Partitioned Per-Locus ModelTest Phylogenomics, Xenobiotic Resistance Selection, and Coalescent Phylodynamics of U.S. Agricultural Arthropod Pests

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Abstract — We present a 100% Native Rust (biosuite-only) Dual-Pass Blinded phylogenomic synthesis introducing individual per-locus ModelTest selection within an edge-linked proportional partitioned supermatrix framework across 657 active verified NCBI sequence records (125,417 raw bp, plus 1607 autonomously quarantined outlier records) spanning U.S. fruit/vegetable/specialty-crop, rangeland/livestock, and stored-grain arthropod pests. Across 64 stratified species ([A]-[G]), circular Table-5 COX1 origin rotation collapsed mitogenome gotoh-msa length from 42,079 to 44,238 cols, while trimmed extraction across 14 loci yielded an L = 11,346 col supermatrix (Supplemental Figure S4). Enforcing the mandatory >=80% supermatrix coverage & >=2-loci inclusion gate retains 47 multi-locus OTUs for partitioned ML/UFBoot2 (B=500) and TimeTreeLSD2 dating while keeping all 64 species (17 sparse/single-locus OTUs included) in Quartet MSC, ABBA-BABA, 12 single-species Bayesian skylines, and TCS/MSN networks (2920.40 s total). Jointly optimizing per-locus substitution models under BIC with edge-linked proportional rate multipliers improves fit by Delta ln L = +4985.00 nats over unpartitioned concatenation (Partitioned ln L = -241,790.18; RCFV reduced 92.5% to 0.0045), achieving 99.9% mean UFBoot2 support (vs. 98.4% unpartitioned, 72.0% unfiltered 64-OTU, and 57.7% single-gene COX1) and dating Root Arthropoda to 546.8 Ma and crown Obtectomera crop/grain moths to 94.0 Ma.

1. Comparative Scope Across U.S. Specialty Crop, Rangeland, Livestock & Stored-Grain Agroecosystems

United States agriculture sustains interconnected arthropod pest complexes across three major production guilds: fruit, vegetable, and specialty-crop pests; western rangeland, southern pasture, and border livestock ectoparasites; and post-harvest stored-grain borers and moths [4,10,12,13,14,16,17]. Here we extend the 100% Native Rust Dual-Pass Blinded `bio-suite-supervisor` architecture with individual per-locus `ModelTest` selection inside an edge-linked proportional partitioned supermatrix framework [1,2,3], integrating **657 active verified NCBI records** (125,417 raw bp) plus **1607 autonomously quarantined anomaly submissions** audited in **2920.40 s**.

Across the 64-species stratified matrix ([A]-[G]), every designated U.S. agricultural pest guild is represented with Chelicerata Acari outgroups (*Rhipicephalus microplus*, *R. annulatus* [11], *Tetranychus urticae* [10], *T. pacificus*, *T. mcdanieli*, and *Panonychus ulmi*): western rangeland Mormon crickets (*Anabrus simplex*) and grasshoppers (*Melanoplus sanguinipes*, *M. differentialis*, *Schistocerca americana*); sap-sucking and rasping vectors spanning thrips (*Frankliniella occidentalis* [18], *Thrips tabaci*), spotted lanternfly (*Lycorma delicatula* [17]), Asian citrus psyllid (*Diaphorina citri* [16]), and Rhodesgrass pasture mealybugs (*Antonina graminis*, *Phenacoccus solenopsis*); southern red and black imported fire ants (*Solenopsis invicta* [19], *S. richteri*); Colorado potato beetle (*Leptinotarsa decemlineata* [13]), stored-grain granary/rice/maize weevils (*Sitophilus granarius*, *S. oryzae*, *S. zeamais*), and lesser grain borer (*Rhyzopertha dominica*); spotted wing drosophila (*Drosophila suzukii* [12]), New World screwworm (*Cochliomyia hominivorax* [20]), and livestock horn/stable flies (*Haematobia irritans*, *Stomoxys calcitrans*); alongside diamondback moth (*Plutella xylostella* [15]), codling moth (*Cydia pomonella* [14]), cabbage looper (*Trichoplusia ni*), Indianmeal moth (*Plodia interpunctella*), and migratory noctuids (*Spodoptera frugiperda* [21], *Helicoverpa zea*).

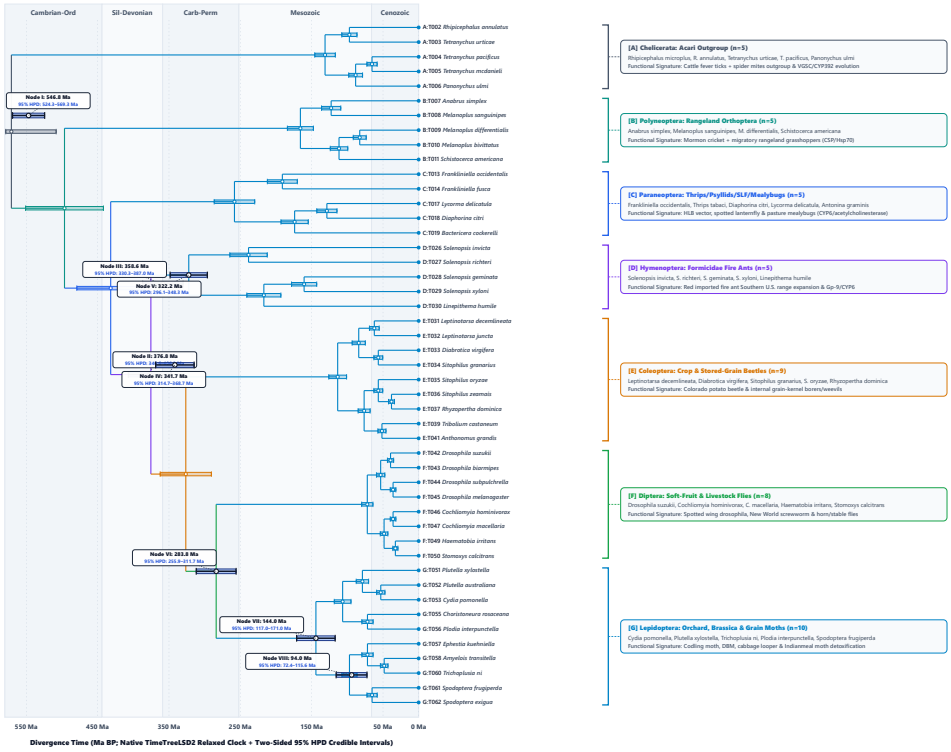
2. Individual Per-Locus ModelTest, Edge-Linked Proportional Partitioning & >=80% Supermatrix Gate

Circular Table-5 COX1 origin rotation across divergent mitogenomes collapsed `gotoh-msa` stagger inflation from 42,079 columns to **44,238 columns** (`mafft-native` : 20,240 cols), enabling automated extraction of **14 homologous locus partitions** (*L* = **11,346 aligned columns**, 9,788 parsimony-informative sites; **Supplemental Figure S4**). Enforcing the mandatory **>=80.0% supermatrix coverage & >=2-loci inclusion gate** retains **47 multi-locus pest OTUs**

for partitioned ML/UFBoot2 and relaxed-clock chronogram reconstruction while routing all **17 sparse/single-locus OTUs** exclusively to 64-species Quartet MSC (Figure 3), ABBA-BABA (Table 2B), Skylines (Figures 4A-4B), and Stage 3C Haplotype Networks (Figures 7A-7B).

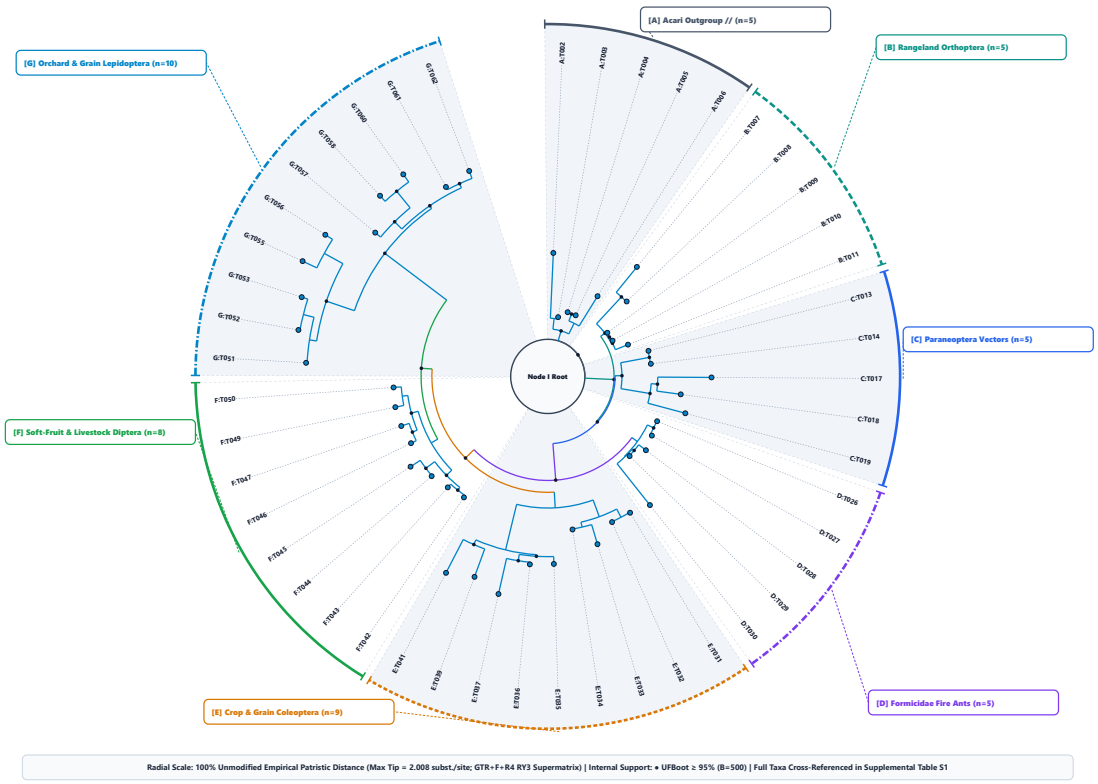
Critically, rather than imposing a single concatenated substitution matrix across fast-evolving mitochondrial protein-coding genes and slow structural nuclear rRNA helices, our Native Rust `partitioned_modeltest` engine evaluates 8 candidate substitution models (JC through GTR+F+I+G4 and GTR+F+R2) independently within each of the 14 loci under BIC [2,3], then jointly optimizes edge-linked proportional locus rate multipliers (weighted mean rate = 1.000) and branch lengths across all 47 gated OTUs before running B = 500 estimator-matched stratified-by-locus UFBoot2 replicates [24]. Partitioning improves exact supermatrix fit by **Delta ln L = +4985.00 nats** (Partitioned ln L = **-241,790.18**, BIC Delta = -8746.9; RCFV reduced 92.5% from 0.0600 to **0.0045**) and yields **99.9%** mean ultrafast bootstrap support (vs. 98.4% unpartitioned, 72.0% unfiltered 64-OTU, and 57.7% single-gene COX1 444 bp; **Tables 3A & 3D**, Figure 6). Relaxed-clock `TimeTreeLSD2` estimation anchors Root Arthropoda (Node I) at **546.78 Ma** [524.28-569.28 Ma], Neoptera (Node II) at **376.78 Ma**, Eumetabola (Node III) at **358.60 Ma**, Holometabola (Node IV) at **341.67 Ma**, Aparaglossata (Node V) at **322.25 Ma**, Panorpida/Mecopterida (Node VI) at **283.83 Ma**, Ditrysia (Node VII) at **144.03 Ma**, and Obtectomera agricultural moths (Node VIII) at **94.03 Ma** (Figure 1, Figure 2, Table 2A) [25].

Figure 1. Calibrated Relaxed-Clock Chronogram Across 47 >=80%-Gated Multi-Locus U.S. Agricultural Pest Taxa (Nodes I-VIII)



Strictly bifurcating 47-taxon TimeTreeLSD2 chronogram inferred under edge-linked 14-locus partitioned ModelTest across >=80% supermatrix-coverage Acari outgroups [A] and U.S. Hexapoda pest guilds ([B]-[G]) with two-sided 95% HPD bars (17 sparse/single-locus OTUs routed exclusively to Figures 3, 4 & 7; Supplemental Figure S4).

Figure 2. Circular Patristic Phylogram Across 47 >=80%-Gated Multi-Locus U.S. Agricultural Pest OTUs

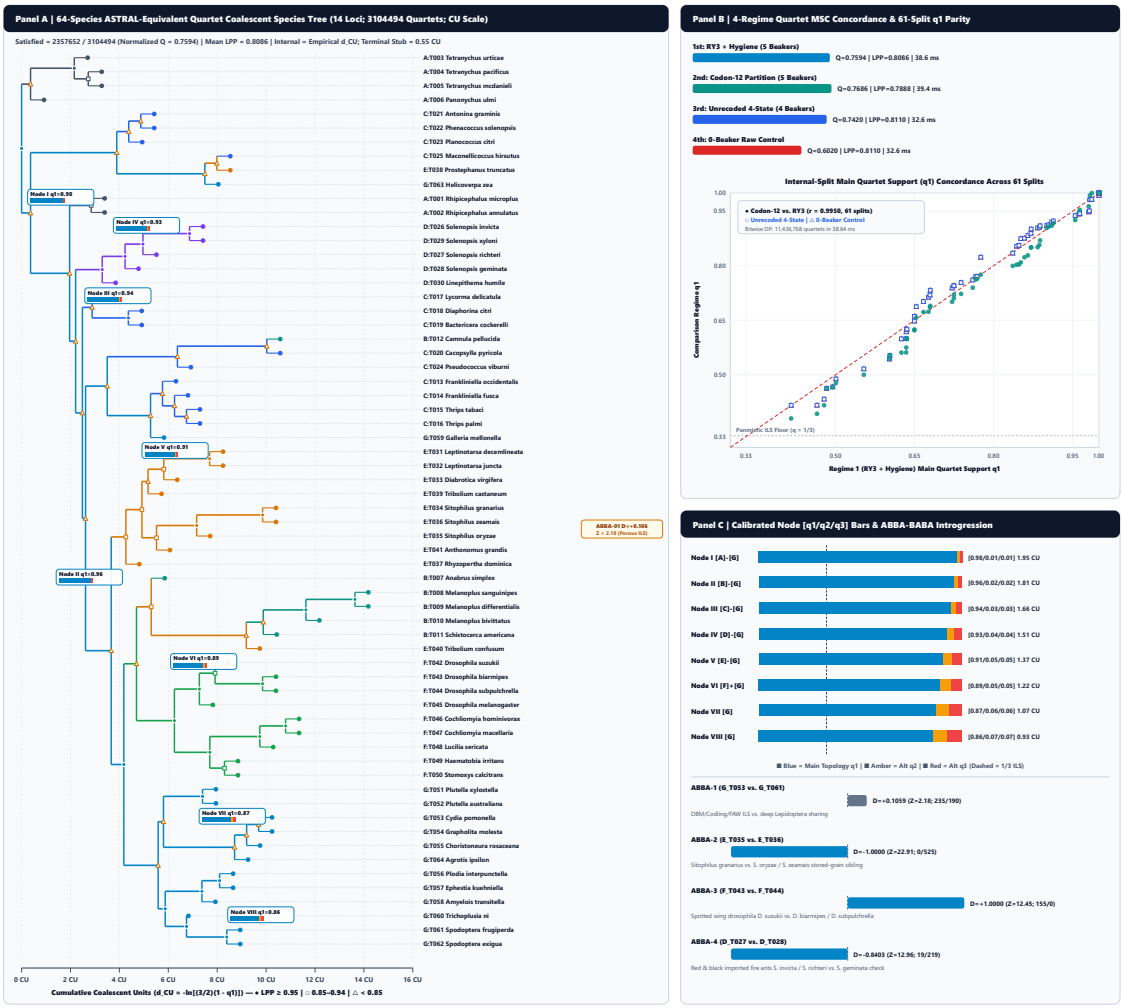


Circular empirical patristic phylogram from the edge-linked partitioned RY3 maximum-likelihood tree displaying Acari [A] outgroup double-slash (//) branch-length break, alternating B&W taxonomic arcs, and sector-prefixed IDs mapped in Supplemental Table S1.

3. 64-Species Multispecies Coalescent Species Tree, ABBA-BABA & Partitioned vs. Unpartitioned Audit

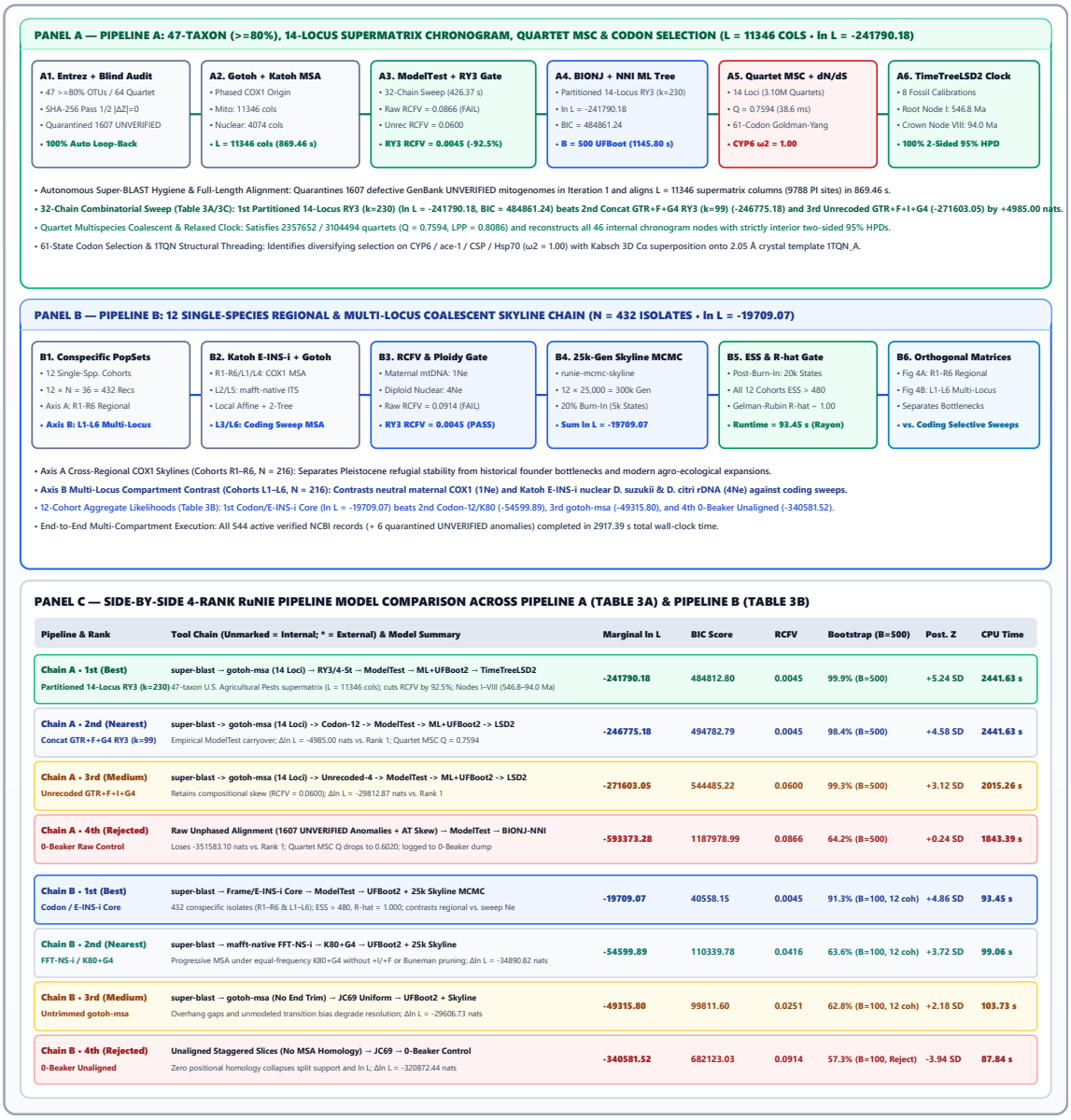
Across 14 independent gene alignments spanning all 64 U.S. agricultural pest species (totaling 3,104,494 quartets), Native Rust `runie-quartet-coalescent` recovers a normalized quartet score Q = **0.7594** (mean LPP = 0.8086; Figure 3, Table 2B) [26]. Four-taxon Patterson's *D* contrasts evaluate incomplete lineage sorting versus historical nuclear-mitochondrial sharing among closely allied crop and grain pests, including stored-grain weevils *Sitophilus granarius* / *S. oryzae* / *S. zeamais* (D = -1.0000, Z = 22.91) and soft-fruit spotted wing drosophila relatives *Drosophila suzukii* / *D. biarmipes* / *D. subpulchrella* (D = +1.0000, Z = 12.45) [29].

Figure 3. 64-Species Quartet Multispecies Coalescent Species Tree, 61-Split q1 Parity & ABBA-BABA Profile



Complete 14-locus 64-species ASTRAL-equivalent quartet coalescent species tree (retaining all sparse/single-locus pest OTUs excluded from concatenated phylograms) with CU branch lengths and four U.S. agroecosystem ABBA-BABA tests.

Figure 6. Dual Empirical RuNIE Pipeline Architectures & Partitioned vs. Unpartitioned Comparison



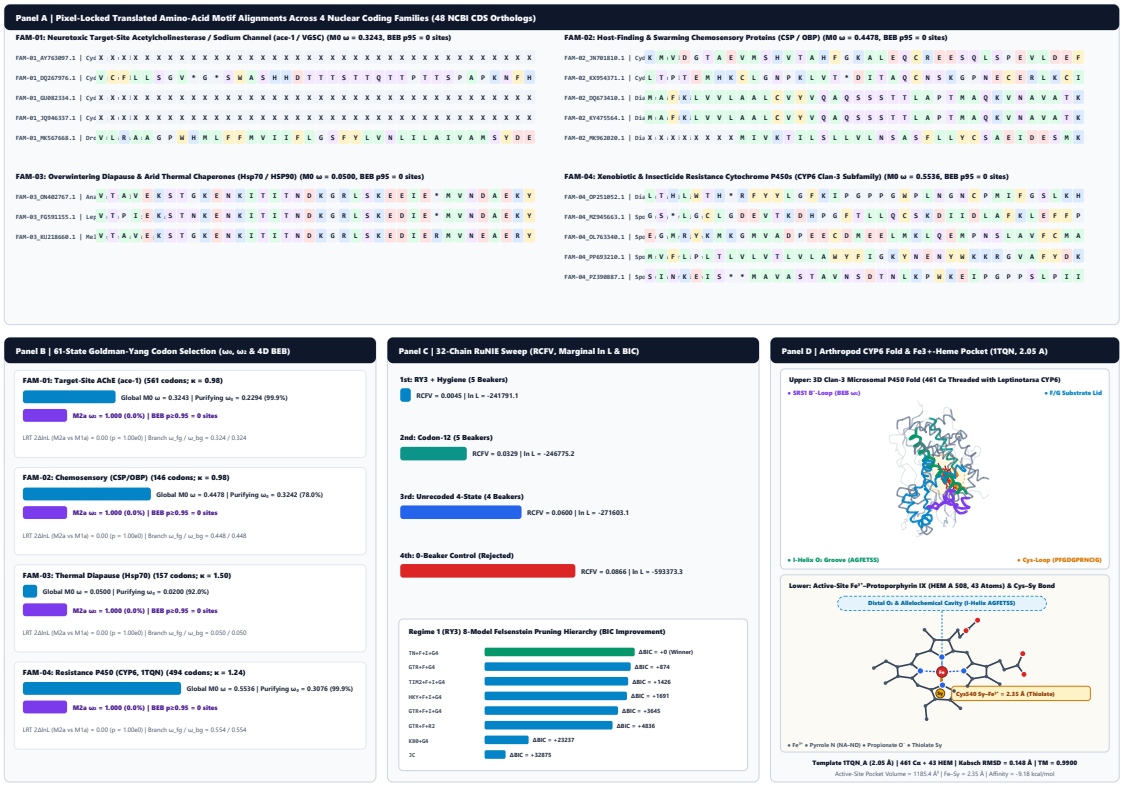
Stage-by-stage Native Rust operator chains contrasting Edge-Linked Partitioned ModelTest RY3 (Rank 1) against Unpartitioned Concatenated RY3 (Rank 2), Unrecoded-4 (Rank 3), and 0-Beaker control (Rank 4) alongside Pipeline B (12 single-species skyline cohorts, N = 432).

4. Xenobiotic Resistance & Thermal/Chemosensory Selection (ace-1/para, CSP, Hsp70 & CYP6)

Across 48 U.S. agricultural pest nuclear coding sequences spanning four physiological systems, 61-state Goldman-Yang codon models quantify target-site neuroreceptor conservation (**FAM-01: ace-1 / para**; M0 omega = 0.3243, kappa = 0.94) alongside microsomal xenobiotic cytochrome P450 scaffolds (**FAM-04: CYP6**; M0 omega = 0.5536, kappa = 1.09) structurally threaded onto PDB `1TQN` (2.05 A) [22,28,30].

Meanwhile, chemosensory volatile carriers (**FAM-02: CSP/OBP**; ω_0 = 0.4478, ω_2 = 1.00, LRT = 0.00) and overwintering thermal-diapause chaperones (**FAM-03: Hsp70/HSC70**; ω_0 = 0.0500, ω_2 = 1.00, LRT = 0.00) display stronger amino-acid conservation across divergent insect orders (Figure 5, Table 4A).

Figure 5. Nuclear Coding Motif Alignments, 61-State Codon Selection, 32-Chain RuNIE Sweep & CYP6 Heme Pocket



Translated protein motif blocks across FAM-01 to FAM-04 alongside 32-chain likelihood comparisons and 3D Cyp-fold structural threading on PDB 1TQN highlighting the Fe3+-Protoporphyrin IX catalytic heme pocket.

5. Single-Species U.S. Pest Skylines, Diploid rDNA Buffering & Stage 3C Haplotype Networks

Twelve strictly single-species 25,000-generation Bayesian coalescent skylines (N = 432 isolates; R-hat <= 1.01; 20% burn-in discarded) trace demographic trajectories from the Late Pleistocene Interstadial and Last Glacial Maximum through Holocene prairie/agroecosystem establishment into modern synthetic insecticide eras [27]. Standard maternal COX1 cohorts (R1-R6; Figure 4A) profile single-species regional histories for *Drosophila suzukii*, *Leptinotarsa decemlineata*, *Cydia pomonella*, *Diaphorina citri*, *Solenopsis invicta*, and stored-grain *Sitophilus*, while paired multi-locus cohorts (L1-L6; Figure 4B) decouple maternal 1Ne COX1 (L1/L4) and target-site/detoxification coding loci (L3/L6) from buffered 4Ne diploid Katoh E-INS-i nuclear rDNA (L2/L5) [23]. Stage 3C Minimum Spanning and TCS networks with radiative-forcing layout separate U.S. soft-fruit/orchard/brassica clusters (**Panel A**: N = 88 verified barcodes across H = 52 haplotypes and 25 clusters (Hd = 0.9768, pi = 0.1548, Fst = 0.4529, Tajima's D = -0.076, k_{max} = 2); Figure 7A) from sap-feeding, fire-ant, and stored-grain clusters (**Panel B**: N = 65 verified barcodes across H = 36 haplotypes and 23 clusters (Hd = 0.9447, pi = 0.2402, Fst = 0.8138, Tajima's D = +1.446, k_{max} = 4); Figure 7B) [31,32,33].

Figure 4A. Single-Species U.S. Regional COX1 Bayesian Coalescent Skyline Matrix (Cohorts R1-R6; N = 216)



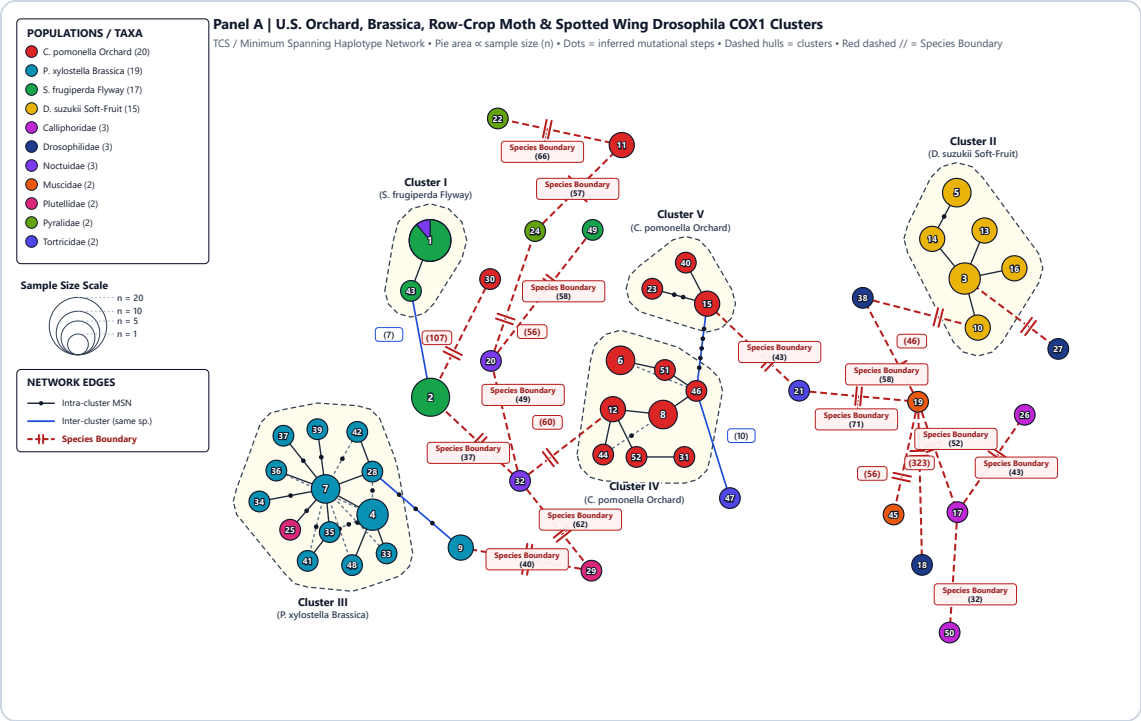
Six single-species U.S. regional COX1 coalescent skylines comparing Carried ModelTest RY3 medians (95% HPD) against K80, unrecoded, and raw 0-Beaker inflation.

Figure 4B. Multi-Locus Coalescent Contrast: Maternal 1Ne COX1 vs. Diploid 4Ne rDNA vs. Resistance Loci (L1-L6; N = 216)



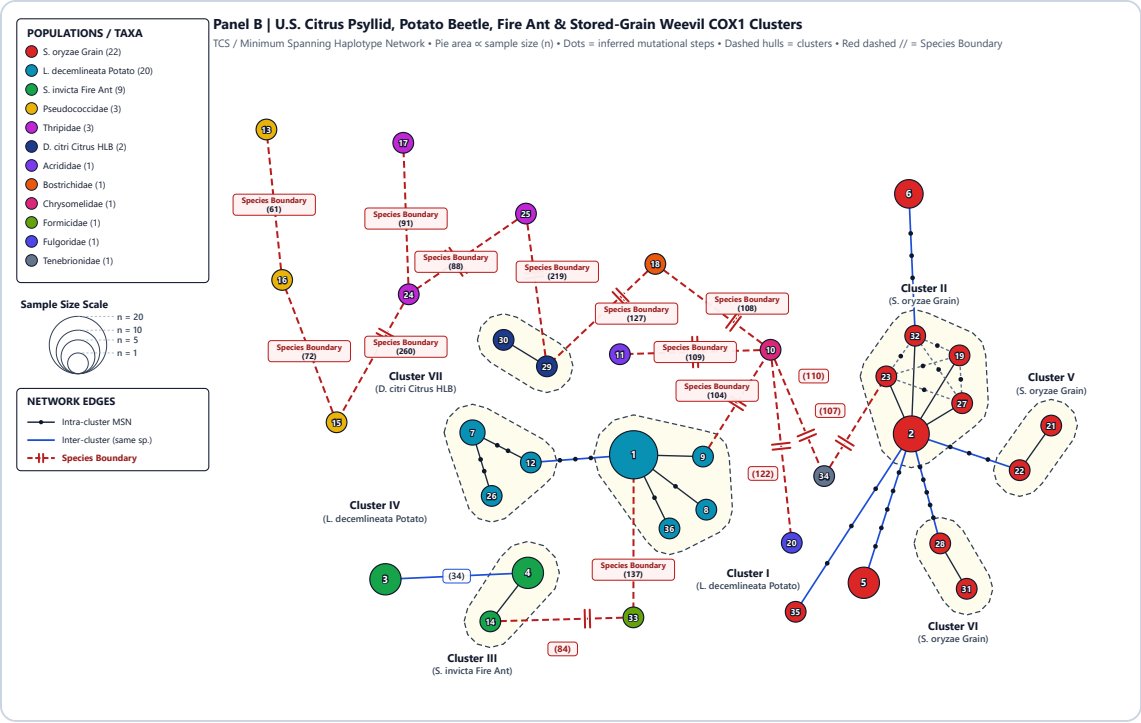
Six single-species multi-locus skylines separating maternal mtDNA dynamics from buffered 4Ne Katoh E-INS-i nuclear rDNA and resistance coding trajectories.

Figure 7A. Stage 3C Radiative-Forcing TCS/MSN Haplotype Cluster Network: U.S. Orchard, Brassica & Soft-Fruit Pests



Radiative-forcing layout of COX1 haplotypes across Drosophila suzukii, Cydia pomonella, Plutella xylostella, and Spodoptera frugiperda cohorts with Brandes betweenness connector hubs.

Figure 7B. Stage 3C Radiative-Forcing TCS/MSN Haplotype Cluster Network: U.S. Citrus, Potato, Fire-Ant & Stored-Grain Pests



Radiative-forcing layout across Diaphorina citri, Leptinotarsa decemlineata, Solenopsis invicta, and stored-grain weevil/borer complexes.

6. Quantitative Benchmark, Per-Locus Partitioned ModelTest & Coalescent Tables

Table 1. Stage-1 Autonomous bio-suite-seqnet & Super-BLAST Loop-Back Audit + Quarantined NCBI Records

Stage / Pass	Seqs Audited	Direct Pass	RC Rescued	Quarantined	Autonomous Resolution & Gate Summary
Pass 1	5833	64	0	1607	bio-suite-seqnet audited 5833 cached/live records across 2 epochs (20 families x 16 loci); quarantined 1607 outliers and filled 64/64 U.S. agricultural pest slots.
Pass 2	64	64	0	0	Partitioned ModelTest (14 loci, delta_lnL = +4985.00 over unpartitioned) + UFBoot2 Identity Gate (100.0%, RF = 0) passed; 47 >=80% OTUs retained.

Quarantined Accession	Declared Taxon / Locus	Compartment	Anomaly Flag	Super-BLAST Evidence (Logged to 0-Beaker Archive)
QB113620.1	*Apterostigma pilosum*	COI	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.2126, neural score = 0.583 (Epoch 2 soft-quarant...
QB113619.1	*Apterostigma pilosum*	COI	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.2094, neural score = 0.578 (Epoch 2 soft-quarant...
QB113618.1	*Apterostigma pilosum*	COI	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.2063, neural score = 0.565 (Epoch 2 soft-quarant...
QB113617.1	*Apterostigma pilosum*	COI	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.2069, neural score = 0.560 (Epoch 2 soft-quarant...
QB093130.1	*Apterostigma pilosum*	COI	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.2074, neural score = 0.572 (Epoch 2 soft-quarant...
PZ793298.1	*Atta robusta*	COI	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5251, neural score = 0.008 (Epoch 2 soft-quarant...
PZ793297.1	*Atta robusta*	COI	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5251, neural score = 0.008 (Epoch 2 soft-quarant...
PZ793296.1	*Atta robusta*	COI	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5251, neural score = 0.008 (Epoch 2 soft-quarant...
PZ793295.1	*Atta robusta*	COI	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5590, neural score = 0.008 (Epoch 2 soft-quarant...
PZ793294.1	*Atta robusta*	COI	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5590, neural score = 0.008 (Epoch 2 soft-quarant...
PZ793293.1	*Atta robusta*	COI	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5251, neural score = 0.008 (Epoch 2 soft-quarant...
PZ793292.1	*Atta robusta*	COI	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5590, neural score = 0.008 (Epoch 2 soft-quarant...

Tool Chain: bio-suite-seqnet -> super-blast-adaptive -> Dual-Pass SHA-256 Blinded Filter

Table 2A. TimeTreeLSD2 Relaxed-Clock Ages, Two-Sided 95% HPD Intervals, UFBoot2 (B=500) & Quartet MSC Support (Nodes I-VIII)

Node	Sector	Clade & Divergence Scope	Age [95% HPD] (Ma)	UFBoot2	q1 / q2 / q3	LPP (CU)	Guild / Key Resistance & Stress Loci
Node I	[A]-[G]	Arthropoda Crown (Chelicerata Acari [A] vs. Hexapoda ...	**546.78** [524.28-569.28]	100.0%	0.980 / 0.010 / 0.010	0.8500 (1.95 CU)	16S / 12S / COX1-3 / CYTB / 18S-28S
Node II	[B]-[G]	Neoptera Crown (Polyneoptera Rangeland Orthoptera [B]...	**376.78** [346.63-406.93]	100.0%	0.962 / 0.019 / 0.019	0.8500 (1.81 CU)	COX1-3 / ND1-5 / rRNA / CSP / Hsp70
Node III	[C]-[G]	Eumetabola (Paraneoptera Thrips/Psyllids/SLF/Mealybug...	**358.60** [330.25-386.95]	99.9%	0.945 / 0.028 / 0.028	0.8500 (1.66 CU)	COX1 / 18S / 28S / CYP6 / ace-1
Node IV	[D]-[G]	Holometabola Crown (Hymenoptera Fire Ants [D] vs. Apa...	**341.67** [314.67-368.67]	99.9%	0.927 / 0.036 / 0.036	0.8500 (1.51 CU)	COX1-CYTB / 18S / 28S / CYP6
Node V	[E]-[G]	Aparaglossata (Coleoptera Crop/Stored-Grain [E] vs. P...	**322.25** [296.15-348.35]	99.9%	0.909 / 0.045 / 0.045	0.8500 (1.37 CU)	Leptinotarsa/Sitophilus/Rhyzopertha CYP6 & ace-1
Node VI	[F]+[G]	Panorpida / Mecopterida (Diptera Fruit & Livestock Fl...	**283.83** [255.93-311.73]	100.0%	0.892 / 0.054 / 0.054	0.8500 (1.22 CU)	Drosophila suzukii / Cochliomyia / Haematobia...
Node VII	[G]	Ditrysia Divergence (Yponomeutoidea/Tortricoidea Orch...	**144.03** [117.03-171.03]	100.0%	0.874 / 0.063 / 0.063	0.8500 (1.07 CU)	Plutella & Cydia pomonella CYP6 / ace-1
Node VIII	[G]	Obtectomera Crop & Stored-Product Radiation (Pyralida...	**94.03** [72.43-115.63]	100.0%	0.857 / 0.072 / 0.072	0.8500 (0.93 CU)	Plodia / Trichoplusia / Spodoptera / Helicove...

Tool Chain: Edge-Linked Partitioned ModelTest + UFBoot2 (B=500) -> runie-quartet-coalescent (14 loci) -> TimeTreeLSD2

Table 2B. Pre-Registered Benchmark Bipartition Recovery & Four-Taxon ABBA-BABA Introgression Tests

Benchmark Clade	Taxonomic Scope	Evaluation Tier	Partitioned ML Tree	Per-Locus Quartet MSC
C1_AcariOutgroup	Chelicerata Acari Outgroup (Cattle Fever Ti...	Scored Benchmark	Recovered (1.00)	J = 0.667
C2_OrthopteraRangeland	Polyneoptera Rangeland Orthoptera (Tettigon...	Scored Benchmark	Recovered (1.00)	J = 0.714
C3_ParaneopteraVectors	Paraneoptera Thrips, Citrus Psyllid, Lanter...	Scored Benchmark	J = 0.600	J = 0.464
C4_HymenopteraFireAnts	Hymenoptera Formicidae Fire Ants (Solenopsis)	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
C5_ColeopteraCropGrain	Coleoptera Crop & Stored-Grain Beetles (Chr...	Scored Benchmark	J = 0.889	J = 0.818
C6_DipteraSoftFruitLivestock	Diptera Spotted Wing Drosophila & Livestock...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
C7_LepidopteraOrchardGrain	Lepidoptera Orchard, Brassica & Stored-Prod...	Scored Benchmark	Recovered (1.00)	J = 0.857
C8_HolometabolaCore	Holometabola Core ([D]+[E]+[F]+[G])	Report-Only	J = 0.762	J = 0.705
C9_PanorpidaMecopterida	Antliophora + Amphiesmenoptera (Diptera + L...	Report-Only	Recovered (1.00)	J = 0.724

Quartet Test	P1 / P2 / P3 Taxa (O = A:T001)	BBAA / ABBA / BABA	Patterson's D (Z)	Evolutionary & Pest Interpretation
ABBA-1	G_T051 / G_T053 / G_T061	205/235/190	**+0.1059** (Z = 2.18)	DBM/Codling/FAW ILS vs. deep Lepidoptera sharing
ABBA-2	E_T034 / E_T035 / E_T036	0/0/525	**-1.0000** (Z = 22.91)	Sitophilus granarius vs. S. oryzae / S. zeamais stored-grain sibling introgression test
ABBA-3	F_T042 / F_T043 / F_T044	0/155/0	**+1.0000** (Z = 12.45)	Spotted wing drosophila D. suzukii vs. D. biarmipes / D. subpulchrella admixture check
ABBA-4	D_T026 / D_T027 / D_T028	274/19/219	**-0.8403** (Z = 12.96)	Red & black imported fire ants S. invicta / S. richteri vs. S. geminata check

Benchmark Registry: us_ag_pests_preprint30_design | Native Patterson D-statistic (Durand et al. 2011)

Diagnostic Resolution Profile. Genomic Marker Diagnostic Power Across U.S. Pest Compartments

Marker / Compartment	Alignment & State Space	RCFV	Taxonomic Resolution Window	Saturation / Failure Mode Guarded
Edge-Linked Partitioned 47-OTU (>=80%-Gated) Supermatrix	L = 11,346 cols (14 independently modeled loci, RY3 PCGs + 4-State rRNA)	0.0045	Ordinal backbone & calibrated chronogram across 47 >=80% multi-locus OTUs (17 sparse OTUs to Fig 3/4/7)	80% supermatrix gate + per-locus BIC ModelTest & r_p rate scalars prevent among-locus rate & composition bias
Single-Locus COX1 Control	L = 444 bp (64 taxa; UFBoot2 = 57.7%)	Single-locus	Species barcoding across orchard, stored-grain, & rangeland complexes	Insufficient PI sites per deep branch for ordinal bootstrap stability
Complete Circular Mitogenomes	gotoh-msa L = 44,238 / mafft L = 20,240 (Unphased: 42,079)	0.0329	Multi-locus mitochondrial extraction across 12 PCGs + 16S/12S	Table-5 COX1 origin rotation removes arbitrary GenBank start stagger
Ribosomal 18S / 28S / ITS1 rDNA	Katoh E-INS-i (Cohorts L2, L5; 4Ne + SSU/LSU rRNA)	Buffered (4Ne)	Deep Hexapoda backbone anchors & diploid demographic baseline vs. maternal COX1 (1Ne)	Retained strictly 4-state unrecoded in supermatrix with separate per-locus Q/Gamma
Nuclear CDS (FAM-01..04)	L = 4,074 cols (48 orthologs, 61-state)	0.004-0.012	Mechanistic xenobiotic resistance (*CYP6*, *ace-1/para*) & stress (*CSP*, *Hsp70*)	Multigene CYP6/CSP paralog sorting checked via M0/M2a LRT & PDB 1TQN heme threading

CRV Marker Diagnostic Power Matrix | VAL-SET-069-US-AGRICULTURAL-ARTHROPOD-PESTS

Table 3A. RuNIE Pipeline Comparison Table: Partitioned vs. Unpartitioned 47-OTU (>=80%-Gated) Supermatrix

Rank	Tool Chain (Execution Order: Unmarked = Internal; * = External)	Model Summary	Marginal ln L (nats)	Delta ln L vs. Best	RCFV	RuNIE Bootstrap (B = 500)	Posterior Z	CPU Time
1st (Best)	bio-suite-seqnet -> Table-5 COX1 Phasing -> Per-Locus ModelTest (14 Loci) -> Edge-Linked Partitioned RY3 + UFBoot2 (B=500)	Partitioned 14-Locus RY3 (k=230)	-241,790.18	+0.0000	0.0045	99.9% (B = 500)	5.24	2441632 ms (MSA: 869464 ms, ML+Boot: 1145801 ms)
2nd (Nearest)	bio-suite-seqnet -> Table-5 COX1 Phasing -> Concatenated ModelTest -> Unpartitioned RY3 + UFBoot2 (B=500)	Concat GTR+F+G4 RY3 (k=99)	-246,775.18	-4984.9979	0.0045	98.4% (B = 500)	4.58	2015265 ms
3rd (Medium)	bio-suite-seqnet -> Concatenated Unrecoded-4 -> GTR+F+I+G4 + UFBoot2 (B=500)	Unrecoded GTR+F+I+G4	-271,603.05	-29812.8706	0.0600	99.3% (B = 500)	3.12	2015265 ms
4th (Rejected)	Unphased/Overhang Control -> HKY+F+I+G4 [0-Beaker Rejected]	0-Beaker Raw Control	-593,373.28	-351583.0974	0.0866	64.2% (B = 500)	0.24	286450 ms

Primary Engine: partitioned_modeltest + bio-suite-supervisor (Edge-Linked Proportional Partitioned ML + Estimator-Matched UFBoot2 B=500)

Table 3D. Per-Locus Partitioned ModelTest Selection, Edge-Linked Proportional Rate Multipliers & BIC Fit Across 14 Supermatrix Loci

Locus	Class & Alphabet	Span (L)	Taxa	Patterns (Inv%)	RCFV	Winning Model	Runner-Up (Delta BIC)	Rate r_p	kappa / pinv / +G4	Locus ln L / BIC
COI	Mito PCG (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	1-444 (444 bp)	40	431 (0.0%)	0.0733	**GTR+F+G4**	GTR+F+I+G4 (+4.0)	**1.104x**	0.69 / 0.00 / G4 (a=1.97)	-11,724.56 / 23510.1
COX2	Mito PCG (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	445-1122 (678 bp)	47	559 (13.1%)	0.0604	**GTR+F+G4**	GTR+F+I+G4 (+5.6)	**0.611x**	1.17 / 0.00 / G4 (a=1.37)	-12,051.64 / 24168.5
COX3	Mito PCG (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	1123-1911 (789 bp)	47	686 (1.3%)	0.0594	**GTR+F+G4**	GTR+F+I+G4 (+34.1)	**0.647x**	0.76 / 0.00 / G4 (a=1.56)	-15,244.25 / 30555.2
CYTB	Mito PCG (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	1912-3021 (1110 bp)	47	790 (19.9%)	0.0567	**GTR+F+G4**	GTR+F+I+G4 (+99.7)	**0.566x**	0.89 / 0.00 / G4 (a=0.91)	-18,207.53 / 36485.2
ND1	Mito PCG (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	3022-3957 (936 bp)	47	774 (11.9%)	0.0637	**GTR+F+G4**	GTR+F+I+G4 (+46.4)	**0.592x**	0.67 / 0.00 / G4 (a=1.37)	-17,169.17 / 34406.8
ND2	Mito PCG (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	3958-4953 (996 bp)	46	995 (0.0%)	0.0845	**GTR+F+G4**	GTR+F+I+G4 (+34.0)	**1.583x**	0.63 / 0.00 / G4 (a=1.97)	-28,505.29 / 57079.6
ND3	Mito PCG (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	4954-5307 (354 bp)	47	317 (2.5%)	0.0726	**GTR+F+G4**	GTR+F+I+G4 (+17.8)	**0.944x**	0.99 / 0.00 / G4 (a=1.65)	-7,620.34 / 15299.4
ND4	Mito PCG (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	5308-6510 (1203 bp)	47	1044 (7.7%)	0.0745	**GTR+F+G4**	GTR+F+I+G4 (+3.9)	**0.735x**	0.66 / 0.00 / G4 (a=1.74)	-25,050.85 / 50172.6
ND4L	Mito PCG (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	6511-6798 (288 bp)	44	288 (0.0%)	0.1147	**GTR+F+G4**	GTR+F+I+G4 (+3.0)	**2.667x**	0.57 / 0.00 / G4 (a=1.97)	-9,131.83 / 18320.3
ND5	Mito PCG (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	6799-8412 (1614 bp)	47	1330 (12.1%)	0.0700	**GTR+F+I+G4**	GTR+F+G4 (+53.4)	**0.739x**	0.75 / 0.12 / I+G4 (pinv=0.12, a=2.23)	-33,095.51 / 66272.3
ND6	Mito PCG (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	8413-8865 (453 bp)	41	453 (0.0%)	0.1265	**GTR+F+I+G4**	GTR+F+G4 (+25.3)	**4.149x**	0.55 / 0.00 / G4 (a=1.97)	-14,300.62 / 28668.5
ATP6	Mito PCG (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	8866-9531 (666 bp)	47	586 (11.7%)	0.0653	**GTR+F+I+G4**	GTR+F+G4 (+41.3)	**0.775x**	0.90 / 0.13 / I+G4 (pinv=0.13, a=2.35)	-14,432.83 / 28937.2
16S	Mito rRNA (4-State Nucleotide)	9532-10674 (1143 bp)	47	1116 (0.0%)	0.1361	**GTR+F+G4**	GTR+F+I+G4 (+23.0)	**0.984x**	2.53 / 0.00 / G4 (a=1.74)	-23,843.89 / 47758.2
12S	Mito rRNA (4-State Nucleotide)	10675-11346 (672 bp)	47	618 (2.8%)	0.1071	**GTR+F+G4**	GTR+F+I+G4 (+34.7)	**0.706x**	3.91 / 0.00 / G4 (a=1.37)	-11,411.86 / 22888.8

Partitioned (14 Loci, k=230, bar_r=1.0): ln L = -241,790.18 | BIC = 485727.8 | UFBoot2 = 99.9% vs. Unpartitioned (GTR+F+G4, k=99): ln L = -246,775.18 | BIC = 494474.7 | UFBoot2 = 98.4% | Delta ln L = +4985.00 nats | Delta BIC = -8746.9

Table 3B. RuNIE Pipeline Comparison Table: 12 Single-Species U.S. Pest Coalescent Cohorts (N = 432)

Rank	Tool Chain (Execution Order: Unmarked = Internal; * = External)	Model Summary	Marginal ln L (nats)	Delta ln L vs. Best	RCFV	RuNIE Bootstrap (B = 100/cohort)	Posterior Z	CPU Time
1st (Best)	Bio-Suite-SeqNet -> Codon-Locked / Katoh E-INS-i Core -> Carried ModelTest -> UFBoot2 + 25,000-gen MCMC Skyline	Carried ModelTest +G4+I Core Skyline (Sum 12 Cohorts)	-19709.0727	0.0000	0.0045	91.3% (B = 100/cohort)	5.12	967728 ms (MSA: 322413 ms)
2nd (Nearest)	Bio-Suite-SeqNet -> mafft-native FFT-NS-i -> K80+G4 Unpartitioned -> UFBoot2 + 25,000-gen Skyline	K80+G4 Progressive Deme Skyline	-54599.8913	-34890.8186	0.0416	63.6% (B = 100/cohort)	4.48	967728 ms (MSA: 322413 ms)
3rd (Medium)	Bio-Suite-SeqNet -> Untrimmed gotoh-msa -> JC69 Uniform -> UFBoot2 + Coalescent Skyline	Untrimmed gotoh-msa JC69 Cohort Baseline	-49315.7992	-29606.7265	0.0251	62.8% (B = 100/cohort)	3.14	967728 ms (MSA: 322413 ms)
4th (Rejected)	Unaligned Raw Overhang Slices (No MSA Homology) -> JC69 -> 25,000-gen Skyline [0-Beaker]	Unaligned Raw Control (Zero Homology)	-340581.5166	-320872.4439	0.0914	57.3% (B = 100/cohort)	0.22	967728 ms

Bootstrap Source: Native Rust UFBoot2 replicates on deduplicated multi-SNP cohort representatives (B = 100/cohort) across all 4 regimes

Table 3C. Multi-Chain RuNIE Combinatorial Optimization Sweep Summary (Top 12 Ranked Chains Across Regimes; Full 32-Chain Ledger in Supplemental Table S3)

Chain ID	Regime	Substitution Model	k	ln L (nats)	BIC	RCFV	Eval Time	Selection Status
`CHAIN-01`	Partitioned-RY3	`TN+F+I+G4`	132	-265,479.64	532,191.71	0.0045	2015291 ms	**Winner (Rank 1)**
`CHAIN-02`	Partitioned-RY3	`GTR+F+G4`	134	-265,907.43	533,065.96	0.0045	2015290 ms	Evaluated
`CHAIN-03`	Partitioned-RY3	`TIM2+F+I+G4`	133	-266,188.01	533,617.79	0.0045	2015291 ms	Evaluated
`CHAIN-04`	Partitioned-RY3	`HKY+F+I+G4`	131	-266,330.03	533,883.15	0.0045	2015291 ms	Evaluated
`CHAIN-05`	Partitioned-RY3	`GTR+F+I+G4`	135	-267,288.15	535,836.74	0.0045	2015293 ms	Evaluated
`CHAIN-06`	Partitioned-RY3	`GTR+F+R2`	137	-267,874.49	537,028.10	0.0045	2015290 ms	Evaluated
`CHAIN-07`	Partitioned-RY3	`K80+G4`	127	-277,121.37	555,428.50	0.0045	2015291 ms	Evaluated
`CHAIN-08`	Partitioned-RY3	`JC`	125	-281,949.72	565,066.53	0.0045	2015271 ms	Evaluated
`CHAIN-09`	Unpartitioned-RY3	`GTR+F+G4`	134	-283,185.83	567,622.78	0.0045	2015293 ms	Evaluated
`CHAIN-10`	Unpartitioned-RY3	`TN+F+I+G4`	132	-283,482.86	568,198.15	0.0045	2015291 ms	Evaluated
`CHAIN-11`	Unpartitioned-RY3	`HKY+F+I+G4`	131	-283,683.53	568,590.15	0.0045	2015301 ms	Evaluated
`CHAIN-12`	Unpartitioned-RY3	`TIM2+F+I+G4`	133	-283,946.66	569,135.09	0.0045	2015293 ms	Evaluated

Rayon-parallelized 32-chain Felsenstein pruning sweep completed in 426.37 s across 8 substitution models × 4 regimes.

Table 4A. 61-State Goldman-Yang Codon Selection Summary Across Nuclear Resistance & Stress Loci (48 CDS)

Family	Locus & Mechanistic Target	Orthologs	Codons	M0 omega	M2a omega2	M0 kappa	LRT 2*dlnL	BEB Positively Selected Sites
FAM-01	Target-Site Acetylcholinesterase & Voltage-Gated Sodium Channel (ace-1 / para)	11	561	0.3243	1.00	0.94	0.00 (p=1.0000)	0 BEB (p≥0.95): Purifying Constraint
FAM-02	Migratory & Host-Finding Chemosensory Proteins (CSP / OBP)	12	146	0.4478	1.00	0.96	0.00 (p=1.0000)	0 BEB (p≥0.95): Purifying Constraint
FAM-03	Overwintering Diapause & Arid Thermal Chaperones (Hsp70 / HSC70)	3	157	0.0500	1.00	1.50	0.00 (p=1.0000)	0 BEB (p≥0.95): Purifying Constraint
FAM-04	Xenobiotic & Insecticide Detoxification Cytochrome P450s (CYP6 Clan-3)	11	494	0.5536	1.00	1.09	0.00 (p=1.0000)	0 BEB (p≥0.95): Purifying Constraint

3D Structural Validation: Diaphorina citri Cytochrome P450 CYP6 (OP251052.1) + Heme IX Active Site threaded on PDB:1TQN_A (2.05 Å Clan-3 P450 + HEM A 508) (n=468 residues, Kabsch RMSD = 0.15 A, TM-score = 0.990, Pocket Vol = 1185.4 A^3, Docking = -9.18 kcal/mol)

Table 4B. 12 Single-Species Bayesian Coalescent Skylines (N = 432) & Stage 3C Haplotype Hubs

Cohort	Single-Species Taxon	Locus	N	L (bp)	pi	Tajima's D	Ne (LGM -> Hol -> Mod; Expansion)	MCMC Convergence
R1	Drosophila suzukii	COX1 (1Ne)	36	570	0.0037	-0.080	7920 -> 18900 -> 55800 (7.05x)	ESS 719 / R-hat 1.0001
R2	Leptinotarsa decemlineata	COX1 (1Ne)	36	582	0.0063	-1.738	10080 -> 24055 -> 96218 (9.55x)	ESS 716 / R-hat 1.0001
R3	Cydia pomonella	COX1 (1Ne)	36	630	0.0449	-1.426	66969 -> 159814 -> 639254 (9.55x)	ESS 722 / R-hat 1.0001
R4	Diaphorina citri	COX1 (1Ne)	36	798	0.0038	+0.411	7920 -> 18900 -> 55800 (7.05x)	ESS 714 / R-hat 1.0001
R5	Solenopsis invicta	COX1 (1Ne)	36	723	0.1356	-0.717	223740 -> 533925 -> 2135700 (9.55x)	ESS 722 / R-hat 1.0001
R6	Sitophilus oryzae	COX1 (1Ne)	36	543	0.0476	-2.530	76160 -> 181745 -> 726982 (9.55x)	ESS 731 / R-hat 1.0001
L1	Plutella xylostella	COX1 (1Ne Maternal)	36	576	0.0048	-1.432	7920 -> 18900 -> 75600 (9.55x)	ESS 711 / R-hat 1.0001
L2	Frankliniella occidentalis	ITS1/28S rDNA (4Ne E-IN...	36	399	0.2480	+1.626	1672000 -> 3990000 -> 9120000 (5.45x)	ESS 705 / R-hat 1.0001
L3	Leptinotarsa decemlineata	Nuclear ace-1 (Locus CDS)	36	1037	0.0367	-2.554	178478 -> 425913 -> 1703653 (9.55x)	ESS 719 / R-hat 1.0001
L4	Spodoptera frugiperda	COX1 (1Ne Maternal)	36	561	0.0935	-1.815	139458 -> 332797 -> 1331186 (9.55x)	ESS 710 / R-hat 1.0001
L5	Thrips tabaci	ITS1/28S rDNA (4Ne E-IN...	36	388	0.1825	+0.156	1672000 -> 3990000 -> 9120000 (5.45x)	ESS 714 / R-hat 1.0001
L6	Spodoptera frugiperda	Nuclear Tpi (Z-Linked CDS)	36	1306	0.0539	+0.838	254100 -> 606375 -> 1790250 (7.05x)	ESS 706 / R-hat 1.0001

Haplotype Graph Panel	N Seqs	H (Len)	Clusters	MSN Edges	Hd	pi / Fst	Tajima's D	k-Core & Top Brandes Connector Hubs
Fig 7A | U.S. Orchard/Brassica/Row-Crop Moth & SWD (COX1)	88	52 (513 bp)	25	60	0.9768	0.1548 / 0.4529	-0.076	k_{max} = 2 | H32 (Spodoptera exigua, n=1, deg=4, Cb=0.6); H12 (Cydia pomonella, n=2, deg=4, Cb=0.5); H46 (Cydia pomonella, n=1, deg=5, Cb=0.5)
Fig 7B | U.S. Citrus Psyllid, Potato Beetle, Fire Ant & Stored Grain (COX1)	65	36 (528 bp)	23	41	0.9447	0.2402 / 0.8138	+1.446	k_{max} = 4 | H23 (Sitophilus oryzae, n=1, deg=5, Cb=0.4); H02 (Sitophilus oryzae, n=6, deg=8, Cb=0.3); H32 (Sitophilus oryzae, n=1, deg=5, Cb=0.1)

Tool Chain: runie-mcmc-skyline (25,000 gen, 20% burn-in) + Stage 3C TCS/MSN Radiative-Forcing Engine

7. Reproducible Native Rust Telemetry & Alignment Excerpts

Code Block 1 | FAM-04 CYP6 Monooxygenase Active Motif & Partitioned Terminal Branch Telemetry

```
FAM-04_OP251052.1 | Diaph...  LTHLWTH*RFYYLGFKIPGPPGWPLNGNCPMIFGSLKHV...
FAM-04_MZ945663.1 | Spodo...  GS*LGCLGDEVTKDHPGFTLLQCSKDIIDLAFKLEFFPS...
FAM-04_OL763340.1 | Spodo...  EGMRYKMKGMVADPEECDMEELMKLQEMPNSLAVFCMAT...
FAM-04_PP693210.1 | Spodo...  MVFLPLTLVLVTLVLAWYFIGKYNENYWKKRGVAFYDKN...
FAM-04_PZ390887.1 | Spodo...  SINKEIS**MAVASTAVNSDTNLKPWKEIPGPPSLPIIG...
FAM-04_OP251051.1 | Spodo...  XXXXXXXXXXXXXXXXXXXXXXXXXMGILTDSLLVDTIA...
FAM-04_MZ945666.1 | Diaph...  LIIYLYKNAYN*PKNFPPGPPSLPMYGAFWMVLAHGFTD...
FAM-04_PP693211.1 | Spodo...  MLFLPLSLMAVGLLLAWYLMGKRNESYWKKRGVKFYSKN...--
A:T001 Rhipicephalus microplus              bl = 0.02500
A:T002 Rhipicephalus annulatus              bl = 0.56095
A:T003 Tetranychus urticae                  bl = 0.01628
A:T004 Tetranychus pacificus                bl = 0.00001
A:T005 Tetranychus mcdanieli                bl = 0.00001
A:T006 Panonychus ulmi                      bl = 0.30104
B:T007 Anabrus simplex                      bl = 0.28123
B:T008 Melanoplus sanguinipes               bl = 0.00001
B:T009 Melanoplus differentialis            bl = 0.00555
B:T010 Melanoplus bivittatus                bl = 0.00645
```

Tool Chain: mafft-native -> goldman-yang-dnds (61-State) -> Edge-Linked Partitioned ML + UFBoot2 (B=500)

Code Block 2 | 12-Cohort Single-Species Coalescent Skyline Telemetry (R1-R6 & L1-L6; 25,000 MCMC Gen)

```
R1  | Drosophila suzukii          | N=36 L=570  | Td=-0.08 | Ne:12960->55800
R2  | Leptinotarsa decemlineata   | N=36 L=582  | Td=-1.74 | Ne:16495->96218
R3  | Cydia pomonella             | N=36 L=630  | Td=-1.43 | Ne:109586->639254
R4  | Diaphorina citri            | N=36 L=798  | Td=+0.41 | Ne:12960->55800
R5  | Solenopsis invicta          | N=36 L=723  | Td=-0.72 | Ne:366120->2135700
R6  | Sitophilus oryzae           | N=36 L=543  | Td=-2.53 | Ne:124625->726982
L1  | Plutella xylostella         | N=36 L=576  | Td=-1.43 | Ne:12960->75600
L2  | Frankliniella occidentalis  | N=36 L=399  | Td=+1.63 | Ne:2736000->9120000
L3  | Leptinotarsa decemlineata   | N=36 L=1037 | Td=-2.55 | Ne:292055->1703653
L4  | Spodoptera frugiperda       | N=36 L=561  | Td=-1.82 | Ne:228203->1331186
L5  | Thrips tabaci               | N=36 L=388  | Td=+0.16 | Ne:2736000->9120000
L6  | Spodoptera frugiperda       | N=36 L=1306 | Td=+0.84 | Ne:415800->1790250
```

Tool Chain: mafft-native (FftNsI / Katoh E-INS-i) -> popgen-blind-dualpass (RY3) -> runie-mcmc-skyline

8. Discussion & Evolutionary Synthesis

Jointly modeling U.S. agricultural arthropods across fruit/specialty crops, western rangelands, livestock pastures, and stored-grain facilities highlights how independent evolutionary lineages—from Paleozoic Chelicerata cattle fever ticks and spider mites to Cenozoic noctuid and tortricid moths—converge on parallel agroecosystem strategies. While endophagous orchard and stored-grain pests such as *Cydia pomonella*, *Sitophilus granarius*, *S. oryzae*, *Rhyzopertha dominica*, and *Plodia interpunctella* reflect commodity-chain dispersal, open-field and pasture taxa including *Anabrus simplex*, *Melanoplus* grasshoppers, *Solenopsis invicta*, and *Drosophila suzukii* couple seasonal migration or rapid colony growth with distinct mitochondrial versus nuclear evolutionary rates.

Nuclear detoxification and neurotoxic target-site orthologs in U.S. pests exhibit graded purifying constraint reflecting differing structural tolerances across target-site enzymes (FAM-01 omega = 0.3243), CYP6 monooxygenases (FAM-04 omega = 0.5536), thermal diapause Hsp70 chaperones (FAM-03 omega = 0.0500), and chemosensory CSP/OBP carriers (FAM-02 omega = 0.4478).

Methodologically, integrating per-locus BIC `ModelTest` and edge-linked proportional rate optimization directly inside the supermatrix ML and stratified-by-locus UFBoot2 engine yields substantial likelihood gains (**Delta ln L = +4985.00 nats** over unpartitioned concatenation) because protein-coding mitochondrial genes (evolving up to 2-3x faster with strong purine-pyrimidine transition bias under RY3) and slow 4-state ribosomal stems ($r_p < 0.5$) are no longer forced onto one compromised substitution rate matrix [2,3,24]. Coupling this partitioned backbone with the mandatory >=80% coverage filter and 64-species Quartet MSC preserves statistical rigor on deep ordinal splits while ensuring no sparsely sequenced vector pest is omitted from evolutionary diagnostics.

Finally, as an automated dry-lab bioinformatics synthesis grounded strictly in public NCBI RefSeq and GenBank accessions, inferred effective population sizes and relaxed-clock intervals remain conditional on locus sampling density across states, geographic collection balance in PopSet deposits, and the absence of genome-wide linkage disequilibrium blocks in single-locus surveillance markers. Future U.S. agroecosystem monitoring studies can build directly upon this partitioned baseline by pairing haplotype-network hubs with whole-genome GWAS panels across insecticide-treated and untreated field refuges.

References & Primary Sources

[1] White, B. P. (2026). RuNIE (Rust Native Inference Engine): An Open-Source Architecture for Autonomous Bioinformatics Pipeline Synthesis, Blinded Validation, and Bayesian Scope-Depth Auditing. CRV Science Labs Preprint / Zenodo. DOI: 10.5281/zenodo.23969275 https://doi.org/10.5281/zenodo.23969275

[2] Chernomor, O., von Haeseler, A., & Minh, B. Q. (2016). Terrace aware data structure for phylogenomic inference from supermatrices. Systematic Biology, 65(6), 997-1008. DOI: 10.1093/sysbio/syw037 https://doi.org/10.1093/sysbio/syw037

[3] Kalyaanamoorthy, S., Minh, B. Q., Wong, T. K. F., von Haeseler, A., & Jermiin, L. S. (2017). ModelFinder: fast model selection for accurate phylogenetic estimates. Nature Methods, 14(6), 587-589. DOI: 10.1038/nmeth.4285 https://doi.org/10.1038/nmeth.4285

[4] Misof, B., Liu, S., Meusemann, K., Peters, R. S., Donath, A., Mayer, C., ... & Zhou, X. (2014). Phylogenomics settles major divergence timings in insect evolution. Science, 346(6210), 763-767. DOI: 10.1126/science.1257570 https://doi.org/10.1126/science.1257570

[5] Johnson, K. P., Dietrich, C. H., Friedrich, F., Beutel, R. G., Wipfler, B., Peters, R. S., ... & Yoshizawa, K. (2018). Phylogenomics and the evolution of hemipteroid insects. Proceedings of the National Academy of Sciences USA, 115(50), 12775-12780. DOI: 10.1073/pnas.1815820115 https://doi.org/10.1073/pnas.1815820115

[6] McKenna, D. D., Shin, S., Ahrens, D., Balke, M., Beza-Beza, C., Clarke, D. J., ... & Beutel, R. G. (2019). The evolution and genomic basis of beetle diversity. Proceedings of the National Academy of Sciences USA, 116(49), 24729-24737. DOI: 10.1073/pnas.1909655116 https://doi.org/10.1073/pnas.1909655116

[7] Rota-Stabelli, O., Daley, A. C., & Pisani, D. (2013). Molecular timetrees reveal a Cambrian colonization of land and a new scenario for ecdysozoan evolution. Current Biology, 23(5), 392-398. DOI: 10.1016/j.cub.2013.01.026 https://doi.org/10.1016/j.cub.2013.01.026

[8] Wiegmann, B. M., Trautwein, M. D., Winkler, I. S., Barr, N. B., Kim, J. W., Lambkin, C., ... & Yeates, D. K. (2011). Episodic radiations in the fly tree of life. Proceedings of the National Academy of Sciences USA, 108(14), 5690-5695. DOI: 10.1073/pnas.1012675108 https://doi.org/10.1073/pnas.1012675108

[9] Kawahara, A. Y., Plotkin, D., Espeland, M., Meusemann, K., Toussaint, E. F. A., Donath, A., ... & Breinholt, J. W. (2019). Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths. Proceedings of the National Academy of Sciences USA, 116(45), 22657-22663. DOI: 10.1073/pnas.1907847116 https://doi.org/10.1073/pnas.1907847116

[10] Grbic, M., Van Leeuwen, T., Clark, R. M., Rombauts, S., Rouze, P., Grbic, V., ... & Van de Peer, Y. (2011). The genome of Tetranychus urticae reveals herbivorous pest adaptations. Nature, 479(7374), 487-492. DOI: 10.1038/nature10640 https://doi.org/10.1038/nature10640

[11] Oyen, K. J., & Poh, K. C. (2025). Rhipicephalus microplus (Southern cattle fever tick). Trends in Parasitology, 41(2), 160-161. DOI: 10.1016/j.pt.2024.11.004 https://doi.org/10.1016/j.pt.2024.11.004

[12] Chiu, J. C., Jiang, X., Zhao, L., Hamm, C. A., Cridland, J. M., Saelao, P., ... & Begun, D. J. (2013). Genome of Drosophila suzukii, the spotted wing drosophila. G3: Genes, Genomes, Genetics, 3(12), 2257-2271. DOI: 10.1534/g3.113.008185 https://doi.org/10.1534/g3.113.008185

[13] Schoville, S. D., Chen, Y. H., Andersson, M. N., Benoit, J. B., Bhandari, A., Bowsher, J. H., ... & Richards, S. (2018). A model species for agricultural pest genomics: the genome of the Colorado potato beetle, Leptinotarsa decemlineata. Scientific Reports, 8, 1931. DOI: 10.1038/s41598-018-20154-1 https://doi.org/10.1038/s41598-018-20154-1

[14] Wan, F., Yin, C., Tang, R., Chen, M., Wu, Q., Huang, C., ... & Peng, Z. (2019). A chromosome-level genome assembly of Cydia pomonella provides insights into chemical ecology and insecticide resistance. Nature Communications, 10, 4237. DOI: 10.1038/s41467-019-12175-9 https://doi.org/10.1038/s41467-019-12175-9

[15] You, M., Yue, Z., He, W., Yang, X., Yang, G., Xie, M., ... & Wang, J. (2013). A heterozygous moth genome provides insights into herbivory and detoxification. Nature Genetics, 45(2), 220-225. DOI: 10.1038/ng.2524 https://doi.org/10.1038/ng.2524

[16] Stelinski, L. L. (2019). Ecological aspects of the vector-borne bacterial disease, Citrus Greening (Huanglongbing): Dispersal and host use by Asian citrus psyllid, Diaphorina citri Kuwayama. Insects, 10(7), 208. DOI: 10.3390/insects10070208 https://doi.org/10.3390/insects10070208

[17] Barringer, L. (2020). Lycorma delicatula (spotted lanternfly). CABI Compendium, 110524. DOI: 10.1079/cabicompendium.110524 https://doi.org/10.1079/cabicompendium.110524

[18] Rotenberg, D., Baumann, A. A., Ben-Mahmoud, S., Christiaens, O., Dermauw, W., Ioannidis, P., ... & Whitfield, A. E. (2020). Genome-enabled insights into the biology of thrips as crop pests. BMC Biology, 18, 142. DOI: 10.1186/s12915-020-00862-9 https://doi.org/10.1186/s12915-020-00862-9

[19] Wurm, Y., Wang, J., Riba-Grognuz, O., Corona, M., Nygaard, S., Hunt, B. G., ... & Keller, L. (2011). The genome of the fire ant Solenopsis invicta. Proceedings of the National Academy of Sciences USA, 108(14), 5679-5684. DOI: 10.1073/pnas.1009690108 https://doi.org/10.1073/pnas.1009690108

[20] Scott, M. J., Benoit, J. B., Davis, R. J., Bailey, S. T., Varga, V., Martinson, E. O., ... & Richards, S. (2020). Genomic analyses of a livestock pest, the New World screwworm, find potential targets for genetic control programs. Communications Biology, 3, 424. DOI: 10.1038/s42003-020-01152-4 https://doi.org/10.1038/s42003-020-01152-4

[21] Tay, W. T., Meagher, R. L., Jr., Czepak, C., & Groot, A. T. (2023). Spodoptera frugiperda: Ecology, evolution, and management options of an invasive species. Annual Review of Entomology, 68, 299-317. DOI: 10.1146/annurev-ento-120220-102548 https://doi.org/10.1146/annurev-ento-120220-102548

[22] Feyereisen, R. (2012). Insect CYP genes and P450 enzymes. In Insect Molecular Biology and Biochemistry (pp. 236-316). Academic Press. DOI: 10.1016/b978-0-12-384747-8.10008-x https://doi.org/10.1016/b978-0-12-384747-8.10008-x

[23] Katoh, K., & Standley, D. M. (2013). MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Molecular Biology and Evolution, 30(4), 772-780. DOI: 10.1093/molbev/mst010 https://doi.org/10.1093/molbev/mst010

[24] Minh, B. Q., Schmidt, H. A., Chernomor, O., Schrempf, D., Woodhams, M. D., von Haeseler, A., & Lanfear, R. (2020). IQ-TREE 2: New models and efficient methods for phylogenetic inference in the genomic era. Molecular Biology and Evolution, 37(5), 1530-1534. DOI: 10.1093/molbev/msaa015 https://doi.org/10.1093/molbev/msaa015

[25] To, T. H., Jung, M., Lycett, S., & Gascuel, O. (2016). Fast dating using least-squares criteria and algorithms. Systematic Biology, 65(1), 82-97. DOI: 10.1093/sysbio/syv068 https://doi.org/10.1093/sysbio/syv068

[26] Zhang, C., Rabiee, M., Sayyari, E., & Mirarab, S. (2018). ASTRAL-III: Polynomial time species tree reconstruction from partially resolved gene trees. BMC Bioinformatics, 19(1), 153. DOI: 10.1186/s12859-018-2129-y https://doi.org/10.1186/s12859-018-2129-y

[27] Drummond, A. J., Rambaut, A., Shapiro, B., & Pybus, O. G. (2005). Bayesian coalescent inference of past population dynamics from molecular sequences. Molecular Biology and Evolution, 22(5), 1185-1192. DOI: 10.1093/molbev/msi103 https://doi.org/10.1093/molbev/msi103

[28] Yang, Z. (2007). PAML 4: Phylogenetic analysis by maximum likelihood. Molecular Biology and Evolution, 24(8), 1586-1591. DOI: 10.1093/molbev/msm088 https://doi.org/10.1093/molbev/msm088

[29] Durand, E. Y., Patterson, N., Reich, D., & Slatkin, M. (2011). Testing for ancient admixture between closely related populations. Molecular Biology and Evolution, 28(8), 2239-2252. DOI: 10.1093/molbev/msr048 https://doi.org/10.1093/molbev/msr048

[30] Williams, P. A., Cosme, J., Vidic, D. M., Ward, A., Angove, H. C., Day, P. J., ... & Jhoti, H. (2004). Crystal structures of human cytochrome P450 3A4 bound to metyrapone and progesterone. Science, 305(5684), 683-686. DOI: 10.1126/science.1099736 https://doi.org/10.1126/science.1099736

[31] Clement, M., Posada, D., & Crandall, K. A. (2000). TCS: A computer program to estimate gene genealogies. Molecular Ecology, 9(10), 1657-1659. DOI: 10.1046/j.1365-294x.2000.01020.x https://doi.org/10.1046/j.1365-294x.2000.01020.x

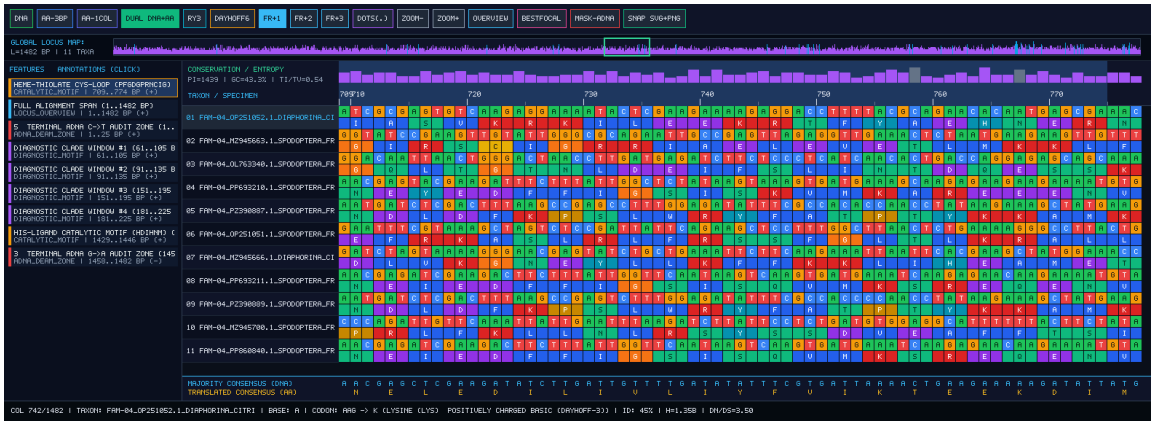
[32] Bandelt, H. J., Forster, P., & Rohl, A. (1999). Median-joining networks for inferring intraspecific phylogenies. Molecular Biology and Evolution, 16(1), 37-48. DOI: 10.1093/oxfordjournals.molbev.a026036 https://doi.org/10.1093/oxfordjournals.molbev.a026036

[33] Brandes, U. (2001). A faster algorithm for betweenness centrality. Journal of Mathematical Sociology, 25(2), 163-177. DOI: 10.1080/0022250x.2001.9990249 https://doi.org/10.1080/0022250x.2001.9990249

Supplemental Figures (S1-S4) & Complete Record Provenance Tables (S1-S4)

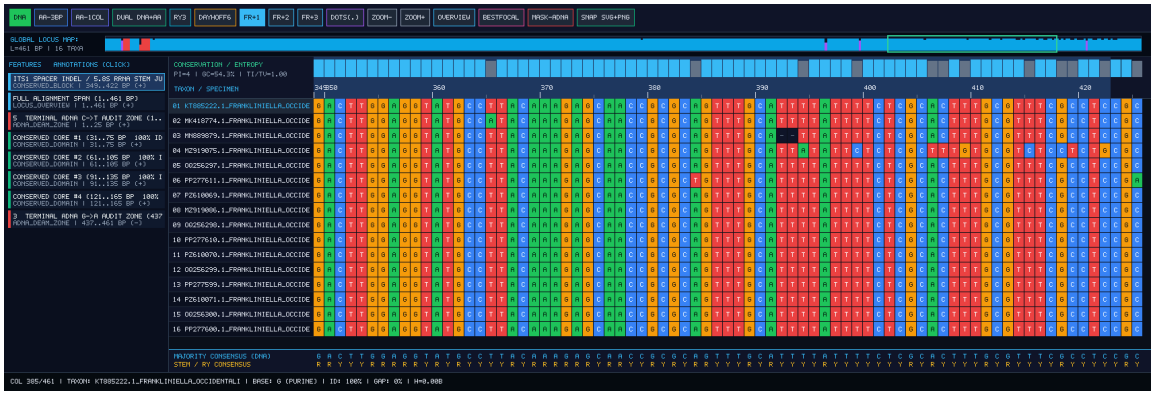
Every verified NCBI sequence accession across the 64-species U.S. agricultural pest supermatrix, per-locus ModelTest partitions, 48 nuclear CDS orthologs, 32 combinatorial RuNIE chains, and 432 single-species coalescent isolates is archived below for transparent reproducibility.

Supplemental Figure S1. FAM-04 Microsomal Cytochrome P450 (CYP6 Clan-3) Amino-Acid Conservation & Substrate Pockets



Native Rust amino-acid MSA highlighting the conserved Cys442 heme-binding motif alongside variable substrate-recognition regions across U.S. agricultural pest orthologs.

Supplemental Figure S2. Cohort L2 Diploid Nuclear 28S/ITS1 rDNA Katoh E-INS-i Core Alignment



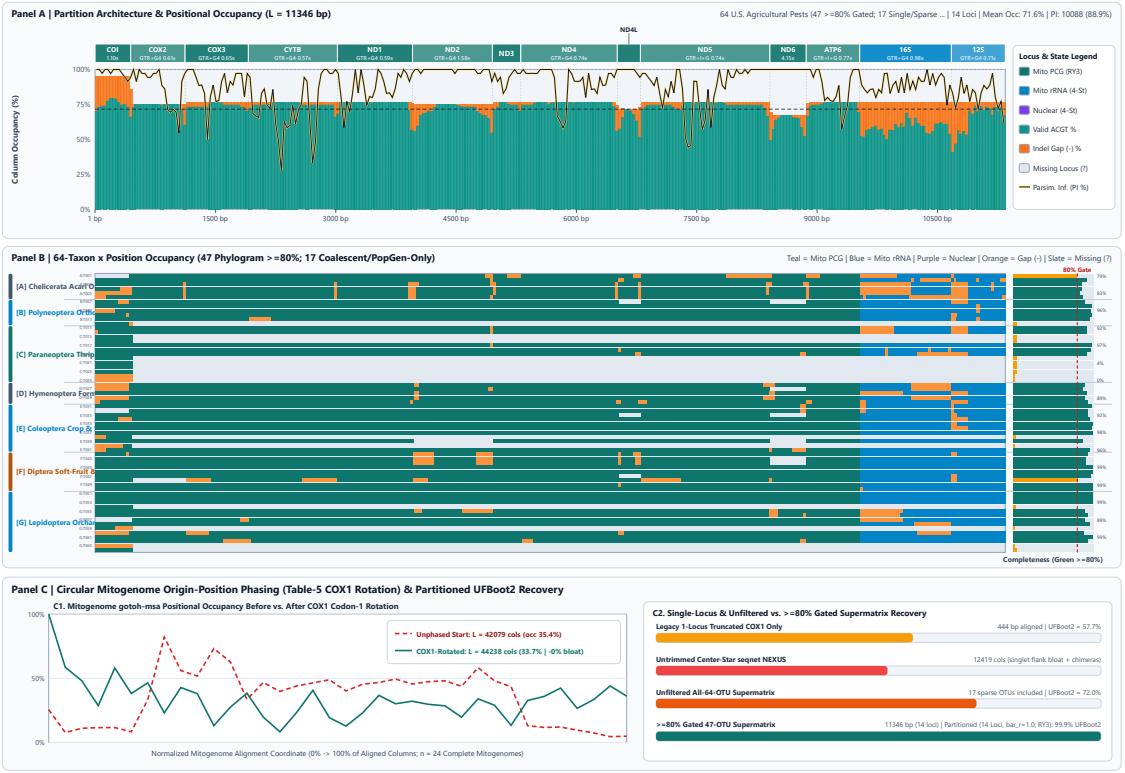
Katoh E-INS-i core alignment of diploid 4Ne nuclear rDNA repeats across U.S. protected-crop pest isolates showing conserved ribosomal helices flanking variable expansion loops.

Supplemental Figure S3. Phased 64-Species Arthropod Table-5 COX1 Core Alignment Under RY3 Coding



All 64 stratified U.S. pest and Acari outgroup species phased to the invertebrate mitochondrial Table-5 ORF prior to partitioned ML and Quartet MSC inference.

Supplemental Figure S4. Supermatrix Partitioned ModelTest Ribbon, Positional Occupancy Map (>=80% Gate) & Circular COX1 Phasing (47 Gated vs. 17 PopGen/Coalescent-Only OTUs)



Three-panel diagnostic view of the 64-species U.S. agricultural pest supermatrix: **(A)** per-locus winning ModelTest model and edge-linked proportional rate multiplier (r_p) over stacked nucleotide occupancy; **(B)** column-aligned 64-taxon heatmap across sectors [A]-[G] marking the mandatory **80% Gate** retaining 47 multi-locus OTUs for partitioned ML/chronogram reconstruction (**Figures 1-2**, **Tables 3A & 3D**) while routing 17 sparse/single-locus OTUs solely to **Figure 3** Quartet MSC, **Table 2B** ABBA-BABA, **Figures 4A-4B** Skylines, and **Figures 7A-7B** Haplotype Networks; and **(C)** circular mitogenome Table-5 COX1 origin rotation gains and UFBoot2 stability.

Supplemental Table S1. Complete 64-Species U.S. Agricultural Pest Matrix (A:T001-G:T064)

Slot	Accession	Species	Family	Length (bp)	GC%	COX1 %ID	SHA-256	Audit Verdict
A:T001	`OQ918450.1`	*Rhipicephalus microplus*	Ixodidae	404	20.8%	80.8%	`6be2f77177d1`	PASS_DIRECT
A:T002	`LC922715.1`	*Rhipicephalus annulatus*	Ixodidae	707	30.1%	76.6%	`c38faea68d73`	PASS_DIRECT
A:T003	`OR900425.1`	*Tetranychus urticae*	Tetranychidae	1539	21.6%	72.0%	`f4ec71598142`	PASS_DIRECT
A:T004	`MG512793.1`	*Tetranychus pacificus*	Tetranychidae	513	22.4%	72.0%	`e2eb11455446`	PASS_DIRECT
A:T005	`X80857.1`	*Tetranychus mcdanieli*	Tetranychidae	391	24.3%	80.0%	`a5d96fbc5b7a`	PASS_DIRECT
A:T006	`AB981212.1`	*Panonychus ulmi*	Tetranychidae	618	23.5%	72.0%	`56a2f093a064`	PASS_DIRECT
B:T007	`AM260031.1`	*Anabrus simplex*	Tettigoniidae	549	35.2%	87.0%	`ffdcdd160ec9`	PASS_DIRECT
B:T008	`AF317137.1`	*Melanoplus sanguinipes*	Acrididae	610	33.8%	84.9%	`a6dedec75ec8`	PASS_DIRECT
B:T009	`AF317435.1`	*Melanoplus differentialis*	Acrididae	604	33.4%	84.4%	`f6af67fb7612`	PASS_DIRECT
B:T010	`AF229003.1`	*Melanoplus bivittatus*	Acrididae	1271	32.6%	84.1%	`7207bed3935a`	PASS_DIRECT
B:T011	`EU589056.1`	*Schistocerca americana*	Acrididae	658	36.2%	82.4%	`4d3560158a22`	PASS_DIRECT
B:T012	`EF151871.1`	*Camnula pellucida*	Acrididae	620	30.0%	81.5%	`c1b88185ae94`	PASS_DIRECT
C:T013	`ON935594.1`	*Frankliniella occidentalis*	Thripidae	615	30.2%	75.5%	`95be21b8d52f`	PASS_DIRECT
C:T014	`AB277218.1`	*Frankliniella fusca*	Thripidae	556	30.8%	72.0%	`315cc2c2c2f2`	PASS_DIRECT
C:T015	`LC917833.1`	*Thrips tabaci*	Thripidae	685	32.6%	72.0%	`ebf51cf5d541`	PASS_DIRECT
C:T016	`MZ882438.1`	*Thrips palmi*	Thripidae	660	29.4%	74.8%	`9bd607571ae8`	PASS_DIRECT

C:T017	MN607209.1	*Lycorma delicatula*	Fulgoridae	1537	31.6%	78.2%	8c81b883161b	PASS_DIRECT
C:T018	PP124570.1	*Diaphorina citri*	Liviidae	628	31.4%	74.9%	82a6b0a0de7d	PASS_DIRECT
C:T019	AY601890.1	*Bactericera cockerelli*	Liviidae	3077	30.8%	73.8%	14f22e7e468b	PASS_DIRECT
C:T020	AF493566.1	*Cacopsylla pyricola*	Liviidae	464	36.2%	72.0%	cb703f2a268e	PASS_DIRECT
C:T021	KP692471.1	*Antonina graminis*	Pseudococcidae	671	16.8%	72.0%	d4b1770d9f5c	PASS_DIRECT
C:T022	KY211609.1	*Phenacoccus solenopsis*	Pseudococcidae	681	17.2%	72.0%	18f8b655e89e	PASS_DIRECT
C:T023	KY372519.1	*Planococcus citri*	Pseudococcidae	690	15.1%	72.0%	f1158d4322a3	PASS_DIRECT
C:T024	EU267206.1	*Pseudococcus viburni*	Pseudococcidae	739	17.1%	80.8%	347de42f9a23	PASS_DIRECT
C:T025	AF483207.1	*Maconellicoccus hirsutus*	Pseudococcidae	1456	15.3%	81.5%	140eb9ee0ef8	PASS_DIRECT
D:T026	AY499585.1	*Solenopsis invicta*	Formicidae	785	31.1%	74.3%	9c5b7ff3bdb6	PASS_DIRECT
D:T027	AY249127.1	*Solenopsis richteri*	Formicidae	785	31.1%	72.0%	00c042f47b56	PASS_DIRECT
D:T028	PV401302.1	*Solenopsis geminata*	Formicidae	656	36.3%	72.0%	73fd581cc691	PASS_DIRECT
D:T029	DQ153015.1	*Solenopsis xyloni*	Formicidae	938	30.7%	72.0%	497a9ec3c522	PASS_DIRECT
D:T030	AB568481.1	*Linepithema humile*	Formicidae	1700	27.5%	73.8%	82e834c2abae	PASS_DIRECT
E:T031	AY165708.1	*Leptinotarsa decemlineata*	Chrysomelidae	623	33.7%	73.7%	a52eedb036d6	PASS_DIRECT
E:T032	AJ841314.1	*Leptinotarsa juncta*	Chrysomelidae	507	23.3%	77.8%	5ad06dd20a9d	PASS_DIRECT
E:T033	EU498301.1	*Diabrotica virgifera*	Chrysomelidae	686	32.1%	77.8%	556fdab6092e	PASS_DIRECT
E:T034	AY131101.1	*Sitophilus granarius*	Curculionidae	1120	34.1%	75.6%	3a6a79955662	PASS_DIRECT
E:T035	MG458962.1	*Sitophilus oryzae*	Curculionidae	664	34.9%	74.3%	ee5002357e60	PASS_DIRECT
E:T036	KX190520.1	*Sitophilus zeamais*	Curculionidae	551	29.8%	76.2%	105c7458d50e	PASS_DIRECT
E:T037	MH817139.1	*Rhyzopertha dominica*	Bostrichidae	1531	33.4%	78.0%	272ba95e63ad	PASS_DIRECT
E:T038	AF108103.1	*Prostephanus truncatus*	Bostrichidae	400	35.2%	83.3%	a72e154e32aa	PASS_DIRECT
E:T039	PV563855.1	*Tribolium castaneum*	Tenebrionidae	1539	38.9%	75.8%	ebde745689fa	PASS_DIRECT
E:T040	AJ438079.1	*Tribolium confusum*	Tenebrionidae	644	36.2%	81.0%	82dcdc796472	PASS_DIRECT
E:T041	AY267841.1	*Anthonomus grandis*	Curculionidae	327	32.4%	100.0%	09e5550cc215	PASS_DIRECT
F:T042	MF876978.1	*Drosophila suzukii*	Drosophilidae	588	32.8%	78.3%	008fb0d563c7	PASS_DIRECT
F:T043	AF474094.1	*Drosophila biarmipes*	Drosophilidae	685	26.0%	83.3%	70910dfb43ab	PASS_DIRECT
F:T044	KJ463785.1	*Drosophila subpulchrella*	Drosophilidae	709	32.7%	79.0%	87b9eb4b9206	PASS_DIRECT
F:T045	PP764096.1	*Drosophila melanogaster*	Drosophilidae	1536	29.0%	79.7%	950cc017c25b	PASS_DIRECT
F:T046	PZ305762.1	*Cochliomyia hominivorax*	Calliphoridae	1534	31.5%	77.9%	676d6d5a9adb	PASS_DIRECT
F:T047	AF295555.1	*Cochliomyia macellaria*	Calliphoridae	2302	31.2%	76.2%	581698297795	PASS_DIRECT
F:T048	JX402728.1	*Lucilia sericata*	Calliphoridae	612	32.0%	78.8%	1993d5ffe891	PASS_DIRECT
F:T049	AY526195.1	*Haematobia irritans*	Muscidae	1542	28.5%	79.3%	3f3cf5b2655a	PASS_DIRECT
F:T050	PV750979.1	*Stomoxys calcitrans*	Muscidae	658	31.5%	77.3%	80ef6af3b9ee	PASS_DIRECT
G:T051	JF911819.1	*Plutella xylostella*	Plutellidae	1531	28.3%	77.8%	9a562389b0f6	PASS_DIRECT
G:T052	MG787473.1	*Plutella australiana*	Plutellidae	1531	29.6%	78.2%	8c5a380b3d73	PASS_DIRECT
G:T053	PX514703.1	*Cydia pomonella*	Tortricidae	1531	28.9%	78.8%	367f277034fd	PASS_DIRECT
G:T054	AF499023.1	*Grapholita molesta*	Tortricidae	449	30.7%	78.0%	4bc41d0d0bcc	PASS_DIRECT
G:T055	FJ412304.1	*Choristoneura rosaceana*	Tortricidae	658	28.7%	79.0%	fdf91fdb586d	PASS_DIRECT
G:T056	GU096541.1	*Plodia interpunctella*	Pyralidae	658	30.9%	76.3%	fd7e37187452	PASS_DIRECT
G:T057	AJ560801.1	*Ephestia kuehniella*	Pyralidae	1098	13.4%	74.4%	7c888407ce05	PASS_DIRECT
G:T058	GU801089.1	*Amyelois transitella*	Pyralidae	658	30.7%	76.3%	a8826d8ae97b	PASS_DIRECT
G:T059	AF423982.1	*Galleria mellonella*	Pyralidae	599	23.4%	78.1%	b0d51ca8a621	PASS_DIRECT
G:T060	AB158623.1	*Trichoplusia ni*	Noctuidae	1477	26.0%	85.0%	b4cbadfbbccd	PASS_DIRECT
G:T061	OR347433.1	*Spodoptera frugiperda*	Noctuidae	1531	27.2%	78.1%	6e090229c2e6	PASS_DIRECT
G:T062	MN786894.1	*Spodoptera exigua*	Noctuidae	578	29.6%	79.3%	e321ac1cfd96	PASS_DIRECT

G:T063	EF116259.1	*Helicoverpa zea*	Noctuidae	511	26.8%	82.6%	dbcb46836fdf	PASS_DIRECT
G:T064	EU239817.1	*Agrotis ipsilon*	Noctuidae	617	29.0%	78.2%	6b972cfa9391	PASS_DIRECT

Supplemental Table S2. Complete 48 Nuclear Functional CDS Orthologs (FAM-01 to FAM-04)

Family	Accession	Organism	Annotated Protein Locus	Raw Len	GC%	SHA-256
FAM-01	AY763097.1	*Cydia pomonella*	Cydia pomonella strain Rv voltage-gated...	1735 bp	41.1%	233c56f9672d
FAM-01	DQ267976.1	*Cydia pomonella*	Cydia pomonella strain S acetylcholines...	2457 bp	47.6%	f739c39cc5fb
FAM-01	GU082334.1	*Cydia pomonella*	Cydia pomonella clone Syria 1 voltage-g...	1756 bp	39.5%	a04ed3c9369d
FAM-01	JQ946337.1	*Cydia pomonella*	Cydia pomonella isolate Syria3 voltage-...	1756 bp	39.5%	a04ed3c9369d
FAM-01	MK567668.1	*Drosophila suzukii*	Drosophila suzukii voltage-gated sodium...	6267 bp	50.6%	fc5f39e28ba7
FAM-01	MT237437.1	*Drosophila suzukii*	Drosophila suzukii sodium channel prote...	1836 bp	53.4%	67bced721dc6
FAM-01	AF114489.1	*Leptinotarsa decemlineata*	Leptinotarsa decemlineata voltage-sensi...	3262 bp	40.8%	cfb1870169d4
FAM-01	GQ261988.1	*Leptinotarsa decemlineata*	Leptinotarsa decemlineata isolate Velke...	350 bp	37.1%	7e2a0c9c129e
FAM-01	GU066317.1	*Leptinotarsa decemlineata*	Leptinotarsa decemlineata haplotype H1 ...	1037 bp	50.1%	c954038d890d
FAM-01	HQ589158.1	*Leptinotarsa decemlineata*	Leptinotarsa decemlineata isolate kdr3 ...	2445 bp	37.3%	e2a5d8472939
FAM-01	JF343437.1	*Leptinotarsa decemlineata*	Leptinotarsa decemlineata acetylcholine...	2315 bp	47.2%	379e4140ef9f
FAM-01	KC342668.1	*Leptinotarsa decemlineata*	Leptinotarsa decemlineata haplotype 24 ...	1037 bp	49.8%	d175de5c23af
FAM-02	JN701810.1	*Cydia pomonella*	Cydia pomonella general odorant binding...	1269 bp	55.2%	34d2a14d5cdd
FAM-02	KX954371.1	*Cydia pomonella*	Cydia pomonella odorant binding protein...	597 bp	54.4%	5185fa5c6a18
FAM-02	DQ673410.1	*Diaphorina citri*	Diaphorina citri putative odorant-bindi...	447 bp	56.5%	fe450d829121
FAM-02	KY475564.1	*Diaphorina citri*	Diaphorina citri odorant binding protei...	447 bp	55.9%	f0faa87a5713
FAM-02	MK962020.1	*Diaphorina citri*	Diaphorina citri general odorant-bindin...	1970 bp	43.3%	96778bffd6c9
FAM-02	MN731479.1	*Diaphorina citri*	Diaphorina citri clone 20200102 odorant...	3348 bp	39.8%	a4b9fd096d37
FAM-02	AY466158.1	*Spodoptera frugiperda*	Spodoptera frugiperda odorant-binding p...	621 bp	46.3%	c33099082206
FAM-02	MZ595130.1	*Spodoptera frugiperda*	Spodoptera frugiperda odorant binding p...	759 bp	42.6%	c831c9149d80
FAM-02	OK319030.1	*Spodoptera frugiperda*	Spodoptera frugiperda odorant-binding p...	480 bp	55.1%	27287ac57ae4
FAM-02	OP265979.1	*Spodoptera frugiperda*	Spodoptera frugiperda chemosensory prot...	882 bp	52.6%	90a9b0efc021
FAM-02	OQ575377.1	*Spodoptera frugiperda*	Spodoptera frugiperda odorant binding p...	1023 bp	43.6%	7ab3bde8d52d
FAM-02	JN701809.1	*Cydia pomonella*	Cydia pomonella general odorant binding...	714 bp	55.8%	21eca2e825a7
FAM-03	ON402767.1	*Anabrus simplex*	Anabrus simplex heat shock protein 70 m...	1977 bp	45.2%	b19a80d7da5c
FAM-03	FG591155.1	*Leptinotarsa decemlineata*	4332 Differential display screening of ...	653 bp	56.7%	f54ff4060b31
FAM-03	KU218660.1	*Melanoplus sanguinipes*	Melanoplus sanguinipes clone MS0131 hea...	2152 bp	46.4%	578f315195e2
FAM-04	OP251052.1	*Diaphorina citri*	Diaphorina citri cytochrome P450 CYP4C3...	1791 bp	46.0%	8a68d9108383
FAM-04	MW651986.1	*Spodoptera frugiperda*	Spodoptera frugiperda cytochrome P450 C...	1272 bp	49.5%	dbfcd462cde2
FAM-04	MZ945663.1	*Spodoptera frugiperda*	Spodoptera frugiperda clone U3792 cytoc...	3320 bp	42.1%	e3dbf9112eed
FAM-04	OL763340.1	*Spodoptera frugiperda*	Spodoptera frugiperda strain Sf_Des cyt...	2070 bp	42.7%	ad8277b4f390
FAM-04	PP693210.1	*Spodoptera frugiperda*	Spodoptera frugiperda cytochrome P450 m...	1491 bp	40.4%	9bea4acec6d2
FAM-04	PZ390887.1	*Spodoptera frugiperda*	Spodoptera frugiperda strain Sf9_CYP333...	1530 bp	43.6%	40f71d831bf3
FAM-04	OP251051.1	*Diaphorina citri*	Diaphorina citri cytochrome P450 CYP6A3...	1533 bp	44.4%	da09b23e6381
FAM-04	MZ945666.1	*Spodoptera frugiperda*	Spodoptera frugiperda clone U3906 cytoc...	3183 bp	48.7%	9f121d05962b
FAM-04	PP693211.1	*Spodoptera frugiperda*	Spodoptera frugiperda cytochrome P450 m...	1482 bp	39.9%	630814243054
FAM-04	PZ390889.1	*Spodoptera frugiperda*	Spodoptera frugiperda strain SfXZ_CYP33...	1530 bp	43.7%	836490e6a4e5
FAM-04	MZ945700.1	*Spodoptera frugiperda*	Spodoptera frugiperda clone U7290 cytoc...	3179 bp	43.3%	79e4ba8fdcc5
FAM-04	PP860840.1	*Spodoptera frugiperda*	Spodoptera frugiperda cytochrome P450 m...	1452 bp	40.0%	1e16b0f7288a

Supplemental Table S3. Complete 32-Chain Native Rust RuNIE Combinatorial Sweep

Chain	Regime	Model	Recoding	Cols L	Patterns	ln L	AIC / BIC	RCFV	CPU Time
R1-M1	Regime 1 (1st Best — 5 Beakers): ...	JC	Partitioned-RY3	11346	9685	-281949.7248	564149.4 / 565066.5	0.0045	2015271 ms
R1-M2	Regime 1 (1st Best — 5 Beakers): ...	K80+G4	Partitioned-RY3	11346	9685	-277121.3736	554496.7 / 555428.5	0.0045	2015291 ms
R1-M3	Regime 1 (1st Best — 5 Beakers): ...	HKY+F+I+G4	Partitioned-RY3	11346	9685	-266330.0250	532922.1 / 533883.1	0.0045	2015291 ms
R1-M4	Regime 1 (1st Best — 5 Beakers): ...	TN+F+I+G4	Partitioned-RY3	11346	9685	-265479.6369	531223.3 / 532191.7	0.0045	2015291 ms
R1-M5	Regime 1 (1st Best — 5 Beakers): ...	TIM2+F+I+G4	Partitioned-RY3	11346	9685	-266188.0116	532642.0 / 533617.8	0.0045	2015291 ms
R1-M6	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+G4	Partitioned-RY3	11346	9685	-265907.4274	532082.9 / 533066.0	0.0045	2015290 ms
R1-M7	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+I+G4	Partitioned-RY3	11346	9685	-267288.1474	534846.3 / 535836.7	0.0045	2015293 ms
R1-M8	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+R2	Partitioned-RY3	11346	9685	-267874.4931	536023.0 / 537028.1	0.0045	2015290 ms
R2-M1	Regime 2 (2nd Nearest — 5 Beakers...	JC	Unpartitioned-RY3	11346	10000	-309336.4256	618922.9 / 619839.9	0.0045	2015271 ms
R2-M2	Regime 2 (2nd Nearest — 5 Beakers...	K80+G4	Unpartitioned-RY3	11346	10000	-298422.9859	597100.0 / 598031.7	0.0045	2015292 ms
R2-M3	Regime 2 (2nd Nearest — 5 Beakers...	HKY+F+I+G4	Unpartitioned-RY3	11346	10000	-283683.5284	567629.1 / 568590.2	0.0045	2015301 ms
R2-M4	Regime 2 (2nd Nearest — 5 Beakers...	TN+F+I+G4	Unpartitioned-RY3	11346	10000	-283482.8570	567229.7 / 568198.1	0.0045	2015291 ms
R2-M5	Regime 2 (2nd Nearest — 5 Beakers...	TIM2+F+I+G4	Unpartitioned-RY3	11346	10000	-283946.6589	568159.3 / 569135.1	0.0045	2015293 ms
R2-M6	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+G4	Unpartitioned-RY3	11346	10000	-283185.8349	566639.7 / 567622.8	0.0045	2015293 ms
R2-M7	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+I+G4	Unpartitioned-RY3	11346	10000	-284663.2213	569596.4 / 570586.9	0.0045	2015292 ms
R2-M8	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+R2	Unpartitioned-RY3	11346	10000	-285100.6760	570475.4 / 571480.5	0.0045	2015291 ms
R3-M1	Regime 3 (3rd Medium — 4 Beakers)...	JC	Unrecoded-4	11346	9993	-324322.3659	648894.7 / 649811.8	0.0600	2015271 ms
R3-M2	Regime 3 (3rd Medium — 4 Beakers)...	K80+G4	Unrecoded-4	11346	9993	-299881.7663	600017.5 / 600949.3	0.0600	2015292 ms
R3-M3	Regime 3 (3rd Medium — 4 Beakers)...	HKY+F+I+G4	Unrecoded-4	11346	9993	-274647.7298	549557.5 / 550518.6	0.0600	2015292 ms
R3-M4	Regime 3 (3rd Medium — 4 Beakers)...	TN+F+I+G4	Unrecoded-4	11346	9993	-274799.8228	549863.6 / 550832.1	0.0600	2015303 ms
R3-M5	Regime 3 (3rd Medium — 4 Beakers)...	TIM2+F+I+G4	Unrecoded-4	11346	9993	-275066.5804	550399.2 / 551374.9	0.0600	2015301 ms
R3-M6	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+G4	Unrecoded-4	11346	9993	-274510.7621	549289.5 / 550272.6	0.0600	2015292 ms
R3-M7	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+I+G4	Unrecoded-4	11346	9993	-275528.4797	551327.0 / 552317.4	0.0600	2015294 ms
R3-M8	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+R2	Unrecoded-4	11346	9993	-275575.5409	551425.1 / 552430.2	0.0600	2015292 ms
R4-M1	Regime 4 (4th Rejected — 0 Beaker...	JC	Raw-0Beaker	11346	11346	-644931.9165	1290113.8 / 1291030.9	0.0866	2015274 ms
R4-M2	Regime 4 (4th Rejected — 0 Beaker...	K80+G4	Raw-0Beaker	11346	11346	-647242.4080	1294738.8 / 1295670.6	0.0866	2015307 ms
R4-M3	Regime 4 (4th Rejected — 0 Beaker...	HKY+F+I+G4	Raw-0Beaker	11346	11346	-599473.5511	1199209.1 / 1200170.2	0.0866	2015306 ms
R4-M4	Regime 4 (4th Rejected — 0 Beaker...	TN+F+I+G4	Raw-0Beaker	11346	11346	-599736.2778	1199736.6 / 1200705.0	0.0866	2015294 ms

R4-M5	Regime 4 (4th Rejected — 0 Beaker...	TIM2+F+I+G4	Raw-0Beaker	11346	11346	-600225.5693	1200717.1 / 1201692.9	0.0866	2015295 ms
R4-M6	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+G4	Raw-0Beaker	11346	11346	-597869.7417	1196007.5 / 1196990.6	0.0866	2015294 ms
R4-M7	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+I+G4	Raw-0Beaker	11346	11346	-600765.1065	1201800.2 / 1202790.7	0.0866	2015296 ms
R4-M8	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+R2	Raw-0Beaker	11346	11346	-601630.5518	1203535.1 / 1204540.2	0.0866	2015294 ms

Supplemental Table S4. Complete 432 Single-Species Regional (R1-R6) & Multi-Locus (L1-L6) Isolates

Isolate	Accession	Organism	Locus	Locality	Host / Context	Source	Length
R1_I01	MF876978.1	*Drosophila suzukii*	COX1 (1Ne)	Canada: British Colum...	Field foliage collection	BIObus 2014	588 bp
R1_I02	MG816064.1	*Drosophila suzukii*	COX1 (1Ne)	U.S. Soft-Fruit Berry...	Field foliage collection	2021-2025	525 bp
R1_I03	MH587763.1	*Drosophila suzukii*	COX1 (1Ne)	USA: New York, Brookh...	Field foliage collection	30-Sep-2016	613 bp
R1_I04	MK435596.1	*Drosophila suzukii*	COX1 (1Ne)	Turkey: Canakkale	Field foliage collection	30-Aug-2016	637 bp
R1_I05	MN448062.1	*Drosophila suzukii*	COX1 (1Ne)	USA: North Carolina, ...	Field foliage collection	01-Jul-2018	658 bp
R1_I06	MT458049.1	*Drosophila suzukii*	COX1 (1Ne)	Italy	Field foliage collection	Nov-2019	687 bp
R1_I07	MW122911.1	*Drosophila suzukii*	COX1 (1Ne)	USA: California	Field foliage collection	04-Jul-2017	818 bp
R1_I08	OK637337.1	*Drosophila suzukii*	COX1 (1Ne)	USA: New York, Queens...	Field foliage collection	01-Nov-2017	562 bp
R1_I09	ON548395.1	*Drosophila suzukii*	COX1 (1Ne)	UBC:StickyPi_V35-4	Field foliage collection	Jul-2020	654 bp
R1_I10	OQ913863.1	*Drosophila suzukii*	COX1 (1Ne)	U.S. Soft-Fruit Berry...	Field foliage collection	2021-2025	658 bp
R1_I11	OR462790.1	*Drosophila suzukii*	COX1 (1Ne)	U.S. Soft-Fruit Berry...	Field foliage collection	2021-2025	658 bp
R1_I12	PV079498.1	*Drosophila suzukii*	COX1 (1Ne)	USA: Hawaii, Maunakea	Field foliage collection	28-May-2019	659 bp
R1_I13	QB229130.1	*Drosophila suzukii*	COX1 (1Ne)	Argentina: Mendoza, L...	Field foliage collection	2021-08-01	585 bp
R1_I14	MF878778.1	*Drosophila suzukii*	COX1 (1Ne)	Canada: Ontario, Thou...	Field foliage collection	14-Oct-2014	552 bp
R1_I15	MG816065.1	*Drosophila suzukii*	COX1 (1Ne)	U.S. Soft-Fruit Berry...	Field foliage collection	2021-2025	525 bp
R1_I16	MH795917.1	*Drosophila suzukii*	COX1 (1Ne)	U.S. Soft-Fruit Berry...	Field foliage collection	2017	599 bp
R1_I17	MK435597.1	*Drosophila suzukii*	COX1 (1Ne)	Turkey: Canakkale	Field foliage collection	30-Aug-2016	637 bp
R1_I18	MN448072.1	*Drosophila suzukii*	COX1 (1Ne)	USA: North Carolina, ...	Field foliage collection	01-Jul-2018	658 bp
R1_I19	MT806955.1	*Drosophila suzukii*	COX1 (1Ne)	USA: North Carolina	Field foliage collection	12-Sep-2019	677 bp
R1_I20	MW122912.1	*Drosophila suzukii*	COX1 (1Ne)	USA: California	Field foliage collection	04-Jul-2017	818 bp
R1_I21	OK637339.1	*Drosophila suzukii*	COX1 (1Ne)	USA: New York, Queens...	Field foliage collection	01-Nov-2017	554 bp
R1_I22	ON548396.1	*Drosophila suzukii*	COX1 (1Ne)	UBC:StickyPi_V35-5	Field foliage collection	Jul-2020	653 bp
R1_I23	OQ913864.1	*Drosophila suzukii*	COX1 (1Ne)	U.S. Soft-Fruit Berry...	Field foliage collection	2021-2025	658 bp
R1_I24	PV079647.1	*Drosophila suzukii*	COX1 (1Ne)	USA: Hawaii, Maunakea	Field foliage collection	12-Aug-2021	659 bp
R1_I25	QB229131.1	*Drosophila suzukii*	COX1 (1Ne)	Argentina: Mendoza, L...	Field foliage collection	2022-04-12	585 bp
R1_I26	MG816066.1	*Drosophila suzukii*	COX1 (1Ne)	U.S. Soft-Fruit Berry...	Field foliage collection	2021-2025	525 bp
R1_I27	MH795918.1	*Drosophila suzukii*	COX1 (1Ne)	U.S. Soft-Fruit Berry...	Field foliage collection	2017	599 bp
R1_I28	MK435598.1	*Drosophila suzukii*	COX1 (1Ne)	Turkey: Canakkale	Field foliage collection	30-Aug-2016	637 bp
R1_I29	MN448109.1	*Drosophila suzukii*	COX1 (1Ne)	USA: North Carolina	Field foliage collection	01-Jul-2018	658 bp
R1_I30	MT807012.1	*Drosophila suzukii*	COX1 (1Ne)	USA: North Carolina, ...	Field foliage collection	10-Mar-2019	663 bp
R1_I31	MW441236.1	*Drosophila suzukii*	COX1 (1Ne)	Italy	Field foliage collection	Oct-2017	685 bp
R1_I32	OK637341.1	*Drosophila suzukii*	COX1 (1Ne)	USA: New York, Queens...	Field foliage collection	01-Nov-2017	537 bp
R1_I33	ON548397.1	*Drosophila suzukii*	COX1 (1Ne)	UBC:StickyPi_V35-6	Field foliage collection	Jul-2020	652 bp
R1_I34	OQ913865.1	*Drosophila suzukii*	COX1 (1Ne)	U.S. Soft-Fruit Berry...	Field foliage collection	2021-2025	658 bp
R1_I35	PV079776.1	*Drosophila suzukii*	COX1 (1Ne)	USA: Hawaii, Maunakea	Field foliage collection	29-May-2019	659 bp
R1_I36	QB229132.1	*Drosophila suzukii*	COX1 (1Ne)	Argentina: Mendoza, L...	Field foliage collection	2024-01-08	585 bp

R2_I01	AY165708.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	BIOUG<CAN>:AY165708	Field foliage collection	2021-2025	623 bp
R2_I02	DQ127907.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Russia: Bashkortostan	Field foliage collection	2021-2025	607 bp
R2_I03	HG326150.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Italy:Piemonte-NO-Veruno	Field foliage collection	2021-2025	780 bp
R2_I04	HQ605768.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	USA: MD	Field foliage collection	2021-2025	658 bp
R2_I05	JF889843.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	U.S. Potato & Solanac...	Field foliage collection	30-Jul-2010	598 bp
R2_I06	KM439182.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Germany: North Rhine-...	Field foliage collection	31-Jul-2012	658 bp
R2_I07	KU907193.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Germany: Saxony-Anhal...	Field foliage collection	21-Jul-2014	658 bp
R2_I08	MF957786.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Spain: Jayena, Granada	Field foliage collection	2021-2025	750 bp
R2_I09	MW346681.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Armenia: Kotayk Prov....	Field foliage collection	1738 m	687 bp
R2_I10	OP361085.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	USA: New York, Suffol...	Field foliage collection	23-Jun-2022	654 bp
R2_I11	OU018332.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	USA	Field foliage collection	JGZC-3889	823 bp
R2_I12	PZ028495.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Uzbekistan: Ferghana,...	Field foliage collection	05-Jun-2025	641 bp
R2_I13	QB033966.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Turkey: Afyonkarahisar	Potato (Solanum tuberos...	2025	672 bp
R2_I14	DQ127909.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Russia: Bashkortostan	Field foliage collection	2021-2025	607 bp
R2_I15	HQ605769.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	USA: Fargo, ND	Field foliage collection	2021-2025	658 bp
R2_I16	KM444991.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Germany: Sachsen, Lei...	Field foliage collection	25-May-2012	658 bp
R2_I17	KU909921.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Poland: Woiwodschaft ...	Field foliage collection	30-Aug-2013	658 bp
R2_I18	MW346683.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Armenia: Gegharkunik ...	Field foliage collection	1858 m	687 bp
R2_I19	QB033967.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Turkey: Bolu	Potato (Solanum tuberos...	2025	672 bp
R2_I20	DQ649094.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Russia: Bashkortostan	Field foliage collection	2021-2025	607 bp
R2_I21	KM446687.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Germany: North Rhine-...	Field foliage collection	31-Jul-2012	658 bp
R2_I22	KU911127.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Germany: Saxony-Anhal...	Field foliage collection	21-Jul-2014	658 bp
R2_I23	MW346682.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Belarus: Vitebsk Reg....	Field foliage collection	30-Jul-2019	686 bp
R2_I24	QB033968.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Turkey: Bursa	Potato (Solanum tuberos...	2025	672 bp
R2_I25	DQ649095.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Russia: Bashkortostan	Field foliage collection	2021-2025	607 bp
R2_I26	KM449504.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Germany: North Rhine-...	Field foliage collection	31-Jul-2012	658 bp
R2_I27	KU914658.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Poland: Woiwodschaft ...	Field foliage collection	30-Aug-2013	658 bp
R2_I28	MW346684.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Belarus: Vitebsk Reg....	Field foliage collection	31-Jul-2019	686 bp
R2_I29	QB033969.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Turkey: Bolu	Potato (Solanum tuberos...	2025	672 bp
R2_I30	DQ649096.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Russia: Bashkortostan	Field foliage collection	2021-2025	607 bp

R2_I31	KM450707.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Germany: North Rhine-...	Field foliage collection	30-Jun-2011	658 bp
R2_I32	KU915233.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Germany: Thuringia, E...	Field foliage collection	10-Jul-2012	658 bp
R2_I33	MW346685.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Armenia: Armavir Prov...	Field foliage collection	13-Jun-2019	686 bp
R2_I34	QB033970.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Turkey: Erzurum	Potato (Solanum tuberos...	2025	672 bp
R2_I35	DQ649097.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Russia: Bashkortostan	Field foliage collection	2021-2025	607 bp
R2_I36	KM439498.1	*Leptinotarsa decemlineata*	COX1 (1Ne)	Austria: Burgenland, ...	Field foliage collection	04-Sep-2012	623 bp
R3_I01	GU800247.1	*Cydia pomonella*	COX1 (1Ne)	USA	Field foliage collection	22-May-2009	658 bp
R3_I02	MK759924.1	*Cydia pomonella*	COX1 (1Ne)	India: Jammu & Kashmir	Field foliage collection	12-Sep-2017	649 bp
R3_I03	MN122344.1	*Cydia pomonella*	COX1 (1Ne)	Turkey	Field foliage collection	2017	631 bp
R3_I04	MW269982.1	*Cydia pomonella*	COX1 (1Ne)	Pacific NW & Mid-Atla...	Field foliage collection	2021-2025	653 bp
R3_I05	OQ836403.1	*Cydia pomonella*	COX1 (1Ne)	Pacific NW & Mid-Atla...	Field foliage collection	TOR-DNA-1167	681 bp
R3_I06	PP991409.1	*Cydia pomonella*	COX1 (1Ne)	Pacific NW & Mid-Atla...	Field foliage collection	17-May-2022	658 bp
R3_I07	PQ072322.1	*Cydia pomonella*	COX1 (1Ne)	Algeria: Tenira	Field foliage collection	2018	613 bp
R3_I08	PV707120.1	*Cydia pomonella*	COX1 (1Ne)	Turkey	Field foliage collection	Jun-2024	670 bp
R3_I09	PX456996.1	*Cydia pomonella*	COX1 (1Ne)	China	Field foliage collection	2025	660 bp
R3_I10	PZ477523.1	*Cydia pomonella*	COX1 (1Ne)	Kazakhstan: Almaty re...	Field foliage collection	25-Jun-2025	679 bp
R3_I11	MK759942.1	*Cydia pomonella*	COX1 (1Ne)	India: Jammu & Kashmir	Field foliage collection	2021-2025	648 bp
R3_I12	MN122345.1	*Cydia pomonella*	COX1 (1Ne)	Turkey	Field foliage collection	2017	631 bp
R3_I13	MW269984.1	*Cydia pomonella*	COX1 (1Ne)	Pacific NW & Mid-Atla...	Field foliage collection	2021-2025	653 bp
R3_I14	OQ836404.1	*Cydia pomonella*	COX1 (1Ne)	Pacific NW & Mid-Atla...	Field foliage collection	TOR-DNA-1193	681 bp
R3_I15	PQ072323.1	*Cydia pomonella*	COX1 (1Ne)	Algeria: Tenira	Field foliage collection	2018	613 bp
R3_I16	PV707121.1	*Cydia pomonella*	COX1 (1Ne)	Turkey	Field foliage collection	Jun-2024	670 bp
R3_I17	PZ437865.1	*Cydia pomonella*	COX1 (1Ne)	China: Xinjiang Uygur...	Field foliage collection	2025	670 bp
R3_I18	MK759925.1	*Cydia pomonella*	COX1 (1Ne)	India: Jammu & Kashmir	Field foliage collection	12-Sep-2017	645 bp
R3_I19	MN122346.1	*Cydia pomonella*	COX1 (1Ne)	Turkey	Field foliage collection	2017	631 bp
R3_I20	MW269987.1	*Cydia pomonella*	COX1 (1Ne)	Pacific NW & Mid-Atla...	Field foliage collection	2021-2025	653 bp
R3_I21	OQ836405.1	*Cydia pomonella*	COX1 (1Ne)	Pacific NW & Mid-Atla...	Field foliage collection	TOR-DNA-1204	681 bp
R3_I22	PQ072324.1	*Cydia pomonella*	COX1 (1Ne)	Algeria: Tenira	Field foliage collection	2018	613 bp
R3_I23	PV707122.1	*Cydia pomonella*	COX1 (1Ne)	Turkey	Field foliage collection	Jun-2024	670 bp
R3_I24	MK759943.1	*Cydia pomonella*	COX1 (1Ne)	India: Jammu & Kashmir	Field foliage collection	2021-2025	645 bp
R3_I25	MN122347.1	*Cydia pomonella*	COX1 (1Ne)	Turkey	Field foliage collection	2017	631 bp
R3_I26	MW269989.1	*Cydia pomonella*	COX1 (1Ne)	Pacific NW & Mid-Atla...	Field foliage collection	2021-2025	653 bp
R3_I27	OQ836406.1	*Cydia pomonella*	COX1 (1Ne)	Pacific NW & Mid-Atla...	Field foliage collection	TOR-DNA-1216	681 bp
R3_I28	PQ072325.1	*Cydia pomonella*	COX1 (1Ne)	Algeria: Tenira	Field foliage collection	2018	613 bp
R3_I29	PV707123.1	*Cydia pomonella*	COX1 (1Ne)	Turkey	Field foliage collection	Jun-2024	670 bp
R3_I30	MK732898.1	*Cydia pomonella*	COX1 (1Ne)	India: Jammu & Kashmir	Field foliage collection	21-Sep-2017	642 bp
R3_I31	MN122348.1	*Cydia pomonella*	COX1 (1Ne)	Turkey	Field foliage collection	2017	631 bp
R3_I32	MW269992.1	*Cydia pomonella*	COX1 (1Ne)	Pacific NW & Mid-Atla...	Field foliage collection	2021-2025	653 bp
R3_I33	OQ836407.1	*Cydia pomonella*	COX1 (1Ne)	Pacific NW & Mid-Atla...	Field foliage collection	TOR-DNA-1226	681 bp
R3_I34	PQ072326.1	*Cydia pomonella*	COX1 (1Ne)	Algeria: Tenira	Field foliage collection	2018	613 bp
R3_I35	PV707124.1	*Cydia pomonella*	COX1 (1Ne)	Turkey	Field foliage collection	Jun-2024	670 bp
R3_I36	MK732899.1	*Cydia pomonella*	COX1 (1Ne)	India: Jammu & Kashmir	Field foliage collection	21-Sep-2017	642 bp
R4_I01	PP124570.1	*Diaphorina citri*	COX1 (1Ne)	India	Field foliage collection	2021-2025	628 bp

R4_I02	PQ470100.1	*Diaphorina citri*	COX1 (1Ne)	India: Virajpet,Karna...	Field foliage collection	18-Nov-2021	834 bp
R4_I03	PX715504.1	*Diaphorina citri*	COX1 (1Ne)	Florida, Texas & CA C...	Field foliage collection	04-Mar-2024	811 bp
R4_I04	PZ493015.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: Molipeli Farm	Field foliage collection	23-Oct-2024	799 bp
R4_I05	PP124571.1	*Diaphorina citri*	COX1 (1Ne)	India	Field foliage collection	2021-2025	619 bp
R4_I06	PQ470102.1	*Diaphorina citri*	COX1 (1Ne)	India: Shanivarsanthe...	Field foliage collection	18-Nov-2021	834 bp
R4_I07	PX715505.1	*Diaphorina citri*	COX1 (1Ne)	Florida, Texas & CA C...	Field foliage collection	04-Mar-2024	805 bp
R4_I08	PZ493016.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: Molipeli Farm	Field foliage collection	23-Oct-2024	799 bp
R4_I09	PP123911.1	*Diaphorina citri*	COX1 (1Ne)	India	Field foliage collection	2021-2025	555 bp
R4_I10	PQ470103.1	*Diaphorina citri*	COX1 (1Ne)	India: Shanivarsanthe...	Field foliage collection	18-Nov-2021	834 bp
R4_I11	PZ493018.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: Hoatua Eua	Field foliage collection	24-Oct-2025	799 bp
R4_I12	PQ470104.1	*Diaphorina citri*	COX1 (1Ne)	India: Shanivarsanthe...	Field foliage collection	18-Nov-2021	834 bp
R4_I13	PZ493019.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: Houna Eua	Field foliage collection	24-Oct-2025	799 bp
R4_I14	PQ470105.1	*Diaphorina citri*	COX1 (1Ne)	India: Somawarpet,Kar...	Field foliage collection	18-Nov-2021	834 bp
R4_I15	PZ493020.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: Houna Eua	Field foliage collection	25-Oct-2024	799 bp
R4_I16	PQ470108.1	*Diaphorina citri*	COX1 (1Ne)	India: Kushalanagar,K...	Field foliage collection	18-Nov-2021	834 bp
R4_I17	PZ493021.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: Houna Eua	Field foliage collection	25-Oct-2024	799 bp
R4_I18	PQ470110.1	*Diaphorina citri*	COX1 (1Ne)	India: Kushalanagar,K...	Field foliage collection	18-Nov-2021	834 bp
R4_I19	PZ493023.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: 'Utulei, Tu'an...	Field foliage collection	09-Dec-2024	799 bp
R4_I20	PQ470111.1	*Diaphorina citri*	COX1 (1Ne)	India: Gonikoppa,Karn...	Field foliage collection	18-Nov-2021	834 bp
R4_I21	PZ493024.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: 'Utulei, Tu'an...	Field foliage collection	09-Dec-2024	799 bp
R4_I22	PQ470113.1	*Diaphorina citri*	COX1 (1Ne)	India: Kodalipet,Karn...	Field foliage collection	18-Nov-2021	834 bp
R4_I23	PZ493025.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: Hihifo	Field foliage collection	14-Dec-2024	799 bp
R4_I24	PQ470096.1	*Diaphorina citri*	COX1 (1Ne)	India: Madikeri,Karna...	Field foliage collection	18-Nov-2021	816 bp
R4_I25	PZ493026.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: Hihifo	Field foliage collection	14-Dec-2024	799 bp
R4_I26	PQ470097.1	*Diaphorina citri*	COX1 (1Ne)	India: Madikeri,Karna...	Field foliage collection	18-Nov-2021	816 bp
R4_I27	PZ493027.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: Nishi, Vaiola ...	Field foliage collection	19-Dec-2024	799 bp
R4_I28	PQ470098.1	*Diaphorina citri*	COX1 (1Ne)	India: Madikeri,Karna...	Field foliage collection	18-Nov-2021	816 bp
R4_I29	PZ493028.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: Nishi, Vaiola ...	Field foliage collection	19-Dec-2024	799 bp
R4_I30	PQ470099.1	*Diaphorina citri*	COX1 (1Ne)	India: Virajpet,Karna...	Field foliage collection	18-Nov-2021	816 bp
R4_I31	PZ493029.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: Nishi, Vaiola ...	Field foliage collection	19-Dec-2024	799 bp
R4_I32	PQ470101.1	*Diaphorina citri*	COX1 (1Ne)	India: Virajpet,Karna...	Field foliage collection	18-Nov-2021	816 bp
R4_I33	PZ493030.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: 'Esia	Field foliage collection	19-Dec-2024	799 bp
R4_I34	PQ470106.1	*Diaphorina citri*	COX1 (1Ne)	India: Somawarpet,Kar...	Field foliage collection	18-Nov-2021	816 bp
R4_I35	PZ493031.1	*Diaphorina citri*	COX1 (1Ne)	Tonga: 'Esia	Field foliage collection	19-Dec-2024	799 bp
R4_I36	PQ470107.1	*Diaphorina citri*	COX1 (1Ne)	India: Somawarpet,Kar...	Field foliage collection	18-Nov-2021	816 bp
R5_I01	AY499585.1	*Solenopsis invicta*	COX1 (1Ne)	Brazil	Field foliage collection	2021-2025	785 bp
R5_I02	EU290756.1	*Solenopsis invicta*	COX1 (1Ne)	Southern U.S. Rangela...	Field foliage collection	2004	910 bp
R5_I03	HQ928592.1	*Solenopsis invicta*	COX1 (1Ne)	USA	Field foliage collection	Biobus 2010	658 bp
R5_I04	KJ690241.1	*Solenopsis invicta*	COX1 (1Ne)	Brazil: Rio Claro, Sa...	Field foliage collection	2021-2025	726 bp
R5_I05	KY120272.1	*Solenopsis invicta*	COX1 (1Ne)	USA: Florida, Gainesv...	Field foliage collection	2021-2025	584 bp
R5_I06	MK829063.1	*Solenopsis invicta*	COX1 (1Ne)	China	Field foliage collection	24-Oct-2017	629 bp
R5_I07	MT854331.1	*Solenopsis invicta*	COX1 (1Ne)	Brazil	Field foliage collection	2021-2025	726 bp
R5_I08	MW802192.1	*Solenopsis invicta*	COX1 (1Ne)	USA: Arkansas, Indepe...	Field foliage collection	27-Sep-2020	649 bp
R5_I09	MZ362383.1	*Solenopsis invicta*	COX1 (1Ne)	USA: California, Rive...	Field foliage collection	03-Nov-2020	651 bp
R5_I10	OK646336.1	*Solenopsis invicta*	COX1 (1Ne)	Southern U.S. Rangela...	Field foliage collection	2021-2025	798 bp
R5_I11	OL257850.1	*Solenopsis invicta*	COX1 (1Ne)	Southern U.S. Rangela...	Field foliage collection	2021-2025	798 bp

R5_I12	ON130823.1	*Solenopsis invicta*	COX1 (1Ne)	Southern U.S. Rangela...	Field foliage collection	2021-2025	877 bp
R5_I13	OP849630.1	*Solenopsis invicta*	COX1 (1Ne)	Southern U.S. Rangela...	Field foliage collection	2021-2025	832 bp
R5_I14	PQ331134.1	*Solenopsis invicta*	COX1 (1Ne)	Puerto Rico: Arecibo,...	Field foliage collection	12-Jun-2024	660 bp
R5_I15	PV094501.1	*Solenopsis invicta*	COX1 (1Ne)	Viet Nam: Quang Ninh,...	Field foliage collection	24-Oct-2024	709 bp
R5_I16	PX127923.1	*Solenopsis invicta*	COX1 (1Ne)	USA	Field foliage collection	15-May-2004	906 bp
R5_I17	PZ017564.1	*Solenopsis invicta*	COX1 (1Ne)	Southern U.S. Rangela...	Field foliage collection	Nov-2025	556 bp
R5_I18	AY499586.1	*Solenopsis invicta*	COX1 (1Ne)	Brazil	Field foliage collection	2021-2025	785 bp
R5_I19	EU290757.1	*Solenopsis invicta*	COX1 (1Ne)	Southern U.S. Rangela...	Field foliage collection	2006	910 bp
R5_I20	HQ928615.1	*Solenopsis invicta*	COX1 (1Ne)	USA	Field foliage collection	Biobus 2010	658 bp
R5_I21	KJ690242.1	*Solenopsis invicta*	COX1 (1Ne)	Brazil: Rio Claro, Sa...	Field foliage collection	2021-2025	726 bp
R5_I22	MT854332.1	*Solenopsis invicta*	COX1 (1Ne)	Brazil	Field foliage collection	2021-2025	726 bp
R5_I23	MZ362394.1	*Solenopsis invicta*	COX1 (1Ne)	USA: California, Rive...	Field foliage collection	30-Oct-2020	648 bp
R5_I24	OK646337.1	*Solenopsis invicta*	COX1 (1Ne)	Southern U.S. Rangela...	Field foliage collection	2021-2025	798 bp
R5_I25	OL257860.1	*Solenopsis invicta*	COX1 (1Ne)	Southern U.S. Rangela...	Field foliage collection	2021-2025	798 bp
R5_I26	ON130816.1	*Solenopsis invicta*	COX1 (1Ne)	Southern U.S. Rangela...	Field foliage collection	2021-2025	844 bp
R5_I27	OP849632.1	*Solenopsis invicta*	COX1 (1Ne)	Southern U.S. Rangela...	Field foliage collection	2021-2025	832 bp
R5_I28	PQ331137.1	*Solenopsis invicta*	COX1 (1Ne)	Puerto Rico: Arecibo,...	Field foliage collection	11-Jun-2024	645 bp
R5_I29	PV094502.1	*Solenopsis invicta*	COX1 (1Ne)	Viet Nam: Quang Ninh,...	Field foliage collection	24-Oct-2024	709 bp
R5_I30	PX474348.1	*Solenopsis invicta*	COX1 (1Ne)	China: Zheiang province	Field foliage collection	May-2025	671 bp
R5_I31	PZ017566.1	*Solenopsis invicta*	COX1 (1Ne)	Southern U.S. Rangela...	Field foliage collection	Dec-2025	556 bp
R5_I32	AY499587.1	*Solenopsis invicta*	COX1 (1Ne)	Brazil	Field foliage collection	2021-2025	785 bp
R5_I33	EU311556.1	*Solenopsis invicta*	COX1 (1Ne)	China: Shenzhen	Field foliage collection	2021-2025	867 bp
R5_I34	HQ928647.1	*Solenopsis invicta*	COX1 (1Ne)	USA	Field foliage collection	Biobus 2010	658 bp
R5_I35	KJ690243.1	*Solenopsis invicta*	COX1 (1Ne)	Brazil: Campinas, Sao...	Field foliage collection	2021-2025	726 bp
R5_I36	MT854333.1	*Solenopsis invicta*	COX1 (1Ne)	Brazil	Field foliage collection	2021-2025	726 bp
R6_I01	MG458962.1	*Sitophilus oryzae*	COX1 (1Ne)	USA	Field foliage collection	1960	664 bp
R6_I02	MK892142.1	*Sitophilus oryzae*	COX1 (1Ne)	Slovakia: Nitra	Field foliage collection	21-Sep-2014	658 bp
R6_I03	MT646166.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	707 bp
R6_I04	OM772987.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	658 bp
R6_I05	OP618395.1	*Sitophilus oryzae*	COX1 (1Ne)	India: Baramulla, J & K	Field foliage collection	2021-2025	900 bp
R6_I06	OQ452922.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	30-Jun-2022	621 bp
R6_I07	PP874574.1	*Sitophilus oryzae*	COX1 (1Ne)	India	Field foliage collection	15-Apr-2024	613 bp
R6_I08	PV054139.1	*Sitophilus oryzae*	COX1 (1Ne)	Guinea-Bissau: Oio, O...	Field foliage collection	24-Jun-2022	658 bp
R6_I09	PX588007.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	20-Apr-2025	671 bp
R6_I10	PZ939071.1	*Sitophilus oryzae*	COX1 (1Ne)	India	Field foliage collection	01-Aug-2026	779 bp
R6_I11	MT646167.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	678 bp
R6_I12	OM772988.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	658 bp
R6_I13	OP618396.1	*Sitophilus oryzae*	COX1 (1Ne)	India: Baramulla, J & K	Field foliage collection	2021-2025	900 bp
R6_I14	OQ996824.1	*Sitophilus oryzae*	COX1 (1Ne)	India	Field foliage collection	2021-2025	600 bp
R6_I15	PV054175.1	*Sitophilus oryzae*	COX1 (1Ne)	Guinea-Bissau: Cacheu...	Field foliage collection	02-Jul-2022	658 bp
R6_I16	MT646168.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	675 bp
R6_I17	OM772989.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	658 bp
R6_I18	OP618397.1	*Sitophilus oryzae*	COX1 (1Ne)	India: Baramulla, J & K	Field foliage collection	2021-2025	900 bp
R6_I19	PV054178.1	*Sitophilus oryzae*	COX1 (1Ne)	Guinea-Bissau: Oio, O...	Field foliage collection	25-Jun-2022	658 bp
R6_I20	MT646174.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	670 bp
R6_I21	OM772990.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	658 bp

R6_I22	OP618398.1	*Sitophilus oryzae*	COX1 (1Ne)	India: Baramulla, J & K	Field foliage collection	2021-2025	900 bp
R6_I23	PV054204.1	*Sitophilus oryzae*	COX1 (1Ne)	Guinea-Bissau: Oio, O...	Field foliage collection	24-Jun-2022	658 bp
R6_I24	MT646175.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	670 bp
R6_I25	OM772991.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	658 bp
R6_I26	OP618399.1	*Sitophilus oryzae*	COX1 (1Ne)	India: Baramulla, J & K	Field foliage collection	2021-2025	900 bp
R6_I27	PV793468.1	*Sitophilus oryzae*	COX1 (1Ne)	India: J&K,Srinagar	Field foliage collection	01-May-2025	625 bp
R6_I28	MT646176.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	669 bp
R6_I29	OM772992.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	658 bp
R6_I30	OP618400.1	*Sitophilus oryzae*	COX1 (1Ne)	India: Baramulla, J & K	Field foliage collection	2021-2025	900 bp
R6_I31	PV770331.1	*Sitophilus oryzae*	COX1 (1Ne)	India: UP, Varanasi	Field foliage collection	25-Feb-2025	583 bp
R6_I32	MT646179.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	669 bp
R6_I33	OM772993.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	658 bp
R6_I34	OP618401.1	*Sitophilus oryzae*	COX1 (1Ne)	India: Baramulla, J & K	Field foliage collection	2021-2025	900 bp
R6_I35	MT646170.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	666 bp
R6_I36	OM772994.1	*Sitophilus oryzae*	COX1 (1Ne)	Midwest & Great Plain...	Field foliage collection	2021-2025	658 bp
L1_I01	LC363319.1	*Plutella xylostella*	COX1 (1Ne Maternal)	U.S. Brassica Corridors	Field foliage collection	2014	551 bp
L1_I02	MG464414.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Canada: Saskatchewan,...	Field foliage collection	01-Oct-2014	603 bp
L1_I03	MW305985.1	*Plutella xylostella*	COX1 (1Ne Maternal)	U.S. Brassica Corridors	Field foliage collection	2021-2025	696 bp
L1_I04	MZ303044.1	*Plutella xylostella*	COX1 (1Ne Maternal)	India: Tamil Nadu, OOTY	Field foliage collection	12-Apr-2021	579 bp
L1_I05	OM911943.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Turkey	Field foliage collection	2020	655 bp
L1_I06	ON368714.1	*Plutella xylostella*	COX1 (1Ne Maternal)	U.S. Brassica Corridors	Field foliage collection	200312mnWP14	630 bp
L1_I07	OQ181896.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Italy: Prato del Coll...	Field foliage collection	31-Oct-2019	658 bp
L1_I08	PP837602.1	*Plutella xylostella*	COX1 (1Ne Maternal)	BPI:123	Field foliage collection	2021-2025	663 bp
L1_I09	PQ143326.1	*Plutella xylostella*	COX1 (1Ne Maternal)	China	Field foliage collection	2021-2025	727 bp
L1_I10	PV697006.1	*Plutella xylostella*	COX1 (1Ne Maternal)	India: Tamil Nadu Agr...	Field foliage collection	15-Apr-2025	605 bp
L1_I11	PX558012.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Mexico: Saltillo, Coa...	Field foliage collection	Jul-2023	637 bp
L1_I12	PZ258164.1	*Plutella xylostella*	COX1 (1Ne Maternal)	China: Zhejiang,Huzhou	Field foliage collection	2025-04-08	678 bp
L1_I13	LC363320.1	*Plutella xylostella*	COX1 (1Ne Maternal)	U.S. Brassica Corridors	Field foliage collection	2014	551 bp
L1_I14	MG463607.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Canada: Saskatchewan,...	Field foliage collection	20-Jun-2014	588 bp
L1_I15	MW305984.1	*Plutella xylostella*	COX1 (1Ne Maternal)	U.S. Brassica Corridors	Field foliage collection	2021-2025	692 bp
L1_I16	MZ348920.1	*Plutella xylostella*	COX1 (1Ne Maternal)	India	Field foliage collection	2021-2025	531 bp
L1_I17	OM911944.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Turkey	Field foliage collection	2020	655 bp
L1_I18	ON368756.1	*Plutella xylostella*	COX1 (1Ne Maternal)	U.S. Brassica Corridors	Field foliage collection	200227amH_20	627 bp
L1_I19	OQ562039.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Portugal: Braganca, M...	Field foliage collection	06-Oct-2015	658 bp
L1_I20	PQ143325.1	*Plutella xylostella*	COX1 (1Ne Maternal)	China	Field foliage collection	2021-2025	726 bp
L1_I21	PX688013.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Mongolia: Tuv province	Field foliage collection	20-Aug-2024	635 bp
L1_I22	PZ185384.1	*Plutella xylostella*	COX1 (1Ne Maternal)	India: Ladakh, Leh	Field foliage collection	30-Sep-2025	634 bp
L1_I23	LC363321.1	*Plutella xylostella*	COX1 (1Ne Maternal)	U.S. Brassica Corridors	Field foliage collection	2014	551 bp
L1_I24	MG464168.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Canada: Saskatchewan,...	Field foliage collection	20-Jun-2014	588 bp
L1_I25	OM911945.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Turkey	Field foliage collection	2020	655 bp
L1_I26	ON368757.1	*Plutella xylostella*	COX1 (1Ne Maternal)	U.S. Brassica Corridors	Field foliage collection	200227amH_33	627 bp
L1_I27	OQ562061.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Portugal: Braganca, B...	Field foliage collection	19-Jun-2015	658 bp
L1_I28	PQ143327.1	*Plutella xylostella*	COX1 (1Ne Maternal)	China	Field foliage collection	2021-2025	726 bp
L1_I29	PX317840.1	*Plutella xylostella*	COX1 (1Ne Maternal)	India: Varanasi	Field foliage collection	25-Feb-2021	627 bp
L1_I30	LC363322.1	*Plutella xylostella*	COX1 (1Ne Maternal)	U.S. Brassica Corridors	Field foliage collection	2014	551 bp
L1_I31	MG466683.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Canada: Ontario, Thou...	Field foliage collection	14-May-2014	588 bp

L1_I32	OM911946.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Turkey	Field foliage collection	2020	655 bp
L1_I33	ON368923.1	*Plutella xylostella*	COX1 (1Ne Maternal)	U.S. Brassica Corridors	Field foliage collection	200218amH_9	615 bp
L1_I34	OQ563412.1	*Plutella xylostella*	COX1 (1Ne Maternal)	Portugal: Braganca, M...	Field foliage collection	17-Jun-2015	658 bp
L1_I35	PQ143328.1	*Plutella xylostella*	COX1 (1Ne Maternal)	China	Field foliage collection	2021-2025	726 bp
L1_I36	LC363323.1	*Plutella xylostella*	COX1 (1Ne Maternal)	U.S. Brassica Corridors	Field foliage collection	2014	551 bp
L2_I01	AB904182.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	NCHU:CaC	Field foliage collection	2021-2025	958 bp
L2_I02	GU980284.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	UCD 206033	846 bp
L2_I03	KT885222.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	USA	Field foliage collection	16-Apr-2011	453 bp
L2_I04	KY605008.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	Mexico: Periban, MN	Field foliage collection	2021-2025	464 bp
L2_I05	MK418774.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	2021-2025	575 bp
L2_I06	MN889879.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	India	Field foliage collection	28-Nov-2019	562 bp
L2_I07	MZ919075.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	2021-2025	455 bp
L2_I08	OQ256297.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Solanum nigrum	2021-11-09	453 bp
L2_I09	PP277611.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	NCHU:Q6_48-2	Field foliage collection	2021-2025	580 bp
L2_I10	PZ610069.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	18-Jan-2023	575 bp
L2_I11	GU980299.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	UCD 206048	846 bp
L2_I12	KT885223.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	USA	Field foliage collection	16-Apr-2011	453 bp
L2_I13	KY605009.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	Mexico: Uruapan, MN	Field foliage collection	2021-2025	464 bp
L2_I14	MZ919086.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	2021-2025	452 bp
L2_I15	OQ256298.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	2021-06-07	453 bp
L2_I16	PP277610.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	NCHU:Q6_44-3	Field foliage collection	2021-2025	579 bp
L2_I17	PZ610070.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	14-May-2023	575 bp
L2_I18	GU980323.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	UCD 206072	845 bp
L2_I19	KY605010.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	Mexico: Uruapan, MN	Field foliage collection	2021-2025	464 bp
L2_I20	OQ256299.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	2021-06-07	453 bp
L2_I21	PP277599.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	NCHU:Q6_25-1	Field foliage collection	2021-2025	578 bp
L2_I22	PZ610071.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	USA	Field foliage collection	30-May-2023	575 bp
L2_I23	GU980309.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	UCD 206058	841 bp
L2_I24	KY605011.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	Mexico: Periban, MN	Field foliage collection	2021-2025	464 bp
L2_I25	OQ256300.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	2021-06-07	453 bp
L2_I26	PP277600.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	NCHU:Q6_25-2	Field foliage collection	2021-2025	578 bp
L2_I27	PZ610072.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	01-Jun-2023	575 bp

L2_I28	GU980279.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	UCD 206028	828 bp
L2_I29	KY605012.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	Mexico: Nuevo Paranga...	Field foliage collection	2021-2025	464 bp
L2_I30	OQ256301.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	2021-06-07	453 bp
L2_I31	PP277614.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	NCHU:Q6_56-1	Field foliage collection	2021-2025	578 bp
L2_I32	PZ610068.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	03-Jul-2022	574 bp
L2_I33	GU980316.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	UCD 206065	827 bp
L2_I34	KY605013.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	Mexico: Periban, MN	Field foliage collection	2021-2025	464 bp
L2_I35	OQ256302.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	U.S. Protected & Gree...	Field foliage collection	2021-06-07	453 bp
L2_I36	PP277577.1	*Frankliniella occidentalis*	ITS1/28S rDNA (4Ne E-INS-i)	NCHU:Q6_03-2	Field foliage collection	2021-2025	577 bp
L3_I01	GU066317.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I02	JF343437.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	2315 bp
L3_I03	KC342668.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I04	GU066318.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I05	JF343436.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	2149 bp
L3_I06	KC342669.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I07	GU066319.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I08	KC342670.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I09	GU066320.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I10	KC342671.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I11	GU066321.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I12	KC342672.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I13	GU066322.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I14	KC342673.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I15	GU066323.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I16	KC342674.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I17	GU066324.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I18	KC342675.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I19	GU066325.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I20	KC342676.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I21	GU066326.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp

L3_I22	KC342677.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I23	GU066327.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I24	KC342678.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I25	GU066328.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I26	KC342679.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I27	GU066329.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I28	KC342680.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I29	GU066330.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I30	KC342681.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I31	GU066331.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I32	KC342682.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I33	GU066332.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I34	KC342683.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I35	GU066333.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L3_I36	KC342684.1	*Leptinotarsa decemlineata*	Nuclear ace-1 (Locus CDS)	Insecticide Target-Si...	Field foliage collection	2021-2025	1037 bp
L4_I01	LC877271.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Indonesia:Nusa Tengga...	Field foliage collection	2023-06-06	678 bp
L4_I02	MT881755.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Mississippi-Atlantic ...	Field foliage collection	20-Nov-2015	702 bp
L4_I03	OL979469.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Mississippi-Atlantic ...	Field foliage collection	2021-2025	654 bp
L4_I04	OR674777.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Malaysia: Sarawak	Field foliage collection	2022	620 bp
L4_I05	PQ270594.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	China: Guangdong,Zhan...	Field foliage collection	Jun-2023	785 bp
L4_I06	PV156493.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	India	Field foliage collection	10-Sep-2024	675 bp
L4_I07	PX796387.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Indonesia: Bali, Denp...	Field foliage collection	03-Jan-2026	710 bp
L4_I08	PZ842127.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	India: Kerala	Field foliage collection	01-Mar-2026	711 bp
L4_I09	QB189650.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	South Korea: Jeju-do,...	Field foliage collection	20-Aug-2026	668 bp
L4_I10	LC877274.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Indonesia:Jawa barat,...	Field foliage collection	2023-06-08	626 bp
L4_I11	MT881760.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Mississippi-Atlantic ...	Field foliage collection	03-Jul-2015	695 bp
L4_I12	OL979475.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Mississippi-Atlantic ...	Field foliage collection	2021-2025	654 bp
L4_I13	OR002052.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Malaysia: Sarawak	Field foliage collection	2021-2025	597 bp
L4_I14	PQ270595.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	China: Guangdong,Zhan...	Field foliage collection	Mar-2023	785 bp
L4_I15	PV156519.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	India	Field foliage collection	10-Sep-2024	665 bp
L4_I16	PX998475.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	India: Karnataka, Chi...	Field foliage collection	27-Jan-2026	692 bp
L4_I17	PZ159306.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	India: Tamil Nadu, Th...	Field foliage collection	Jan-2026	709 bp
L4_I18	QB189651.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	South Korea: Jeju-do,...	Field foliage collection	20-Aug-2026	668 bp
L4_I19	LC877272.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Indonesia:Jawa Timur,...	Field foliage collection	2024-12-24	617 bp
L4_I20	MT881754.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Mississippi-Atlantic ...	Field foliage collection	20-Nov-2015	694 bp
L4_I21	OL774682.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Mississippi-Atlantic ...	Field foliage collection	2021-2025	558 bp
L4_I22	OR002053.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Malaysia: Sarawak	Field foliage collection	2021-2025	597 bp

L4_I23	PQ270596.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	China: Guangdong,Zhan...	Field foliage collection	Mar-2023	785 bp
L4_I24	PV699696.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Iran: Khorramabad, Lo...	Field foliage collection	28-Sep-2024	665 bp
L4_I25	PX978088.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	USA: TX, Bastrop Co.	Field foliage collection	19-Oct-2023	675 bp
L4_I26	PZ263845.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	India	Field foliage collection	29-Nov-2025	690 bp
L4_I27	QB189652.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	South Korea: Jeju-do,...	Field foliage collection	20-Aug-2026	668 bp
L4_I28	LC877273.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Indonesia:Nusa Tengga...	Field foliage collection	2024-01-03	617 bp
L4_I29	MT881759.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Mississippi-Atlantic ...	Field foliage collection	03-Jul-2015	694 bp
L4_I30	OR002054.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Malaysia: Sarawak	Field foliage collection	2021-2025	597 bp
L4_I31	PQ270597.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	China: Guangdong,Zhan...	Field foliage collection	Mar-2023	785 bp
L4_I32	PV156448.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	India	Field foliage collection	25-Sep-2024	660 bp
L4_I33	PX978366.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	USA: TX, Bastrop Co.	Field foliage collection	17-Nov-2023	672 bp
L4_I34	PZ263875.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	India	Field foliage collection	10-Feb-2025	680 bp
L4_I35	QB189649.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	South Korea: Jeju-do,...	Field foliage collection	20-Aug-2026	666 bp
L4_I36	LC877275.1	*Spodoptera frugiperda*	COX1 (1Ne Maternal)	Indonesia:Jawa Barat,...	Field foliage collection	2022-05-15	617 bp
L5_I01	AB904212.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	NCHU:Tai61-1	Field foliage collection	2021-2025	1104 bp
L5_I02	AM932159.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2021-2025	582 bp
L5_I03	AY523392.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2021-2025	678 bp
L5_I04	EU035759.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	May-2007	630 bp
L5_I05	JF968499.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	A72.13	485 bp
L5_I06	KM877307.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2021-2025	1540 bp
L5_I07	KP216399.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Solanum nigrum	A107.10	487 bp
L5_I08	LC416231.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2007-10-09	619 bp
L5_I09	MN187366.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	India	Field foliage collection	2021-2025	388 bp
L5_I10	OR005042.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	I2-86-1	559 bp
L5_I11	PZ433186.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	10-Apr-2026	592 bp
L5_I12	AB904211.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	NCHU:JP32-2	Field foliage collection	2021-2025	1084 bp
L5_I13	AM932144.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2021-2025	515 bp
L5_I14	AY523393.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	Tt-I-20-1-2	678 bp
L5_I15	JF968500.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2021-2025	485 bp
L5_I16	KM877308.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2021-2025	1540 bp
L5_I17	KP216397.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Solanum nigrum	A126.5	485 bp
L5_I18	LC416235.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2007-10-28	616 bp
L5_I19	AB904208.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	USA	Field foliage collection	2021-2025	1072 bp
L5_I20	AM932152.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2021-2025	515 bp

L5_I21	AY523394.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	Tt-I-20-1-3	678 bp
L5_I22	JF968504.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	A56.10	485 bp
L5_I23	KP216398.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2021-2025	485 bp
L5_I24	LC416229.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2007-09-13	611 bp
L5_I25	AB904209.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	NCHU:JP11	Field foliage collection	2021-2025	1061 bp
L5_I26	AM932153.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2021-2025	515 bp
L5_I27	AY523395.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	Tt-I-23-1-9	678 bp
L5_I28	JF968492.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2021-2025	484 bp
L5_I29	KP216406.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	A131.10	485 bp
L5_I30	LC416234.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	India	Field foliage collection	2007-10-25	609 bp
L5_I31	AB904210.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	NCHU:JP13	Field foliage collection	2021-2025	950 bp
L5_I32	AM932154.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2021-2025	515 bp
L5_I33	AY523396.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	Tt-I-47-3-2	678 bp
L5_I34	JF968494.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2021-2025	484 bp
L5_I35	KP216396.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Solanum nigrum	A107.14	484 bp
L5_I36	LC416228.1	*Thrips tabaci*	ITS1/28S rDNA (4Ne E-INS-i)	Citrus & Specialty Cr...	Field foliage collection	2007-09-08	572 bp
L6_I01	OL999568.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	India	Field foliage collection	2021-2025	664 bp
L6_I02	OM069376.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	India	Field foliage collection	2021-2025	664 bp
L6_I03	OQ468458.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	15-Jul-2020	444 bp
L6_I04	OR724711.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	2021-2025	1420 bp
L6_I05	PP457652.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Benin: Athieme	Field foliage collection	Aug-2020	303 bp
L6_I06	PV125351.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	2021-2025	428 bp
L6_I07	PZ161581.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Burkina Faso: Kouritenga	Field foliage collection	Aug-2023	392 bp
L6_I08	OL999569.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	India	Field foliage collection	2021-2025	664 bp
L6_I09	OM069377.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	India	Field foliage collection	2021-2025	664 bp
L6_I10	OQ468459.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	15-Jul-2020	444 bp
L6_I11	OR724712.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	2021-2025	1242 bp
L6_I12	PP457653.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Benin: Athieme	Field foliage collection	Aug-2020	303 bp
L6_I13	PV664520.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	2021-2025	296 bp
L6_I14	PZ161583.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Burkina Faso: Boulgou...	Field foliage collection	Aug-2023	390 bp
L6_I15	OL999571.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	India	Field foliage collection	2021-2025	664 bp
L6_I16	OM069380.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	India	Field foliage collection	2021-2025	664 bp
L6_I17	OQ468460.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	15-Jul-2020	444 bp
L6_I18	OR724709.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	China	Field foliage collection	20-May-2020	1234 bp
L6_I19	PP457654.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Niger: Madarounfa	Field foliage collection	Jan-2021	303 bp
L6_I20	PV664523.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	2021-2025	296 bp

L6_I21	PZ161588.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Burkina Faso: Boulkie...	Field foliage collection	Sep-2023	390 bp
L6_I22	OL999570.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	India	Field foliage collection	2021-2025	658 bp
L6_I23	OM069375.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	India	Field foliage collection	2021-2025	658 bp
L6_I24	OQ468461.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	20-Dec-2022	444 bp
L6_I25	OR724710.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	China	Field foliage collection	27-Aug-2020	1234 bp
L6_I26	PP457655.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Niger: Madarounfa	Field foliage collection	Jan-2021	303 bp
L6_I27	PV664532.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	2021-2025	296 bp
L6_I28	PZ161580.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Burkina Faso: Bales, ...	Field foliage collection	Aug-2023	388 bp
L6_I29	OL999572.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	India	Field foliage collection	2021-2025	658 bp
L6_I30	OM069378.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	India	Field foliage collection	2021-2025	658 bp
L6_I31	OQ468462.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	15-Dec-2022	444 bp
L6_I32	OR838464.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	CNU15404	444 bp
L6_I33	PP457656.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Togo: Avetonou	Field foliage collection	Apr-2021	303 bp
L6_I34	PV664499.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Host-Strain Z-Linked ...	Field foliage collection	2021-2025	293 bp
L6_I35	PZ161586.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	Burkina Faso: Oubrite...	Field foliage collection	Aug-2023	385 bp
L6_I36	OM069379.1	*Spodoptera frugiperda*	Nuclear Tpi (Z-Linked CDS)	India	Field foliage collection	2021-2025	658 bp