Non-technical abstract for NSF DEB-2127744

Bees are vitally important to agriculture, food security, and the preservation of natural ecosystems due to their pollination services. Over 85% of the 325,000 flowering plant species on the planet depend on animal pollination and the vast majority is carried out by bees. In the U.S.A. alone bees are responsible for the commercial production of 130 crop plants, generating over $11 billion in annual revenue. The value of bees to nature and human well-being is abundantly clear. The partnership between bees and flowering plants formed over 100 million years ago, and since that time, bees have radiated globally into an astounding 20,000+ different species, many of which are specialist pollinators of particular plant species or families. The study of bee biodiversity is urgently needed because there is growing evidence that some bee species are in decline and baseline knowledge of bee diversity, distribution, and family relationships is incomplete. The Bees of the World project has the potential to significantly improve knowledge of bee biodiversity and to establish a guide to interpret key traits of bees, such as their host-plant associations. By utilizing recent advances in DNA sequencing technology, a comprehensive tree-of-life for bees will be generated for the first time, providing a framework from which to study bee diversity and their relationships with plants. To disseminate results and general bee knowledge, the project will engage in multiple outreach efforts with professional and non-professional audiences. Activities include creation of a virtual bee course, teaching of a molecular methods workshop, and, in collaboration with the Natural History Museum of Utah, development of exhibits and youth education activities focused on pollinators.

The project will use cutting edge molecular and analytical methods and engage a global network of collaborators to assemble a comprehensive phylogenomic dataset for bees. The project aims are to: (1) resolve remaining uncertainties in higher-level bee phylogeny and classification, (2) incorporate fossils to reconstruct the global biogeographic history of bees, revealing the origin and spread of bee diversity over time, and (3) analyze patterns of host-plant use across bees and at lower taxonomic levels, revealing how host-plant specialization has evolved and impacted rates of diversification. To resolve the phylogeny of bees with improved confidence, the research team will use next-generation DNA sequencing approaches and novel laboratory methods to sequence bee species from across the globe. The project will generate low coverage genomes for most bee genera and ultraconserved element (UCE) data for over 3,000 species, filling in sampling gaps. The resulting bee phylogeny will serve as a framework to study bee classification, biogeography, and host-plant evolution. Comprehensive databases of bee fossil, distribution, and host-plant information will be created and made available to other researchers. Combining results from each component of the project will provide a comprehensive understanding of how bees have diversified and dispersed over time and how their partnership with plants has shaped their evolutionary trajectory.