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The potential role of long non-coding RNAs and micro RNAs in insects: From junk to luxury

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Abstract

Noncoding RNAs (ncRNAs) play an important role in almost all biological processes and comprise a layer of internal signals that have a potential control on various levels of gene expression. The research in the field of ncRNAs has progressed a lot owing to the recent developments in sequencing methods and information analysis. A large number of ncRNAs have been identified in insects from the RNA-Seq data or transcriptomes and they have important regulatory functions at the epigenetic, transcriptional, or post-transcriptional levels. The technological innovations have made it possible to discover ncRNAs from both beneficial (honeybees, silkworm, etc.) and harmful insects (Plutella xylostella, Helicoverpa armigera, Bactrocera species, aphids etc.). The characterization and utilization of ncRNAs in the field of insect science have become a worldwide research focus and they are believed to have potential applications in insect pest management and the prevention and management of diseases of beneficial insects.

Keywords: Gene regulation, Insect, Pest, Management, ncRNA, miRNA.

1. Introduction

Ribonucleic acid (RNA) molecules were thought to be nothing more than a messenger between DNA and protein, but that is no longer the case as a messenger between DNA and protein for decades, but now it's well established that they have key role in almost all biological processes. There are broadly two types of RNAs viz. Coding and Non-coding. The coding RNAs generally refer to RNAs which encode proteins and it includes the messenger RNA (mRNA) only. Non-coding RNA molecules (ncRNAs) arise from the transcription of DNA but do not get translated into protein molecules. The amount of noncoding RNA

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varies among species and proportionally increases with increasing complexity of organism. The ncRNA contains information and remains functionally active by regulating other genes and their function is assessed based on their low coding potential [1]. The regulatory role of non-coding RNAs is thought to be responsible for many of the intricate genetic relationships and differences between species. They have a spatio-temporal expression and are mostly unconserved from species to species. The ncRNAs are involved in various biological and pathological processes [2,3] and can have either DNA binding sites, protein binding sites, or both. The ncRNAs are of many types such as ribosomal RNA (rRNA), transfer RNA (tRNA), small nuclear RNA (snRNA), small nucleolar RNA (snoRNA), endogenous small interfering RNA (siRNA), PIWI-interacting RNA (piRNA), microRNA (miRNA), long non-coding RNA (lncRNA), circular RNA (circRNA), etc. [4].

The advancement in high-throughput sequencing technologies has gained popularity as a way to determine the level of RNA in cells and provides a snapshot of a cell type or tissue at a specific moment of time. The researchers now can comprehend the complexity and diversity of insect transcriptomic data. According to the recent study, around 156 insect genomes from Diptera, Lepidoptera, and Hymenoptera are sequenced and submitted to the genome database of NCBI [5]. However, the Encyclopedia of DNA Elements (ENCODE) Program revealed that the large chunk of the insect genome generates a plethora of non-protein-coding RNAs, termed as noncoding RNA (ncRNA) [6] (Figure 1). Recent years have seen a paradigm shift as an increasing number of non-coding RNAs has been identified and characterized. The discovery of RNA interference (RNAi) has resulted in a surge of knowledge on the identification of ncRNAs and also how these ncRNAs interact with one another. Non-coding RNAs (ncRNAs) include RNAs that are transcribed from DNA but not translated into proteins. ncRNAs, earlier misidentified as “background noise” or “evolutionary junk”, are emerging as key elements that participate in various biological processes. ncRNAs have gotten a lot of interest recently because of their roles at the epigenetic, transcriptional, and post-transcriptional levels in insects. The recent explosion in science suggests that the repertoire of ncRNAs is still poorly characterized in insects. Here, we provide an overview of two main classes of insect ncRNAs viz., microRNAs and long ncRNAs, and for each class; we describe their biogenesis mechanisms and highlight their certain functions in different insect groups to provide their comprehensive understanding.

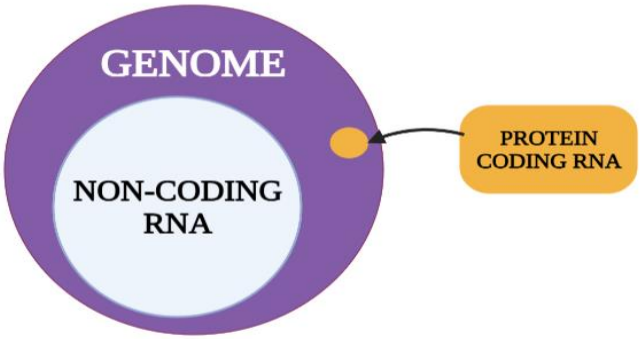

Figure 1. Non-coding RNAs comprise a larger portion of the insect genome.

2. Diversity of insect ncRNAs

The presence of ncRNAs has been witnessed in a broad range of insect species. According to a relatively broad size threshold, ncRNAs have been classified into into two subclasses viz. small ncRNAs and long ncRNAs (Figure 2a). ncRNAs typically less than 200 nucleotides in length are called small or short ncRNAs viz., miRNAs, siRNAs, etc. whereas the which are more than 200 nt in length are called long ncRNAs (lncRNAs). Based on functionality, ncRNAs include regulatory ncRNAs and housekeeping ncRNAs. Ribosomal RNAs (rRNAs) and transfer RNAs (tRNAs) fall in the category of housekeeping ncRNAs and regulatory ncRNAs include long non-coding RNAs (lncRNAs), microRNAs (miRNAs), small interfering RNAs (siRNAs), piwi-interacting RNAs (piRNAs), and small nuclear RNAs

(snRNAs) (Figure 2b) [7]. Nonetheless, due to the cross-over of properties, categorization of ncRNAs remains difficult.

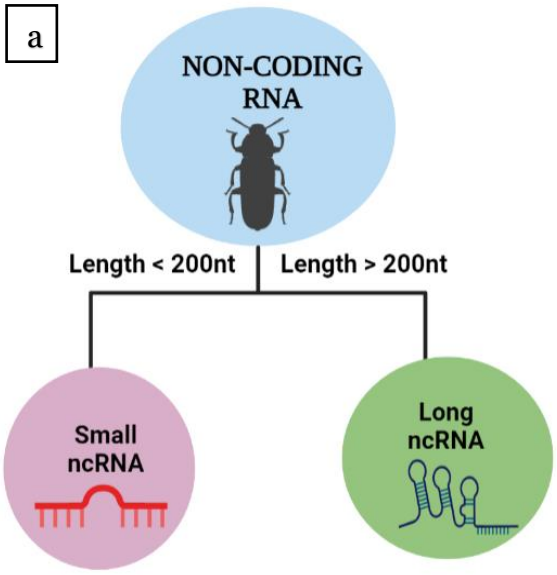

Figure 2a: Classification of ncRNAs based on the size of the transcript

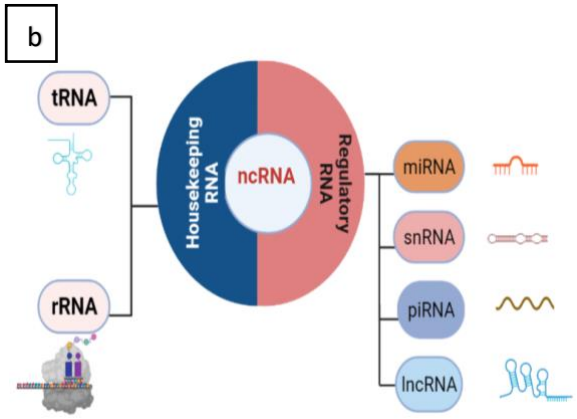

Figure 2b. Classification of ncRNAs based on functionality

3. Identification of ncRNAs

Because of the tremendous transcription power of mammalian genomes and the diverse processes of ncRNA synthesis, the ncRNA world is still loaded of unanswered questions in which unknown RNA species could play some key roles. Thanks to the advancements in technology, more unique functional ncRNAs are being found.

Next-generation sequencing methods, particularly RNA-seq, enable the identification of novel and unusual transcripts such as long noncoding RNAs (lncRNAs) by providing genome-wide expression profiling. Many RNA-seq studies have now been conducted to characterize lncRNAs and their potential role in cell development and differentiation in various animals, cell types, and tissues. RNA-seq is a whole-transcriptome sequencing technique that assesses gene expression across a broad range of values. It has been widely used in the model organism and human research in the past, and it overcomes the limitations of microarray technology. A reference library of approximately 8000 humans long intergenic noncoding RNAs using RNA-seq data has been created by Cabili et al., [8] the vast majority of which had never been described before. Long noncoding RNAs can now be annotated and characterized owing to the recent improvements in RNA-seq and computational techniques for reconstructing transcriptomes. RNA-seq has led to the discovery of a large number of lncRNAs [9]. As a result, enormous amounts of RNA-seq data have enabled us to fully identify and quantify ncRNAs (also protein-coding RNAs), as well as describe their functions. High throughput sequencing was used by Liao et al., [10] to identify a total of 62 lncRNA, 332 miRNA, and 366 mRNA profiles between coronary heart disease and healthy control in humans. Using a combination of next-generation sequencing and bioinformatics, Tonge et al., [11] could identify thousands of lncRNAs located throughout the human genome, based solely on their function using the approach of next generation sequencing technologies aided with bioinformatics.

4. Insect ncRNA research

ncRNAs have been extensively researched in mammals, however their roles in insects are still to be clearly understood. The advent of high-throughput technology has facilitated the sequencing of various insects' genomes and transcriptomes, resulting in the finding of several key ncRNAs in insects. Nowadays,

tens of thousands of ncRNAs have been discovered in insects, thanks to the approaches like RNA sequencing technologies, which provide a basis for the structural and functional research of ncRNA in invertebrates such as insects. Insect ncRNA research previously was focussed on model insects, however, now the researchers are focussing on identifying and deciphering the role of various ncRNAs in non-model insects.

5. MicroRNAs (miRNAs)

MicroRNAs (miRNAs) are small, single-stranded RNAs (ss ncRNAs), about 22-24 nucleotides, with a characteristic hairpin structure. Lin-4 was the first miRNA to be discovered 1993 in Caenorhabditis elegans by the Ambros and Ruvkun groups. Lin-4 was initially thought to be a protein-coding gene, but it was later demonstrated to produce small RNAs and to influence developmental timing in C.elegans [12]. Tens of thousands of miRNAs have been discovered since then, and are now stored in the miRBase database (www.mirbase.org) [13]. Since this first discovery of the lin-4 gene, it has become clear that miRNAs have many different functions. miRNAs are the most studied in humans followed by model organisms from other groups. These miRNAs are believed to serve critical roles in development, apoptosis, cell differentiation, reproduction, behavior, and physiology in eukaryotes, including plants and animals [14-16]. Researchers have previously shown that miRNAs have a key role in a wide range of biological processes in insects, including oogenesis, embryogenesis, mounting, metamorphosis, immunity, behavior, and host-pathogen interactions [17-22]. While miRNA activity is conserved across significantly different species, the functions of miRNAs in the model species fruit fly, Drosophila melanogaster have been thoroughly investigated [23-25]. Understanding the role of miRNA in insects other than fruit fly, on the other hand, is an emerging trend in insect research.

Biogenesis of microRNAs in insects: miRNA biogenesis in insects involves numerous processing steps, viz., Transcription of miRNA loci, Pri-miRNA processing by the microprocessor complex, nuclear export of pre-miRNA, Pre-miRNA processing by Dicer and MicroRNA strand selection, and Argonaute loading (Figure 3). Monocistronic, bicistronic, and polycistronic miRNA transcripts can produce mature miRNAs. These transcripts fold into pri-miRNA viz., primary miRNA hair-loop structures, that are processed in the nucleus by an enzyme, RNase III, which liberates the pre-miRNA, precursor miRNA. Once this pre-miRNA is transferred to the cytoplasm and digested by yet another RNaseIII enzyme, the miRNA-miRNA* pair is synthesized. Although the biogenesis of miRNAs has been extensively researched in model insects such as Drosophila; nonetheless, new findings of non-canonical miRNA production and processing in other species is emerging day by day [26,27].

Steps of miRNA biogenesis:

1. Transcription of miRNA genes

The initial step of miRNA biogenesis is the transcription of miRNA genes. The resulting primary transcripts, also known as primiRNAs, are often several kilobases (kb) long and undergo extensive processing during the formation of the functional 21 nt miRNA [23]. Earlier, it was presumed that RNA polymerase III (pol III) assisted in the transcription of most miRNA sites because it is reported to synthesize the majority of smaller non-coding RNAs including such tRNAs and U6 snRNAs [16]. As suggested by miRNA gene structure and explicit experimental data, miRNA loci appear to act as class-II genes, with polymerase II (pol II) being the principal RNA polymerase facilitating miRNA loci transcription in animal species. Hence, RNA polymerase II transcribes the significant proportion of miRNA genes, while RNA polymerase III transcribes a small percentage of miRNAs. RNA

polymerase III, for example, transcribes miRNAs from the human Chromosome 19 group [26].

2. Processing of primary transcripts (primiRNA) by the microprocessor complex

Pri-miRNAs are usually several kilobases long, with local stem-loop structures, and are polyadenylated and capped, although the cap and the poly (A) tail are removed during miRNA processing [28]. These primiRNA undergo an endonucleolytic cleavage at the stem of the hairpin structure, thereby releasing a 60–70 nt hairpin known as the pre-miRNA by the microprocessor complex. This microprocessor complex (about 500KDa) comprises of an assembly of three components viz., i) an enzyme RNase III, ii) Drosha, and iii) Pasha, its double-stranded RNA (dsRNA) binding partner, otherwise known as DGCR8 in case of mammals and nematode, C. elegans [29-33]. The cleavage of pri-miRNA transcript takes place by the activity of Drosha and its partner protein, Pasha/DGCR8. Pasha/DGCR8 targets the precursor pri-miRNA, hooks to the flanking ssRNA and dsRNA stem junctions, and identifies location 11bp into the stem wherein Drosha's activity centre is located to fragment the pri-miRNA [34]. Drosha-Pasha/DGCR8 processing can be bypassed by a non-canonical class of miRNAs termed miRtrons [35]. Drosha-Pasha/DGCR8 processing can be bypassed by a set of non-canonical of miRNAs termed miRtrons (Ruby et al., 2007). These miRtrons have been heavily studied in Drosophila. The pri-miRNA is converted into pre-miRNA (about 70 nt) by Drosha-Pasha processing.

i. Nuclear export of pre-miRNA

Pre-miRNA is crucial for nuclear transport and is transported into the cytoplasm from the nucleus with the aid of Exportin-5 (Exp-5). Exp-5, a Ran guanosine triphosphate (RanGTP)-dependent dsRNA-binding receptor, enables pre-miRNA outflow by targeting the 2 nt miRNA's 3' tail in the nucleus [36,37]. Exp-5 not only works as an element of nuclear export for pre-miRNAs, but that also shields pre-miRNAs with nuclease degradation [37].

ii. Cytoplasmic processing of pre-miRNA by Dicer

Pre-miRNAs are processed into mature 22 nt miRNA-miRNA* duplexes by Dicer, RNase III type enzyme in the cytoplasm [38]. The miRNA and miRNA* duplexes are the two strands of the dsRNA product of dicer processing of the stem-loop precursor miRNA. Dicer was first discovered in *Drosophila* as an important enzyme in the RNAi pathway [39]. The *Drosophila* genome encodes two Dicer enzymes, Dcr-1 and Dcr-2, each having a unique role in the miRNA and siRNA pathways respectively.

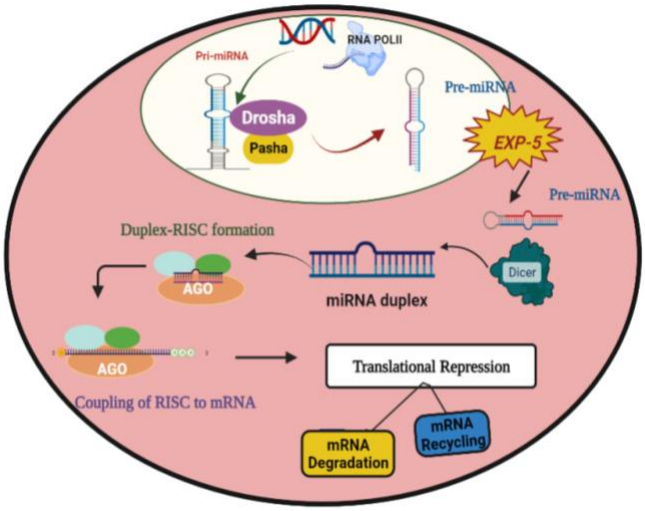

Figure 3. Stepwise Biogenesis of miRNA in insects**, a.** Transcription of miRNA genes into the primary miRNA (pri-miRNA) by RNA polymerase **b.** Processing of pri-miRNA into pre-miRNA by Drosha in association with Pasha **c.** Transport of pre-miRNA into cytoplasm by Exportin 5 **d.** Incorporation of miRNA duplex into the RISC complex followed by translational repression.

iii. Formation of miRNA containing RNA Induced Silencing Complex

After the cleavage of the pre-miRNA to form miRNA-miRNA* duplex by the action of Dcr-1, one of the strands is loaded into the RISC. The Argonaute family of sRNA-guided RNA-binding proteins forms the core part of the RISC. The miRNA-Ago complex is ready to operate on the vast majority of the target sequences of

insect miRNAs; however, certain miRNAs require further processing following Ago loading. Typically, the miRNA-Ago complexes silence the gene expression after transcription by either inhibiting translation or degrading mRNA.

Role of miRNAs in insects:

MiRNAs have an extensive role in various insect biological processes viz., development, immunity, host-pathogen interactions. Some of the miRNA roles in insects have been discussed below:

1.Insect Germ Cell Development

The significance of miRNAs in the developmental processes of insects has received the glaring attention in comparison to other areas of insect biology, owing to their conserved functions in the development of animals. The model insect *Drosophila melanogaster*, which has a plethora of genetic tools at its disposal, has been the focus of miRNA study, particularly concerning insect development. Experimental evidence reveals that proteins involved in controlling germ cell development work in tandem with the miRNA pathway to control important signaling pathways that govern the fate of progenitor cells. In *Drosophila*, loss of miR-184 results in failure of oogenesis coupled with defects in early embryogenesis [40]. For proper differentiation of germ stem cells (GSCs) in *Drosophila,* the repression of miR-7 caused by Maelstrom protein is a must and the absence of which inhibits differentiation of GSCs into primary spermatocytes in the testes [41]. miRNAs have a role to play in the panoistic type of oogenesis in *Drosophila,* apart from the meroistic type. Experimental findings in the German cockroach, *B. germanica* revealed that miRNAs play an important role in the regulation of oogenesis in panoistic ovaries. The sterile females were found to be developed due to the depletion of Dicer-1 in B. germanica [42].

2.Muscle development

A microRNA, miR-1, regulates heart function in *Drosophila* and mice by maintaining the transcript levels of the RhoGTPase Cdc42 gene, that in turn is essential for cardiac output and the maintenance of myofibrillar architecture in the heart [43]. Besides this, miR-1 is also responsible for keeping the muscular integrity in insects [23]. Because of the profound evolutionary conservation of miRNAs, Drosophila has been used as a model to better comprehend the signaling pathways associated with muscle development, the heart muscles in particular, in order to efficiently manage relevant disorders or ailments.

3.Apoptosis

Research shows that some of the miRNAs viz., Bantam, miR-14, miR-2, and miR-13 supposedly are cell death inhibitors in Drosophila [18]. Besides this, members of the miR-2 family, specifically miR-2/6/11/13/308, are vital for the regulation of cell death during the process of embryogenesis in Drosophila [44].

4.Host-pathogen interactions

The role of insect miRNAs in host-pathogen interactions is now well established [45]. Experimental evidence suggests that miRNAs can target host-pathogen interactions either by targeting the pathogen directly or by changing the expression of host genes which are beneficial to the pathogen [46,47]. In the case of Anopheles gambiae, after the attack and invasion by the parasite Plasmodium berghei, expression patterns of four miRNAs produced in the midgut of the mosquito was significantly modified [48].

5. miRNAs in insect pest management

Only a handful amount of studies, though promising, have been reported on the utilization and successful exploitation of miRNAs for the insect pest management. The trans-kingdom RNA interference (RNAi) approach utilizing miRNAs have been utilized for pest control. This method entails miRNAs being

delivered through kingdoms by food to receptive species, wherein they subsequently execute their biological function. *Escherichia coli has been engineered to express precursors for artificial miRNAs (amiRNAs) that target insects for the purpose of pest control using TK-RNAi/bacterial-mediated miRNA expression. An amiRNA is an altered endogenous miRNA progenitor with sequences tailored to inhibit any predetermined target gene in place of the miRNA: miRNA duplex. Larvae of H. armigera fed with E. coli-expressing a precursor for an amiRNA that targets Ecdysone Receptor EcR, showed considerable mortality, decrease in the rate of oogenesis, and the developmental abnormalities. During feeding, H. armigera is thought to have ingested the E. coli-expressed precursor backbone, which was then changed into the mature amiRNA that targeted EcR and resulted in the visible effects. This strategy is less expensive in comparison to the synthesised miRNA mimics for insect pest control* [49].

6. Long non-coding RNAs (lncRNAs)

NcRNAs of size greater than 200 nt belong to the category of lncRNAs and are believed to be present in all the eukaryotic organisms including insects. LncRNAs are categorized in four groups based on the genomic location from which they are transcribed: a) Sense lncRNAs; b) antisense lncRNAs; c) Intergenic lncRNAs and d) Intronic (bidirectional) lncRNAs [50] (Figure 4). LncRNAs transcribed from the sense strand of protein-coding genes are termed sense lncRNAs. On the contrary, antisense lncRNAs are transcribed from the antisense strand of protein-coding genes. Intergenic lncRNAs are transcribed from Intergenic locations from both the strands while Intronic lncRNAs are transcribed entirely from introns of protein-coding genes. As compared to other classes of ncRNAs in insects, lncRNAs have been extensively studied.

Biogenesis of LncRNAs:

The biogenesis of most of the lncRNAs is similar to that of mRNAs. It is believed that in eukaryotes, the majority of the lncRNAs get transcribed by RNA polymerase II. However, it is found that some of the novel lncRNAs get also transcribed by RNA polymerase III. Most of the lncRNAs are capped, polyadenylated, and spliced by the canonical mode. They can also be metabolized in non-canonical ways, perhaps by cleaving them with ribonuclease P (RNase P) to yield mature 3′ ends, capping them with snoRNA-protein (snoRNP) complexes at their ends, and forming of the circular structures [51].

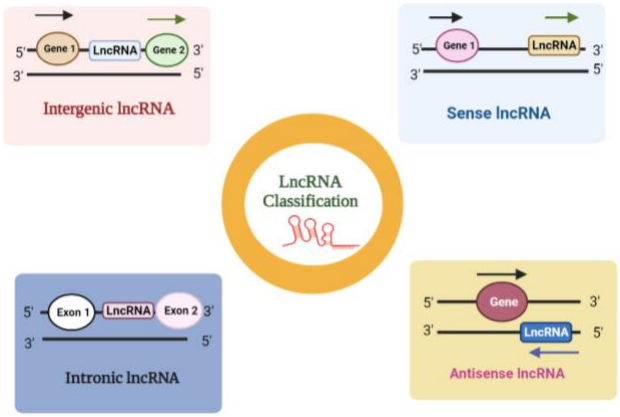

Figure 4. Classification of lncRNAs based on genomic locations.

Mode of action of LncRNA: Three major paradigms for characterizing lncRNA function have emerged: guides, dynamic scaffolds, and molecular decoys.

LncRNAs as Guides: LncRNA as guides are necessary for the appropriate localization and organization of the factors at specific genomic loci for genome regulation. These transcripts connect to regulatory or enzymatically functional proteins, including such transcriptional regulators and chromatin modifiers, to channel them to designated locations in the genome at either cis or trans sites from their transcription locus [52].

LncRNAs as Scaffolds: LncRNAs as "molecular scaffolds", play an important structural role in assembling multi-protein complexes such as short-

lived ribonucleoprotein (RNP) complexes. LncRNAs, which operate as dynamic molecular scaffolds, serve a structural role in the transitory assembly of numerous enzymatic complexes as well as other regulatory co-factors. RNP complexes can repress or enhance transcription depending on the presence and type of the RNAs and proteins involved once they've been fully assembled [53].

LncRNAs as Decoys: The primary purpose of decoy lncRNAs is to act as a molecular sink, limiting the availability of certain regulatory components. RNA-binding proteins, transcription factors, mirnas, catalytic proteins, and components of larger modifying complexes are sequestered by this RNA class, thus modulating the gene expression [54].

Role of lncRNAs in insects: Due to the development of a computational pipeline to identify lncRNAs from RNA-Seq data, a great number of lncRNAs have been identified in insects in these recent years. The role of lncRNAs in the development of insects, insecticide resistance, and anti-viral defense has been studied in various insect pests [55].

i. Dosage compensation and genomic imprinting

i) Dosage compensation and genomic imprinting

Dosage compensation is a technique that organisms use to alter the dose and so balances the X-chromosome (or Z-chromosome) genes expression levels in both males and females of a species. In animals, the dosage compensation acts by epigenetically silencing one of it's x - chromosome in females through the Xist lncRNA in cis form. In Drosophila, the male-specific dosage compensation complex (DCC) activates the majority of genes on the single X chromosome. It is involved in the global acetylation of histone H4 at lysine 16 (H4K16ac), ultimately resulting in a two-fold increase in their expression in order to match the expression from the two X chromosomes in females [56].

ii. Waggle dance in *Apis mellifera*

Based on RNA sequencing of four sets of the honey bee brains, it was discovered that about 2877 lncRNAs and 9647 mRNAs were identified from honey bee brains. The comparison of waggling dancers and non-dancing bees revealed nine differently expressed lncRNAs. A comparison study revealed that two lncRNAs (MSTRG.6803.3 and XR 003305156.1) that were likely engaged in the honey bee waggle dance controlled ten genes via the *cis*-regulatory mechanism [57].

iii. Other functions

LncRNAs are found to be involved in the transition of the larvae during metamorphosis in Drosophila [54]. In Apis mellifera, an abundance of four lncRNA in the brain such as; Nb-1, Ks-1, AncR-1, and kakusei, play a key role in regulating their foraging behavior [58]. Insect lncRNAs have also been implicated in fecundity and pesticide resistance in *N. lugens* [59,60]. Some lncRNAs were shown to be substantially expressed in insecticide-resistant strains [61,62] and some were attributed to chlorantraniliprole resistance in the diamondback moth [61,62].

Conclusion

The ncRNAs are functional and important regulatory molecules in almost all biological processes. The recent advances in the high-throughput sequencing technology has helped the researchers to discover the novel types of ncRNAs and to study their functions. A number of ncRNAs have been reported from insects, but their utilization towards the development of eco-friendly and effective insect pest management practices are lacking. Many studies have also been conducted on the ncRNAs involved in the diseases of beneficial insects such as honeybees and silkworm. Therefore, the research on the structure, function and diversity of ncRNAs in insects deserves special attention to exploit

their role in insect pest management and also in the prevention and management of diseases of beneficial insects.

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References

1- Gardini A, Shiekhattar R. The many faces of long noncoding RNAs. FEBS J 2015; 282:1647-57.
2-Batista PJ, Chang HY. Long noncoding RNAs: cellular address codes in development and disease. Cell 2013;152:1298–1307.
3- Rinn JL, Chang HY. Genome Regulation by Long Noncoding RNAs. Annu Rev Biochem 2012;81:145-166.
4- Lauressergues D, Couzigou JM, Clemente HS, Martinez Y, Dunand C, Bécard G, Combier JP. Primary transcripts of microRNAs encode regulatory peptides. Nature. 2015;2520(7545):90-3.
5- Coordinators NR. Database resources of the national center for biotechnology information. Nucleic acids research 2015;43(Database issue):D6.
6- Hemberger M, Redies C, Krause R, Oswald J, Walter J, Fundele RH. H19 and Igf2 are expressed and differentially imprinted in neuroectoderm-derived cells in the mouse brain. Dev Gene Evol 1998;208:393-402.
7- Dozmorov MG, Giles CB, Koelsch KA, Wren JD. Systematic classification of non-coding RNAs by epigenomic similarity. In BMC bioinformatics 2013; 14:1-12
8- Cabili MN, Trapnell C, Goff L, Koziol M, Tazon-Vega B, Regev A, et al. Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses. Genes & development 2011;25(18):1915-1927.
9- Li X, Xu J, Xiao Y, Ning S, Zhang Y. (Eds.). Non-coding RNAs in Complex Diseases: A Bioinformatics Perspective 2018, (Vol. 1094). Springer.
10- Liao J, Wang J, Liu Y, Li J, Duan L. Transcriptome sequencing of lncRNA, miRNA, mRNA and interaction network constructing in coronary heart disease. BMC medical genomics, 2019;12(1):1-12.
11- Tonge DP, Darling D, Farzaneh F, Williams GT. Whole-genome-scale identification of novel non-protein-coding RNAs controlling cell proliferation and survival through a functional forward genetics strategy. Scientific reports 2022;12(1):1-13.
12- Lee RC, Feinbaum RL, Ambros V. The C. elegans heterochronic gene lin-4 encodes small RNAs with antisense complementarity to lin-14. Cell 1993;75(5):843-854.
13- Kozomara A, Griffiths-Jones S. miRBase: integrating microRNA annotation and deep-sequencing date. Nucleic Acids Res 2011;39(S1):D152-D157.
14- Ambros V. The functions of animal microRNAs. Nature 2004;431(7006):350-355.
15- Lucas K, Raikhel AS. Insect microRNAs: biogenesis, expression profiling and biological functions. Insect biochemistry and molecular biology 2013;43(1):24-38.
16- Moran Y, Agron M, Praher D, Technau U. The evolutionary origin of plant and animal micro-RNAs. Nat Ecol Evol 2017;1: 0027.
17- Aravin AA, Lagos-Quintana M, Yalcin A, Zavolan M, Marks D, Snyder B., et al. The small RNA profile during Drosophila melanogaster development. Developmental cell 2003;5(2):337-350.
18- Asgari S. MicroRNA functions in insects. Insect biochemistry and molecular biology 2013;43(4):388-397.
19- Chawla G, Sokol NS. Hormonal activation of let-7-C microRNAs via EcR is required for adult Drosophila melanogaster morphology and function. Development 2012;139(10):1788-1797.
20- Skalsky RL, Cullen BR. Viruses, microRNAs, and host interactions. Annual review of microbiology, 2010;64:123-141.
21- Lu LF, Liston A. MicroRNA in the immune system, microRNA as an immune system. Immunology 2009;127(3):291-298.
22- Wei Y, Chen S, Yang P, Ma Z, Kang L. Characterization and comparative profiling of the small RNA transcriptomes in two phases of locust. Genome biology 2009;10(1):1-18.
23- Chawla G, Sokol NS. MicroRNAs in Drosophila development. International review of cell and molecular biology 2011;286:1-65.
24- Luhur A, Chawla G, Sokol NS. MicroRNAs as components of systemic signaling pathways in Drosophila melanogaster. Current topics in developmental biology 2013;105:97-123.
26- Borchert GM, Lanier W, Davidson BL. RNA polymerase III transcribes human microRNAs. Nature structural & molecular biology 2006;13(12):1097-1101.
27- Waldron JA, Newbury SF. The roles of miRNAs in wing imaginal disc development in Drosophila. Biochemical Society Transactions 2012;40(4):891-895.
28- Belles X, Cristino AS, Tanaka ED, Rubio M, Piulachs MD. Insect MicroRNAs: from molecular mechanisms to biological roles. In Insect molecular biology and biochemistry 2012, pp. 30-56. Academic Press.
29- Denli AM, Tops BB, Plasterk RH, Ketting RF, Hannon, GJ. Processing of primary microRNAs by the Microprocessor complex. Nature 2004;432(7014):231-235.
30- Gregory RI, Yan KP, Amuthan G, Chendrimada T, Doratotaj B, Cooch N., Shiekhattar R. The Microprocessor complex mediates the genesis of microRNAs. Nature 2004;432(7014):235-240.
31- Han J, Lee Y, Yeom KH, Kim YK, Jin H, Kim VN. The Drosha-DGCR8 complex in primary microRNA processing. Genes & development 2004;18(24):3016-3027.
32- Landthaler M, Yalcin A, Tuschl T. The human DiGeorge syndrome critical region gene 8 and Its D. melanogaster homolog are required for miRNA biogenesis. Current biology 2004;14(23):2162-2167.
33- Lee Y, Ahn C, Han J, Choi H, Kim J, Yim J, et al. The nuclear RNase III Drosha initiates microRNA processing. Nature 2003;425(6956):415-419.
34- Han J, Lee Y, Yeom KH, Nam JW, Heo I, Rhee JK, et al. Molecular basis for the recognition of primary microRNAs by the Drosha-DGCR8 complex. Cell 2006;125(5):887-901.
35- Ruby JG, Stark A, Johnston WK, Kellis M, Bartel DP, Lai EC. Evolution, biogenesis, expression, and target predictions of a substantially expanded set of Drosophila microRNAs. Genome research, 2007;17(12):1850-1864.
36- Bohnsack MT, Czaplinski K, Görlich D. Exportin 5 is a RanGTP-dependent dsRNA-binding protein that mediates nuclear export of pre-miRNAs. RNA 2004;10(2):185-191.
37- Lund E, Guttinger S, Calado A, Dahlberg JE, Kutay U. Nuclear export of microRNA precursors. Science 2004;303(5654):95-98.
38- Hutvagner G, McLachlan J, Pasquinelli AE, Bálint É, Tuschl T, Zamore PD. A cellular function for the RNA-interference enzyme Dicer in the maturation of the let-7 small temporal RNA. Science 2001;293(5531):834-838.
39-Bernstein E, Caudy AA, Hammond SM, Hannon GJ. Role for a bidentate ribonuclease in the initiation step of RNA interference. Nature 2001;409(6818):363-366.

40- Iovino N, Pane A, Gaul U. miR-184 has multiple roles in Drosophila female germline development. Developmental cell 2009;17(1):123-133.
41- Pek JW, Lim AK, Kai T. Drosophila maelstrom ensures proper germline stem cell lineage differentiation by repressing microRNA-7. Developmental cell 2009;17(3):417-424.
42- Tanaka ED, Piulachs MD. Dicer-1 is a key enzyme in the regulation of oogenesis in panoistic ovaries. Biol Cell 2012;104(8):452-461.
43- Qian L, Wythe JD, Liu J, Cartry J, Vogler G, Mohapatra B et al. Tinman/Nkx2-5 acts via miR-1 and upstream of Cdc42 to regulate heart function across species. J Cell Biol 2011;193(7):1181-1196.
44- Leaman D, Chen PY, Fak J, Yalcin A, Pearce M, Unnerstall U, et al. Antisense-mediated depletion reveals essential and specific functions of microRNAs in Drosophila development. Cell 2005;121(7):1097-1108.
45- Asgari S. Role of microRNAs in insect host–microorganism interactions. Front Physio 2011;2:48.
46- Pedersen IM, Cheng G, Wieland S, Volinia S, Croce CM, Chisari FV, et al. Interferon modulation of cellular microRNAs as an antiviral mechanism. Nature 2007;449(7164):919-922.
47- Xiao C, Rajewsky K. MicroRNA control in the immune system: basic principles. Cell 2009;136(1):26-36.
48- Winter F, Edaye S, Hüttenhofer A, Brunel C. Anopheles gambiae miRNAs as actors of defence reaction against Plasmodium invasion. Nucleic acids research 2007;35(20):6953-6962.
49- Yogindran S, Rajam MV. Artificial miRNA-mediated silencing of ecdysone receptor (EcR) affeTablects larval development and oogenesis in Helicoverpa armigera. Insect biochemistry and molecular biology 2016;77:21-30.
50- Dai X, Kaushik AC and Zhang J. The Emerging Role of Major Regulatory RNAs in Cancer Control. Front Oncol 2019;9:920.
51- Liu Y, Ding W, Yu W, Zhang Y, Ao X, Wang J. Long non-coding RNAs: Biogenesis, functions, and clinical significance in gastric cancer. Molecular Therapy-Oncolytics 2021;23:458-476.
52- Balas MM, Johnson AM. Exploring the mechanisms behind long noncoding RNAs and cancer. Non-coding RNA research 2018;3(3):108-117.
53- Guttman M, Rinn JL. Modular regulatory principles of large non-coding RNAs. Nature, 2012;482(7385):339-346.
54- Chen B, Zhang Y, Zhang X, Jia S, Chen S, Kang L. Genome-wide identification and developmental expression profiling of long noncoding RNAs during Drosophila metamorphosis. Scientific reports 2016;6(1):1-8.
55- Wang Y, Xu T, He W, Shen X, Zhao Q, Bai J, et al. Genome-wide identification and characterization of putative lncRNAs in the diamondback moth, Plutella xylostella (L.). Genomics 2007;110(1):35-42.
56- Conrad T, Akhtar A. Dosage compensation in Drosophila melanogaster: epigenetic fine-tuning of chromosome-wide transcription. Nature Reviews Genetics 2012;13(2):123-134.
57- Feng W, Huang J, Zhang Z, Nie H, Lin Y, Li Z, et al. Understanding of Waggle Dance in the Honey Bee (Apis mellifera) from the Perspective of Long Non-Coding RNA. Insects 2022;13(2):111.
58- Sawata M, Yoshino D, Takeuchi H, Kamikouchi A, Ohashi K, Kubo T. Identification and punctate nuclear localization of a novel noncoding RNA, Ks-1, from the honeybee brain. RNA 2002;8(6):772-785.
59- Xiao H, Yuan Z, Guo D, Hou B, Yin C, Zhang W, et al. Genome-wide identification of long noncoding RNA genes and their potential association with fecundity and virulence in rice brown planthopper, Nilaparvata lugens. BMC genomics 2015;16(1):1-16.
60- Zhu KA, Liu MH, Fu Z, Zhou Z, Kong Y, Liang HW, et al. Plant microRNAs in larval food regulate honeybee caste development. PLoS Genetics 2017;13:e1006946.
61- Etebari K, Furlong MJ, Asgari S. Genome wide discovery of long intergenic non-coding RNAs in Diamondback moth (Plutella xylostella) and their expression in insecticide resistant strains. Scientific reports 2015;5(1):1-14.
62- Liu F, Guo D, Yuan Z, Chen C, Xiao H. Genome-wide identification of long non-coding RNA genes and their association with insecticide resistance and metamorphosis in diamondback moth, Plutella xylostella. Scientific reports 2017;7(1):1-11.