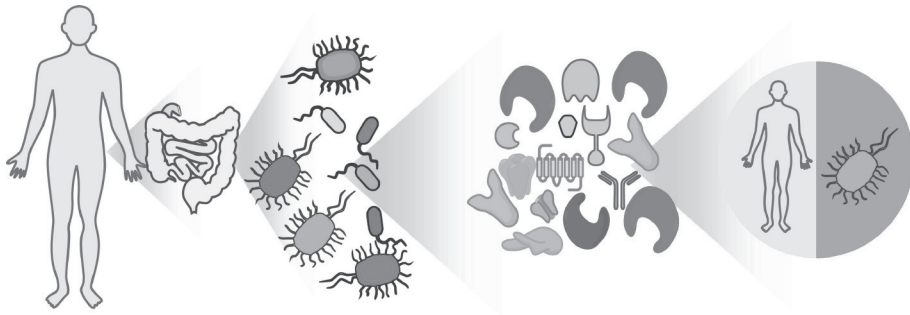


Proteomik Arařtırmalarının Konak Baęırsak Mikrobiyotasına Etkisi

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1. Giriř

Mikroplar tm ekosistemlerde bulunur ve biyojeokimyasal dng ile insan saęlıęında nemli roller oynarlar. İnsan vcudu, vcudun farklı kısımlarını kolonize eden trilyonlarca mikrobun varlıęında iřlev grr. Ortalama bir insan vcudunda tahmini 37 trilyon hcre vardır ve mikrobiyomun biraz daha fazla hcreden oluřtuęu ve ortalama sayının 39 trilyon olduęu tahmin edilmektedir (Sender ve ark. 2016). İnsan baęırsaęının mikroplar tarafından kolonizasyonu, insan ve baęırsak mikrobiyotası arasındaki iliřkinin birlikte evriminin bir sonucudur (řekil 1). İnsan baęırsaęında bulunan mikroplar "baęırsak mikrobiyotası" ve bunlar tarafından ifade edilen genler veya proteinler "baęırsak mikrobiyomu" olarak adlandırılır (Turnbaugh ve ark.2006,2007). Genel olarak, bu tr iliřkiler simbiyotiktir ve baęırsak, mikrobiyal hcreler ile konakçı hcreler arasında dinamik bir etkileřim iin karmařık bir ortam saęlar (Moeller ve ark. 2016). Bu etkileřim, normal doęum sonrası geliřimden yetiřkin saęlıęına kadar insan fiziolojisinin birok ynn modle eder (Moeller ve dięerleri 2016; Gordo 2019).



řekil 1. İnsan baęırsaęı mikrobiyomu analizi tipik olarak, baęırsaktan izolatların (Tablo 1'de mukozal lmen ara yznn dıřkı malzemeleri) rneklenmesi yoluyla gerekleřtirilir. Ortaya ıkan protein izolatları, insan hcrelerinin yanı sıra karmařık bir bakteri topluluęundan elde edilir.

İnsan saęlıęı, baęırsakta yařayan mikropların bileřiminden olumlu veya olumsuz etkilenebilir (Mohajeri ve ark. 2018). Deęiřen baęırsak mikrobiyomları obezite, diya-

belirlemek için kritik adımlardır. Bu, doldurulması zor bir alandır ve büyük işbirlikçi çabalar gerektirecektir. Peptitlerin tandem MS spektral kütüphanelerini oluşturmak ve kullanmak için çabalara ihtiyaç vardır. Ayrıca protein ekstraksiyonu, LC-MS numune hazırlama, depolama ve LC-MS verilerinin biyoinformatik analizi de dahil olmak üzere bağırsak mikrobiyolojik analizi için proteomik iş akışını standartlaştırmaya ihtiyaç vardır. Mikrobiyom alanında proteomik uygulamaların çoğaldığına dair şüphe yoktur, ancak bu tekniğin potansiyel faydalarını tam olarak gerçekleştirmek için ele alınması gereken birçok zorluk vardır. Yüksek kaliteli ve kapsamlı bir spektral kütüphane veritabanı oluşturmak ve mevcut iş akışlarına tutarlı spektral kütüphane arama araçlarını eklemek, bu alanı ilerletmek için kritik öneme sahiptir. Bağırsak mikrobiyotası ve insan sağlığı arasındaki bağlantıya dair artan kanıtlarla birlikte, gelecekteki çalışmalar, bağırsak mikrobiyotası ve mikrobiyom temelli terapötiklerin geliştirilmesi hakkında işlevsel bilgiler sağlamak için sıralı genomların ve spektral kütüphane veritabanlarının artan kullanılabilirliği ile birlikte gelişmiş analitik ve hesaplama araçlarından tam olarak yararlanacaktır.

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