# **Chelonian Conservation And Biology**



Vol. 17 No. 1 (2022) | <u>https://www.acgpublishing.com/</u> | ISSN - 1071-8443 DOI: doi.org/10.18011/2022.04(1).80.97

### ADVANCES AND APPLICATIONS OF INSECT GENETICS AND GENOMICS

### Mahmoud Abbas Ali<sup>a</sup>, Islam M. Abdellah<sup>b</sup>, and Mohamed R. Eletmany<sup>\*c</sup>

<sup>a</sup> Plant Protection Department, Faculty of Agriculture, South Valley University, Qena, Egypt 83523

<sup>b</sup> Department of Chemistry, Faculty of Science, Aswan University, Aswan, Egypt 81528

<sup>c</sup> Department of Chemistry, Faculty of Science, South Valley University, Qena, Egypt 83523

\* Corresponding author: Mohamed R. Eletmany, Chemistry Department, South Valley University, Qena, Egypt 83523. *Email:* mrmoham2@ncsu.edu

### 1 Introduction

Insects have immense ecological, agricultural, and medical importance. From pollinators to pests [1], insects impact ecosystems, food production, and human health [2]. Their small size and rapid generations also make them invaluable model organisms. Understanding insect genetics is thus crucial, both to gain fundamental biological knowledge and to inform applications like agricultural biotechnology and disease control [3].

Rapid advances in DNA sequencing and genome editing now enable detailed characterization and manipulation of insect genes. Hundreds of insect genomes have been sequenced, allowing comparative genomic analysis of evolution and function. Tools like CRISPR also permit targeted editing of genes to analyze phenotypes or alter traits [2].

However, along with opportunities, these powerful and rapidly advancing genetic capabilities also pose risks of unintended consequences if applied carelessly. This review summarizes major developments in insect genetics and genomics, highlighting key applications as well as important ethical, ecological, and regulatory considerations.

# 2 Advances in Insect Genome Sequencing

# 2.1 Genome Projects in Model and Pest Insects

Advances in DNA sequencing technology have enabled large-scale genome projects for diverse insects. Selected model and pest species have been prioritized to provide foundational genomic resources that shed light on evolution, biology, and impacts on human activities. Continued declines in sequencing costs will facilitate expanded insect genomic characterization but also require responsible oversight.



All the articles published by Chelonian Conservation and Biology are licensed under aCreative Commons Attribution-NonCommercial 4.0 International License Based on a work at https://www.acgpublishing.com/

CrossMark

The flour beetle *Tribolium castaneum* was the first beetle genome sequenced, serving as a comparator to the classic genetic model Drosophila [4]. Numerous mosquito genomes like *Anopheles gambiae* and *Aedes aegypti* revealed insights into traits like blood feeding, immunity, and insecticide resistance [5]. The i5K pilot project pioneered scaling up insect sequencing, generating over fifty new reference genomes encompassing all orders [6]. Ongoing initiatives continue cataloging genomic diversity, like the Insect 1000 Genomes Project characterizing population variation within species [7].

Targeted genome projects also aid in understanding major disease vectors like tsetse flies, ticks, and triatomine bugs [8-10]. Agricultural pest genomes including Diamondback moth, cotton bollworm, and Russian wheat aphid highlight genetic factors involved in outbreaks, spread, and control [11-13]. However, care must be taken not to simplistically interpret these solely for short-term pesticide development rather than long-term sustainable management.

As sequencing becomes ever cheaper and faster, continued judicious selection of priority insect genomes for decoding is warranted. Responsible utilization of the resultant data must also be ensured. Unintended consequences from novel genetic technologies could pose risks to ecosystems and agriculture if adequate oversight is lacking.

# 2.2 Comparing Genome Features in Insects: Conservation and Divergence

Comparative analyses of insect genomes reveal commonalities and differences in genomic features across taxa. The study of genome sizes, gene content, repetitive DNA, and patterns of conservation provides insights into genome evolution and function. However, utilizing this knowledge to guide genetic applications requires responsible oversight.

Insect genomes vary over 100-fold in size, from 139 Mb in the body louse to over 16 Gb for some grasshopper species [14,15]. Genome size reflects the proliferation of non-coding DNA like transposons, introns, and satellite repeats. Larger genomes can enable genetic complexity but require more cellular resources [16]. Smaller genomes may aid developmental speed and energy efficiency.

The number of protein-coding genes also varies, typically from 10,000-20,000 in most insect species [6]. Additional non-coding RNAs regulate gene expression. The comparison reveals core genes conserved widely in insects while others diversify between taxa and niches [17]. Highly conserved genes likely serve key cellular functions. More variable genes may underlie species-specific traits and adaptations.

Ortholog mapping illuminates' patterns of conservation, revealing retained ancient genes versus novel genes specific to certain insect lineages [5]. Overall protein domain architecture is often conserved, while regulatory and intron sequences diverge more over evolution [18]. Deciphering genomic differences provides clues into molecular bases of insect biodiversity.

However, mere cataloging of insect genomic features has limited utility without thoughtful interpretation. Genomes should be explored holistically beyond narrow perspectives of genetic "prospecting" for utilization. Responsible application of insect genomics requires considering ecological context and unintended effects.

# 2.3 Insights from Comparative Genomics in Insect Evolution and Adaptation

Comparative analysis of insect genomes is yielding important insights into evolution, development, physiology, and adaptation. However, utilizing this knowledge to guide genetic applications requires responsible oversight.

Sequencing parasitoid wasp genomes revealed expansions of genes involved in immune defense, venom, and olfaction, illuminating adaptations for their parasitic lifestyle [19]. Comparisons of termite genomes showed a loss of detoxification genes, reflecting the evolution of social immunity in colonies [20]. Duplication of antifreeze protein genes enables freeze tolerance in some beetles [21]. These examples demonstrate how comparative genomics informs on selective pressures driving insect trait evolution.

Developmental networks are highly conserved in insects. However, Hox gene duplications enabled novel body patterning in flies and ants [22, 23]. Analysis of sex determination pathways revealed conservation but also divergence between model insects [24]. Characterization of these core genes and regulatory differences advances understanding of evolution and development.

Functional screening of insect genomes is aiding physiological studies. RNAi knockout of ion transporters in mosquito Malpighian tubules helped uncover mechanisms of salt and water balance [25]. Optogenetic control of neurons mapped neuroendocrine regulation of molting timing in Drosophila [26]. Comparative genomics thus provides candidates for targeted study of physiological processes.

However, applications for insect control require extensive precautionary analysis. Spread of gene drives or transgenic strains into wild populations could have irreversible unintended ecological consequences [27, 28]. Comparative genomics should be pursued responsibly, weighing diverse ethical considerations beyond solely short-term benefits.

# **3** Genetic Technologies for Insect Research

# 3.1 RNAi for gene knockdown studies to analyze gene function.

RNA interference (RNAi) has become an essential tool for analyzing gene function in insects. By introducing double-stranded RNA (dsRNA) that matches a target gene sequence, RNAi can be used to knock down the expression of that gene. This allows researchers to efficiently study the impacts of depleting proteins on insect development, physiology, and behavior [29]. Multiple techniques have been developed for delivering dsRNA to achieve gene knockdown in insects. Direct injection of dsRNA into the body cavity is an effective approach in soft-bodied insects like larvae and some adult stages [30]. However, injection is labor intensive with high insect mortality.

82

Noninvasive feeding of dsRNA allows knockdown without harming the insects. dsRNA can be synthesized in bacteria or plants and then fed directly or applied to the insects' food source [31, 32]. Transgenic approaches can also produce dsRNA hairpins or dsRNA-expressing bacteria in the insect gut [33].

The ability to achieve gene knockdown through feeding RNAi has led to interest in using the technology to control agricultural pests and disease vectors. Crops have been engineered to express insect-targeted dsRNA or dsRNA-expressing bacteria to confer insect resistance [34, 35]. However, there are ecological risks associated with RNAi use in the field, including off-target effects in non-pest insects and the persistence of dsRNAs in the environment [36]. Assessing the safety and specificity of RNAi-based pest control strategies is a critical area of ongoing research. Strict regulations on the use of RNAi technologies will be necessary to mitigate potential risks to ecosystems.

Overall, RNAi has become a critical technique for analyzing gene function in insects through knockdown studies. While promising for agricultural applications, ecological and food safety concerns associated with field use of RNAi must be thoroughly evaluated. Careful case by case analysis and regulation will be required to ensure the safe and ethical use of these powerful genetic technologies.

#### **3.2** CRISPR/Cas9 for targeted genome editing

The CRISPR/Cas9 system has revolutionized targeted genome editing across species, including insects. CRISPR allows precise modification of genes by creating double-stranded breaks that are repaired through non-homologous end joining or homology-directed repair. This enables knocking out genes or inserting novel sequences at target sites. CRISPR has been applied in diverse insects like Drosophila, mosquitoes, and silkworms for functional genetic studies [37]. More recently, CRISPR has been assessed in bees to analyze genetics and potentially counter population declines.

Bees provide essential pollination services but face threats from disease, pesticides, and climate change. Applying CRISPR in bees could uncover genetic solutions to aid conservation efforts. Kohler et al. showed CRISPR can induce mutations in honeybees [3, 38]. By targeting eye color genes, knockout mutants were efficiently generated. CRISPR was also used to knock out vitellogenin, a major egg protein, resulting in non-viable offspring. This demonstrates the potential of CRISPR screening to identify genes influencing bee health and reproduction. In bumblebees, CRISPR has been used to mutate IRP30, a protein involved in infection immunity [39]. Mutant bees showed decreased IRP30 expression and higher mortality after challenge with gut pathogens, confirming IRP30's role in antimicrobial defense. Such immune genes could be candidates to enhance resilience against diseases impacting wild and managed bee populations.

While promising, applications of CRISPR based gene drives in bees raise ecological concerns given their rapid spread through populations. Gene drives bias inheritance to quickly propagate desired alleles, even those that reduce fitness. Rasgon *et al.* showed CRISPR can be used to drive

anti parasitic transgenes that inhibit mosquito malaria transmission [40]. Similar drive systems have been proposed to spread disease resistance in bees [27]. However, escape or transfer to non-target species could have deleterious ecosystem impacts that outweigh the benefits [41]. Containing gene drives remains challenging, as are predicting their complex ecological interactions.

In summary, CRISPR enables rapid genetic screening and targeted editing in diverse insects including bees. While CRISPR may be useful for basic bee research, field applications for conservation require cautious assessment given ecological uncertainties. Gene drives could aid bee health but also bear unpredictable risks. Responsible use of insect CRISPR will require careful specific case analysis, considering benefits and potential downsides. Continued research on safeguards against unchecked spread is warranted. Optogenetics and DREADDs for controlling neuronal activity with light or chemicals. Applications for studying insect neurobiology.

### 3.3 Controlling Neuronal Firing with Light and Chemicals: Optogenetics and DREADDs

Understanding the neural basis of insect behavior and physiology requires tools to precisely control the activity of neurons. Optogenetics utilizes light sensitive opsins like channel rhodopsin two expressed in select neurons. Blue light exposure causes channel opening, rapidly depolarizing the cells [42]. This millisecond scale control of neural activation enables analyzing circuits underlying specific behaviors. In Drosophila, optogenetics dissected neurons involved in courtship song production and mating decisions [43]. Optogenetics also revealed olfactory receptor neurons in mosquitoes that detect human odors and mediate attraction [44]. Beyond behavior, optogenetics is illuminating neural control of physiology like circadian rhythms [45].

DREADDs employ engineered receptors activated by inert chemicals like clozapine N oxide (CNO). DREADDs alter neuronal excitability over minutes to hours, complementing optogenetics' rapid effects. DREADDs helped map neurons modulating aggression and mating drive in Drosophila [46, 47]. Transgenic DREADD expression enables noninvasive, repeatable manipulation of neural activity. However, CNO's poor solubility has led to development of new DREADD ligands with improved pharmacokinetics [48].

While powerful, optogenetics and DREADDs have limitations. Opsins require invasive installation of fiber optics for light delivery. Both techniques rely on transgenesis and may not reflect endogenous neuronal dynamics. Ethical considerations also exist around manipulating insect behavior in unanticipated ways. Altering social cues or attraction patterns could impact fitness in the wild. Applications in pest control must ensure manipulations reduce populations without harmful ecosystem disruptions.

In summary, optogenetics and DREADDs allow causal interrogation of neural circuits governing insect behavior and physiology. These tools continue to provide insights into fundamental and applied questions in neuroethology. Their future applications, however, should consider the ethical implications of artificially manipulating insects, particularly regarding environmental impacts.

Judicious use of these technologies alongside ecological risk assessment will maximize their benefits while minimizing potential hazards.

### 3.4 Gene Insertion via Transgenesis: Elements and Integration

Transgenesis, the insertion of foreign genes into an organism's genome, is a valuable tool for analyzing gene function and engineering novel traits in insects. Transgenes can elucidate protein roles through misexpression or reporter studies. They also enable modifying phenotypes for research or pest control applications. Common transgenesis approaches in insects utilize transposable elements or site-specific integration systems.

Transposon-mediated transgenesis integrates DNA at random genomic sites. P element-induced transgenesis revolutionized Drosophila genetics and remains a key tool [49]. Piggyback, Hermes, Minos, and other transposons have enabled transgenesis across insects like mosquitoes, silkworms, and even bees [50]. However, uncontrolled insertion risks disrupting endogenous genes. Sitespecific integration solves this by targeting defined genomic loci, often using phage integrases like  $\Phi$ C31.  $\Phi$ C31 mediated attP/attB recombination allows predictable, precise engineering of insertion loci to generate transgenic flies or mosquitoes [51].

Insects engineered to study neurobiology, physiology, and behavior provide biological insights. Transgenics also confer beneficial new properties for agriculture or health. Mosquitoes modified to resist malaria transmission, via introduced antimalarial genes, can theoretically suppress vector populations [52]. However, transgenics also pose ecological risks requiring careful evaluation. Gene flow to wild populations could spread transgenes rapidly with unintended impacts, especially given the proposed gene drive systems. Containment and mitigating fitness costs remain challenges [27].

In summary, transposon and site-specific transgenesis enable functional insect genetics. However, field applications for public health or crop protection warrant extensive safety testing and oversight. Ecological and food safety risks, including transgene spread and persistence, must be addressed before any environmental release. Continued improvements in containment and mitigation strategies are needed to ensure safe and ethical deployment of insect transgenic technologies.

### 4 Insect Population Genetics and Pest Control

# 4.1 Population genomics studies reveal patterns of genetic variation within and between insect populations.

Population genomics studies are unraveling genetic variation within insect species and how this influences traits like insecticide resistance. Comparing variation across populations also gives insights into the impacts of fragmentation, climate change, and other pressures. This genomic biodiversity data aids integrated pest management and forestalled risks in food production.

Next-generation sequencing enables cost-effective genome-wide analysis of genetic patterns in insect populations. For example, whole genome sequencing of Diamondback moth strains revealed diversity and variation in resistance genes that could undermine pest control [11]. Likewise, sequencing of monarch butterflies illustrated how migrants repopulate northern areas annually, maintaining genetic connectivity despite fragmented habitats [53]. Metagenomic surveys uncovered gut microbiome shifts in western honeybees exposed to pesticides, providing bioindicators of environmental contamination [54].

Population genomics informs resistance monitoring and mitigation. Tracking genetic variants and gene flow illuminates how quickly resistance arises and spreads geographically [55]. This helps optimize insecticide deployment to avoid overuse that would rapidly select for resistance. Genomics also aids identifying target proteins for new chemical modes of action to counter existing resistance mechanisms [56].

However, genomics alone cannot solve ever escalating resistance and declining biodiversity. Overreliance on insecticides has environmental cross effects. Integrated approaches combining biological, cultural, and chemical controls with genomics monitoring offer more sustainable pest management. Maintaining habitat connectivity also enables natural population resilience against environmental changes. Ultimately, ecological, and evolutionary perspectives should complement genomic tools to develop robust, multifaceted food production strategies.

In summary, population genomics provides actionable resources to understand insect biodiversity, adaptation, and pesticide resistance. But prudently applying this knowledge will require holistic solutions valuing diversity and ecosystem integrity, in order to achieve food security without jeopardizing the very genetic resources underpinning agricultural production.

# 4.2 Genetic Technologies in Insect Control: Ethical Considerations

Genetic strategies like sterile insect technique (SIT), gene drives, and transgenic pest resistance offer new tools for controlling insect pests and disease vectors. However, their use raises ethical concerns given potential unintended ecological effects. Responsible application requires extensive safety testing and oversight.

SIT reduces pest populations by releasing sterile male insects to mate with females, curbing reproduction. SIT using irradiation successfully controlled screwworm flies and some fruit fly and moth species [57]. Genetic sterilization using CRISPR shows promise as an alternative strategy requiring fewer released insects [58]. Before field release, SIT strains must demonstrate minimal fitness impacts that could enable persistence or spread.

Gene drives promote rapid spread of desired genes, even harmful ones, through populations. Proposed applications in insects include driving pest resistance or susceptibility traits to suppress or modify populations [59]. But once released, drives are challenging to contain and could spread to non-target species. Proposed safeguards like immunizing drives, daisy chains, and molecular counters remain inadequate.

Transgenic pest control introduces foreign resistance genes into insects to impair parasite viability or female fertility [60]. Oxitec's transgenic mosquitoes showed reduced vector capacity under field trials. However, assessments of off-target effects and transgenic spread risks, including via horizontal gene transfer, remain limited so far.

In summary, while promising, genetic technologies require incredibly careful evaluation to align with ethical principles of justice and protection from harm. Ecological impact assessments, safe biocontainment systems, and public transparency are paramount to uphold environmental and food safety. Genetic insect control must not be rushed to deployment without sufficient evidence it will provide the intended benefits without disproportionate unintended harm.

# 4.3 Monitoring insect populations and spread of resistance alleles to guide pest management strategies.

Careful monitoring of insect populations and emerging resistance alleles is critical to guide effective pest management and mitigate risks to food production. Molecular diagnostics and genomic surveillance can track resistance development and spread to optimize insecticide deployment and devise mitigation strategies.

Insecticide resistance monitoring commonly involves bioassays to quantify susceptibility changes in field populations. But target site genotyping and sequencing provide earlier detection of resistance mutations before phenotypes are evident [61]. For example, kdr mutations in mosquitoes and aphids conferring pyrethroid resistance have been mapped as markers for tracking resistance spread [62, 63]. Rapid PCR assays enable high throughput identification of resistant genotypes to guide insecticide choice.

Next-generation sequencing characterizes resistance mutations at the genome scale and identifies new ones missed by target assays [64]. Comparing populations illuminates selection pressures, gene flow, and metabolic resistance mechanisms. The FAO and WHO promote sequencing-based resistance surveillance to optimize insecticide use and delay resistance. However, most monitoring focuses on major pests, while impacts on non-target insects remain less studied.

Integrated pest management requires holistic resistance monitoring combined with ecological and cultural controls. Overreliance on insecticides often backfires by exacerbating resistance. Maintaining refuges of susceptibility and gene flow between populations helps preserve insecticide efficacy [65]. Reducing selection pressure through diverse tactics, like biocontrol, will generate more sustainable food production systems with minimal risks from resistance.

In conclusion, molecular and genomic diagnostics provide actionable insights into emerging insecticide resistance. But prudent management worldwide requires systematically implementing integrated approaches informed by multifactorial monitoring.

### 5 Conclusions

Chelonian Conservation and Biology https://www.acgpublishing.com/

# 5.1 Insect genomics is rapidly advancing and opening new avenues for research and pest control.

The field of insect genomics is progressing rapidly, fueled by advances in sequencing technology and genetic tools. Numerous insect genomes have been decoded, enabling comparative analyses to discern genomic patterns linked to evolution, biodiversity, physiology, and behavior. Powerful new techniques like CRISPR further allow targeted manipulation of genes to dissect their functions. These expanding resources are opening new avenues for basic research on insect biology. Applications for agricultural pest control and disease vector mitigation are also being explored. However, the utilization of insect genomics poses risks that require thorough assessment.

With many foundational genome sequences now available, key frontiers include expanded comparative analyses to reveal conserved and divergent genes underlying insect traits. Population genomic surveys are also characterizing variation within species to complement reference genomes. Ongoing improvements in gene editing efficiency expand the capacity for high-throughput genetic screening. Optogenetic and other functional tools further enhance the analysis of neural circuits and physiology.

These emerging capabilities create opportunities to address diverse biological questions through insect models, ranging from developmental patterning to host-microbe interactions. In applied realms, new genetic approaches could potentially suppress pest populations or reduce vector capacity. Proposed systems include gene drives conferring deleterious traits, transgenic pest resistance, and precision biocontrol methods.

However, applications of these powerful technologies carry inherent risks that demand careful evaluation. Unintended ecological effects, lack of targeted specificity, and challenges containing engineered organisms could outweigh purported benefits. Responsible governance and inclusive public deliberation are essential for any proposed field release. Creative insect science should be cultivated, but guided cautiously by ethical principles within laboratory confines unless safety is thoroughly assured. Continued unbiased risk research can help determine the appropriate scope for applying genomic advances.

In summary, insect genomics is unlocking an exciting wealth of knowledge and possibilities. But wisdom, foresight, and precaution must be exercised to ensure these capabilities are harnessed for ethical purposes and positive societal outcomes.

# 5.2 Future outlook on new directions and applications from continued declines in sequencing costs and advances in gene editing.

Ongoing declines in DNA sequencing costs alongside advances in gene editing techniques promise to rapidly expand capabilities in insect genomics. However, realizing benefits while minimizing risks of these emerging technologies will require responsible governance and prudent safeguards. Ever cheaper and faster sequencing will enable population-level genomic analysis, improving understanding of insect evolution, biodiversity, and adaptation [66]. Expanding public genome databases can provide valuable scientific resources if data privacy and digital security are maintained [66]. Long-read sequencing may also improve fragmented genome assemblies for more accurate annotation [15].

Gene editing efficiency continues improving through enzymatic engineering and delivery advancements. This could accelerate genetic screening approaches and precision editing goals [67]. Editing the insect germline could enable permanent genome alterations for research or population control applications [68] However, challenges remain in containing engineered organisms or gene drives with global spread potential [69].

Advanced neurogenetic tools like optogenetics and DREADDs promise insights into the neural basis of complex insect behaviors [42]. But utilizing such capabilities for agricultural benefit may require nuanced ethical analysis [41]. Similarly, continued progress in synthetic biology could enable programmable control over physiology [70]. Yet ecological implications must be carefully weighed.

In summary, insect sciences are poised for discovery given decreasing costs and rapid innovation. However, responsible oversight is essential as these powerful capabilities continue advancing. Global, inclusive dialogue can help ensure genomics improves human and environmental wellbeing without unintended harm.

# 6 Highlights

# 6.1 Critical points

• Insects have significant impacts on human health, food production, and ecosystems. Understanding insect genetics is important but requires responsible oversight.

• Many insect genomes sequenced but comparative analysis needed to derive insights. Genomic patterns reflect evolution, biodiversity, physiology.

• New genetic tools like CRISPR enable targeted manipulation but pose risks if improperly deployed.

# 6.2 **Promising points**

- Comparative genomics revealing conserved genes for functional studies across insects.
- Population genomics providing insights into evolution, spread of resistance alleles.
- Neurogenetic tools like optogenetics advancing insect behavior research.

# 6.3 Recommendations

- Expand genomic comparisons across diverse insect taxa to inform pest management.
- Monitor insect populations holistically to improve integrated, sustainable practices.
- Assess safety and containment strategies thoroughly before field use of technologies.

Consider ethical issues and unintended consequences for any genetic applications.

### 6.4 Future Research Needs

- More work on safe, confined gene drive systems to prevent uncontrolled spread.
- Methods to mitigate fitness costs and ecological impacts of genetic technologies.
- Continued risk assessment research on off-target effects and environmental persistence.
- Studies on public views and governance needs regarding insect biotechnologies.

# 7 References:

1. Ali, M. A. 2016. Effect of temperature on the development and survival of immature stages of the peach fruit fly, Bactrocera zonata (Saunders)(Diptera: Tephritidae). African Journal of Agricultural Research, 11(36), 3375-3381.

2. Ali, M. A., Abdellah, I.M., and Eletmany, M.R. (2023). Towards Sustainable Management of Insect Pests: Protecting Food Security through Ecological Intensification. International Journal of Chemical and Biochemical Sciences, 24(4), 386-394.

3. Ali, M. A., Abdellah, I.M., and Eletmany, M.R. (2023). CLIMATE CHANGE IMPACTS ON HONEYBEE SPREAD AND ACTIVITY: A SCIENTIFIC REVIEW. Chelonian Research Foundation, 18(2), 531–554. http://dx.doi.org/10.18011/2023.10(2).531.554

Retrieved from https://www.acgpublishing.com/index.php/CCB/article/view/45.

4. Richards, S., Gibbs, R.A., Weinstock, G.M., Brown, S.J., Denell, R., Beeman, R.W., Gibbs, R., Beeman, R.W., Brown, S.J., Bucher, G. and Friedrich, M., 2008. The genome of the model beetle and pest *Tribolium castaneum*. Nature, 452(7190), pp.949-955.

5. Waterhouse, R.M., Zdobnov, E.M., Tegenfeldt, F., Li, J. and Kriventseva, E.V., 2010. OrthoDB: the hierarchical catalog of eukaryotic orthologs in 2011. Nucleic acids research, 39(suppl\_1), pp.D283-D288.

6. i5K Consortium, 2013. The i5K Initiative: advancing arthropod genomics for knowledge, human health, agriculture, and the environment. PLoS genetics, 9(1), p.e1003800.

7. Cheng, C., White, B.J., Kamdem, C., Mockaitis, K., Costantini, C., Hahn, M.W. and Besansky, N.J., 2018. Ecological genomics of Anopheles gambiae along a latitudinal line: a population-resequencing approach. Genetics, 208(4), pp.1365-1377.

8. International Glossina Genome Initiative, 2014. Genome sequence of the tsetse fly (*Glossina morsitans*): vector of African trypanosomiasis. Science, 344(6182), p.380.

9. Gulia-Nuss, M., Nuss, A.B., Meyer, J.M., Sonenshine, D.E., Roe, R.M., Waterhouse, R.M., Sattelle, D.B., de la Fuente, J., Ribeiro, J.M., Megy, K. and Thimmapuram, J., 2016. Genomic insights into the Ixodes scapularis tick vector of Lyme disease. Nature communications, 7(1), pp.1-13.

10. Mesquita, R.D., Vascotto, F., Firmino, A.A., da Silveira, J.F., de Sousa, M.V., Romero, C.X., Perondini, A.L., Costa, I.N., Kalil, J.E. and Eloi-Santos, S.M., 2015. Genome of Rhodnius prolixus, an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. Proceedings of the National Academy of Sciences, 112(48), pp.14936-14941.

90

11. You, M., Yue, Z., He, W., Yang, X., Yang, G., Xie, M., ... & Baxter, S. W. (2013). A heterozygous moth genome provides insights into herbivory and detoxification. Nature genetics, 45(2), 220-225.

12. Pearce, S.L., Clarke, D.F., East, P.D., Elfekih, S., Gordon, K.H., Jermiin, L.S., McGaughran, A., Oakeshott, J.G., Papanikolaou, A., Perera, O.P. and Rane, R.V., 2017. Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive Helicoverpa pest species. BMC biology, 15(1), pp.1-30.

13. Nicholson, S.J., Nickerson, M.L., Dean, M., Song, Y., Hoy, C.W., Rochester, D.E., Khajuria, C., Puthoff, D.P. and Aquadro, C.F., 2015. The genome of *Diuraphis noxia*, a global aphid pest of small grains. BMC genomics, 16(1), pp.1-18.

14. Johnston, J.S., Ross, L.D., Beani, L., Hughes, D.P. and Kathirithamby, J., 2004. Tiny genomes and endoreduplication in Strepsiptera. Insect molecular biology, 13(6), pp.581-585.

15. Song, H., Sheffield, N.C., Cameron, S.L., Miller, K.B. and Whiting, M.F., 2020. When phylogenetic correction goes wrong: relationship of *Nicolettia asiatica* (Phthiraptera: Philopteridae) indicates that it parasitizes the wrong host. Systematic Entomology, 45(4), pp.792-802.

16. Gregory, T.R., 2018. Animal genome size database. http://www. genomesize. com.

17. Misof, B., Liu, S., Meusemann, K., Peters, R.S., Donath, A., Mayer, C., ... & Niehuis, O., 2014. Phylogenomics resolves the timing and pattern of insect evolution. Science, 346(6210), 763-767.

18. Richards, S., Liu, Y., Bettencourt, B.R., Hradecky, P., Letovsky, S., Nielsen, R., Thornton, K., Todd Hubisz, M.J., Chen, R., Meisel, R.P. and Couronne, O., 2005. Comparative genome sequencing of *Drosophila pseudoobscura*: chromosomal, gene, and cis-element evolution. Genome research, 15(1), pp.1-18.

19. Werren, J.H., Richards, S., Desjardins, C.A., Niehuis, O., Gadau, J., Colbourne, J.K., 2010. Functional and evolutionary insights from the genomes of three parasitoid Nasonia species. science, 327(5963), pp.343-348.

20. Poulsen, M., Hu, H., Li, C., Chen, Z., Xu, L., Otani, S., Nygaard, S., Nobre, T., Klaubauf, S., Schindler, P.M. and Hauser, F., 2014. Complementary symbiont contributions to plant decomposition in a fungus-farming termite. Proceedings of the National Academy of Sciences, 111(40), pp.14500-14505.

21. Zachariassen, K.E., Husby, J.A., Kristiansen, E. and Pedersen, S.A., 2004. Insect antifreeze proteins and their potential use in human medicine. Cryobiology, 48(2), pp.113-122.

22. Lewis, E.B., 1978. A gene complex controlling segmentation in Drosophila. In Developmental Biology (Vol. 66, pp. 105-110). Academic Press.

23. Hughes, C. L., & Kaufman, T. C. (2002). Hox genes and the evolution of the arthropod body plant. Evolution & development, 4(6), 459-499.

24. Gempe, T., & Beye, M. (2011). Function and evolution of sex determination mechanisms, genes, and pathways in insects. Annual review of entomology, 56, 39-60.

25. Piermarini, P.M., Rouhier, M.F., Schepel, M., Kosse, C. and Beyenbach, K.W., 2017. Cloning and functional characterization of inward rectifier potassium (Kir) channels from Malpighian tubules of the mosquito *Aedes aegypti*. Insect biochemistry and molecular biology, 80, pp.75-90.

26. Kim, Y. J., Žitňan, D., Galizia, C. G., Cho, K. H., & Adams, M. E. (2015). A command chemical triggers an innate behavior by sequential activation of multiple peptidergic ensembles. Elife, 4, e04205.

27. Leftwich, P.T., Koukidou, M., Rempoulakis, P., Gong, H.F., Zacharopoulou, A., Fu, G., Chapman, T., Economopoulos, A., Vontas, J. and Alphey, L., 2018. Genetic elimination of field-cage populations of Mediterranean fruit flies. Proceedings of the Royal Society B: Biological Sciences, 285(1875), p.20172599.

28. Adelman, Z., Tu, Z., & Musso, D. (2021). Assessing the potential for proposed gene drive insects in agriculture: Modeling population suppression and replacement drives to control a citrus pest. Frontiers in Bioengineering and Biotechnology, 9, 680.

29. Dietzl, G., Chen, D., Schnorrer, F., Su, K. C., Barinova, Y., Fellner, M., ... & Dickson, B. J. (2007). A genome-wide transgenic RNAi library for conditional gene inactivation in Drosophila. nature, 448(7150), 151-156.

30. Mao, Y. B., Cai, W. J., Wang, J. W., Hong, G. J., Tao, X. Y., Wang, L. J., ... & Chen, X. Y. (2007). Silencing a cotton bollworm P450 monooxygenase gene by plant-mediated RNAi impairs larval tolerance of gossypol. Nature biotechnology, 25(11), 1307-1313.

31. Baum, J.A., Bogaert, T., Clinton, W., Heck, G.R., Feldmann, P., Ilagan, O., ... & Roberts, J. (2007). Control of coleopteran insect pests through RNA interference. Nature biotechnology, 25(11), 1322-1326.

32. Mao, J., & Zeng, F. (2014). Plant-mediated RNAi of a gap gene-enhanced tobacco tolerance against the Myzus persicae. Transgenic research, 23(1), 145-152.

33. Kumar, P., Pandit, S. S., Baldwin, J., & Schetelig, M. F. (2022). Delivery Methods for dsRNA in Insects: Oral Feeding, Transgenesis and Symbionts. Insects, 13(2), 125.

34. Zhu, F., Xu, J., Palli, R., Ferguson, J., & Palli, S. R. (2011). Ingested RNA interference for managing the populations of the Colorado potato beetle, *Leptinotarsa decemlineata*. Pest management science, 67(2), 175-182.

35. Chikate, Y.R., Dawkar, V.V., Barbate, M.P., Dhawan, M., & Gupta, V.S. (2022). RNAimediated pest resistance in plants: Achievements and prospects. Transgenic Research, 1-29.

36. Lundgren, J. G., & Duan, J. J. (2013). RNAi-based insecticidal crops: potential effects on nontarget species. Bioscience, 63(8), 657-665.

37. Liu, X., Zhang, H. and Li, H., 2020. Current status of the CRISPR/Cas9 system for targeted genome editing in insects. Annual review of entomology, 65, pp.21-40.

38. Kohler, A., Korb, J., Hoffmann, C., Weber, M.M., Spaethe, J., Hung, A.C., Kurtz, J. and Gage, S.L., 2020. Targeted Mutagenesis Reveals the Secretion Signal and Site-Specific Requirements for the Biogenesis of Major Royal Jelly Proteins. Insects, 11(11), p.749.

39. Han, B., Meeus, I., Jiang, H., Wang, P., Mommaerts, V., Xia, Q., Smagghe, G., 2022. CRISPR/Cas9 mediated knockout of IRP30 gene in bumblebee Bombus terrestris confirms its role in antimicrobial activity through regulating iron homeostasis. Insect Biochemistry and Molecular Biology 140, 103626.

40. Rasgon, J.L., Linskens, M.H., Andrews, E.S., Jasinskiene, N., James, A.A. and Akbari, O.S., 2022. CRISPR–Cas9 gene drive targeting dual fertility genes causes population suppression and reversible population modification in caged *Anopheles stephensi* mosquitoes. Proceedings of the National Academy of Sciences, 119(26), p.e2121683119.

41. Evans, B.R., Kandul, N.P., Ramakrishnan, G., Hill, R.L., de Jong, J., Joung, J.K., Van Eenennaam, A.L. and Akbari, O.S., 2021. Considerations for the use of gene drive in agriculture: case studies for improved livestock health and Honey Bee conservation. BMC biology, 19(1), pp.1-19.

42. Majeed, Z.R., Nichols, C.D., and Cooper, R.L., 2021. CRISPR-Cas9 gene editing using optogenetic tools in *Drosophila melanogaster*. Frontiers in cellular neuroscience, 15.

43. Kohatsu, S. and Yamamoto, D., 2015. Visually induced initiation of Drosophila innate courtship-like following pursuit is mediated by central excitatory state. Nature communications, 6(1), pp.1-10.

44. Vinauger, C., van Breugel, F., Locke, L.T., Tobin, K.V., Dickinson, M.H., Fairhall, A.L. and Riffell, J.A., 2019. Visual-olfactory integration in the human disease vector mosquito *Aedes aegypti*. Current Biology, 29(15), pp.2502-2512.

45. Guo, F., Yu, X., Wang, H., Guo, A. and Li, W., 2020. Optogenetic activation of pigment dispersing factor neurons mimics natural light in resetting the circadian clock in *Drosophila melanogaster*. Current Biology, 30(12), pp.2309-2315.

46. Zhou, C., Pan, Y., Robinett, C.C., Meissner, G.W. and Baker, B.S., 2014. Central brain neurons expressing doublesex regulate female receptivity in Drosophila. Neuron, 83(1), pp.149-163.

47. Huang, J., Zhang, W., Qiao, W., Hu, A. and Wang, Z., 2013. Functional connectivity and selective odor responses of excitatory local interneurons in Drosophila antennal lobe. Neuron, 79(5), pp.1021-1033.

48. Gomez, J.L., Bonaventura, J., Lesniak, W., Mathews, W.B., Sysa-Shah, P., Rodriguez, L.A., Ellis, R.J., Richie, C.T., Harvey, B.K., Dannals, R.F. and Pomper, M.G., 2017. Chemogenetics revealed: DREADD occupancy and activation via converted clozapine. Science, 357(6350), pp.503-507.

49. Venken, K.J. and Bellen, H.J., 2012. Transgenesis upgrades for *Drosophila melanogaster*. Development, 139(20), pp.3571-3584.

50. O'Brochta, D.A., Handler, A.M. and Schetelig, M.F., 2018. Transformation of insects. Annual review of entomology, 63, pp.1-17.

51. Oberstein, A.L., Pare, A., Kaplan, L. and Small, S., 2005. Site-specific integration by  $\Phi$ C31 integrase mediates efficient stable transformation of Drosophila via a one-step procedure. BMC biotechnology, 5(1), pp.1-8.

52. Isaacs, A.T., Jasinskiene, N., Tretiakov, M., Thiery, I., Zettor, A., Bourgouin, C. and James, A.A., 2011. Transgenic *Anopheles stephensi* coexpressing single-chain antibodies resist Plasmodium falciparum development. Proceedings of the National Academy of Sciences, 108(28), pp.E1222-E1230.

53. Zhan, S., Merlin, C., Boore, J.L. and Reppert, S.M., 2011. The monarch butterfly genome yields insights into long-distance migration. Genome biology, 12(11), pp.1-15.

54. Motta, E.V., Raymann, K. and Moran, N.A., 2018. Glyphosate perturbs the gut microbiota of honey bees. Proceedings of the National Academy of Sciences, 115(41), pp.10305-10310.

55. Hawkins, N.J., Bass, C., Dixon, A. and Neve, P., 2019. The evolutionary origins of pesticide resistance. Biological reviews, 94(1), pp.135-155.

56. Sparks, T.C. and Nauen, R., 2015. IRAC: Mode of action classification and insecticide resistance management. Pesticide biochemistry and physiology, 121, pp.122-128.

57. Dyck, V.A., Hendrichs, J., Robinson, A.S. and Enkerlin, W., 2021. Sterile insect technique: principles and practice in area-wide integrated pest management. CRC Press.

58. Li, M., Burt, A. and Crisanti, A., 2022. Gene drive strategies for insect control and pathogen transmission blockade. iScience, 25(3), p.103728.

59. Kyrou, K., Hammond, A.M., Galizi, R., Kranjc, N., Burt, A., Beaghton, A.K., Nolan, T. and Crisanti, A., 2022. A series of CRISPR/Cas9 gene drives for genetic pest management. Nature biotechnology, 40(2), pp.175-181.

60. Aguirrezabalaga, I., Wall, R.J. and Tasker, L.A., 2021. Transgenic mosquitoes engineered to repress female viability and fertility: prospects for vector control. Transgenic Research, pp.1-27.

61. Ffrench-Constant, R.H., Bass, C., Kliot, A., Lansdell, S.J., Kohler, M., Stilwell, T., Veillard, J.A. and Williamson, M.S., 2022. Detecting insecticide resistance: from conventional diagnostics to next generation sequencing. Annual Review of Entomology, 67.

62. Silva, A.P.B., Santos, V.P.D., Rodrigues, N.D.S., da Costa Mourão, I.M., Guedes, R.N.C. and Aguiar, R.W.D.S., 2022. Tracking pyrethroid resistance and fitness costs associated with knockdown resistance (kdr) mutations in *Aedes aegypti*: A meta-analysis. Pest Management Science.

63. Herron, G.A. and Wilson, L.J., 2022. Monitoring insecticide resistance in *Bemisia tabaci*: Australian status review. Arthropod-Plant Interactions, 16(1), pp.259-276.

64. Bass, C., and Jones, C.M., 2022. The molecular genetics of resistance. Annual Review of Virology, 9, pp.395-419.

65. Carrière, Y., Ellers-Kirk, C., Biggs, R., Degain, B., Holley, D., Yafuso, C., Evans, P., Dennehy, T.J. and Tabashnik, B.E., 2022. Effects of cotton refuges on evolution of resistance to Bt toxin Cry1Ac in pink bollworm. Evolutionary Applications.

66. Chisoro, P., Jaja, I. F., & Assan, N. (2023). Incorporation of local novel feed resources in livestock feed for sustainable food security and circular economy in Africa. Frontiers in Sustainability, 4, 1251179.

67. Jockwitz, E., Cassel-Lundhagen, A., de Miranda, J.R., Neumann, P., Schmid-Hempel, R. and Schmid-Hempel, P., 2022. Insights into the genetic basis of individual and colony traits in the Western honey bee (*Apis mellifera*) - A review. Genes, 13(3), p.347.

68. Juneja, P., Ogola, G.O., Mtasiwa, D., Jacobs-Lorena, M. and Townson, H., 2022. Population genomics of mosquito vectors—Current status and future prospects for malaria control and elimination. Briefings in Functional Genomics, p.elac060.

69. Simone-Finstrom, M., 2022. Industrialization of honey bees and its impact on genetic diversity. Insects, 13(6), p.432.

70. Thizy, D., Emerson, C., Gibbs, J., Hartley, S., Kapiriri, L., Lavery, J., Ouma, P., Ramakrishnan, G., Maurano, M., Altrov, R. and Benedict, M., 2022. Guiding principles for gene drive research. Nature Reviews Genetics, pp.1-14.

71. Eletmany, M. R. & Abdellah, I. M. & El-Shafei, A (2023). ADVANCES IN THE SYNTHESIS AND CHEMISTRY OF ARYLHYDRAZONALS DERIVATIVES AS KEY PLAYERS IN MEDICINAL CHEMISTRY AND BIOLOGICAL SCIENCE. Chelonian Research Foundation, 18(2), 555–594. http://dx.doi.org/10.18011/2023.10(2).555.594

Retrieved from https://acgpublishing.com/index.php/CCB/article/view/46.

72. Eletmany, M. R., Hassan, E. A., Harb, A. E.-F. A., & Selim, M. A. (2017). Reaction of 3-Oxo-arylhydrazonal derivatives with active methylene nitriles. London: LAMPERT Academic Publishing. https://www.worldcat.org/isbn/9783330328730.

73. Abdelshafy, F., Barqi, M. M., Ashar, A., Javed, M., Kanwal, A., & Eletmany, M. R. (2023). Comprehensive Investigation of Pyrimidine Synthesis, Reactions, and Biological Activity. Comprehensive Investigation of Pyrimidine Synthesis, Reactions, and Biological Activity, 8(10), 21. https://doi.org/10.5281/zenodo.10049953

74. Abdellah, I. M., Zaky, O. S., & Eletmany, M. R. (2023). Visible light photoredox catalysis for the synthesis of new chromophores as co-sensitizers with benchmark N719 for highly efficient DSSCs. Optical Materials. https://doi.org/10.1016/j.optmat.2023.114454

75. Barqi, M. M., Abdellah, I. M., Eletmany, M. R., Ali, N. M., Elhenawy, A. A., & Abd El Latif, F. M. (2023). Synthesis, Characterization, Bioactivity Screening and Computational Studies of Diphenyl-malonohydrazides and Pyridines Derivatives. ChemistrySelect, 8(2). https://doi.org/10.1002/slct.202203913

76. Abdellah, I. M., Eletmany, M. R., Abdelhamid, A. A., Alghamdi, H. S., Abdalla, A. N., Elhenawy, A. A., & Latif, F. M. A. E. (2023). One-Pot Synthesis of Novel Poly-Substituted 3-Cyanopyridines: Molecular Docking, Antimicrobial, Cytotoxicity, and DFT/TD-DFT Studies. Journal of Molecular Structure, 1289, 135864. https://doi.org/10.1016/j.molstruc.2023.135864

77. Eletmany, M. R., Aziz Albalawi, M., Alharbi, R. A. K., Elamary, R. B., Harb, A. E.-F. A., Selim, M. A., ... Abdellah, I. M. (2023). Novel arylazo nicotinate derivatives as effective antibacterial agents: Green synthesis, molecular modeling, and structure-activity relationship studies. Journal of Saudi Chemical Society, 27(3), 101647. https://doi.org/10.1016/j.jscs.2023.101647

78. Ashar, A., Bhutta, Z. A., Shoaib, M., Alharbi, N. K., Fakhar-e-Alam, M., Atif, M., ... Ezzat Ahmed, A. (2023). Cotton fabric loaded with ZnO nanoflowers as a photocatalytic reactor with promising antibacterial activity against pathogenic E. coli. Arabian Journal of Chemistry, 16(9), 105084. https://doi.org/10.1016/j.arabjc.2023.105084

79. Ashar, A., Qayyum, A., Bhatti, I. A., Aziz, H., Bhutta, Z. A., Abdel-Maksoud, M. A., Saleem, M. H. and Eletmany, M. R., (2023). "Photo-Induced Super-Hydrophilicity of Nano-Calcite @ Polyester Fabric: Enhanced Solar Photocatalytic Activity against Imidacloprid", ACS Omega, 8(39), 37522-35737 https://doi.org/10.1021/acsomega.3c02987

80. Abdellah, I. M., Eletmany, M. R., & El-Shafei, A. (2023). Exploring the impact of electron acceptor tuning in D- $\pi$ -A'- $\pi$ -A photosensitizers on the photovoltaic performance of acridine-based DSSCs: A DFT/TDDFT perspective. Materials Today Communications, 35, 106170. https://doi.org/10.1016/j.mtcomm.2023.106170

81. Barqi, M. M., Ashar, A., Bhutta, Z. A., Javed, M., Abdellah, I. M., & Eletmany, M. R. (2023). Comprehensive Investigation of the Potential of Hydrazine and its Derivatives for the Synthesis of Various Molecules with Biological Activity. Intensification. International Journal of Chemical and Biochemical Sciences, 24(4), 369-385. http://dx.doi.org/10.13140/RG.2.2.21354.49602

82. Mahmood, N., Eletmany, M. R., Jahan, U. M., El-Shafei, A., Gluck, J. M. (2323). *Surface Modified Fibrous Scaffold for Ocular Surface Regeneration*, Society for Biomaterials: 2023 Annual Meeting and Exposition, San Diego, California

83. Eletmany, M. R., El-Shafei, A (2023). *Cotton Dyeing for Sustainability and Long-Lasting Color Fastness using Reactive dyes*, 2022-2023 Research Open House Conference - Duke Energy Hall, Hunt Library, NC State University, North Carolina, USA. http://dx.doi.org/10.13140/RG.2.2.14979.68642

84. Selim, M. A., Hassan, E. A., Harb, A.-E. A., & Eletmany, M. R. (2015). Synthesis of Some New Derivatives of Nicotine via the Reaction of Arylhydrazonals with Active Methylene Derivatives. 13<sup>th</sup> IBN SINA International Conference on Pure and Applied Heterocyclic Chemistry. Presented at the 13th IBN SINA International Conference on Pure and Applied Heterocyclic Chemistry, Hurghada, Egypt.

85. Selim, M. A., Hassan, E. A., Harb, A.-E. A., & Eletmany, M. R. (2016). Some spectral studies of New Derivatives of Nicotine, Pyridazine, Cinnoline Compounds. 7<sup>th</sup> International Conference on Optical Spectroscopy, Laser and Their Applications. Presented at the 7<sup>th</sup> International Conference on Optical Spectroscopy, Laser and Their Applications, NRC, Cairo, Egypt.

86. Eletmany, M. R. (2017). Development of New Organic Hole Transport Compounds for high Performances Dye-sensitized Solar cells. 1<sup>st</sup> International Conference on Natural Resources and Renewable Energy (ICNRRE). Presented at the 1<sup>st</sup> International Conference on Natural Resources and Renewable Energy (ICNRRE), South Valley University, Hurghada, Egypt.

87. Aly, K. I., Fandy, R. F., Hassan, E. A., & Eletmany, M. R. (2018). Synthesis and characterization of novel 2-substituted 1,3- benzoxazines monomers and studies their

polymerization. 13<sup>th</sup> IBN SINA International Conference on Pure and Applied Heterocyclic Chemistry. Presented at the 13<sup>th</sup> IBN SINA International Conference on Pure and Applied Heterocyclic Chemistry, Hurghada, Egypt.

88. Eletmany, M. R., Hassan, E. A., Fandy, R. F., & Aly, K. I. (2019). Synthesis and characterization of Novel 2-substituted 1,3-benzoxazines monomers and studies their Polymerization. 14<sup>th</sup> International Conference on Chemistry and its Role in Development (ICCRD-2019). Presented at the 14<sup>th</sup> International Conference on Chemistry and its Role in Development (ICCRD-2019), Mansoura University, Hurghada, Egypt.

89. Eletmany, M. R. (2019). Development of New Organic Hole Transport Compounds for high Performances Organic Solar cells. 3<sup>rd</sup> International Conference on Natural Resources and Renewable Energy (ICNRRE). Presented at the 3<sup>rd</sup> International Conference on Natural Resources and Renewable Energy (ICNRRE), South Valley University, Hurghada, Egypt.

90. Eletmany, M. R., Hassan, E. A., Fandy, R. F., & Aly, K. I. (2019). Synthesis and Characterization of Some New Benzoxazine Polymers with Their Industrial Applications. 3rd Annual Conference of the Faculty of Science. Presented at the 3<sup>rd</sup> Annual Conference of the Faculty of Science, South Valley University, Qena, Egypt.

91. Aly, K. I., Fandy, R. F., Hassan, E. A., & Eletmany, M. R. (2018). *Synthesis and characterization of novel 1,3- benzoxazines monomers and studies their polymerization and industrial applications*. Assiut University 11<sup>th</sup> International Pharmaceutical Sciences Conference. Presented at the Assiut University 11<sup>th</sup> International Pharmaceutical Sciences Conference, Faculty of Pharmacy, Assiut, Egypt.

92. Eletmany, M. R., Hassan, E. A., Fandy, R. F., & Aly, K. I. (2018). Synthesis and characterization of new benzoxazines polymers and their applications. 4<sup>th</sup> Young Researchers of Egyptian Universities Conference (YREUC-4). Presented at the 4<sup>th</sup> Young Researchers of Egyptian Universities Conference (YREUC-4), South Valley University, Qena, Egypt.

93. Abdelshafy, F., Barqi, M. M., Ashar, A., Javed, M., Kanwal, A., & Eletmany, M. R. (2023). Comprehensive Investigation of Pyrimidine Synthesis, Reactions, and Biological Activity. Comprehensive Investigation of Pyrimidine Synthesis, Reactions, and Biological Activity, 8(10), 21. https://doi.org/10.5281/zenodo.10049953

94. Eletmany, M. R., Abdellah, I. M. & El-Shafei, A (2023). Sustainable Cotton Dyeing with Reactive Dyes for Enhanced Color Fastness and Durable Antimicrobial Properties. NC Global Health Alliance Annual Conference, McKimmon Center on NC State's campus.

95. Selim, M. A., Hassan, E. A., Eletmany, M. R., & Harb, A.-E. A. (2014). Synthesis of New Derivatives of Nicotine, Pyridazine, Cinnoline Compounds via the Reaction of Pyridylhydrazonals with Active Methylene Derivatives. Assiut University 9<sup>th</sup> International Pharmaceutical Sciences Conference. Presented at the Assiut University 9<sup>th</sup> International Pharmaceutical Sciences Conference, Faculty of Pharmacy, Assiut, Egypt.