

Enflamasyon ve Kronik Enterik Enfeksiyonlarda Bağırsak Mikrobiyomu

Arpita Aditya, Catherine Galleher, Yeal Ad, Mitchell Coburn ve Aaron Zweig

1. Giriş

İnsan vücutu, kendi hücrelerinden ortalama 10 kat fazla olan yaklaşık 10.000 türde trilyonlarca mikroorganizma barındırır (Eckburg ve ark. 2005; Savage 1977). Bu mikroplar topluca insan mikrobiyomu olarak bilinir ve bunlar genellikle insan vücudunun olası her bölümünde uyum içinde yaşayan bakterileri, virusleri, protozoaları ve mantarları içerir; mikrobiyom, insan beyninin ağırlığından 2 kg daha ağırdır (Hallen-Adams ve Suhr 2016). İnsan vücudunun yaklaşık %2'sini oluşturan küçük bir kiracı olan bu mikroorganizmalar, konakçıya bazen "ekstra organ" olarak kabul edilen pek çok fayda sağlar. İnsan Mikrobiyom Projesi (HMP), insan bağırsak mikrobiyotası hakkında kapsamlı bilgi edinmek için 2007 yılında başlatılmıştır. HMP'nin sonuçlarının, mikrobiyomun insan sağlığı, bağışıklık, beslenme ve hastalıktaki rolünün daha iyi bir açıklamasını vermesi beklenmektedir.

Sağlıklı bir şekilde dengelenmiş bir bağırsak mikroflorası; bağırsak bariyer fonksiyonunun korunmasına, bağışıklık sistemini eğitmeye ve olgunlaştmaya, iltihabı önlemeye, besinler ve reseptör proteinler için patojenlere karşı doğrudan rekabet etmeye, hormon ve vitaminler (örneğin, K vitamini, biyotin ve folat) üretmeye yardımcı olur (Marchesi 2014). ; McKenney ve Pamer 2015). Üç ana bileşen (konak bağışıklığı, patojen ve konağın bağırsak mikrobiyotası) arasındaki karmaşık sürekli etkileşim, enterik enfeksiyonlara yol açabilir. Karmaşık etkileşimin verimliliğine bağlı olarak, enterik enfeksiyon çözülebilir veya enfekte konağın kronik patojen kolonizasyonuna ve hatta konağın ölümüne yol açabilir (Sekirov ve Finlay 2009). Bağırsak mikrobiyotası, bellenmedik bir şekilde patojenlerin kolonizasyonunu destekleyen metabolitler üreterek akut veya kronik enterik enfeksiyonları teşvik edebilir. Simbiyotik *Bacteroides thetaiotaomicron*, *Clostridium rodentium*'u rekabetçi bir şekilde dışlayabilir, ancak bağırsak epitel dokusunun müsinin sialik asit parçalarından süksinat üreterek *Clostridium difficile*'nin kolonizasyonuna yardımcı olabilir (Ferreyra ve diğerleri 2014; Ng ve diğerleri. 2013; Rolhion ve Chassaing 2016). *C. difficile* ayrıca bağırsak ortamındaki endosporlardan gelişmek için safra tuzunu da kullanabilir (Giel ve ark. 2010). Dihidrojen ve etanolamin (bir nitrojen kaynağı olarak) gibi bağırsak mikrobiyomunun çeşitli diğer

kan sonuçlar, gıda alerjileri ve hassasiyetlerinin kaynağı olarak bağırsak mikrobiyomunu işaret etmeye devam etmektedir. Bağırsak bariyerinin nasıl çalıştığını ve nasıl hasar görebileceğini anlamak, alerjilerin nasıl ortaya çıktığını açıklayabilir. Bu aynı zamanda romatoid artrit ve lupus gibi otoimmün hastalıkların daha iyi anlaşılmasını sağlayabilir (Mudd ve Brenchley 2016). Bu, bugünün tedavi edilemeyen hastalıklarına gelecekte çare bulma umidini göstermektedir.

5. Sonuç

İnsan vücutunun önemli bir bileşeni olarak bağırsak mikroorganizmalarının rolü, sağlık ve hastalıklarda daha belirgin hale gelmektedir. Bunların uygun biyoaktif metabolitler ve farmabiyotik molekül kaynakları oldukları zaten tespit edilmiştir. Ancak belirtmek gerekmek, insan modellemesi olmadıkları için bugüne kadar edindiğimiz bilgiler öncelikle *in vitro* ve *in vivo* hayvan modeli çalışmalarına dayanmaktadır. Bir insan vücutu, bağılıklık sistemindeki, genetik arka plandaki, çevredeki, yaştaşı, bağırsak yapısındaki ve en önemlisi, kronik metabolik hastalıklardan nöronal bozukluklara kadar birçok komplikasyona yol açabilen yerli bağırsak mikrobiyal bileşimindeki varyasyonla ilişkili olabilecek bağırsak mikrobiyal bileşiminde oluşan herhangi bir bozulmaya farklı tepkiler gösterir. İnsanlarda mikrobiyal kolonizasyon tarihinin tam olarak anlaşılmasının, öbiyozu sürdürmek ve birçok istenmeyen hastalığı önlemek için etkili stratejiler tasarlamaya yardımcı olacağı varsayılmaktadır.

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