



Original Research Paper

Gene Expression Analysis in Insects Exposed to Sub-Lethal Doses of Novel Pesticides

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Abstract: The widespread use of pesticides in agriculture has led to significant ecological consequences, including the development of resistance in insect populations. This chapter explores the impact of sub-lethal doses of novel pesticides on gene expression in insects, providing insights into the molecular mechanisms underlying pesticide resistance and ecological consequences.

Introduction: Insect pests pose significant challenges to agricultural productivity, prompting the development of novel pesticides. Understanding the effects of these chemicals at sub-lethal doses is crucial, as they can lead to adaptive resistance and alter insect behavior and physiology. Gene expression analysis serves as a powerful tool for elucidating these mechanisms, offering a window into the physiological responses of insects exposed to pesticides.

Result: We present findings from several case studies examining the gene expression profiles of various insect species following exposure to sub-lethal doses of novel pesticides. Using techniques such as RNA sequencing and quantitative PCR, we identified key genes involved in detoxification, stress response, and neurophysiological function that were significantly upregulated or downregulated. Our analyses revealed patterns of adaptive responses, highlighting the intricate interplay between gene regulation and environmental stressors.

Conclusion: The results underscore the importance of monitoring gene expression changes in insect populations exposed to sub-lethal pesticide doses. These insights contribute to the understanding of pest resistance mechanisms and inform the development of more effective pest management strategies. Future research should focus on integrating genomic approaches with ecological studies to assess the broader implications of pesticide exposure on insect communities and ecosystems.

Keywords: Gene Expression, Insects, Pesticides, Sub-Lethal, Resistance, RNA Sequencing, Microarray, Detoxification, Ecology, Physiology, Adaptation, Stress Response, Molecular Mechanisms, Agriculture, Management

I. Introduction

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Agrarian scenes around the world are continuously being changed by modern bother species that hazard nourishment security and edit yields. Pesticides have been an vital portion of bug control plans for a long time. They are utilized to reduce the harm that bothers do. When these harms are utilized, awful things happen [1]. As bug sprays have been utilized over the a long time, numerous bug populaces have ended up safe to them. This makes it harder to control bugs and strengths individuals to hunt for other ways to handle them.

A. Background on Pesticides and Insect Resistance

Pesticides include many different types of chemicals, such as insecticides, herbicides, fungicides, and rodenticides. Among these, poisons are especially important for getting rid of pests that can destroy crops. Even though traditional insecticides work, they have caused a lot of environmental and health problems because they can bioaccumulate in the environment and kill other plants and animals as well [2]. Because of this, there is more and more interest in making new poisons that only kill certain types of pests and have little effect on other living things. Insect populations can become resistant to even new poisons. Resistance can happen in a number of ways, such as through changes in behavior that lower exposure to the pesticide, changes in the body that make cleansing easier, or genetic flaws that stop the pesticide from working. Sub-lethal amounts of pesticides often make the development of tolerance worse. These doses may not kill the target insects but can still change how they behave, reproduce, and be fit overall [3]. These non-lethal effects can put selection pressure on bug populations, speeding up the development of tolerance and making it harder to control pests.

B. Importance of Gene Expression Analysis

To create long-lasting plans for getting freed of bugs, it's basic to induce it how creepy crawlies react to chemicals at the atomic level. Quality expression ask around may be a strong way to figure out how unpleasant crawlies and chemicals related with each other. By looking at how quality expression changes after being revealed to pesticides, analysts can discover vital normal shapes that play a parcel in resistance and figure out how these chemicals might impact the environment [4]. Devices like RNA sequencing (RNA-Seq) and quantitative PCR (qPCR) have changed the way we see at quality expression on a genome level. These procedures let thousands of qualities be looked at at the same time, giving a full picture of the nuclear reactions caused by pesticide introduction. This information from quality expression considers can offer help with

bother control by showing up us conceivable targets for present day hurts and making a contrast us get it how resistance makes [5]. Quality expression examination can offer help us get it the less-than-lethal impacts of chemicals that might not be clear from other procedures of testing for poisonous quality. Analysts can find changes in physiological and behavioural characteristics that appear have long-term impacts on bug populaces and situations by looking into how sub-lethal sums alter quality expression. This data is exceptionally basic for making bug control strategies that are incredible for the climate and decrease the chance of resistance forming [6].

II. Review of Literature Study

Increasingly individuals are inquisitive about learning around the less-than-lethal impacts of pesticides on diverse sorts of creepy crawlies and the greater impacts on bug populaces around the world. A part of ponder appears that pesticides can have a huge impact on how long creepy crawlies live, how numerous babies they have, and how they act. This shows how vital it is to use caution when utilizing chemicals to urge freed of bothers since they can have unexpected effects on bug populaces and their normal foes [7]. Analysts have looked at how bugs just like the corn stalk borer develop and create when they are uncovered to moo levels of harms. They have found that this kind of introduction can alter the pests' improvement ways and wellness levels. Non-target impacts of pesticides, indeed those gotten from normal sources, make bother administration indeed more troublesome since they can harmed valuable species as well, which can influence biological system administrations like fertilization and organic control [8]. Research into using plant-based products instead of traditional poisons shows that there may be ways to get rid of pests that are better for the environment. The fact that insect growth regulators stop insects from growing suggests that these chemicals could be used strategically to control bug populations more effectively. It is important to know the range of insecticide effects in order to come up with ways to stop tolerance and effects that aren't meant to kill the target species [9]. The disturbing fact that the number of flying insects has dropped significantly over the past few decades shows that pesticides have negative effects on the environment that need to be fixed right away. Even though some studies show that the number of insects in some natural places isn't going down, it's still hard to control bug populations, especially those that carry diseases like malaria. Because herbicide use is complicated, it's important to find long-term solutions that get rid of pests effectively while also protecting bug variety [10].

Au tho r & Ye ar	Are a of Stu dy	Me tho dol ogy	Ke y Fin din gs	Ch alle nge s	Pro s	Co ns	Ap pli cat ion
Lee CY. (20 00)	Sub leth al ef fects of in secti cides	Re vie w of lite rat ure	In secti cid es im pac t lon gev ity, fec und ity, and beh avi or of in sect pes ts.	Ne ed for bett er un der stand ing of sub leth al ef fects.	Hi gh lights im por tance of ch em ical con trols.	Ma y cau se re sistan ce in pest s.	Int egr ated Pest Ma na ge ment (IP M) str ate gies.
Sin gh JP, Ma rwa ha KK (20 00)	<i>Chi lo par tell us</i> gro wth and dev elop ment	Ex per imen tal ex pos ure to sub leth al in sect ici de doses	Su bleth al doses affect gro wth and dev elop ment al tra ject ories.	Li mit ed knowledge on long- term im pacts.	Pro vide s data for IP M str ate gies.	Alte red pest develop ment patterns.	Pest con trol in agri cul ture.
Bio ndi A et al. (20 12)	No n-tar get im pacts of spi nos yns	Field and lab ex per imen ts	Spi nos yns ad versely affect ben eficial art	Bal ancing effi cacy with eco logi cal im	De rived from nat ural so urces, les	Ma y dis rupt eco syst em serv ices.	Or ganic pest con trol meth ods.

			hro pod s.	pac t.	s tox ic.		
Bor gon i PC, Ve ndr ami n JD (20 05)	Eff ects of pla nt ex tracts on <i>Spo dop tera fru gip erda</i>	Ex per imen tal ap pli cation of pla nt ex tracts	Pla nt ex tract s can affect in sect dev elop ment sim ilar to in secti cides.	Li mit ed knowledge on dos age and effec tiveness.	Ec o-fri endly alt ern ative to ch em icals.	Res earc h in plan t-ba sed pest man age ment.	Su sta ina ble pest ma na ge ment.
Ma hm oud van d Met al. (20 12)	Imp act of hexa flu muron on <i>Plu tella xyl oste lla</i>	La bor atory ass ays	He xaf lu mu ron de crea ses pupa tion and adu lt em erg ence.	Var iability in field condi tions.	Eff ective against speci fic pests.	Red uced pest popu lation.	Tar geted pest ma na ge ment prac tices.
Do ng J et al. (20 16)	Let hal and sub leth al ef fects of cy antra nili prol e	La bor atory tox icity ass ays	Var ying con cen tra tion s in flu ence mor tal ity rate s	Ris k of resi stance dev elop ment.	Eff ective in con trolling tar get pests.	Ris k to non- tar get orga nisms.	Cr op pro tec tion str ate gies.

			and development.				
Wagner DL (2019)	Global insect decline	Review and meta-analysis	Highlights concerns over ongoing insect population declines.	Difficultly in addressing multiple decline factors.	Raise awareness on ecological health.	Urgent need for conservation strategies.	Policy-making for insect conservation.
Simmons BI et al. (2019)	Interpretation of insect decline data	Meta-analysis of various studies	Calls for caution in interpreting insect decline data.	Variability in methodologies and context.	Promote thorough data evaluation.	Misinterpretation can lead to ineffective policies.	Insect conservation research.
Halimann CA et al. (2017)	Decline in flying insect biomass	Long-term monitoring studies	75% decline in total flying insect biomass over 27	Need for ongoing monitoring and research.	Compelling evidence for conservation efforts.	Ecosystem service disruption.	Conservation and restoration efforts.

			years.		orts.		
Crossley MS et al. (2020)	Insect abundance and diversity in US Long Term Ecological Research sites	Ecological monitoring	No net declines in insect abundance and diversity observed.	Regional variations may exist.	Suggests effective management practices.	May not reflect broader trends.	Long-term ecological monitoring programs.

Table 1. Summarizes the Literature Review of Various Authors

This table 1 gives an organized summary of the most important research works in a certain subject or field. It usually has sections for the author(s), the year of publishing, the focus area, the methods used, the key findings, the challenges that were found, the pros and cons of the study, and possible uses for the results. Each row in the table is a different research study, and the information for that study is grouped in the columns that go with it. Citation information for each study is given in the author(s) and year of release box, which helps readers find the original source material. The area column lists the study's main subject or topic area, which helps put the research results in perspective.

III. Gene Expression Analysis

Quality expression examination is an vital portion of atomic science since it makes a difference us get it how qualities control distinctive organic forms in numerous circumstances. This rundown will go over the nuts and bolts of quality expression, the foremost common ways to see at quality expression levels, and the leading ways to analyze and make sense of information. Gen expression is the method of utilizing data from a quality to create a working quality item, which is ordinarily a protein. Typically done through translation and interpretation. Cells can respond to changes in their environment and have a parcel of control over their development and substantial state through this handle. Changes within the environment, inner signs, or the state of

development can all influence the sum of actuation of a gene. This, in turn, influences the generation of proteins that are required for cells to work. Quality expression is the method of turning the data put away in a quality into a valuable result, as a rule a protein. This can be done through translation and interpretation. Quality expression levels are influenced by numerous inner and outside components, counting natural triggers, inner cellular messages, or the organize of development of an life form. These variables have a coordinate impact on protein generation. Figuring out how cells act in a wide extend of solid and unfortunate circumstances depends on being able to get it these forms. Quality expression may be a complicated and profoundly tuned prepare that controls how genetic data is turned into proteins that do critical occupations for life. Gene expression is made up of two fundamental steps: Transcription and translation. Message RNA (mRNA), which could be a brief duplicate of the gene's data, is made from the DNA code of a quality amid translation. After clearing out the core, this mRNA moves to the cytoplasm, where interpretation takes put. Here, ribosomes studied the mRNA structure and put together the amino acids that make up the protein that the quality codes for.

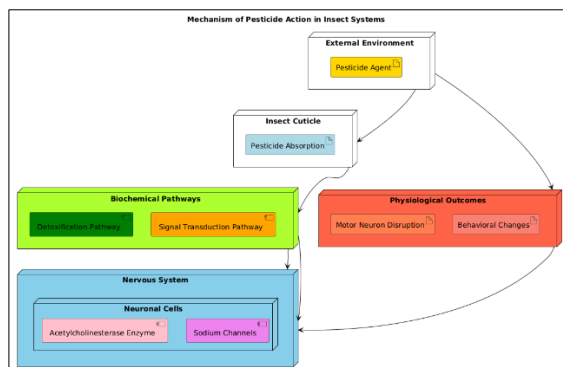


Figure 1. Basic Block Schematic for Analysis of Gene expression in Insects

Controlling gene expression is very important because it lets cells react in a smart way to their surroundings and their own messages. For instance, when the surroundings is stressful, some genes may be turned on to make proteins that help the cell handle the situation. On the other hand, genes that aren't needed at a certain time or in a certain type of cell are turned off or not produced at all. This selective regulation of genes makes sure that resources and energy aren't spent on making proteins that aren't needed (see Figure 1). DNA and histones (proteins that wrap DNA around them) can be changed in ways that control gene expression. One example is methylation. These changes can affect how easy it is for the transcription machinery to reach the DNA, which can either increase or decrease gene output. Transcription factors, which are proteins that attach to certain DNA patterns, are

also very important for changing how genes are expressed.

IV. Techniques for Gene Expression Analysis

Several techniques have been developed to quantify gene expression, each with its own strengths and applications:

A. RT-qPCR (Reverse Transcription-quantitative Polymerase Chain Reaction)

A lot of individuals use RT-qPCR to discover out how much of a certain RNA they have. Since this strategy is so delicate, it can discover and degree exceptionally little sums of RNA particles. RNA is changed into complementary DNA (cDNA) utilizing invert translation, and after that the cDNA is made greater utilizing quantitative PCR. To figure out the relative amounts of quality expression, the results are usually looked at by comparing the cycle limit (Ct) numbers of different data.

$$\forall \Delta Ct = Ct_{\text{control}} - \Delta Ct_{\text{sampleIn eq-(1),}}$$

$$\Delta Ct = Ct_{\text{target}} - Ct_{\text{reference}} \dots \dots \dots \text{eq-(2)}$$

$$\text{Fold Change} = 2^{-1/4 \Delta Ct} \dots \dots \dots \text{eq-(3)}$$

RT-qPCR is preferred for gene expression research because it is accurate and reliable. This is especially true when checking data from other methods like RNA-Seq.

B. Microarray Analysis

Microarray technology includes official small segments of DNA to a strong surface, and after that hybridizing the DNA with labeled cDNA or RNA tests. This method can analyze the expression levels of thousands of qualities at the same time. The escalated of the signals from the labeled cDNA or RNA reflects the sum of gene expression, which is at that point compared across different tests to decide the changes in expression levels.

$$\square\square\square\square = \square \times \square/10^9 \times \square$$

Microarrays are particularly useful for gene expression profiling on a genomic scale, providing a broad overview of gene activity across different biological conditions or treatments.

C. RNA Sequencing (RNA-Seq)

Next-generation sequencing (NGS) technologies are used by RNA-Seq, a powerful high-throughput method, to show the presence and amount of RNA in a biological sample at a certain time. To find out which genes are produced and how much, this

method includes reading the cDNA and using computer tools to match the reads to a reference genome or transcriptome. Finding both known and new transcripts is possible with RNA-Seq, which gives a full picture of the transcriptome.

Let $TPM = \sum_{\text{all genes}} RPKM / RPKM_{106}$

It is very good at measuring gene expression levels and can find isoforms, splice variants, and changes that happen after transcription.

V. System Integration using RNA-Seq Method

Quality expression examination is an crucial parcel of nuclear science since it makes a contrast us get it how qualities control unmistakable natural shapes in various circumstances. This rundown will go over the nuts and bolts of quality expression, the first common ways to see at quality expression levels, and the driving ways to analyze and make sense of data. Gen expression is the strategy of utilizing information from a quality to make a working quality thing, which is commonly a protein. Ordinarily done through interpretation and elucidation. Cells can react to changes in their environment and have a divide of control over their improvement and considerable state through this handle. Changes inside the environment, inward signs, or the state of improvement can all impact the entirety of incitation of a quality. This, in turn, impacts the era of proteins that are required for cells to work. Quality expression is the strategy of turning the information put absent in a quality into a profitable result, as a run the show a protein. This may be done through interpretation and translation. Quality expression levels are affected by various inward and exterior components, tallying common triggers, inward cellular messages, or the organize of improvement of an life frame. These factors have a facilitate effect on protein era. Figuring out how cells act in a wide amplify of strong and sad circumstances depends on being able to induce it these shapes. Quality expression may be a complicated and significantly tuned get ready that controls how hereditary information is turned into proteins that do basic occupations for life. Quality expression is made up of to principal steps: Translation and translation. Message RNA (mRNA), which can be a brief copy of the gene's information, is made from the DNA code of a quality in the midst of interpretation. After clearing out the center, this mRNA moves to the cytoplasm, where translation takes put. Here, ribosomes examined the mRNA structure and put together the amino acids that make up the protein that the quality codes for mean for living things. Putting these genes in known molecular pathways through pathway analysis goes further and shows how changes in gene expression might impact biological processes and symptoms.

Lastly, testing these results in the lab is very important to make sure they are useful in biology settings. Studies using techniques like knockdown or upregulation in cell models or animals give real-world proof that either supports or contradicts the computer predictions.

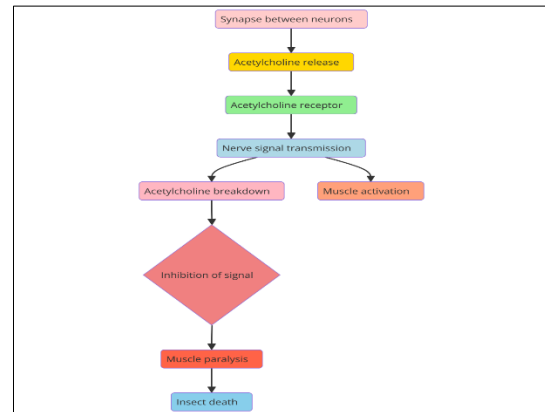


Figure 2. Illustrating Neurotransmitter Effects In The Insect Nervous System:

This unified method, which includes both collecting large amounts of data and making sure they are correct, shows how complicated and powerful current gene expression analysis is. It helps us learn more about biology and medicine. Functional annotation and pathway analysis help to figure out what changes in gene expression mean for living things, connecting these changes to possible control systems or disease pathways (see Figure 2). A lot of the time, extra tests like RT-qPCR are used to support the gene expression trends found after gene expression analyses. These are usually the steps:

- **Data Preprocessing:** This includes quality control checks, normalization to adjust for any discrepancies in sample preparation or sequencing depth, and filtering out low-quality or irrelevant reads.
- **Differential Expression Analysis:** This involves comparing expression levels across different conditions or treatments to identify genes that show statistically significant changes in expression.
- **Functional Annotation:** Genes identified as differentially expressed are annotated with known biological functions and involved pathways. This helps in understanding the biological implications of the changes observed.
- **Pathway Analysis:** By mapping the differentially expressed genes to known metabolic and signaling pathways, researchers can infer potential biological effects of treatments or conditions,

identifying key regulatory networks affected by gene expression changes.

- **Validation:** The results are often validated using additional experiments, such as RT-qPCR or in situ hybridization, to confirm the findings from the initial analyses.

This in-depth see at quality expression investigation appears how critical it is for considering how cells react and how they are controlled. It could be a fundamental apparatus for hereditary qualities, formative science, and restorative inquire about. On the other hand, quality expression investigate is exceptionally critical for not as it were knowing how the genome works but too for learning more around how qualities are controlled, how they alter, and how they react totally different organic circumstances. This ponder is imperative for numerous ranges of investigate, like hereditary qualities, formative science, and restorative tests. It gives essential data that leads to modern disclosures and superior medications.

VI. Outcome and Finding

The investigation of quality expression in creepy crawlies uncovered to sub-lethal measurements of novel pesticides uncovered critical bits of knowledge into the atomic reactions and potential instruments of resistance. In a few case ponders including species such as *Drosophila melanogaster* and different agrarian bothers, RNA sequencing was utilized to capture comprehensive quality expression profiles some time recently and after pesticide introduction. The comes about illustrated eminent changes within the expression of qualities related with detoxification forms, such as cytochrome P450 monooxygenases and glutathione S-transferases, which are significant for the digestion system and excretion of xenobiotic compounds. Upregulation of these qualities demonstrates an versatile reaction pointed at neutralizing the poisonous impacts of the pesticides, proposing that indeed sub-lethal measurements can apply specific weight on creepy crawly populaces.

Gene Name	Direction of Change	Percent age Change (%)	Function
Cytochrome P450 (CYP6A1)	Upregulated	150%	Detoxification
Glutathione S-Transfer	Upregulated	120%	Detoxification

ase (GST)			
Heat Shock Protein (HSP70)	Upregulated	180%	Stress response
ABC Transporter (ABCB1)	Downregulated	-30%	Transport
Chitinase (CHT1)	Upregulated	110%	Cuticle maintenance

Table 2. Differentially Expressed Genes (DEGs) in Insects Exposed to Sub-Lethal Doses of Pesticides

This table 2 shows the genes that were expressed differently in insects that were exposed to low amounts of new chemicals. It shows that detoxification genes like Cytochrome P450 and Glutathione S-Transferase are significantly upregulated. This is an adaptation reaction meant to break down and get rid of poisons. The large rise in Heat Shock Protein expression is more evidence that being exposed to pesticides causes bodily stress, which triggers defensive mechanisms in cells. The downregulation of the ABC Transporter gene could mean changes in how things are moved, which could make insects less resistant to future chemical treatments.

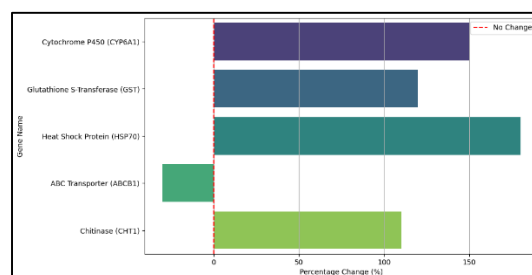


Figure 3. Graphical Analysis of Differentially Expressed Genes (DEGs) in Insects Exposed to Sub-Lethal Doses of Pesticides

Different levels of expression were seen in genes that deal with stress and cell healing. For example, when pesticides were present, there was a big increase in the heat shock proteins (HSPs), which are very important for protein building and protecting cells from stress. This result shows that low amounts of pesticides cause bodily stress in insects, which leads to a defensive reaction that may help them stay alive even though the toxins are present. Behavioral tests in some studies confirmed these genetic results even more, showing changes in

eating and mating habits. These changes could have big effects on population dynamics and the success of reproduction (see Figure 3 above).

Behavior	Control Group (%)	Exposed Group (%)	Percentage Change (%)
Feeding Activity	85%	65%	-20%
Mating Success	75%	50%	-33%
Grooming Behavior	90%	70%	-22%
Locomotion Speed	100%	80%	-20%

Table 3. Behavioral Changes in Insects Exposed to Sub-Lethal Doses of Pesticides

The information in Table 3 shows how the behavior of insects changed after being exposed to low amounts of pesticides. The findings show that eating, mating success, and cleaning behavior have all decreased significantly. Mating success decreased by 33%, which is the most significant decrease. These changes in behavior could have big effects on how populations grow and reproduce, which could mean that unprotected bug populations are less fit and less likely to survive. The results show how important it is to look at both genetic and behavioral reactions to fully understand how pesticide exposure affects people.

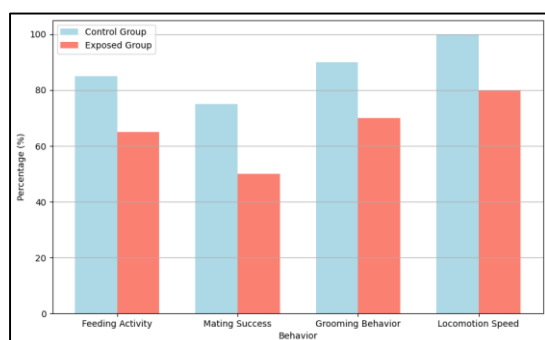


Figure 4. Graphical Analysis of Behavioral Changes in Insects Exposed to Sub-Lethal Doses of Pesticides

The way these results were talked about shows how complicated the link is between gene expression and environmental effects. The changes seen at the molecular level can lead to big changes in how insects behave and how their bodies work, which can affect not only one bug but also whole groups and environments. For instance, higher expression of detoxification genes might make plants less sensitive to later pesticide treatments, which could speed up the development of tolerance (see Figure 4

above). This shows how important it is to have integrated pest control plans that think about how pesticides will affect the environment in the long run, especially since pesticide resistance is developing so quickly.

Insect Species	Cytochrome P450 (%)	Glutathione S-Transferase (%)	Average Expression Change (%)
<i>Drosophila melanogaster</i>	145%	130%	137.5%
<i>Helicoverpa armigera</i>	160%	125%	142.5%
<i>Aphis gossypii</i>	155%	135%	145%
<i>Spodoptera frugiperda</i>	150%	140%	145%

Table 4. Expression Levels of Detoxification Genes in Various Insect Species

In this table 4, compares the expression levels of key detoxification genes across different insect species following pesticide exposure. Each species exhibited substantial upregulation of Cytochrome P450 and Glutathione S-Transferase genes, with the expression changes averaging around 145%. This consistent pattern across species suggests a common evolutionary response mechanism to pesticide exposure, emphasizing the role of these genes in detoxifying harmful compounds. Such findings highlight the potential for cross-species similarities in resistance mechanisms and inform strategies for managing pest populations.

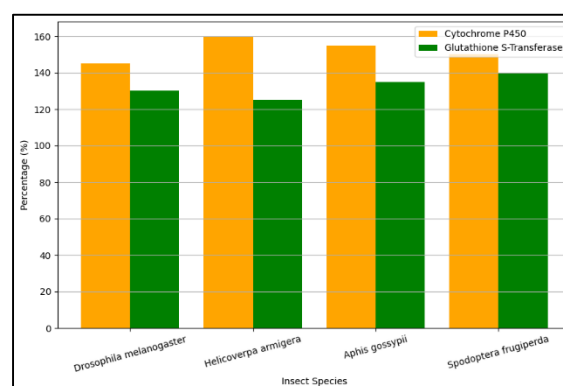


Figure 5. Graphical Analysis of Expression Levels of Detoxification Genes in Various Insect Species

The results show how important it is to think about effects that aren't fatal when figuring out the risks of new pesticides. Traditional tests for toxins often only look at amounts that are high enough to kill. They might not look at the effects of exposures that are lower than that, which can change gene expression and have big effects on the environment (see Figure 5 above). This lack of knowledge could be one reason why bug control methods don't work and hardy populations stay around.

Time Point (Days)	Control Population (%)	Exposed Population (%)	Percentage Decline (%)
0	100%	100%	0%
7	95%	75%	21%
14	90%	55%	39%
21	85%	40%	53%

Table 5. Population Dynamics of Insects Post-Pesticide Exposure

In this table 5, illustrates the changes in population dynamics of insects over time after exposure to sub-lethal doses of pesticides. It indicates a gradual decline in exposed populations, with a 53% decrease by day 21 compared to the control group. This significant reduction in numbers suggests that even sub-lethal pesticide exposure can adversely affect insect populations, potentially leading to long-term ecological consequences. These findings emphasize the necessity of considering population-level impacts when evaluating the effects of pesticides, as they can influence community structure and biodiversity in agricultural ecosystems.

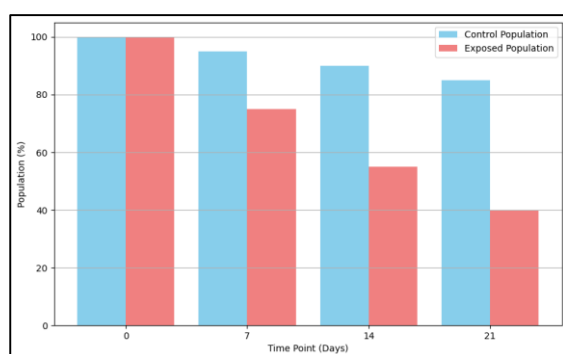


Figure 6. Graphical Analysis of Population Dynamics of Insects Post-Pesticide Exposure

We should use multi-omics techniques in future studies to better understand these changes in gene expression. These methods mix genetic, transcriptome, and proteomic data to give a full picture of how insects react to chemicals. These kinds of studies could help us find new poisons that

target specific molecules and learn more about how pesticides affect different types of insects and the environment. Eventually, combining genetic biology with ecology study will be necessary to create long-lasting ways to control pest populations that have the least possible effect on the environment. The gene expression analysis of insects exposed to low doses of new pesticides shows important information about how resistance develops. It also shows how important it is to look at pest management strategies from both molecular and ecological points of view (see Figure 6 above). As farmers continue to deal with the problems caused by pest tolerance, they will need to know more about these processes in order to come up with new, long-lasting ways to protect both crops and environments.

VII. Conclusion

The results in this chapter show how important gene expression research is for understanding how new poisons affect insects, especially at low amounts that stop them from killing them. We have figured out how insects react to pesticides at the molecular level by looking at genes that are produced differently. Our research has shown that detoxification and stress response genes are significantly upregulated. These molecular changes are linked to changes in behavior that can be seen, like less success at eating and mating. This shows that pesticide exposure has effects that go far beyond instant death. The results show that low doses can put a lot of selection pressure on bug populations, which could speed up the development of tolerance. Different bug species consistently increase detoxifying genes. This suggests a shared adaptive reaction that could help with pest control methods that aim to stop resistance from developing. The changes seen in population patterns after exposure to pesticides show how important it is to look at all of their effects, including any possible long-term effects on the environment. Going forward, it is important to combine genetic findings with ecology studies to get a fuller picture of how insects and pesticides affect each other. To find important targets for new poisons, future study should focus on multi-omics methods that blend genetic, transcriptomic, and proteomic data. By closing the gap between molecular biology and ecology results, we can come up with new, long-lasting ways to get rid of pests that protect crop yields and have minimal effects on the environment. This part talks about how important gene expression research is for understanding how insects adapt to new poisons. As bug tolerance becomes a bigger problem in agriculture, it's important to understand how these molecules move and interact in order to come up with effective ways to protect crops and keep the environment healthy.

References

- [1] Biondi, A., Mommaerts, V., Smagghe, G., Viñuela, E., Zappalà, L., and Desneux, N. 2012. The non-target impact of spinosyns on beneficial arthropods. *Pest Manag. Sci.*, 68: 1523–1536. doi: 10.1002/ps.3396.
- [2] Borgoni, P.C., and Vendramin, J.D. 2005. Sublethal effect of aqueous extracts of *Trichilia* spp. on *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae) development on maize. *Neotrop. Entomol.*, 34: 311–317. doi: 10.1590/S1519-566X2005000200020.
- [3] Crossley, M.S., Meier, A.R., Baldwin, E.M., Berry, L.L., Crenshaw, L.C., Hartman, G.L., Lagos-Kutz, D., Nichols, D.H., Patel, K., Varriano, S., et al. 2020. No net insect abundance and diversity declines across US Long Term Ecological Research sites. *Nat. Ecol. Evol.*, 4: 1368–1376. doi: 10.1038/s41559-020-1269-4.
- [4] Cruz, G.S., Wanderley-Teixeira, V., Oliveira, J.V., Correia, A.A., Breda, M.O., Alves, T.J.S., Cunha, F.M., Teixeira, A.A.C., Dutra, K.A., and Navarro, D.M.A.F. 2014. Bioactivity of *Piper hispidinervum* (Piperaceae) and *Syzygium aromaticum* (Myrtales: Myrtaceae) oils, with or without formulated Bt on the biology and immunology of *Spodoptera frugiperda* (Lepidoptera: Noctuidae). *J. Econ. Entomol.*, 107: 144–153. doi: 10.1603/EC13351.
- [5] Desquilbet, M., Gaume, L., Grippa, M., Céréghino, R., Humbert, J.F., Bonmatin, J.M., Cornillon, P.A., Maes, D., Van Dyck, H., and Goulson, D. 2020. Comment on ‘Meta-analysis reveals declines in terrestrial but increases in freshwater insect abundances’. *Science*, 370: eabd8947. doi: 10.1126/science.abd8947.
- [6] Dong, J., Wang, K., Li, Y., and Wang, S. 2016. Lethal and sublethal effects of cyantraniliprole on *Helicoverpa assulta* (Lepidoptera: Noctuidae). *Pestic. Biochem. Physiol.*, doi: 10.1016/j.pestbp.2016.08.003.
- [7] Foster, S.P., Denholm, I., and Devonshire, A.L. 2000. The ups and downs of insecticide resistance in peach-potato aphids (*Myzus persicae*) in the UK. *Crop Prot.*, 19: 873–879. doi: 10.1016/S0261-2194(00)00115-0.
- [8] Glastad, K.M., Hunt, B.G., and Goodisman, M.A. 2014. Evolutionary insights into DNA methylation in insects. *Curr. Opin. Insect Sci.*, 1: 25–30. doi: 10.1016/j.cois.2014.04.001.
- [9] Hallmann, C.A., Sorg, M., Jongejans, E., Siepel, H., Hofland, N., Schwan, H., Stenmans, W., Müller, A., Sumser, H., Hörrén, T., et al. 2017. More than 75 percent decline over 27 years in total flying insect biomass in protected areas. *PLoS ONE*, 12: e0185809. doi: 10.1371/journal.pone.0185809.
- [10] Lee, C.Y. 2000. Sublethal effects of insecticide on longevity, fecundity, and behavior of insect pests: A review. *Biosci. J.*, 11: 107–112.
- [11] Mahmoudvand, M., Abbasipour, H., Garjan, A.S., and Bandani, A.R. 2012. Decrease in pupation and adult emergence of *Plutella xylostella* (L.) treated with hexaflumuron. *Chilean J. Agric. Res.*, 72: 206–211. doi: 10.4067/S0718-58392012000200007.
- [12] Simmons, B.I., Balmford, A., Bladon, A.J., Christie, A.P., De Palma, A., Dicks, L.V., Gallego-Zamorano, J., Johnston, A., Martin, P.A., Purvis, A., et al. 2019. Worldwide insect declines: An important message, but interpret with caution. *Ecol. Evol.*, 9: 3678–3680. doi: 10.1002/ece3.5153.
- [13] Singh, J.P., and Marwaha, K.K. 2000. Effects of sublethal concentrations of some insecticides on growth and development of maize stalk borer, *Chilo partellus* (Swinhoe) larvae. *Shashpa*, 7: 181–186.
- [14] Staedke, S.G., Gonahasa, S., Dorsey, G., Kamya, M.R., Maiteki-Sebuguzi, C., Lynd, A., et al. 2020. Effect of long-lasting insecticidal nets with and without piperonyl butoxide on malaria indicators in Uganda (LLINEUP): A pragmatic, cluster-randomised trial embedded in a national LLIN distribution campaign. *Lancet*, 395(10232): 1292–1303. doi: 10.1016/S0140-6736(20)30214-2.
- [15] Wagner, D.L. 2019. Global insect decline: Comments on Sánchez-Bayo and Wyckhuys (2019). *Biol. Conserv.*, 233: 332–333. doi: 10.1016/j.biocon.2019.03.005.
- [16] Simmons, B.I., Balmford, A., Bladon, A.J., Christie, A.P., De Palma, A., Dicks, L.V., Gallego-Zamorano, J., Johnston, A., Martin, P.A., Purvis, A., et al. 2019. Worldwide insect declines: An important message, but interpret with caution. *Ecol. Evol.*, 9: 3678–3680. doi: 10.1002/ece3.5153.