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Genomic adaptation to polyphagy and insecticides in a major East Asian noctuid pest

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Supplementary Information

Section 1: Genome sequencing, assembly and annotation

An inbred stock of *Spodoptera litura* from Ishihara, Japan, was obtained through 24 generations of sib mating. We used genomic DNA from male moths to construct sequence libraries using a whole-genome shotgun strategy and sequenced on the Illumina HiSeq 2000 platform. We obtained a total of 49.09 gigabases (Gb) after filtering low-quality bases, low-quality reads, adapter, and PCR duplicates. The genome size was estimated to be 444.44 Mb by *K*-mer depth distribution of short reads (Supplementary Fig. 1c), and the C-value of *S. litura* was estimated at 0.469 ± 0.049 pg (SD) using flow-cytometry. Based on the C-value, the genome size of *S. litura* was estimated to be 458.68 ± 47.92 Mb, which is near the estimated 444.44 Mb by *K*-mer analysis. The genome was assembled *de novo* into contigs and scaffolds by the software program Allpaths-LG¹, resulting in a final assembly of 438.32Mb, representing 98.6% of the *S. litura* genome. The assembly consists of 13636 contigs with N50 sizes of 68.35 kilobases (Kb) and 3597 scaffolds with N50 sizes of 915.47 Kb. More than 90% of the assembly consisted of scaffolds with lengths more than 200 Kb. There were 10.30 Mb of Ns introduced in the scaffolding process; the relatively low percent of gaps (2.35%) in this assembly speaks to its general high quality.

Three evaluation methods showed that our assemblies are quite complete and reliable. The sequencing depth of 96% of the assembly was more than 20-fold (Supplementary Fig. 1d), ensuring high accuracy at the nucleotide level. Base coverage of the assembly was 97.89% and 93.27% by 57293 RNA-seq transcripts and 7785 Sanger-derived ESTs, respectively (Supplementary Table 5). The completeness of the genome and gene sets of *S. litura* reached 86% and 92%, respectively, better than the other four Lepidoptera genomes compared by BUSCO evaluation (Supplementary Table 6). The distribution of GC content in the *S. litura* genome (36.5%) is higher than that of *D. plexippus*, and close to those of *B. mori* and *P. xylostella*.

Genome annotation of the assembly was performed as described in methods. Approximately 136.2 Mb (31.8%) of *S. litura* genome was identified as repetitive elements, including DNA transposons, LTR, LINE, and SINE repetitive elements (Supplementary Table 4). SINEs comprised only 1.99% of the *S. litura* genome, obviously lower than *B. mori* (10.56%). The *S. litura* genome is predicted to contain 15317 protein-coding genes (Supplementary Table 3) and 1017 non-coding RNAs (Supplementary Table 7). 96.94% of predicted genes were found to be functional by several annotation methods (Supplementary Table 8). Compared with three other sequenced lepidopteran species, the *S. litura* genome has a longer average CDS length (Supplementary Fig. 1e). 4812 families including 9986 *S. litura* predicted genes are shared by the four lepidopteran insects, whereas 406 *S. litura*-specific families with 615 genes are smaller in number than the others (Supplementary Fig. 1a). By analyzing single-copy orthologous groups, we constructed a phylogenetic tree involving *S. litura* and nine other species (Supplementary Fig. 1b). As expected, *S. litura* placed within moths and split from two other Lepidoptera, butterfly and silkworm, about 104.7 million years ago, whereas the older lepidopteran, *P. xylostella*, diverged from them approximately 147 million years ago, and Lepidoptera and Diptera diversified approximately 258 million year ago^{2,3}, which is consistent with other divergent time estimates.

Section 2: Linkage analysis and construction of a linkage map

Two genetically contrasting strains of *S. litura*, one developed at the University of Delhi, India (called India strain) and another available at the National Institute of Agrobiological Sciences, Japan (called Ishihara strain), were employed in generating a mapping population (Supplementary Fig. 2a). Crossing over is non-existent in lepidopteran females, resulting in all genes and related markers on the identical maternally acquired chromosomes being completely linked, and hence segregating together^{4,5}. Crossing over between non-sister chromatids during meiosis occurs only in males, facilitating linkage map construction and deducing the distance between the markers. We obtained F1 offspring by crossing an India male and a Ishihara female followed by crossing an F1 male with an Ishihara female in a backcross (BC1). We used genomic DNA from 116 BC1 offspring to develop RAD libraries which we sequenced using an Illumina HiSeq 2000 platform. RAD sequencing generated about 98.94GB of raw data and filtering resulted in the generation of 81.13GB of clean data after removing adaptor sequences and low quality reads. The genotypes of each individual at every genomic site were calculated by SOAP2⁶. We retained markers that followed a Mendelian segregation pattern to identify a total of 87,120 RAD markers. We carried out further filtering by selecting only SNP markers with a missing rate of <0.09 and by selecting SNPs separated by at least 2000bp. After such stringent filtering we obtained a total of 6088 SNP markers. We used JoinMap 4.1 to develop a linkage map with these markers. We set the Limit of Detection (LOD) $LOD\ score = Z = \log [probability\ of\ sequence\ with\ linkage / probability\ of\ sequence\ with\ no\ linkage]$ for linkage to e^{-4-20} (start-end). By applying the indicated parameters we eventually narrowed the map down to 31 linkage groups (Supplementary Fig 2b) with a total map of length 3971.7cM and a mean distance of 0.652cM between markers. We observed a wide range of marker distances, from 70cM on LG3 to 332cM on LG14, and variable linkage group lengths, from the shortest of 45.4cM (LG28) to the longest of 201.5cM (LG15). Haploid chromosome numbers vary in Lepidoptera from $n=7$ to $n=220$, with most ranging from $n=29-31$ ⁷. *S. litura* has a WZ/ZZ sex chromosome system with 31 chromosomes. A total of 639 scaffolds covering approximately 380.89 Mb were anchored on the 31 linkage groups defined by genetic mapping.

To further guide anchoring and rearrange disordered markers, we established syntenic relationships between *S. litura* and *B. mori*. Fifteen scaffolds showed strong synteny with *B. mori* chromosome 1 (sex chromosome Z) and were outside the other 30 linkage groups. Using these 15 scaffolds, we built a pseudo-chromosome Z for *S. litura* by syntenic order and orientation with *B. mori* sex chromosome Z. Since the karyotype of *S. litura* contained 31 pairs of chromosomes⁷, we integrated *Slitu* LG28 and LG31, based on the distribution of scaffold 22 markers on two linkage groups and good synteny with *B. mori* chromosome 11. Based on *S. litura* chromosomes, we compared inter-genome collinearity between *S. litura* ($n=31$) and *B. mori* ($n=28$)⁸, *H. melpomene* ($n=21$)⁹ and *Papilio xuthus* ($n=30$)¹⁰ (Supplementary Fig. 2c; Supplementary Table 10). We used whole-genome BLASTP results

and the genome annotation file to compute collinear blocks for all possible pairs of chromosomes by MCSan software¹¹. We designated a region with at least five syntenic genes and no more than 15 gapped genes as a syntenic block. In total, we analyzed 8020, 6539, and 7595 syntenic genes from *S. litura* to *B. mori*, to *H. melpomene*, and to *P. xuthus*, corresponding to 341, 480, and 398 syntenic blocks, respectively. Based on the yield of syntenic genes from *S. litura* to *B. mori* and to *H. melpomene*, we determined genomic syntenies and made chromosome-level visualisations using CIRCOS¹². We found that six *S. litura* chromosomes (chr3 and chr28, chr19 and chr25, chr13 and chr26) were fused to three *B. mori* chromosomes (chr11, chr23, and chr24). Between *S. litura* and *H. melpomene*, twenty *S. litura* chromosomes (chr3 and chr21, chr28 and chr10, chr19 and chr14, chr25 and chr4, chr13 and chr27, chr26 and chr15, chr5 and chr16, chr6 and chr12, chr7 and chr24, chr9 and chr18) were fused to ten *H. melpomene* chromosomes (chr6, chr7, chr20, chr18, chr17, chr1, chr10, chr12, chr19, chr13) (Supplementary Fig. 2c; Supplementary Table 11). *S. litura* has the same haploid chromosome number as the Glanville fritillary butterfly (*Melitaea cinxia*), which showed an identical pattern of chromosome fusion¹³. These observations suggests two different modal chromosomal fusions occurred in basal lepidopteran ancestors, one leading to the ancestors of butterflies and the other to moths.

Section 3: Chemosensory receptor gene families

Chemosensory genes play an essential role in host plant recognition of herbivores; gustatory receptors (GR) and olfactory receptors (OR) are key receptors. Especially, GRs are highly variable among species, which could be a major factor for host plant adaptation. GRs are categorized into three classes, CO₂ receptors, sugar receptors and bitter receptors, among which bitter receptors are most variable, while CO₂ and sugar receptors are conserved among species¹⁴⁻¹⁶. In addition, expression of GRs is extremely low and usually limited to perception organs, which hinders annotation of precise gene structure and transcriptome analysis^{17,18}. To annotate GRs and ORs in the *S. litura* genome assembly, we performed BLASTp and tBLASTn queries with insect GRs and ORs published in NCBI as well as those identified in the *S. frugiperda* genome¹⁹ for BLASTp and tBLASTn. We also used automatically annotated genes. This procedure yielded 73 ORs and 237 GRs in the *S. litura* genome assembly and 73 ORs and 76 GRs in that of the silkworm (Supplementary Table 12,13). A large expansion of GRs, essentially in the so-called bitter receptor family, was obvious in *Spodoptera* species (Table 2), whereas in the other Lepidoptera species investigated to date only 45 ~ 80 GRs are reported^{3,9,15,16,20,21}. Most of these previously annotated genomes are from monophagous and oligophagous species, whereas *S. litura* and *S. frugiperda* present an extreme polyphagy with most host plants being monocots covering more than 40 different plant families with over 100 plants²². Thus, the difference in the number of GRs is likely to be related to species' diets. As such, a recent study reported expansion of the *Gr* gene family in the armyworm *Helicoverpa armigera* (Lepidoptera: Noctuidae), another polyphagous Noctuid, with a description of up to 197 genes²³ (Table 2). Taken together, these observations support the hypothesis that the vast

expansion of *GRs* may be linked to polyphagy.

Phylogenetic analysis showed clearly that bitter *GRs* made distinctive clades between *B. mori* and *S. litura*, the latter species exhibiting many more bitter *GR* clades. By contrast, the CO₂ receptor (*BmGR1-3*) and the sugar receptor (*BmGR4-10*) from *B. mori* provided a clear 1:1 correspondence with *SlituGRs*, i.e., they are conserved between the two species, except for *BmGR4*, which has expanded into three *SlituGRs* (Fig. 1a). Most of the numerous bitter receptor genes of *S. litura* formed large gene clusters: 124 *SlituGRs* were found on chr12: 838021-1801668 spanning 1Mb, 14 *GRs* on chr14 spanning 76kb, 9 *GRs* in 49kb on chr27 and 7 *GRs* in scaffold725. The phylogenetic analysis showed that putative bitter *GR* duplications occurred after *S. litura* and *B. mori* separated, indicating that bitter receptors may have evolved faster than other chemosensory genes. This strongly suggests that bitter receptors make a significant contribution to adaptation of Lepidoptera to novel ecological niches.

Expression and functional studies of *GRs* in Lepidoptera are scarce compared to research on *Drosophila GRs*²⁴. Only two studies have conducted large scale *Gr* expression analyses in Lepidoptera: one focused only on adult tissues¹⁶ and the other analyzing both adult and larval tissues²³. Only three *GRs* have been functionally characterized in *B. mori*, all responding to sugars^{20,25,26}. To understand why *S. litura* contains such a large expanded *GR* set, we analyzed RNA-Seq data derived from 9 tissues of larvae and moths including antenna, maxilla, fat body, epipharynx, legs, midgut, moth proboscis and pheromone gland (Fig. 1d). We chose these because *GRs* contribute to host plant selection, mating behavior and decision on egg-laying sites. Transcripts were detected for 122 out of 237 *GRs*, among which 109 were putative bitter receptors, although expression levels of bitter receptor genes were fairly low. Bitter *GRs* were mainly expressed in larval maxilla, followed by moth proboscis, by which *S. litura* sucks flower nectar to obtain energy for flying. Six putative bitter *GRs* associated with the major *GR* cluster on chr12, *SlituGR39*, 47, 59, 122, 140 and 148, were expressed in larval antenna, maxilla, midgut and legs. It is notable that *SlituGR47* was highly expressed in larval midgut. Intriguingly, *SlituGR012*, 167, 168 and 169, which formed a cluster on chr25, were expressed mainly in the moth proboscis where several sugar *GRs* were also highly expressed. In the phylogenetic tree (Fig. 1a) these four *GRs* formed a clade corresponding to *BmGr53*, indicating that the four *SlituGRs* could have been copied by recent gene duplication events to form a cluster with the same expression profile. By contrast, the corresponding silkworm gene, *BmGr53*, was expressed in larval maxilla and legs²⁷. Since *S. litura* moths require sugar water or nectar to obtain energy for flight whereas silkworms do not feed, this expansion may represent an adaptation for this aspect of adult feeding. In addition, *BmGr53* and the four *SlituGRs* are single exon genes which strongly indicates they had a common ancestor, and after the species separated a basal *SlituGR* duplicated into four genes with a common ecological niche. Similarly, 14 bitter *GRs*, *SlituGR160-161* and *SlituGR224-235*, forming a cluster on chr14, were expressed mainly in proboscis as well as in larval maxilla, whereas the corresponding *BmGr55-57* on chr10 expressed in maxilla²⁵ form a separate clade in the phylogenetic tree (Fig. 1a), indicating that after the species separated the expanded gene cluster was formed by recent gene duplication events (Fig. 1b). Male and female moths feed on flower nectar of host plants which contains various toxic plant secondary metabolites. In the butterfly, *H. melpomene*, 44 bitter *GRs* are expressed in proboscis¹⁶. Our observations

suggest that the *S. litura* chr14 and 25 bitter *GRs* expressed mainly in moth proboscis could be used to detect and initiate detoxification of xenobiotics found in nectar.

The extensive expansion of *bitter GRs* in *S. litura* is consistent with the idea that this polyphagous pest has taken a strategy to increase new bitter *GRs* with altered ligand specificity to enable the identification of a large number of toxins and bitter compounds in host plants. Since large expansions of *bitter GRs* are reported in other polyphagous pests, such as *S. frugiperda*¹⁹ and *H. armigera*²³, this strategy could be a unique adaptation of the extremely polyphagous Noctuidae, which are different from *Drosophila* where the use of coreceptors for perception of bitter tastants allows detection of bitter compounds with a relatively small number of bitter *GRs*^{28,29}.

Detection of toxic compounds involved in foods must be crucial for insects to survive. After detection of toxins or bitter tastants in food, insects rapidly inhibit or continue feeding. Polyphagous lepidopteran pests take the latter course of behavior, for which they should have powerful detoxification processes as described in the next section to be able to ingest a large number of different host plants. Therefore, identification of toxins and bitter compounds in host plants must be critical for this extremely polyphagous pest. The *bitter GRs* are likely involved in this process. Ligand binding on the extracellular domain of *GRs* has been reported to activate downstream signaling pathways in *Drosophila* and *B. mori*^{20,30}; however, such downstream signaling pathways in Lepidoptera are largely unknown. Detailed mechanisms underlying the function and/or potential participation of *bitter GRs* in inducing the detoxification process by ligand binding of toxic or bitter compounds are important subjects for future research.

Section 4: Cytochrome P450

The detoxification process of xenobiotics usually involves several distinct detoxification pathways, from active metabolism of toxins³¹ to enhanced excretion activity by ABC transporters^{32,33}. To elucidate these mechanisms, we have annotated the *cytochrome P450* (*P450*), *carboxylesterase* (*COE*), *glutathione-S-transferase* (*GST*), *aminopeptidase N* (*APN*) and *ABC transporter* (*ABC*) gene families in the *S. litura* genome. Table 1 presents a comparison of detoxification-related genes among lepidopteran species where large expansions were found in *P450*, *COE* and *GST* in extremely polyphagous *Spodoptera* species. *Cytochrome P450* or *CYP* genes constitute one of the largest gene families with representatives in nearly all living organisms from viruses, Archaea, bacteria, fungi, plants and vertebrates to insects³⁴. *CYP* are heme-containing monooxygenases that generally catalyze the insertion of an oxygen atom into a substrate after activation of molecular oxygen. Many insect *CYPs* are involved in the metabolism of key endogenous substrates such as steroid hormones and lipids but *CYP* are also associated with the metabolism or detoxification of xenobiotics such as plant natural products and pesticides. Accordingly, insect *CYPs* are key components for successful adaptation to their host plants³⁵. We annotated 138 *P450* genes in the *S. litura* genome (Supplementary Table 14). Based on their sequence identity *CYPs* are classified into 4 clans: the *CYP2* clan, the *CYP3* clan, the *CYP4* clan and the mitochondrial clan. We focus our discussion on key genes that might orchestrate *S. litura* adaptation to its host plants and chemical environment.

Evolutionarily conserved mitochondrial (11 *CYP*) and *CYP2* (7 *CYP*) clans showed a strict

orthology between the *S. litura* and *B. mori* genomes (Supplementary Fig. 4). Genes of these 2 clans play basic physiological roles in insect development via ecdysteroid synthesis and regulation, but they are also involved in chemosensory roles with CYP303A1, a rare 1:1 ortholog between insects^{36,37}, and in detoxification of xenobiotics with the Lepidoptera specific CYP333A, CYP333B and CYP428A sub-families. Members of the CYP333B sub-family are involved in detoxification of chemical insecticides and plant compounds^{38,39}. In *P. xylostella*, *CYP428A1* is reported to display a higher expression level in an insecticide-resistant strain in comparison to a susceptible one³⁸. In the experiments reported here, *SlCYP333A12* (*SlituP450-001*), *SlCYP333B3-B4* (*SlituP450-002, 003*) and *SlCYP428A1* (*SlituP450-44*) showed different tissue specific expression patterns and after ricin treatment were repressed to a higher level in midgut and Malpighian tubules (Supplementary Figs. 4 & 5b).

CYP3 clan members are involved in xenobiotic metabolism and insecticide resistance^{40,41}, and showed more diversity than CYP2 and mitochondrial clans (Table 1; Supplementary Fig. 4). Compared with *B. mori*, CYP3 showed a nearly 2-fold expansion to 61 copies in *S. litura* from 32 of *B. mori*. Phylogenetic tree analysis revealed expansions in 6 families, *CYP6AE9* (*SlituP450-72~76*), *CYP6B* (*SlituP450-85~89*), *CYP9A* (*SlituP450-95~107*), *CYP321B* (*SlituP450-114~118*), *CYP324* (*SlituP450-119~121*) and *CYP321A* (*SlituP450-91~94*) (Fig. 2a; Supplementary Fig. 5a), whereas 9 families showed 1:1 orthology between *S. litura* and *B. mori* (Supplementary Fig. 4). These expansions, which formed gene clusters, most probably resulted from serial duplication events in the *S. litura* genome. *CYP6B48* is induced by flavone and xanthotoxin⁴² and *SfCYP6B39* is induced by xanthotoxin and indole³⁹. *Manduca sexta* *MsCYP6B46* is induced by nicotine⁴³. *BmCYP6AE9* and 22 are expressed in fat body and regulated by both insecticides and plant allelochemicals^{31,44}. In *H. armigera*, several *CYP6AE* are involved in catabolism and detoxification of gossypol^{45,46}, and *CYP6AE11* is involved in tolerance to deltamethrin⁴⁷. These data suggest that the function of *Spodoptera* *CYP6AEs* might be linked to pesticide detoxification and adaptation to plant allelochemicals. Our observation of the increased expression of expanded *CYP6AE* and *CYP6B* clusters in larvae treated with toxins is consistent with this hypothesis (Supplementary Fig. 5a). We observed a large expansion of *SlituCYP9A* in a gene cluster composed of *SlituP450-95~107* on chromosome 29 (Fig. 2a). We also found similar clustering of the *CYP9A* family in a syntenic region of *S. frugiperda* (14-15 genes)³⁹ and *B. mori* (4 genes on chromosome 17), indicating a recent extensive expansion of this cluster in *Spodoptera*. Interestingly, the *SlituCYP9A* gene cluster co-localized with two bitter *GRs* (*SlituGR176* and *177*) and was flanked by a gene cluster of 4 *alcohol dehydrogenase (ADH)* genes which was also located in *CYP9A* gene cluster of *B. mori*. This genomic region of *S. litura* including *CYP9As*, *GRs* and *ADHs* is linked to host plant adaptation (Fig. 2a; see also Section 9 Population Genetic Analysis). Supplementary Figure 5a shows other expansions of *CYP337A1*, *3337A2*, *CYP6B29* and *6AE9* in *S. litura*.

We studied expression profiles of *SlituP450s* of fat body, midgut and Malpighian tubule of larvae fed with imidacloprid, ricin and xanthotoxin by RNA-Seq (Supplementary Fig. 5b). Most of the duplicated *S. litura* CYP3 genes were inducible with toxins (Fig. 2a; Supplementary Fig. 5a), suggesting their contribution to detoxification ability. In contrast, most conserved *SlituCYP3* with 1:1 orthology between *S. litura* and *B. mori*, namely,

SlituP450-15, 17, 34, 77, 80, 84, 90, 108 and 124, showed no expression or induction in fat body, midgut or Malpighian tubule with toxins, except for *SlituP450-80* which were induced by flavone and xanthotoxin⁴² (Supplementary Fig. 5b). This contrast clearly indicated that *CYP3* expansion is dedicated to increasing the detoxification ability of this pest. The *ADH* gene cluster flanked by the *CYP9A* cluster on chromosome 29 was also induced highly by xanthotoxin (Supplementary Fig. 5c). The high conservation of this *ADH* cluster within the *BmCYP9A* cluster (Fig. 2a) suggests its function may also be associated with a *CYP9A* detoxification pathway.

In order to verify the link between *CYP clan3* expansion and the increase of detoxification ability in this pest, we selected *P450-74, 88, 92 and 98* as members of *P450 clan3* for knock-down experiments. After knock down of each *CYP* by siRNA injection, we fed knock-down insects with artificial diet containing imidacloprid (50µg/g). We observed an increase in sensitivity to the insecticide in the treated larvae compared to controls and confirmed the increase of sensitivity against imidacloprid in all knockdown samples (Supplementary Fig. 7a-d).

In insects, the *CYP4* clan is a highly-diversified group of enzymes with roles in pesticide metabolism, development and chemical communication such as odorant metabolism and cuticular hydrocarbon biosynthesis^{40,48}. Compared with *B. mori*, this clan showed as great an expansion in the *S. litura* genome as the *CYP3* clan. We assigned the *CYP4* clan to 7 families expansions by gene duplication events, *CYP340* (*SlituP450-63~68*), *CYP340A* (*SlituP450-129~130*), *CYP340K1* (*SlituP450-133~136*), *CYP367A* (*SlituP450-36-40*), *CYP340K1* (*SlituP450-133~136*), *CYP4L6* (*SlituP450-49~51*) and *CYP4M* (*SlituP450-52-55*). Supplementary Figure 5d presents the genomic organization of the 21 member *CYP4* gene cluster on chromosome 24 which was split into three parts: *CYP340* (9 genes), *CYP340A* (6 genes) and *CYP340K1* family (6 genes). This large *CYP4* cluster is syntenic to a region of *B. mori* chr26 containing 9 *CYPs*. Thirteen genes among the 21 gene clusters are *Spodoptera* specific (Supplementary Fig. 5d), representing expansions in *Spodoptera*, whereas the other eight *CYP4s* correspond to the *B. mori* *CYP4* cluster on chr26 with no expansion. *SlituP450-21* and 27 located in the left side of the *Spodoptera*-specific *CYP4* cluster could have been translocated from the right side of the cluster, since in *B. mori*, *thioredoxine peroxidase* is located on the right side of the *CYP4* cluster. Three genes, *SlituP450-26, 132 and 127*, were induced by ricin and imidacloprid, while other members showed no induction or no expression in fat body, midgut or Malpighian tubule by toxins (Supplementary Fig. 5d). Other expansions of *CYP4* clusters presented diverse variations in expression profiles with toxin-treatment (Supplementary Fig. 5e). Genes from the *CYP4L* family are suggested to have a role as odorant-degrading enzymes in *Mamestra brassicae* and *S. littoralis*^{40,48}; however, in *S. litura* all members of the *CYP4L* cluster on chr13 were induced with toxin-treatment. In Lepidoptera, *CYP4Ms* are expressed in several larval stages and in different tissues, and are regulated by pesticides and plant allelochemicals^{49,50}, which was also observed in the *S. litura* *CYP4M* cluster. *CYP341B14* is involved in the biosynthesis of sex pheromone in *Hyphantria cunea*⁵¹. Interestingly, *SlituP450-65 and 66* of the *SlCYP341B1* cluster on chr9 shared the same induced expression in midgut in larvae treated with ricin, but other members of the cluster had no expression in fat body, midgut or Malpighian tubule. We also observed an expansion of the *CYP367A* family. We could not detect any expression of these genes in our

experiments, but in *P. xylostella* the two *CYP367A* orthologs are mainly expressed in head³⁸. For the *CYP4* clan, expanded *CYP4* clusters presented various expression profiles and different tissue expression patterns, indicating diverse functions of this clan including detoxification. The differential expansion of each *CYP4* family observed in *S. litura* might be associated with adaptation to various conditions required in this pest.

Our results show that *CYP* expansions of clans 3 and 4 are involved in xenobiotic metabolism. These genes exhibit extensive enhanced *S. litura* detoxification activity which can enable this pest to eat a wide-range of plants and become highly tolerant to insecticides. Phylogenetic analysis indicates that large expansions of *CYPs* occurred in each *Spodoptera* species, supporting their adaptation to novel ecological niches.

Section 5: Carboxylesterase (COE)

Carboxylesterases (COE) are classified into three functional groups, dietary detoxification, pheromone/hormone degradation and neurodevelopment, and play an important role in the metabolism of a wide range of xenobiotics associated with plants and insecticides^{31,52-54}. For plant allelochemicals, *COEs* are induced by phenolic glycosids in *Papilio*⁵⁵, rutin in *S. litura*⁵⁶, gramine in aphid⁵⁷ and quercetin in *Bemisia tabaci*⁵⁸. By sequence homology search and phylogenetic tree analysis of insect *COEs*, we annotated 110 *SlituCOEs* in the *S. litura* genome (Supplementary Table 15) which were divided into 10 subgroups^{53,59,60}. Insect α -esterases are known to be involved in organophosphate resistance^{53,61}. By comparison with *B. mori*, *COEs* (Table 1) revealed major expansions in *S. litura* in groups categorized as “lepidopteran esterases” and “ α -esterases,” whereas the other esterases were completely conserved. This tendency is clearly seen in the phylogenetic tree (Supplementary Fig. 6a). Figure 2b presents a large/major expansion of *SlituCOE* gene clusters on chr2 composed of 23 lepidopteran *esterase* genes, adjacent to one *acetylcholinesterase* and four *neuroligin COEs* (not shown) on the right side. The corresponding silkworm *COE* gene clusters located on chr15 are composed of 5 lepidopteran *esterases*, one *acetylcholinesterase* and four *neuroligins* in the same order. The conservation of *acetylcholinesterase* and *neuroligins* was obvious; in contrast, the lepidopteran *esterase COEs* were extensively expanded. *-esterase COEs* also provided a major expansion on chr25 in the *S. litura* genome compared with *B. mori* (Supplementary Fig. 6b).

To investigate the relationship between *COE* expansions and enhancement of detoxification ability, we performed transcriptome analysis of toxin-treated larvae by RNA-Seq. Most members of the lepidopteran *esterase COE* cluster on chr2 were induced by xanthotoxin and imidacloprid (Fig. 2b). Half of the α -esterase *COE* cluster showed induction by toxins, but the other half was not expressed or had no induction with toxins (Supplementary Fig. 6b), suggesting they may have different functions. By contrast, 17 *SlituCOEs* of both lepidopteran and α -esterase groups showing a 1:1 orthologous relationship between *S. litura* and *B. mori* (*SlituCOE005, 006, 007, 025, 029, 038, 039, 044, 072, 078, 088, 089, 090, 092, 097, 098* and *109*) showed almost no expression in fat body, midgut or Malpighian tubule or no induction with toxins with only three exceptions (*SlituCOE089.090* and *092*) (Supplementary Fig. 6c). This also clearly indicates that *COE* expansion occurred to strengthen the ability to detoxify allelochemicals associated with host plants and pesticides. Oakeshott *et al* reported that insecticide resistance was attained by mutations in *COEs* or by amplification of *COE* genes in

this group⁵³. To confirm the relationship of the expansion of lepidopteran *COEs* with increased detoxification ability, we knocked down *COE-57* and *COE-58* by siRNA injection, and then fed the injected larvae with artificial diet containing imidacloprid (5mg/g). This treatment resulted in increased sensitivity to the insecticide compared to controls (Supplementary Fig. 7e, f). These results provide support for the hypothesis that in *S. litura*, esterase gene amplification contributes significantly to the detoxification ability of this pest.

Section 6: Glutathione-S transferase (GST)

GSTs catalyze a conjugation reaction of reduced glutathione with endo- and exogenous compounds for homeostasis or making them more water-soluble and more easily excreted^{62,63}. Insect GSTs are classified into six classes, delta, epsilon, omega, sigma, theta and zeta⁶⁴, among which delta and epsilon are insect-specific. For *S. litura*, Deng et al.⁶⁵ suggested two epsilon-class GSTs (*GSTepsilons*) might play roles in detoxification of various insecticides. We annotated 47 *GSTs* in the *S. litura* genome, which are listed in Supplementary Table 16 and compared with *B. mori* *GSTs* (Table 1). It is obvious that *GSTepsilon* shows a large expansion. This can be seen explicitly in the phylogenetic tree (Fig. 3a) and in the *GSTepsilon* gene clusters on chr9 and chr14 (Fig. 3b, c), suggesting strongly that *GSTepsilon* contributes to the ecological adaptation of this pest. We investigated whether these *GSTepsilon* expansions are toxin-inducible by transcriptome analysis via RNA-Seq of larvae fed with toxins. Both expanded *GSTepsilon* clusters showed induction by xanthotoxin (Fig. 3b, c), suggesting strongly that the large expansion of *GSTepsilon* genes enhanced detoxification activity in this insect. To verify these expanded *GSTepsilon* clusters actually enhanced the detoxification process, we employed siRNA knock-down together with insecticide binding assays. For these tests, we chose *SlituGST-20* and *SlituGST-7* as representatives of the two *GSTepsilon* gene clusters (Fig. 3a). We injected *SlituGST07/SlituGST20* siRNA into larvae vs water for controls, and then observed larval lethality after imidacloprid-treatment via artificial diet feeding. Most siRNA-injected larvae were affected by imidacloprid-treatment, while all water-injected control larvae were alive after feeding on toxin-treated diet (Fig. 3d, e). We performed the same knock-down experiments for *SlituGST07* and *SlituGST20* using pesticide injection instead of imidacloprid-treatment by artificial diet feeding; this yielded the same results (Data not shown). These results indicated that knockdown of *SlituGST07* and 20 increased sensitivity to this insecticide, consistent with the idea that expansion of *GSTepsilon* genes made this pest more tolerant to the insecticide.

We examined the inhibitory effects of imidacloprid on *SlituGST07* and *SlituGST20* using 1-chloro-2,4-dinitrobenzene (CDNB) and glutathione (GSH) as standard substrates. A competitive assay revealed that the activity of both proteins was inhibited by imidacloprid (Fig. 3f, g), and residual activity decreased in proportion to the increasing amounts of each substrate. In the presence of 1 mM imidacloprid, *SlituGST07* and *SlituGST20* showed about 20% of its original activity. These results indicated the expansion of *SlituGSTepsilon* genes enhanced detoxification activity extensively and conferred more powerful insecticide tolerance on this pest.

In addition, we observed expansion of the sigma-class *GSTs* in *S. litura* (Table 1). The sigma-class *GSTs* are involved in prostaglandin metabolism which functions in body temperature⁶⁶ and physiological sleep-wake cycle⁶⁷ in vertebrates. In insects, prostaglandin

exerts an effect on the immune response against bacterial, fungal and viral infections⁶⁸. This suggests that expanded sigma-class *GSTs* may play roles in cellular defense in *S. litura*.

Section 7: Aminopeptidase N (APN)

The APN family is a class of enzymes that cleaves neutral amino acids from the N terminus of polypeptides. They serve a variety of functions in a wide range of species, but in the lepidopteran larval midgut, they work in cooperation with endopeptidases and carboxypeptidases to digest proteins derived from the diet⁶⁹. In addition to being studied for their role in digestion, APNs have been extensively studied as putative Cry toxin receptors. We annotated 18 *SlituAPN* genes in the *S. litura* genome (Supplementary Table 17). On chr21, 15 *SlituAPN* genes made a gene cluster which corresponded to the *APN* gene cluster on chr9 of *B. mori* (Supplementary Fig. 8a). Among the cluster, three members, *SlituAPN08*, *09* and *10*, were expanded by gene duplication events in *S. litura* (Supplementary Fig. 8b) and were inducible by xanthotoxin. Compared with *P450*, *COE* and *GST*, *APN* did not show a large expansion, which may result from a different mechanism of Cry protein toxicity. Thus, the standard model is that active Cry protein binds to a receptor in the midgut, followed by insertion into the membrane, formation of a pore, and cellular lysis⁷⁰. Therefore, mutation of the receptor could confer resistance against Cry protein in this pest. Mutations in *APN* which is a possible Cry protein receptor could be responsible for Cry toxin resistance, without the need for increasing gene number by amplification.

From our population genetic studies, *SlituAPN13* and *SlituAPN16* are variable genes assigned to the class 1 group. In *M. sexta* and *S. exigua*, class1 APNs are reported to bind to Cry proteins and identified as receptors (see Section 9, Population genetic analysis; Supplementary Table 21)^{71,72}. Therefore, *SlituAPN13* and *SlituAPN16* may be good candidates for Bt-toxin resistance. RNA-Seq analysis of larvae fed with toxins revealed that *SlituAPN06*, *10*, *11*, *14*, *15* and *18* were highly induced by ricin (Supplementary Fig. 8c), suggesting that these aminoesterases may have a role in ricin detoxification.

Section 8: ABC transporter (ABC)

ABC transporter genes are among the largest protein superfamilies found in all living organisms. They are typically involved in transporting various molecules across cell membranes using ATP for energy⁷³⁻⁷⁵. *ABC* genes are classified into eight subfamilies (A-H), of which subfamilies A, B, C, and G have been shown to be related to resistance to xenobiotics, including allelochemicals, multiple drugs and insecticides^{33,74-77}. We identified 54 *SlituABC* genes in the predicted genes of *S. litura* (Supplementary Table 18). As shown in Table 1, the number of *ABC* genes in *S. litura* is close to that of *B. mori* (51 *ABC* genes), whereby *S. litura* has only one additional gene in each of the *ABCB*, *ABCC* and *ABCG* subfamilies. Phylogenetic analysis showed that most of the *ABC* genes in the two lepidopteran insects have a one-to-one ortholog relationship (Supplementary Fig. 9a). Furthermore, we identified highly conserved chromosomal synteny of the *ABC* genes between the two insects in two scaffolds of *S. litura* and chr15 of *B. mori* where the largest number of *ABCC* subfamilies are located (Supplementary Fig. 9b). These results indicate that the *ABC* genes are highly conserved between the two species. On the other hand, we identified four

ABC genes (*SlituABCA3-4*, *SlituABCB1-2*, *SlituABCC4-6* and *SlituABCG4-4*) which have no one-to-one ortholog in *B. mori* and thus these genes might contribute to *S. litura* specific features. *SlituABCG4-4* is a half *ABC transporter* (containing one pair of a nucleotide-binding domain (NBD) and a transmembrane domain (TMD)); the remaining three genes are full *ABC transporters* (containing two pairs of NBD and TMD). *SlituABCA3-4* is similar to orthologs of the human *ABCA3* gene which has been considered to be involved in multidrug resistance (MDR)⁷⁶. *SlituABCA3-4* shares similar identity with top-hit genes of *S. litura* (29% with *SlituABCA3-2*) and *B. mori* (30% with *BmABCA3-1*). Since the average identity of all the *ABC* genes between the two insects is 73.5%, *SlituABCA3-4* shows very low identity. Furthermore, we found no one-to-one orthologs of *SlituABCA3-4* in the publicly available gene sets of other lepidopteran insects (*P. xylostella*⁷⁸, *M. sexta* (<http://www.agripestbase.org/>), and *H. melpomene*⁷⁹). This suggests that *SlituABCA3-4* is a novel *ABCA3-like* gene which is related to some *S. litura* specific feature of resistance to xenobiotics. *S. litura* has two *ABCB* genes (*SlituABCB1-1* and *SlituABCB1-2*) which are similar to orthologs of the human *ABCB1* (*MDR1*) gene, which is one of the best characterized *ABC* genes⁷³⁻⁷⁵. Of these, *SlituABCB1-2* shares similar identity with top-hit genes of *S. litura* (59% with *SlituABCB1-1*) and *B. mori* (58% with *BmABCB1*), while no one-to-one orthologs were found in the other lepidopteran insects. This suggests *SlituABCB1-2* may be a novel *MDR1-like* gene. In two noctuid insects, *Heliothis virescens* and *H. armigera*, a higher expression level of an *MDR1* gene has been considered to contribute to resistance to several insecticides⁷⁷. Since *S. litura* has two genes similar to *MDR1*, it may have a potential for resistance to a greater number of insecticides. Finally, *S. litura* has four tandemly repeated *ABCC4* genes whose order and orientation are highly conserved with *B. mori* (Supplementary Fig. 9b). Of these, only *SlituABCC4-6* has no corresponding gene in *B. mori* and thus *SlituABCC4-6* is likely to be an *S. litura* specific duplicated gene derived from one of the neighboring *ABCC4* genes. The *ABCC4* genes of *S. litura* are similar to genes orthologous to the human *ABCC4* gene, known as multidrug resistance-associated protein 4 (MRP4). Again, these observations are consistent with the hypothesis that gene duplications contribute to a higher level of resistance to xenobiotics in *S. litura*.

Transcriptome analysis showed that 13 *ABC transporter* genes were induced by imidacloprid-treatment, among which seven genes were induced in Malpighian tubule (Supplementary Fig. 9c). This could be related to the main function of *ABC transporter* proteins that bind and hydrolyze ATP while transporting a wide range of xenobiotics including insecticides across lipid membranes^{33,77}. Interestingly, *SlituABCA3-4* was highly induced in the midgut by imidacloprid-treatment. This suggests that *SlituABCA3-4* may be an *S. litura* specific insecticide tolerance-related gene. Another interesting feature was that 20 *ABC transporter* genes were induced by ricin. Other detoxification related gene families like *P450*, *COE* and *GST* families rarely showed induction by ricin, suggesting that *ABC transporter* proteins could function with exposure to different types of xenobiotics.

Section 9: Population genetics analysis

Genetic diversity A large number of SNPs enabled precise estimation of the genomic nucleotide diversity π for each surveyed local population (Supplementary Table 22), which ranged between 0.013 and 0.016 for most local populations. The diversity was a little lower in

Delhi in northern India (0.0086 ± 0.0001), and was an order of magnitude lower at two sampling locations in Hunan province in China: Hunan1 (0.0018 ± 0.0000) and Guangzhou2 (0.0019 ± 0.0000).

High east-west gene flow ranging across South India, South China, and Japan Figures 4a shows the cluster analysis based on the extent of gene flow between them (Supplementary Table 23). An east-west high gene flow was observed ranging between South India, South China and Japan. Notably, the pairwise F_{ST} values were below 0.01 between Hyderabad in India, Fujian in China, Okinawa and Tsukuba in Japan (Fig. 4a): $F_{ST}(\text{Hyderabad, Okinawa}) = 0.002 \pm 0.004$, $F_{ST}(\text{Okinawa, Tsukuba}) = 0.005 \pm 0.006$, $F_{ST}(\text{Hyderabad, Fujian}) = 0.006 \pm 0.011$, $F_{ST}(\text{Fujian, Tsukuba}) = 0.008 \pm 0.011$, $F_{ST}(\text{Fujian, Okinawa}) = 0.008 \pm 0.011$ and $F_{ST}(\text{Hyderabad, Tsukuba}) = 0.008 \pm 0.005$. The three local populations, Delhi, Hunan1, and Guangzhou2, which had lower genetic diversity, had little genetic exchange among each other and with the other local populations. The gene flow among the other local populations in China was mild: $0.1 < F_{ST} < 0.4$.

Wan *et al.*⁸⁰ investigated the DNA sequence variation of *S. litura* in 11 local populations in China and Korea, and observed a high gene flow of nuclear ITS2 sequences between the two countries. Consistent with the current results, the geographical map (Supplementary Fig. 12) also implies that the east-west gene flow is even stronger than north-south gene flow within China. Tojo *et al.*⁸¹ studied overseas migration of *S. litura* from May to mid-July in four regions in East Asia: western Japan, South Korea, China, and Taiwan. Using the world wind record and a simulation model, they estimated the trajectory of insects that resulted in the abrupt increase of catch in western Japan, and found that catch increases coincide with the arrival of southwesterly air currents from southern China and/or Taiwan. Our results (Fig. 4a) imply an even longer distance trip from southern India to China and Japan⁸⁰.

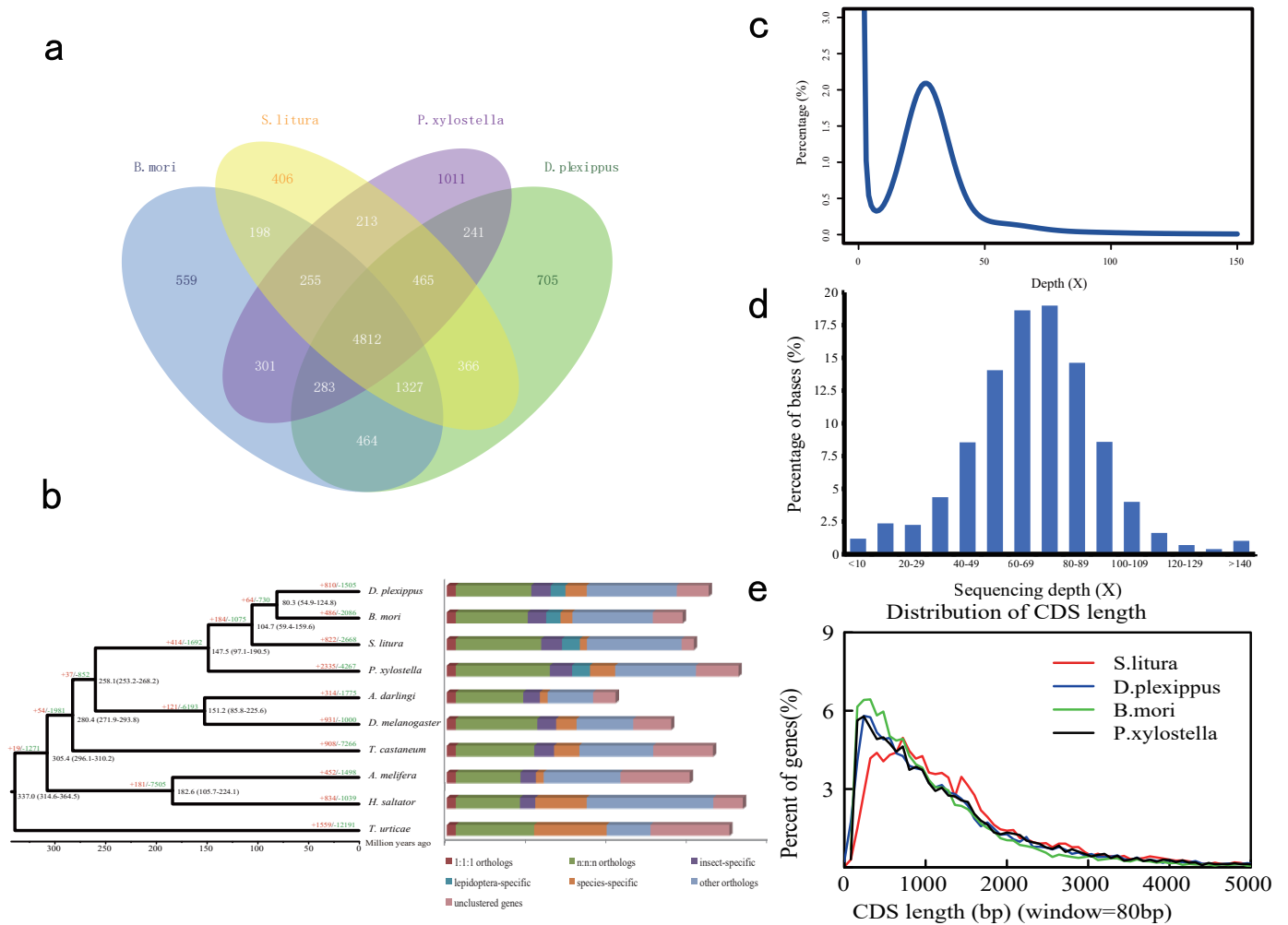
The model-based structure analysis⁸² provided the predicted population structure which is consistent with the F_{ST} -based cluster analysis (Supplementary Fig. 10, see Methods). By incorporating the estimated allele frequency divergence between the ancestral populations, we obtained a very stable picture of population structure against the assumed number of the ancestral populations, K . Here again, extremely high gene flow between central India (Hyderabad and Matsyapuri), the southeast coast of mainland China (Zhejiang, Guangzhou and Fujian), and Japan (Okinawa and Tsukuba) were observed. The assignments of individual genomes to the ancestral populations gave a detailed picture on the gene flows (Fig. 4b, Supplementary Fig. 10b). These results are consistent with the study of DNA sequence variation of *S. litura* among populations of *S. litura* in China and Korea⁸⁰. In addition, overseas migration from southern China to western Japan driven by typhoons was reported^{81,83}. Geographical data on Asian monsoon in July-August⁸⁴ may support our result, an even longer distance trip from southern India to China and Japan.

To further understand the global migration route pattern, we analyzed the joint allele frequency spectrums (Fig. 4c) by $\partial a \partial i$ (diffusion approximation for demographic inference)⁸⁵. Based on the F_{ST} -based population structure and the model based assignment of the individual genomes, we constructed six population groups: two population groups in India (India_local and India_migrate), three population groups in China (China_isolate, China_local, and China_migrate), and Japan. By applying the isolation with migration model⁸⁶ to each of the pairs of population groups, we identified a global route from the Indian migrating population

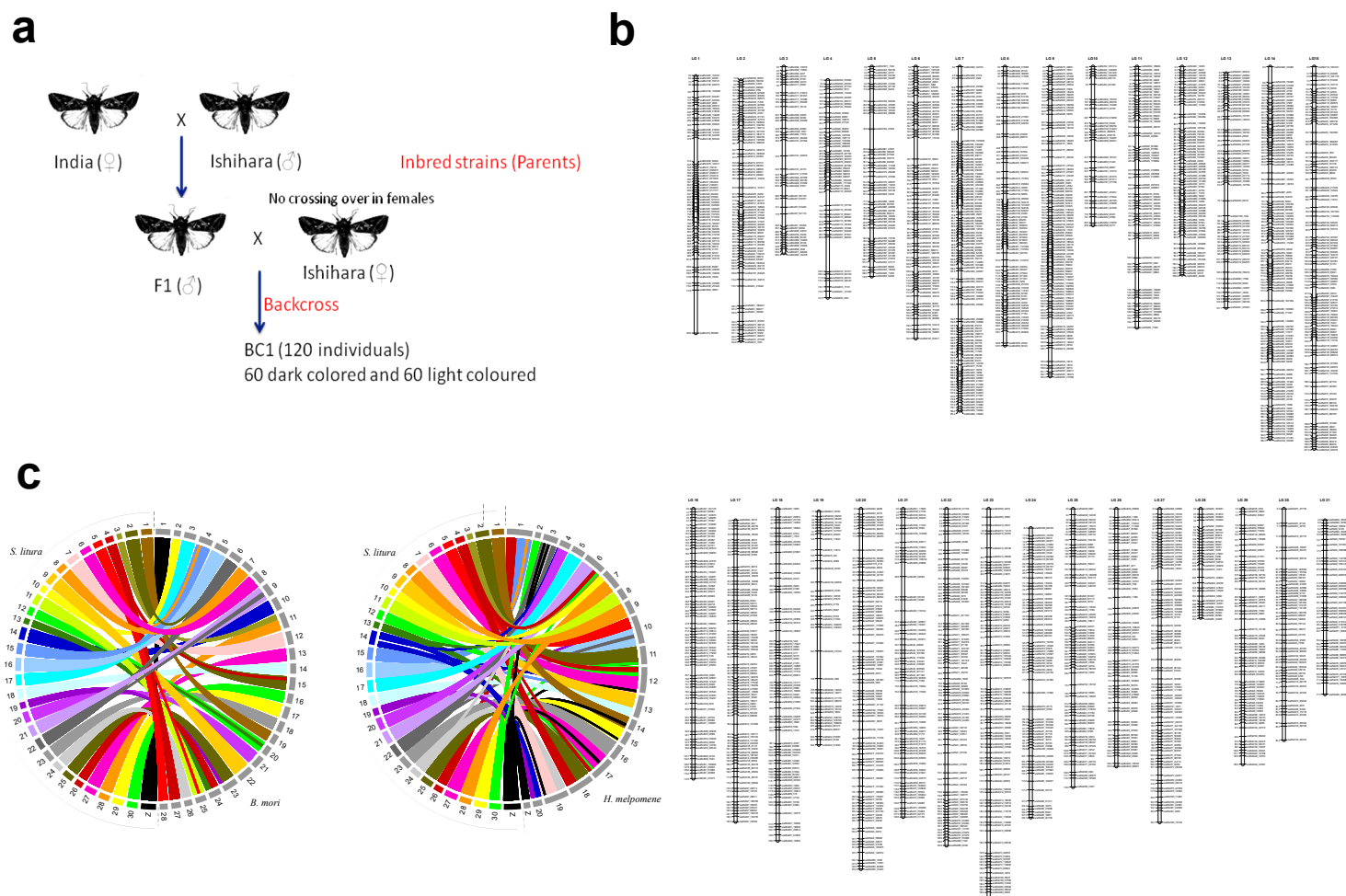
through the Chinese local population, which ranges from south at Hainan to north at Hubei (Fig. 4d). This Chinese local population has a large number of migrants to and from the Chinese migrating population. Moderate numbers of migrants from China to Japan and from China to India were observed. Also, the local populations in India and China have been shrinking significantly since 2000-3000 years ago. In contrast, the Japanese population has been expanding for the last 5000 years (Supplementary Table 24).

Section 10: Conclusion

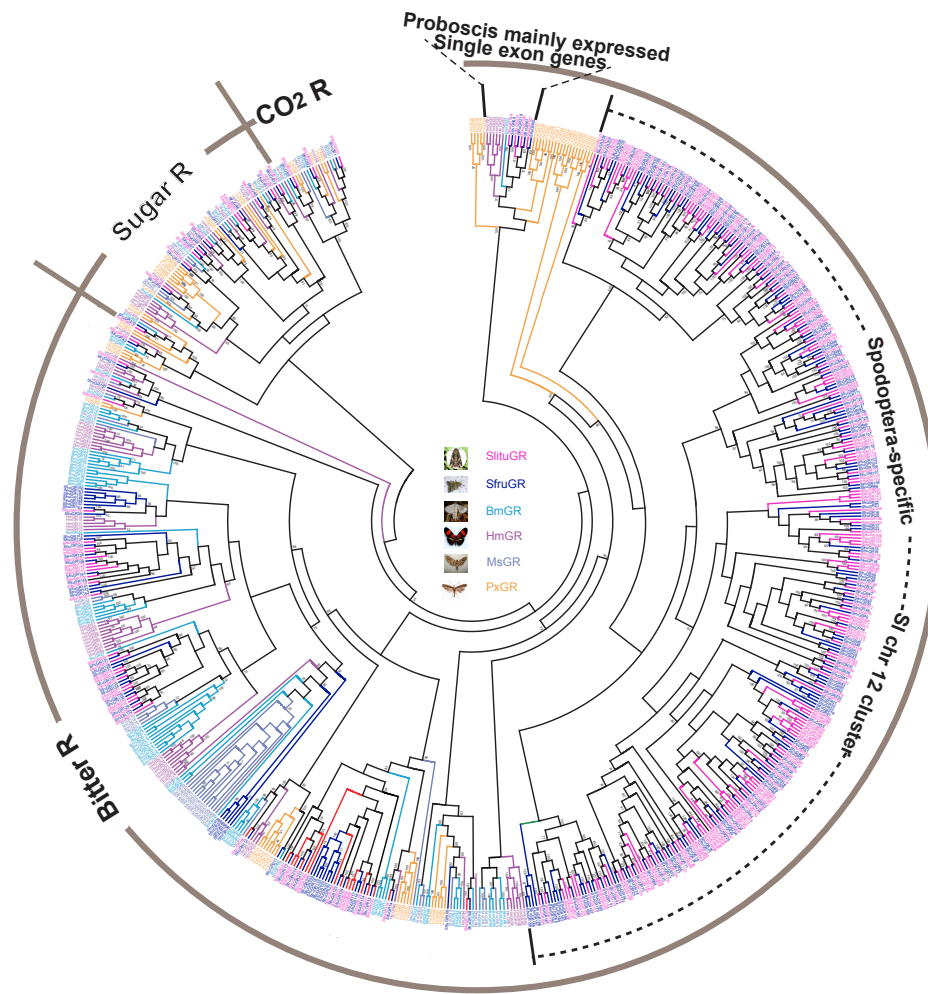
The complete genome sequence of the extremely polyphagous noctuid pest, *S. litura*, revealed large expansions of detoxification-related gene families, *cytochrome P450*, *COE* and *GST*, resulting in highly enhanced detoxification ability of this pest as evidenced by transcriptome analysis, RNAi and binding assays. As another outstanding feature of this pest, we found a huge expansion of *bitter receptor* genes whose products which can bind various kinds of ligands to detect a large number of allelochemicals associated with host plants, and subsequently activate powerful detoxification pathways to detoxify and excrete them. In addition, population genetic analysis showed a high east-west gene flow between South India, South China and Japan. Considered with the geographic data, supporting the idea that this pest undergoes an extremely long distance migration, likely aided by seasonal monsoons or typhoons. Taken together, our evidence suggests that the extreme flight ability of *S. litura* enables it to migrate to many places across East Asia where it encounters and must adapt to highly diverse ecological conditions. We conclude that this this scenario has contributed to the hugely expanded detoxification systems of this pest to deal with the large number of host plants and potential pesticides it encounters.



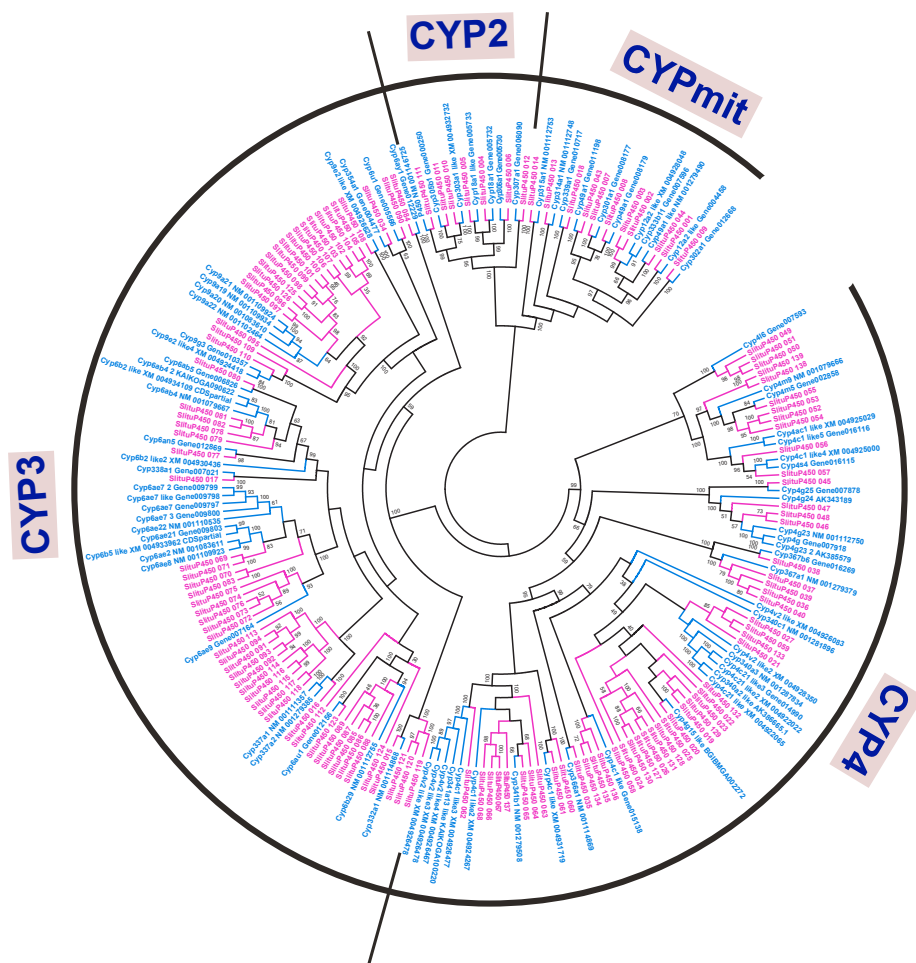
Supplementary Figure 1 | Comparative genome structure of *S. litura* with other Lepidoptera. **a**, Venn Diagram illustrating the unique and shared gene family clusters in *S. litura*, *B. mori*, *P. xylostella*, and *D. plexippus*. **b**, Phylogenetic tree, divergence time and expansion and contraction of ten species. 1:1:1 orthologs include the common orthologs with the same number of copies in ten species, N:N:N orthologs include the common orthologs with different copy numbers in the different species. **c**, Genome size and sequence depth estimation based on the K-mer spectrum. X-axis, sequencing depth; Y-axis, proportion of a K-mer at a given sequencing depth. **d**, Distribution of sequencing depth across the assembled genome. Y-axis, proportion of the genome at a given sequencing depth. **e**, Gene feature showing the distribution of CDS length in four Lepidoptera species.



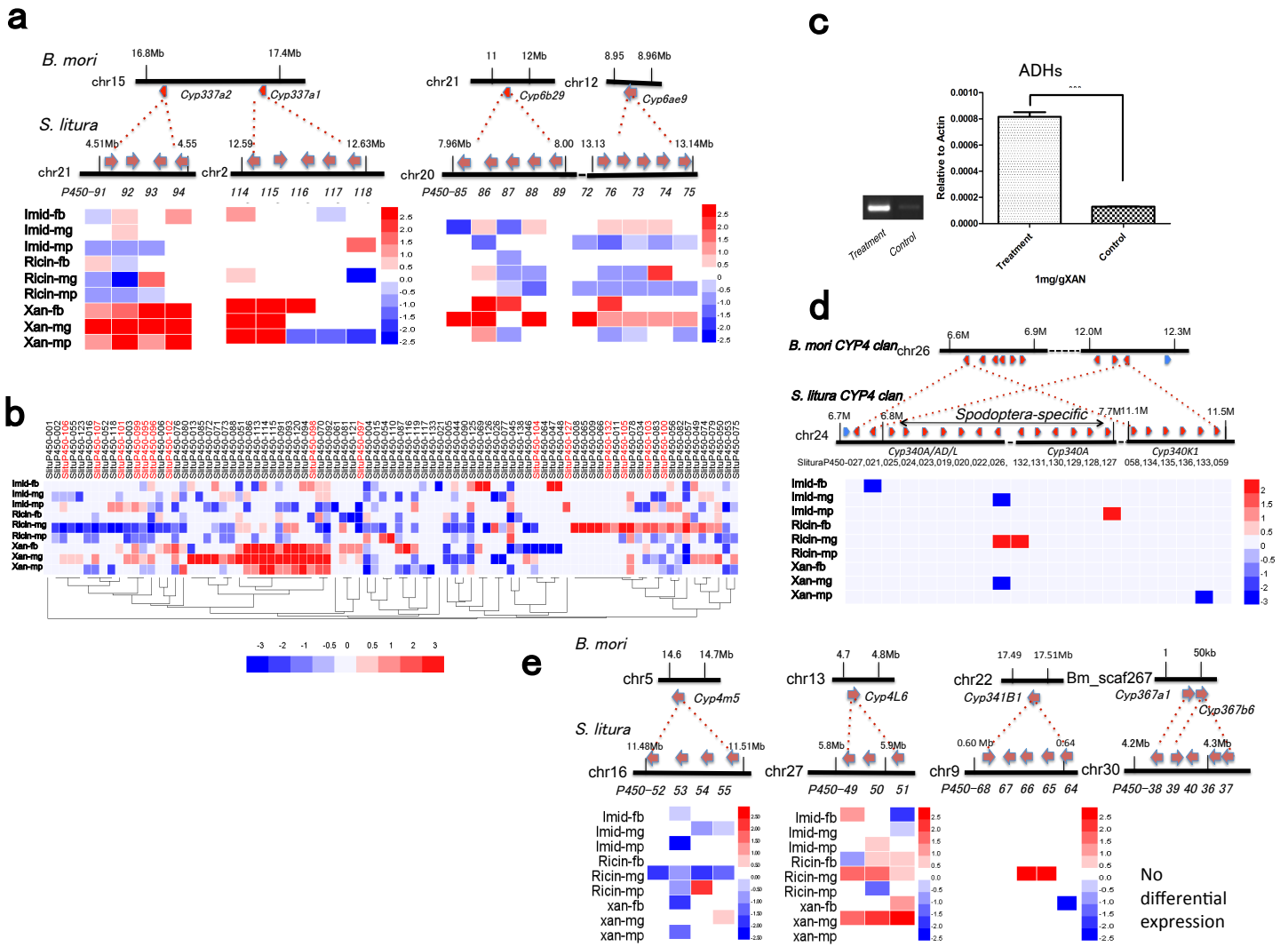
Supplementary Figure 2 | Linkage analysis and syntenic relationship with other Lepidoptera. **a**, Schematic of mapping population developed for preparing a linkage map of the *S. litura* genome. F1 offspring were obtained by crossing an India male and an Ishihara female. BC1 individuals were obtained by crossing an F1 male and an Ishihara female. The same number of dark and light colored BC1 individuals was chosen for RAD-seq analysis. **b**, Linkage map of *S. litura* developed using RAD-seq based genotyping. Positions in cM are shown on the left of the linkage group. The linkage mapping markers and their targeted scaffolds are shown on the right. **c**, Circos diagram illustrating syntenic relationships between *S. litura* and *B. mori* (left)/*H. melpomene* (right). Each line connects a syntenic block.



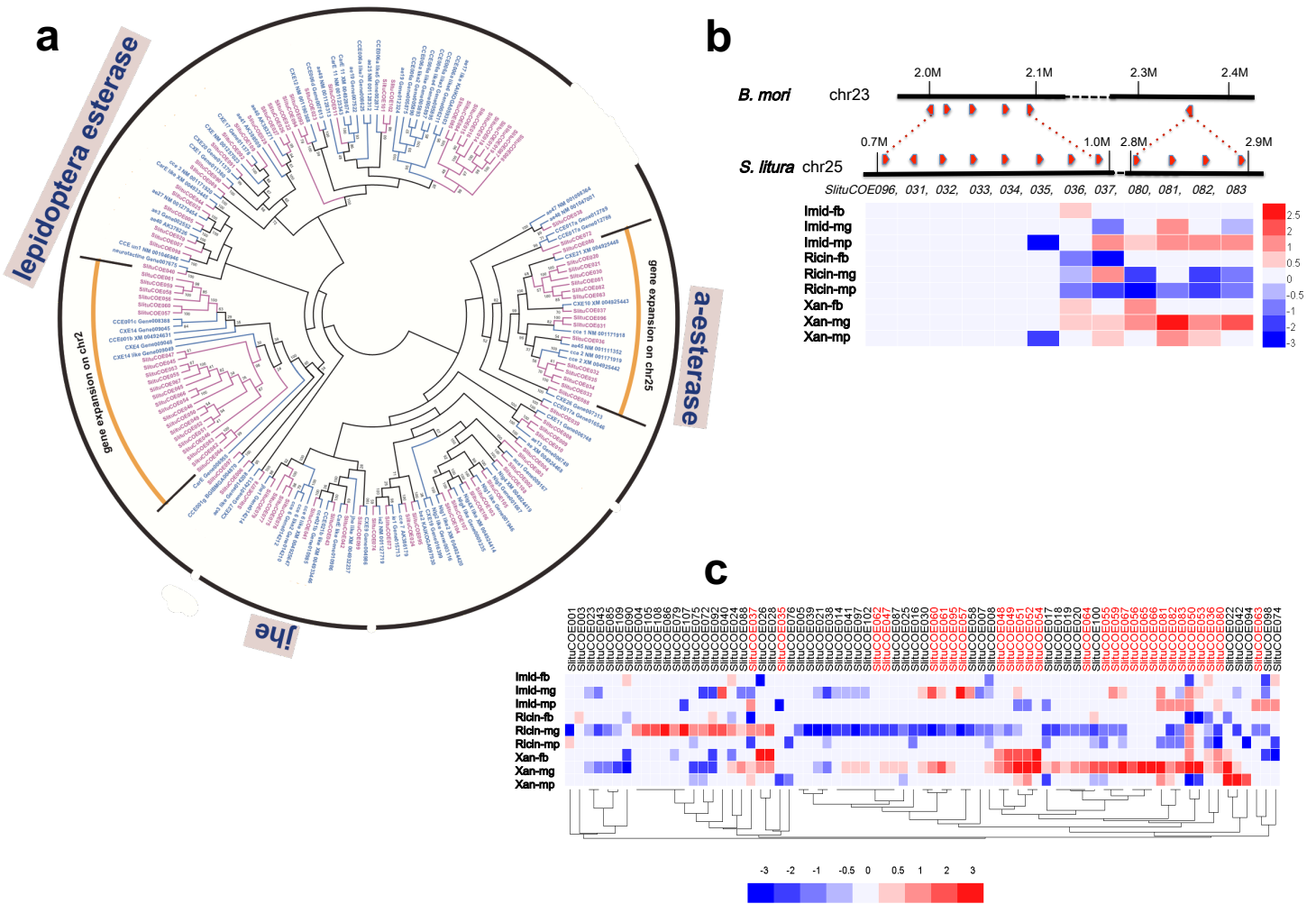
Supplementary Figure 3 | Phylogenetic analysis of gustatory receptors of 6 lepidopteran species with sequenced genomes. *S. litura* (magenta), *B. mori* (light blue), *S. frugiperda* (dark blue), *H. melpomene* (purple), *M. sexta* (grey) and *P. xylostella* (yellow). The phylogenetic tree was built using MEGA6 with a bootstrap of 100 replicates. The single-exon bitter GR clade is shown.



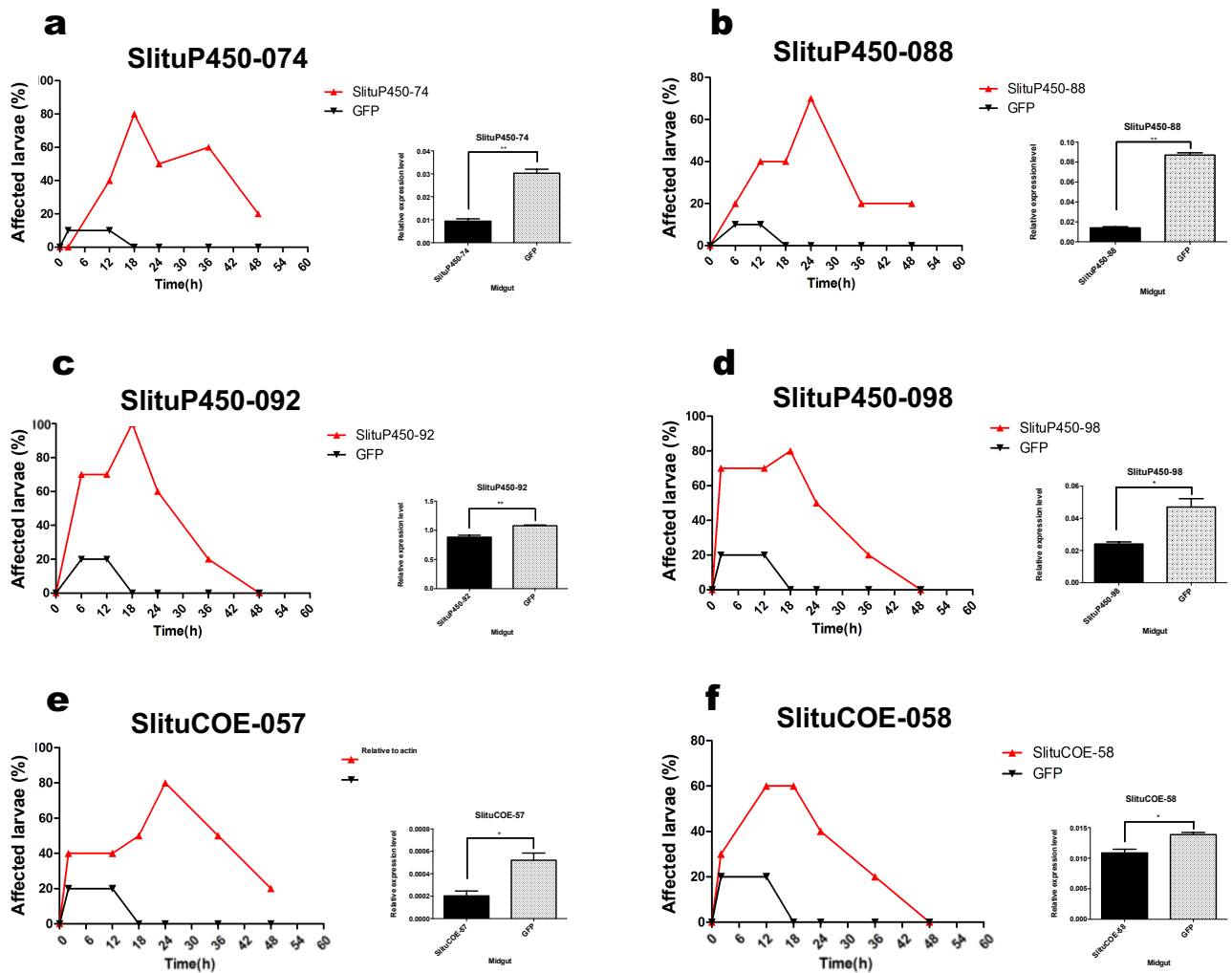
Supplementary Figure 4 | Phylogenetic tree of cytochrome P450s of *S. litura* and *B. mori*.
SlitP450: magenta, *BmorP450*: blue. Bootstrap was 1000 replicates.



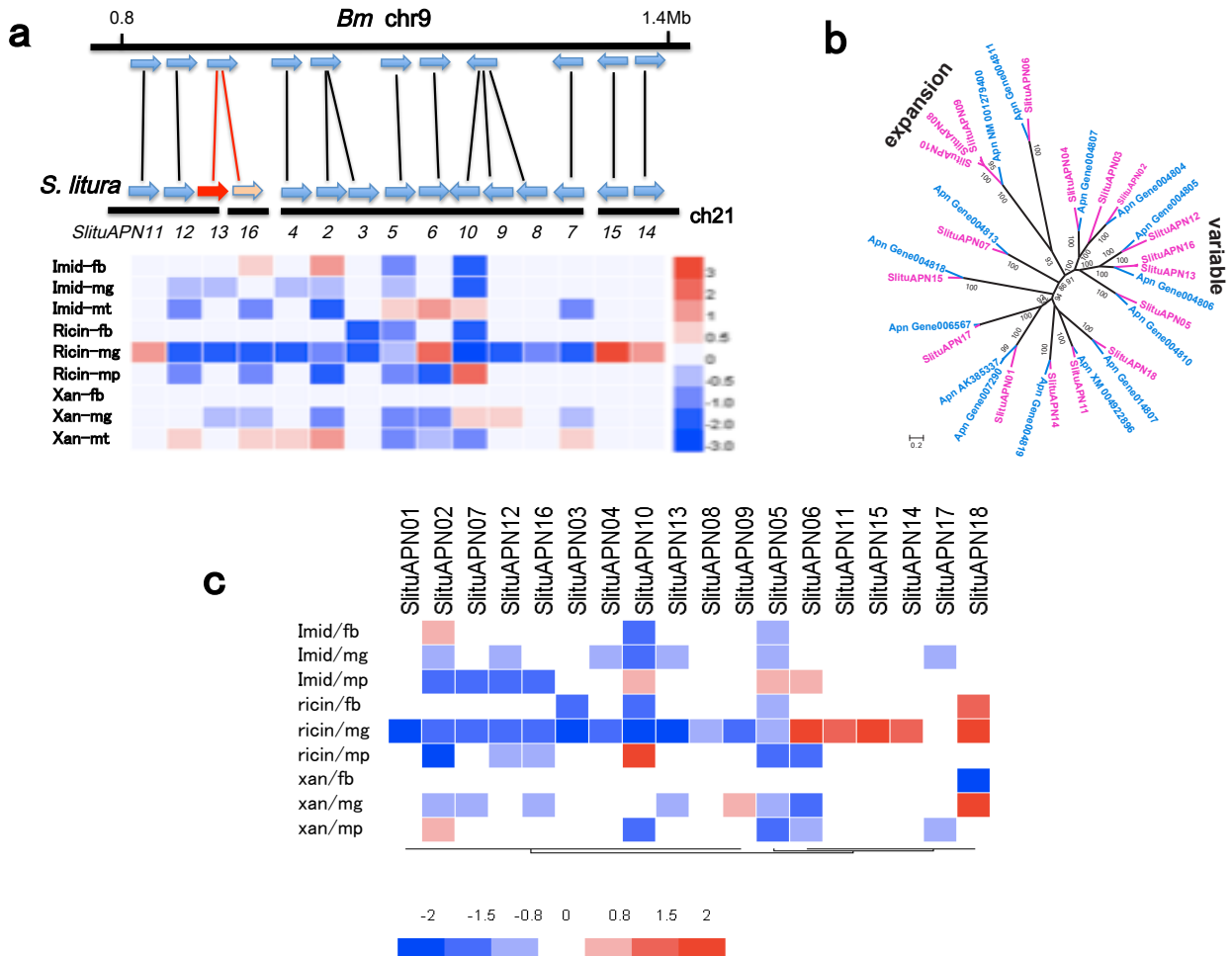
Supplementary Figure 5 | Expansion of *S. litura* CYP3 clan and CYP4 clan gene clusters and toxin induction of their expression. **a**, Four expansions of CYP3 clan, *Cyp337a1*, *Cyp337a2*, *Cyp6b* and *Cyp6ae9* in *S. litura*. Upper panel, genomic alignments. Lower panel, toxin induction of *Cyp3* gene expression. Toxin: Imidacloprid (Imid), ricin and xanthotoxin (Xan). Tissue: fat body (fb), midgut (mg) and Malpighian tubule (mp). **b**, Expression profiles of *S. litura* P450s with toxin-treatment. **c**, Xanthotoxin-induction of the *ADH* gene cluster flanking the *Cyp9a* gene cluster on chr29 (Fig. 2a). Expression level of *ADH* was measured by RT-qPCR. In the heatmap, red shows induced expression with toxin-treatment; blue shows reduced expression with toxin-treatment.



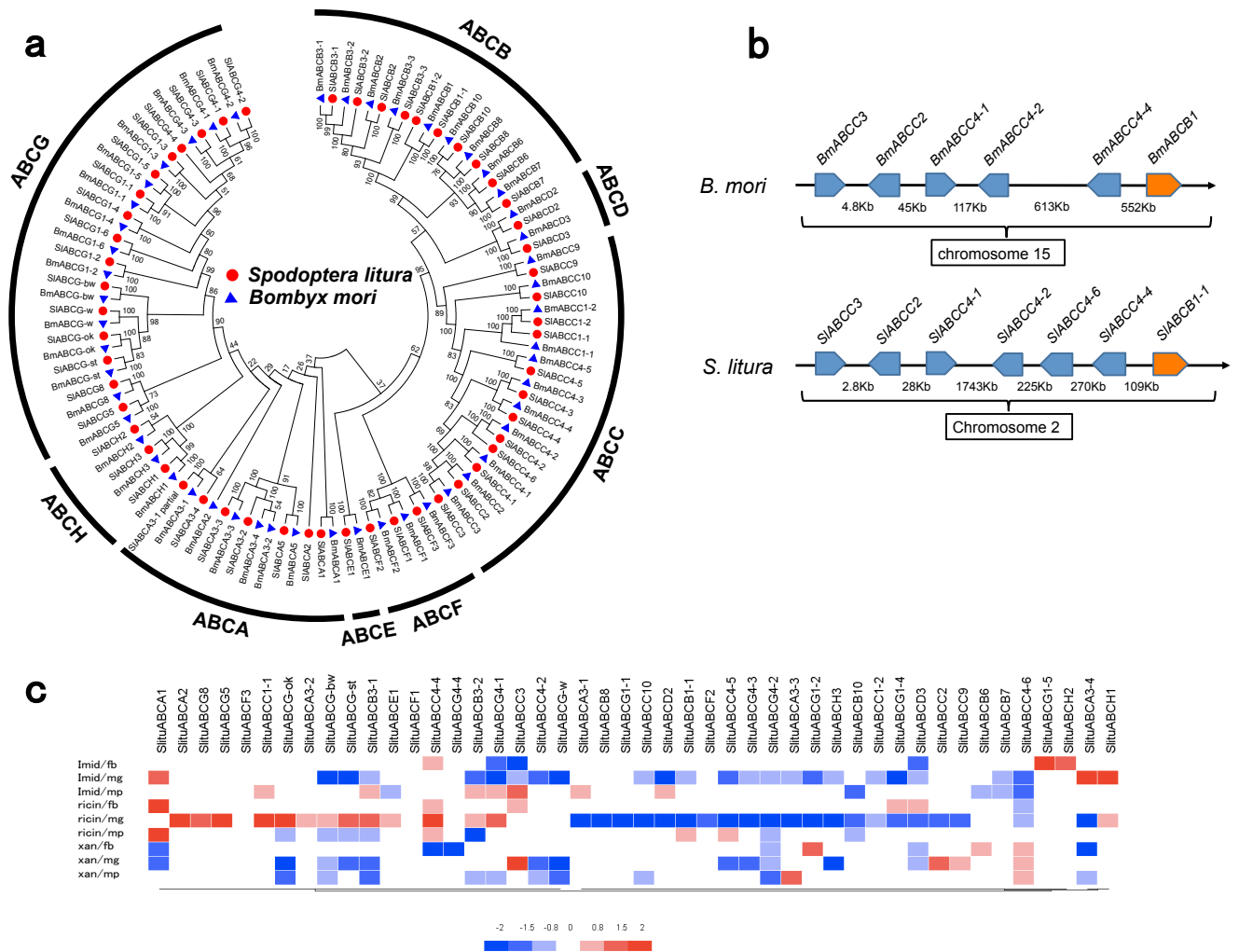
Supplementary Figure 6 | Large expansion of *S. litura* COEs. **a**, Phylogenetic tree of COE genes of *S. litura* and *B. mori*. Phylogenetic analysis shows large expansions of lepidopteran esterase genes on chr20 and α -esterase genes on chr25. *S. litura* COE: magenta, *B. mori* COE: blue. **b**, A large expansion of α -esterase genes on chr25. Upper panel, genomic organization of the expanded COE gene cluster on *S. litura* chr25 compared with *B. mori* chr23. Lower panel, heatmap of the expanded *S. litura* chr25 COE expression profiles with toxin-treatment. **c**, Heatmap of *S. litura* COE expression profiles following toxin-treatment. In the heatmap, red shows induced expression with toxin-treatment, blue shows reduced expression with toxin-treatment. Toxin: Imidacloprid (Imid), ricin and xanthotoxin (Xan). Tissue: fat body (fb), midgut (mg) and Malpighian tubule (mp).



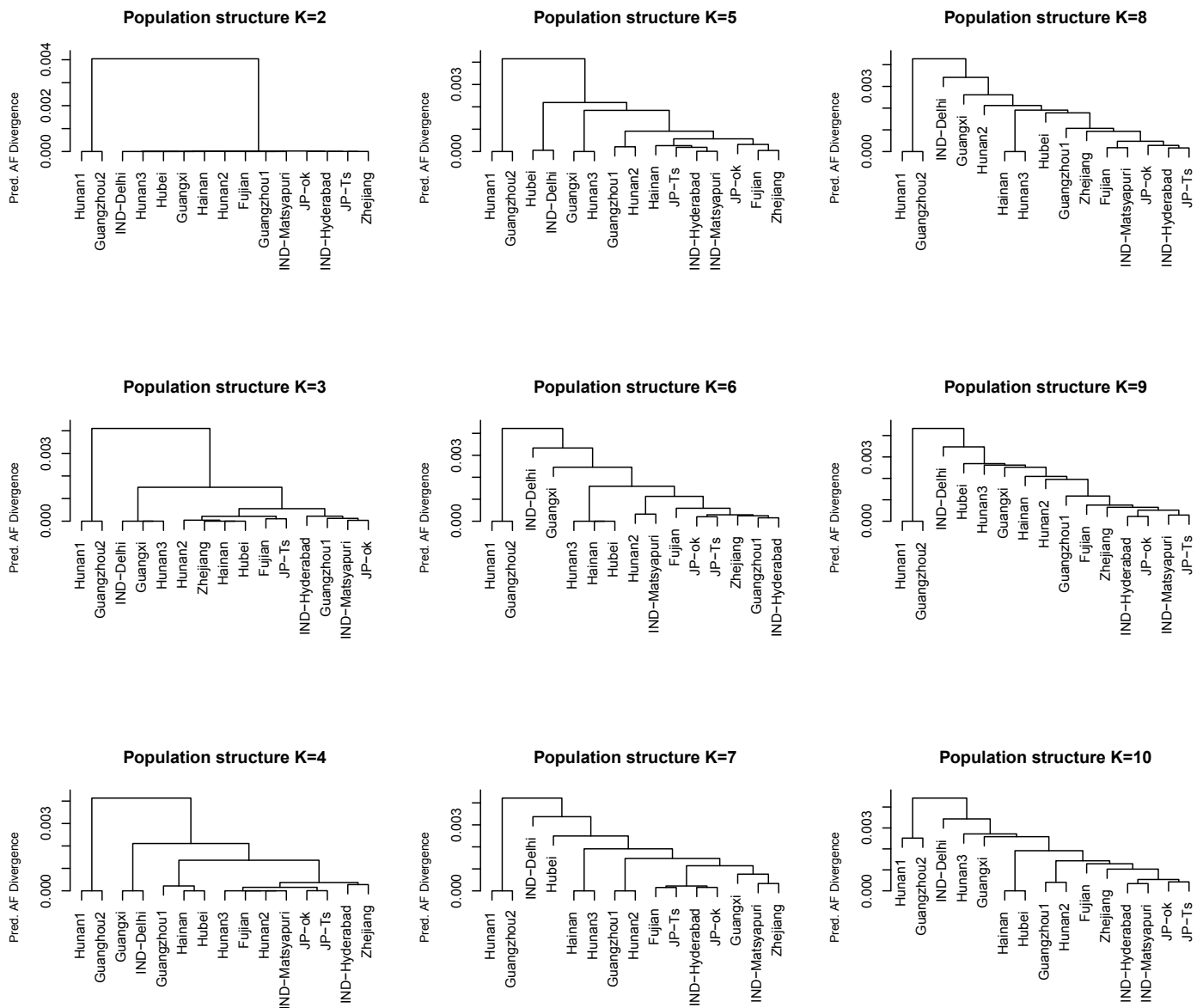
Supplementary Figure 7 | Preliminary experimental results on induced sensitivity to the pesticide imidacloprid caused by *SlituP450* and *COE* knock-down. Knock-down was performed by siRNA injection and confirmed by RT-qPCR. Each 5th instar larva was injected with 4μl (100pm/μl) of *siSlituRNA*; control larvae were injected with *siGFP*. At 24hr after injection, all larvae were fed artificial diet containing imidacloprid (50μg/g). Larval condition was scored at 2h, 6h, 12h, 18h, 24h, 36h and 48h after feeding to determine the effect of toxin-treatment. “Affected” means that larvae rounded up and when touched did not move for a couple of hours, as if dead (suspended animation). However, several hours later, many affected larvae recovered from their suspended state, probably due to detoxification of ingested imidacloprid. **a–f**: Left panel, percent of larvae affected by feeding on imidacloprid. For each siRNA, 30 larvae were used. Right panel, knock-down reduction rate measured by RT-qPCR. Error bars denote the Standard Deviation from three independent experiments with 3 larvae each, using a student’s t-test, * $P < 0.05$, ** $P < 0.01$.



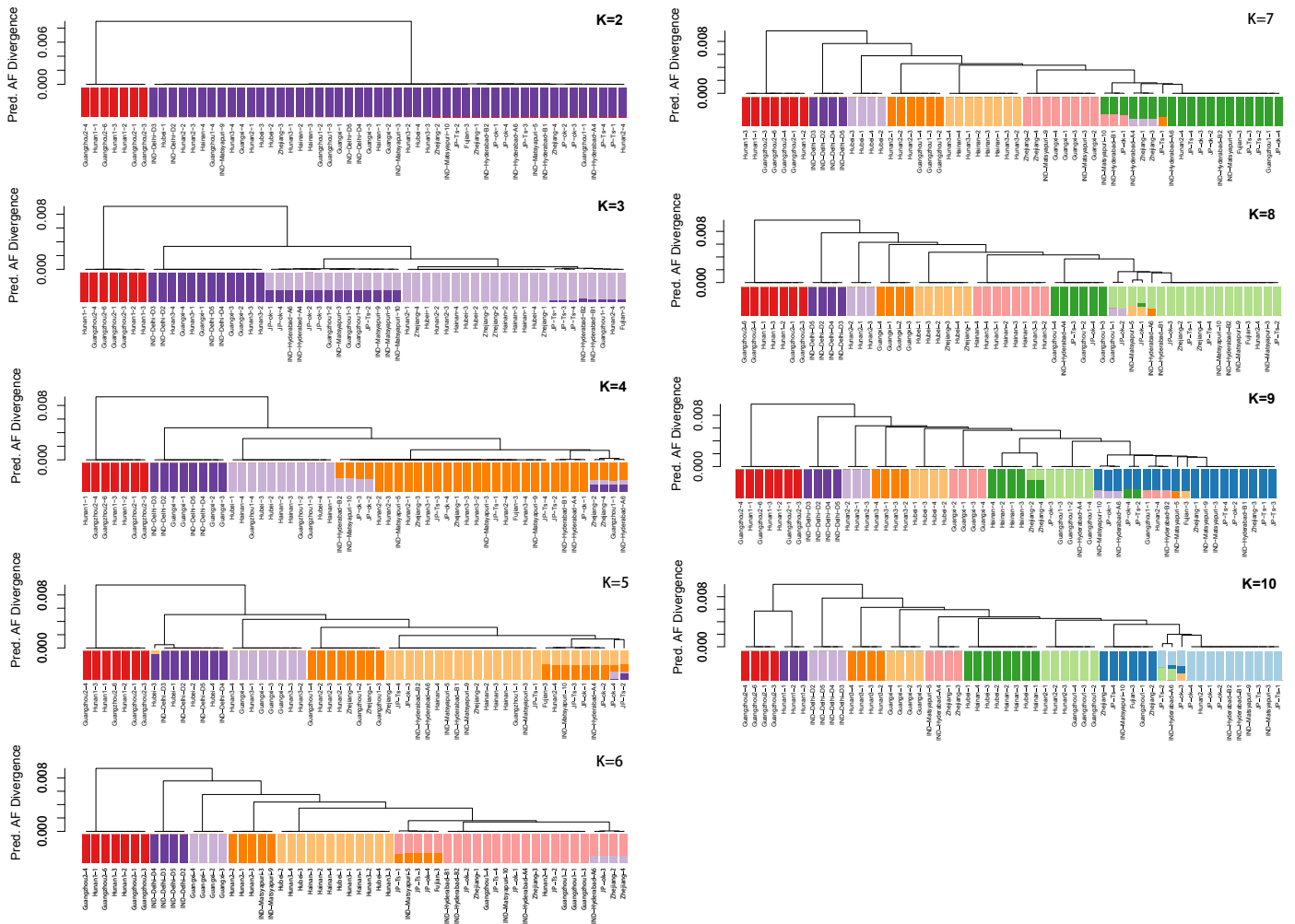
Supplementary Figure 8 | *S. litura* Aminopeptidase *N* genes. **a**, Expansion of the *S. litura* APN gene cluster on chr21. Upper panel, a comparative alignment of the largest APN gene clusters between *S. litura* and *B. mori*. Expanded APNs were mostly induced by toxin-treatment. *SlituAPN-13* and *16* (red, pink) are estimated to be variable among local populations based on population genetic analysis and to be important for adaptation. **b**, Phylogenetic tree of deduced APN protein genes in *S. litura* (magenta) and *B. mori* (blue). **c**, Heatmap of *S. litura* APN gene expression with toxin-treatment. Toxin: Imidacloprid (Imid), ricin and xanthotoxin (Xan). Tissue: fat body (fb), midgut (mg) and Malpighian tubule (mp).



Supplementary Figure 9 | Comparison of ABC transporter genes between *S. litura* and *B. mori*. **a**, Phylogenetic tree of deduced ABC transporter protein genes of *S. litura* and *B. mori*. The phylogenetic tree was built with MEGA6 with a bootstrap of 1000 replicates. Red circles, *S. litura*; blue triangles, *B. mori*. **b**, Highly conserved syntenic between ABC genes in *B. mori* chr15 gene cluster and in *S. litura* chr2 gene cluster. **c**, Heatmap of *S. litura* ABC transporter gene expression under toxin-treatment. Toxin: Imidacloprid (Imid), ricin and xanthotoxin (Xan). Tissue: fat body (fb), midgut (mg) and Malpighian tubule (mp).



Supplementary Figure 10a | Structure analysis of populations and individual genomes: long distance gene flow and diversifying selection. Cluster analysis of populations based on the predicted allele frequency divergence (see Methods).



Supplementary Figure 10b | Structure analysis of populations and individual genomes: long distance gene flow and diversifying selection. Assignment of the individual genomes in the samples to the ancestral populations predicted by structure.



Supplementary Figure 12 | Long distance gene flow. Gene flows of nuclear ITS2 sequences among local populations, which are consistent with the picture obtained by the present study. The location pairs with high gene flow ($F_{ST} < 0.05$) are connected by segments. The sampling locations were as follows. In China (province): Nanning (Guangxi), Changsha (Hunan), Jianli (Hubei), Wuhan (Hubei), and Nantong (Jiangsu). In Korea (province): Kangreung (Kangwon), Ansung (Gyeonggi), Cheongwon (Chungbuk), Milyang (Gyeongnam), Noan (Chonnam), and Jeju Island.

Supplementary Tables

Supplementary Table 1 | Summary of *S. litura* genome sequencing data

Library	Raw Reads					Qualified Reads				
	Raw reads	Total	Read	Sequence	Physical	Clean reads	Total	Read	Sequence	Physical
	Insert Size	Data (Gb)	Length (bp)	Coverage (X)	Coverage (X)		Data (Gb)	Length (bp)	Coverage (X)	Coverage (X)
170bp	68740935	13.43	100	30.55	25.97	63439128	12.39	100	28.20	23.97
300bp	34643123	6.77	100	15.40	23.10	31475850	6.15	100	13.99	20.98
500bp	29401520	5.74	100	13.07	32.67	25981489	5.07	100	11.55	28.87
800bp	64599723	12.62	100	28.71	114.84	49722792	9.71	100	22.10	88.40
2kb	242133292	47.29	100	107.61	1076.15	102574123	10.02	50	22.79	455.88
5kb	61667081	12.04	100	27.41	685.19	28295291	2.76	50	6.29	314.39
10kb	188203356	36.76	100	83.65	4182.30	30542258	2.98	50	6.79	678.72
Total	689389030	134.65	--	306.40	--	332030931	49.09	--	111.70	--

* Assumed genome size to be 450 Mb

Supplementary Table 2 | Summary of the *S. litura* genome assembly

	Contigs*		Scaffold*	
	Size (bp)	Number	Size (bp)	Number
N90	16 608	6538	208 387	512
N80	28 995	4625	376 883	362
N70	41 354	3395	531 654	266
N60	54 157	2488	740 983	196
N50	68 350	1784	915 465	143
Longest	638 354	--	4 425 893	--
Total	428 021 750	13 636	438 317 887	3597

*Only contigs and scaffolds ≥ 200 bp were included in the genome assembly

Supplementary Table 3 | General statistics of predicted protein-coding genes from *S. litura* genome

Gene set		Number	Average gene length (bp)	Average CDS length (bp)	Average exon per gene	Average exon length (bp)	Average intron per gene	Average intron length (bp)
De novo	AUGUSTUS	35524	8464.42	1077.2	4.06	265.01	3.06	2410.45
	SNAP	39060	15010.62	1076.56	6.08	177.04	5.08	2742.46
Homolog	<i>A. gambiae</i>	10723	5455.93	1001.87	4.28	234.02	3.28	1357.54
	<i>D. melanogaster</i>	10343	5612.7	1025.07	4.39	233.47	3.39	1353.08
	<i>B. mori</i>	18953	3934.25	986.85	3.94	250.45	2.94	1002.38
	<i>A. pisum</i>	12459	4468.5	1000.89	3.63	275.37	2.63	1316.11
	<i>D. plexippus</i>	16604	5374.45	1102.61	4.36	252.51	3.36	1268.91
RNA-SEQ	cufflinks/ cuffmerge*	9834	12511.63	1539.16	6.61	232.86	5.61	1955.97
	cufflinks/ cuffmerge	20882	12783.66	1321.16	6.13	215.51	5.13	2234.25
GLEAN		15317	12494.19	1565.19	6.64	235.78	6.64	1938.35

* The longest ORF of each gene locus was selected

Supplementary Table 4 | The content of repeat elements in the *S. litura* genome

Type of repeat	copy number	total length	% of repeats	% of genome
DNA elements	46097	8399327	6.168	1.962
Helitron	24090	3608652	2.650	0.843
hAT-Tip100	1916	695970	0.511	0.163
TcMar-Mariner	1365	606539	0.445	0.142
TcMar-Tc1	926	388438	0.285	0.091
Sola	1600	369869	0.272	0.086
hAT-Ac	1132	243054	0.178	0.057
TcMar-Fot1	957	149943	0.110	0.035
Zator	691	144893	0.106	0.034
hAT-Charlie	1050	141766	0.104	0.033
CMC-Transib	558	86777	0.064	0.020
PiggyBac	286	81651	0.060	0.019
CMC-EnSpm	359	64377	0.047	0.015
Academ	154	53559	0.039	0.013
Other	11013	1763839	1.295	0.412
LTR elements	3677	2413943	1.773	0.564
Gypsy	1912	1309886	0.962	0.306
Pao	749	490395	0.360	0.115
Copia	496	373623	0.274	0.087
DIRS	246	179386	0.132	0.042
Other	274	60653	0.045	0.014
Non-LTR elements	226333	46270290	33.980	10.810
LINE	173130	37759168	27.730	8.822
CR1	66906	13479658	9.899	3.149
L2	23844	7403220	5.437	1.730
R1	25503	6190668	4.546	1.446
Dong-R4	13222	2245170	1.649	0.525
CR1-Zenon	14151	2226163	1.635	0.520
RTE-RTE	10502	1886428	1.385	0.441
RTE-BovB	7488	1268697	0.932	0.296
CRE-II	6300	917177	0.674	0.214
Jockey	1157	613663	0.451	0.143
Proto2	1083	596886	0.438	0.139
I	1478	586961	0.431	0.137
Other	1496	344477	0.253	0.080
SINE	53203	8511122	6.250	1.988
tRNA	44554	7181279	5.274	1.678

5S-Deu	584	67907	0.050	0.016
Other	8065	1261936	0.927	0.295
Unknown Interspersed Repeats	476073	73889173	54.263	17.263
Total Interspersed Repeats	752180	130972733	96.185	30.599
small RNA	675	75457	0.055	0.018
Satellite	82	7309	0.005	0.002
Simple Repeats	90074	4522325	3.321	1.057
Low_complexity	12412	589705	0.433	0.138
Total	855423	136167529	100	31.813

Supplementary Table 5 | Genome coverage evaluated by EST and transcriptome datasets

Data set*	Length	Number	Total length (bp)	Bases covered by assembly (%)	Sequences covered by assembly (%)	with $\geq 90\%$ sequence in one scaffold		with $\geq 50\%$ sequence in one scaffold	
						Number	Percent	Number	Percent
RNA-seq	All	57,293	50,674,239	97.89	99.36	53,360	93.14	56,557	98.72
	>200bp	57,293	50,674,239	97.89	99.36	53,360	93.14	56,557	98.72
	>500bp	22,599	40,326,383	97.92	99.71	20,924	92.59	22,389	99.07
	>1000bp	13,218	33,810,296	97.91	99.92	12,140	91.84	13,122	99.27
	>2000bp	6,633	24,408,466	97.66	99.98	5,985	90.23	6,579	99.19
	>5000bp	1,102	7,584,914	96.32	99.91	941	85.39	1,081	98.09
	p								
EST	All	7,785	4,174,901	93.27	96.87	6,074	78.02	7,157	91.93
	>200bp	7,474	4,126,847	93.46	97.44	5,892	78.83	6,914	92.51
	>500bp	4,416	2,948,115	94.86	99.09	3,676	83.24	4,164	94.29
	>1000bp	216	421,421	98.88	100.00	199	92.13	215	99.54
	>2000bp	65	209,700	98.54	100.00	58	89.23	64	98.46
	>5000bp	10	58,066	99.77	100.00	9	90.00	10	100.00
	p								

*RNA-seq data were assembled using Trinity without a genome reference. Each EST collection was aligned to the assembly with BLAT; only alignments with identity ≥ 0.9 and coverage ≥ 0.5 were kept.

Supplementary Table 6 | Assessment of genome assemblies and gene sets in BUSCO notation
(C:complete [D:duplicated], F:fragmented, M:missing, n:gene number)

Species	Genome size/ Gene set	BUSCO notation assessment results	Complete Single-Copy BUSCOs	Complete Duplicated BUSCOs	Fragmented BUSCOs	Missing BUSCOs	Total BUSCO groups searched
<i>D. melanogaster</i>	142.57 Mbp	C:98%[D:6.3%],F:1.0%, M:0.3%,n:2675	2639	170	27	9	2675
	30362 genes	C:99%[D:6.1%],F:0.0%, M:0.0%,n:2675	2673	1641	1	1	2675
<i>B. mori</i>	431.72 Mbp	C:80%[D:3.9%],F:12%, M:7.1%,n:2675	2155	106	329	191	2675
	14623 genes	C:75%[D:7.0%],F:14%, M:10%,n:2675	2024	118	381	270	2675
<i>D. plexippus</i>	272.28 Mbp	C:87%[D:11%],F:9.3%, M:3.5%,n:2675	2329	331	250	96	2675
	16254 genes	C:86%[D:9.0%],F:9.5%, M:3.8%,n:2675	2318	241	255	102	2675
<i>H. melpomene</i>	269.65 Mbp	C:85%[D:4.3%],F:8.5%, M:6.0%,n:2675	2282	116	230	163	2675
	12829 genes	C:74%[D:7.0%],F:14%, M:10%,n:2675	1998	189	385	292	2675
<i>P. xylostella</i>	337.41 Mbp	C:75%[D:16%],F:10%, M:13%,n:2675	2024	442	280	371	2675
	18073 genes	C:66%[D:18%],F:12%, M:21%,n:2675	1787	489	321	567	2675
<i>S. litura</i>	428.02 Mbp	C:86%[D:5.6%],F:7.7%, M:5.4%,n:2675	2323	150	207	145	2675
	15317 genes	C:92%[D:10%],F:4.7%, M:2.7%,n:2675	2475	280	127	73	2675

Supplementary Table 7 | Non-coding RNA (tRNA, rRNA, snRNA, and miRNA) genes in the *S. litura* genome

Type		Copy number	Average length (bp)	Total length (bp)	Percentage of the genome
miRNA (precursor)		55	82.45	4,535	1.01E-05
tRNA		667	75.62	50,441	1.12E-04
rRNA		147	133.92	19,820	4.40E-05
	18S	16	129.25	2,068	4.60E-06
	28S	27	246.19	6,647	1.48E-05
	5.8S	4	153	612	1.36E-06
	5S	100	104.92	10,492	2.33E-05
snRNA		148	144.68	21,414	4.76E-05
	CD-box	31	174.93	5,423	1.21E-05
	HACA-box	4	133.25	533	1.18E-06
	splicing	113	136.78	15,458	3.44E-05

Supplementary Table 8 | Statistics on functional annotation of *S. litura* predicted genes

	Gene number	Percent (%)
Total	15,317	100%
Annotated	14,848	96.94
Swissprot	11,631	75.94
TrEMBL	14,848	96.94
InterPro	13,637	89.03
inver_Refseq	14,811	96.70
KEGG	8,781	57.33
GO	11,440	74.69
Unannotated	469	3.06

Supplementary Table 9 | Summary of gene families in 10 insects

Species	#Total genes (>30aa)	#Clustered genes	#Unclustered genes	#Families	#Uniq families (gene number)	#Ave.genes per families
<i>Anopheles darlingi</i>	10457	9066	1391	5684	314(475)	1.60
<i>Tetranychus urticae</i>	17521	12626	4895	5317	1239(4501)	2.37
<i>Drosophila melanogaster</i>	13900	11559	2341	6281	586(1277)	1.84
<i>Apis mellifera</i>	15052	10750	4302	7317	270(474)	1.47
<i>Spodoptera litura</i>	15313	14556	757	8042	264(436)	1.81
<i>Tribolium castaneum</i>	16496	12788	3708	6943	562(1561)	1.84
<i>Plutella xylostella</i>	18073	15438	2635	7581	808(1577)	2.04
<i>Danaus plexippus</i>	16223	14247	1976	8663	542(1315)	1.64
<i>Bombyx mori</i>	14621	12772	1849	8199	392(725)	1.56
<i>Harpegnathos saltator</i>	18361	16516	1845	7812	790(3183)	2.11

Supplementary Table 10 | Summary of syntenic comparisons between *S. litura* (Slitu) and *B. mori* (Bmor), *H. melpomene* (Hmel), and *P. Xuthus* (Pxut)

Comparison	No. of syntenic genes	No. of syntenic genes in compared genome	Syntenic blocks	Average No. of paired genes in block	No. of genes in largest block	Length of the largest block (Mb)
Slitu-Bmor	8020	8029	341	24.47	230	2.54
Slitu-Hmel	6539	6487	480	14.61	89	1.72
Slitu-Pxut	7595	7528	398	21.42	182	2.87

Supplementary Table 11 | Summary of chromosome homology among *S. litura* and *B. mori*, *H. melpomene*, and *P. xuthus*

<i>S. litura</i> Chr	<i>B. mori</i> Chr	No. of orthologues on homologous linkage groups	<i>H. melpomene</i> Chr	No. of orthologues on homologous linkage groups	<i>P. xuthus</i> Chr	No. of orthologues on homologous linkage groups
Chr1	Chr19	261	Chr14	243	Chr7	331
Chr2	Chr15	475	Chr11	431	Chr12	491
Chr3	Chr11	120	Chr6	167	Chr28	86
Chr4	Chr27	151	Chr18	152	Chr25	161
Chr5	Chr28	179	Chr10	153	Chr4	181
Chr6	Chr8	333	Chr12	328	Chr5	327
Chr7	Chr12	338	Chr19	295	Chr11	361
Chr8	Chr7	234	Chr9	196	Chr27	239
Chr9	Chr22	282	Chr13	246	Chr21	341
Chr10	Chr2	170	Chr7	164	Chr8	169
Chr11	Chr25	321	Chr8	258	Chr15	327
Chr12	Chr20	198	Chr12	206	Chr24	230
Chr13	Chr24	110	Chr17	117	Chr29	137
Chr14	Chr10	436	Chr20	138	Chr6	454
Chr15	Chr4	381	Chr1	345	Chr1	386
Chr16	Chr5	429	Chr10	438	Chr23	406
Chr17	Chr3	333	Chr5	274	Chr2	297
Chr18	Chr14	177	Chr13	111	Chr18	185
Chr19	Chr23	140	Chr20	69	Chr8	164
Chr20	Chr21	250	Chr4	152	Chr22	264
Chr21	Chr9	271	Chr6	249	Chr20	288
Chr22	Chr6	257	Chr3	256	Chr9	249
Chr23	Chr18	250	Chr16	239	Chr16	279
Chr24	Chr26	197	Chr19	199	Chr17	223
Chr25	Chr23	260	Chr18	244	Chr14	258
Chr26	Chr24	144	Chr1	128	Chr26	168
Chr27	Chr13	346	Chr17	287	Chr3	306
Chr28	Chr11	308	Chr7	257	Chr19	342
Chr29	Chr17	287	Chr15	237	Chr13	294
Chr30	Chr16	302	Chr2	116	Chr10	327
ChrZ	Chr1	362	ChrZ	95	Chr30	103

Supplementary Table 12 | Manually annotated Olfactory receptor genes of *S. litura* (*SlituOR*)

Gene Name	Gene ID	chr #	chromosomal position		Dir	CDS (bp)	aa length	# of Ex
SlituOR08	SWUSI0008350	1	7473456	7476584	-	1229	409	4
SlituOR09	SWUSI0013060	2	5810354	5816239	-	1188	396	9
SlituOR10	SWUSI0013740	2	7343763	7348278	+	1106	368	7
SlituOR11	SWUSI0020270	4	2313497	2317369	+	1168	389	5
SlituOR12	none	4	2319446	2322689	-	1168	389	5
SlituOR13	none	4	2326701	2331002	-	1186	395	5
SlituOR14	none	4	2346900	2350432	-	1405	468	5
SlituOR15	SWUSI0022630	5	1663030	1669007	-	1157	385	4
SlituOR16	SWUSI0023790	5	6673340	6679789	+	1232	410	7
SlituOR17	SWUSI0024440	5	8561638	8569951	+	1196	398	7
SlituOR18	SWUSI0024450	5	8594781	8598007	+	1217	405	7
SlituOR19	SWUSI0024450	5	8603506	8607058	+	1185	395	7
SlituOR20	SWUSI0029550	6	12419943	12426699	-	1180	393	9
SlituOR21	SWUSI0029700	6	12693577	12697126	+	1240	413	8
SlituOR22	none	7	5349170	5351716	-	1263	421	6
SlituOR23	none	7	6446720	6448409	+	1231	410	5
SlituOR24	SWUSI0038380	8	10271563	10275737	-	1198	399	5
SlituOR25	none	8	10284898	10287117	-	1193	397	4
SlituOR26	none	9	1094560	1098802	+	1189	396	5
SlituOR27	SWUSI0040540	9	4138079	4140836	-	1195	398	8
SlituOR28	SWUSI0040850	9	5398437	5401739	-	1201	400	8
SlituOR29	SWUSI0040850	9	5402793	5407562	-	1195	398	8
SlituOR31	none	11	3298199	3300913	-	1166	388	7
SlituOR32	SWUSI0048350	11	3302576	3305632	-	1119	373	7
SlituOR33	SWUSI0063990	14	11214591	11216194	+	1657	552	4
SlituOR34	SWUSI0063990	14	11218707	11222469	+	1157	385	4
SlituOR35	SWUSI0064040	14	11305487	11307787	-	1198	399	2
SlituOR36	none	16	5504561	5506271	-	1157	385	4
SlituOR37	none	16	5511139	5512700	-	1186	395	4
SlituOR38	none	16	5515752	5518942	-	1214	404	4
SlituOR39	SWUSI0073230	16	5527480	5529420	-	1345	448	4
SlituOR40	SWUSI0077890	16	16247723	16253899	-	1307	435	10
SlituOR41	SWUSI0077890	16	16257008	16266158	-	1214	404	10
SlituOR42	none	17	12938576	12944997	+	1241	413	4
SlituOR43	none	17	12945779	12948634	+	1253	417	4

SlituOR44	SWUSI0082570	17	12951249	12954157	+	1252	417	5
SlituOR45	SWUSI0082580	17	12958338	12960407	+	1223	407	4
SlituOR03	SWUSI0083370	18	2319002	2324001	+	1185	395	8
SlituOR04	none	18	2327981	2337922	+	1548	516	7
SlituOR05	none	18	2346268	2350427	+	1290	430	9
SlituOR06	SWUSI0083520	18	3275315	3285191	+	1285	428	9
SlituOR07	SWUSI0083530	18	3289319	3296404	-	1289	429	9
SlituOR46	none	19	2320456	2326053	-	1301	433	8
SlituOR47	SWUSI0090240	20	5211176	5215707	+	1157	385	7
SlituOR48	none	20	7427853	7428839	-	759	253	2
SlituOR49	SWUSI0090720	20	7571836	7577665	+	1275	425	9
SlituOR50	none	20	11919144	11923106	-	1206	402	6
SlituOR51	SWUSI0093450	21	3635077	3642437	-	1319	439	4
SlituOR52	none	21	4219482	4221841	-	1204	401	5
SlituOR53	none	21	4224469	4226778	-	1178	392	5
SlituOR54	SWUSI0095380	21	9606208	9619380	-	1280	426	8
SlituOR55	none	21	9757534	9768534	-	1925	641	9
SlituOR56	SWUSI0095440	21	9773703	9785478	-	1220	406	9
SlituOR57	none	21	10024726	10030090	-	1294	431	9
SlituOR58	none	21	11932099	11934099	-	1186	395	5
SlituOR59	SWUSI0096730	21	13525970	13528773	-	1208	402	7
SlituOR60	SWUSI0096730	21	13528997	13531712	-	1208	402	7
SlituOR61	SWUSI0096740	21	13533753	13536499	+	1202	400	7
SlituOR62	SWUSI0096740	21	13538047	13540843	+	1177	392	8
SlituOR63	SWUSI0099510	22	6882522	6889647	-	1167	389	9
SlituOR64	none	23	11441271	11448882	+	1150	383	8
SlituOR65	SWUSI0107650	24	4497271	4515612	+	1289	429	12
SlituOR66	SWUSI0108920	24	9756289	9763282	-	1237	412	5
SlituOR67	SWUSI0119500	27	8881451	8885153	+	1199	399	7
SlituOR68	SWUSI0119510	27	8885969	8888685	+	3177	1059	8
SlituOR02	SWUSI0133170	30	4808968	4827988	-	1492	497	10
SlituOR69	SWUSI0133920	30	6926379	6948668	+	1222	407	11
SlituOR70	SWUSI0136150	30	11538690	11541363	-	1342	447	8
SlituOR01	SWUSI0003740	Z	12640503	12643794	-	1417	472	8
SlituOR71	SWUSI0139930	scaffold476	72783	75045	+	1177	392	5
SlituOR72	SWUSI0140620	scaffold518	66033	73220	-	2153	717	5
SlituOR73	none	scaffold472	180227	184820	+	1225	408	7

Supplementary Table 13 | Manually annotated *S. litura* Gustatory receptor genes (*SlituGR*)

Gene Name	Gene ID	chr #	chromosomal position		Dir	CDS (bp)	aa length	# of Ex
SlituGR239	none	1	1818928	1822924	+	1162	387	5
SlituGR007	SWUSI0015330	2	9587112	9590476	+	619	206	5
SlituGR236	none	2	9605751	9619993	-	1311	437	10
SlituGR010	SWUSI0016460	2	11698358	11711256	+	1216	405	8
SlituGR237	none	2	11608673	11616780	+	1424	474	10
SlituGR006	SWUSI0016450	2	11579796	11595320	-	1190	396	10
SlituGR238	none	2	11564574	11574023	+	1284	428	9
SlituGR004	SWUSI0016440	2	11555206	11562059	+	1287	429	9
SlituGR005	SWUSI0016430	2	11541931	11553330	+	1281	427	9
SlituGR011	none	3	5319454	5322855	+	740	246	4
SlituGR013	none	6	3903320	3912070	+	1235	411	4
SlituGR002	SWUSI0028390	6	7572131	7580402	-	1293	431	9
SlituGR014	SWUSI0028750	6	8669602	8671364	-	1018	339	2
SlituGR015	none	8	2606904	2609325	+	1032	344	3
SlituGR016	none	8	2611221	2622447	-	1085	361	4
SlituGR017	none	8	2627723	2630739	-	783	261	3
SlituGR018	none	8	2631487	2634977	-	1020	340	3
SlituGR019	none	8	2661025	2664730	-	1158	386	3
SlituGR020	none	8	2665462	2667222	-	1118	372	4
SlituGR021	none	8	2667777	2669506	-	1052	350	4
SlituGR022	none	8	2669717	2671676	+	1035	345	3
SlituGR023	none	8	2671937	2676050	+	1109	369	4
SlituGR024	none	8	2689884	2691528	-	1223	407	4
SlituGR025	none	8	2774828	2776894	-	1094	364	4
SlituGR003	SWUSI0037120	8	6300635	6303681	+	1423	474	5
SlituGR026	none	9	5450690	5451766	-	1076	358	1
SlituGR027	none	11	10519553	10521776	-	927	309	3
SlituGR028	none	11	10522452	10524181	-	1011	337	3
SlituGR029	none	11	10526324	10534294	-	993	331	3
SlituGR030	none	11	10557341	10558861	+	1005	335	3
SlituGR031	none	11	10559554	10561308	+	1050	350	3
SlituGR032	none	11	10564297	10567074	-	951	317	3
SlituGR033	none	11	10567413	10570136	+	1002	334	3
SlituGR034	none	12	838021	839044	+	471	157	3
SlituGR035	SWUSI0052670	12	839944	843001	+	1131	377	3

SlituGR036	SWUSI0052670	12	843121	845013	+	1121	373	4
SlituGR037	none	12	845400	847247	+	1122	374	3
SlituGR038	none	12	847734	849863	+	1122	374	3
SlituGR039	none	12	856402	859441	+	1127	375	4
SlituGR040	none	12	861032	863217	+	1071	357	3
SlituGR041	none	12	864442	867157	-	1044	348	3
SlituGR042	none	12	1045141	1046743	+	396	132	3
SlituGR043	none	12	1047201	1050666	+	3136	1045	4
SlituGR044	none	12	1052235	1054491	+	1217	405	4
SlituGR045	none	12	1056917	1060017	+	1193	397	4
SlituGR046	none	12	1066452	1069310	-	1172	390	4
SlituGR047	none	12	1075501	1078867	+	1079	359	4
SlituGR048	none	12	1082577	1085692	-	1207	402	4
SlituGR049	none	12	1086255	1088478	+	1187	395	4
SlituGR050	none	12	1089431	1094029	+	1157	385	4
SlituGR051	none	12	1096428	1099861	+	1089	363	3
SlituGR052	none	12	1101831	1104020	-	1220	406	4
SlituGR053	none	12	1106163	1107899	+	1146	382	4
SlituGR054	none	12	1121709	1128092	-	1197	399	4
SlituGR055	none	12	1136211	1138026	+	1163	387	4
SlituGR056	none	12	1139813	1142339	-	1004	334	4
SlituGR057	none	12	1142839	1148092	-	1166	388	4
SlituGR058	none	12	1148814	1150751	-	1190	396	4
SlituGR059	none	12	1146464	1155457	-	1046	348	4
SlituGR060	none	12	1156158	1158248	-	1187	395	4
SlituGR061	none	12	1159300	1161619	+	1092	364	3
SlituGR062	none	12	1162189	1163838	-	1083	361	3
SlituGR063	none	12	1164450	1167934	-	1112	370	4
SlituGR064	none	12	1169528	1172715	-	1193	397	4
SlituGR065	none	12	1173166	1176622	-	1130	376	4
SlituGR066	none	12	1177058	1179879	-	1142	380	5
SlituGR067	none	12	1180871	1184455	-	1205	401	4
SlituGR068	none	12	1188810	1191841	-	1071	357	3
SlituGR069	none	12	1202244	1207586	-	1170	390	3
SlituGR070	none	12	1210215	1211766	-	893	297	2
SlituGR071	none	12	1213164	1215340	-	1056	352	3
SlituGR072	none	12	1216450	1217924	-	1196	398	4
SlituGR073	none	12	1218798	1221057	-	1163	387	4

SlituGR074	none	12	1222172	1223956	-	1145	381	4
SlituGR075	none	12	1224523	1227811	-	1166	388	4
SlituGR076	none	12	1229037	1231434	+	1038	346	3
SlituGR077	none	12	1232032	1234739	+	1044	348	3
SlituGR078	none	12	1235042	1237439	-	1133	377	4
SlituGR079	none	12	1238776	1240604	-	1154	384	4
SlituGR080	none	12	1241836	1244202	+	1097	365	4
SlituGR081	none	12	1246294	1254084	-	1163	387	4
SlituGR082	none	12	1259779	1262422	+	1208	402	4
SlituGR083	none	12	1262878	1265463	+	1119	373	3
SlituGR084	none	12	1269313	1272870	+	1157	385	4
SlituGR085	none	12	1274004	1276170	+	1199	399	4
SlituGR086	none	12	1366265	1369109	+	964	321	2
SlituGR087	none	12	1382103	1387387	+	1047	349	3
SlituGR088	none	12	1387769	1390440	+	1123	374	2
SlituGR089	none	12	1391159	1393737	-	1271	423	4
SlituGR090	none	12	1396470	1399904	+	1205	401	4
SlituGR091	none	12	1404458	1407063	-	1200	400	4
SlituGR092	none	12	1407796	1410407	-	1056	352	3
SlituGR093	none	12	1410738	1413501	-	1148	382	4
SlituGR094	none	12	1414671	1416968	-	1223	407	4
SlituGR095	none	12	1417500	1420126	-	1190	396	4
SlituGR096	none	12	1421134	1422759	-	1068	356	3
SlituGR097	none	12	1433317	1437080	-	1163	387	4
SlituGR098	none	12	1437799	1444015	-	1193	397	4
SlituGR099	none	12	1447348	1450943	+	1065	355	3
SlituGR100	none	12	1451585	1454263	+	960	320	3
SlituGR101	none	12	1455290	1458466	+	1014	338	3
SlituGR102	none	12	1459475	1463465	-	1135	378	4
SlituGR103	none	12	1464511	1468064	-	1116	372	3
SlituGR104	none	12	1469903	1472306	-	1116	372	3
SlituGR105	none	12	1476346	1480474	-	1086	362	3
SlituGR106	none	12	1484989	1487402	-	1095	365	3
SlituGR107	none	12	1489125	1496767	-	1438	479	5
SlituGR108	none	12	1516937	1519665	-	1095	365	3
SlituGR109	none	12	1522872	1525557	-	1071	357	3
SlituGR110	none	12	1528584	1530634	-	1172	390	4
SlituGR111	none	12	1535203	1539710	-	1148	382	4

SlituGR112	none	12	1540480	1543104	-	1202	400	4
SlituGR113	none	12	1543524	1547745	-	1214	404	4
SlituGR114	none	12	1549114	1551735	-	1163	387	4
SlituGR115	none	12	1553246	1556276	-	1098	366	4
SlituGR116	none	12	1557035	1560666	-	1184	394	4
SlituGR117	none	12	1562120	1564702	-	1119	373	4
SlituGR118	none	12	1567347	1570341	-	1620	540	4
SlituGR119	none	12	1570958	1575067	-	1178	392	4
SlituGR120	none	12	1583860	1585419	-	1082	360	4
SlituGR121	none	12	1587604	1591242	+	993	331	3
SlituGR122	none	12	1596000	1598885	+	1171	390	4
SlituGR123	none	12	1601553	1604041	+	1098	366	3
SlituGR124	none	12	1604329	1606625	+	1057	352	3
SlituGR125	none	12	1607505	1610805	+	1064	354	3
SlituGR126	none	12	1612135	1615587	+	1145	381	4
SlituGR127	none	12	1615923	1618479	+	1136	378	4
SlituGR128	none	12	1621888	1626220	+	1142	380	4
SlituGR129	none	12	1637745	1640125	+	1340	446	3
SlituGR130	none	12	1640820	1644825	+	1193	397	4
SlituGR131	none	12	1649280	1654607	+	1167	389	4
SlituGR132	none	12	1657194	1660132	+	1041	347	3
SlituGR133	none	12	1662509	1668429	+	1172	390	4
SlituGR134	none	12	1670495	1675373	-	1173	391	4
SlituGR135	none	12	1682253	1685536	+	1190	396	4
SlituGR136	none	12	1690165	1693267	-	1204	401	4
SlituGR137	none	12	1700816	1703171	+	1262	420	4
SlituGR138	none	12	1703930	1707046	-	1014	338	3
SlituGR139	none	12	1708669	1711287	-	1062	354	3
SlituGR140	none	12	1712327	1714737	+	1166	388	4
SlituGR141	none	12	1715137	1718060	-	1525	508	4
SlituGR142	none	12	1719367	1722315	-	1077	359	3
SlituGR143	none	12	1724464	1727189	-	1220	406	4
SlituGR144	none	12	1728817	1731356	-	1084	361	3
SlituGR145	none	12	1732100	1735320	-	1187	395	4
SlituGR146	none	12	1745315	1747952	+	1034	344	4
SlituGR147	none	12	1748152	1751552	+	1092	364	3
SlituGR148	none	12	1752208	1758052	+	1131	377	3
SlituGR149	none	12	1759306	1762502	+	1193	397	4

SlituGR150	none	12	1763223	1765429	-	1178	392	4
SlituGR151	none	12	1766078	1769169	+	1142	380	4
SlituGR152	none	12	1769950	1773643	+	1142	380	4
SlituGR153	none	12	1773967	1777030	+	1014	338	3
SlituGR154	none	12	1777452	1780871	+	1178	392	4
SlituGR155	none	12	1783087	1785310	+	1256	418	4
SlituGR156	none	12	1792302	1795608	+	1226	408	4
SlituGR157	none	12	1798438	1801668	+	1178	392	4
SlituGR158	none	12	2088258	2092194	-	919	306	2
SlituGR159	none	13	1798074	1801329	-	952	317	2
SlituGR224	none	14	12796625	12798422	-	1130	376	4
SlituGR225	none	14	12790929	12794015	-	1163	387	4
SlituGR226	none	14	12787238	12789616	-	1151	383	4
SlituGR227	none	14	12782842	12784702	-	1122	374	4
SlituGR228	none	14	12779561	12782108	-	1136	378	4
SlituGR229	none	14	12777253	12778751	-	1118	372	4
SlituGR230	none	14	12773765	12776319	-	1151	383	4
SlituGR231	none	14	12771077	12772805	-	1139	379	4
SlituGR232	none	14	12764053	12769813	-	1130	376	4
SlituGR160	none	14	12759814	12762336	-	1154	384	4
SlituGR233	none	14	12755576	12759037	-	1157	385	4
SlituGR161	none	14	12751361	12754326	-	1148	382	4
SlituGR234	none	14	12745471	12749314	-	1163	387	4
SlituGR235	none	14	12721232	12724316	-	1124	374	4
SlituGR162	none	20	6579729	6581802	+	1058	352	4
SlituGR163	none	20	5871031	5873345	+	1040	346	4
SlituGR165	none	22	1154687	1158434	+	1212	404	4
SlituGR012	SWUSI0112650	25	9073789	9075033	-	1244	414	1
SlituGR167	SWUSI0112660	25	9076442	9077701	-	1259	419	1
SlituGR168	none	25	9080876	9082111	-	1235	411	1
SlituGR169	SWUSI0112660	25	9083121	9084368	-	1247	415	1
SlituGR001	SWUSI0112760	25	9579071	9591573	+	1369	456	9
SlituGR170	none	27	2394142	2397603	-	924	308	3
SlituGR171	none	27	2400205	2402180	-	1025	341	4
SlituGR172	none	27	2402702	2404937	-	1031	343	4
SlituGR173	none	27	2408032	2415360	-	1028	342	4
SlituGR219	none	27	2416421	2420136	-	951	317	3
SlituGR220	none	27	2420483	2430735	+	1147	382	5

SlituGR221	none	27	2440222	2443147	+	1040	346	4
SlituGR222	none	27	2444602	2448049	+	1049	349	4
SlituGR223	none	27	2448490	2452848	+	972	324	3
SlituGR174	SWUSI0119740	27	9426641	9428378	-	1193	397	4
SlituGR175	SWUSI0121130	27	13846526	13848538	+	1214	404	4
SlituGR176	none	29	995359	998137	-	1137	379	3
SlituGR177	none	29	998905	1001393	+	1149	383	3
SlituGR178	none	29	9201955	9205819	-	1136	378	4
SlituGR179	none	30	4251639	4253803	+	1140	380	3
SlituGR009	SWUSI0135150	30	9338783	9343690	-	1394	464	10
SlituGR008	SWUSI0135160	30	9357745	9365139	+	1437	479	10
SlituGR180	none	scaffold470	6766	10696	-	1017	339	3
SlituGR181	none	scaffold470	13398	16225	-	1072	357	3
SlituGR182	none	scaffold470	17572	20898	-	1001	333	3
SlituGR183	none	scaffold470	22099	25892	-	1107	369	3
SlituGR184	none	scaffold470	26597	32870	-	1080	360	3
SlituGR185	none	scaffold470	33826	37191	-	1068	356	3
SlituGR186	none	scaffold470	38015	40449	-	1038	346	3
SlituGR187	none	scaffold470	41524	44195	-	1080	360	3
SlituGR188	none	scaffold470	44963	48199	-	1035	345	3
SlituGR189	none	scaffold470	50317	54195	-	1076	358	4
SlituGR190	none	scaffold1183	167	2409	-	1190	396	4
SlituGR191	none	scaffold1183	3636	7966	+	1188	396	4
SlituGR192	none	scaffold851	3014	7236	-	700	233	4
SlituGR193	none	scaffold851	1248	1772	-	524	174	1
SlituGR194	none	scaffold2905	744	1585	-	841	280	1
SlituGR195	none	scaffold2818	5	1673	-	759	253	3
SlituGR196	none	scaffold479	122515	127014	+	1080	360	3
SlituGR197	none	scaffold479	176422	177067	+	835	278	2
SlituGR198	none	scaffold479	177322	179453	+	1201	400	4
SlituGR199	none	scaffold479	180331	182905	+	1239	413	3
SlituGR200	none	scaffold479	188745	191462	+	1189	396	5
SlituGR201	none	scaffold479	194319	198668	+	1215	405	3
SlituGR202	none	scaffold479	199468	201422	+	1193	397	4
SlituGR203	none	scaffold479	202733	205953	+	1053	351	3
SlituGR204	none	scaffold131	41011	46762	-	1005	335	3
SlituGR205	nonw	scaffold131	47939	51412	-	1292	430	4
SlituGR206	none	scaffold131	57804	59307	-	1086	362	3

SlituGR207	none	scaffold131	60038	63423	+	1092	364	3
SlituGR208	none	scaffold131	94639	95373	−	734	244	1
SlituGR209	none	scaffold131	96825	99298	−	1050	350	3
SlituGR210	none	scaffold131	109290	114417	−	1061	353	4
SlituGR211	none	scaffold131	353653	358149	+	1179	393	3
SlituGR212	none	scaffold725	20207	23104	−	1097	365	3
SlituGR213	none	scaffold725	24667	26558	−	1257	419	3
SlituGR214	none	scaffold725	28124	34191	+	1092	364	3
SlituGR215	none	scaffold725	34455	39205	+	1122	374	3
SlituGR216	none	scaffold725	40429	42318	+	1041	347	3
SlituGR217	none	scaffold725	55191	56659	+	1038	346	3
SlituGR218	none	scaffold725	58497	59267	+	770	256	1

Supplementary Table 14 | Manually annotated *S. litura* Cytochrome P450 genes (*SlituP450*)

Gene Name	Gene ID	Type_CLAN	chr#	chromosomal position		dir	CDS (bp); aa length	Exon #
SlituP450-043	SWUSI0008840	CYP49A1_CLAN-mit	chr01	8794103	8798075	+	1413bp; 470aa	7
SlituP450-015	SWUSI0012760	CYP332A1_CLAN3	chr02	5444659	5455334	+	1587bp; 528aa	8
SlituP450-114	SWUSI0016820	CYP321B1_CLAN3	chr02	12592166	12593653	-	1488bp, 495aa	1
SlituP450-115	SWUSI0016840	CYP321B3_CLAN3	chr02	12610515	12611999	+	1485bp, 494aa	1
SlituP450-116	SWUSI0016850	CYP321B3_CLAN3	chr02	12616587	12618074	-	1488bp, 495aa	1
SlituP450-117	SWUSI0016860	CYP321B4_CLAN3	chr02	12621782	12623272	-	1491bp, 496aa	1
SlituP450-118	none	CYP321B4_CLAN3	chr02	12626118	12627555	-	1428bp, 475aa	2
SlituP450-125	SWUSI0016970	CYP9A75_CLAN3	chr02	12837528	12844188	-	1599bp, 532aa	10
SlituP450-126	SWUSI0016980	CYP9A75_CLAN3	chr02	12856868	12862687	-	1599bp, 532aa	10
SlituP450-012	SWUSI0018470	CYP307A2_CLAN2	chr03	3037347	3047120	+	1620bp; 539aa	2
SlituP450-001	SWUSI0028040	CYP333A12_CLAN-mit	chr06	6159062	6162603	-	1503p; 500aa	8
SlituP450-014	SWUSI0027190	CYP315A1_CLAN-mit	chr06	4360469	4364976	-	1356bp; 451aa	7
SlituP450-044	SWUSI0029140	CYP428A1_CLAN-mit	chr06	9889253	9931441	-	1623bp; 540aa	10
SlituP450-138	SWUSI0030870	CYP4CG18_CLAN4	chr07	2958660	2974434	-	1512bp; 503aa	9
SlituP450-139	SWUSI0030860	CYP4CG18_CLAN4	chr07	2951585	2958003	-	1494bp; 497aa	9
SlituP450-017	SWUSI0033980	CYP338A1_CLAN3	chr07	12083575	12090954	+	1398bp; 465aa	2
SlituP450-137	SWUSI0039220	CYP341B22_CLAN4	chr09	101364	108696	-	1506bp; 501aa	10
SlituP450-068	SWUSI0039320	CYP341B16_CLAN4	chr09	601373	606216	+	1515bp; 504aa	10
SlituP450-067	SWUSI0039330	CYP341B_CLAN4	chr09	607317	613226	-	1527bp; 508aa	10
SlituP450-066	SWUSI0039340	CYP341B_CLAN4	chr09	627498	633157	-	1527bp; 508aa	10
SlituP450-065	SWUSI0039350	CYP341B18_CLAN4	chr09	635083	642834	-	1515bp; 504aa	10
SlituP450-064	SWUSI0039360	CYP341B_CLAN4	chr09	648950	660380	-	1506bp;501aa	10
SlituP450-063	SWUSI0039370	CYP341B15_CLAN4	chr09	667221	674340	-	1476bp; 491aa	9
SlituP450-113	SWUSI0039660	CYP321A15_CLAN3	chr09	1855612	1862183	+	1401bp, 466aa	2
SlituP450-077	SWUSI0040050	CYP6AN4_CLAN3	chr09	2868842	2871904	-	1554bp; 517aa	2
SlituP450-062	SWUSI0040860	CYP341A11_CLAN4	chr09	5434046	5446583	-	1533bp; 510aa	10
SlituP450-009	SWUSI0041680	CYP302A1_CLAN-mit	chr09	6718602	6728685	-	1446bp; 481aa	7
SlituP450-081	SWUSI0047540	CYP6AB58_CLAN3	chr10	8457348	8459362	+	1542bp; 513aa	2
SlituP450-082	SWUSI0047560	CYP6AB12_CLAN3	chr10	8472941	8474868	-	1533bp; 510aa	2
SlituP450-124	SWUSI0050360	CYP6CT1_CLAN3	chr11	8196154	8201745	-	1554bp, 517aa	5
SlituP450-004	SWUSI0061770	CYP18A1_CLAN2	chr14	5902505	5905004	-	1614bp; 537aa	6
SlituP450-005	SWUSI0061780	CYP18B1_CLAN2	chr14	5969942	5972420	-	1485bp; 494aa	7
SlituP450-006	SWUSI0061760	CYP306A1_CLAN2	chr14	5896345	5900839	+	1620bp; 539aa	7
SlituP450-090	SWUSI0063110	CYP6AW1_CLAN3	chr14	9090846	9092947	-	1488bp; 495aa	2
SlituP450-055	SWUSI0075930	CYP4M18_CLAN4	chr16	11480004	11484604	-	1500bp; 499aa	9
SlituP450-054	SWUSI0075940	CYP4M17_CLAN4	chr16	11487992	11492733	-	1506bp;501aa	9

SlituP450-053	SWUSI0075950	CYP4M15_CLAN4	chr16	11494141	11497766	-	1509bp; 502aa	9
SlituP450-052	SWUSI0075970	CYP4M14_CLAN4	chr16	11499093	11503605	-	1512bp; 503aa	9
SlituP450-035	SWUSI0082530	CYP366A1_CLAN4	chr17	12923490	12929925	+	1524bp; 507aa	10
SlituP450-060	SWUSI0080450	CYP4AU1_CLAN4	chr17	6503634	6511235	+	1458bp; 485aa	10
SlituP450-061	SWUSI0080440	CYP4AU2_CLAN4	chr17	6490618	6499513	-	1485bp; 494aa	10
SlituP450-007	SWUSI0084290	CYP301A1_CLAN-mit	chr18	5347747	5371397	+	1590bp; 529aa	8
SlituP450-008	SWUSI0084300	CYP301B1_CLAN-mit	chr18	5393411	5426519	+	1635bp; 544aa	12
SlituP450-083	SWUSI0085910	CYP6AE68_CLAN3	chr18	11023744	11025613	+	1572bp; 524aa	2
SlituP450-078	SWUSI0088490	CYP6AB59_CLAN3	chr20	46074	47889	+	1557bp; 518aa	2
SlituP450-079	SWUSI0088510	CYP6AB60_CLAN3	chr20	65346	67461	-	1548bp; 515aa	2
SlituP450-085	SWUSI0090930	CYP6B38_CLAN3	chr20	7966839	7968997	-	1512bp; 503aa	2
SlituP450-086	SWUSI0090940	CYP6B38_CLAN3	chr20	7979207	7981263	-	1512bp; 503aa	2
SlituP450-087	SWUSI0090950	CYP6B40_CLAN3	chr20	7985680	7987470	-	1515bp; 504aa	2
SlituP450-088	SWUSI0090960	CYP6B41_CLAN3	chr20	7988797	7990961	-	1515bp; 504aa	2
SlituP450-089	SWUSI0090970	CYP6B42_CLAN3	chr20	7993175	7994828	-	1515bp; 504aa	2
SlituP450-123	SWUSI0091720	CYP6B50_CLAN3	chr20	10831837	10833674	-	1509bp; 502aa	2
SlituP450-121	SWUSI0091890	CYP324A18_CLAN3	chr20	11184648	11197038	+	1506bp; 501aa	9
SlituP450-084	SWUSI0091950	CYP365A1_CLAN3	chr20	11947197	11977059	-	1692bp; 563aa	9
SlituP450-056	SWUSI0092180	CYP4S8_CLAN4	chr20	12230820	12260284	+	1488bp; 495aa	9
SlituP450-057	SWUSI0092200	CYP4S9_CLAN4	chr20	12302136	12342897	+	1473bp; 490aa	9
SlituP450-072	SWUSI0092450	CYP6AE9_CLAN3	chr20	13129766	13131169	+	1404bp; 467aa	1
SlituP450-076	none	CYP6AE9_CLAN3	chr20	13131504	13132871	+	1368bp; 455aa	1
SlituP450-073	SWUSI0092460	CYP6AE70_CLAN3	chr20	13133624	13135054	+	1431bp; 476aa	1
SlituP450-074	SWUSI0092470	CYP6AE71_CLAN3	chr20	13135373	13136773	+	1401bp; 466aa	1
SlituP450-075	SWUSI0092470	CYP6AE74_CLAN3	chr20	13137463	13140172	+	1563bp; 520aa	2
SlituP450-091	SWUSI0093710	CYP321A9_CLAN3	chr21	4521907	4523400	+	1467bp; 497aa	1
SlituP450-092	SWUSI0093720	CYP321A7_CLAN3	chr21	4527517	4529004	+	1488bp; 495aa	1
SlituP450-093	SWUSI0093730	CYP321A8_CLAN3	chr21	4533205	4534695	-	1491bp; 496aa	1
SlituP450-094	SWUSI0093740	CYP321A10_CLAN3	chr21	4540858	4542351	-	1494bp; 497aa	1
SlituP450-112	SWUSI0102880	CYP3097A1_CLAN3	chr23	4445416	4447265	+	1506bp; 501aa	2
SlituP450-018	SWUSI0104750	CYP339A1_CLAN-mit	chr23	8667874	8671323	-	1737bp; 578aa	10
SlituP450-027	SWUSI0108250	CYP340AD4_CLAN4	chr24	6729711	6742133	-	1467bp; 488aa	10
SlituP450-021	SWUSI0108260	CYP340A_CLAN4	chr24	6753454	6771096	-	1491bp; 496aa	10
SlituP450-025	SWUSI0108270	CYP340L_CLAN4	chr24	6827175	6844243	+	1458bp; 485aa	10
SlituP450-024	SWUSI0108290	CYP340AB1_CLAN4	chr24	6869565	6896515	+	1518bp; 505aa	10
SlituP450-023	SWUSI0108300	CYP340L_CLAN4	chr24	6909689	6923732	+	1476bp; 491aa	10
SlituP450-019	SWUSI0108320	CYP340L_CLAN4	chr24	6926314	6958006	+	1359bp; 452aa	8
SlituP450-020	SWUSI0108320	CYP340L_CLAN4	chr24	6957960	6965044	+	1362bp; 453aa	9

SlituP450-022	SWUSI0108340	CYP340L_CLAN4	chr24	6967487	6979716	-	1467bp; 488aa	10
SlituP450-026	SWUSI0108350	CYP340A_CLAN4	chr24	6985420	7000238	-	1476bp; 491aa	10
SlituP450-132	SWUSI0108480	CYP340A_CLAN4	chr24	7548610	7557420	-	1455bp; 484aa	10
SlituP450-131	SWUSI0108490	CYP340A_CLAN4	chr24	7577503	7587764	+	1479bp; 492aa	10
SlituP450-130	SWUSI0108500	CYP340A_CLAN4	chr24	7600712	7609820	-	1482bp; 493aa	10
SlituP450-129	SWUSI0108510	CYP340A_CLAN4	chr24	7626259	7651152	+	1494bp; 497aa	11
SlituP450-128	SWUSI0108520	CYP340A_CLAN4	chr24	7662490	7674887	+	1479bp; 492aa	10
SlituP450-127	none	CYP340A_CLAN4	chr24	7687750	7697958	+	1344bp; 447aa	10
SlituP450-058	SWUSI0109350	CYP340Q4_CLAN4	chr24	11189543	11194418	+	1464bp; 487aa	10
SlituP450-134	SWUSI0109370	CYP421B1_CLAN4	chr24	11211764	11215537	+	1500bp; 499aa	10
SlituP450-135	SWUSI0109380	CYP421B1_CLAN4	chr24	11218708	11222739	+	1488bp; 495aa	10
SlituP450-136	SWUSI0109390	CYP421B1_CLAN4	chr24	11223377	11234602	+	1365bp; 454aa	9
SlituP450-133	SWUSI0109450	CYP340K14_CLAN4	chr24	11435269	11444388	+	1482bp; 493aa	10
SlituP450-059	SWUSI0109460	CYP340K14_CLAN4	chr24	11447359	11453976	+	1473bp; 490aa	10
SlituP450-002	SWUSI0118050	CYP333B4_CLAN-mit	chr27	5751944	5759654	+	1530bp; 509aa	10
SlituP450-003	SWUSI0118060	CYP333B3_CLAN-mit	chr27	5761939	5782575	+	1506bp; 501aa	10
SlituP450-049	SWUSI0118070	CYP4L12_CLAN4	chr27	5844985	5863209	-	1479bp; 492aa	
SlituP450-050	SWUSI0118080	CYP4L9_CLAN4	chr27	5865448	5875072	-	1482bp; 493aa	11
SlituP450-051	SWUSI0118090	CYP4L13_CLAN4	chr27	5877371	5882439	-	1482bp; 493aa	11
SlituP450-045	SWUSI0119530	CYP4G75_CLAN4	chr27	8918912	8923759	-	1671bp; 556aa	8
SlituP450-046	SWUSI0119860	CYP4G106_CLAN4	chr27	9745809	9751653	+	1692bp; 563aa	10
SlituP450-047	SWUSI0119870	CYP4G74_CLAN4	chr27	9758567	9765836	+	1692bp; 563aa	10
SlituP450-048	SWUSI0119880	CYP4G109_CLAN4	chr27	9775380	9784972	+	1701bp; 566aa	10
SlituP450-111	SWUSI0124430	CYP15C1_CLAN2	chr28	7425529	7430263	+	1476bp; 491aa	9
SlituP450-080	SWUSI0123210	CYP6AB61_CLAN3	chr28	5114695	5116936	-	1536bp; 511aa	2
SlituP450-110	SWUSI0126430	CYP9G3_CLAN3	chr29	189147	192962	-	1494bp; 497aa	9
SlituP450-109	SWUSI0126440	CYP9G17_CLAN3	chr29	194314	201497	-	1479bp; 492aa	9
SlituP450-107	SWUSI0126650	CYP9A60_CLAN3	chr29	977628	981924	-	1602bp; 533aa	11
SlituP450-106	SWUSI0126650	CYP9A59_CLAN3	chr29	984808	988079	-	1596bp; 531aa	10
SlituP450-105	SWUSI0126650	CYP9A58_CLAN3	chr29	990597	993260	-	1593bp; 530aa	10
SlituP450-104	SWUSI0126670	CYP9A25_CLAN3	chr29	1001666	1004872	-	1590bp; 529aa	10
SlituP450-103	SWUSI0126680	CYP9A26_CLAN3	chr29	1006487	1009321	-	1593bp; 530aa	10
SlituP450-102	SWUSI0126690	CYP9A27_CLAN3	chr29	1012760	1016075	-	1587bp; 523aa	10
SlituP450-101	SWUSI0126700	CYP9A28_CLAN3	chr29	1019125	1023793	-	1596bp; 531aa	10
SlituP450-100	SWUSI0126710	CYP9A29_CLAN3	chr29	1029907	1033402	-	1596bp; 531aa	10
SlituP450-099	SWUSI0126720	CYP9A30_CLAN3	chr29	1037027	1039397	-	1584bp; 527aa	10
SlituP450-098	SWUSI0126720	CYP9A31_CLAN3	chr29	1042088	1045456	-	1566bp; 521aa	10
SlituP450-097	SWUSI0126730	CYP9A91_CLAN3	chr29	1052728	1056968	-	1593bp; 530aa	10

SlituP450-096	SWUSI0126740	CYP9A91_CLAN3	chr29	1061345	1066393	-	1593bp; 530aa	10
SlituP450-095	SWUSI0126760	CYP9A32_CLAN3	chr29	1085539	1091761	+	1593bp; 530aa	10
SlituP450-108	SWUSI0126880	CYP9AJ1_CLAN3	chr29	1649885	1660461	+	1539bp; 512aa	10
SlituP450-038	SWUSI0132920	CYP367B11_CLAN4	chr30	4230516	4241252	-	1503p; 500aa	10
SlituP450-039	SWUSI0132930	CYP367A12_CLAN4	chr30	4257663	4262919	+	1527bp; 508aa	10
SlituP450-040	SWUSI0132940	CYP367A12_CLAN4	chr30	4268932	4270594	-	936bp; 311aa	6
SlituP450-036	SWUSI0132970	CYP367A12_CLAN4	chr30	4299178	4309316	-	1491bp; 496aa	10
SlituP450-037	SWUSI0132980	CYP367A12_CLAN4	chr30	4315223	4333211	-	1488bp; 495aa	10
SlituP450-071	SWUSI0136230	CYP6AE43_CLAN3	chr30	11678685	11680728	+	1578bp; 525aa	2
SlituP450-070	SWUSI0136240	CYP6AE44_CLAN3	chr30	11687560	11692495	-	1581bp; 526aa	2
SlituP450-069	SWUSI0136250	CYP6AE75_CLAN3	chr30	11716571	11720158	+	1578bp; 525aa	2
SlituP450-011	SWUSI0002060	CYP305B1_CLAN2	chrZ	8489672	8507751	-	1464bp; 487aa	8
SlituP450-120	SWUSI0141330	CYP324A16_CLAN3	scaffold541	138098	125498		1518bp; 505aa	9
SlituP450-119	SWUSI0141340	CYP324A16_CLAN3	scaffold541	160555	147584		1503bp; 500aa	9
SlituP450-010	SWUSI0137740	CYP303A1_CLAN2	scaffold228	615277	618250		1506bp;501aa	3
SlituP450-013	SWUSI0138390	CYP314A1_CLAN-mit	scaffold390	40096	58650		1554bp; 517aa	9
SlituP450-016	SWUSI0145310	CYP337B5_CLAN3	scaffold700	66266	68573		1479bp; 492aa	2
SlituP450-034	SWUSI0145930	CYP354A14_CLAN3	scaffold729	10317	1939		1545bp; 514aa	9

Supplementary Table 15 | *S. litura* Carboxylesterase genes (*SlituCOE*)

Gene Name	Gene ID	class	chr #	chromosomal position		Dir	CDS (bp)	aa length	# of Ex
SlituCOE025	SWUSI0006690	lep	1	3431509	3445413	+	1668	556	3
SlituCOE041	SWUSI0006980	jhe	1	4048066	4050992	-	1890	630	3
SlituCOE042	SWUSI0006990	jhe	1	4052721	4055387	-	1749	583	3
SlituCOE043	SWUSI0007000	jhe	1	4059642	4062382	-	1757	585	3
SlituCOE044	SWUSI0007010	lep	1	4063197	4065535	+	1683	561	3
SlituCOE089	SWUSI0010430	lep	1	13136623	13139642	-	1668	556	3
SlituCOE090	SWUSI0010440	lep	1	13146687	13153078	-	1680	560	3
SlituCOE091	SWUSI0010450	lep	1	13169265	13172708	-	1635	545	3
SlituCOE092	SWUSI0010460	lep	1	13185521	13188249	+	1656	552	3
SlituCOE056	SWUSI0015220	lep	2	9526023	9528183	+	1617	539	3
SlituCOE057	SWUSI0015230	lep	2	9530327	9531624	+	811	270	3
SlituCOE058	SWUSI0015240	lep	2	9532315	9534480	+	1770	590	3
SlituCOE059	SWUSI0015240	lep	2	9535873	9538009	+	1734	578	3
SlituCOE060	SWUSI0015250	lep	2	9541992	9544182	+	1707	569	3
SlituCOE061	SWUSI0015260	lep	2	9547060	9549028	+	1710	570	3
SlituCOE062	SWUSI0015270	lep	2	9550437	9553004	+	1659	553	3
SlituCOE063	SWUSI0015280	lep	2	9555094	9563907	+	1659	553	3
SlituCOE064	SWUSI0015290	lep	2	9564857	9566791	-	1643	547	4
SlituCOE065	SWUSI0015300	lep	2	9574372	9576470	+	1644	548	3
SlituCOE066	SWUSI0015310	lep	2	9577806	9580153	+	1674	558	3
SlituCOE067	SWUSI0015320	lep	2	9582334	9584403	-	1677	559	3
SlituCOE045	SWUSI0016230	lep	2	11087868	11090292	+	1695	565	3
SlituCOE046	SWUSI0016240	lep	2	11092071	11096369	-	1647	549	3
SlituCOE047	SWUSI0016250	lep	2	11097937	11100292	-	1662	554	3
SlituCOE048	SWUSI0016260	lep	2	11105430	11107193	-	1462	487	2
SlituCOE049	SWUSI0016270	lep	2	11108348	11112031	-	1671	557	3
SlituCOE050	SWUSI0016280	lep	2	11112392	11115630	-	1680	560	3
SlituCOE051	SWUSI0016290	lep	2	11117462	11120910	-	1680	560	3
SlituCOE052	SWUSI0016300	lep	2	11122861	11125096	-	1689	563	3
SlituCOE053	SWUSI0016310	lep	2	11135167	11137447	-	1668	556	3
SlituCOE054	SWUSI0016320	lep	2	11139877	11142089	-	1674	558	3
SlituCOE055	SWUSI0016330	lep	2	11146784	11149542	+	1749	583	3
SlituCOE002	SWUSI0016510	ace	2	11840415	11845779	-	2082	694	3
SlituCOE108	SWUSI0017210	Nlg	2	14334490	14373406	-	4416	1472	12
SlituCOE106	SWUSI0017130	Nlg	2	13439428	13493855	-	2681	893	10

SlituCOE107	SWUSI0017190	Nlg	2	13955735	13976615	+	2987	995	10
SlituCOE104	SWUSI0017300	Nlg	2	14714083	14762650	+	2701	900	11
SlituCOE029	SWUSI0018610	lep	3	3424175	3427781	+	1620	540	3
SlituCOE022	SWUSI0019220	lep	3	5190914	5196732	+	1539	513	3
SlituCOE074	SWUSI0022080	ie	5	11749	16593	-	1750	583	11
SlituCOE024	SWUSI0025790	beta	6	1369375	1402304	-	1664	554	10
SlituCOE072	SWUSI0039380	alpha	9	683478	685688	-	1623	541	3
SlituCOE026	SWUSI0044710	lep	9	14662946	14665397	+	1632	544	3
SlituCOE027	SWUSI0044720	lep	9	14665823	14667905	+	1638	546	3
SlituCOE028	SWUSI0044720	lep	9	14670001	14672410	+	1617	539	3
SlituCOE004	SWUSI0050210	alpha	11	7992047	8014610	-	1928	642	10
SlituCOE097	SWUSI0051410	lep	11	10693398	10696439	-	1674	558	3
SlituCOE014	SWUSI0052130	lep	11	12774359	12776889	+	1647	549	3
SlituCOE015	SWUSI0052140	lep	11	12777143	12780683	+	1647	549	3
SlituCOE016	SWUSI0052150	lep	11	12781168	12783443	+	1599	533	3
SlituCOE017	SWUSI0052160	lep	11	12784203	12786571	+	1641	547	3
SlituCOE018	SWUSI0052170	lep	11	12787450	12789443	+	1647	549	3
SlituCOE019	SWUSI0052180	lep	11	12789798	12792361	+	1626	542	3
SlituCOE006	SWUSI0052260	lep	11	13040940	13044631	-	1694	564	4
SlituCOE007	SWUSI0052270	lep	11	13045152	13048920	-	2034	678	3
SlituCOE075	SWUSI0052280	jhe	11	13051821	13054238	-	2069	689	7
SlituCOE076	SWUSI0052290	jhe	11	13060594	13063949	-	1721	573	7
SlituCOE077	SWUSI0052300	jhe	11	13070122	13074048	-	1722	574	7
SlituCOE078	SWUSI0052310	lep	11	13076612	13080945	-	1507	502	5
SlituCOE079	SWUSI0052320	jhe	11	13082537	13088595	-	1698	566	6
SlituCOE030	SWUSI0052680	alpha	12	850953	853003	-	1620	540	3
SlituCOE093	SWUSI0055220	lep	12	7128303	7131386	-	1560	520	3
SlituCOE094	SWUSI0055220	lep	12	7135496	7142529	-	1575	525	3
SlituCOE105	SWUSI0066080	Nlg	15	990941	1003923	-	2136	712	12
SlituCOE109	SWUSI0066490	lep	15	2565349	2568123	-	1635	545	3
SlituCOE103	SWUSI0068140	Nlg	15	6626219	6646035	-	2750	916	13
SlituCOE005	SWUSI0072580	lep	16	3995113	3999262	-	1890	630	3
SlituCOE101	SWUSI0075240	lep	16	10243029	10245819	+	1710	570	3
SlituCOE102	SWUSI0075250	lep	16	10246646	10250008	+	1641	547	3
SlituCOE001	SWUSI0076190	un	16	11853965	11857408	-	861	287	3
SlituCOE099	SWUSI0084700	alpha	18	7316847	7319505	+	1659	553	3
SlituCOE038	SWUSI0087010	alpha	19	2511980	2516763	+	1790	596	4
SlituCOE039	SWUSI0087020	alpha	19	2529060	2532067	-	1578	526	3

SlituCOE003	SWUSI0093870	gli	21	4956778	4994478	+	1911	637	6
SlituCOE100	SWUSI0094060	alpha	21	5425961	5428689	-	1659	553	3
SlituCOE098	SWUSI0098320	un	22	3371441	3377289	+	2030	676	11
SlituCOE096	SWUSI0110110	alpha	25	796279	805680	+	1566	522	4
SlituCOE032	SWUSI0110180	alpha	25	1014529	1016692	+	1646	548	4
SlituCOE033	SWUSI0110190	alpha	25	1020902	1024237	+	1673	557	4
SlituCOE034	SWUSI0110200	alpha	25	1026542	1028397	+	1194	398	6
SlituCOE035	SWUSI0110210	alpha	25	1033511	1036431	+	1667	555	4
SlituCOE036	SWUSI0110220	alpha	25	1043130	1045492	+	1614	538	3
SlituCOE037	SWUSI0110230	alpha	25	1053763	1055972	+	1614	538	3
SlituCOE031	SWUSI0110120	alpha	25	831698	835010	-	1637	545	4
SlituCOE080	SWUSI0110740	alpha	25	2858123	2860522	+	1623	541	3
SlituCOE081	SWUSI0110750	alpha	25	2862984	2866281	+	1611	537	3
SlituCOE082	SWUSI0110760	alpha	25	2867509	2872142	+	1608	536	3
SlituCOE083	SWUSI0110770	alpha	25	2873619	2876703	+	1611	537	3
SlituCOE023	SWUSI0117900	alpha	27	5066562	5069977	-	1578	526	3
SlituCOE040	SWUSI0117310	alpha	27	3775740	3779424	+	1928	642	4
SlituCOE010	SWUSI0123340	alpha	28	5441756	5443974	-	1602	534	3
SlituCOE009	SWUSI0123350	alpha	28	5445101	5447382	-	1596	532	3
SlituCOE008	SWUSI0123360	alpha	28	5451275	5453833	+	1596	532	3
SlituCOE011	SWUSI0135610	lep	30	10621709	10623852	+	1629	543	3
SlituCOE095	SWUSI0003240	beta	Z	11627821	11635663	+	1543	514	9
SlituCOE084	SWUSI0145150	lep	scaffold687	46446	49012	+	1812	604	4
SlituCOE085	SWUSI0145160	lep	scaffold687	49730	53341	+	1593	531	3
SlituCOE086	SWUSI0145170	lep	scaffold687	55479	58019	+	1617	539	3
SlituCOE087	SWUSI0145180	lep	scaffold687	68307	71045	-	1260	420	3
SlituCOE110	none	jhe	scaffold687	71320	72508	-	519	173	2
SlituCOE088	SWUSI0145080	alpha	scaffold688	584	3090	+	1584	528	3
SlituCOE020	SWUSI0146110	alpha	scaffold688	44418	48149	+	1745	581	4
SlituCOE021	SWUSI0146120	alpha	scaffold725	50962	53462	+	1547	515	4
SlituCOE012	none	ie	5	1240471	1242133	-	712	237	5
SlituCOE013	none	un	17	8513537	8538736	+	1845	615	3
SlituCOE068	none	ace	16	8280680	8293502	-	2651	883	16
SlituCOE069	none	Nlg	16	14083668	14108364	+	2613	871	15
SlituCOE112	none	ie1	2	13179317	13197253	+	1571	523	4
SlituCOE111	none	ie1	5	255	4801	+	1249	416	8
SlituCOE073	none	ie1	5	6531	8329	-	1672	557	11

Supplementary Table 16 | *S. litura* Glutathione-S-transferase genes (*SlituGST*)

Gene Name	Gene ID	class	chr #	chromosomal position		Dir	CDS (bp)	aa length	# of Ex
SlituGST25	SWUSI0005600	e	1	531597	532591	+	665	221	4
SlituGST09	SWUSI0006580	d	1	3187156	3188483	+	642	214	3
SlituGST14	SWUSI0010470	e	1	13317695	13318348	-	653	217	1
SlituGST15	SWUSI0010470	e	1	13318943	13319596	-	653	217	1
SlituGST37	SWUSI0012570	z	2	5057096	5070191	+	634	211	5
SlituGST11	SWUSI0038400	e	8	10321805	10326229	+	652	217	5
SlituGST12	SWUSI0038410	e	8	10332682	10335687	+	652	217	5
SlituGST13	SWUSI0038420	e	8	10339038	10345951	+	709	236	5
SlituGST17	SWUSI0040700	e	9	4678314	4680061	+	649	216	5
SlituGST18	SWUSI0040710	e	9	4682852	4685215	+	629	209	6
SlituGST19	SWUSI0040710	e	9	4687068	4690177	+	649	216	5
SlituGST22	SWUSI0040720	e	9	4693109	4695473	+	646	215	5
SlituGST23	SWUSI0040720	e	9	4698433	4700600	+	652	217	5
SlituGST16	SWUSI0040730	e	9	4705097	4709145	+	649	216	5
SlituGST20	SWUSI0040740	e	9	4712090	4713430	-	646	215	5
SlituGST21	SWUSI0040750	e	9	4718079	4719368	+	646	215	5
SlituGST36	SWUSI0048160	z	11	2620364	2622396	+	658	219	5
SlituGST29	SWUSI0057590	o	13	2698649	2707656	+	717	239	6
SlituGST06	SWUSI0064750	e	14	13215716	13218910	-	667	222	5
SlituGST05	SWUSI0064760	e	14	13222147	13227227	-	655	218	5
SlituGST08	SWUSI0064770	e	14	13235917	13238164	-	542	180	4
SlituGST07	SWUSI0064780	e	14	13239382	13242758	-	686	228	5
SlituGST30	SWUSI0078740	s	17	2536734	2545249	-	611	203	4
SlituGST31	SWUSI0078730	s	17	2530159	2532138	-	1227	409	4
SlituGST32	none	s	17	2515936	2517807	-	602	200	4
SlituGST33	SWUSI0078720	s	17	2523854	2526883	-	611	203	4
SlituGST24	SWUSI0091750	e	20	10892830	10895547	-	682	227	5
SlituGST35	SWUSI0098350	u	22	3398505	3402981	-	694	231	5
SlituGST02	SWUSI0099820	d	22	7949952	7958370	+	717	239	6
SlituGST03	SWUSI0101090	d	22	13129548	13134349	+	647	215	4
SlituGST04	SWUSI0101100	d	22	13134906	13136696	-	662	220	4
SlituGST10	SWUSI0108040	e	24	6049086	6049727	+	641	213	1
SlituGST27	SWUSI0123690	o	28	6331290	6334540	-	760	253	5
SlituGST28	SWUSI0123700	o	28	6337383	6341652	+	844	281	5
SlituGST26	SWUSI0003500	d	Z	12197860	12213249	-	1131	377	6

SlituGST34	SWUSI0141850	t	scaffold559	98272	101011	–	697	232	5
SlituGST38	SWUSI0005590	u	1	528405	529792	–	574	191	5
SlituGST39	SWUSI0146240	u	scaffold741	53426	55684	+	883	294	5
SlituGST40	SWUSI0100390	s	22	10760851	10765334	+	635	211	4
SlituGST42	SWUSI0100380	s	22	10756109	10758369	–	617	205	4
SlituGST43	SWUSI0100400	s	22	10769417	10771779	+	614	204	4
SlituGST44	SWUSI0081630	u	17	10806298	10808773	+	2278	759	2
SlituGST45	SWUSI0014150	micro	2	8251764	8252219	+	455	151	1
SlituGST46	SWUSI0014170	micro	2	8257757	8258209	+	452	150	1
SlituGST47	SWUSI0014160	micro	2	8254918	8255370	+	452	150	1
SlituGST48	none	micro	25	3646740	3647144	–	404	134	1
SlituGST49	SWUSI0110960	micro	25	3650664	3651011	–	347	115	1

Supplementary Table 17 | *S. litura* Aminopeptidase N genes (*SlituAPN*)

Gene Name	Gene ID	chr #	chromosomal position		Dir	CDS (bp)	aa length	# of Ex
SlituAPN01	SWUSI0031540	7	5334227	5345802	+	2740	913	17
SlituAPN14	SWUSI0092900	21	1675216	1689516	–	3142	1047	14
SlituAPN15	SWUSI0092910	21	1728508	1746114	+	2805	935	14
SlituAPN07	SWUSI0092950	21	1954757	1964031	+	2910	970	15
SlituAPN08	SWUSI0092960	21	1969857	1977237	+	2923	974	14
SlituAPN09	SWUSI0092970	21	1986268	1999543	+	3075	1025	14
SlituAPN10	SWUSI0078570	21	2005366	2015004	+	4197	1399	14
SlituAPN06	SWUSI0092990	21	2016419	2038041	–	2540	846	13
SlituAPN05	SWUSI0092990	21	2042710	2058390	–	2797	932	14
SlituAPN03	SWUSI0093000	21	2063629	2078901	–	3002	1000	16
SlituAPN02	SWUSI0093010	21	2083602	2095883	–	2845	948	15
SlituAPN04	SWUSI0093020	21	2100658	2111418	–	2874	958	15
SlituAPN18	SWUSI0106440	24	469566	488982	–	2904	968	19
SlituAPN17	SWUSI0123980	28	6949504	6955952	+	2781	927	12
SlituAPN13	SWUSI0143290	scaffold604	115000	120720	+	1141	380	6
SlituAPN11	SWUSI0143270	scaffold604	56403	82162	+	2963	987	13
SlituAPN12	SWUSI0143280	scaffold604	91883	105964	+	3022	1007	14
SlituAPN16	SWUSI0148040	scaffold867	6258	22066	–	4213	1404	15

Supplementary Table 18 | *S. litura* ABC transporter genes (*SIABC*)

Gene ID	Auto-annotated gene ID	Chr location	Dir	CDS (bp); aa length
SIABCB3-1	SWUSI0003640	Z:12448398-12464154	+	3918bp; 1305aa
SIABCB3-2	SWUSI0003650	Z:12469934-12483547	+	3918bp; 1305aa
SIABCF2	SWUSI0001200	Z:4885568-4901126	-	1863bp; 620aa
SIABCC9	SWUSI0062100	14:7163497-7176343	-	4968bp; 1655aa
SIABCF3	SWUSI0147730	scaffold834:9449-19598	-	2118bp; 705aa
SIABCG-st	SWUSI0060830	14:2985622-3023847	-	1983bp; 660aa
SIABCG-w	SWUSI0060840	14:3042002-3068679	-	2064bp; 687aa
SIABCG1-1	SWUSI0123270	28:5246629-5309443	-	1887bp; 628aa
SIABCC10	SWUSI0033370	7:9926005-9938353	-	4428bp; 1475aa
SIABCC1-1	SWUSI0145100	scaffold688:8390-25784	+	4545bp; 1514aa
SIABCC1-2*	SWUSI0145110	scaffold688:30142-64632	+	4551bp; 1516aa
SIABCG4-3	SWUSI0030660	7:2681947-2717360	+	1953bp; 650aa
SIABCG4-4	SWUSI0030650	7:2630888-2674409	-	1881bp; 626aa
SIABCG1-3	SWUSI0031020	7:3311789-3332668	+	1911bp; 636aa
SIABCG4-2	SWUSI0030980	7:3195081-3245963	+	2064bp; 687aa
SIABCG1-5	SWUSI0033940	7:11802461-11881771	+	2001bp; 666aa
SIABCG1-6	SWUSI0032770	7:8516185-8553151	+	1902bp; 633aa
SIABCG1-4*	SWUSI0031750	7:8560390-8560507 + 7:5812728-5849250	+	1863bp; 620aa
SIABCG1-2	SWUSI0031760	7:5854082-5869512	+	1821bp; 606aa
SIABCA1	SWUSI0086020*	18:11553111-11593207	+	12177bp; 4058aa
SIABCB2	SWUSI0084160*	18:5076003-5098671	-	3999bp; 1332aa
SIABCB1-1	SWUSI0013860	2:7728285-7750322	-	3903bp; 1300aa
SIABCB1-2*	SWUSI0026910 + SWUSI0026920	6:3881307-3893786	-	3540bp; 1179aa
SIABCC4-3	SWUSI0015840*	2:10535858-10549860	+	3936bp; 1311aa
SIABCF1	SWUSI0140110	scaffold490:35514-46252	+	2763bp; 920aa
SIABCC3	SWUSI0013240	2:6674276-6698477	-	4080bp; 1359aa
SIABCC2	SWUSI0013230	2:6659432-6671454	+	4035bp; 1344aa
SIABCC4-1	SWUSI0013210*	2:6591164-6632146	-	4185bp; 1394aa
SIABCC4-2	SWUSI0014290	2:8396054-8421914	+	4086bp; 1361aa
SIABCC4-6	SWUSI0123710	28:6344649-6358523	-	4113bp; 1370aa
SIABCC4-4	SWUSI0013920	2:7858761-7897496	+	4236bp; 1411aa
SIABCA5	SWUSI0134070	30:7245882-7304704	-	5559bp; 1852aa
SIABCA3-2	SWUSI0141140	scaffold529:50935-71603	-	5097bp; 1698aa
SIABCA3-3	SWUSI0141130	scaffold529:34387-46567	+	5238bp; 1745aa
SIABCB10	SWUSI0104570	23:8225298-8239559	-	2121bp; 706aa
SIABCB8	SWUSI0010010	1:11667258-11680946	-	2097bp; 698aa

SIABCA3-1*	SWUSI0050300 + SWUSI0148730	11:8092402-8114091 + scaffold951:1118-13873	+	4026bp; 1342<aa
SIABCA3-4*	SWUSI0009900	1:10905780-10943311	+	4428bp; 1475aa
SIABCD3	SWUSI0043710	9:11288691-11309542	-	2004bp; 667aa
SIABCG5	SWUSI0043830	9:11560428-11572877	-	1926bp; 641aa
SIABCB7	SWUSI0044350	9:13395559-13405196	-	2274bp; 757aa
SIABCG8	SWUSI0043840	9:11620816-11627884	+	2742bp; 913aa
SIABCB3-3*	SWUSI0086400	19:23466-75213	-	3951bp; 1316aa
SIABCC4-5	SWUSI0086980	19:2373770-2412843	-	4275bp; 1424aa
SIABCG4-1*	SWUSI0030300	7:1066455-1066609(+) + 7:1004105-1010247(-)	-	2235bp; 744aa
SIABCH1	SWUSI0107250	24:3177498-3212587	-	2373bp; 790aa
SIABCH2	SWUSI0107270	24:3346433-3378462	+	2163bp; 720aa
SIABCH3	SWUSI0106480	24:556552-635431	-	2298bp; 765aa
SIABCD2	SWUSI0021440	4:8727684-8741691	+	2298bp; 765aa
SIABCA2*	SWUSI0071790 + SWUSI0071810	16:2078027-2119477	-	5022bp; 1673aa
SIABCG-ok*	SWUSI0072390	16:2995545-3014065	+	1932bp; 643aa
SIABCG-bw	SWUSI0072400	16:3016956-3042808	-	1779bp; 592aa
SIABCE1*	SWUSI0037280 + SWUSI0037290	8:6452510-6460379	-	1827bp; 608aa
SIABCB6	SWUSI0027500*	6:4808959-4826060	-	2541bp; 846aa

*Predicted gene sequences were manually modified.

Supplementary Table 19 | RT-PCR primers for *SlituGSTs*, *P450s* and *COEs*

Name	Primer	Sequence (5'-3')	Product (bp)
SlituGST-07	F	TAGTGGACCAGTGCATGTTCTTC	118
	R	ATTCCTGTATGTGTTGGGCTGT	
SlituGST-20	F	CCAAGTCCCTGTTATGGAAGATG	93
	R	GAGTCATCCTTTCCGTAGGTGTC	
SlituP450-74	F	CTCACTCCAAGCCCACATTCT	150
	R	GTATAAGTACAGGTTCCGTGCCA	
SlituP450-88	F	GCTGGACTTCAGTAACCGAGG	180
	R	ACTTGGCATTTCAGTGCTAACATA	
SlituP450-92	F	TTTtaggcagtcacccagatg	152
	R	TGGAGGGAATACTCTCATTGCTT	
SlituP450-98	F	TACCCTTTATGATAGAGGTCGGAG	133
	R	GAGGCAATCACATCGTTAGCATA	
SlituCOE-57	F	CTCCATCTACGAGGAACACTACC	117
	R	AACATGCCAATGGTAACTACAAT	
SlituCOE-58	F	ATGCCATACTAAATAATGAAGGGG	177
	R	CACTCAATCTCACTGAACCATCC	

Supplementary Table 20 | siRNA primers for *SlituGSTs*, *P450s* and *COEs*

Name	Primer	siRNA sequence (5'-3')
SlituGST-07	F1	GCCACGCCATAATGAAGTATT
	R1	UACUUCAUUAUGGCGUGGCTT
SlituGST-07	F2	CACATACAGGAAATAGAGATT
	R2	UCUCUAUUUCCUGUAUGUGTT
SlituGST-20	F1	CGUGCGCUUGUUAACCAAATT
	R1	UUUGGUUAACAAGCGCACGTT
SlituGST-20	F2	GACAUUGGCCUGGUUAGAATT
	R2	UUCUAACCAGGCCAAUGUCTT
SlituP450-74	F1	GGAUCCAGAAAUAUUAAATT
	R1	UUUAAUUAUUUCUGGAUCCTT
Slitu P450-74	F2	GACACGAUUUCGUAGAUCUTT
	R2	AGAUCUACGAAAUCGUGUCTT
SlituP450-88	F1	CAUACGAGUCUAUUAAGGATT
	R1	UCCUUAUUAGACUCGUAUGTT
Slitu P450-88	F2	GGACUUCGAUGCUUUCACUTT
	R2	AGUGAAAGCAUCGAAGUCCTT
SlituP450-92	F1	CUCUUAUGAUGUUCUGUAATT
	R1	UUACAGAACAUCAUAAGAGTT
Slitu P450-92	F2	CUCCGACACUGUUUGUCAUTT
	R2	AUGACAAACAGUGUCGGAGTT
SlituP450-98	F1	GGAUGGCUCCGUAGACUUATT
	R1	UAAGUCUACGGAGCCAUCCTT
Slitu P450-98	F2	CAGAGAGUUGAAGAAUAUUTT
	R2	AAUAUUCUUAACUCUCUGTT
SlituCOE-57	F1	GAAAUUCUCAGACUUCUUATT
	R1	UAAGAAGUCUGAGAAUUUCTT
SlituCOE-57	F2	CCGAUGCACGAUUUCCAUUTT
	R2	AAUGGAAAUCGUGCAUCGGTT
SlituCOE-58	F1	CUGGAGCUGACAGAUUAUATT
	R1	UUUAUAUCUGUCAGCUCCAGTT
SlituCOE-58	F2	GCUGAAGAUCGCAAGAUUATT
	R2	UAAUCUUGCGAUCUUCAGCTT
GFP	F	AUAGACGUUGUGGCUGUUGUA
	R	CAACAGCCACAACGUCUAUUU

Supplementary Table 21 | SNP calling statistics of *S. litura* samples

strains	raw reads (PE)	clean reads (PE)	duplicated reads	mapped reads	mapped rated	proper mapped reads	proper mapped rate	snp number	sequencing depth	mapped depth
Fujian-1	49,976,530	42,306,047	0	490,655	0.01	318,862	0.01	116,612	20.15	0.15
Fujian-2	51,437,693	45,606,736	0	517,373	0.01	342,009	0.01	130,098	21.72	0.16
Fujian-3	49,948,303	44,107,681	0	35,436,430	0.80	32,327,026	0.73	8,124,993	21.00	15.39
Fujian-4	56,326,502	46,466,958	0	535,580	0.01	348,517	0.01	130,863	22.13	0.17
Guangxi-1	35,750,378	32,036,579	0	25,723,709	0.80	23,132,531	0.72	7,234,759	15.26	11.02
Guangxi-2	48,723,692	42,947,177	0	33,926,158	0.79	30,922,626	0.72	8,124,265	20.45	14.73
Guangxi-3	62,134,773	47,002,718	0	36,975,608	0.79	33,685,761	0.72	8,140,494	22.38	16.04
Guangxi-4	55,131,064	42,079,721	0	32,586,493	0.77	28,870,445	0.69	7,778,236	20.04	13.75
Guangzhou1-1	47,386,490	42,216,265	0	34,248,270	0.81	31,561,816	0.75	8,131,573	20.10	15.03
Guangzhou1-2	47,381,820	40,157,888	0	32,436,370	0.81	29,420,791	0.73	7,956,124	19.12	14.01
Guangzhou1-3	45,033,758	39,008,158	0	31,502,649	0.81	28,628,638	0.73	7,851,254	18.58	13.63
Guangzhou1-4	57,568,725	40,067,496	0	31,293,992	0.78	26,690,066	0.67	7,304,105	19.08	12.71
Hainan-1	51,056,695	45,376,894	0	36,760,076	0.81	33,858,898	0.75	7,491,604	21.61	16.12
Hainan-2	54,047,603	47,904,337	0	39,094,511	0.82	36,075,498	0.75	7,552,831	22.81	17.18
Hainan-3	46,008,347	40,307,969	0	32,355,487	0.80	29,700,856	0.74	7,744,977	19.19	14.14
Hainan-4	50,603,807	46,002,285	0	36,598,359	0.80	33,433,698	0.73	7,993,360	21.91	15.92
Hubei-1	49,345,780	45,220,663	0	36,826,994	0.81	33,620,501	0.74	8,287,003	21.53	16.01
Hubei-2	54,087,204	49,506,361	0	39,501,848	0.80	36,470,734	0.74	8,362,355	23.57	17.37
Hubei-3	52,698,155	48,320,917	0	39,322,915	0.81	36,265,071	0.75	8,459,224	23.01	17.27
Hubei-4	47,512,918	44,390,732	0	36,152,586	0.81	32,843,142	0.74	8,241,445	21.14	15.64
Hunan1-1	81,700,483	72,218,263	0	62,745,560	0.87	59,757,501	0.83	3,891,026	34.39	28.46
Hunan1-2	60,686,520	53,677,051	0	46,795,734	0.87	44,421,858	0.83	3,712,569	25.56	21.15
Hunan1-3	64,703,715	54,961,001	0	47,675,134	0.87	44,211,495	0.80	3,753,051	26.17	21.05

Hunan2-1	50,470,982	44,611,111	0	35,640,396	0.80	32,101,416	0.72	8,322,765	21.24	15.29
Hunan2-2	52,404,186	46,163,099	0	36,510,372	0.79	32,745,225	0.71	8,341,661	21.98	15.59
Hunan2-3	43,402,282	38,977,494	0	30,374,820	0.78	27,299,048	0.70	7,794,440	18.56	13.00
Hunan2-4	55,912,648	47,414,470	0	30,705,799	0.65	27,931,073	0.59	7,880,633	22.58	13.30
Hunan3-1	48,990,487	41,192,802	0	33,590,574	0.82	30,291,627	0.74	8,044,493	19.62	14.42
Hunan3-2	50,229,123	44,862,146	0	36,297,763	0.81	33,108,909	0.74	8,312,814	21.36	15.77
Hunan3-3	50,716,451	44,306,245	0	34,772,829	0.78	31,237,038	0.71	8,137,196	21.10	14.87
Hunan3-4	53,245,925	45,271,935	0	35,359,429	0.78	32,089,594	0.71	8,125,632	21.56	15.28
Delhi-D2	45,470,129	39,185,015	0	31,064,654	0.79	28,277,730	0.72	6,362,407	18.66	13.47
Delhi-D3	50,612,852	45,357,166	0	36,054,545	0.79	33,011,849	0.73	6,572,110	21.60	15.72
Delhi-D4	45,986,924	41,410,120	0	30,760,537	0.74	28,330,630	0.68	6,258,570	19.72	13.49
Delhi-D5	51,582,952	47,472,715	0	37,817,715	0.80	34,802,556	0.73	6,896,841	22.61	16.57
Hyderabad-A4	46,884,810	39,238,965	0	32,127,550	0.82	29,216,363	0.74	7,519,482	18.69	13.91
Hyderabad-A6	47,091,801	42,418,756	0	34,503,418	0.81	31,656,569	0.75	8,032,265	20.20	15.07
Hyderabad-B1	55,832,656	47,981,022	0	39,281,217	0.82	36,156,785	0.75	8,202,457	22.85	17.22
Hyderabad-B2	46,099,846	40,007,539	0	32,626,711	0.82	29,915,620	0.75	7,722,991	19.05	14.25
Matsyapuri-10	57,342,652	52,727,420	0	42,125,065	0.80	38,465,011	0.73	8,510,713	25.11	18.32
Matsyapuri-3	50,118,978	45,345,602	0	36,159,791	0.80	33,048,725	0.73	8,247,509	21.59	15.74
Matsyapuri-5	52,786,173	47,604,291	0	37,341,849	0.78	34,213,035	0.72	8,277,465	22.67	16.29
Matsyapuri-9	36,295,165	32,835,667	0	25,812,178	0.79	22,565,857	0.69	7,029,474	15.64	10.75
Okinawa-1	51,654,458	46,222,609	0	38,734,303	0.84	35,898,735	0.78	7,825,348	22.01	17.09
Okinawa -2	47,838,019	42,336,323	0	31,380,499	0.74	28,892,016	0.68	7,428,300	20.16	13.76
Okinawa -3	49,965,394	44,612,911	0	31,348,557	0.70	28,999,815	0.65	7,164,361	21.24	13.81
Okinawa -4	48,707,090	43,735,977	0	36,564,393	0.84	33,864,080	0.77	7,713,099	20.83	16.13
Taukuba-1	48,263,663	44,420,687	0	36,125,059	0.81	33,058,064	0.74	8,101,444	21.15	15.74
Taukuba -2	52,254,680	47,779,350	0	38,849,898	0.81	35,638,552	0.75	8,331,715	22.75	16.97

Taukuba -3	52,937,991	48,787,767	0	39,695,769	0.81	36,563,660	0.75	8,200,433	23.23	17.41
Taukuba -4	47,096,266	43,512,206	0	35,471,372	0.82	32,595,059	0.75	8,009,079	20.72	15.52
Guangzhou2-1	50,846,850	44,192,423	0	38,202,920	0.86	36,116,233	0.82	3,839,755	21.04	17.20
Guangzhou2-3	51,563,295	42,930,224	0	36,276,947	0.85	34,010,428	0.79	3,786,539	20.44	16.20
Guangzhou2-4	53,090,372	43,010,360	0	30,423,631	0.71	28,937,163	0.67	3,459,342	20.48	13.78
Guangzhou2-6	47,565,655	39,574,037	0	34,192,979	0.86	32,200,676	0.81	3,701,912	18.84	15.33
Shanxi-1	51,400,340	45,301,995	0	551,395	0.01	337,786	0.01	111,125	21.57	0.16
Shanxi-2	50,321,398	43,381,251	0	525,796	0.01	322,528	0.01	100,042	20.66	0.15
Shanxi-3	50,520,937	44,561,566	0	555,056	0.01	348,610	0.01	110,525	21.22	0.17
Shanxi-4	46,829,572	40,656,569	0	484,623	0.01	292,545	0.01	85,946	19.36	0.14
Zhejiang-1	46,159,946	33,699,742	0	26,655,266	0.79	23,213,443	0.69	6,995,633	16.05	11.05
Zhejiang-2	43,664,509	32,686,893	0	26,158,959	0.80	23,418,477	0.72	7,079,637	15.57	11.15
Zhejiang-3	54,964,512	39,792,819	0	31,446,445	0.79	27,678,321	0.70	7,652,171	18.95	13.18
Zhejiang-4	52,198,930	36,667,317	0	28,488,732	0.78	24,353,271	0.66	7,086,138	17.46	11.60

The proper mapped rate was about 70% percent except for three individuals of the Fujian sample and the four individuals of Shangxhi sample (shaded). These seven individuals were excluded from the population genomic analysis.

Supplementary Table 22 | Genomic nucleotide diversities π of the individuals of each sampling location.

	pi	se
Fujian	0.01489	0.00044
Guangxi	0.01308	0.00019
Guangzhou1	0.01512	0.00021
Hainan	0.01351	0.00021
Hubei	0.01309	0.00020
Hunan1	0.00180	0.00003
Hunan2	0.01433	0.00022
Hunan3	0.01294	0.00021
Delhi	0.00857	0.00013
Hyderabad	0.01616	0.00026
Matsyapuri	0.01566	0.00023
Okinawa	0.01604	0.00026
Tsukuba	0.01621	0.00025
Guangzhou2	0.00194	0.00003

Supplementary Table 23 | Pairwise F_{ST} values among the localities

	Fujian	Guangxi	Guangzhou1	Hainan	Hubei	Hunan1	Hunan2	Hunan3	Delhi	Hyderabad	Matsyapuri	Okinawa	Tsukuba	Guangzhou2	Zhejiang
Fujian		0.2352	0.0789	0.1447	0.2316	0.8142	0.1438	0.2444	0.4281	0.0063	0.0480	0.0084	0.0075	0.8120	0.0914
Guangxi	0.0125		0.1580	0.2085	0.2399	0.5520	0.1927	0.2445	0.3638	0.1212	0.1435	0.1203	0.1237	0.5760	0.1619
Guangzhou1	0.0125	0.0051		0.1290	0.1613	0.4693	0.1134	0.1666	0.2866	0.0413	0.0643	0.0402	0.0443	0.5001	0.0812
Hainan	0.0124	0.0075	0.0059		0.2112	0.5184	0.1648	0.2163	0.3362	0.0926	0.1151	0.0921	0.0959	0.5476	0.1333
Hubei	0.0107	0.0070	0.0086	0.0067		0.5524	0.1965	0.2480	0.3665	0.1251	0.1468	0.1245	0.1281	0.5769	0.1659
Hunan1	0.0129	0.0138	0.0106	0.0085	0.0123		0.5039	0.5580	0.6882	0.4304	0.4520	0.4309	0.4310	0.6539	0.4737
Hunan2	0.0122	0.0047	0.0063	0.0047	0.0070	0.0081		0.2006	0.3200	0.0766	0.0988	0.0762	0.0797	0.5321	0.1173
Hunan3	0.0121	0.0077	0.0062	0.0072	0.0070	0.0105	0.0039		0.3710	0.1288	0.1516	0.1292	0.1324	0.5818	0.1704
Delhi	0.0125	0.0082	0.0166	0.0106	0.0107	0.0120	0.0064	0.0064		0.2467	0.2689	0.2494	0.2532	0.7036	0.2914
Hyderabad	0.0108	0.0067	0.0051	0.0056	0.0062	0.0073	0.0049	0.0069	0.0062		0.0242	0.0021	0.0082	0.4641	0.0445
Matsyapuri	0.0103	0.0048	0.0050	0.0051	0.0112	0.0088	0.0046	0.0080	0.0098	0.0038		0.0252	0.0309	0.4843	0.0674
Okinawa	0.0113	0.0063	0.0034	0.0079	0.0070	0.0135	0.0044	0.0187	0.0064	0.0044	0.0041		0.0054	0.4644	0.0435
Tsukuba	0.0107	0.0053	0.0044	0.0053	0.0038	0.0076	0.0045	0.0042	0.0122	0.0051	0.0038	0.0064		0.4649	0.0480
Guangzhou2	0.0101	0.0094	0.0084	0.0123	0.0093	0.0064	0.0101	0.0081	0.0080	0.0095	0.0089	0.0106	0.0087		0.5043
Zhejiang	0.0118	0.0090	0.0048	0.0062	0.0079	0.0125	0.0076	0.0074	0.0083	0.0052	0.0043	0.0033	0.0051	0.0093	

The upper-right figures above the diagonal are F_{ST} values and the lower-left figures below the diagonal are standard errors.

Supplementary Table 24| The estimated population histories based on the analysis of two dimensional allele frequency spectra. The size of a population (N) represents the number of chromosomes. The migration rate (M) is the number of migrating chromosomes per generation. The time of the population split is the number of years before present. The figures after $\pm$ are the standard errors obtained by parametric bootstrap (see Method).

population 1 population 2	China_local China_migrate	China_migrate India_migrate	China_migrate Japan_migrate	India_migrate Japan_migrate	China_local India_migrate	China_local Japan_migrate	India_local India_migrate
N_{anc}	1.38×10^7 $\pm 5.84 \times 10^5$	1.26×10^7 $\pm 6.68 \times 10^5$	1.45×10^7 $\pm 1.44 \times 10^7$	1.08×10^7 $\pm 5.94 \times 10^5$	1.41×10^7 $\pm 6.31 \times 10^5$	1.38×10^7 $\pm 6.16 \times 10^5$	1.14×10^7 $\pm 5.54 \times 10^5$
T_{anc}	9.49×10^5 $\pm 5.47 \times 10^4$	9.17×10^5 $\pm 7.35 \times 10^4$	6.99×10^5 $\pm 3.10 \times 10^6$	9.13×10^5 $\pm 7.54 \times 10^4$	9.28×10^5 $\pm 5.69 \times 10^4$	9.19×10^5 $\pm 5.60 \times 10^4$	8.42×10^5 $\pm 7.10 \times 10^4$
T_{split}	1.16×10^3 $\pm 4.62 \times 10^1$	8.88×10^3 $\pm 1.43 \times 10^3$	2.30×10^5 $\pm 1.32 \times 10^5$	2.89×10^3 $\pm 3.06 \times 10^{-7}$	2.20×10^2 ± 3.36	5.54×10^3 $\pm 1.87 \times 10^2$	2.50×10^3 $\pm 1.49 \times 10^2$
N_{pop1_split}	1.32×10^7 $\pm 5.71 \times 10^5$	3.28×10^6 $\pm 3.92 \times 10^5$	1.40×10^7 $\pm 1.38 \times 10^7$	9.53×10^6 $\pm 5.92 \times 10^5$	1.41×10^7 $\pm 6.31 \times 10^5$	1.38×10^7 $\pm 6.15 \times 10^5$	6.17×10^6 $\pm 2.79 \times 10^5$
$N_{pop1_current}$	8.24×10^3 $\pm 1.75 \times 10^3$	1.04×10^6 $\pm 1.20 \times 10^4$	5.81×10^6 $\pm 3.22 \times 10^7$	3.37×10^5 $\pm 1.02 \times 10^4$	1.17×10^3 $\pm 8.96 \times 10^1$	4.92×10^4 $\pm 8.72 \times 10^3$	6.83×10^2 $\pm 5.47 \times 10^1$
N_{pop2_split}	5.68×10^5 $\pm 1.36 \times 10^4$	9.31×10^6 $\pm 2.78 \times 10^5$	4.63×10^5 $\pm 6.56 \times 10^5$	1.22×10^6 $\pm 2.38 \times 10^3$	3.92×10^3 $\pm 4.98 \times 10^1$	4.86×10^4 $\pm 7.05 \times 10^2$	5.23×10^6 $\pm 2.75 \times 10^5$
$N_{pop2_current}$	1.20×10^4 ± 258.96	3.62×10^5 $\pm 6.08 \times 10^4$	5.54×10^6 $\pm 5.17 \times 10^6$	3.98×10^5 $\pm 9.33 \times 10^3$	9.17×10^4 ± 470.79	2.13×10^8 $\pm 2.96 \times 10^6$	4.15×10^4 $\pm 1.83 \times 10^3$
$M_{pop1 \leftarrow pop2}$	6.44×10^2 $\pm 1.84 \times 10^1$	9.00×10^{-4} ± 0.024	1.91×10^1 ± 3.29	2.83×10^{-3} ± 0.064	2.64×10^3 ± 5.89	6.91×10^1 ± 1.20	4.45×10^1 ± 0.458
$M_{pop2 \leftarrow pop1}$	6.90×10^2 ± 7.93	9.00×10^{-4} ± 0.013	1.88×10^1 ± 25.16	2.83×10^{-3} ± 0.019	1.28×10^2 ± 248.75	1.36×10^2 ± 2.16	4.45×10^1 ± 0.454

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