

# BÖLÜM 1

## COVID-19 VE AŞILAR

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### GİRİŞ

Çin'in Wuhan kentinde yeni beta-koronavirüs (SARS-CoV-2) ile ilişkili pnömoni vakaları ilk olarak Kasım 2019'da tespit edilmiştir.<sup>1</sup> Hastalardan alınan bronko-alveoler lavaj sıvısı örneklerinden virüs izolasyonu, PCR ve tam genom sekans analizi yapılmış ve etken Dünya Sağlık Örgütü (DSÖ) tarafından 2019-yeni koronavirüs (2019-nCoV) olarak isimlendirilmiştir.<sup>2</sup> Çin'den başlayarak birçok ülkeye yayılmasıyla DSÖ tarafından 11 Mart 2020 tarihinde pandemi ilan edildi. Günümüz itibariyle dünyada toplam 233.127.914 vaka ve 4.770.204 ölüm bulunmaktadır.<sup>3</sup> Virüsün genetik sekansı 10 Ocak 2020 tarihinde yayınlandıktan sonra hastalık için ilk aşı denemeleri (NCT04283461) Mart 2020'de başladı.<sup>4</sup> Bu tarihten itibaren aşı çalışmaları hız kazanmış olup güncel veriler doğrultusunda dünya genelinde faz 1 aşamasında 54, faz 2 aşamasında 47 faz 3 aşamasında 35, ruhsatlı 13 ve tam kullanım için onaylanmış 8 aşı çalışması bulunmaktadır.<sup>5</sup> Dünya genelinde halka açık 20 çeşit aşı mevcut ve 180 ülkede 6.13 milyar dozdan fazla COVID-19 aşısı uygulanmıştır.<sup>6</sup>

### ETİYOLOJİ VE EPİDEMİYOLOJİ

Koronavirüsler *Coronaviridae* ailesi, *Orthocoronavirinae* alt ailesinde *Alfa-*, *Beta-*, *Gamma-* ve *Deltacoronavirus* olarak 4 cinse ayrılmıştır. İnsan patojenlerini kapsayan alfa- ve beta- alt ailelerindeki HCoV-229E (alfaCoV), HCoV-NL63 (alfaCoV), HCoV-OC43 (betaCoV) ve HCoV-HKU1 (betaCoV) hafif solunum yolu enfeksiyonuna ve pnömونيye, SARS-CoV-1 (betaCoV), SARS-CoV-2 (betaCoV) ve MERS-CoV (betaCoV) ise şiddetli solunum yolu enfeksiyonuna neden olarak büyük salgın ve pandemilere neden olmaktadır.<sup>7</sup> Büyük yapılı (80-200 nm) virion zarflı olup genomu pozitif polariteli, tek iplikçikli, 20-32 kb uzunluğunda linear RNA karakterindedir. SARS-CoV-2 genomu, çoğu bilinmeyen işlevlere sahip 11 açık okunabilir bölgeyi (open reading frame-ORF) barındırır (Şekil 1). Genomun

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## SONUÇ

COVID-19 enfeksiyonu hızla yayılmaya ve toplum sağlığını tehdit etmeye devam etmektedir. Her ne kadar virüs varyantlarının yayılmasını önlemeye yönelik politikalar uygulansa da, RNA virüsünün yüksek mutasyon oranı ve varyantlarının hızla ortaya çıkması neticesinde gelecekteki varyantların erken tanımlanması için genomik sürveyans çalışmalarının yapılması büyük önem arz etmektedir. Aşı etkinliğini değerlendirmek için mevcut ve gelecekteki olası varyantlara karşı nötralize edici aktiviteyi ortaya çıkarmak enfeksiyonları önlemek için bir zorunluluk olarak kabul edilmektedir. Virüsün yayılmasını yavaşlatmak için önemli düzeyde toplum bağışıklığını (en az %60 aşılama) elde etmeye odaklanılmalıdır.

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