Journal of
HIV/AIDS & Infectious Diseases

JScholar
Fostering Scholarly Communication

Research Article Open Access

The Main Reservoir of HIV Hidden in Carriers after HAART is in the Intestinal Tract, WhereVaccines Cannot Eliminate it

Vladimir Zajac*

Associate Professor, Former researcher at the Cancer Research Institute, BMC, SAS, SAV, Bratislava, Slovakia

***Corresponding author:** Vladimir Zajac, Associate Professor, Former researcher at the Cancer Research Institute, BMC, SAS, SAV, Dúbravská cesta 9, 84505, Bratislava, Slovakia, Tel: 0908281354, E-mail: vladimir.zajac@savba.sk

Received Date: February 24, 2022 **Accepted Date:** March 23, 2021 **Published Date:** March 24, 2021

Citation: Vladimir Zajac (2022) The Main Reservoir of HIV Hidden in Carriers after HAART is in the Intestinal Tract, Where Vaccines Cannot Eliminate it. J HIV AIDS Infect Dis 9: 1-5.

Abstract

All viruses, including HIV, are parasites. They cannot exist by themselves and fully depend on theircarriers. This is the basic condition of their existence. Very little is still known about how they can jump from one species to another and finally spread to humans. After all, a parasite must have its host, a living cell. It is generally claimed that a virus can exist for as little as 2-5 seconds during which it spreads to another species. But this goes against the basic dogma that a virus cannot exist without a living cell. Naturally, tracking these viral journeys is not easy and has not been fully researched. However, this is a key issue, the solution of which can lead to a fundamental reversal in how we view viruses.

Keywords: HIV; Bacteria; Carriers; Intestinal Tract; Elimination; Antibiotics

Introduction

What living cell carries viruses? We have been looking for an answer to that question for over 30 years, when we started working on the diagnosis of leukosis in cows caused by bovine leukemia virus (BLV) with the aim of its nationwide eradication in Czechoslovakia. A stable was set up in theVeterinary College, in which the progress of infection to healthy animals was monitored. Finally, after many years of research, it has been concluded that bacterial cells may be vectors of the virus and its hosts. This theory was experimentally tested and the results confirmed. By DNA hybridization were identificated BLV-like sequences in bacteria of BLV infected animals using BLV *gag, pol* and *env* fragments as probes. Consequently, based on the project for NIH, was started analysing carriers of HIV in the laboratory of prof. Flossie Wong-Staal (UCSD, USA). In this model, too, the bacterial cells of the intestinal tract were found to be the host of the virus. Evidence was confirmed at the DNA level by hybridization and PCR using commercial, diagnostic primers and consequent sequencing [1,2] By the sequencing of PCR products synthesized on the template ofpatient's bacterial DNA using primers for *env, gag and pol* HIV-1 gene, homology for more than 90% with HIV-1 isolate HXB2 (HIVHXB2CG) were revealed [1-12]. At the protein level, HIV- like proteins were confirmed by Western blotting using commercial monoclonal antibodies againstHIV antigens [4-12]. Bacteria of USA HIV/AIDS 15 patients and 25 Slovak patients most often were identified as *Escherichia coli (35%), Proteus mirabilis (15%),* followed by *Citrobacter freundii* (10%), *Staphylococcus sp.* (7%) and *Enterococcus aerogenes* (4%).

In the nasopharingeal swabs of 39 Cambodian and 28 Kenyan HIV positive children bacteria of 16Cambodian (41%) and 8 Kenyan (31%) children patients were found to be positive in colony, dot- blot DNA hybridization and in PCR using commercial diagnostic primers and consequent sequencing. HIV-like proteins were detected by Western blotting using commercial monoclonal antibodies against HIV antigens. Hybridized bacteria were mostly *Klebsiella pneumoniae* (31%), *Escherichia coli* (20%), *Staphylococcus aureus (*MRSA) (20%), *yeasts Candida albicans* (10%), *Klebsiella pneumonie* (9%). Surprisingly, *Candida albicans* in Cambodian HIV patients was positive in 60%, but negative in samples from Kenya HIV patients [4-7]. Information on the detection of retroviral sequences in bacteria has not yet been recorded. The obtained results presentthe first experimental evidence for the detection of HIV sequences in bacteria isolated from the colon of HIV/AIDS patients.

Intestinal bacteria of Slovak and American HIV/AIDS patients were tested for capacity to internalize cell of HL-60 cell line and normal human lymphocytes as well. In a study, a gentamicin protection assay found that a specific characteristic of these bacteria is a strong ability to internalizeHL-60 cells and human lymphocytes [8-12]. In comparison with intestinal bacteria isolated from patients with colorectal cancer, their capacity to internalized normal human lymphocytes is 10-25 times higher and compared with negative control it is 500 times higher. Internalization frequently resulted in partial or complete lysis (50-60%) of HL-60 cells and normal human lymphocytes. This phenomenon has not been described in the literature and its verification on other cell lines is very necessary, because the ability of bacteria containing HIV sequences to penetrate HL-60 cells or human lymphocytes represents an ideal model for study of viral pathways.

After transmission to humans, HIV enters hematopoietic cells containing the CD4 receptor and co- receptor (either CCR5 or CXCR4) on the host cell. Upon contact of viral grippers located on the surface of HIV bacteria with this receptor, the virus enters the recipient cell, where it induces the process of its destruction. After overcoming the infection and eliminating the virus in the recipient's cells by a conventional drug-based treatment approach such as HAART and activation of the immune system, the infection is suppressed and the patient can be pronounced cured So far, there is no evidence that HIV-infected people have been completely free of the virus after HAART therapy. The reason is the existence of reservoirs in which the virus cannot be destroyed. Itis generally stated that the hidden reservoir of HIV is a group of immune cells in the body that are infected with HIV but are not actively producing new HIV. HIV can hide out inside these cells for years, forming a latent HIV reservoir. At any time, cells in the latent reservoir can become active again and start making more HIV.

Results

According to our results, the main reservoir of HIV genetic information located in viral carriers is inthe gastrointestinal and respiratory tract. And this is the reason why so far there is no vaccine that would completely rid the infected person of the virus, because no vaccine in the gut and respiratory tract has an effect on HIV hidden in the carrier. Whenever the immune system is weakened due to injury, disease, drugs, medicines, HIV-transmitting bacteria multiply, penetrate the body and infect *de novo* not only the host, but they can also be transmitted

in the feces to other people. Surprisingly,no attention is currently being paid to a possible fecal infection. However, history provides us witha lot of evidence about the importance of disinfection and disposal of faeces during epidemics. This important approach has been proven many times in history and has helped to overcome epidemics.

Analysis of possible participation of bacteria bearing HIV in immunodeficiency, reduction of their amount (quantity) in intestinal tract of HIV/AIDS patients was performed by per oral application of probiotics bacteria *Escherichia coli* strain Nissle 1917 [14]. For this pilot study 18 HIV-infected ART-naïve patients were selected. The probiotics were applied per diem in a period of 3 months. The presence of probiotics bacteria in patient's intestinal tract was checked by the PCR and DNA hybridization. After three months of probiotics treatment the viral load decreased or remained on the detection limit (<400 c/ml) at 57.5% of tested patients. The viral load of patients in the study completely trimmed down about 67%. The probiotics bacteria were not detected in tampons of threepatients. The viral load of the control group of 8 asymptomatic patients increased by 77% over the corresponding time. The reached results were statistically significant (p = 0,036). Detection of probiotics bacteria in patients micro-flora was in close correlation with the remission of the viral load [16].

It is generally accepted that the HIV was transferred to humans from contact with monkeys about 70 to 100 years ago. However, this claim has not been sufficiently confirmed statistically and epidemiologically. The spread and incubation period and other symptoms of the Black Death have led to the theory that epidemic may have been caused by hemorrhagic viruses [13]. Having examined detailed historical data, we have concluded that the bacterium *Yersenia pestis* was an infectious agent in the epidemic, together with another agent which we suggest was HIV [10-12].Our considerations are strongly supported by the CCR5 delta 32 mutation, which protects against HIV infection and and based on mathematical model has been present in the Caucasian population for over 2000 years [14]. The combination of the two infectious agents led to a devastating Black Death epidemic. The plague ultimately resulted in a reduction in the number of HIV carriers and an increase in the number of CCR5D32 mutations in the Caucasian population to 10% or to 15% to 20% in the northern regions of Europe (15). In sub-Saharan Africa, this epidemic and the subsequent sanitation process did not take place, what explains the absence of the CCR5D32 mutation. This results in a much higher level of HIV genetic information in this population.

Conclusion

A virus, just like a parasite, is not a full-fledged biological form and thus hard to fight. Its main weakness is that it is hosted by bacteria or yeast. Bacteria and yeasts are a complete biological form and they can be eliminated. Based on our results, several bacterial strains may be carriers of HIV. Their detection is expected to be complicated as it may vary from individual to individual. In our experimental experience, HIV-containing bacteria are largely resistant and multidrug-resistant. Therefore, it is not easy to remove them, it requires very complex studies. By destroying microbes carrying a virus, the virus ceases to exist. Thus, many viral infections can be stopped. Confirmationof the assumption that bacteria or yeasts can serve as a reservoir of HIV genetic information, their elimination by antibiotics or competent displacement with probiotics can improve the health of treated patients.

Based on these results, it was concluded that many viruses, including HIV and novel coronavirus, can be transmitted by bacteria, yeast or by other single-celled organisms [17-20]. They can survivefor months or years in carriers and, in addition, can mutate in them without restriction, independent of the carrier. It is thought that the virus, after suppressing the infection, can enter the intestinal tract, settle and in the event of a weakened immune system, infect the host *de novo* as well as other people

Acknowledgment

Author is grateful to L. Wachsmannova, S. Ciernikova, K. Hainova, Z. Adamcikova and V. Stevurkova for participation in this work. I am also grateful to A. Liskova and H. Komjathy for support and stimulating discussion.

This work was supported by these grants: APPV-06-46-11, VEGA 2/0096/11 and VEGA 2/0170/13.This publication is also the result of the project implementation: SF ITMS project code: 26240220058 supported by the Research & Development Operational Programme funded by the ERDF.

Declaration of conflicting interest

The author declares that there is no conflict of interest.

References

1. V Zajac V, Kovac M, Ciernikova S, Mego M, Rauko P, Stevurkova V, et al. (2005) Detection of HIV sequences in colon bacteria of AIDS positive patients. Clin. Microbiol Infec 11: 53.

2. Zajac V, Mego M, Kovac M, Stevurkova V, Ciernikova S, et al. (2006) Testing of bacteria isolated from HIV/AIDS patients in Experimental models. Neuro Endocrinol Lett 27: 101-4.

3. Zajac V, Stevurkova V, Matelova L, Ujhazy E (2007) Detection of HIV-1 sequences in intestinal bacteria of HIV/AIDS patients. Neuro Endocrinol Lett 28: 591-5.

4. Zajac V, Adamcikova Z, Holec V, Hainova K, Stevurkova V, et al. (2011) Chapter in a book: Microbes, viruses and parasites in AIDS process". Editor: Vladimir Zajac. Printed in INTECH 375-90.

5. Zajac V, Matelova L, Liskova A, Mego M, Holec V, et al. (2011) Confirmation of HIV-like sequences in respiratory tract bacteria of and HIV- positive pediatric patients. Med Sci Monit 17: 154-8.

6. Hainova K, Mego M, Wachsmannova L, Adamcikova Z, Stevurkova V, et al. (2013) Microflora of intestinal and respiratory tract in AIDS process, J Antivir Antiretrovir 15: 1–6.

7. Hainova K, Adamcikova Z, Ciernikova S, Stevurkova V, Krcmery V, et al. (2014) Detection of proteins homologous with HIV-1 antigens in bacteria of positive patients - phase II. Neuro Endocrinol Lett 35: 101–6.

8. Zajac V (2014) The fundamental role of bacteria and yeasts in AIDS progression. J Vaccines Vaccin 5: 4.

9. Wachsmannova L, Ciernikova S, Majek J, Mego M, Stevurkova V, et al. (2016) Internalization property of intestinal bacteria in colon cancer and HIV/AIDS patients. Neuro Endocrinol Letters 37: 245-50.

10. Zajac V (2018) Evolutionary view of the AIDS process. J Int Med Res 46: 4032- 8.

11. Vladimir Zajac (2020) Can CCR5 delta 32 mutation be a proof of possible HIV participation in the Black Dead epidemic? J Clinical Microbiology and Infectious Diseases. 2020: 3.

12. Vladimir Zajac (2020) An Overview on the Fundamental Role of Bacteria and Yeasts in AIDS Progression. Current Topics in Medicine and Medical Research. 2020: 3.

13. Duncan SR, Scott S and Duncan CJ (2005) Reappraisal of the historical selective pressures for the CCR5-D32 mutation. J Med Genet 42: 205-8.

14. Michael NL, Louie LG, Rohrbaugh AL, Schultz KA, Dayhoff DE, et al. (1997) The role of CCR5 and CCR2 polymorphisms in HIV-1 transmission and disease progression. Nature Medicine 3: 1160–2.

15. Mecsas J, Franklin G, Kuziel WA, Brubaker RR, Falkow S, Mosier DE (2004) CCR5 mutation and plague protection. Nature 427: 606.

16. Vladimir Zajac (2019) AIDS process from an evolutionary perspective. Lecture at the "9th EuroSciCon Conference on Microbiology and Virology", 22 to 23 April 2019, Athens, Greece.

17. Vladimir Zajac (2020) Elimination ot the new coronavirus and the prevention of the second wave of infection. World Journal of Advances Research and Reviews 08: 148-50.

18. V Zajac (2020) The Role of Bacteria in Viral Transmission. Japanesse Journal of Gastroenterology and Hepathology 4: 1-2.

19. Vladimir Zajac (2021) The irreplaceable role of coronavirus carriers in its transmission and in second wave of infection. World Journal of Advances Research and Reviews 9: 226-8.

20. Anna Liskova, Vladimir Zajac (2021) Identification of a new coronavirus in rectal swabs from persons infected 15-25 days ago. World Journal of Advances Research and Reviews 10: 356-9.