

# Bölüm 5

## AĞRI GENETİĞİ

Duygu ONUR CURA<sup>1</sup>

### GİRİŞ

Ağrı, fiziksel, duygusal, davranışsal ve sosyokültürel faktörlerin karmaşık etkileşimleriyle şekillenen bir deneyimdir (1). Birçok hastalığın ana bileşeni olup poliklinik başvurularında karşılaşılan en sık semptomlardan biridir. Araştırmalar, toplumun % 15–50'sinin yaşamının herhangi bir döneminde ağrı deneyimlediğini göstermektedir (2). Ağrıya neden olan uyaranlar, nosiseptörler denilen periferik ağrı reseptörleri tarafından tespit edilir ve bu nosiseptif sinyaller aksonlarla beyine iletilerek ağrı olarak algılanır. Bu bölümde, genetik temelleri bilinen ailesel ağrı sendromları yanı sıra çok sayıda gendeki varyantlarla ilişkilendirilmiş kronik ağrı durumları, temporomandibular eklem hastalıklarının genetik temeli ve epigenetik değişikliklerin ağrıdaki rolü güncel genetik çalışmalar ışığında irdelenmiştir.

### AĞRI VE GENETİK

Ağrı, dokusal bütünlüğün zarar görmesine neden olabilecek dış etkenlere karşı doğal bir koruyucu mekanizma olarak görev yaparken ağrının kronik formu, içsel patoloji işareti olarak görülür ve bireylerin işlevselliğini olumsuz yönde etkiler (3). Ağrı algısı, bireyler arasında farklılıklar göstermektedir. Bu farklılıklar cinsiyetler arasında belirgin olduğu gibi ırk ve etnik kökenle de ilişkili olduğu gösterilmiştir (2). Ayrıca çeşitli ağrı durumlarında, genetik olarak tanımlanmış farklı periferik nöron gruplarının ve mekanizmaların rol aldığı bilinmektedir (4).

Genomdaki varyasyonlar, bireyler arasındaki farklılıkların temelini oluşturmaktadır. Bu varyasyonlardan en yaygın olanı tek nükleotid değişiklikleridir (SNP: Single Nucleotide Polimorphism). Genomda belli bir yerdeki bir nükleoti-

<sup>1</sup> Tıbbi Genetik Uzmanı, Dokuz Eylül Üniversitesi Sağlık Bilimleri Enstitüsü, Moleküler Tıp Anabilim Dalı, duyguonur\_05@hotmail.com

## KAYNAKLAR

1. Schmid AB, Adhikari K, Ramirez-Aristeguieta LM, et al. Genetic components of human pain sensitivity: a protocol for a genome-wide association study of experimental pain in healthy volunteers. *BMJ Open*. 2019;9(4):e025530. doi:10.1136/bmjopen-2018-025530.
2. Young EE, Lariviere WR, Belfer I. Genetic basis of pain variability: recent advances. *J Med Genet*. 2012;49(1):1-9. doi:10.1136/jmedgenet-2011-100386.
3. Sexton JE, Cox JJ, Zhao J, et al. The Genetics of Pain: Implications for Therapeutics. *Annu Rev Pharmacol Toxicol*. 2018;58:123-142. doi:10.1146/annurev-pharmtox-010617-052554.
4. Minett MS, Nassar MA, Clark AK, et al. Distinct Nav1.7-dependent pain sensations require different sets of sensory and sympathetic neurons. *Nat Commun*. 2012;3:791. doi:10.1038/ncomms1795.
5. Nussbaum RL, McInnes RR, Willard HF. (2016). Human Genetic Diversity: Mutation and Polymorphism. In. *Thompson & Thompson Genetics in Medicine* (8th ed., pp. 43-57). Canada: Elsevier Inc.
6. Strachan T, Read AP. (2011). Human Genetic Variability and Its Consequences. In. *Human Molecular Genetics* (4th ed., pp. 405-441). United States: Garland Science/Taylor & Francis Group.
7. Nussbaum RL, McInnes RR, Willard HF. (2016). The Human Genome: Gene Structure and Function. In. *Thompson & Thompson Genetics in Medicine* (8th ed., pp. 21-43). Canada: Elsevier Inc.
8. Lodish H, Berk A, Kaiser CA, et al. (2013). Epigenetic regulation of Transcription. In. *Molecular Cell Biology* (7th ed., pp. 327-336). United States: W.H. Freeman and Company.
9. Belfer I. Nature and nurture of human pain. *Scientifica* (Cairo). 2013;2013:415279. doi:10.1155/2013/415279.
10. Denk F, McMahon SB, Tracey I. Pain vulnerability: a neurobiological perspective. *Nat Neurosci*. 2014;17(2):192-200. doi:10.1038/nn.3628.
11. Zorina-Lichtenwalter K, Meloto CB, Khoury S, et al. Genetic predictors of human chronic pain conditions. *Neuroscience*. 2016;338:36-62. doi:10.1016/j.neuroscience.2016.04.041.
12. Cox JJ, Kurth I, Woods CG (2019) Human Genetics of Pain. In: Wood JN, editor. *The Oxford Handbook of the Neurobiology of Pain*.
13. James S. Human pain and genetics: some basics. *Br J Pain*. 2013;7(4):171-178. doi:10.1177/2049463713506408.
14. Nahorski MS, Chen YC, Woods CG. New Mendelian Disorders of Painlessness. *Trends Neurosci*. 2015;38(11):712-724. doi:10.1016/j.tins.2015.08.010.
15. Young EE, Kelly DL, Shim I, et al. Variations in COMT and NTRK2 Influence Symptom Burden in Women Undergoing Breast Cancer Treatment. *Biol Res Nurs*. 2017;19(3):318-328. doi:10.1177/1099800417692877.
16. Hu B, Zhang X, Xu G, et al. Association between COMT Polymorphism Val158Met and Opioid Consumption in Patients with Postoperative Pain: A Meta-Analysis. *Neurosignals*. 2018;26(1):11-21. doi:10.1159/000487038.
17. Albury CL, Stuart S, Haupt LM, et al. Ion channelopathies and migraine pathogenesis. *Mol Genet Genomics*. 2017;292(4):729-739. doi:10.1007/s00438-017-1317-1.
18. Skerratt SE, West CW. Ion channel therapeutics for pain. *Channels* (Austin). 2015;9(6):344-351. doi:10.1080/19336950.2015.1075105.
19. Carreno O, Corominas R, Fernandez-Morales J, et al. SNP variants within the vanilloid TRPV1 and TRPV3 receptor genes are associated with migraine in the Spanish population. *Am J Med Genet B Neuropsychiatr Genet*. 2012;159B(1):94-103. doi:10.1002/ajmg.b.32007.
20. Binder A, May D, Baron R, et al. Transient receptor potential channel polymorphisms are associated with the somatosensory function in neuropathic pain patients. *PLoS One*. 2011;6(3):e17387. doi:10.1371/journal.pone.0017387.

21. Bennett DL, Woods CG. Painful and painless channelopathies. *Lancet Neurol.* 2014;13(6):587-599. doi:10.1016/S1474-4422(14)70024-9.
22. Kurzawski M, Rut M, Dziejewski V, et al. Common Missense Variant of SCN9A Gene Is Associated with Pain Intensity in Patients with Chronic Pain from Disc Herniation. *Pain Med.* 2018;19(5):1010-1014. doi:10.1093/pm/pnx261.
23. Duan G, Xiang G, Guo S, et al. Genotypic Analysis of SCN9A for Prediction of Postoperative Pain in Female Patients Undergoing Gynecological Laparoscopic Surgery. *Pain Physician.* 2016;19(1):E151-162.
24. Duan G, Han C, Wang Q, et al. A SCN10A SNP biases human pain sensitivity. *Mol Pain.* 2016;12. doi:10.1177/1744806916666083.
25. Ambrosini A, D'Onofrio M, Buzzi MG, et al. Possible Involvement of the CACNA1E Gene in Migraine: A Search for Single Nucleotide Polymorphism in Different Clinical Phenotypes. *Headache.* 2017;57(7):1136-1144. doi:10.1111/head.13107.
26. Nielsen LM, Christrup LL, Sato H, et al. Genetic Influences of OPRM1, OPRD1 and COMT on Morphine Analgesia in a Multi-Modal, Multi-Tissue Human Experimental Pain Model. *Basic Clin Pharmacol Toxicol.* 2017;121(1):6-12. doi:10.1111/bcpt.12757.
27. Manfredini D, Guarda-Nardini L, Winocur E, et al. Research diagnostic criteria for temporomandibular disorders: a systematic review of axis I epidemiologic findings. *Oral Surg Oral Med Oral Pathol Oral Radiol Endod.* 2011;112(4):453-462. doi:10.1016/j.tripleo.2011.04.021.
28. Graff-Radford SB, Abbott JJ. Temporomandibular Disorders and Headache. *Oral Maxillofac Surg Clin North Am.* 2016;28(3):335-349. doi:10.1016/j.coms.2016.03.004.
29. Michelotti A, Liguori R, Toriello M, et al. Catechol-O-methyltransferase (COMT) gene polymorphisms as risk factor in temporomandibular disorders patients from Southern Italy. *Clin J Pain.* 2014;30(2):129-133. doi:10.1097/AJP.0b013e318287a358.
30. Smith SB, Mir E, Bair E, et al. Genetic variants associated with development of TMD and its intermediate phenotypes: the genetic architecture of TMD in the OPPERA prospective cohort study. *J Pain.* 2013;14(12 Suppl):T91-101 e101-103. doi:10.1016/j.jpain.2013.09.004.
31. Bonato LL, Quinelato V, Pinheiro Ada R, et al. ESRRB polymorphisms are associated with comorbidity of temporomandibular disorders and rotator cuff disease. *Int J Oral Maxillofac Surg.* 2016;45(3):323-331. doi:10.1016/j.ijom.2015.10.007.
32. Smith SB, Reenila I, Mannisto PT, et al. Epistasis between polymorphisms in COMT, ESR1, and GCH1 influences COMT enzyme activity and pain. *Pain.* 2014;155(11):2390-2399. doi:10.1016/j.pain.2014.09.009.
33. Smith SB, Maixner DW, Greenspan JD, et al. Potential genetic risk factors for chronic TMD: genetic associations from the OPPERA case control study. *J Pain.* 2011;12(11 Suppl):T92-101. doi:10.1016/j.jpain.2011.08.005.
34. Furquim BD, Flamengui LMSP, Repeke CEP, et al. Influence of TNF-alpha-308 G/A gene polymorphism on temporomandibular disorder. *American Journal of Orthodontics and Dentofacial Orthopedics.* 2016;149(5):692-698. doi:10.1016/j.ajodo.2015.10.026.
35. Xiao JL, Meng JH, Gan YH, et al. Association of GDF5, SMAD3 and RUNX2 polymorphisms with temporomandibular joint osteoarthritis in female Han Chinese. *J Oral Rehabil.* 2015;42(7):529-536. doi:10.1111/joor.12286.
36. Slade GD, Smith SB, Zaykin DV, et al. Facial pain with localized and widespread manifestations: separate pathways of vulnerability. *Pain.* 2013;154(11):2335-2343. doi:10.1016/j.pain.2013.07.009.
37. Sanders AE, Jain D, Sofer T, et al. GWAS Identifies New Loci for Painful Temporomandibular Disorder: Hispanic Community Health Study/Study of Latinos. *J Dent Res.* 2017;96(3):277-284. doi:10.1177/0022034516686562.
38. Niederberger E, Resch E, Parnham MJ, et al. Drugging the pain epigenome. *Nat Rev Neurol.* 2017;13(7):434-447. doi:10.1038/nrneuro.2017.68.

39. Gombert S, Rhein M, Eberhardt M, et al. Epigenetic divergence in the TRPA1 promoter correlates with pressure pain thresholds in healthy individuals. *Pain*. 2017;158(4):698-704. doi:10.1097/j.pain.0000000000000815.
40. Odell DW. Epigenetics of pain mediators. *Curr Opin Anaesthesiol*. 2018;31(4):402-406. doi:10.1097/ACO.0000000000000613.
41. Cheng YY, Kao CL, Ma HI, et al. SIRT1-related inhibition of pro-inflammatory responses and oxidative stress are involved in the mechanism of nonspecific low back pain relief after exercise through modulation of Toll-like receptor 4. *J Biochem*. 2015;158(4):299-308. doi:10.1093/jb/mvv041.
42. Lopez-Gonzalez MJ, Landry M, Favereaux A. MicroRNA and chronic pain: From mechanisms to therapeutic potential. *Pharmacol Ther*. 2017;180:1-15. doi:10.1016/j.pharmthera.2017.06.001.
43. Pereira CM, Sehnem D, da Fonseca EO, et al. miRNAs: Important Targets for Oral Cancer Pain Research. *Biomed Res Int*. 2017;2017:4043516. doi:10.1155/2017/4043516.
44. Liang L, Lutz BM, Bekker A, et al. Epigenetic regulation of chronic pain. *Epigenomics*. 2015;7(2):235-245. doi:10.2217/epi.14.75.