Tracking sources of blood meals using unidentified tandem mass spectral libraries

Abstract:

Identifying the species on which hematophagous arthropods feed is crucial for studying the factors that affect pathogen distributions and that can aid public health. Here we describe a protocol to identify the species a parasitic arthropod has previously fed upon by identifying the source of the remnants of a previous blood meal via shotgun proteomics and spectral matching. The protocol is a nontargeted approach that uses the entire detected blood proteome for source identification; it does not require a priori knowledge of genome or protein sequences. Instead, reference spectral libraries are compiled from the blood of multiple host species by using SpectraST, which takes ∼4 d; the identification of the species from which a previous blood meal of a hematophagous arthropod was taken is achieved with spectral matching against the reference spectral libraries, which takes approximately another 4 d. This method is robust against random degradation of the blood meal and can identify unknown blood remnants months after the feeding event.