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Experimental Diagenesis of Proteins Fossilizing in Tree Resin

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DNA sequencing has revolutionized our understanding of microbial life on Earth, but the reach of this revolution into the geologic past has been limited. DNA is diagenetically degraded relatively quickly and it can be difficult to distinguish authentic ancient molecules from younger contamination. For lipids, taxonomic resolution can be limited, leaving ambiguities about the connections between environment and organisms. Proteins, like DNA, can preserve taxonomic and metabolic information but are more durable over geologic time in a variety of depositional contexts. However, the use of protein molecular fossils as recorders of microbial evolution and as environmental proxies is in its infancy. There is an outstanding need in the field for methods to discriminate truly ancient proteins from modern contamination, which hinges on a clearer molecular-level understanding of protein diagenesis in a wider array of preservational settings. The preservation of proteins might be maximized in certain especially durable geologic archives, such as amber (fossil tree resin), where they are isolated from diagenetic alteration. Previous work has successfully isolated amino acids from amber, which suggests that higher-molecular weight protein may survive as well. In this project, we analyzed natural sub-fossil resin samples and experimentally encased protein in tree resin to develop protein isolation and sequencing methods and understand protein diagenesis in fossil resins. Preliminary results indicate that proteins can be extracted and sequenced from fossil resins, suggesting that amber may preserve valuable molecular fossil records of ancient microbial taxa and past environments.