A new international study co-authored by a University of Florida researcher describes one of the most comprehensive analyses of Lepidoptera evolutionary relationships to date, and could have broad implications in the fields of genetics, agriculture and conservation.

With nearly 175,000 described species serving as herbivores, pollinators and prey, Lepidoptera affect humans as agricultural pests and essential pollinators for production of many food crops, said co-author Akito Kawahara, assistant curator of Lepidoptera at the Florida Museum of Natural History's McGuire Center for Lepidoptera and Biodiversity on the UF campus.

"The new study provides one of our best estimates of the evolutionary relationships of butterflies and moths," Kawahara said. "When trying to conserve a butterfly or moth species, the biology of that particular species might not be well known because it's so rare, but if you have a family tree, you can infer these traits based on closely related species."

The study, funded by the National Science Foundation's Assembling the Tree of Life program, was authored by 16 researchers from five countries. The researchers collected and analyzed DNA sequences of 483 taxa spanning 115 families of the Ditrysia group, which comprises about 98 percent of described butterfly and moth species. Each specimen was chosen to represent a major family of butterflies or moths.

Kawahara collected specimens and assisted with DNA sequence analysis as a doctoral candidate at the University of Maryland. Published online in the journal PLOS One March 12, the study shows molecular evidence broadly supports the relationships determined by analyzing physical features, but more extensive data is needed to gain complete understanding of Lepidoptera evolution, Kawahara said.

"A big chunk of the tree is still largely uncertain," Kawahara said. "The collaborative team has made major headway, but there's still more to do."

Provided by University of Florida