

# Factors that Consistently Contribute to the Evolution and Spread of Zoonotic Viruses

## Case Study: HIV-1 M and Avian Flu

### INTRODUCTION

In this study, articles were compiled to research the evolution and spread of HIV-1 M and the Avian Flu. The two zoonoses were broken into categories and analyzed in order to determine which respective factors contributed to their success as developing epidemics, with respect to their genetics and environment. This study utilizes an expository approach to review keystone literature regarding these topics.

### OBJECTIVES

The objective of this project was to compile information regarding the different factors that contribute to the evolution and spread of the two diseases studied: mode of transfer, population demographic, rate of mutation, and the medical understanding of the area.

### AVIAN FLU

- Avian flu (also known as H5N1) was detected in contaminated geese in Guangdong, China and was known as A/Goose/Guangdong/1/96<sup>10</sup>
  - the first outbreak of the flu was documented in Hong Kong in 1997<sup>10</sup>
- Evolved from reassortant genes of the A/Goose/Guangdong/1/96 and H9N2/H6N1 genes dominant in quail<sup>10</sup>
- Avian flu has been transmitted to humans by way of frequent contact with affected fowl who have the virus (mainly chickens), quail, geese, etc.
- Avian flu becomes a zoonotic disease when the segmented genome is able to undergo reassortment, therefore creating new pathways for a different strain to be made (antigenic change)<sup>10</sup>
  - Doing so allows the virus to avoid certain pathways that would lead to the viral cells dying

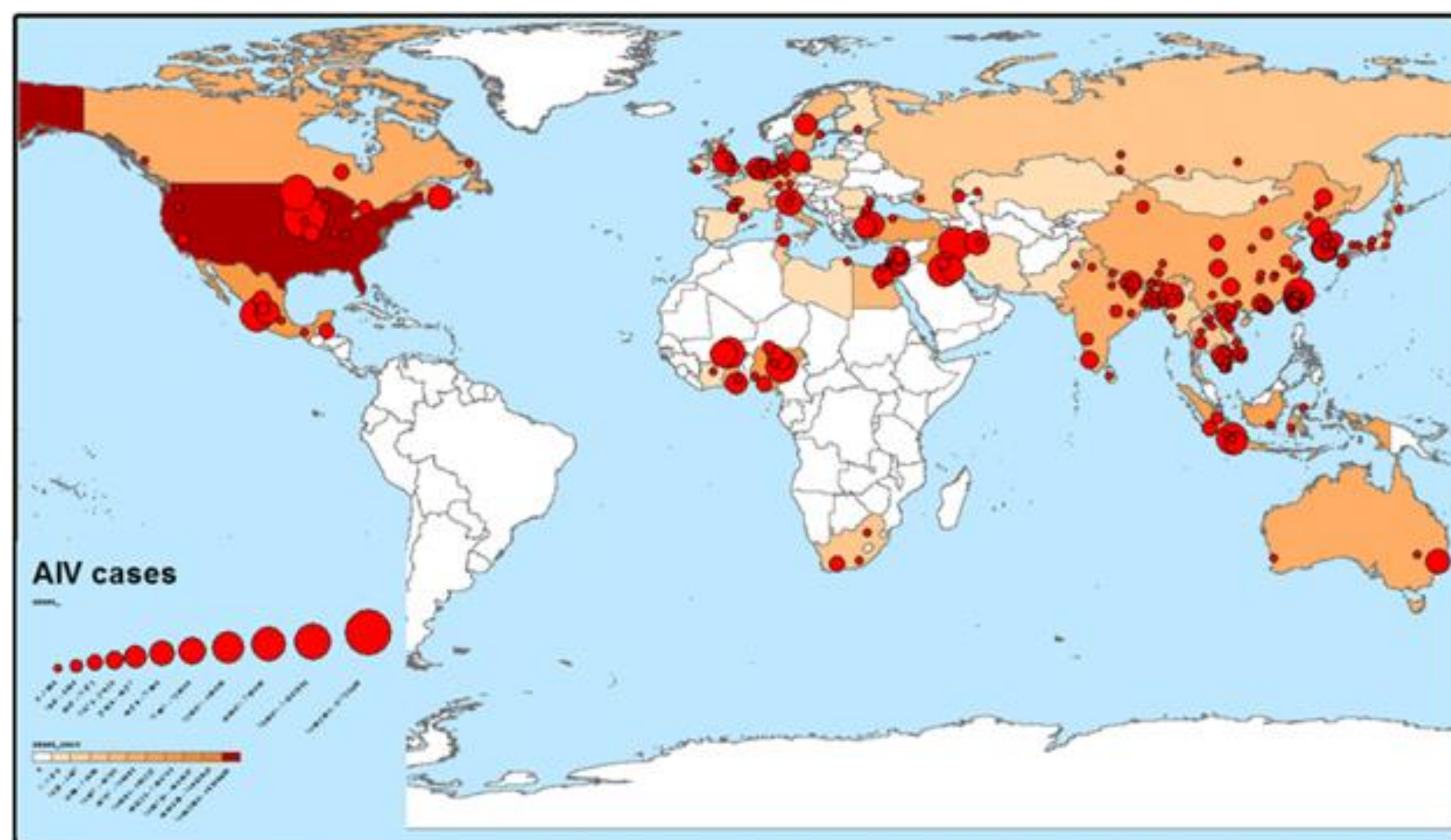


Figure 1. Global distribution of avian influenza outbreaks

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- Birds kept in close quarters and unclean conditions such as that seen in the live poultry markets of Asia makes poultry susceptible to infection. Spread is severe because it can be airborne and contracted via eyes nose and mouth. A study in 2016 which monitored these Chinese Poultry Markets concluded that these are the most prominent “breeding grounds” for the virus.<sup>4</sup>
- Dense amounts of human traffic near birds kept in these conditions, as well as a mass consumption of birds kept in these conditions creates a large possibility of contracting the virus, making avian flu a concern for humans. samples of chicken carcasses from live poultry markets contained more than 50% more viral RNA than those from traditional supermarkets. Consuming animals in a way in which human contact is not made before consumption, and avoiding contact with wild birds can ensure safety.<sup>4</sup>

### HIV-1 M

The Evolution of HIV-1 M

- Evolved from SIVcpz Ptt in chimpanzees from Southern Cameroon, Africa, around 1910-1930<sup>7</sup>
- Has the highest mutation rate of any biological organism, evolving one million times faster than mammalian DNA<sup>8</sup>, leading to over 60 strains found worldwide
- Extended contact with SIV the result of the hunting and human consumption of infected primates<sup>5</sup>
  - 80% of meat consumed by humans in rainforests is primate, society of humans required to be in contact with potentially infected animals in order to survive.<sup>5</sup>
- In order to become zoonotic, SIVcpz Ptt developed genetic circumventions to cross-species transmission obstacles
  - Most importantly was group M’s anti-tetherin (BST-2) defense system, allowing HIV-1 to bud and release virions from infected CD4 cells<sup>9</sup>

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- Disease is incurable and requires specific rotations of drugs, (HAART) to manage
  - Virus rapidly develops resistance to antivirals used alone
- Mode of transfer differs between cultures, but the main cause of exposure is sexual contact
  - Heterosexual sex in Africa, homosexual sex in U.S. and Europe, contaminated needles in China



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### CONCLUSIONS

The most vital contributors to a viral zoonotic epidemic involve multiple facets of healthcare, education, and medicine. Primarily, viral machinery and replication rates, access to proper medical treatment, animal health and husbandry, and educated awareness regarding these viruses are the key to preventing, or treating, future zoonotic outbreaks.

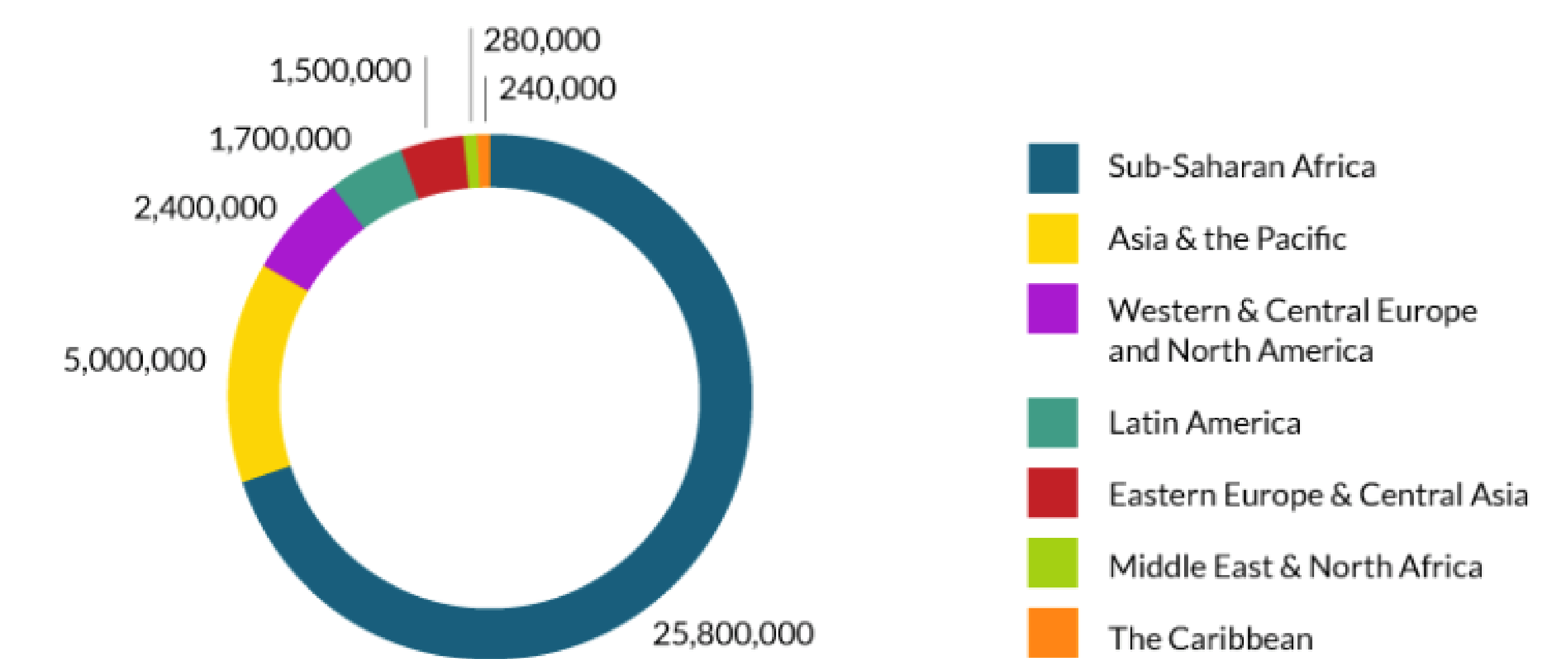


Figure 2. HIV global distribution

### FUTURE WORK

In the future, we hope to further research underlying genetic factors of zoonotic viruses. This could possibly include genetic sequencing of HIV or Avian Flu strains in order to identify the mutations that allow strains to become public health hazards.

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