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Avian Influenza in Asia: Descriptive Epidemiology Based on FAO EMPRES-i Data (2015–2024)

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Abstract

Based on publicly available data from the FAO EMPRES-i database, this paper provides a descriptive epidemiological analysis of avian influenza outbreaks in Asia that were reported between 2015 and 2024. A total of 27,311 outbreak data were examined in order to find patterns in the distribution of serotypes, geographic dispersion, impacted species, and zoonotic impact. The top three impacted nations were China, Vietnam, and Indonesia. H5N1 HPAI was the most prevalent serotype, and the most commonly aflicted species were chickens. Additionally, 2108 human cases with 646 fatalities were reported in the study. This study shows how open-source technologies like Python and publicly available data may be used to extract useful insights for public health and veterinary surveillance.

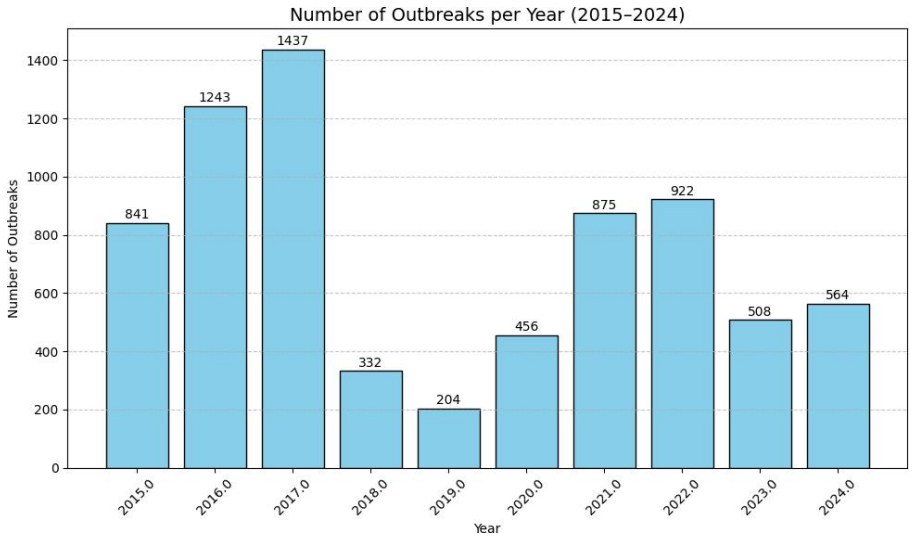
Keywords: Avian Influenza, H5N1, Python, Zoonosis, Descriptive Analysis, Veterinary Epidemiology

Introduction

Avian influenza (AI) is a highly contagious viral disease that caused by Avian influenza virus. It mostly affects birds with specific serotypes of the Avian influenza virus. It can cause serious sickness and even death in humans and poultry. Globally, the highly pathogenic avian influenza (HPAI) strains—particularly H5N1—have raised concerns about public health. Disease control and preparation depend on knowing and tracking outbreak trends. Using information from the FAO's EMPRES-i platform, this study attempts to conduct a descriptive epidemiological analysis of avian influenza outbreaks recorded from 2015 to 2024. Outbreak frequency over time, dominant serotypes, geographic hotspots, impacted species, and zoonotic effects are the main topics of the investigation.

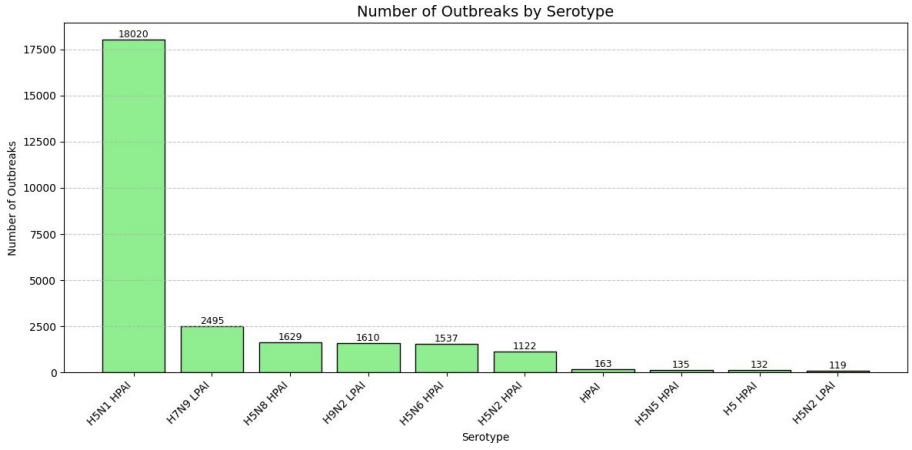
Results

Outbreak trends by year



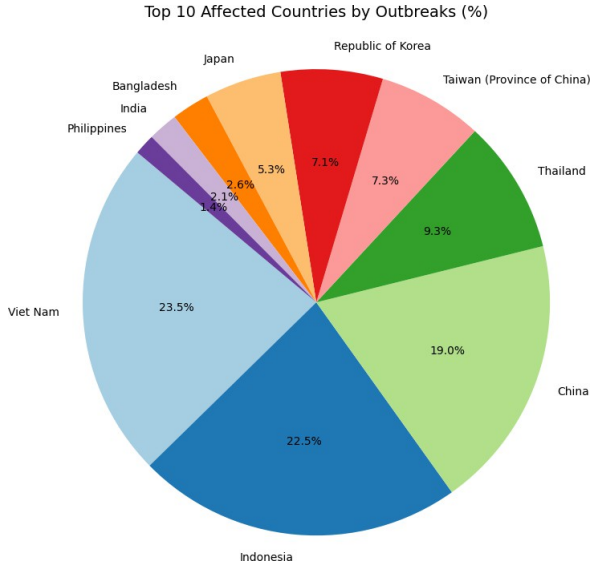
The highest number of reported outbreaks in 2017, with 1,437 cases. The lowest number was observed in 2019, with 204 cases. The years 2021 and 2022 showed an increase in cases compare to previous years. However, a decline was observed in 2023 and 2024.

Common Serotypes



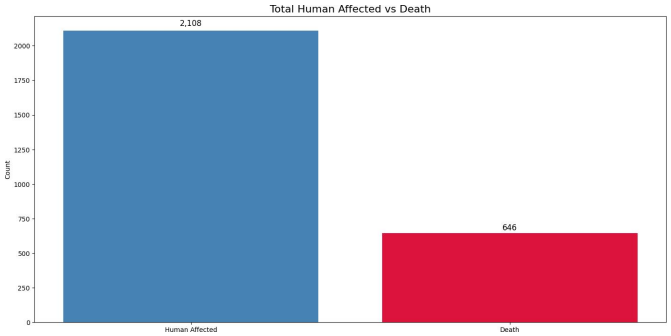
The most prevalent highly pathogenic avian influenza (HPAI) serotype was H5N1. 18020 number of outbreaks are caused by H5N1 HPAI.

Top Affected Countries



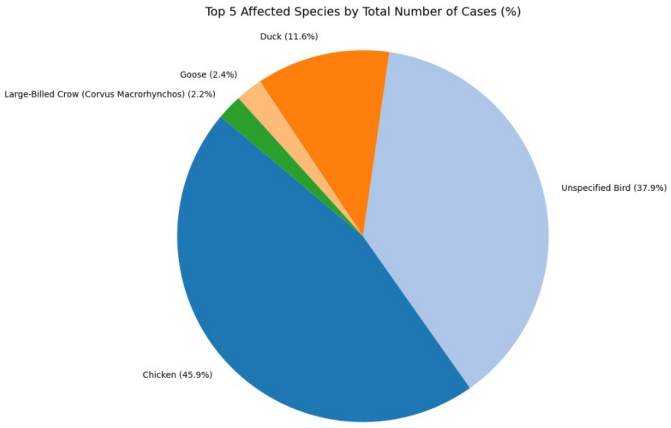
The top three affected countries in Asia were Vietnam, Indonesia, China. Among the top ten affected countries Vietnam was responsible for 23.5% of outbreaks, Indonesia for 22.5% and China for 19%.

Human Cases and Deaths



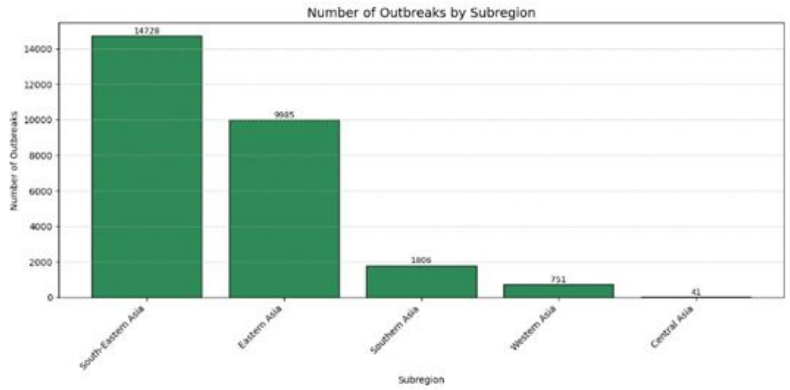
A total of 2,108 human cases of avian influenza were reported, with 646 resulting in death.

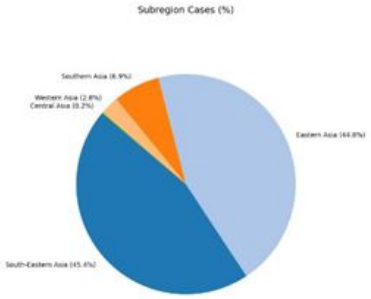
Most Affected Species



Chickens were the most affected species. Among top five affected species, 37.9% of cases were recorded in unspecified birds, while ducks were responsible for 11.6%.

Outbreak trends by Subregion





A total of 14,728 number of outbreaks were observed in South Eastern Asia. South Eastern Asia and Eastern Asia were the most affected sub region of Asia. South Asia was also significantly concerning, while central Asia accounted for only 0.2% of the total recorded outbreaks.

Discussion

Python was used for data cleaning, exploratory data analysis and data visualization. This study provides the descriptive epidemiological analysis of Avian influenza in Asia. The disease is worldwide concerning but, in this paper, it only represents the Asian region. The years 2016 and 2017 saw the highest number of outbreaks, dominated by the serotype H5N1 HPAI. South Eastern Asia and Eastern Asia were the most affected subregion and the Vietnam, Indonesia and China are the most affected countries. Chickens were the primary affected species. A total of 2,108 human cases were recorded, with 646 deaths.

Conclusion

Avian influenza is a worldwide serious issue, affecting both poultry and human. In Asia with the densely populated country are most vulnerable. This study shows the effect of Avian influenza in poultry and human. Data-driven approaches such as this can inform policy, biosecurity practices, and early warning systems. More advanced modeling is recommended in future studies.

References

1. AO EMPRES-i. https://empres-i.apps.fao.org/diseases