık 6000 civarında olup dünya nüfusunun %6-10'unu etkilemektedir (1).

25 milyon civarında Amerikan vatandaşı ve 10 milyon civarında da Çin vatandaşı, nadir hastalık-

lardan etkilenmiştir. Söz konusu nadir hastalıkların %80'i genetik geçişli olup bir kısmı tek gen diğer bir bölümü de çoklu gen mutasyonlarına bağlı gelişmektedirler (2,3).

İnsan genomu 23 çift kromozomdan oluşmaktadır ve bunun 22'si otozom hücrelerden diğer bir kromozom da gonozom hücrelerden olmak üzere toplam 46 kromozomdan oluşmaktadır (4,5). Bu kromozomlar ortalama 80-300 bin baz çiftinden meydana gelmektedirler. Her bir kromozom kendi özdeş kromozomu ile karşı karşıya gelerek büyükten küçüğe doğru sıralanmakta ve "karyotip" olarak isimlendirilir. Kromozomlar içerisinde DNA'lar, DNA'lar içerisinde de genler yer almaktadırlar. DNA ise genetik materyaldir ve DNA (Deoksiribonükleik Asit) nükleotidlerin karşı karşıya gelmesi sonucu iki iplikten oluşan çift sarmallı bir yapıdadır. Nükleotidler; bir fosfat grubu, bir azotlu baz (Adenin, Timin, Guanin ve Sitozin gibi) ve bir pentoz (5 Karbonlu şekerden) oluşur. Adenin ve Guanin pürin bazı, Timin ve Sitozin pirimidin bazlarıdır. Adenin bazının karşısında Timin, Guanin bazının karşısına ise Sitozin gelmektedir. DNA'da saklanan genetik bilgilerin, RNA'ya aktarılmasına "Transkripsiyon" denir. Transkripsiyon ile RNA'ya kopyalanan genetik bilgilerin bir protein molekülü haline çevrilmesine de "Translasyon" denir. Bu olayların tamamı gen ekspresyonu olarak ifade edilir (6,7).

¹ Uzman Doktor, Malatya Eğitim ve Araştırma Hastanesi İç Hastalıkları Kliniği dr_bulentuyaprak@hotmail.com

² Uzman Doktor, Malatya Eğitim ve Araştırma Hastanesi, Nöroloji Kliniği dr.sibel_ciplak@hotmail.com

³ Uzman Doktor, Özel Medipol hastanesi Genetik Kliniği ,drserhatseyhan@gmail.com

mu 12p11.2-q13.1 kromozomundaki *LRRK2* genindeki mutasyonlara bağlı PARK8'dir (106,107).

LRRK2'nin en sık mutasyonu olan G2019S bulguları idiyopatik parkinsonizme benzer bulgular göstermektedir(108,109).

Parkin (PARK2) gen mutasyonları, otozomal resesif kalıtım gösterir. Hastalık semptomları 50 yaşından önce başlar ve de distoni ve postural instabilite çok daha erken görülmektedir(110,111).

Mitokondriyal PTEN aracılı Kinaz 1 geninin (PINK1,PARK6) mutasyonları da otozomal resesif geçişlidir (112,113).

Mitokondriyal *DJ-1* geninin (*PARK7*) mutasyonları, otozomal resesif kalıtım paternine uymaktadır(114,115). Tüm bu gen mutasyonları Parkinson hastalığı ile ilişkili başlıca genetik faktörler arasında yer almaktadırlar.

MİGREN

Migren episodik, şiddetli baş ağrıları ile karakterize yaygın sık görülen ve işlevselliği etkileyen en sık görülen nörolojik hastalıklardan biridir (116,117).

Trigeminal afferentlerin uyarılması ve inflamatuvar maddelerin salınımı sonucunda, vazodilatasyon ve ağrı meydana gelir. Aile öyküsü bulunanlarda 2-3 kat daha sık görülmektedir (43,45).

Familiyal hemiplejik migren (FHM)'de, motor güçsüzlük ve sık auralı migren atakları görülür. CACNA1A (Kalsiyum kanalı), ATP1A2 (Sodyum-potasyum ATP pompası) ve SCN1A (Sodyum kanalı) iyon kanallarında otozomal dominant mutasyon ile karakterizedir (118,119).

NOTCH3 geninde mutasyon sonucu gelişen vasküler değişiklikler, demans, migren ve enfarkt görülen tablo CADASIL olarak adlandırılmaktadır (120).

SONUÇ

Nörogenetik tıpta hızlı gelişmekte ve gelecekte umut vaat etmektedir. Gelişmekte olan pek çok genetik testlerle monogenik ve poligenik birçok genetik hastalığın tanısını koyma konusunda önemli aşamalar kaydedilmiştir. Spinal müsküler

atrofi gibi birçok hastalığın tedavisinde de önemli gelişmeler tespit edilmiştir. Bununla birlikte nörogenetik alanında gelecekte de pek çok genetik hastalığın tanı ve tedavisinde ilerlemeler sağlanacağı konusunda, çok merkezli çalışmaların devam edeceğini ve yeni hedefler göstermesini bekliyoruz.

Anahtar Kelimeler: Nöro-genetik, otozomal dominant, otozomal resesif, X'e bağlı geçiş

KAYNAKLAR

1. Dos Santos Luz G, Da Silva MRS, De Montigny F. Rare diseases: Diagnostic and therapeutic journey of the families of affected people. ACTA Paul Enferm. 2015;28(5):395-400.
2. Rhee TG. Policymaking for orphan drugs and its challenges. Vol. 17, AMA Journal of Ethics. 2015. p. 776-9.
3. Gong S, Jin S. Current progress in the management of rare diseases and orphan drugs in China. Intractable Rare Dis Res. 2012;1(2):45-52.
4. Collins FS, Lander ES, Rogers J, et al. Finishing the euchromatic sequence of the human genome. Nature. 2004;431(7011):931-45.
5. Lander ES, Linton LM, Birren B, et al. Initial sequencing and analysis of the human genome. Nature. 2001;409(6822):860-921.
6. Ng P, Tan JJS, Ooi HS, et al. Multiplex sequencing of paired-end ditags (MS-PET): A strategy for the ultra-high-throughput analysis of transcriptomes and genomes. Nucleic Acids Res. 2006;34(12).
7. Ng P, Wei C-L, Ruan Y. Paired-End diTagging for Transcriptome and Genome Analysis. In: Current Protocols in Molecular Biology. 2007.
8. McCarthy MI, Abecasis GR, Cardon LR, Goldstein DB, Little J, Ioannidis JPA, et al. Genome-wide association studies for complex traits: Consensus, uncertainty and challenges. Vol. 9, Nature Reviews Genetics. 2008. p. 356-69.
9. Klepper J. GLUT1 deficiency syndrome in clinical practice. Epilepsy Res. 2012;100(3):272-7.
10. Faber CG, Hoeijmakers JGJ, Ahn HS, Cheng X, Han C, Choi JS, et al. Gain of function Na V1.7 mutations in idiopathic small fiber neuropathy. Ann Neurol. 2012;71(1):26-39.
11. Goldberg YP, Macfarlane J, Macdonald ML, Thompson J, Dube MP, Mattice M, et al. Loss-of-function mutations in the Nav1.7 gene underlie congenital indifference to pain in multiple human populations. Clin Genet. 2007;71(4):311-9.
12. EURORDIS Rare Diseases Europe. What Is a Rare Disease? Rare Dis Eur. 2007;14-5.
13. Upadhyaya M, Cooper DN. Molecular diagnosis of facioscapulohumeral muscular dystrophy. Expert Rev Mol Diagn. 2002 Mar;2(2):160-71.
14. Lunt PW, Jardine PE, Koch M, Maynard J, Osborn M, Williams M, et al. Phenotypic-genotypic correlation will assist genetic counseling in 4q35-facioscapu-

- lohumeral muscular dystrophy. *Muscle Nerve*. 1995 Jan;18(S13):S103-9.
15. Dundar M. TIBBİ GENETİK VE KLİNİK UYGULAMALARI. 2016. 1-1222 p.
 16. Lemmers RJ, Miller DG, van der Maarel SM. Facioscapulohumeral Muscular Dystrophy. *GeneReviews*®. University of Washington, Seattle; 1993.
 17. Chen H. Atlas of genetic diagnosis and counseling. Atlas of Genetic Diagnosis and Counseling. 2017. 1-3080 p.
 18. Blumen SC, Sadeh M, Korczyn AD, Rouche A, Nisipeanu P, Asherov A, et al. Intranuclear inclusions in oculopharyngeal muscular dystrophy among Bukhara Jews. *Neurology*. 1996 May;46(5):1324-8.
 19. Brais B, Bouchard J-P, Gosselin F, Xie Y-G, Fardeau M, Tomé FMS, et al. Using the full power of linkage analysis in 11 French Canadian families to fine map the oculopharyngeal muscular dystrophy gene. *Neuromuscul Disord*. 1997 Oct;7:S70-4.
 20. Tennyson CN, Klamut HJ, Worton RG. The human dystrophin gene requires 16 hours to be transcribed and is cotranscriptionally spliced. *Nat Genet*. 1995 Feb;9(2):184-90.
 21. Jacobs PA, Hunt PA, Mayer M, Bart RD. Duchenne muscular dystrophy (DMD) in a female with an X/autosome translocation: Further evidence that the DMD locus is at Xp21. *Am J Hum Genet*. 1981 Jul;33(4):513-8.
 22. Chelly J, Marlhens F, Le Marec B, Jeanpierre M, Lambert M, Hamard G, et al. De novo DNA microdeletion in a girl with Turner syndrome and Duchenne muscular dystrophy. *Hum Genet*. 1986 Oct;74(2):193-6.
 23. Quan F, Janas J, Toth-Fejel S, Johnson DB, Wolford JK, Popovich BW. Uniparental disomy of the entire X chromosome in a female with Duchenne muscular dystrophy. *Am J Hum Genet*. 1997 Jan;60(1):160-5.
 24. Katayama Y, Tran VK, Hoan NT, Zhang Z, Goji K, Yagi M, et al. Co-occurrence of mutations in both dystrophin- and androgen-receptor genes is a novel cause of female Duchenne muscular dystrophy. *Hum Genet*. 2006 Jun;119(5):516-9.
 25. Worton RG, Thompson MW. Genetics of Duchenne Muscular Dystrophy. *Annu Rev Genet*. 1988 Dec;22(1):601-29.
 26. Yan J, Feng J, Buzin CH, Scaringe W, Liu Q, Mendell JR, et al. Three-tiered noninvasive diagnosis in 96% of patients with Duchenne muscular dystrophy (DMD). *Hum Mutat*. 2004 Feb;23(2):203-4.
 27. Dent KM, Dunn DM, von Niederhausern AC, Aoyagi AT, Kerr L, Bromberg MB, et al. Improved molecular diagnosis of dystrophinopathies in an unselected clinical cohort. *Am J Med Genet Part A*. 2005 Apr;134A(3):295-8.
 28. Den Dunnen JT, Grootsholten PM, Bakker E, Blonden LA, Ginjaar HB, Wapenaar MC, et al. Topography of the Duchenne muscular dystrophy (DMD) gene: FIGE and cDNA analysis of 194 cases reveals 115 deletions and 13 duplications. *Am J Hum Genet*. 1989 Dec;45(6):835-47.
 29. White S, Kalf M, Liu Q, Villerius M, Engelsma D, Kriek M, et al. Comprehensive Detection of Genomic Duplications and Deletions in the DMD Gene, by Use of Multiplex Amplifiable Probe Hybridization. *Am J Hum Genet*. 2002 Aug;71(2):365-74.
 30. Bennett RR, den Dunnen J, O'Brien KE, Darras BT, Kunkel LM. Detection of mutations in the dystrophin gene via automated DHPLC screening and direct sequencing. *BMC Genet*. 2001;2(1):17.
 31. Mendell JR, Buzin CH, Feng J, Yan J, Serrano C, Sangani DS, et al. Diagnosis of Duchenne dystrophy by enhanced detection of small mutations. *Neurology*. 2001 Aug;57(4):645-50.
 32. Darras BT, Urion DK, Ghosh PS. Dystrophinopathies. *GeneReviews*®. University of Washington, Seattle; 1993.
 33. Essen AJ van, Mulder IM, Vlies P van der, Hout AH van der, Buys CHCM, Hofstra RMW, et al. Detection of point mutation in dystrophin gene reveals somatic and germline mosaicism in the mother of a patient with Duchenne muscular dystrophy. *Am J Med Genet*. 2003 Apr;118A(3):296-8.
 34. Bonne G, Leturcq F, Ben Yaou R. Emery-Dreifuss Muscular Dystrophy. *GeneReviews*®. University of Washington, Seattle; 1993.
 35. Emery AEH. Emery-Dreifuss syndrome. *J Med Genet*. 1989 Oct;26(10):637-41.
 36. Bécane HM, Bonne G, Varnous S, Muchir A, Ortega V, Hammouda EH, et al. High incidence of sudden death with conduction system and myocardial disease due to lamins A and C gene mutation. *Pacing Clin Electrophysiol*. 2000 Nov;23(11 Pt 1):1661-6.
 37. Bonne G, Mercuri E, Muchir A, Urtizberea A, Bécane HM, Recan D, et al. Clinical and molecular genetic spectrum of autosomal dominant Emery-Dreifuss muscular dystrophy due to mutations of the lamin A/C gene. *Ann Neurol*. 2000 Aug;48(2):170-80.
 38. Mercuri E, Brown SC, Nihoyannopoulos P, Poulton J, Kinali M, Richard P, et al. Extreme variability of skeletal and cardiac muscle involvement in patients with mutations in exon 11 of the lamin A/C gene. *Muscle Nerve*. 2005 May;31(5):602-9.
 39. Benedetti S, Menditto I, Degano M, Rodolico C, Merlini L, D'Amico A, et al. Phenotypic clustering of lamin A/C mutations in neuromuscular patients. *Neurology*. 2007 Sep;69(12):1285-92.
 40. OMIM - Online Mendelian Inheritance in Man.
 41. Dinçer P, Leturcq F, Richard I, Piccolo F, Yalnizoğlu D, De Toma C, et al. A biochemical, genetic, and clinical survey of autosomal recessive limb girdle muscular dystrophies in Turkey. *Ann Neurol*. 1997 Aug;42(2):222-9.
 42. Richard I, Brenguier L, Dinçer P, Roudaut C, Bady B, Burgunder JM, et al. Multiple independent molecular etiology for limb-girdle muscular dystrophy type 2A patients from various geographical origins. *Am J Hum Genet*. 1997 May;60(5):1128-38.
 43. Beckmann JS, Richard I, Hillaire D, Broux O, Antignac C, Bois E, et al. A gene for limb-girdle muscular dystrophy maps to chromosome 15 by linkage. *C R Acad Sci III*. 1991;312(4):141-8.
 44. Vissing J, Barresi R, Witting N, Van Ghelue M, Gammelgaard L, Bindoff LA, et al. A heterozygous 21-bp deletion in CAPN3 causes dominantly inherited limb girdle muscular dystrophy. *Brain*. 2016 Aug;139(8):2154-63.
 45. Angelini C, Fanin M. Calpainopathy. *GeneReviews*®. University of Washington, Seattle; 1993.
 46. Liu J, Aoki M, Illa I, Wu C, Fardeau M, Angelini C, et al. Dysferlin, a novel skeletal muscle gene, is mutated in

- Miyoshi myopathy and limb girdle muscular dystrophy. *Nat Genet.* 1998 Sep;20(1):31–6.
47. Aoki M. Dysferlinopathy. *GeneReviews*®. University of Washington, Seattle; 1993.
 48. ten Dam L, Frankhuizen WS, Linssen WHJP, Straathof CS, Niks EH, Faber K, et al. Autosomal recessive limb-girdle and Miyoshi muscular dystrophies in the Netherlands: The clinical and molecular spectrum of 244 patients. *Clin Genet.* 2019 Aug;96(2):126–33.
 49. Penttilä S, Palmio J, Udd B. ANO5-Related Muscle Diseases [Internet]. *GeneReviews*®. University of Washington, Seattle; 1993. Available from: <http://www.ncbi.nlm.nih.gov/pubmed/23193613>
 50. MacDonald ME, Ambrose CM, Duyao MP, Myers RH, Lin C, Srinidhi L, et al. A novel gene containing a trinucleotide repeat that is expanded and unstable on Huntington's disease chromosomes. *Cell.* 1993;72(6):971–83.
 51. Gil JM, Rego AC. Mechanisms of neurodegeneration in Huntington's disease. Vol. 27, *European Journal of Neuroscience.* 2008. p. 2803–20.
 52. Trottier Y, Devys D, Imbert G, Saudou F, An I, Lutz Y, et al. Cellular localization of the Huntington's disease protein and discrimination of the normal and mutated form. *Nat Genet.* 1995;10(1):104–10.
 53. Dayalu P, Albin RL. Huntington Disease: Pathogenesis and Treatment. Vol. 33, *Neurologic Clinics.* 2015. p. 101–14.
 54. Semaka A, Kay C, Doty C, Collins JA, Bijlsma EK, Richards F, et al. CAG size-specific risk estimates for intermediate allele repeat instability in Huntington disease. *J Med Genet.* 2013;50(10):696–703.
 55. Andrew SE, Goldberg YP, Kremer B, Telenius H, Theilmann J, Adam S, et al. The relationship between trinucleotide (CAG) repeat length and clinical features of Huntington's disease. *Nat Genet.* 1993;4(4):398–403.
 56. Lee JM, Ramos EM, Lee JH, Gillis T, Mysore JS, Hayden MR, et al. CAG repeat expansion in Huntington disease determines age at onset in a fully dominant fashion. *Neurology.* 2012;78(10):690–5.
 57. Wexler NS, Lorimer J, Porter J, Gomez F, Moskowitz C, Shackell E, et al. Venezuelan kindreds reveal that genetic and environmental factors modulate Huntington's disease age of onset. *Proc Natl Acad Sci U S A.* 2004;101(10):3498–503.
 58. Arning L, Kraus PH, Valentin S, Saft C, Andrich J, Eppelen JT. NR2A and NR2B receptor gene variations modify age at onset in Huntington disease. *Neurogenetics.* 2005;6(1):25–8.
 59. Furtado S, Schowinsky O, Barry Rewcastle N, Graham L, Klimek M Lou, Garber A. Relationship between trinucleotide repeats and neuropathological changes in Huntington's disease. *Ann Neurol.* 1996;39(1):132–6.
 60. Rosenblatt A, Liang KY, Zhou H, Abbott MH, Gourley LM, Margolis RL, et al. The association of CAG repeat length with clinical progression in Huntington disease. *Neurology.* 2006;66(7):1016–20.
 61. Bates GP, Dorsey R, Gusella JE, Hayden MR, Kay C, Leavitt BR, et al. Huntington disease. Vol. 1, *Nature Reviews Disease Primers.* 2015.
 62. Duyao M, Ambrose C, Myers R, Novelletto A, Persichetti F, Frontali M, et al. Trinucleotide repeat length instability and age of onset in Huntington's disease. *Nat Genet.* 1993;4(4):387–92.
 63. Telenius H, Almqvist E, Kremer B, Spence N, Squitieri F, Nichol K, et al. Somatic mosaicism in sperm is associated with intergenerational (CAG)_n changes in huntington disease. *Hum Mol Genet.* 1995;4(2):189–95.
 64. Renaud M, Tranchant C, Martin JVT, Mochel F, Synofzik M, van de Warrenburg B, et al. A recessive ataxia diagnosis algorithm for the next generation sequencing era. *Ann Neurol.* 2017;82(6):892–9.
 65. Manto MU. The wide spectrum of spinocerebellar ataxias (SCAs). Vol. 4, *Cerebellum.* 2005. p. 2–6.
 66. Trottier Y, Lutz Y, Stevanin G, Imbert G, Devys D, Cancel G, et al. Polyglutamine expansion as a pathological epitope in huntington's disease and four dominant cerebellar ataxias. *Nature.* 1995;378(6555):403–6.
 67. Bird TD. Myotonic Dystrophy Type 1. *GeneReviews*®. University of Washington, Seattle; 1993.
 68. Liquori CL, Ricker K, Moseley ML, Jacobsen JF, Kress W, Naylor SL, et al. Myotonic dystrophy type 2 caused by a CCTG expansion in intron 1 of ZNF9. *Science.* 2001 Aug;293(5531):864–7.
 69. Liquori CL, Ikeda Y, Weatherspoon M, Ricker K, Schorer BGH, Dalton JC, et al. Myotonic Dystrophy Type 2: Human Founder Haplotype and Evolutionary Conservation of the Repeat Tract. *Am J Hum Genet.* 2003 Oct;73(4):849–62.
 70. Carey JC, Laub JM, Hall BD. Penetrance and variability in neurofibromatosis: a genetic study of 60 families. *Birth Defects Orig Artic Ser.* 1979;15(5B):271–81.
 71. Friedman JM. Epidemiology of neurofibromatosis type 1. *Am J Med Genet.* 1999 Mar;89(1):1–6.
 72. Carmen Valero M, Martín Y, Hernández-Imaz E, Marina Hernández A, Meleán G, María Valero A, et al. A Highly Sensitive Genetic Protocol to Detect NF1 Mutations. *J Mol Diagnostics.* 2011 Mar;13(2):113–22.
 73. Evans DG, Bowers N, Burkitt-Wright E, Miles E, Garg S, Scott-Kitching V, et al. Comprehensive RNA Analysis of the NF1 Gene in Classically Affected NF1 Affected Individuals Meeting NIH Criteria has High Sensitivity and Mutation Negative Testing is Reassuring in Isolated Cases With Pigmentary Features Only. *EBioMedicine.* 2016 May;7:212–20.
 74. Maruoka R, Takenouchi T, Torii C, Shimizu A, Misu K, Higasa K, et al. The Use of Next-Generation Sequencing in Molecular Diagnosis of Neurofibromatosis Type 1: A Validation Study. *Genet Test Mol Biomarkers.* 2014 Nov;18(11):722–35.
 75. van Minkelen R, van Bever Y, Kromosoeto JNR, Withagen-Hermans CJ, Nieuwlaet A, Halley DJJ, et al. A clinical and genetic overview of 18 years neurofibromatosis type 1 molecular diagnostics in the Netherlands. *Clin Genet.* 2014 Apr;85(4):318–27.
 76. Kluwe L, Siebert R, Gesk S, Friedrich RE, Tinschert S, Kehrer-Sawatzki H, et al. Screening 500 unselected neurofibromatosis 1 patients for deletions of the NF1 gene. *Hum Mutat.* 2004 Feb;23(2):111–6.
 77. Pasmant E, Sabbagh A, Spurlock G, Laurendeau I, Grillo E, Hamel M-J, et al. NF1 microdeletions in neurofibromatosis type 1: from genotype to phenotype. *Hum Mutat.* 2010 May;31(6):E1506–18.

78. Sloan JB, Fretzin DF, Bovenmyer DA. Genetic counseling in segmental neurofibromatosis. *J Am Acad Dermatol.* 1990 Mar;22(3):461-7.
79. Evans DG. Neurofibromatosis 2. GeneReviews®. University of Washington, Seattle; 1993.
80. Evans DgR. Neurofibromatosis type 2 (NF2): A clinical and molecular review. *Orphanet J Rare Dis.* 2009 Dec;4(1):16.
81. Halliday D, Emmanouil B, Pretorius P, MacKeith S, Painter S, Tomkins H, et al. Genetic Severity Score predicts clinical phenotype in NF2. *J Med Genet.* 2017;54(10):657-64.
82. Smith MJ, Urquhart JE, Harkness EF, Miles EK, Bowers NL, Byers HJ, et al. The Contribution of Whole Gene Deletions and Large Rearrangements to the Mutation Spectrum in Inherited Tumor Predisposing Syndromes. *Hum Mutat.* 2016 Mar;37(3):250-6.
83. Kluwe L, Mautner V, Heinrich B, Dezube R, Jacoby LB, Friedrich RE, et al. Molecular study of frequency of mosaicism in neurofibromatosis 2 patients with bilateral vestibular schwannomas. *J Med Genet.* 2003 Feb;40(2):109-14.
84. Moyhuddin A, Baser ME, Watson C, Purcell S, Ramsden RT, Heiberg A, et al. Somatic mosaicism in neurofibromatosis 2: Prevalence and risk of disease transmission to offspring. *J Med Genet.* 2003 Jun;40(6):459-63.
85. Evans DGR, Ramsden RT, Shenton A, Gokhale C, Bowers NL, Huson SM, et al. Mosaicism in neurofibromatosis type 2: an update of risk based on uni/bilaterality of vestibular schwannoma at presentation and sensitive mutation analysis including multiple ligation-dependent probe amplification. *J Med Genet.* 2007 Jan;44(7):424-8.
86. Evans D, Bowers N, Huson S, Wallace A. Mutation type and position varies between mosaic and inherited NF2 and correlates with disease severity. *Clin Genet.* 2013 Jun;83(6):594-5.
87. Northrup H, Wheless JW, Bertin TK, Lewis RA. Variability of expression in tuberous sclerosis. *J Med Genet.* 1993 Jan;30(1):41-33.
88. Sancak O, Nellist M, Goedbloed M, Elfferich P, Wouters C, Maat-Kievit A, et al. Mutational analysis of the TSC1 and TSC2 genes in a diagnostic setting: genotype – phenotype correlations and comparison of diagnostic DNA techniques in Tuberous Sclerosis Complex. *Eur J Hum Genet.* 2005 Jun;13(6):731-41.
89. Au KS, Williams AT, Roach ES, Batchelor L, Sparagana SP, Delgado MR, et al. Genotype/phenotype correlation in 325 individuals referred for a diagnosis of tuberous sclerosis complex in the United States. *Genet Med.* 2007 Feb;9(2):88-100.
90. Jones AC, Shyamsundar MM, Thomas MW, Maynard J, Idziaszczyk S, Tomkins S, et al. Comprehensive Mutation Analysis of TSC1 and TSC2—and Phenotypic Correlations in 150 Families with Tuberous Sclerosis. *Am J Hum Genet.* 1999 May;64(5):1305-15.
91. Dabora SL, Jozwiak S, Franz DN, Roberts PS, Nieto A, Chung J, et al. Mutational Analysis in a Cohort of 224 Tuberous Sclerosis Patients Indicates Increased Severity of TSC2, Compared with TSC1, Disease in Multiple Organs. *Am J Hum Genet.* 2001 Jan;68(1):64-80.
92. Rose VM, Au K-S, Pollom G, Roach ES, Prashner HR, Northrup H. Germ-Line Mosaicism in Tuberous Sclerosis: How Common? *Am J Hum Genet.* 1999 Apr;64(4):986-92.
93. Mosser J, Douar AM, Sarde CO, Kioschis P, Feil R, Mosser H, et al. Putative X-linked adrenoleukodystrophy gene shares unexpected homology with ABC transporters. *Nature.* 1993;361(6414):726-30.
94. McGuinness MC, Lu J-F, Zhang H-P, Dong G-X, Heinzer AK, Watkins PA, et al. Role of ALDP (ABCD1) and Mitochondria in X-Linked Adrenoleukodystrophy. *Mol Cell Biol.* 2003;23(2):744-53.
95. Wanders RJA, Waterham HR. Peroxisomal disorders: The single peroxisomal enzyme deficiencies. Vol. 1763, *Biochimica et Biophysica Acta - Molecular Cell Research.* 2006. p. 1707-20.
96. van Roermund CWT, Visser WF, IJlst L, van Cruchten A, Boek M, Kulik W, et al. The human peroxisomal ABC half transporter ALDP functions as a homodimer and accepts acyl-CoA esters. *FASEB J.* 2008;22(12):4201-8.
97. Mercer JFB. The molecular basis of copper-transport diseases. Vol. 7, *Trends in Molecular Medicine.* 2001. p. 64-9.
98. Singleton AB, Farrer MJ, Bonifati V. The genetics of Parkinson's disease: Progress and therapeutic implications. Vol. 28, *Movement Disorders.* 2013. p. 14-23.
99. Tanner CM, Ottman R, Goldman SM, Ellenberg J, Chan P, Mayeux R, et al. Parkinson disease in twins: An etiologic study. *J Am Med Assoc.* 1999;281(4):341-6.
100. Klein C, Schlossmacher MG. Parkinson disease, 10 years after its genetic revolution: Multiple clues to a complex disorder. Vol. 69, *Neurology.* 2007. p. 2093-104.
101. Sidransky E, Nalls MA, Aasly JO, Aharon-Peretz J, Annesi G, Barbosa ER, et al. Multicenter analysis of glucocerebrosidase mutations in Parkinson's disease. *N Engl J Med.* 2009;361(17):1651-61.
102. Murphy KE, Gysbers AM, Abbott SK, Tayebi N, Kim WS, Sidransky E, et al. Reduced glucocerebrosidase is associated with increased α -synuclein in sporadic Parkinson's disease. *Brain.* 2014;137(3):834-48.
103. Stefanis L. α -Synuclein in Parkinson's disease. *Cold Spring Harb Perspect Med.* 2012;2(2).
104. Polymeropoulos MH, Higgins JJ, Golbe LI, Johnson WG, Ide SE, Di Iorio G, et al. Mapping of a gene for Parkinson's disease to chromosome 4q21-q23. *Science (80-).* 1996;274(5290):1197-9.
105. Polymeropoulos MH, Lavedan C, Leroy E, Ide SE, Dehejia A, Dutra A, et al. Mutation in the α -synuclein gene identified in families with Parkinson's disease. *Science (80-).* 1997;276(5321):2045-7.
106. Funayama M, Hasegawa K, Kowa H, Saito M, Tsuji S, Obata F. A new locus for Parkinson's Disease (PARK8) maps to chromosome 12p11.2-q13.1. *Ann Neurol.* 2002;51(3):296-301.
107. Paisán-Ruiz C, Jain S, Evans EW, Gilks WP, Simón J, Van Der Brug M, et al. Cloning of the gene containing mutations that cause PARK8-linked Parkinson's disease. *Neuron.* 2004;44(4):595-600.
108. Trinh J, Zeldenrust FMJ, Huang J, Kasten M, Schaake S, Petkovic S, et al. Genotype-phenotype relations for the Parkinson's disease genes SNCA, LRRK2, VPS35: MDS- Gene systematic review. Vol. 33, *Movement Disorders.*

2018. p. 1857–70.

109. Healy DG, Falchi M, O'Sullivan SS, Bonifati V, Durr A, Bressman S, et al. Phenotype, genotype, and worldwide genetic penetrance of LRRK2-associated Parkinson's disease: a case-control study. *Lancet Neurol.* 2008;7(7):583–90.
110. Lücking CB, Dürr A, Bonifati V, Vaughan J, De Michele G, Gasser T, et al. Association between early-onset Parkinson's disease and mutations in the parkin gene. *N Engl J Med.* 2000;342(21):1560–7.
111. Doherty KM, Silveira-Moriyama L, Parkkinen L, Healy DG, Farrell M, Mencacci NE, et al. Parkin disease: A clinicopathologic entity? *JAMA Neurol.* 2013;70(5):571–9.
112. Valente EM, Abou-Sleiman PM, Caputo V, Muqit MMK, Harvey K, Gispert S, et al. Hereditary early-onset Parkinson's disease caused by mutations in PINK1. *Science* (80-). 2004;304(5674):1158–60.
113. Valente EM, Salvi S, Ialongo T, Marongiu R, Elia AE, Caputo V, et al. PINK1 mutations are associated with sporadic early-onset Parkinsonism. *Ann Neurol.* 2004;56(3):336–41.
114. Bonifati V, Rizzu P, Van Baren MJ, Schaap O, Breedveld GJ, Krieger E, et al. Mutations in the DJ-1 gene associated with autosomal recessive early-onset parkinsonism. *Science* (80-). 2003;299(5604):256–9.
115. Hague S, Rogaeva E, Hernandez D, Gulick C, Singleton A, Hanson M, et al. Early-onset Parkinson's disease caused by a compound heterozygous DJ-1 mutation. *Ann Neurol.* 2003;54(2):271–4.
116. Olesen J. The international classification of headache disorders. Vol. 48, *Headache.* 2008. p. 691–3.
117. Steiner TJ, Stovner LJ, Vos T. GBD 2015: migraine is the third cause of disability in under 50s. Vol. 17, *Journal of Headache and Pain.* 2016.
118. Wieser T, Mueller C, Evers S, Zierz S, Deufel T. Absence of known familial hemiplegic migraine (FHM) mutations in the CACNA1A gene in patients with common migraine: Implications for genetic testing. *Clin Chem Lab Med.* 2003;41(3):272–5.
119. Kirchmann M, Thomsen LL, Olesen J. The CACNA1A and ATP1A2 genes are not involved in dominantly inherited migraine with aura. *Am J Med Genet - Neuropsychiatr Genet.* 2006;141 B(3):250–6.
120. Tan RYY, Markus HS. CADASIL: Migraine, encephalopathy, stroke and their inter-relationships. *PLoS One.* 2016;11(6).