

Research on HIV Spreading by Macroscopic Based on Molecular Phylogeny in Anhui Province, China

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Research Article

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Abstract

Background

Acquired Immune Deficiency Syndrome (AIDS) is a global pandemic. The disease remains the most challenging public health issue of common concern in all countries because of its high fatality rate, the widespread susceptibility of the entire population to HIV, and the lack of an effective vaccine or cure. Therefore, it is of great significance to study and analyze the spread of HIV/AIDS.

Methods

We applied Bayesian phylogenetic methods to the gene sequence of the two main subtypes (CRF 01AE and CRF 07BC, 340 in total) of the HIV virus in Anhui Province to infer the nearest ancestor and its effective reproduction number (R_e) to trace the history of HIV transmission in Anhui Province. Based on the characteristics of HIV transmission between heterosexuals and homosexuals, we established a dynamic model to predict the future trend of HIV drug resistance transmission. Through fitting the two effective reproduction numbers (R_e) from the two different methods above, we got some important parameter values. By analyzing the sensitive factors affecting the transmission situation, we proposed relevant measures to reduce the transmission of HIV-resistant strains and effectively prevent and control the HIV epidemic.

Results

Through the study of gene sequences, it was inferred that the nearest ancestor of the 150 CRF 01AE subtypes was in 1982, while the nearest ancestor of the 190 CRF 07BC subtypes was later (1992). Moreover, the effective reproduction number R_e of HIV transmission in Anhui Province has been stable at first, then increased, and then remained stable, from 1.33 in 1992 to 2.20 in 2018. The study of macro-transmission dynamics model found that simply increasing the treatment rate had little effect on reducing the infection rate of the entire population, but would lead to the increase of drug resistance rate instead. This may be due to the inverse ratio between the prevalence of HIV and the lifespan of infected patients after treatment. According to the Sensitivity analysis, a more effective way to control transmission is reducing the number of sexual partners of the MSM population. In addition, we also have unexpected new findings regarding the traditional belief that "bisexual men play a bridge role in the transmission of HIV virus": if simply cutting off the sexual relationship between women and bisexual men, the HIV epidemic will be significantly enhanced instead.

Conclusion

Study on gene sequences told us the history of HIV/AIDS spreading in Anhui province and the dynamic model told us its future. The link between them is the effective reproduction number R_e .

Full Text

Figures

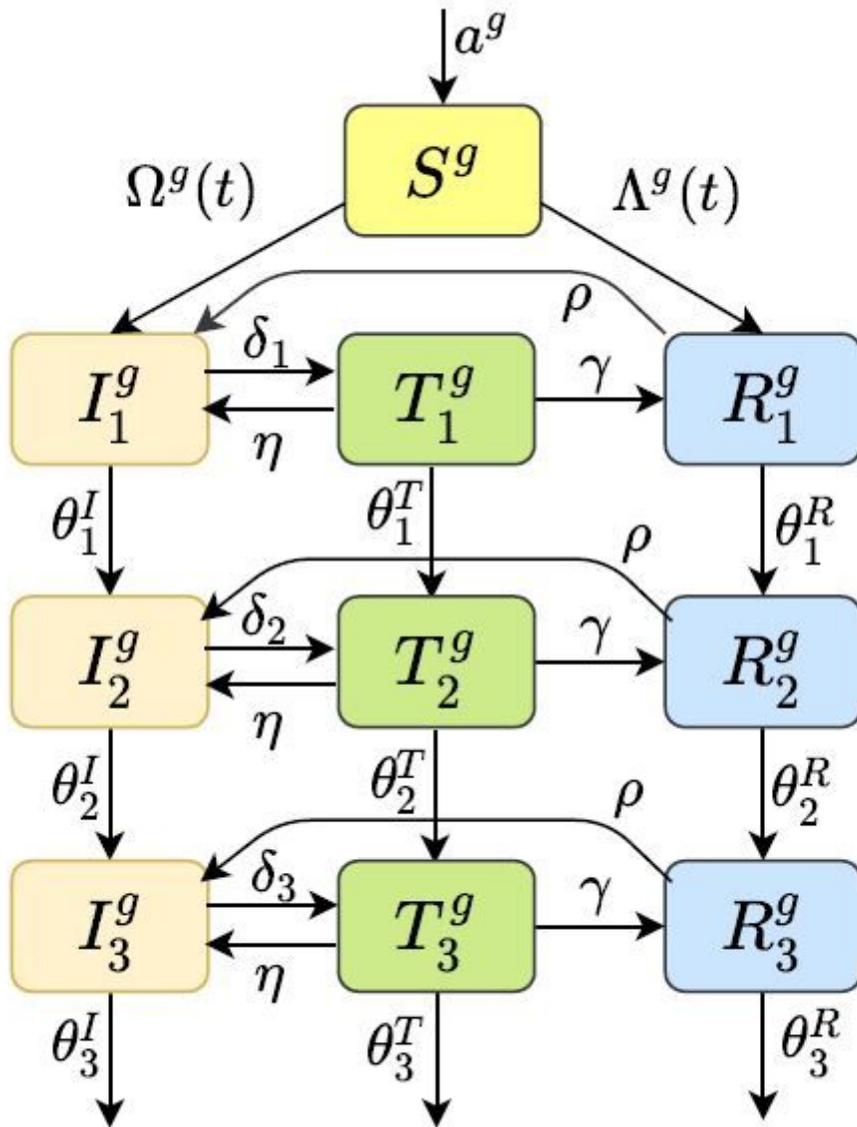


Figure 1

Transmission process diagram

Re with time

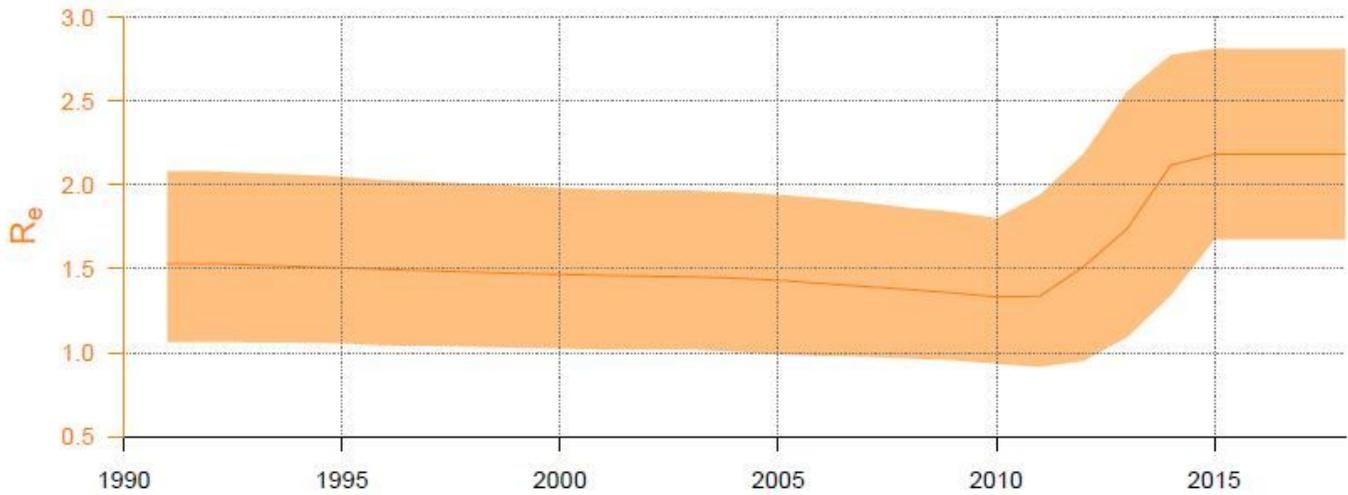


Figure 2

Dynamics of effective reproduction number R_e over time

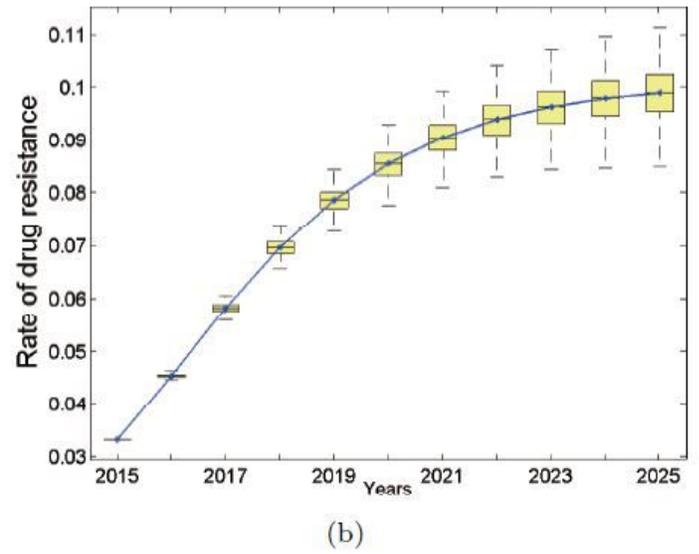
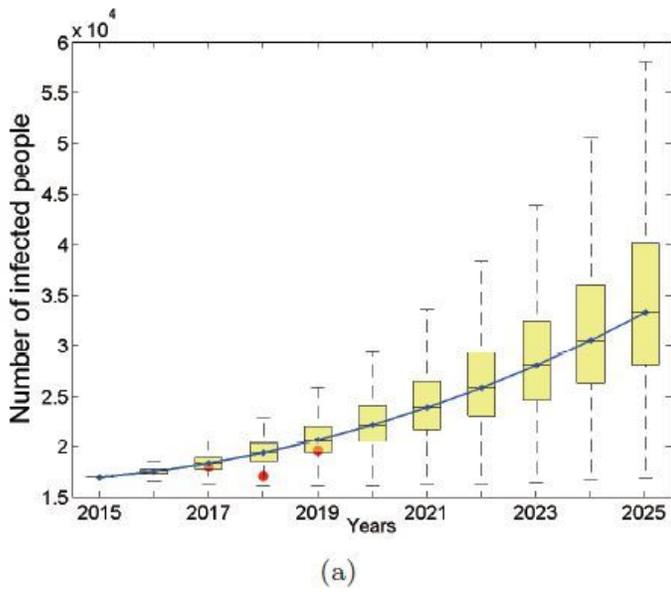
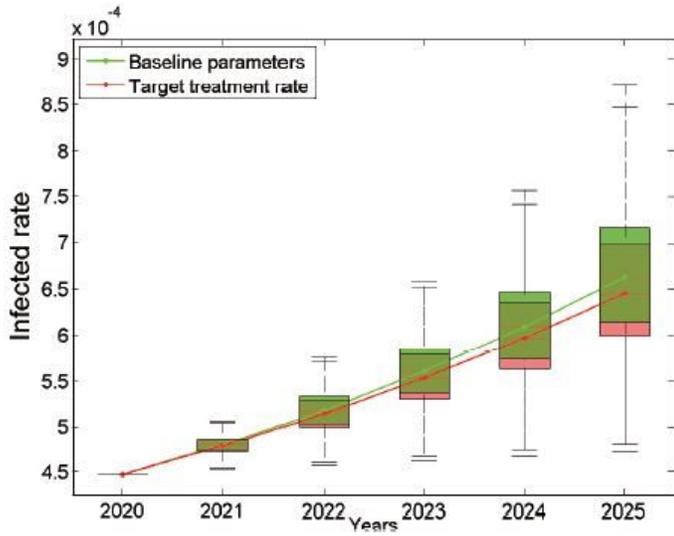
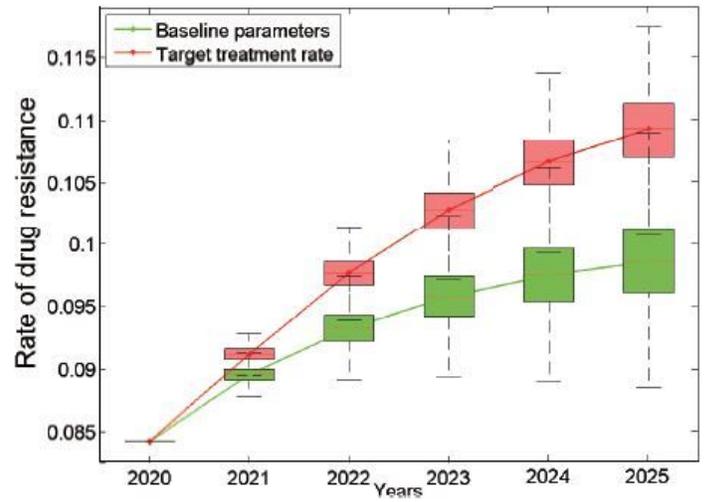


Figure 3

The number of HIV-positive people in the whole population (a) and drug resistance rate (b), where the continuous curve is the median line.



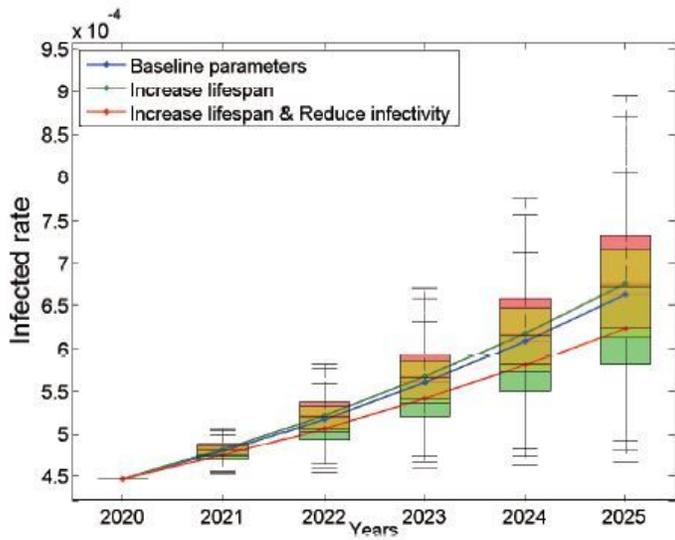
(a)



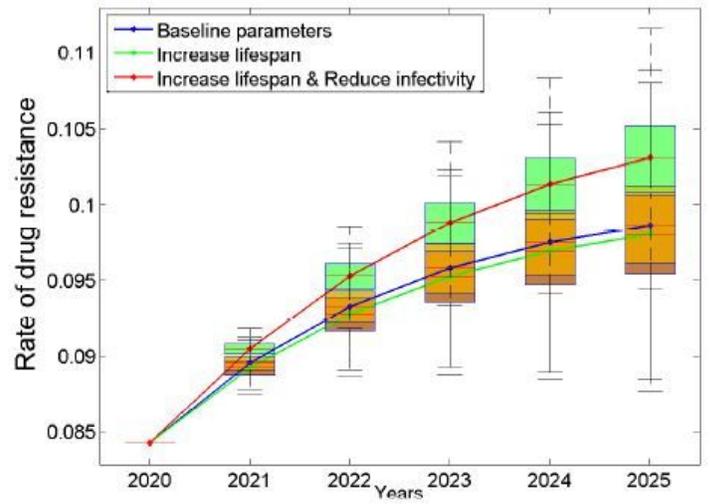
(b)

Figure 4

The impact of target treatment rates on the HIV/AIDS epidemic



(a)



(b)

Figure 5

The impact of improving the treatment effect on the HIV/AIDS epidemic

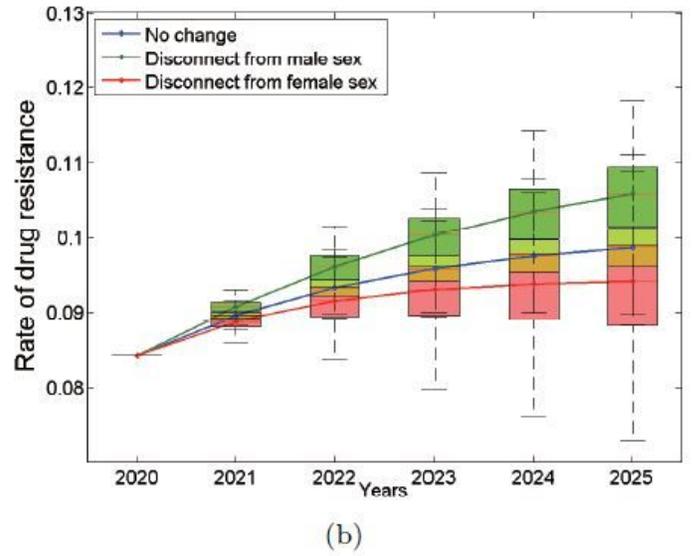
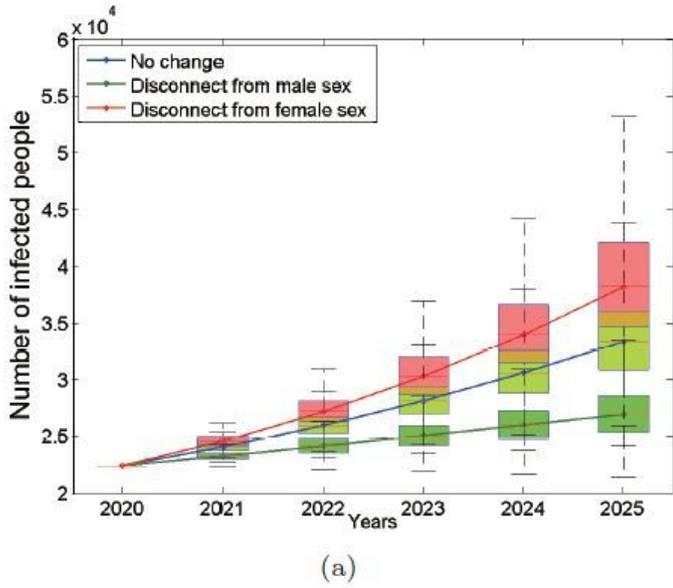


Figure 6

The impact of changing the sexual preferences of bisexual men on the HIV/AIDS epidemic.

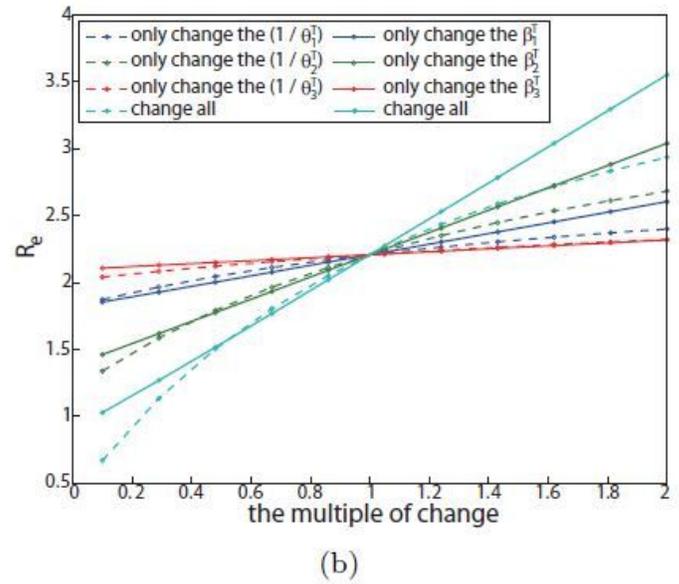
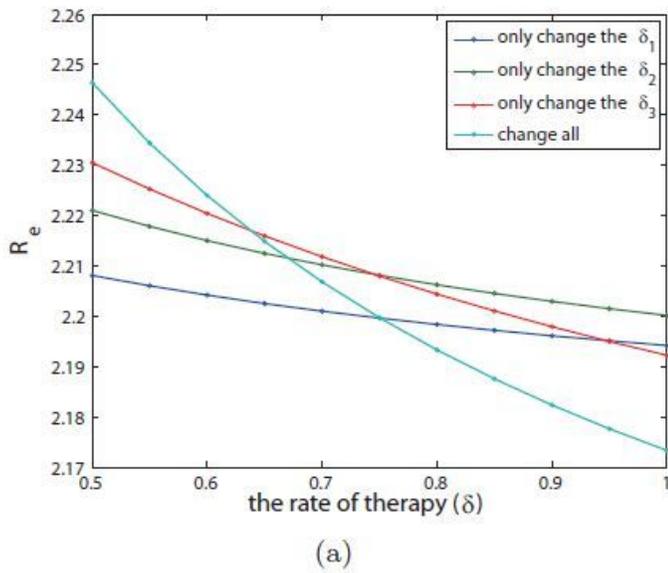


Figure 7

Sensitivity analysis of treatment rate (a), infection rate after treatment (solid line in (b)) and course of the disease after treatment(dotted line in (b)) to R_e

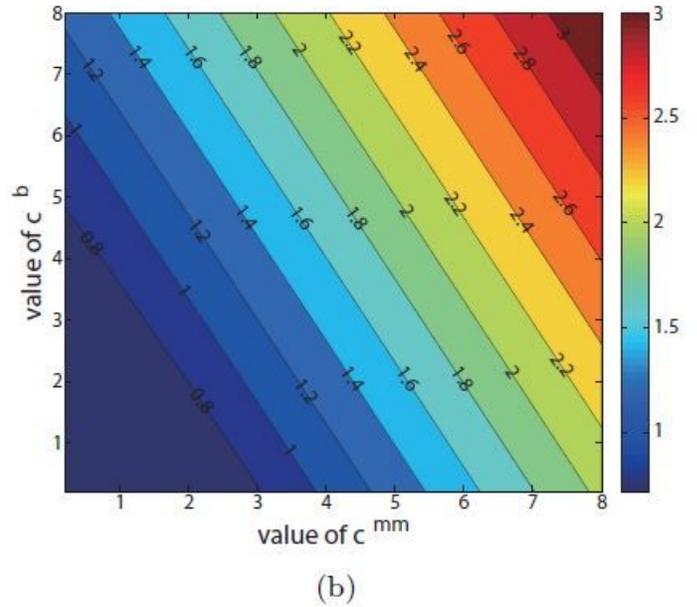
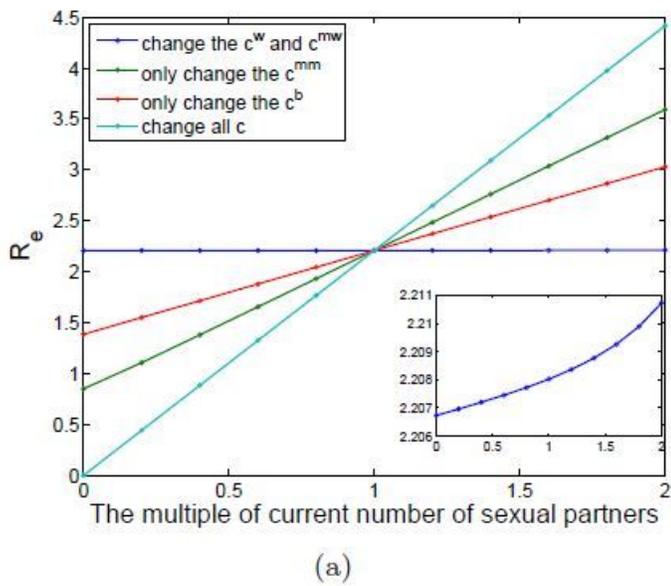


Figure 8

Sensitivity analysis of sexual partners to R_e

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- [Appendix.pdf](#)