Research Progress on Oviposition-Related Genes in Insects

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Abstract

Oviposition-related genes have remained a consistent focus of insect molecular biology. Previous research has gradually clarified our mechanistic understanding of oviposition-related genes, including those related to oviposition-gland-related genes, oogenesis-related genes, oviposition-site-selection-related genes, and genes related to ovulation and hatching. Moreover, some of this research has revealed how the expression of single oviposition-related genes affects the expression of related genes, and more importantly, how individual node genes function to link the expression of upstream and downstream genes. However, the research to date is not sufficient to completely explain the overall interactions among the genes of the insect oviposition system. Through a literature review of a large number of studies, this review provides references for future research on oviposition-related genes in insects and the use of RNAi or CRISPR/Cas9 technology to verify the functions of oviposition-related genes and to prevent and control harmful insects.

Graphical Abstract

In order to control the population size of insect pests by molecular biology technology, the oviposition-related gene families were divided into four categories according to the functional characteristics of oviposition-related genes participating in physiological and biochemical reactions in pests: oviposition-gland-related genes, oogenesis-related genes, oviposition-site-selection-related genes, and genes related to ovulation and hatching.

Key words: gland, oogenesis, location, ovulation, hatching

Female insects, particularly certain outbreak pests, have a very high reproductive capacity and can oviposit hundreds to thousands of eggs each. For example, in Glenea cantor (Coleoptera: Cerambycidae: Lamiinae), some females may have multiple matings, and the number of eggs laid by these females is often higher than that laid by other females; thus, the high reproductive capacity of this insect...
directly results in expansion of the damage range in kapok plants, this study can be found that the females fecundity of eggs laid by females, and even oviposition-related genes, play a key role in the continuation of insect populations (Lu et al. 2013). Insect oviposition is controlled by a genetic pathway formed by oviposition-related genes, and many kinds of genes control insect oviposition. The relationship between upstream and downstream genes is complex, and one or several key genes may determine whether insect oviposition can proceed normally. Therefore, the oviposition-related genes of female insects are the key entry point allowing researchers to analyze the oviposition process from the perspective of molecular biology and formulate new strategies for pest control. Although great progress has been made in understanding the functions of oviposition-related genes, at present, there is no effective method to inhibit the expression of these genes due to their high variation in structure and function. How to apply gene silencing technology to pest control on a large scale also remains to be determined.

The oviposition-related genes of insects are mainly divided into four categories: the genes controlling oviposition-related glands, the egg surface, oviposition-site-selection-related, and ovulation and egg hatching; these genes may directly or indirectly affect the oviposition of insects (Du et al. 2019, Guo et al. 2019, Ma et al. 2019, Peng et al. 2020). To date, RNA interference (RNAi) and CRISPR/Cas9 have been used to study some oviposition-related genes in detail; the combination of RNAi and other methods to control plant diseases and injurious pests is especially important, and a small amount of commercial application has begun (Killiny and Kishk 2017, Yu et al. 2017, Dao and Illny 2018, Yu and Killiny 2018a, Abdullaha et al. 2019, Avelar et al. 2019, Chen et al. 2019a, Fandino et al. 2019, Hao et al. 2019, Liu et al. 2019a, Lin et al. 2019, Lu et al. 2019a, Ortega and Killiny 2019, Richard et al. 2019, Wang et al. 2019a, Dias et al. 2020). Compared with the vast number of genes in the insect gene bank, only a small number of oviposition-related genes have been studied thus far, and research on oviposition-related genes has not been systematic. Understanding the functions of oviposition-related genes in different kinds of insects will be a focus of future research. In this review, the progress of research examining the oviposition-related genes of insects was reviewed, and oviposition-site-selection-related genes, oviposition-related genes, oogenesis-related genes, and oviposition and egg hatching genes of insects were systematically discussed. This information could provide a reference for using RNAi and CRISPR/Cas9 technology to control pests in the future.

**Oviposition-Related Gland Genes**

Oviposition-related gland genes refer to the genes that control the physiological and biochemical activities of oviposition-related organs and secretory glands of female insects, for example vitellogenin gene is highly expressed in ovary and salivary gland (Nunes et al. 2013, Huang et al. 2016). The transformation from the larva or nymph to the female adult insect occurs through a series of physiological and biochemical reactions, which promote the formation of oviposition-related organs (Fig. 1). Many kinds of genes are already known to be related to the metabolism of organs controlling oviposition in insects or other oviparous animals, especially the ovary. For example, in Apis mellifera (Hymenoptera: Apidae), the Vitellogenin (Vg) gene is considered to be the key gene regulating hormone signal transduction, feeding- and oviposition-related behavior, immunity, stress resistance, and life span in females, and interference of Vg gene expression can lead to lipid loss in females, including lipid accumulation in ovaries; these factors can directly or indirectly affect ovary development (Nunes et al. 2013, Ghosh et al. 2018; Fig. 2; Table 1). The expression of the Transformer-2 (Tra-2) gene of *Nasonia vitripennis* (Diptera: Muscidae) has a direct impact on the ovary development, and interference with the expression of this gene will reduce the number of eggs laid by females or increase the egg mortality rate during development (Geeverink et al. 2017). In addition, Glucose dehydrogenase (GLD) gene is also a gene that needs to be focused on. The transcriptomic study of *N. vitripennis* found that GLD protein is involved in the storage and release of *N. vitripennis* sperm, which provides a possible candidate protein for controlling female sex distribution during female oviposition, and GLD protein also affects the metabolic activity of female ovaries (Pannebakker et al. 2013). However, due to the large number of glands involved in oviposition and the complex relationships among the relevant genes and their expression, the existing research has not yet completely elucidated the connection between the genetic network regulating insect oviposition glands, unlike the research on insect oviposition-related genes.

First, egg production by the female requires the mobilization of nutrients for the egg cells in the ovary to produce Vitellogenin, while the semen provided by the male to the female contains substances that promote female oviposition. In the study of the *Selenoprotein F-like* (SPF-L) gene in male *Nilaparvata lugens* (Hemiptera: Delphacidae), it was found that the male accessory gland (MAG) contained a kind of Selenoprotein F (SPF-L), which could improve female reproductive ability and interfere with that of the male through RNA, and after knockdown of the SPF-L gene in males, the oocytes and ovaries of females that received semen from these males were stunted, resulting in a decrease in female reproductive ability and egg hatching rate (Ge et al. 2019; Fig. 2). It has been reported that the expression of oviposition-related genes in some females is affected by the expression of related genes in the semen of males. It has also been found that if the female needs to eat before oviposition, gene expression in the salivary gland affects ovary development. In the study of microRNA1000 (miR-1000) gene action in the salivary gland of *Drosophila melanogaster* (Diptera: Drosophilidae), it was found that after miR-1000 gene silencing, the feeding efficiency of females decreased significantly, and this phenomenon indirectly affected the development of the ovaries (Sadninan et al. 2020). This result also shows that salivary glands participate in the oviposition process. In this process, autophagy-related protein (ATG) can redistribute the nutrients stored in the ovary, regulate the balanced development of each part of the ovary, and prevent follicle overdevelopment from damaging the ovary. For example, RNAi technology was used to silence the expression of *Autophagy-related protein 8* (ATG8) gene of *Rhodnius prolixus* (Hemiptera: Reduviidae), and it was found that the inhibition of ATG8 protein synthesis impairs autophagy in oocytes and directly hinders follicle development (Pereira et al. 2020). The ATG8 gene and its related genes have potential as key research subjects for the study of insect-oviposition-related regulatory hormones in the future.

During oviposition-related metabolism, the ovaries continuously obtain nutrients from oviposition-related organs in the body to promote oviposition-related physiological processes in the ovaries, including the development of oocytes, the absorption of Vg protein by ovarian follicles, and the development of sexual maturity in the ovaries; these processes involve many genes that determine the physiological activities of the ovaries (Dao and Illny 2018, Chen et al. 2019b, Liu et al. 2019b, Xavier et al. 2019). For example, it was found that interfering with the expression of the Protein snail homing Sna-like (PSHS-like) gene of *Henosepilachna*
vigintioctopunctata (Coleoptera: Coccinellidae) could prolong the preoviposition period in females and effectively inhibit the growth of the next-generation population (Guo et al. 2019). An investigation of the characteristics and functions of the Small heat shock protein (SHSP) genes of Tribolium castaneum (Coleoptera: Tenebrionidae) showed that the Heat shock protein 18.3 (hsp18.3) gene was expressed in all stages of adult development and highly expressed in the early pupal stage and late adult stage, especially in the ovary and fat body of adults, and that reproductive capacity was significantly reduced after Tchsp18.3 gene silencing (Xie et al. 2019a). Knockout of the Tudor gene in Bactrocera dorsalis (Diptera: Trypetidae) led to a decrease in ovarian development, mating rate, and oviposition and interfered with the corresponding expression of downstream genes and the expression of primordial germ cells (Xie et al. 2019b). The above research shows that genes related to ovarian development control reproductive capacity, the secretion of oviposition hormones, and the physiological activities of female insects in the early stage of oviposition. Additional genes with similar or related functions represent key research subjects for gene interference in the future.

Many genes in the oviposition-related glands of insects jointly regulate the physiological metabolism of oviposition in female insects, and these genes can be studied using RNAi technology, which has revealed the functions of a certain number of oviposition-gland-related genes and the involvement of some upstream and downstream genes. At present, the difficulties in studying the functions of oviposition-related genes and their interactions lie in the large number and different types of oviposition-gland-related genes and their expression in multiple insect organs; it has so far been impossible to systematically study the complex regulatory relationships among oviposition-gland-related genes.

**Oogenesis-Related Genes**

During the process of ovarian development, oocytes continuously obtain nutrients to promote the formation of ova. Existing studies have revealed the dynamic landscape of gene regulation during oogenesis, and a total of 1,932 genes were identified to be differentially expressed among different stages, most of which occurred during the transition from late vitellogenesis to early choriogenesis, and discuss the genes involved in all aspects of oogenesis (Carter et al. 2013). Including vitellogenesis and choriogenesis, plus those implicated in hormonal control of oogenesis and transgenerational hormonal effects in great detail (Zhang et al. 2017). The Vg gene is an important factor in oocyte development and determines whether the oocytes can obtain enough nutrition and whether oocytes can be formed through continuous division (Fig. 1). The Vg protein is a kind of yolk precursor glycolipid protein that is expressed in almost all females of oviparous animal species, such as fishes, amphibians, reptiles, birds, and insects. For insects, it is usually expressed in only adult females and not in larvae or males (Tufail and Takeda 2008). It is related to the food quality of the females; high-quality food can induce the expression of vitellogenin, while low-quality food can inhibit ovary development and the expression of vitellogenin.
During oogenesis, Vg protein is synthesized in the fat body, secreted into the hemolymph, and then incorporated into the developing oocytes through vitellogenin receptor (VgR)-mediated endocytosis (Tufail and Takeda 2008; Fig. 2; Table 1). At this stage, multiple genes become involved. A study found that adipokinetic hormones (AKHs) could promote the uptake of Vg protein in the oocytes of *N. lugens*. AKHs also function to mobilize lipids and carbohydrates in the progress of insect oviposition, and they may be involved in the reproductive regulation of oocytes. Inhibition of AKHR gene expression by RNAi leads to not only a decrease in AKH content in the circulating hemolymph but also an increase in Vg protein accumulation in the hemolymph and a decrease in Vg protein deposition in the ovaries, which is not conducive to the formation of ova (Lu et al. 2019b). However, how the VgR receptor releases Vg protein into the hemolymph and how it affects the biochemical reaction of oocytes during oogenesis, as well as the localization mechanism of the VgR mRNA and protein in cells, are unknown (Rika et al. 2019).

In addition to the above, the expression of certain genes directly or indirectly affects the absorption of Vg protein by oocytes. A study found that the destruction of sex-specific exons resulted in male- and female-specific defects in *Agrotis ipsilon* (Lepidoptera: Noctuidae). The *Doublesex* (*DSX*) gene is a downstream gene in the sex determination pathway of insects and a key regulator of sexual development and behavior in various insects. The Vg gene is the direct target of the DSX protein, and the synthesis of the Vg protein is directly affected by the DSX protein (Chen et al. 2019c). A study found that the ecdysone receptor complex is the key to the reproductive success of the female desert locust *Schistocerca gregaria* (Orthoptera: Catantopidae). The *Ecdysone* receptor (*EcR*) gene is expressed in all insect oocytes as an important component of embryogenesis, and the production of yolk requires ecdysone signaling, which is directly involved in the formation of the yolk envelope of the primary follicle at the end of oogenesis (Lenaerts et al. 2019; Fig. 2). If the expression of the Vg gene is silenced by RNAi technology, female reproductive capacity is reduced (Moriyama et al. 2016). These examples show the potential of the Vg protein in pest control and provide a theoretical basis for using gene interference technology to control pests in the future.
Overall, the oogenesis-related gene research to date clearly illustrates that almost all genes related to ovum formation directly or indirectly regulate the expression of the Vg protein. The Vg gene is a node among both upstream and downstream genes related to egg formation.

Oviposition-Site-Selection-Related Genes

After the ovaries are fully developed, it is often necessary to identify female oviposition sites that can provide sufficient food for the next generation of larvae or nymphs (Sétamou et al. 2016; Fig. 1). In the process of finding an oviposition site, females mainly rely on the abundant sensilla on the antennae, and these sensilla often express various types of olfactory genes. The olfactory-related proteins encoded by these genes play key roles in female mating and the location of suitable oviposition sites (Alonso et al. 2019). Research indicates that female olfactory ability is the basis of host recognition, mating, and oviposition.

At present, the major genes related to olfactory proteins and receptors in female insects are Odorant-binding proteins (OBPs), Chemosensory proteins (CSPs), Odorant-degrading enzymes (ODEs), Odorant receptors (ORS), Ionomotropic receptors (IRs), and Sensory neuron membrane proteins (SNMPs). The proteins encoded by these genes are the main proteins responsible for chemical signaling (Leal 2013, Cheng et al. 2019a, González et al. 2019, Li et al. 2019, Zhang et al. 2019). Among them, the research on OBPs is the most detailed, including the construction of a phylogenetic tree of OBP genes among different species of female insects; transcriptome analysis and the functions of related proteins have also been reported. The OBP genes control the first step in female sensing of airborne odor molecules through their antennae (Cheng et al. 2019b). For example, the high expression of OBP genes in the antennae of Anoplophora glabripennis (Coleoptera: Cerambicidae) females suggests that OBP genes may play important roles in identifying host plants or finding volatiles that indicate suitable oviposition sites (Wang et al. 2019b). OBP genes are highly expressed not only in the antennae but also in the legs, wings, and other parts, indicating that these tissues may also be involved in the host location by female insects (Li et al. 2016). Compared with the OBP genes, the CSP genes have similar functions, and CSP proteins allow the antennae to receive chemical signals and then transmit the signals to the ORs. Compared with the OBP genes, the CSP genes have broader expression, including the antennae and maxillary palps and labial palps (Sheng et al. 2017, Angelica et al. 2019). Some nonolfactory tissues, such as the pheromone glands, feet, and wings, also express these genes (Cui et al. 2017). When a chemical signal is received by the ORs on the antennae, odor signals are transmitted through heteromeric ligand-gated ion channels and cyclic-nucleotide-activated cation channels, which promote neurons to respond to the signals quickly, briefly, sensitively, and effectively to complete the efficient location of the host oviposition site (Crava et al. 2019; Fig. 2). After the neuron receives the signal, the signal substance that activated the nerve impulse must be degraded, and thus, the ODE enzymes begin to play their role. ODE enzymes can quickly degrade volatiles after the neurotransmitter binds to the receptor, halting the nerve impulse and facilitating the next stage of signal transmission. After the above-mentioned signal transmission process generates an action potential through the Sensilla on antennae which recognition of volatile compounds, the signal is transmitted to the primary olfactory center and antennal lobe of the female brain and then to the protocerebrum; at this time, the female responds by carrying out the corresponding positioning behavior (Leal 2013). OBP, CSP, OR, and ODE genes are involved in the host location activities of almost all kinds of insects, but there are few systematic studies of the roles of SNMP and IR genes in host location. However, research on the OBP, CSP, OR, and ODE genes has illuminated some functions of the SNMP and IR genes. For example, one study mentioned that the SNMP1CD36 genes of insects can be divided into three categories: the SNMP genes belong to the third category and can be further divided into two subgroups, SNMP1 and SNMP2 (Nichols and Vogt 2008). The SNMP1 subgroup is expressed in the antennae, and its members are related to pheromone-specific olfactory sensilla neurons (OSNs). Members of the SNMP2 subgroup are expressed in neurons and particularly in sensory neurons (Vogt et al. 2009); in a study of the functional structure of the olfactory ionotropic glutamate receptor, the IR genes were shown to play an important role in regulating IR sensory ciliary targeting and IR-based sensory channels (Abuin et al. 2011). The specific roles of these two gene families in host location by female insects and the function of their proteins in oviposition location are not yet clear and remain to be further studied in the future.

In addition to the olfactory genes in the antennae, taste genes, visual genes, olfactory genes, and foraging genes in the female body also play key roles in oviposition. For example, by studying the function of the gustatory receptor 11 (Gr11) gene of Ni. lugens, it was found that the Gr11 gene could enhance the reproductive capacity of Ni. lugens through adenosine monophosphate-activated protein kinase (AMPK) and phosphorylation of the protein kinase B (AKT) receptor; this study was also the first to find that a taste receptor could regulate reproductive capacity in insects, and thus, it identified a potential target gene for pest control (Chen et al. 2019a). By studying the mechanism by which the Opsin Rh6 (Rh6) visual gene regulates host location in Bactrocera minax (Diptera: Tephritidae), we found that the Rh6 protein is a green-sensitive opsin; after RNAi

Table 1. Two important gene families

| Gene types       | Two important related genes   | Function                                                                 |
|------------------|-------------------------------|--------------------------------------------------------------------------|
| Oviposition gland| Vitellogenin (Vg)             | Directly or indirectly affect the development of ovary (Ibanez et al. 2017). |
|                  |                               | Egg formation, oviposition behavior, and other physiological activities of oviposition are affected (Lu et al. 2019b). |
|                  |                               | It is highly expressed in the ovary (Yao et al. 2018).                     |
|                  |                               | Transport VG protein (Du et al. 2019).                                     |
|                  | Vitellogenin receptor (VgR)   | Promote ovarian growth and oviposition (Jing et al. 2018).                 |
|                  |                               | Showed the highest abundance in the ovaries (Rika et al. 2019).            |

Vitellogenin (Vg) and Vitellogenin receptor (VgR) genes are two gene families that need to be focused on. Some literatures have done a detailed study on the functions of these two genes.
technology was used to interfere with the expression of the gene, the number of B. minax eggs in citrus crops decreased significantly (Wang et al. 2019c). A study of pheromone receptor expression in female moth ovipositors found that the Pheromone binding protein (PBP2) and Pheromone receptor HR13 (HR13) genes were expressed at the top of the ovipositor, and an immunohistochemical analysis with a specific antiserum showed multiple types of receptors, some of which had the function of locating the oviposition site, around the top of the ovipositor (Widmayer et al. 2009; Fig. 2). The foraging gene of insects has been studied to some extent, such as it was found in the research of feeding and oviposition sites of Manduca sexta by odorant receptor coreceptor gene (Orco), after the Orco gene was knocked out, the Orco gene KO gravid female displayed reduced attraction toward a nonflowering plant (Fandino et al. 2019). Studies have shown that more than half of hawkmoths were able to use characteristic odor-directed flight orientation and ovipositor on the host plant that is suggested that the expression of foraging gene and olfactory genes may be two independent processes, but the correlation between these two groups of genes needs further study (McConnell and Fitzpatrick 2017).

Many papers have discussed the roles of olfactory genes, taste genes, visual genes, and foraging genes in oviposition location; the functions of these genes include feeding, detoxification, courtship, mating, oviposition, and so on. However, except for the genes related to olfactory, there are relatively few studies of the other genes related to oviposition-site-selection-relevant genes, and currently, it is impossible to establish a functional gene network; only individual taste, vision genes, and foraging genes have been studied in the existing literature. In the future, additional efforts can be made to study the correlations among olfactory, gustatory, visual, and foraging genes and establish a gene bank of these four types of genes to lay a foundation for the practical application of RNAi and CRISPR/Cas9 technology in the field to control pests.

Genes Related to Oviposition and Hatching

Most kinds of insects reproduce via oviposition, which includes the two stages of egg laying and egg hatching (Fig. 1). When a female finds the right place to oviposit on a host, she lays one or more eggs. During this process, abundant genes control the physiological and behavioral activities of the female, including ovulation, maintaining humidity on the egg surface and a stable internal environment in the eggs (Hu et al. 2019, Wang et al. 2019d).

At present, the field of ovulation-related gene research is still in the stage of studying the functions of single genes (Azmal et al. 2019, Zhou et al. 2019). For example, a study found that the recombinant Homeobox protein akr (Akr) gene reduced the oviposition amount of Dermatobia hominis (Acarina: Dermatophagoideidae), and the application of recombinant Deg-akr protein produced by the Akr gene to the adult body surface of D. hominis affected egg-laying behavior, resulting in a 42% reduction in oviposition (Lima-Barbero et al. 2019). A study found that DOPA decarboxylase is an essential enzyme for corneous tanning in R. prolisus and affects its molting, survival, and reproduction; knockout of the Aromatic amino acid decarboxylase 2 (AADC-2) gene resulted in delayed ovulation, decreased hatchability, and higher mortality in the nymphs that successfully hatched (Sterkel et al. 2019; Fig. 2). Some studies have confirmed that DOPA decarboxylase has been conducted to clarify the participation of biogenic amines in ovulation and egg laying; in the study on dopa decarboxylase in Drosophila sechellia (Diptera: Drosophilidae) and Plutella xylostella (Lepidoptera: Plutellidae), it was found that DOPA decarboxylase can affect the survival rate of larvae and the reproductive activity of female adults, and the silence of Dopa decarboxylase genes will reduce the number of individuals in the next generation, which indicates that DOPA decarboxylase plays an important role in the oviposition of female adults (Ellango et al. 2018, Lanno et al. 2019).

After the egg leaves the female’s body, genes related to hatching begin to act, mainly by controlling the metabolism of the egg, indirectly maintaining the stability of its inner environment to ensure hatching and other physiological activities (Tang et al. 2019). Current research focuses on genes related to environmental stability and hatching. For example, one study performed RNAi-mediated Transformer-2 homologue (Tra-2) gene knockout, leading to a reduction in reproduction of Diaphorina citri (Kuwayama) (Hemiptera: Lividiidae); when Tra-2 were silenced, RNAi females lay fewer eggs, with a mean of 12.44, and the hatching rate of laid eggs is reduced approximately by 29.86% compared with the control (Yu and Killiny 2018b). Another study found that myxoid protein is a necessary protein for Ni. lugens oviposition, and Mucin (Muc) genes encode eggshell-related proteins necessary for normal oviposition. After gene expression in females was repressed by using dsMuc, the resulting eggs did not hatch at 45–55% humidity, indicating that the Muc gene plays an important role in maintaining the humidity tolerance of eggs (Lou et al. 2019; Fig. 2). In a study of Aedes aegypti (Diptera: Culicidae) control examining ion channels related to oviposition in fresh water, the pickpocket (Ppk301) gene was shown to have great significance for maintaining osmotic stability inside eggs, especially for females that oviposit in water, and it is of great significance to study how to maintain the osmotic pressure of eggs in the external water environment under different salt concentrations (Matthews et al. 2019).

The ovulation and hatching of insects determine whether the next generation of larvae or nymphs can grow normally. Crucially, each female must discharge a large number of eggs from the ovipositor into an appropriate position through the regulation of abdominal muscles. In addition, the physiological and biochemical substances distributed inside and outside the eggshell are key to maintaining the stability of the egg environment (Lou et al. 2019). It can be seen that RNAi technology to destroy the stability of the egg environment has a certain application value for pest control. In the future, we can develop gene insecticides for egg killing in this research direction, which is helpful for the prevention and control of pest population.

Conclusion

Studies on insect oviposition have been recorded around the 1950s. Since the early 1990s, the research on molecular biology in insects began to rise after the ‘human genome project’.

The latest research on oviposition-related genes in insects has made considerable progress, but the mechanisms controlling ovarian development, the physiological metabolism of oviposition, and the location of oviposition sites through the antennae during the process of ovulation and egg hatching are not as simple as expected. A single gene cannot control the oviposition behavior of females in every respect, but many genes cooperate with each other to control oviposition behavior overall. In this process, several key genes, such as OBP and Vg genes, often appear. In the future research, we can focus on the relationship between these genes and upstream and downstream genes, which is very helpful for the study of insect oviposition-related genes. These key genes are often nodes connecting upstream and downstream genes, but
to date, the research in this field has not systematically analyzed how these genes affect the expression of multiple additional genes, and the molecular basis of the interactions among these genes remains unknown. In the future, we can use these key oviposition-related genes to begin to study how the expression of each gene affects oviposition in female insects. In addition to exploring new nodes, we must also study the relationships among upstream and downstream genes and build a gene bank of oviposition-gland-related genes. Another important direction for the study of insect oviposition behavior in the future is to use RNAi/Cas9 technology to verify the roles of newly discovered genes in female oviposition behavior. Research on oviposition-related genes will remain an important field in the future.

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Author Contributions

H-LI, X-YW, WL, and X-LZ planned, designed, and wrote the paper and helped in data collection and diagram preparation. H-LI recognized the opportunity to develop this review and pilot its writing with significant input from X-YW, WL, and X-LZ. Each colleague contributed their own unique expertise and experience in the realm of Modern Agricultural Industry Technology System Guangxi.

Conflict of Interest

The authors declare that they have no conflicts of interest.

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