Wireworms are a common soil-dwelling pest of corn (*Zea mays* L.) in the midwestern United States. Wireworms are a problematic group to control and study due to the difficulty involved in identification. The objectives of our research are to identify morphologically cryptic species of wireworms using molecular diagnostic techniques, construct a phylogeny of economically important wireworm species, and determine the genetic structure of *Melanotus depressus* populations in the Midwest. Wireworms were collected from a wide variety of locations through the midwestern United States. Adult museum specimens were sequenced for the identification of cryptic larvae. Using polymerase chain reaction, the cytochrome oxidase I gene gene from mtDNA was sequences from over 300 individuals. The species analyzed include all economically important members of the genus *Melanotus* as well as *Conoderus lividus*. The morphologically cryptic species were successfully separated using nucleotide *p*-distances, and the sequences were then used in phylogenetic analyses. Maximum parsimony, maximum likelihood, and minimum evolution trees were constructed. Molecular data exhibited convergence with morphological data. *M. depressus* population structure was analyzed using analysis of molecular variance. There was more genetic variation within populations than among populations. Our results suggest that wireworms may disperse through mechanisms other than simple flight. The data presented here represent an initial phylogenetic hypothesis concerning economically important wireworms, as well as an initial view of *M. depressus* populations in the Midwest. Our results indicate that the mitochondrial COI gene provides a fast and accurate method of separating morphologically cryptic wireworm species. By increasing the ease and accuracy of identification, we hope to facilitate further investigations into their biology and control.