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Digital DNA Tags: QR Code Generation for Insect Pest Species in Seri-Ecosystem

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Abstract

Accurate and rapid identification of insect species is vital for biodiversity assessment, ecological research, and effective pest management. Traditional identification methods, which often depend on morphological examination can be time-consuming, labor-intensive, and susceptible to human error. This study introduces an innovative approach that leverages the mitochondrial Cytochrome-c-oxidase I (COI) gene - a widely accepted molecular marker - for insect species identification, integrated with a QR code generation system using Python. The COI gene is highly conserved within species yet variable across taxa, making it a reliable genetic marker for distinguishing insect species. In this approach, COI gene sequences are extracted from reference databases and encoded into QR codes, which contain key taxonomic and ecological information such as species name, classification hierarchy, and habitat data. Upon scanning, the QR code provides immediate access to this information, facilitating quick identification and data retrieval in both laboratory and field settings. The system is developed using Python, incorporating bioinformatics tools for sequence analysis and a QR code generation library to convert genetic and taxonomic data into scannable codes. This integrated platform offers a fast, automated, and user-friendly alternative to conventional identification methods. Designed for entomologists, ecologists, and field researchers, it enhances the efficiency of species monitoring and supports real-time biodiversity documentation. The study demonstrates the potential of merging molecular techniques with digital technologies to streamline species identification and support conservation and ecological research efforts.

INTRODUCTION

Insect species identification is essential across various domains, including biodiversity monitoring, ecological research, pest management, conservation, and agriculture. Given the vast diversity and abundance of insects, accurate species identification supports a wide range of scientific and practical applications. Quick Response (QR) codes, first developed in 1994 by Denso Wave in Japan, are a form of two-dimensional matrix barcodes capable of encoding significantly more information than traditional one-dimensional barcodes (Tigor Naul et al., 2015). These codes consist of black and white square patterns divided into two main regions: the encoding region, which stores the data and error-correction information, and the function pattern region, which assists in decoding and orientation (Kinjal H. Pandya et al., 2014). The function region includes finder patterns, alignment patterns, and timing patterns. Finder patterns - located in three corners - enable correct orientation; timing patterns guide decoding software along rows and columns and alignment patterns help correct distortions during scanning. A 'quiet zone' surrounding the QR code ensures the scanner can distinguish it from its background. QR codes can store diverse data types, including URLs, plain text, numeric values, and even image data. In the context of biological sciences, QR codes can serve as quick-access links to DNA sequences, specimen metadata, images, maps, and database entries such as those in GenBank (NCBI). Unlike DNA barcodes that store data in one direction (linear format), QR codes store information both horizontally and vertically, allowing for greater data density and compactness (Faridah Hanim Yahya et al., 2018). This dual-direction capability makes QR codes especially valuable for efficient species identification and data sharing. All living organisms possess genomic DNA composed of nucleotide bases-adenine (A), thymine (T), cytosine (C), and guanine (G) - which encode the organism's genetic information. DNA barcoding involves sequencing a short, standardized region of DNA to serve as a species-specific genetic marker. In animals, the mitochondrial cytochrome c oxidase subunit I (COI) gene is widely used as a universal barcode due to its high interspecies variability and ease of amplification. COI sequences are typically obtained via PCR amplification using species-specific primers, followed by Sanger sequencing.

The resulting COI sequences are compared with reference databases using tools such as NCBI’s BLAST (Basic Local Alignment Search Tool), which identifies sequence similarity through optimal alignments that account for matches, mismatches, and gaps. BLASTN further supports hierarchical clustering and diagnostic identification, aiding in the classification of unknown species.

Mulberry (genus *Morus*) is a crucial host plant for the silkworm (*Bombyx mori*), forming the foundation of sericulture. However, its productivity is severely threatened by various insect pests that feed on its leaves, stems, and roots. These pests can cause significant qualitative and quantitative damage to mulberry foliage, directly affecting leaf yield and, consequently, cocoon production and silk quality.

32 Key insect pests namely *Diaphania pulverunlentalis, Delius eucharis, Acraea violae, Etiella behrii, Eressa strepsimeris, Cleora repulsaria, Olene mendosa, Pyla imposter, Tymbophora peltastis, Spodoptera litura, Attagenus fasciatus, Paracoccus marginatus, Toxoptera odinae, Acrosternum gramineum, Holymorpha picus, Aphis glycines, Maconellicoccus hirsutus, Aleurodicus disperses, Dieuches schmitzi, Eocanthecona furcellata, Nizara virudula, Spelobia bifrons, Exorista sorbillins, Myllocerus viridanus, Illeis cincta, Calvia championorum, Calvia quaturodecimguttata, Coccinellidae, Cryptoleamus monotrouzeri, Hexocentrus Japonicus, Neothacris Acuticeps,* and *Meranoplus magrettii* are known to infest mulberry and other important food plants. Leaf-eating caterpillars and sap- sucking pests reduce the photosynthetic capacity of the plant, lower leaf biomass, and may lead to plant wilting, defoliation, and death in severe cases. Yield losses due to insect pest infestation in mulberry plantations can range from 15% to 40%, depending on pest type, population density, and climatic conditions. In extreme cases, particularly under poor pest management practices, losses can exceed 50%, seriously impacting silkworm rearing and overall sericultural productivity. Effective identification and timely control of these pests are vital for maintaining healthy mulberry crops and ensuring the sustainability of sericulture. Molecular tools such as DNA barcoding combined with digital technologies like QR code-based data retrieval can enhance pest monitoring and rapid species identification, leading to more targeted and efficient pest management strategies. This study addresses a key limitation of conventional DNA barcoding-the difficulty in retrieving or interpreting raw DNA sequence data due to its length and complexity. To overcome this, we developed a method to encode DNA barcode sequences into QR codes, providing a compact, scannable format that links genetic data with taxonomic information. This QR-based approach improves accessibility and enhances the practical application of DNA barcoding in species identification (S. Vimala et al., 2020).

METHODOLOGY

2.1 Generation of DNA Barcodes:

32 Insect pest species were considered in the study. The mitochondrial COI gene sequencing was performed using DNA isolation and PCR experiments (K Haripriya et al., 2023). The obtained partial COI gene sequences were edited, trimmed, and were submitted to Barcode of Life Data System (BOLD) for through verification and validation by preparing sequence file, trace file, taxonomy details file. Further, the accession numbers are specified to each gene sequence of specimen in the form of BIN number. The respective DNA barcodes were assigned to each COI gene sequence of insect species by the BOLD system database (Ratnasingham S etal., 2024).

2.2 DNA based QR codes for automatic species identification

Quick reading codes were developed to each insect species selected for this study for their automatic identification by common people. These QR codes are created based on their COI gene sequence information. Here, the python program might have been used to design for the creation of QR code in the form of displaying Insect specimen picture, its taxonomic classification, its life cycle, COI marker gene sequence and DNA barcode when it scanned through QR code machine. The python programming details which were used in QR coding were explained. Anaconda-Python stand-alone Jupiter platform was used for programming.

2.2.1 ANACONDA-PYTHON:

Anaconda (Python distribution) is a standard platform with python programming language. For the use of scientific computations like Data sciences, data processing, predictive analytics. Anaconda distribution comes with conda package and virtual environment manager called “Anaconda Navigator. Anaconda Navigator is a desktop graphical user interface (GUI) that was maintained under anaconda distribution.

It allows users to launch applications and environments and channels without using command-line in command prompt. In built cells lead to run through the programme. For DNA based QR code development “JUPYTER NOTEBOOK” application was used and this application and is available as default in Navigator. Jupyter is browser-based interpreters that permit to users to interactively work with Python. Jupyter acts as a digital notebook which can allow the user to execute commands by taking input and display the output in the form of charts. It is primarily used by Data Scientists. From the Launcher tab, Python 3 kernel was opened in the Notebook area. A new Jupyter notebook file with an empty code cell opened in a separate tab. The python program was then entered in the code cell. To execute the program, a new code cell was added below the program and selected the cell in the notebook from the toolbar.

2.2.2 Preparation of data set using COI gene Sequences

The sequence information of COI gene of each selected specimen for the current study were retrieved from BOLD Database. To retrieve each DNA sequence from BOLD database, the keyword ‘barcode’ was used as a query. Some DNA sequences were directly taken from the complete genome in the form of CDS for COI gene. The DNA barcode sequences of all insect fauna were chosen as reference barcodes. The DNA sequence with BOLD index numbers: were chosen as test set (Different insect samples).

2.2.3 Encoding of QR code with DNA sequences QR code has the best compression efficiency in encoding DNA barcode sequences than the other 2D codes (Matrix). The open source QR Code Library in Jupyter-Python kernel version (Anaconda) was adapted for developing program to encode the DNA sequences. To generate QR code, a new python JUPYTER notebook in kernel version is created at first to write QR code collecting commands for running the programme. At this stage it is called as encode. In the encode method, four settings are found; the text to the DNA sequence (encode), QR code (barcode type) and the desired width and height (in pixels) of the image are produced. The applications of general commercial QR codes are endless. They are used to identify and classify magazines, advertisements, product wrappings, T-shirts, passports, business cards etc. The insect fauna collected from various sericulture research centres and mulberry garden were considered. The partial COI gene sequence that acts as marker gene sequence and amplified from total genomic DNA is taken as input sequence. In addition to that sequence information, species name, image, taxonomic data and its life cycle image were also taken as inputs. By using above programming code, the DNA based QR code is developed for every respective insect fauna considered for this study. The protocol used to create DNA based QR codes were displayed as a flowchart. From installation of Python software to generation of QR codes were explained.

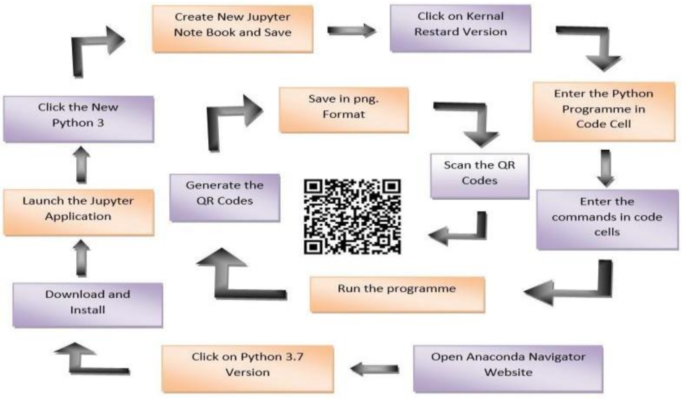


Figure 1: Operational flow chart to generate QR Code using python programme.

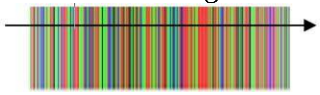
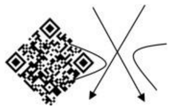
2.3 Comparison of DNA barcodes and DNA based QR code:

The applications of DNA based QR codes are vast than DNA barcoding. DNA barcode holds the information in vertical direction only. Whereas QR code holds the information both horizontally and vertically. DNA barcode only considered alphabets as input source. But QR code consider alphanumeric as input source. From DNA barcode, only molecular information was present. But in QR code, taxonomic information also generated. Differences and application of DNA barcode and QR code are tabulated in table 1 and pictorially mentioned in table 2.

Table: 1 Comparison of DNA barcode and DNA based QR code

S.No	DNA Barcode	DNA based QR Code
1	DNA Barcode contains the information in vertical direction	QR code holds the information in both horizontal and vertical directions.
2	DNA Barcode can maintain as much as information that could be limited to the number of specific DNA bases and position.	The capacity of QR code is hundreds of times higher in storing and linking the information than a DNA barcode [2].
3	DNA barcode consider alphabetical information as input only.	While QR code takes up information in Alphanumeric.
4	Taxonomic information and meta data cannot be included only gene sequence information is needed	Organism's taxonomic information can be included which explains the entire binomial nomenclature, species type and genus name and common name too.
5	Image data and meta data cannot be included in a DNA barcode	QR code can be generated with not only alphanumeric information but also image and meta data too.
6.	Scanners for DNA barcodes are not available and need to be designed specifically.	QR code can be scanned with any publicly available QR code scanner. Hence it can reach out to the common man

Table: 2 Comparisons between DNA barcode and DNA based QR code

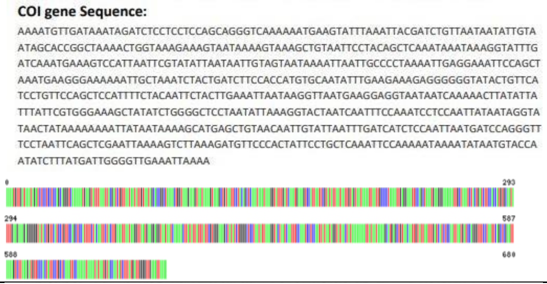
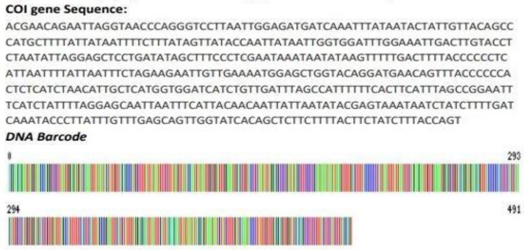
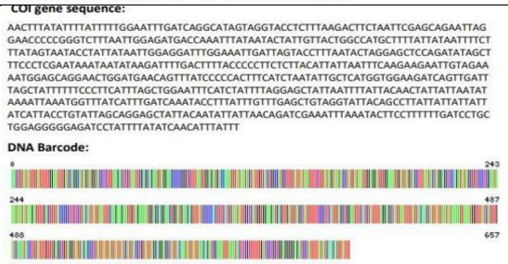
Features of the code	DNA barcode	DNA based QR code
High capacity	650-680 bases Alpha	Upto 7089 numeric digits
Durability against soil and damage	Reading is impossible	Reading is possible (upto 30% damaged)
Reduced space	10 digits numeric (approx. 50 mm X 20 mm)	40digits Numeric (approx. 5mm X 5mm)
360° reading	Horizontal reading 	Supports 360° reading 
Language supported	Alpha/sequence based ATGCGACTACTCGCATGCTTG	Numeric alphanumeric kanji, kana #%$@& 123AGB x_{y^2} €£¥

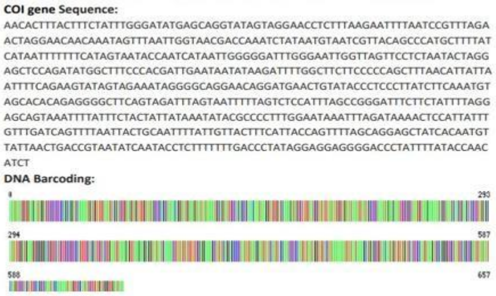
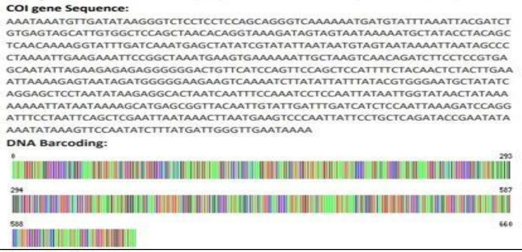
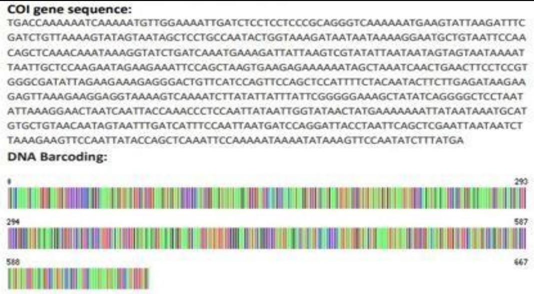
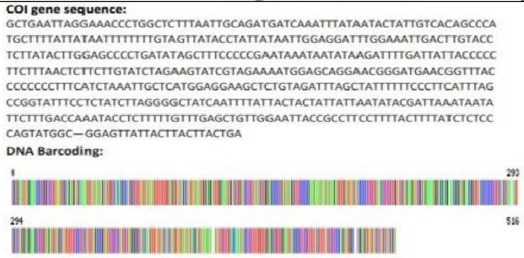
RESULTS

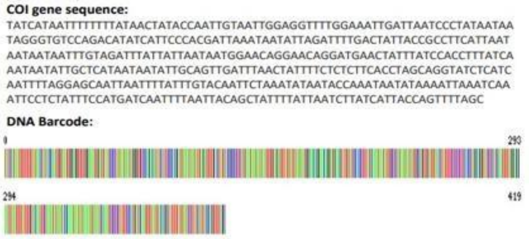
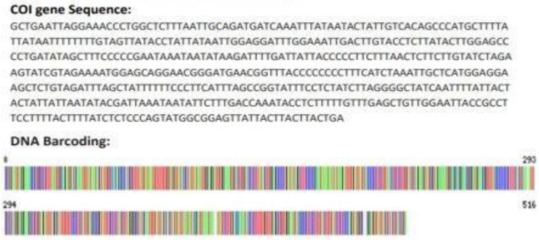
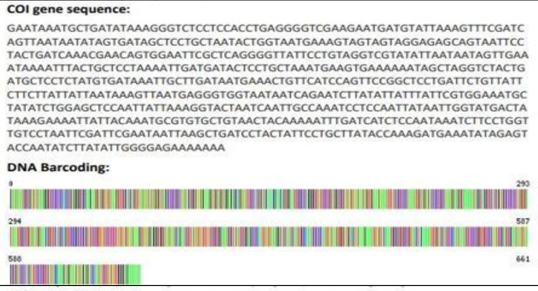
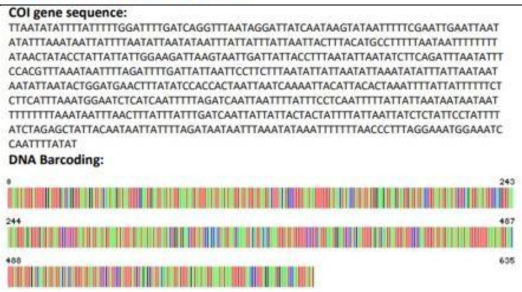
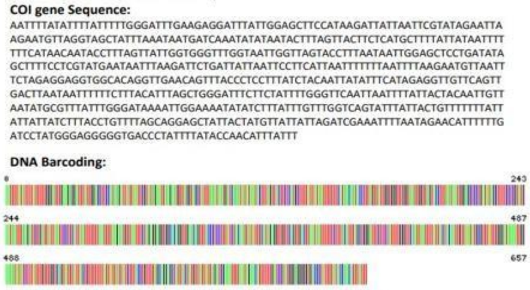
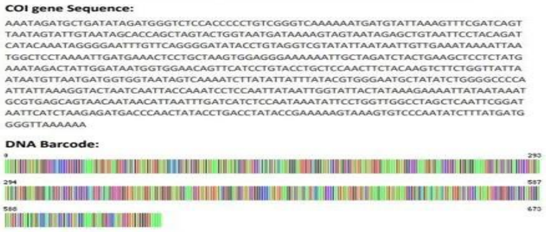
DNA based QR codes of the samples look darker than the common QR codes due to pixel density. In the present study partial COI gene sequences of 36 various insect fauna collected from different Sericulture research centers and mulberry gardens were taken for the current study. As seen in Table: 2, to keep more data into QR code, the more rows and columns of modules (the little black squares) will be needed. Therefore, the minimum width of printed QR code image depends on the size of individual module when viewed by the camera (from a distance at some resolution). We found that the minimum width of a printed DNA QR code is 2.8cm, below that minimum width, the scanner cannot read the DNA QR code correctly.

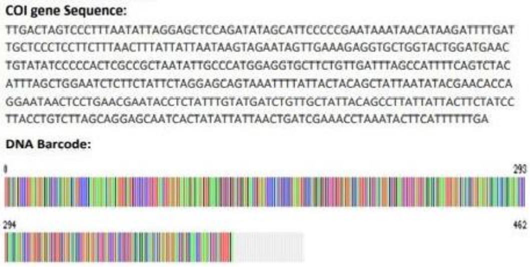
3.1 DNA based QR code scanning

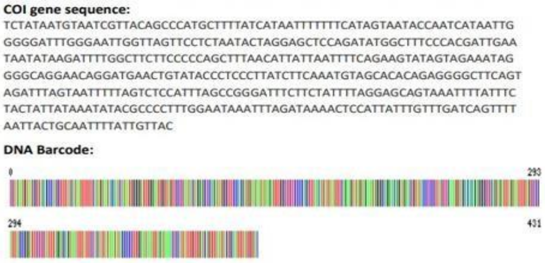
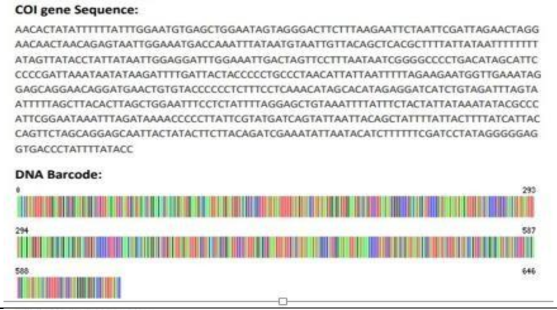
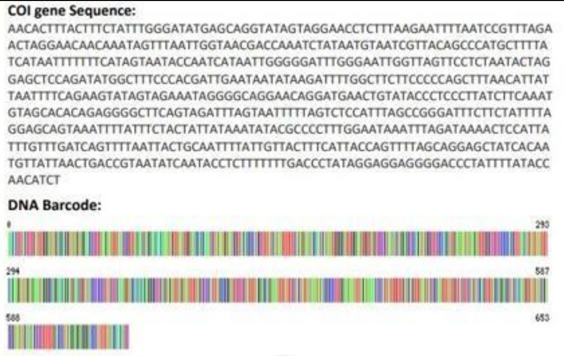
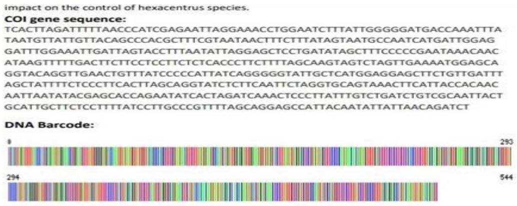
DNA based QR code must be scanned with QR scanner apps which can be download from google play into a store in to a Smart phone using the matrix can be read quickly using QR code scanner app. For some applications it requires internet connection. When the application has started, it shows blank rectangle in the middle of the device screen and captioned buttons place at the bottom. By touching the scan button, the screen switched to the camera interface. User can place the DNA QR code inside the viewfinder. The scanner captured the DNA QR code and decoding back into DNA sequences including its taxonomical data and its genus/species name.

S.No.	Species Name	COI Gene Sequence	QR Code
1	*Diaphania pulverunlentalis*	 **COI gene Sequence:** AAAATGTTGATAAATAGATCTCCTCCTCCAGCAGGGTCAAAAAATGAAGTATTTAAATTACGATCTGTTAATAATATTGTA ATAGCACCGGCTAAAACTGGTAAAGAAAGTAATAAAAGTAAAGCTGTAATTCCTACAGCTCAAATAAATAAAGGTATTTG ATCAAATGAAAGTCCATTAATTCGTATATTAATAATTGTAGTAATAAAATTAATTGCCCCTAAAATTGAGGAAATTCCAGCT AAATGAAGGGAAAAAATTGCTAAATCTACTGATCTTCCACCATGTGCAATATTTGAAGAAAGAGGGGGTATACTGTTCA TCCTGTTCCAGCTCCATTTTCTACAATTCTACTTGAAATTAATAAGGTTAATGAAGGAGGTAATAATCAAAAACTTATATTA TTTATTCGTGGGAAAGCTATATCTGGGGCTCCTAATATTAAAGGTACTAATCAATTTCCAAATCCTCCAATTATAATAGGTA TAACTATAAAAAAAATTATAATAAAAGCATGAGCTGTAACAATTGTATTAATTTGATCATCTCCAATTAATGATCCAGGGTT TCCTAATTCAGCTCGAATTAAAAGTCTTAAAGATGTTCCCACTATTCCTGCTCAAATTCCAAAAATAAAATATAATGTACCA ATATCTTTATGATTGGGGTTGAAATTAAAA 0 293 294 587 588 680	
2	*Delius eucharis*	 CAGGATCATTAATTGGTGATGACCAAATTTATAATACCATTGTTACAGCTCATGCTTTTATTATAATTTTCTTTAT AGTTATACCTATAATAATTGGAGGTTTTGGAAATTGACTAGTACCTCTAATACTTGGAGCCCCTGATATAGCCT TTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCATTAACCCTTTTAATTTCGAGAAGAATTGTAG AAAATGGAGCAGGAACAGGATGAACAGTTTACCCCCCACTTTCATCTAATATCGCTCATAGAGGGTCATCAGT TGACTTAGCTATTTTCTCTTTACATCTTGCTGGTATTTCCTCAATTCTTGGAGCAATTAATTTTATTACTACTATTA TTAATATACGAATTAATAATATATCTTTTGATCAAATACCTTTATTTGTATGAGCTGTAGGAATCACTGCTCTTCT TCTTCTTCTTTCTTTACCTGTTCTT 0 293 294 475	
3	*Acraea violae*	 **COI gene Sequence:** ACGAACAGAATTAGGTAACCCAGGGTCCTTAATTGGAGATGATCAAATTTATAATACTATTGTTACAGCC CATGCTTTTATTATAATTTTCTTTATAGTTATACCAATTATAATTGGTGGATTTGGAAATTGACTTGTACCT CTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTC ATTAATTTTATTAATTTCTAGAAGAATTGTTGAAAATGGAGCTGGTACAGGATGAACAGTTTACCCCCCA CTCTCATCTAACATTGCTCATGGTGGATCATCTGTTGATTTAGCCATTTTTTCACTTCATTTAGCCGGAATT TCATCTATTTTAGGAGCAATTAATTTCATTACAACAATTATTAATATACGAGTAAATAATCTATCTTTTGAT CAAATACCCTTATTTGTTTGAGCAGTTGGTATCACAGCTCTTCTTTTACTTCTATCTTTACCAGT ***DNA Barcode*** 0 293 294 491	
4	*Etiella behrii*	 **COI gene sequence:** AACTTTATATTTTATTTTTGGAATTTGATCAGGCATAGTAGGTACCTCTTTAAGACTTCTAATTCGAGCAGAATTAG GAACCCCCGGGTCTTTAATTGGAGATGACCAAATTTATAATACTATTGTTACTGGCCATGCTTTTATTATAATTTTCT TTATAGTAATACCTATTATAATTGGAGGATTTGGAAATTGATTAGTACCTTTAATACTAGGAGCTCCAGATATAGCT TTCCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCTCTTACATTATTAATTTCAAGAAGAATTGTAGAA AATGGAGCAGGAACTGGATGAACAGTTTATCCCCCACTTTCATCTAATATTGCTCATGGTGGAAGATCAGTTGATT TAGCTATTTTTTCCCTTCATTTAGCTGGAATTTCATCTATTTTAGGAGCTATTAATTTTATTACAACTATTATTAATAT AAAATTAAATGGTTTATCATTTGATCAAATACCTTTATTTGTTTGAGCTGTAGGTATTACAGCCTTATTATTATTATT ATCATTACCTGTATTAGCAGGAGCTATTACAATATTATTAACAGATCGAAATTTAAATACTTCCTTTTTTGATCCTGC TGGAGGGGGAGATCCTATTTTATATCAACATTTATTT **DNA Barcode:** 0 243 244 487 488 657	

5	*Eressa strepsimeris*	**COI gene Sequence:** AACACTTTACTTTCTATTTGGGATATGAGCAGGTATAGTAGGAACCTCTTTAAGAATTTTAATCCGTTTAGA ACTAGGAACAACAAATAGTTTAATTGGTAACGACCAAATCTATAATGTAATCGTTACAGCCCATGCTTTTAT CATAATTTTTTTCATAGTAATACCAATCATAATTGGGGGATTTGGGAATTGGTTAGTTCCTCTAATACTAGG AGCTCCAGATATGGCTTTCCCACGATTGAATAATATAAGATTTTGGCTTCTTCCCCCAGCTTTAACATTATTA ATTTTCAGAAGTATAGTAGAAATAGGGGCAGGAACAGGATGAACTGTATACCCTCCCTTATCTTCAAATGT AGCACACAGAGGGGCTTCAGTAGATTTAGTAATTTTTAGTCTCCATTTAGCCGGGATTTCTTCTATTTTAGG AGCAGTAAATTTTATTTCTACTATTATAAATATACGCCCCTTTGGAATAAATTTAGATAAAACTCCATTATTT GTTTGATCAGTTTTAATTACTGCAATTTTATTGTTACTTTCATTACCAGTTTTAGCAGGAGCTATCACAATGT TATTAACTGACCGTAATATCAATACCTCTTTTTTTGACCCTATAGGAGGAGGGGACCCTATTTTATACCAAC ATCT **DNA Barcoding:**	
6	*Cleora repulsaria*	**COI gene Sequence:** AAATAAATGTTGATATAAGGGTCTCCTCCTCCAGCAGGGTCAAAAAATGATGTATTTAAATTACGATCT GTGAGTAGCATTGTGGCTCCAGCTAACACAGGTAAAGATAGTAGTAATAAAAAATGCTATACCTACAGC TCAACAAAAGGTATTTGATCAAATGAGCTATATCGTATATTAATAATGTAGTAATAAAATTAATAGCCC CTAAAATTGAAGAAATTCCGGCTAAATGAAGTGAAAAAATTGCTAAGTCAACAGATCTTCCTCCGTGA GCAATATTAGAAGAGAGAGGGGGGACTGTTCATCCAGTTCCAGCTCCATTTTCTACAACTCTACTTGAA ATTAAAAGAGTAATAGATGGGGGAAGAAGTCAAAATCTTATATTATTTATACGTGGGAATGCTATATC AGGAGCTCCTAATATAAGAGGCACTAATCAATTTCCAAATCCTCCAATTATAATTGGTATAACTATAAA AAAAATTATAATAAAAGCATGAGCGGTTACAATTGTATTGATTTGATCATCTCCAATTAAAGATCCAGG ATTTCCTAATTCAGCTCGAATTAATAAACTTAATGAAGTCCCAATTATTCCTGCTCAGATACCGAATATA AAATATAAAGTTCCAATATCTTTATGATTGGGTTGAATAAAA **DNA Barcoding:**	
7	*Olene mendosa*	**COI gene sequence:** TGACCAAAAAATCAAAAATGTTGGAAAATTGATCTCCTCCTCCCGCAGGGTCAAAAAATGAAGTATTAAGATTTC GATCTGTTAAAAGTATAGTAATAGCTCCTGCCAATACTGGTAAAGATAATAATAAAAGGAATGCTGTAATTCCAA CAGCTCAAACAAATAAAGGTATCTGATCAAATGAAAGATTATTAAGTCGTATATTAATAATAGTAGTAATAAAAT TAATTGCTCCAAGAATAGAAGAAATTCCAGCTAAGTGAAGAGAAAAAATAGCTAAATCAACTGAACTTCCTCCGT GGGCGATATTAGAAGAAAGAGGGACTGTTCATCCAGTTCCAGCTCCATTTTCTACAATACTTCTTGAGATAAGAA GAGTTAAAGAAGGAGGTAAAAGTCAAAATCTTATATTATTTATTCGGGGGAAAGCTATATCAGGGGCTCCTAAT ATTAAAGGAACTAATCAATTACCAAACCCTCCAATTATAATTGGTATAACTATGAAAAAAATTATAATAAATGCAT GTGCTGTAACAATAGTAATTTGATCATTTCCAATTAATGATCCAGGATTACCTAATTCAGCTCGAATTAATAATCT TAAAGAAGTTCCAATTATACCAGCTCAAATTCCAAAAATAAAATATAAAGTTCCAATATCTTTATGA **DNA Barcoding:**	
8	*Pyla imposter*	**COI gene sequence:** AGTAGGGACCTCTTTAAGACTTCTAATTCGAGCAGAATTAGGAACCCCCGGGTCTTTAATTGGAGATG ATCAAATTTATAATACTATTGTTACTGGCCATGCTTTTATTATAATTTTCTTTATAGTAATACCTATTATA ATTGGAGGATTTGGAAATTGATTAGTACCTTTAATGCTAGGAGCTCCAGATATAGCTTTCCCTCGAATA AATAATATAAGATTTTGACTTTTACCCCCCTCTCTTACATTATTAATTTCAAGAAGAATTGTAGAAAATG GAGCAGGAACTGGATGAACAGTTTATCCCCCACTTTCATCTAATATTGCTCATGGTGGAAGATCAGTTG ATTTAGCTATTTTCTCTCTTCATTTAGCTGGAATTTCATCTATTTTAGGAGCTATTAATTTTATTACAACTA TTATTAATATAAAATTAAATGGTTTATCATTTGATCAAATACCTTTATTTGTTTGAGCTGTAGGTATTACA GCCTTATTATTATTACTATCATTACCTCTATTAACAGGAGCTAT **DNA Barcoding:**	
9	*Tymbophora peltastis*	**COI gene sequence:** GCTGAATTAGGAAACCCTGGCTCTTTAATTGCAGATGATCAAATTTATAATACTATTGTCACAGCCCA TGCTTTTATTATAATTTTTTTTGTAGTTATACCTATTATAATTGGAGGATTTGGAAATTGACTTGTACC TCTTATACTTGGAGCCCCTGATATAGCTTTCCCCCGAATAAATAATATAAGATTTTGATTATTACCCCC TTCTTTAACTCTTCTTGTATCTAGAAGTATCGTAGAAAATGGAGCAGGAACGGGATGAACGGTTTAC CCCCCCCTTTCATCTAAATTGCTCATGGAGGAAGCTCTGTAGATTTAGCTATTTTTTCCCTTCATTTAG CCGGTATTTCCTCTATCTTAGGGGCTATCAATTTTATTACTACTATTATTAATATACGATTAAATAATA TTCTTTGACCAAATACCTCTTTTTGTTTGAGCTGTTGGAATTACCGCCTTCCTTTTACTTTTATCTCTCC CAGTATGGC—GGAGTTATTACTTACTTACTGA **DNA Barcoding:**	
10	*Spodoptera litura*	**COI gene sequence:** ATAATTCGAGCTGAATTAGGAACTCCAGGGTCATTAATTGGAGATGATCAAATTTATAATACTATTGTAACAGC TCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTGGAAATTGACTTGTACCTTTA ATATTAGGAGCTCCTGATATAGCTTTCCCACGTTTAAATAATATAAGTTTTTGACTTTTACCACCTTCTTTAACCT TACTAATTTCAAGTAGAATTGTAGAAAATGGAGCAGGAACTGGATGAACAGTTTACCCCCCCCTCTCCTCTAAT ATTGCTCATGGTGGAAGATCAGTAGATTTAGCTATTTTTTCCCTTCACCTAGCTGGAATTTCATCTATTTTAGGA GCTATTAACTTTATTACTACTATTATTAATATACGATTAAATAATTTATCATTTGATCAAATACCTTTATTTGTTT GAGCTGTAGGAATTACTGCATTTTTAATAGTATTATCTTTACCTGTTTTAGCTGGAGCTATTATCTATATTATTA ACTGATTGAAATTTAAATACATCATTTTTTGATCCAGCAGGAGGAGGTGACCCATATTTTTTTTTTCTCCTTTTG **DNA Barcode:**	
11	*Paracoccus marginatus*	**COI gene sequence:** ACTTATATATTTAATTTTTGGATTTTGATCAAGATTAATAGGTTTATCAATAAGTTTTATTATTCGAATTGAATTA ATAAATTTAAATAATAATTTTAATAATAATATAATTTATTATATAATAATTACTATTCATGCTTTTATTATAATTTT TTTTATAACTATACCTATTATTATTGGAAGATTAAGTAATTGATTATTACCTTTAATATTAATATCTTCAGATTTA ATTTTTCCTCGTTTAAATAATTTTAGATTTTGATTATTAATTCCATCTTTAATTTTTATAATATTAAATATATTATT AAATAATAATATTAATACTGGATGAACATTATATCCTCCTTTAATTAATCAAAATTTTATTACATTAAATTTTATT ATTTTTTCATTACATTTAAATGGTTTATCTTCAATTTTTAGATCTATTAATTTTATTTCATCTATTTTTATTATTAAT AATAATAATTTTTTTTTAAATAATTTTTCTTTATATATTTGATCAATTATTGTTACTACAATTTTATTAATTATTTCA ATTCCTATTTTATCTAGAGCTATTACTATAATTATTTTAGATAATAATTTAAACATAAATTTTTTTAATCCAATAG GAAATGGTAATCCTATTTTATATCAACATTTATTT **DNA Barcoding:**	

12	*Toxoptera odinae*	 **COI gene sequence:** TATCATAATTTTTTTTATAACTATACCAATTGTAATTGGAGGTTTTGGAAATTGATTAATCCCTATAATAA TAGGGTGTCCAGACATATCATTCCCACGATTAAATAATATTAGATTTTGACTATTACCGCCTTCATTAAT AATAATAATTTGTAGATTTATTATTAATAATGGAACAGGAACAGGATGAACTATTTATCCACCTTTATCA AATAATATTGCTCATAATAATATTGCAGTTGATTTAACTATTTTCTCTCTTCACCTAGCAGGTATCTCATC AATTTTAGGAGCAATTAATTTTATTTGTACAATTCTAAATATAATACCAAATAATATAAAATTAAATCAA ATTCCTCTATTTCCATGATCAATTTTAATTACAGCTATTTTATTAATCTTATCATTACCAGTTTTAGC **DNA Barcode:** 	
13	*Acrosternum gramineum*	 **COI gene Sequence:** GCTGAATTAGGAAACCCTGGCTCTTTAATTGCAGATGATCAAATTTATAATACTATTGTCACAGCCCATGCTTTTA TTATAATTTTTTTTGTAGTTATACCTATTATAATTGGAGGATTTGGAAATTGACTTGTACCTCTTATACTTGGAGCC CCTGATATAGCTTTCCCCCGAATAAATAATATAAGATTTTGATTATTACCCCCTTCTTTAACTCTTCTTGTATCTAGA AGTATCGTAGAAAATGGAGCAGGAACGGGATGAACGGTTTACCCCCCCCTTTCATCTAAATTGCTCATGGAGGA AGCTCTGTAGATTTAGCTATTTTTCCCTTCATTTAGCCGGTATTTCCTCTATCTTAGGGGCTATCAATTTTATTACT ACTATTATTAATATACGATTAAATAATATTCTTTGACCAAATACCTCTTTTTGTTTGAGCTGTTGGAATTACCGCCT TCCTTTTACTTTTATCTCTCCCAGTATGGCGGAGTTATTACTTACTTACTGA **DNA Barcoding:** 	
14	*Holymorpha picus*	 **COI gene sequence:** GAATAAATGCTGATATAAAGGGTCTCCTCCACCTGAGGGGTCGAAGAATGATGTATTAAAGTTTCGATC AGTTAATAATATAGTGATAGCTCCTGCTAATACTGGTAATGAAAGTAGTAGTAGGAGAGCAGTAATTCC TACTGATCAAACGAACAGTGGAATTCGCTCAGGGGTTATTCCTGTAGGTCGTATATTAATAATAGTTGAA ATAAAATTTACTGCTCCTAAAATTGATGATACTCCTGCTAAATGAAGTGAAAAAATAGCTAGGTCTACTG ATGCTCCTCTATGTGATAAATTGCTTGATAATGAAACTGTTCATCCAGTTCCGGCTCCTGATTCTGTTATT CTTCTTATTATTAATAAAGTTAATGAGGGTGGTAATAATCAGAATCTTATATTATTTATTCGTGGAAATGC TATATCTGGAGCTCCAATTATTAAAGGTACTAATCAATTGCCAAATCCTCCAATTATAATTGGTATGACTA TAAAGAAAATTATTACAAATGCGTGTGCTGTAACTACAAAAATTTGATCATCTCCAATAAATCTTCCTGGT TGTCCTAATTCGATTCGAATAATTAAGCTGATCCTACTATTCCTGCTTATACCAAAGATGAAATATAGAGT ACCAATATCTTATATTGGGGAGAAAAAAA **DNA Barcoding:** 	
15	*Aphis glycines*	 **COI gene Sequence:** TACATCATTTTTCGATCCAGCAGGTGGAGGAGATCCTATTCTTTATCAACATTTATTTTGATTTTTTGGA CATCCAGAAGTATATATTTTAATTCTTCCAGGATTTGGATTAATTTCACATATTATTAGACAAGAAAGAA ATAAAAATGAAACATTTGGTAATATTAGAATAATTTATGCAATATTAACTATTGGATTATTAGGATTTAT TGTTTGAGCTCATCATATATTTACAATTGGAATAGACGTTGATACACGAGCTTATTTTACATCAGCAACT ATAATCATTGCTATTCCTACAGGAATTAAAATTTTTAGATGACTAGCAACTATTTATGGATCTAAAATTA ACTTTTCACCATCAACTATTTGAGCTTTAGGATTTATTTTTTTATTTACAATTGGGGGATTAACAGGAGT AATTTTAGCCAATTCATCTATTGATATTATTCTACATGATACTTATTATGTAGTAGCCCATTTCCACTACG TATTATCAATAGGAATTGTATTTGCAATTATTGCCAGTTTAATTCACTGATTCCCAATTTTCACAGGATTT TCAATAAATAACTTCATTTTAAAAATTCAATTTATTTTAATGTTTATTGGAGTAAATTTAACTTTCTTCCC **DNA Barcoding:** 	
16	*Maconellicoccus hirsutus*	 **COI gene sequence:** TTAATATATTTTATTTTTGGATTTTGATCAGGTTTAATAGGATTATCAATAAGTATAATTTTTCGAATTGAATTAAT ATATTTAAATAATTATTTTAATATTAATATAATTTATTATTTATTAATTACTTTACATGCCTTTTTAATAATTTTTTTT ATAACTATACCTATTATTATTGGAAGATTAAGTAATTGATTATTACCTTTAATATTAATATCTTCAGATTTAATATTT CCACGTTTAAATAATTTTAGATTTTGATTATTAATTCCTTCTTTAATATTATTAATATTAAATATATTTATTAATAAT AATATTAATACTGGATGAACTTTATATCCACCACTAATTAATCAAAATTACATTACACTAAATTTTATTATTTTTTCT CTTCATTTAAATGGAATCTCATCAATTTTTAGATCAATTAATTTTATTTCCTCAATTTTTATTATTAATAATAATAAT TTTTTTTTAAATAATTTAACTTTATTTATTTGATCAATTATTATTACTACTATTTTATTAATTATCTCTATTCCTATTTT ATCTAGAGCTATTACAATAATTATTTTAGATAATAATTTAAATATAAATTTTTTTAACCCTTTAGGAAATGGAAATC CAATTTTATAT **DNA Barcoding:** 	
17	*Aleurodicus dispersus*	 **COI gene Sequence:** AATTTTATATTTTATTTTTGGGATTTGAAGAGGATTTATTGGAGCTTCCATAAGATTATTAATTCGTATAGAATTA AGAATGTTAGGTAGCTATTTAAATAATGATCAAATATATAATACTTTAGTTACTTCTCATGCTTTTATTATAATTTT TTTCATAACAATACCTTTAGTTATTGGTGGGTTTGGTAATTGGTTAGTACCTTTAATAATTGGAGCTCCTGATATA GCTTTTCCTCGTATGAATAATTTAAGATTCTGATTATTAATTCCTTCATTAATTTTTTTAATTTTAAGAATGTTAATT TCTAGAGGAGGTGGCACAGGTTGAACAGTTTACCCTCCTTTATCTACAATTATATTTCATAGAGGTTGTTCAGTT GACTTAATAATTTTTTCTTTACATTTAGCTGGGATTTCTTCTATTTTGGGTTCAATTAATTTTATTACTACAATTGTT AATATGCGTTTATTTGGGATAAAATTGGAAAATATATCTTTATTTGTTTGGTCAGTATTTATTACTGTTTTTTTATT ATTATTATCTTTACCTGTTTTAGCAGGAGCTATTACTATGTTATTATTAGATCGAAATTTTAATAGAACATTTTTTG ATCCTATGGGAGGGGGTGACCCTATTTTATACCAACATTTATTT **DNA Barcoding:** 	
18	*Dieuches schmitzi*	 **COI gene Sequence:** AAATAGATGCTGATATAGATGGGTCTCCACCCCCTGTCGGGTCAAAAAATGATGTATTAAAGTTTCGATCAGT TAATAGTATTGTAATAGCACCAGCTAGTACTGGTAATGATAAAAGTAGTAATAGAGCTGTAATTCCTACAGAT CATACAAATAGGGGAATTTGTTCAGGGGATATACCTGTAGGTCGTATATTAATAATTGTTGAAATAAAATTAA TGGCTCCTAAAATTGATGAAACTCCTGCTAAGTGGAGGGAAAAAATTGCTAGATCTACTGAAGCTCCTCTATG AAATAGACTATTGGATAATGGTGGAACAGTTCATCCTGTACCTGCTCCAACTTCTACAAGTCTTCTGGTTATTA ATAATGTTAATGATGGTGGTAATAGTCAAAATCTTATATTATTTATACGTGGGAATGCTATATCTGGGGCCCCA ATTATTAAAGGTACTAATCAATTACCAAATCCTCCAATTATAATTGGTATTACTATAAAGAAAATTATAATAAAT GCGTGAGCAGTAACAATAACATTAATTTGATCATCTCCAATAAATATTCCTGGTTGGCCTAGCTCAATTCGGAT AATTCATCTAAGAGATGACCCAACTATACCTGACCTATACCGAAAAAGTAAAGTGTCCCAATATCTTTATGATG GGGTTAAAAAA **DNA Barcode:** 	

19	*Eocanthecona furcellata*	**COI gene sequence:** AAAAGTAGGATCCGCTATAAGACTAATTATTCGTATTGAAGTAGGTCAACCTGGAAGATTTATTGGG GATGACCAAATTTATAATGTAGTCGTTACTGCACACGCTTTTGTTATAATTTTCTTTATAGTTATACCA ATTATAATTGGAGGATTTGGTAATTGACTAGTACCTTTAATAATTGGAGCACCAGATATAGCATTTCC ACGAATAAATAATATAAGATTCTGATTACTACCCCCTTCTCTTACCCTACTAATAGTAAGAAGATTAGC TGAAGCTGGAGCTGGAACCGGGTGAACAGTTTACCCTCCATTATCAAGCAATTTATCCCATAGAGGT GCTTCAGTAGACGTAGCTATTTTTTCCTTACATTTAGCAGGAGTATCTTCAATTTTAGGTGCTGTAAAT TTTATTTCTACCATTATTAATATACGGCCCGCGGGGATAATTCCAGAACGGATTCCCTTATTTGTTTGA TCAGTTGGAATTACAGCTCTGCTACTATTATTATCTTTACCAGTTTTAGCAGGAGCTATTACGATATTA TTAACAGATCGAAATTTTAATACATCCTTTTTTGATCCCTCATGAGGAGGAGATCCAATTTTGTATCAA CACTTATTCTGATTTTTTGGTCACCTGA **DNA Barcode:** 	
20	*Nizara virudula*	**COI gene sequence:** CAGGTGACCAAAAAATCAAAATAAGTGTTGATAAAGAGGGGTCTCCCCCTCCTGAAGGGTCAAAGAATGATGTA TTAAAGTTTCGATCTGTTAATAATATTGTAATTGCACCTGCTAGTACAGGTAATGAAAGTAGTAATAATAGTGCT GTGATTCCAACTGATCAAACAAATAGTGGCACTCGTTCTGGAGTTATACCTGTTGGTCGTATATTAATAATAGTT GAAATGAAATTTACTGCACCTAAAATTGATGATACTCCTGCTAGATGTAATGAAAAAATAGCTAAATCCACTGAA GCTCCTCTATGGGATAAGTTACTAGATAAAGGAGGATCAGTTCATCCTGTCCCTGCTCCAGATTCTGCTAATCTTC TTACTATTAAAAGGGTTAATGATGGGGGTAATAGTCAGAATCTTATATTGTTTATTCGAGGGAATGCTATGTCTG GGGCACCAATCATTAAAGGTACTAATCAATTTCCAAATCCTCCAATTATGATTGGCATTACTATAAAGAAAATTAT TACAAATGCGTGAGCTGTTACTACTACATTATTTTGATCATCTCCAATAAATCTTCCGGGTTGTCCTAGTTCAATTC GAATAATTAGTCTTATTGCTGATCCTACTATTCCTGCTCATATACCAAATAAATATAAGGTTCCAATATCTTTATGA **DNA Barcode:** 	
21	*Spelobia bifrons*	**COI gene sequence:** ATATAGGTGTTGGTATAAAAGGGTCTCCTCCTCCTGCTGGATCAAAGAAAGAGGTATTTAAATTTCGATCTGTCAA TAATATTGTAATAGCTCCGGCTAATACTGGTAGAGATAGTAATAATAATAATGCTGTAATTACTACTGATCACACAA ATAATGGTATTCGGTCAAAAGTAATTCCAGTGGATCGTATATTAATGACAGTTGTAATAAAATTTACAGCTCCTAAA ATTGAAGAGATTCCTGCTAAATGAAGAGAGAAAATTGCTAAATCTACTGAAGCTCCTCCATGGGCAATTCCAGAA GATAGAGGAGTTCAACCTGTACCAGCCCCATTTTCCACTATACTACTAACTAATAGTAGTGTAAGAGAAGGAGGCA GTAATCAAAAACTTATATTATTTATTCGTGGAAAAGCTATATCAGGAGCTCCTAATATTAAAGGAACGAGTCAATTT CCGAATCCACCAATTATAATAGGTATTACTATAAAAAAAATTATTACAAAAGCATGTGCTGTAATTACATTATTTTG ATCATCTCCAATTAAAGCACCTGGATGACCTAGTTCAGCTCGAATTAAAATACTAAGAGAAGTACCTACTATTCCG GCTCAAGCTCCAAATATGAAAAGAGTACCAATATCTTTAGGGGGGAAAAAAAA **DNA Barcoding:** 	
22	*Exorista sorbillins*	**COI gene sequence:** AGCTGAATTAGGACATCCTGGATCATTAATTGGTGATGATCAAATTTATAATGTAATTGTTACAGCTCA TGCATTCATTATAATTTTTTTTATAGTTATACCAATTATAATTGGAGGATTTGGTAACTGACTAGTTCCTT TAATATTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGTTTTTGATTACTTCCTCCTTC TTTAACACTTTTGTTAACAAGTAGTATAGTTGAAAATGGAGCCGGAACTGGATGAACAGTTTATCCACC TTTATCTTCAGTAATCGCCCACGGAGGAGCATCTGTTGATTTAGCAATTTTTTCTCTTCATTTAGCTGGG ATTTCATCAATTTTAGGTGCTGTAAATTTTATTACAACAGTAATTAATATACGATCAATAAATTTTACATT AGACCGAATACCTTTATTTGTATGATCTGTAGTTATTACTGCTTTATTATTACTATTATCATTACCTGTAT TAGCTGGAGCAATTACTATACTTTTAACAGACCGAAATTTAAATA **DNA Barcode:** 	
23	*Myllocerus viridanus*	**COI gene sequence:** GGGTGACCAAAAAATCAAAATAAATGCTGGAGAATAGGGTCTCCCCCTCCTGCCGGGTCAAAAAAAGATGTATT AATATTACGATCTGTTAATAGCATAGTGATAGCCCCTGCTAGGACAGGTAAAGATAAAAGAAGTAAGATGGCAG TAATTTTTACTGCTCATACAAATAGAGGTAGACGATCAAATGATATTCCAGCAGGTCGTATATTAATAACGGTAG AAATAAAATTTACTGCCCCAAGAATAGAAGATACTCCAGCTATATGAAGTCTAAAGATGGCTAAATCAACTGATG AGCCTTCATGAGCGATATTAGCCGATAGAGGGGGAACCGTTCATCCTGTCCCAGCTCCTTTGTCTACAATTCTTCT TATAAGTAAGAGAGATAAAGAGGGGGGTAAAAGTCAAAATCTTATATTATTAAGTCGGGGGAAGGCTATATCA GGAGCTCCTAGTATAAGAGGGACTAATCAATTTCCGAATCCCCCAATTATTATAGGTATAACTATAAAGAAAATT ATAATGAAAGCGTGAGCTGTAACAATTACTTATAGATTTGGTCATCTCCAATTAAGGATCCTGGGTTTCCTAGTTC TGTTCGAATTAAAATTCTTAATGAAGTTCCTACTATTCCGGATCATGCTCCAAAAAGGTTCCAATATCTTTAT **DNA Barcode:** 	
24	*Attagenus fasciatus*	**COI gene Sequence:** TTGACTAGTCCCTTTAATATTAGGAGCTCCAGATATAGCATTCCCCCGAATAAATAACATAAGATTTTGAT TGCTCCCTCCTTCTTTAACTTTATTATTAATAAGTAGAATAGTTGAAAGAGGTGCTGGTACTGGATGAAC TGTATATCCCCCACTCGCCGCTAATATTGCCCATGGAGGTGCTTCTGTTGATTTAGCCATTTTCAGTCTAC ATTTAGCTGGAATCTCTTCTATTCTAGGAGCAGTAAATTTTATTACTACAGCTATTAATATACGAACACCA GGAATAACTCCTGAACGAATACCTCTATTTGTATGATCTGTTGCTATTACAGCCTTATTATTACTTCTATCC TTACCTGTCTTAGCAGGAGCAATCACTATATTATTAACTGATCGAAACCTAAATACTTCATTTTTTGA **DNA Barcode:** 	

25	*Illeis cincta*	 **COI gene sequence:** TCTATAATGTAATCGTTACAGCCCATGCTTTTATCATAATTTTTTTCATAGTAATACCAATCATAATTG GGGGATTTGGGAATTGGTTAGTTCCTCTAATACTAGGAGCTCCAGATATGGCTTTCCCACGATTGAA TAATATAAGATTTTGGCTTCTTCCCCCAGCTTTAACATTATTAATTTTCAGAAGTATAGTAGAAATAG GGGCAGGAACAGGATGAACTGTATACCCTCCCTTATCTTCAAATGTAGCACACAGAGGGGCTTCAGT AGATTTAGTAATTTTTAGTCTCCATTTAGCCGGGATTTCTTCTATTTTAGGAGCAGTAAATTTTATTTC TACTATTATAAATATACGCCCCTTTGGAATAAATTTAGATAAAACTCCATTATTTGTTTGATCAGTTTT AATTACTGCAATTTTATTGTTAC **DNA Barcode:** 	
26	*Calvia championorum*	 **COI gene Sequence:** AAATAGGTGTTGTTATAAAATCGGGTCACCTCCTCCTATAGGATCGAAAAAAGATGTATTAATATTACGGT CAGTTAATAGTATAGTAATAGCTCCCGCCAGTACTGGTAAGGAAAGAAGTAAAAGAATTGCTGTAATTAA AACTGACCATACAAATAAAGGGGTCTTATCTAAATTTATCCCAAAAGGACGTATATTTATAATAGTAGAAA TAAAGTTTACTGCTCCTAAAATTGAAGAGATTCCTGCTAAGTGAAGGCTAAAAATTACTAGATCTACTGAG GCACCTCTATGAGCTACGTTAGAAGATAGAGGGGGATACACAGTTCATCCTGTTCCTGCCCCTATTTCTAC TATTCTTCTAAAAATTAATAATGTTAAAGCTGGGGGTAGCAACCAAAATCTTATATTATTTAATCGTGGAA ATGCTATATCGGGGGCTCCTAGTATTAGAGGAACCAATCAGTTTCCAAATCCTCCAATTATAATTGGTATT ACTATAAAAAAAATTATAATAAAAGCATGAGCTGTGACAATAAAGATTTGGTCGTTTCCAATTAAACTATT TGTTGTCCCTAATTCTAATCGAATTAAAATTCTTAAAGAAGTTCCTACTATTCCTGCTCATATACCAAATAA GAAAAGTGTTCCAATATCTTATATTGGGGAGAAAAATT **DNA Barcode:** 	
27	*Calvia quaturodecimguttata*	 **COI gene Sequence:** AACACTATATTTTTTATTTGGAATGTGAGCTGGAATAGTAGGGACTTCTTTAAGAATTCTAATTCGATTAGAACTAGG AACAACTAACAGAGTAATTGGAAATGACCAAATTTATAATGTAATTGTTACAGCTCACGCTTTTATTATAATTTTTTT ATAGTTATACCTATTATAATTGGAGGATTTGGAAATTGACTAGTTCCTTTAATAATCGGGGCCCCTGACATAGCATTC CCCCGATTAAATAATATAAGATTTTGATTACTACCCCCTGCCCTAACATTATTAATTTTTAGAAGAATGGTTGAAATAG GAGCAGGAACAGGATGAACTGTGTACCCCCCTCTTTCCTCAAACATAGCACATAGAGGATCATCTGTAGATTTAGTA ATTTTTAGCTTACACTTAGCTGGAATTTCCTCTATTTTAGGAGCTGTAAATTTTATTTCTACTATTATAAATATACGCCC ATTCGGAATAAATTTAGATAAAACCCCCTTATTCGTATGATCAGTATTAATTACAGCTATTTTATTACTTTTATCATTAC CAGTTCTAGCAGGAGCAATTACTATACTTCTTACAGATCGAAATATTAATACATCTTTTTTCGATCCTATAGGGGGAG GTGACCCTATTTTATACC **DNA Barcode:** 	
28	*Coccinellidae*	 **COI gene Sequence:** AACACTTTACTTTCTATTTGGGATATGAGCAGGTATAGTAGGAACCTCTTTAAGAATTTTAATCCGTTTAGA ACTAGGAACAACAAATAGTTTAATTGGTAACGACCAAATCTATAATGTAATCGTTACAGCCCATGCTTTTA TCATAATTTTTTTCATAGTAATACCAATCATAATTGGGGGATTTGGGAATTGGTTAGTTCCTCTAATACTAG GAGCTCCAGATATGGCTTTCCCACGATTGAATAATATAAGATTTTGGCTTCTTCCCCCAGCTTTAACATTAT TAATTTTCAGAAGTATAGTAGAAATAGGGGCAGGAACAGGATGAACTGTATACCCTCCCTTATCTTCAAAT GTAGCACACAGAGGGGCTTCAGTAGATTTAGTAATTTTTAGTCTCCATTTAGCCGGGATTTCTTCTATTTTA GGAGCAGTAAATTTTATTTCTACTATTATAAATATACGCCCCTTTGGAATAAATTTAGATAAAACTCCATTA TTTGTTTGATCAGTTTTAATTACTGCAATTTTATTGTTACTTTCATTACCAGTTTTAGCAGGAGCTATCACAA TGTTATTAACTGACCGTAATATCAATACCTCTTTTTTTGACCCTATAGGAGGAGGGGACCCTATTTTATACC AACATCT **DNA Barcode:** 	
29	*Cryptoleamus monotrouzeri*	 **COI gene Sequence:** TTTATTCAAACCGTTTTCCGGAAAGAAAAACAACGGTTCTTTTTTAGGTATCCTATATCTTTAATTGGAAA TGATCAAATTTATAATGTTATTGTAACTGCCCATGCTTTCATTATAATTTTTTTTATAGTTATGCCTATTAT AATTGGAGGATTTGGAAATTGATTAGTACCTTTAATAATTGGAGCCCCTGATATAGCCTTCCCTCGACTT AATAATATAAGATTTTGACTTCTTCCTCCTGCCTTAACTTTATTAATTATAAGATCAATTGTAGAAAGAGG AGCAGGAACTGGTTGAACAGTCTATCCACCTTTATCTTCTAATTTAGCTCATAGAGGGCCTTCTGTAGAT TTAGCTATTTTTAGACTTCATTTAGCAGGTATTTCATCTATTTTAGGAGCAATTAATTTTATTACTACAATT TTAAATATACGTCCATATTTAATAACACTTGAAAAAATACCATTATTTGTATATCTGTTTTAATTACAGCTG TTCTTCTTCTTCTTTCCTTACCTGTTTTAGCAGGAGCTATTACAATACTTTTAACTGATCGAA **DNA Barcode:** 	
30	*Hexocentrus Japonicus*	 impact on the control of hexacentrus species. **COI gene sequence:** TCACTTAGATTTTTAACCCATCGAGAATTAGGAAACCTGGAATCTTTATTGGGGGATGACCAAATTTA TAATGTTATTGTTACAGCCCACGCTTTCGTAATAACTTTCTTTATAGTAATGCCAATCATGATTGGAG GATTTGGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCCCGAATAAACAAC ATAAGTTTTTGACTTCTTCCTCCTTCTCTCACCCTTCTTTTAGCAAGTAGTCTAGTTGAAAATGGAGCA GGTACAGGTTGAACTGTTTATCCCCCATTATCAGGGGGTATTGCTCATGGAGGAGCTTCTGTTGATTT AGCTATTTTCTCCCTTCACTTAGCAGGTATCTCTTCAATTCTAGGTGCAGTAAACTTCATTACCACAAC AATTAATATACGAGCACCAGAATATCACTAGATCAAACTCCCTTATTTGTCTGATCTGTCGCAATTACT GCATTGCTTCTCCTTTTATCCTTGCCCGTTTTAGCAGGAGCCATTACAATATTATTAACAGATCT **DNA Barcode:** 	

31	*Neothacris Acuticeps*	 **COI gene Sequence:** AAATAAATGTTGATATAAGATTGGGTCCCCTCCTCCTGCAGGGTCGAAAAATGATGTATTTAAGTTTCGGTCTGTTAGTAA TATTGTGATTGCTCCTGCAAGAACAGGTAACGATAAGAGTAATAATAGTGCTGTAATAATTACTGATCATACAAATAGAG GGGTTTGGTCTATATTTATTAATGATGATCGTATATTGATTGCTGTTGTAATAAAGTTTACTGCCCCTAGGATTGATGAAAC ACCAGCTAAGTGAAGAGAAAAAATTGCTAAATCTACTGATCTACCTCCATGTGCAATGGCTCCGCTAAAGGTGGATATACT GTTCAGCCCGTACCCACTCCTATATCAATTATCGATGATGTTATTAGTAATGTTAAAGATGGTGGTAATATTCAAAATCTTA TGTTATTTATTCGTGGAAATGCTATATCTGGGGCCCCAATTATTAAAGGGACTAGTCAATTTCCGAATCCTCCAATTATGGG CACCAAGAAAATTATGACAAATGCATGTGAGATTACATTGTATATTTGATCATCACCAATTAATTGTCCAGGTTGCCCTAAT TCTGTTCGGATTAATAATCTATAGATGTACCCACTATTCCAGACCGCTCCGAATAAAAAGTATATTGTTCCAATATCTTATG AGGGGGTTAAAAAAATA **DNA Barcode:**	
32	*Meranomplus magrettii*	 **COI gene sequence:** AGGTGACCAAAAAATCAAAATAGATGTTGATATAGTAGGGTCTCCCCCCCCGGAAGGGTCAAAAAT GAAGATTACGATCAGTTAATATATGGTGATTGCTCCAAAGACGGGCAAGGAAAGGAAAATGGCTGT AATTATAATTGATCAAAAAAGAGTAATTTTGAAGGAAAAATTTTTGTGGTGTATGAGAATAGTGGAA ATGAAATTAATGGCAATAGAAGATATACCAGCAATAAGTGAAAAAATAGACATGTCAACAGAGGGG CCACTATGAAAAATATTTGATGGGGGGTAAATGGTCCATCCGGTTCCTACTCCTGATCCAATAAAATT TCTAAAAGTAATAGTGAGAGAGATGGGGGTAATAATCAAAATCTTATATTATTTATTCGGGGGTATG CTATGTCAGGTGATCCGAGTATTAAGGGAACTAGAAAATTGCCAAATCCACCGATTATAAAAGGCAT AACTATAAAGAAAATTATAATGAAGGCATGACTAGTTACTATAGAATTAATTTGGTCATTATTAATAA AGATTCACATGTGCCTAATTCTAATCGAATTATACTTATTGAGGATCCAATTATCCCTGCTCAGATTGC TAGTAAAAAGAATACCAATATCTTTATGATTTGTTGACCCA **DNA Barcode:**	

If the scanner failed to decode the DNA QR code, the rectangle contains some random numbers only. In this case, the user should repeat the scanning again for deciphering the coded information. The created QR codes are supplied to QR code scanner, itdisplays the Insect scientific name, image, taxonomic classification, life cycle, COI gene sequence and its DNA barcode. DNA based QR code of each insect species was shown in figure

DISCUSSION

DNA-based QR codes offer a unique approach to storing and accessing biological data efficiently. Unlike conventional barcodes, QR codes can encode multiple types of data-including numeric and alphanumeric characters, Kanji, Hiragana, Katakana, symbols, binary, and control codes. These codes can store up to 7,089 numeric characters or 4,296 alphanumeric characters, which is hundreds of times more than the capacity of traditional one-dimensional (1D) barcodes (ISO/IEC 18004:2015). Owing to their compact nature, QR codes require only one-tenth the space of a regular DNA barcode, making them ideal for field-based biological applications. They support high-speed scanning, are readable from any orientation due to position detection patterns, and function effectively even in the presence of background interference. Moreover, QR codes include built-in error correction capabilities, allowing up to 30% of the code to be damaged without data loss. This is achieved through four standardized error correction levels: Level H (30%), Level Q (25%), Level M (15%), and Level L (7%).An additional advantage is compartmentalization, allowing data to be segmented into up to 16 individual areas, thus enabling miniaturized QR prints suitable for various labeling purposes. These codes are also highly accessible, as they can be scanned using any smartphone, tablet, or computer with a camera, supported by freely available QR code reader applications.Several studies support the use of QR codes in molecular taxonomy and DNA barcoding. For example, Chang Liu et al. (2012) conducted a comparative analysis between 1D and 2D barcode systems using gene regions such as ITS2, rbcL, matK, psbA-trnH, and COI, and concluded that QR codes are the most appropriate symbology for encoding DNA barcodes. Ravi Prabhakar et al. (2016) developed a matK-based QR classifier to identify plant species using the matK gene as a DNA barcoding marker. Similarly, Barbi Gogoi et al. (2020) demonstrated the field utility of DNA-based QR codes by creating a system to identify *Clerodendrum* species, enabling even non-specialists to recognize plant species by scanning QR codes with mobile devices.Building upon these advancements, the present study developed DNA-based QR codes for insect pest species collected from the sericultural ecosystem, using partial mitochondrial COI gene sequences. A Python-based software system was implemented to generate output that displays the insect species name, image, taxonomic classification, COI gene sequence, and corresponding DNA barcode within a scannable QR format.This system holds substantial promise for practical use, especially by farmers and field professionals, as it allows for easy pest identification at any life stage. By scanning these QR codes through mobile devices, users can quickly access critical information to accurately identify pest species and take timely and appropriate pest control measures. This approach can substantially reduce crop losses in mulberry plantations and safeguard silkworm rearing, thereby enhancing the overall productivity and sustainability of sericulture.By integrating molecular diagnostics with digital technology, this method bridges the gap between scientific research and on-ground agricultural application, empowering farmers with real-time, reliable pest identification gears.

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