# Fruit Fly-A Microscopic Window Bridging Life Sciences and Human Disease Research

#### Sijia Cai

Trinity College

Abstract: This article provides an in-depth exploration of the pivotal role that Drosophila melanogaster, commonly known as the fruit fly, plays in biomedicine. Originating as a genetic research model in the early 20th century, Drosophila has evolved into a preferred subject in genetics, developmental biology, and neurobiology. This study aims to comprehensively explore Drosophila's applications through a meticulous literature review, shedding light on its contributions to developmental biology, biochemistry, molecular biology, and neuroscience. In addition, this article explores and explains the intersection of modern technology and fruit fly research. This study found that remarkable progress in Drosophila genome manipulation technology has led to the development of unique techniques with cross-species applications, expanding its potential in various scientific domains. The groundbreaking milestone of its genome sequencing in contemporary times solidifies its position as a crucial model for comprehending human biology and disease processes.

Keywords: Drosophila Melanogaster; Biomedicine; Genome Manipulation Technology; Cross-Species Applications.

## **1. INTRODUCTION**

The fruit fly (Drosophila melanogaster) is a globally distributed small insect. Since its selection as a genetic research model by Morgan in the early 20th century [1], it has progressively become the preferred subject of study in various scientific disciplines, including genetics, developmental biology, and neurobiology. Drosophila boasts an extensive history in genetic research, and its unparalleled knowledge of chromosome composition, phenotype, gene encoding, and location surpasses that of other organisms. In contemporary times, Drosophila melanogaster achieved a groundbreaking milestone as the first complex organism to undergo genome sequencing [2]. This not only significantly influenced the field of Drosophila research, but also a few years later, when the human genome was sequenced, the observed homology between the two genomes reinforced its role as a pivotal model for comprehending human biology and disease processes.

Since the 1980s, there has been remarkable progress in Drosophila genome manipulation technology. Researchers have pioneered a range of highly effective techniques in Drosophila, many of which have successfully found application in other metazoans. Despite these cross-species applications, Drosophila research retains a set of unique technologies. Notably, enhancer trap technology, site-directed homologous recombination technology, two-component ectopic gene expression system, chimera analysis technology, and gene site-directed knockout technology are specific to Drosophila [3, 4]. These exclusive techniques significantly broaden the potential applications of Drosophila as a research model. Benefiting from its transparent genetic background and adaptable genetic manipulation methods, Drosophila holds irreplaceable value across diverse scientific domains such as developmental biology, biochemistry, and molecular biology. Its utilization in the field of neuroscience is also increasingly prevalent. Over nearly a century, Drosophila melanogaster has maintained a pivotal role in biological research and earned the reputation of an ideal model organism. Whether in the past, present, or future, its enduring and valuable contributions to humanity's profound exploration of the mysteries of life remain steadfast. This article aims to comprehensively explore the application of Drosophila in the realms of different area through a meticulous review of pertinent literature. Also, this study delves into the nuances of techniques, shedding light on their applications and implications in the broader scientific landscape. Furthermore, the article showcasing the adaptability and relevance of this model organism in advancing our understanding of complex biological systems. By critically analyzing the advancements and unique features of Drosophila genome manipulation technology, the study seeks to elucidate the enduring and valuable contributions of Drosophila melanogaster to the fields of genetics and biology.

#### 2. THE CHARACTERISTICS OF DROSOPHILA AS A MODEL ORGANISM.

The fruit fly, a diminutive insect measuring approximately 3mm, derives its name from its frequent presence around decaying fruits. Renowned as a model organism, the fruit fly offers numerous advantages that contribute to its widespread utilization in scientific research. These advantages encompass its small size, straightforward



operability, ease of maintenance, cost-effectiveness, brief life cycle lasting around two weeks, robust reproductive capacity, and prolific offspring production. The simplicity of phenotyping and uncomplicated laboratory upkeep further enhances its appeal [5].

In a significant milestone in 2000, the entire genome of Drosophila melanogaster was successfully sequenced. Spanning approximately 165 Mb, the genome comprises around 13,600 protein-coding genes [6]. Notably, nearly half of these proteins exhibit sequence homology with their mammalian counterparts. This starkly contrasts with another model organism, nematode nematodes, where the proportion is a mere 36%. Remarkably, over 60% of human disease genes find direct homologues in Drosophila, particularly those associated with tumors, neurological disorders, malformation syndromes, metabolic irregularities, and kidney diseases. This positioning of Drosophila as an ideal model for investigating the pathogenesis of these human diseases is underscored by the substantial overlap in genetic components [7].

# 3. THE APPLICATIONS OF DROSOPHILA AS A MODEL ORGANISM.

#### **3.1 Application of Drosophila in Genetics**

Drosophila, a venerable model for genetic research, occupies a pivotal role in elucidating fundamental principles and concepts within eukaryotic genetics. This encompasses unraveling the chromosomal foundations of sex determination, genetic linkage, chromosomal dynamics, and behavior. Since the 1970s, Drosophila melanogaster has been extensively employed in developmental biology research, providing insights into the intricate processes transforming a relatively simple fertilized egg into a complex organism. These revelations extend across embryonic development and the formation of various adult organs, including the eye, wings, legs, brain, and heart. Beyond its contributions to developmental biology, Drosophila has emerged as an outstanding model in the field of neurobiology. Its utilization facilitates the study of nervous system development and delves into the mechanisms governing advanced neural activity and behavior [8-11]. Through these multifaceted applications, Drosophila continues to be a cornerstone in advancing our understanding of genetic and biological phenomena.

#### 3.2 Utilizing Drosophila in the Study of Circadian Rhythms

Drosophila melanogaster has long served as a pivotal model organism in the exploration of circadian rhythms. A significant breakthrough occurred in 1971 when Konopka and Benzer, through the application of chemical mutagens, identified the first per mutant associated with the Drosophila circadian clock [12]. This groundbreaking study marked a turning point in understanding the molecular intricacies of circadian rhythms. Subsequent research has revealed intriguing parallels between the sleep characteristics of Drosophila and mammals [13]. Notably, Drosophila's sleep patterns exhibit enduring quiescence, an elevated arousal threshold, and responsiveness to drugs like caffeine, modafinil, isopropylamine, and antihistamines. Furthermore, Drosophila's sleep is intricately linked to brain activity and undergoes various gene expression changes [14].

Circadian rhythms wield substantial influence over Drosophila's sleep patterns, with the internal environment acting as a complementary factor in determining the timing and intensity of sleep, particularly following periods of sleep deprivation. Hendricks [15] observed that, akin to mammals and humans, young fruit flies experience more prolonged periods of sleep, which gradually become fragmented with age. Intriguingly, in contrast to humans, the total daily sleep duration in fruit flies does not diminish with aging. Furthermore, certain molecular markers regulated by sleep and wakefulness in mammals demonstrate analogous effects in Drosophila.

Collectively, the quiescent phase (sleep) of Drosophila shares numerous fundamental properties with mammals across behavioral, pharmacological, molecular biological, and genetic dimensions. Leveraging Drosophila as a model organism for sleep research holds significant promise for in-depth analyses of sleep mechanisms and the advancement of sleep-related pharmaceuticals.

# 4. MODERN BIOLOGICAL TECHNIQUES FOR INVESTIGATING FRUIT FLIES

#### 4.1 Harnessing CRISPR/Cas9 in Drosophila Research

CRISPR/Cas9, originating from the bacterial immune system, has evolved into a transformative gene-editing technology. Originally employed by bacteria to recognize and cleave viral DNA invading their genome, CRISPR/Cas9 has become a versatile tool for precisely targeting the genomes of various organisms. In the realm

of Drosophila research, this technology enables researchers to pinpoint and modify specific sequences within the fruit fly genome.

A noteworthy example of CRISPR/Cas9 application in Drosophila comes from the work of Xu et al. [16]. They conducted genome-wide CRISPR-Cas9-mediated knockout screening in Drosophila S2R+ cells, successfully identifying Visgun (Vsg) as the typical receptor for P. luminescens Tc toxin (pTc). This discovery shed light on the contribution of Tc toxin to the pathogenicity of P. luminescens. Moreover, the study established a groundbreaking genome-wide CRISPR screening method, providing a powerful approach for investigating insecticidal toxins and pathogens.

The application of CRISPR/Cas9 in Drosophila research not only showcases its potential for unraveling intricate biological mechanisms but also underscores its role in advancing our understanding of insect-pathogen interactions and facilitating the development of targeted genetic modifications in fruit flies.

#### 4.2 Integrating Machine Learning in Fruit Fly Studies

In the era of advancing technology, the integration of machine learning into Drosophila research is burgeoning, offering biologists robust tools to address intricate biological challenges. Machine learning proves instrumental in analyzing and predicting gene expression patterns in Drosophila, facilitating the inference of gene functions. This approach enhances our comprehension of the specific roles that genes play in various biological processes and pathways.

Machine learning algorithms, particularly those associated with deep learning, have found extensive application in the microscopic image analysis of Drosophila melanogaster. Automation of tasks such as the identification and tracking of fruit fly movements, classification of fruit fly morphology, and determination of their sex has become possible through these algorithms. A notable contribution comes from Chola et al. [17], who introduced an innovative automated system for classifying the sex of Drosophila using microscopic images (abdominal view). The system processes the input image into a grayscale format to extract texture features, employing machine learning classifiers such as Support Vector Machine (SVM), Naive Bayes (NB), and K-Nearest Neighbors (KNN) to categorize flies as male or female. In a real microscopic image dataset evaluation, the results indicated that the KNN classifier achieved an accuracy of 90%, surpassing the accuracy of the SVM classifier.

This application of machine learning not only expedites data analysis but also enables the feasibility of conducting large-scale experiments. By automating labor-intensive tasks and providing accurate classifications, machine learning contributes significantly to the efficiency and depth of Drosophila research.

## 5. UTILIZING FRUIT FLIES TO EXPLORE HUMAN DISEASES

#### 5.1 Unraveling Neurodegenerative Diseases through Drosophila Research

Drosophila flies emerge as pivotal model organisms in the exploration of various diseases, including aging, neurological degeneration, sleep disorders, cancer, obesity, and cardiovascular diseases. This small flying insect plays a huge role in the process of discovering new drugs, speeding up the pace of drug development and making a significant contribution to shortening the cycle of drugs from the laboratory to the market.Neurodegenerative diseases, characterized by progressive neuronal loss and the accumulation of toxic proteins, often elude early detection in human postmortem analyses of the brain and spinal cord. In contrast, the Drosophila model replicates the entire disease progression, providing a unique perspective on the developmental mechanisms of neurodegenerative diseases. Since the identification of the P transposon in the Drosophila genome in 1988, this model has gained prominence for studying degenerative diseases [18].

#### 5.2 Drosophila Contributions to Human Cancer Research

Drosophila, as a model organism, offers a more efficient approach to modeling mammalian tumor development compared to traditional mouse models, contributing to the discovery of novel cancer pathways. Numerous crucial genes (e.g., Notch gene) and signaling pathways (e.g., Hedgehog signaling pathway) related to tumors were initially identified in Drosophila and later validated in humans [19]. Presently, Drosophila tumor models have played a crucial role in screening and identifying effective compounds. Notable examples include vandetanib, inhibiting the development of multiple endocrine neoplasia type I, and asivir, which prevents tumor formation in



Drosophila models [20][21]. These findings underscore the immense potential and application value of Drosophila as an experimental model in unveiling new targets for tumor research and developing innovative anti-cancer drugs.

# 6. CONCLUSION

In this comprehensive exploration, this study have delved into the pivotal role that Drosophila research plays in the field of biomedicine. Through an extensive literature review, this article illuminates the transformative journey of Drosophila melanogaster as an exemplary experimental model. The unparalleled status of Drosophila stems from the seamless integration of its genome and the simplicity of its operability, rendering it an ideal subject for investigating diverse scientific realms, including genetics, developmental biology, and behavior. The significance of Drosophila extends beyond its historical roots, particularly as scientific and technological advancements continue to unfold. Breakthroughs in gene editing and computational biology have further widened the horizons of Drosophila research, offering unprecedented opportunities to address complex scientific queries. From deciphering the intricacies of molecular-level life to unraveling the origins and progressions of diseases, the Drosophila model stands poised to perpetuate its irreplaceable role in shaping the landscape of future life science research. However, it is crucial to acknowledge the limitations of this study. The depth of coverage in the literature review, while comprehensive, may not encompass every facet of Drosophila research due to the sheer breadth of the field. Additionally, as scientific understanding evolves, new developments may emerge that could impact the perspectives presented here.

# ACKNOWLEDGMENTS

We acknowledge the invaluable contributions of countless scientists, past and present, whose dedicated work in genetics, developmental biology, and neurobiology has propelled Drosophila melanogaster to its status as an exemplary experimental model. The groundbreaking milestone of the genome sequencing of Drosophila melanogaster in contemporary times has opened new horizons in understanding human biology and disease processes.

# REFERENCES

- G.M. Rubin, E.B. Lewis, A brief history of Drosophila's contributions to genome research, Science 287(5461) (2000) 2216-8.
- [2] M.D. Adams, The genome sequence of Drosophila melanogaster, Science 287(5461) (2000) 2185-95.
- [3] D. St Johnston, The art and design of genetic screens: Drosophila melanogaster, Nat Rev Genet 3(3) (2002) 176-88.
- [4] M.D. Adams, J.J. Sekelsky, From sequence to phenotype: reverse genetics in Drosophila melanogaster, Nat Rev Genet 3(3) (2002) 189-98.
- [5] E. Bier, R. Bodmer, Drosophila, an emerging model for cardiac disease, Gene 342(1) (2004) 1-11.
- [6] T.E. Lloyd, J.P. Taylor, Flightless flies: Drosophila models of neuromuscular disease, Ann N Y Acad Sci 1184 (2010) e1-20.
- [7] E. Bier, Drosophila, the golden bug, emerges as a tool for human genetics, Nat Rev Genet 6(1) (2005) 9-23.
- [8] Lewis, B. E., A gene complex controlling segmentation in Drosophila, Nature 276(5688) (1978) 565-70.
- [9] C. Nüsslein-Volhard, E. Wieschaus, Nusslein-Volhard, C.W.E. Mutations affecting segment number and polarity in Drosophila. Nature 287, 795-801, Nature 287(5785) (1980) 795-801.
- [10] Dom, Iacute, M. Nguez, Iacute, F. Casares, Organ specification–growth control connection: New insights from the Drosophila eye–antennal disc, Developmental Dynamics 232(3) (2005) 673–684.
- [11] J.A. Lengyel, D.D. Iwaki, It takes guts: the Drosophila hindgut as a model system for organogenesis, Developmental Biology 243(1) (2002) 1-19.
- [12] R.J. Konopka, S. Benzer, Konopka R, Benzer S. Clock mutants of Drosophila melanogaster. Proc Natl Acad Sci USA 68: 2112-2116, Proceedings of the National Academy of Sciences 68(9) (1971) 2112-2116.
- [13] E.Y. Kim, K. Bae, F.S. Ng, N.R.J. Glossop, P.E. Hardin, I. Edery, Drosophila CLOCK protein is under posttranscriptional control and influences light-induced activity, Neuron 34(1) (2002) 69-81.
- [14] C. Cirelli, D. Bushey, S. Hill, R. Huber, R. Kreber, B. Ganetzky, G. Tononi, Reduced sleep in Drosophila Shaker mutants, Nature 434(7037) (2005) 1087-92.

- [15] Hendricks, Joan, C., Sumei, Lu, Kume, Kazuhiko, Jerry, C.-P., Yin, Gender Dimorphism in the Role of cycle (BMAL1) in Rest, Rest Regulation, and Longevity in Drosophila melanogaster, Journal of Biological Rhythms (2003).
- [16] Y. Xu, R. Viswanatha, O. Sitsel, D. Roderer, H. Zhao, C. Ashwood, C. Voelcker, S. Tian, S. Raunser, N. Perrimon, M. Dong, CRISPR screens in Drosophila cells identify Vsg as a Tc toxin receptor, Nature 610(7931) (2022) 349-355.
- [17] C. Chola, J.V.B. Benifa, D.S. Guru, A.Y. Muaad, J. Hanumanthappa, M.A. Al-Antari, H. AlSalman, A.H. Gumaei, Gender Identification and Classification of Drosophila melanogaster Flies Using Machine Learning Techniques, Comput Math Methods Med 2022 (2022) 4593330.
- [18] J.P. Castro, C.M.A. Carareto, Drosophila melanogaster P transposable elements: mechanisms of transposition and regulation, Genetica 121(2) (2004) 107-118.
- [19] C. Gonzalez, Drosophila melanogaster: A model and a tool to investigate malignancy and identify new therapeutics, Nature Reviews Cancer 13(3) (2013).
- [20] T. Das, R. Cagan, Drosophila as a novel therapeutic discovery tool for thyroid cancer, Thyroid 20(7) (2010) 689.
- [21] L.F. Willoughby, T. Schlosser, S.A. Manning, J.P. Parisot, A.M. Brumby, An in vivo large-scale chemical screening platform using Drosophila for anti-cancer drug discovery, Disease Models and Mechanisms 6(2) (2012) 521-529.