

# DNA Barcode of Thief Ant Complex (Hymenoptera: Formicidae)<sup>1</sup>

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**Abstract** The thief ant, *Solenopsis molesta* (Say), a common nuisance species found throughout the United States is genetically related to red imported fire ants, *S. invicta* Buren. Therefore, its identification at the molecular level is very important. The deoxyribonucleic acid (DNA) barcoding, a recent technique was used to identify thief ant complex at species and subspecies levels using a short DNA sequence from the cytochrome oxidase subunit 1 (COI) mitochondrial region. The DNA from thief ants collected from 9 states was extracted using Qiagen's Genra PUREGENE® DNA Isolation Kit. The polymerase chain reactions (PCR) were run on the extracted DNA to amplify partial sequence of COI using primers Lep-F1 (forward) and Lep-R1 (reverse). The resulting DNA products were concentrated, purified and sequenced. The 600 bp sequences of the COI generated were submitted to GenBank that issued accession numbers from HM179641 to HM179653. The sequences associated with these accession numbers were used as DNA barcodes for distinguishing species and subspecies. Based on this molecular analysis, thief ants collected from New York, Indiana and 1 location in Nebraska were separated in 1 group as *S. molesta validiuscula* (Emery) and another with ants from Louisiana identified as *S. carolinensis* (Forel). The third group was comprised of ants from South Dakota, Washington, New Jersey, Tennessee, Kansas and 2 other locations in Nebraska was identified as *S. molesta molesta* (Say).

**Key Words** thief ants, *Solenopsis* sp., molecular genetics, DNA barcode

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Ants are one of the leading causes for complaints to pest management professionals (PMPs) from homeowners. The PMPs generated approx. US \$1.7 billion annually to manage ant populations (Field et al. 2007). The thief ants (*Solenopsis molesta* Say) are included within the group of ants known as nuisance pests (Bennett et al. 2005, Klotz et al. 2008). Because thief ants are genetically related to red imported fire ants, *S. invicta* Buren, it is critical to identify these ants accurately at species level. DNA barcoding, a relatively new taxonomic approach, uses a short sequence from the mitochondrial DNA (mDNA) region as a molecular diagnostic tool for identification of species (Hebert et al. 2003). DNA barcoding sequences a section (600 bp to 650 bp) of the cytochrome oxidase subunit 1 (COI). This is relatively short compared with the mDNA genome (>16,000 bp) (Hajibabaei et al. 2007). The mDNA region suggested for the use in DNA barcoding is highly conserved and relatively easy to isolate and sequence. Several researchers have reported that COI sequence variability is low and closely related to species difference, making it possible to confidently identify species and resolve most species-level differences (Hebert et al. 2004, Rohlfritsch and Borsa

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2005, Ward et al. 2005, Hajibabaei et al. 2006, Hye et al. 2006, Tavares and Baker 2008).

DNA barcoding offers a standardized method for identifying species using a short mtDNA sequence from the COI gene to provide a 'barcode'. DNA barcoding popularized by Hebert et al. (2003) has since gained acceptance, leading to public databases of DNA barcodes, such as the 'Barcode of Life' and 'GenBank', where the mitochondrial COI gene sequences ('barcodes') for species are stored (Hebert et al. 2003). These databases provided a central location where gene sequences for identifying species can be easily and quickly accessed.

The use of mtDNA for barcoding and identification is not foolproof. DNA barcoding relies on the low levels of mtDNA sequence variation within species as compared with between species. The presence of symbionts such as *Wolbachia* can disrupt this pattern by contributing mtDNA sequence to their host (Hurst and Jiggins 2005, Whitworth et al. 2007). Additionally, because mtDNA are maternally inherited markers, it would be unreliable if male and female histories differ in a species. Also, with conserved primers, there is the possibility of nuclear genome integrations into mtDNA sequence, confounding the potential to clearly identify species. The presence of pseudogenes in mtDNA and its inconsistent evolutionary rate among lineages are also disadvantageous in relying on COI as the sole marker for taxonomic identification (Chu et al. 2009).

The advantages of DNA barcoding are far greater than the disadvantages previously described. The use of DNA barcoding for species identification and population genetics is important as numerous cryptic species are misidentified. Because the DNA sequences of a species are unique, the DNA barcode developed for any species could be used to separate cryptic species (Hebert et al. 2004, Smith et al. 2006, 2007). Most cryptic species are, as Bickford et al. (2007) described, in 'morphological stasis' – limited or no changes due to selection, adaptation and/or environmental condition. Hajibabaei et al. (2006) used COI DNA barcodes to differentiate among lepidopteran families from Costa Rica and found that 97.9% (of 521) species have distinctive COI barcodes.

DNA barcoding also may be used for the early detection of invasive species and their spread such as the big-headed ant, *Pheidole megacephala* F., a pest ant registered in the list of the '100 of the world's worst invasive alien species' (Fournier et al. 2008). This technique will help with faster, more accurate species identification which could accelerate implementation of proper control methods and, thus, reduce their geographic movement. DNA barcoding can identify a species throughout its entire life cycle, whereas morphological identification of a species is based mostly on adult features. Numerous researchers have used this method to identify alien, cryptic or invasive species in entomology, botany, ornithology, ichthyology, etc.; for example, Chown et al. (2008) with lepidopteran species in Marion Island, South Africa; Hebert et al. (2004) with neotropical skipper butterfly; Lahaye et al. (2008) with plant biodiversity at 2 hotspots (southern Africa and Mesoamerica); Kerr et al. (2007) with North American birds; Ward et al. (2005) with Australian fishes, etc.

Accurate identification of the thief ants relied heavily of the morphological features of the queen of each species. Because the queens are not easily available, molecular technique using the abundant worker caste could be used for species identification. The objective of this research was to develop DNA barcodes for identifying the thief ants within the *S. molesta* complex using workers for a fast and reliable tool to identify thief ants at species and subspecies levels.

## Materials and Methods

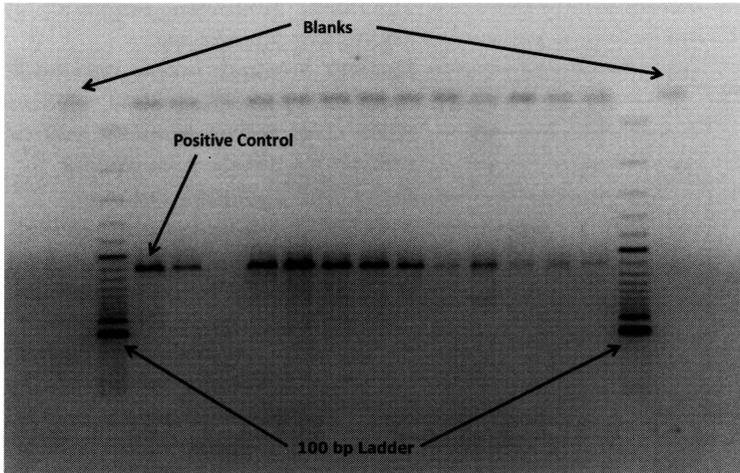
**Ant collection.** Thief ants, *S. molesta*, were collected from 3 locations in Lancaster Co., Nebraska and other states including: Indiana, Kansas, Louisiana, New Jersey, New York, South Dakota, Tennessee and Washington (Table 1). Thief ants in Nebraska were collected using the techniques described by Husen et al. (2008). All thief ant specimens were preserved in 95% ethyl alcohol and stored at -20°C in VWR freezer (VWR, West Chester, PA) for DNA extraction, COI amplification and sequencing.

**DNA extraction and isolation.** Thief ant workers stored in 95% ethyl alcohol at -20°C were removed, and the ethanol was allowed to dry. DNA was extracted from ants using PUREGENE® DNA Isolation Kit (Invitrogen, Carlsbad, CA) and tissue method modified from PUREGENE® DNA Isolation manual included in the kit. Standard primers (Smith et al. 2007) (*Forward Primer* >*LepF1 ATTCAACCAATCATAAAGATATTGG*; *Reverse primer* >*LepR1 TAAACTTCTGGATGTCCAAAAAATCA*) (Invitrogen, Carlsbad, CA) were used to amplify and sequence the mitochondrial COI from thief ants. Additional solutions and reagents required for DNA extraction and PCR amplification were prepared according to protocols of Sambrook et al. (1989). After completion of the amplification process, 5.0 µL PCR product was loaded into 1.0% agarose gel in 0.5x TBE, stained with 0.1% ethidium bromide, electrophoresed at 100 V for approx. 1 h. The gel was viewed and photographed (Fig. 1) on a Bio-Rad Gel Doc System (Bio-Rad, Hercules, CA). The DNA, once rehydrated, was stored at 4.0°C until PCR amplification was completed. The concentration of the extracted DNA was determined using a NanoDrop 1000 spectrophotometer (Thermo Scientific, Waltham, MA), and an equivalent of 80 - 100 ng/µl was used as template for the PCR reaction.

**PCR amplification program and DNA sequencing.** Polymerase chain reactions (PCR) amplification program and DNA sequencing were performed according to

**Table 1. Thief ants collected from various states were used for species identification.**

State	Zip Code	Latitude	Longitude	Collector
Louisiana	71051	32.3309	-93.4801	L. Hooper-Bui
Louisiana	70714	30.5922	-91.1161	L. Hooper-Bui
South Dakota	57701	44.1454	-103.1510	R. Narain
Tennessee	37721	36.1259	-83.8261	K. Vail
Nebraska	68516	40.7369	-96.6531	R. Narain
New Jersey	08901	40.4879	-74.4467	C. Wang
Kansas	66503	39.2327	-96.6852	S. Dobesh
Washington	99224	47.6733	-117.5328	L. Hensen
Nebraska	68505	40.8247	-96.6157	R. Narain
New York	11741	40.7942	-73.0700	S. Narain
Nebraska	68583	40.8002	-96.6667	R. Narain
Indiana	47907	40.4253	-86.9155	G. Buczkowski



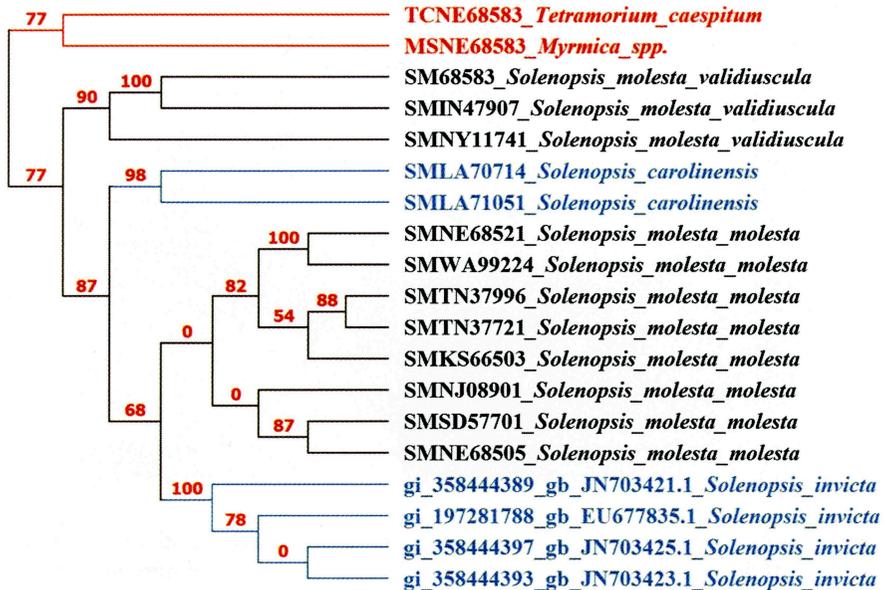
**Fig. 1.** Image of 1% agarose gel showing some successful and unsuccessful PCR amplification of COI DNA from thief ants, primer dimers shown as a band at the top of the gel.

protocol of Narain et al. (2012). Additional sequences of *S. invicta* used for comparison were downloaded from GeneBank, accession numbers EU677835, JN703421, JN703423 and JN703425.

## Results and Discussion

**Species genetic identification.** Phylogenetic tree (Fig. 2) analysis using programs at [www.phylogeny.fr](http://www.phylogeny.fr) (Dereeper et al. 2008) separates the COI sequences collected into 3 groups of thief ants previously identified (Narain et al. 2012). Included in the Neighbor Joining tree are *S. invicta* COI sequences, which were used to compare its relationship to that of thief ants. *Tetramorium caespitum* (L.), and *Myrmica* spp. (Latreille) were used as out-groups for the phylogenetic trees. The phylogenetic tree (Fig. 2) showed that red imported fire ants, *S. invicta*, were more closely (68%) related to *S. molesta molesta* than to the other groups of thief ants from this study. An 82% homology for the sequences was calculated in MEGA 4 ( $p$ -distance = 0.18). The changes in the sequences were assumed to be made by (1) taxa joined together have descended from a common ancestor, (2) random mutation in nucleotides occurs in lineages over time, (3) the random mutation transpires at an approximately constant rate, and (4) the mutations are independent (Thorpe 1982). This is especially true when the species are minute or degrade with time in storage.

The use of COI sequences as DNA barcodes to identify unknown or undetermined species would greatly increase the efficiency of minute specimen of insects. For example, the revision of the thief ants by Pacheco (2007) listed 83 species. From a previous 149 available taxa, the author recognizes 72 valid species and identified 11 new species. COI sequence generated and the protocol used in this research could be reproduced on thief ant specimens collected in other locations. This could aid in identification of the species, reducing the difficulty associated with morphologic identification of such tiny ants.

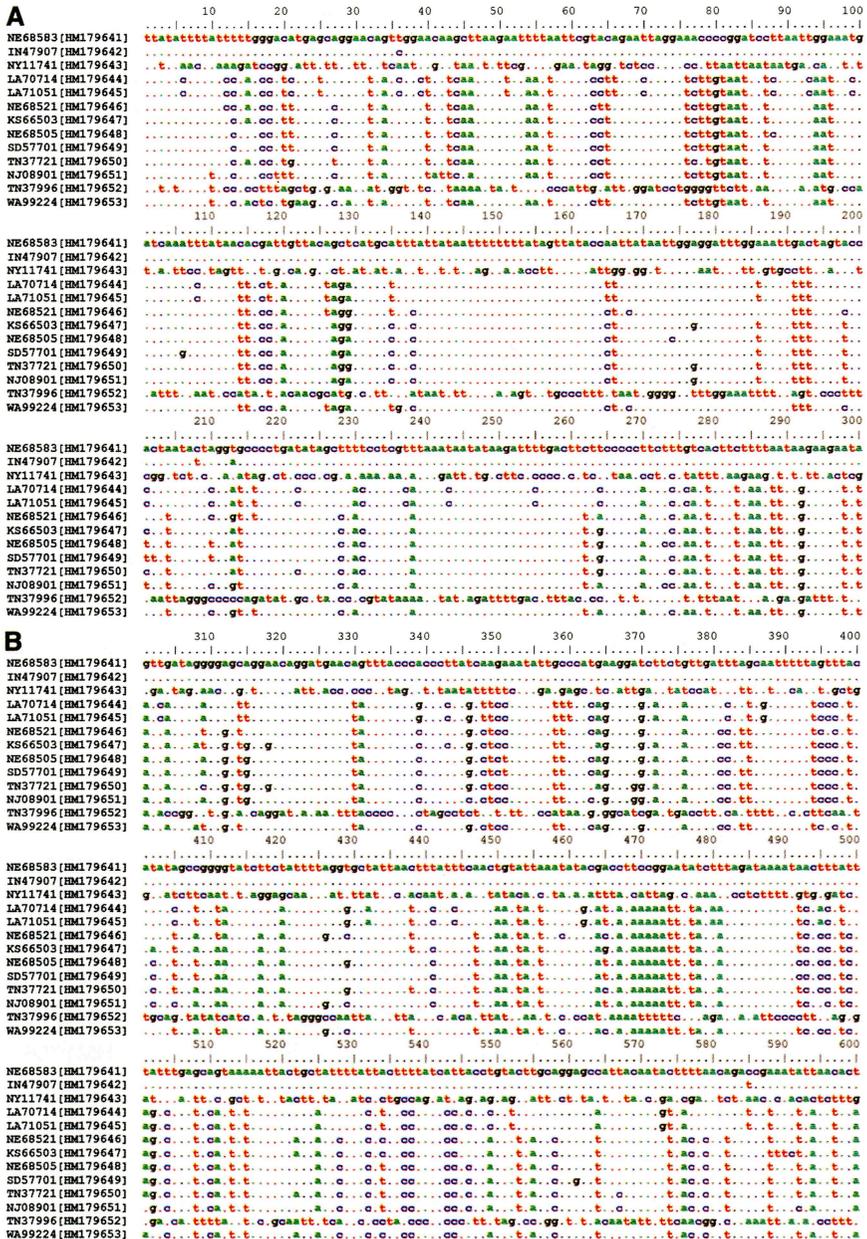


**Fig. 2.** Maximum Likelihood phylogenetic tree of thief ants collected from 13 locations in 9 states across its distribution range; compared with red imported fire ants; rooted with *Tetramorium caespitum* and *Myrmica* spp. Numbers represent branch supporting values (as percent).

**DNA barcode.** Cytochrome oxidase subunit I (COI) sequences of thief ants from 13 locations in 9 states were submitted to GenBank. The frequency and percent of the nucleotides were: A: 2859 (29.9%); C: 1824 (19.1%); G: 1253 (13.1%) and T: 3,612 (37.8%) (MEGA 4.0 Tamura et al. 2007). The sequences are comprised of 8,107 bp, 32.29% G+C content with an average length of 638 bp per submission. The COI sequences of the thief ant are shown in Fig. 3. Periods in the sequence letters represents conserved bases between populations from each location. Conserved bases are indicative of similarities between populations whereas the different bases account for separation of the different populations within and between species.

These results indicate that a COI-based identification system could be effective in identifying thief ants. These DNA barcodes could be used to determine related species, to identify cryptic species (Hebert, et al. 2004, Burns, et al. 2008) or invasive species (Rubinoff 2006, Darling and Blum 2007). The COI sequences DNA barcodes generated during from this research is a valuable tool to be used in future research on thief ants.

The GenBank accession numbers from HM179641 to HM179653 for the COI sequences obtained from this study are presented in Table 2. The DNA sequences associated with these accession numbers were used as DNA barcodes in this study. The use of these DNA barcodes for identification would reduce or help rectify the discrepancy associated with identification of this group of ants whereas enumerating the number of species of ants in this group.



**Fig. 3.** Thief ants: States, Accession numbers and base sequences with an average length of 638 bp. Periods between bases represented conserved bases. (Ant collection locations: IN = Indiana, KS = Kansas, LA = Louisiana, NE = Nebraska, NJ = New Jersey, NY = New York, SD = South Dakota, TN = Tennessee, WA = Washington followed by zip codes).

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Based on literature reviewed, this is the first submission of COI generated DNA barcodes for thief ants to GenBank. This would help to identify thief ants in other states and also determine the number of thief ant species (subspecies) found within the USA and possibly identify new species of thief ants. The COI sequences DNA barcodes generated would facilitate easier identification of each species and reduce the conflict generated when morphological identification is used to separate specimen.

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