Project summary

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Overview.
Integrating the cross-scale drivers of the distribution of biodiversity requires an understanding of both how that biodiversity evolved and how it changes in the ecological present. Evolution is the context within which ecological processes take place: there can be no macro-scale synthesis of present-day ecology without addressing its evolutionary context. This proposal will integrate local-scale ecological community assembly with macro-scale regional assembly and trait evolution. Specifically, the proposal's three key scientific objectives are:

1. Assemble novel phylogenies and functional trait databases that subsequent analyses depend upon
2. Quantify the role of macro-scale ecological processes and evolutionary constraints in determining the local-scale composition of plant, beetle, mammal, and bird communities across North America
3. Model the evolution, and so make better predictions of ecological pattern, of cross-trophic interactions and co-occurrences in plant–beetle and mammal–tick assemblages across North America

Intellectual merit.
Biologists have long-recognized that present-day ecological processes operate within the context of past evolutionary history. For example, in biogeography, great progress has been made quantifying the extent to which the evolutionary origin of species affects the ecological niche(s) and distributions species occupy today, but progress in community ecology has been more mixed. Community ecologists have tried to incorporate evolutionary dynamics through eco-phylogenetic (or community phylogenetic) analyses, but the field has had difficulty moving from correlative studies to generate mechanistic insights. Addressing this challenge requires a synthetic framework that integrates differing mechanisms of the macro-evolution of species' traits with macro- and local-scale assembly processes based upon those traits. This proposal uses phylogeny as a lynch-pin to both construct and empirically test such a synthetic framework. Going further, this framework will also be used to advance the study of cross-guild interactions. Biologists are frequently forced to overlook temporal and spatial variation in species' interactions and associations, assuming that species that do not interact have not evolved to do so. Using this proposal's synthetic framework, it is possible to examine of the evolution of interactions within the context of ecological opportunity to interact. This will provide critical insight into how cross-guild interactions evolve and ecologically assemble.

Broader impacts.
This proposal will enhance infrastructure for research, contribute to pest monitoring, and engage under-represented groups in science. As species move ever-more freely around the globe in the Anthropocene, there is a growing need for prediction of interactions and community structure in under-studied species. Objective 3 (see "Overview"), by focusing on phylogeny, will allow for policy-relevant prediction of beetle pests (relevant for ecosystem services) and mammal parasites (relevant for human health), even in unstudied species. Objective 1 (see "Overview") will result in the release of data to support further fundamental and applied research into the macro-scale distribution and structure of biodiversity. Finally, this proposal will enhance Utah State University's Native American STEM Mentorship Program (NASMP), helping members of this group that has been historically under-represented within STEM complete four-year degree programs. Members of the project team will mentor NASMP participants, teaching a data science course focused on using NEON data and helping them complete a research project using NEON data. This program will culminate in a trip to the Moab NEON site, giving students an insight into both the analysis and collection of macro-scale data.