

SPATIOTEMPORAL DISTRIBUTION AND PUBLIC HEALTH IMPLICATIONS OF THE SYNANTHROPIC FLY *MUSCA DOMESTICA* IN PAKISTAN BASED ON GBIF OCCURRENCE RECORDS (2010–2025)

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ABSTRACT

Musca domestica (housefly) is a medically important synanthropic insect with a well-documented role in the mechanical transmission of human pathogens. This study investigates the spatiotemporal distribution and seasonal dynamics of *M. domestica* in Pakistan using occurrence records obtained from the Global Biodiversity Information Facility (GBIF) for the period 2010–2025. After data filtering, 18,739 georeferenced records were analyzed. Temporal trends revealed a substantial increase in occurrence records after 2018, with a peak in 2024, indicating intensified reporting and/or expansion of synanthropic populations. Spatial analysis demonstrated widespread distribution across Pakistan, with pronounced clustering in densely populated and agriculturally active regions. Density-based hotspot analysis identified high-risk zones associated with urban centers, livestock operations, and waste accumulation sites. Seasonal patterns showed peak occurrence during late summer and early autumn, followed by a marked decline in winter, reflecting environmental constraints on population dynamics. These findings highlight the strong association of *M. domestica* with human-modified environments and underscore its potential role in pathogen transmission in high-density regions. This study demonstrates the utility of open-access biodiversity data in identifying vector hotspots and provides a baseline framework for integrating ecological surveillance into public health risk assessment and vector control strategies.

Keywords: *Musca domestica*, housefly, synanthropic insects, temporal trends, spatial distribution, seasonal variation, Pakistan, biodiversity databases

INTRODUCTION

Synanthropic insects are species that thrive in close association with human environments and play significant roles in ecological processes and public health. Among these, *Musca domestica* (housefly) is one of the most widely distributed insect species, commonly found in urban, rural, and agricultural settings (Graczyk et al., 2001). Its ability to exploit a wide range of organic substrates

for feeding and breeding has contributed to its global success and persistence across diverse ecological conditions (Moon, 2002).

The ecological importance of *M. domestica* is closely linked to its role as a mechanical vector of pathogens. Due to its feeding habits and frequent contact with waste materials, it can carry and transmit a wide range of microorganisms,

including bacteria, viruses, and parasites (Olsen, 2001; Graczyk et al., 2001). This characteristic makes it a species of considerable concern in both veterinary and human health contexts, particularly in regions with inadequate sanitation and waste management systems (Nazni et al., 2005).

The distribution and abundance of *M. domestica* are strongly influenced by environmental factors such as temperature, humidity, and availability of breeding substrates. Seasonal fluctuations in population density have been reported in several studies, with higher abundance typically observed during warmer months when environmental conditions favor rapid development and reproduction (Kaufman et al., 2000; Lysyk, 1998). In addition, anthropogenic factors such as urbanization, livestock farming, and waste accumulation further enhance habitat suitability for this species (Keiding, 1986).

Recent advances in biodiversity informatics have enabled large-scale analyses of species occurrence data. Open-access platforms such as the Global Biodiversity Information Facility provide extensive datasets that facilitate the study of spatial and temporal distribution patterns of species (Edwards et al., 2000). Such databases have been increasingly used to assess ecological trends, although challenges related to sampling bias and data completeness remain (Yesson et al., 2007).

Despite the availability of global data, region-specific analyses of *M. domestica* distribution remain limited, particularly in developing countries such as Pakistan. The country encompasses a wide range of climatic zones and ecological conditions, providing diverse habitats that can influence insect distribution patterns. Understanding the occurrence dynamics of *M. domestica* in this context is essential for ecological monitoring and for assessing its potential sanitary impact.

The present study aims to analyze the occurrence patterns of *Musca domestica* in Pakistan using biodiversity records from 2010 to 2025. By integrating spatial, temporal, and seasonal analyses, this study provides a comprehensive assessment of the distribution dynamics of this synanthropic species and highlights the role of

biodiversity data in ecological and public health research.

MATERIALS AND METHODS

Data Source

Occurrence data for *Musca domestica* were obtained from the Global Biodiversity Information Facility, an open-access platform that provides global biodiversity records. Data were retrieved using the scientific name *Musca domestica*, and only records corresponding to Pakistan were included in the analysis.

Data Filtering and Preparation

The downloaded dataset was filtered to include records from the period 2010 to 2025 to ensure the use of recent and relevant occurrence data. Records lacking geographic coordinates (latitude and longitude) were excluded. Additionally, entries with zero or invalid coordinates were removed to maintain spatial accuracy.

Duplicate records based on identical geographic coordinates were eliminated to avoid spatial redundancy. After data cleaning, a total of **18,739 occurrence records** were retained for further analysis.

Data Processing and Analysis

Data processing and analysis were performed using the RStudio environment (R version 4.x). Descriptive statistical analyses were conducted to evaluate occurrence patterns.

Temporal analysis was performed by extracting the year from the event date and summarizing the number of records per year to assess trends over time. Seasonal variation was examined by extracting monthly information from the dataset and analyzing the distribution of records across months.

Spatial analysis was conducted by mapping occurrence records based on geographic coordinates. Country-level distribution was assessed by examining the spatial spread of records within Pakistan.

Spatial Visualization

Spatial visualization of occurrence data was performed using R-based graphical packages. A Pakistan-focused distribution map was generated

to illustrate the geographic spread of *M. domestica*. A density-based heatmap was created using kernel density estimation to identify areas of high occurrence concentration. This approach enabled the identification of hotspot regions associated with human activity. Additionally, temporal and seasonal trends were visualized using line graphs to represent annual and monthly variation in occurrence records. All graphical outputs were generated in high resolution suitable for publication.

Software and Tools

All data processing, statistical analysis, and visualization were conducted using RStudio with relevant packages including **dplyr**, **ggplot2**, and **maps**. Data handling and preliminary inspection were optionally supported using Microsoft Excel. All analyses were conducted using reproducible scripts to ensure transparency and repeatability.

RESULTS

A total of **18,739 occurrence records** of *Musca domestica* were analyzed after data cleaning and filtering. All records corresponded to Pakistan,

representing a comprehensive country-level dataset for the period 2010–2025.

Temporal Trends

The temporal analysis revealed pronounced variation in annual occurrence records over the study period (Figure 1). From 2010 to 2015, the number of records remained relatively low, with minor fluctuations and a noticeable peak around 2012. This was followed by a gradual increase beginning in 2016, indicating a shift toward higher reporting or population presence. A substantial rise in occurrence records was observed after 2018, with a sharp increase between 2019 and 2020. The highest number of records was recorded in **2024**, representing the peak of the dataset. This upward trend suggests either increased sampling effort, improved data reporting, or a genuine rise in *M. domestica* occurrence linked to environmental or anthropogenic factors. However, a decline was observed in **2025**, which may reflect incomplete data for the year or reduced sampling intensity rather than an actual decrease in population.

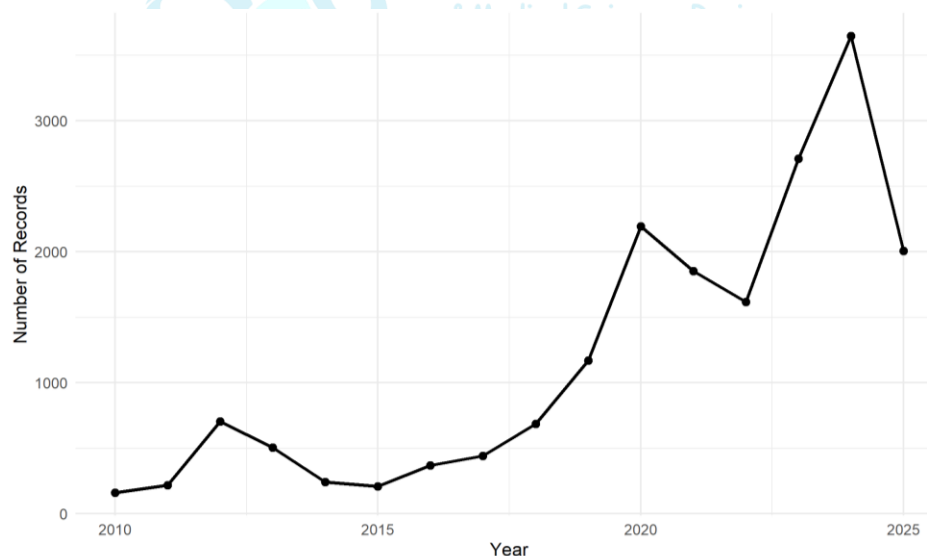


Figure 1. Temporal trend of *Musca domestica* occurrence records in Pakistan from 2010 to 2025, showing variation in annual record counts

Spatial Distribution Patterns

The spatial distribution map demonstrates that *Musca domestica* is widely distributed across Pakistan (Figure 2). Occurrence records are

densely clustered in the **eastern and central regions**, particularly in areas associated with high human population density.

Notable clustering is observed in:

- Punjab region
- Northern plains
- Urban and peri-urban zones

In contrast, **western and sparsely populated regions** exhibit fewer records, likely reflecting both lower sampling effort and reduced human-associated habitats.

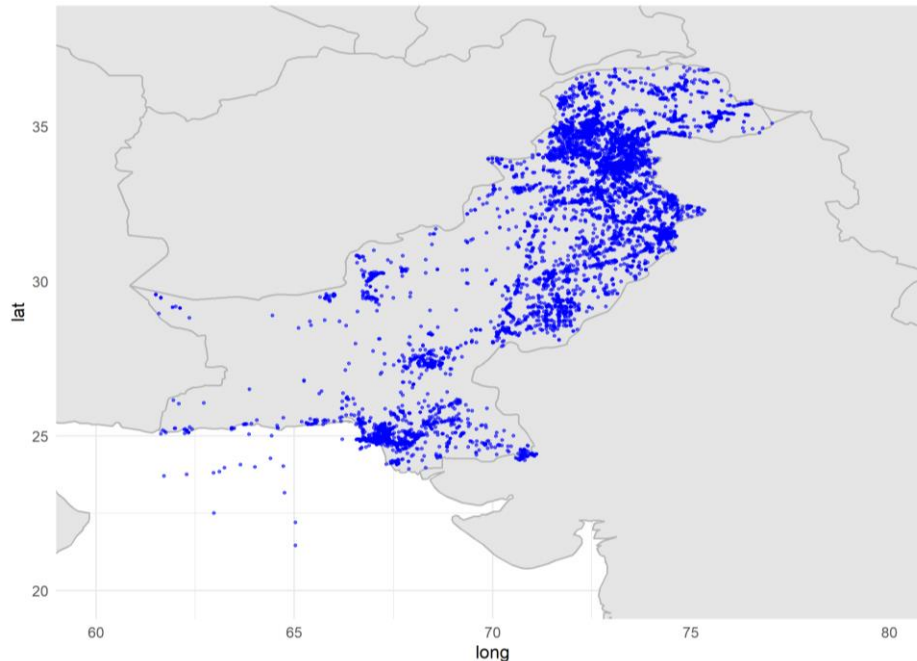


Figure 2. Spatial distribution of *Musca domestica* occurrence records across Pakistan based on GBIF data.

Density (Hotspot) Analysis

The density-based heatmap further refines spatial interpretation by identifying **hotspot regions** of occurrence (Figure 3). High-density clusters are concentrated in regions with intensive human activity, supporting the synanthropic nature of *M. domestica*.

These hotspots likely correspond to:

1. Urban centers
2. Agricultural zones
3. Livestock-associated environments

The heatmap clearly indicates that the distribution of *M. domestica* is not random but strongly structured by anthropogenic factors.

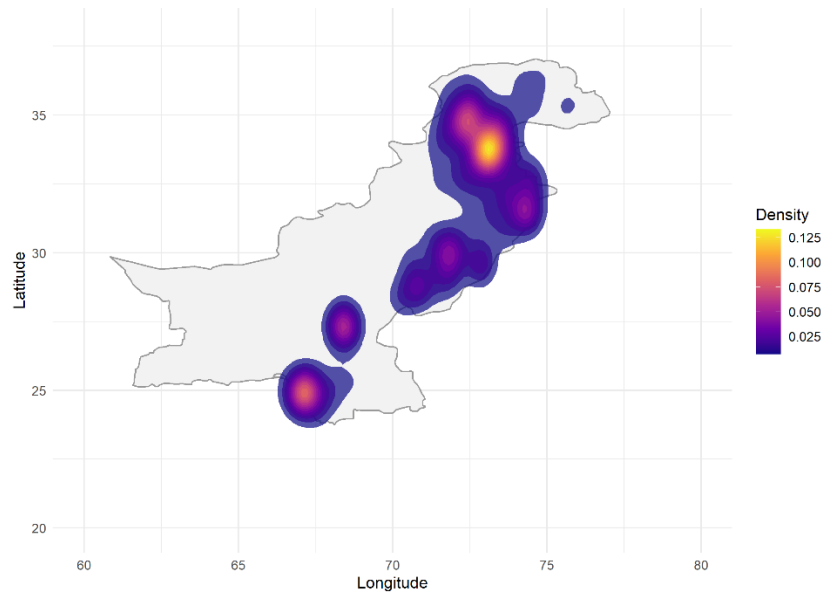


Figure 2. Density distribution (heatmap) of *Musca domestica* occurrence records in Pakistan, highlighting areas of high record concentration.

Seasonal (Monthly) Variation

Monthly analysis revealed distinct seasonal variation in occurrence records (Figure 4). The number of records gradually increased from early months of the year, reaching a peak during **late summer and early autumn (August–September)**. After this peak, a gradual decline was observed toward the winter months. This pattern suggests

that *M. domestica* activity is strongly influenced by seasonal environmental conditions, particularly temperature and humidity. Lower occurrence during winter months likely reflects reduced activity or survivability under cooler conditions.

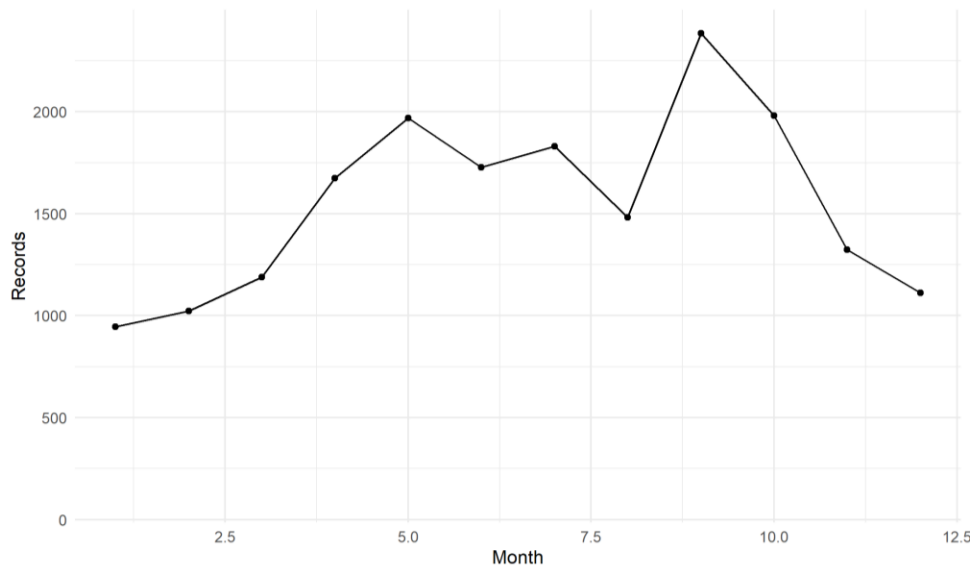


Figure 4. Monthly variation in *Musca domestica* occurrence records, illustrating seasonal patterns in distribution.

The dataset used in this study consisted of a total of **18,739 occurrence records**, all originating from Pakistan and spanning the years 2010 to 2025 (Table 1). This provides a robust foundation for analyzing both spatial and temporal patterns of *M. domestica*.

DISCUSSION

The present study provides a comprehensive analysis of the occurrence patterns of *Musca domestica* in Pakistan using biodiversity records spanning the period 2010–2025. The observed spatiotemporal distribution of *Musca domestica* in Pakistan demonstrates a strong association with densely populated urban centers, agricultural landscapes, and livestock-associated environments, highlighting its close linkage with human-modified habitats. The identification of high-density hotspots in these areas, coupled with pronounced seasonal peaks during late summer and early autumn, suggests periods and locations of increased vector activity where the risk of mechanical transmission of pathogens may be elevated. Given the species' known capacity to carry and disseminate a wide range of microorganisms through contact with contaminated substrates, these patterns have direct implications for public health, particularly in regions with inadequate sanitation and waste management infrastructure. Integrating such ecological occurrence data into vector surveillance frameworks can support targeted intervention strategies aimed at reducing disease transmission risks associated with synanthropic flies. The results demonstrate a widespread distribution of this synanthropic species across the country, reflecting its strong ecological adaptability and close association with human-modified environments. The temporal analysis revealed a clear increase in occurrence records over recent years, with a marked rise after 2018 and a peak in 2024. This trend may be attributed to a combination of factors, including increased sampling effort, improved reporting through digital biodiversity platforms, and potential environmental changes that favor the proliferation of *M. domestica*. Similar trends have been observed in biodiversity datasets, where temporal increases in occurrence records

often reflect both ecological dynamics and advancements in data collection systems (Beck et al., 2014).

The spatial distribution patterns indicate that *M. domestica* is extensively distributed across Pakistan, with higher concentrations in densely populated and agriculturally active regions. The clustering of records in eastern and central parts of the country highlights the influence of human population density and associated environmental conditions on the distribution of this species. As a synanthropic insect, *M. domestica* thrives in environments such as urban settlements, livestock farms, and waste disposal sites, which provide abundant breeding and feeding opportunities (Scott et al., 2014).

The density-based heatmap further emphasizes the non-random distribution of *M. domestica*, revealing distinct hotspot regions associated with anthropogenic activities. This spatial structuring supports the ecological characterization of *M. domestica* as a species closely linked to human environments, with its distribution largely driven by resource availability and habitat suitability.

Seasonal analysis demonstrated a clear pattern of increased occurrence during late summer and early autumn, followed by a decline in winter months. This seasonal variation is consistent with the biology of *M. domestica*, which is strongly influenced by temperature and humidity conditions that affect its reproduction and survival (Lysyk et al., 1998). Warmer conditions during summer months promote rapid population growth, while colder temperatures in winter reduce activity levels.

Although this study focuses primarily on ecological patterns, the widespread occurrence of *M. domestica* has important sanitary implications. The species is known to act as a mechanical carrier of various pathogens, including bacteria, viruses, and parasites, thereby posing potential risks to human health (Khamesipour et al., 2018). Therefore, understanding its distribution and occurrence dynamics is essential for both ecological monitoring and public health management.

Despite its strengths, this study has certain limitations. The use of occurrence data from open-

access databases may introduce biases related to uneven sampling effort, geographic data gaps, and variability in reporting intensity (Beck et al., 2014). Additionally, the absence of detailed environmental variables limits the ability to establish direct causal relationships between distribution patterns and ecological drivers. Future research could integrate climatic and environmental datasets to provide a more comprehensive understanding of the factors influencing *M. domestica* distribution.

CONCLUSION

This study presents a data-driven assessment of the occurrence patterns of *Musca domestica* in Pakistan using biodiversity records from 2010 to 2025. The findings demonstrate the widespread distribution and ecological persistence of this species across diverse regions of the country. Temporal and seasonal analyses highlight its consistent presence and strong dependence on environmental conditions, while spatial patterns emphasize its close association with human-modified habitats. The study underscores the value of open-access biodiversity databases in supporting rapid and cost-effective ecological research and provides a foundation for future investigations into the ecological and sanitary significance of synanthropic insects.

ABBREVIATIONS

GBIF – Global Biodiversity Information Facility
GIS – Geographic Information System
CSV – Comma-Separated Values
R – Statistical Computing Environment

DECLARATION SECTION

Ethics Approval and Consent to Participate

Not applicable.

Consent for Publication

Not applicable.

Availability of Data and Materials

The datasets analyzed during the current study are publicly available from the Global Biodiversity Information Facility (GBIF).

Competing Interests

The author declares no competing interests.

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Authors' Contributions

The author solely conceived the study, performed data analysis, interpreted the results, and wrote the manuscript.

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