Short Communication
Volume 15:05, 2024

Journal of AIDS & Clinical Research

ISSN: 2155-6113 Open Access

Mechanisms of HIV-associated Malignancies and Oncogenic Proteomics Strategies for Translational Research

Cintori Kerol*

Department of Oncology, IRCCS Azienda Ospedaliero-Universitaria di Bologna, Policlinico S. Orsola Malpighi, 40126 Bologna, Italy

Introduction

Human Immunodeficiency Virus (HIV) infection has long been recognized for its profound effects on the immune system. However, over the past few decades, it has become increasingly clear that HIV is also associated with a higher risk of developing various types of malignanciesa broader spectrum of cancers influenced by the immunocompromised state induced by HIV and its treatments. The underlying mechanisms of HIV-associated malignancies are complex and multifactorial, involving direct and indirect viral effects, chronic inflammation, immune dysregulation, and viral co-infections. which have improved life expectancy for people living with HIV, the incidence of HIV-associated malignancies remains elevated compared to the general population. This has spurred considerable interest in the molecular and proteomic changes that contribute to the development of HIV-associated cancers. In this article, we will explore the mechanisms behind HIV-associated malignancies, the role of oncogenic proteomics in understanding these cancers, and the potential applications of proteomic strategies in translational research to improve diagnosis, treatment and prevention of these cancers in HIV-infected individuals. Translational research aims to bridge the gap between laboratory findings and clinical applications. In the context of HIV-associated malignancies, proteomic strategies are increasingly being integrated into clinical research to develop personalized treatment approaches, improve cancer detection, and predict therapeutic responses. Proteomics can also be used to identify protein signatures that predict how well a patient will respond to specific therapies, including chemotherapy, immunotherapy, and ART. For example, certain proteomic profiles may indicate resistance to immune checkpoint inhibitors, helping to tailor immunotherapy regimens for HIV-infected cancer patients [1,2].

Description

HIV primarily targets orchestrating immune responses against malignancies. The depletion of these cells leads to a weakened immune system, impairing the body's ability to detect and eliminate tumor cells. while improving immune function, does not completely restore immune surveillance, making HIV-infected individuals more vulnerable to cancers. HIV infection induces persistent immune activation and inflammation, even in the presence of ART. Chronic inflammation is a known risk factor for the development of cancer because it can lead to DNA damage, mutations, and the promotion of an environment conducive to cancer growth. These viruses can directly induce cellular transformation, promote cancer cell proliferation, and evade immune responses, compounding the cancer risk in individuals with HIV. In HIV-infected individuals, the compromised immune system may also limit the effectiveness of modern cancer therapies, such as immune checkpoint inhibitors, which rely on robust immune responses. The combination of immune dysregulation, chronic viral replication, and immune evasion strategies employed by both HIV and oncogenic viruses complicates the use of immunotherapy [3-5].

Conclusion

Proteomics is the large-scale study of proteins, particularly with respect to their functions and interactions in biological systems. It involves techniques such as mass spectrometry, two-dimensional gel electrophoresis, and protein microarrays to identify and quantify proteins within cells, tissues, or body fluids. In the context of HIV-associated malignancies, oncogenic proteomics refers to the use of proteomic technologies to identify proteins and signaling pathways that contribute to the initiation, progression, and metastasis of HIV-related cancers. Proteomics can provide valuable insights into the molecular mechanisms underlying cancer development, allowing researchers to identify biomarkers for early detection, understand the pathogenesis of cancer in HIV-infected individuals, and discover new therapeutic targets. By analyzing the differences in protein expression and post-translational modifications between cancerous and non-cancerous tissues in HIV-infected individuals, oncogenic proteomics can highlight key drivers of malignancy that may be missed using traditional genomic approaches.

Acknowledgement

None.

Conflict of Interest

None.

References

1. Geretti, Anna Maria, Gary Brook, Claire Cameron and David Chadwick, et al. "British HIV Association guidelines on the use of vaccines in HIV-positive adults 2015." *HIV Med* 17 (2016): S2-S81.
2. Crum-Cianflone, Nancy F. and Eva Sullivan. "Vaccinations for the HIV-infected adult: A review of the current recommendations, part I." *Infect Dis Ther* 6 (2017): 303-331.
3. Rubin, Lorry G., Myron J. Levin, Per Ljungman and E. Graham Davies, et al. "2013 IDSA clinical practice guideline for vaccination of the immunocompromised host." *Clin Infect Dis* 58 (2014): e44-e100.
4. Bruzzesi, Elena, Laura Galli, Andrea Poli and Simona Bossolasco, et al "Prevalence and risk factors of anal HPV infection in MSM living with HIV: Identifying the target groups to prioritize for immunization." *J Aids* 91 (2022): 226-231.
5. Sadlier, Corinna, Anna O'Rourke, Alison Carr and Colm Bergin. "Seroepidemiology of hepatitis A, hepatitis B and varicella virus in people living with HIV in Ireland." *J Infect Public Heal* 10 (2017): 888-890.

***Address for Correspondence:** Cintori Kerol, Department of Oncology, IRCCS Azienda Ospedaliero-Universitaria di Bologna, Policlinico S. Orsola Malpighi, 40126 Bologna, Italy, E-mail: kerolc@gmail.com*

Received: 03 October, 2024, Manuscript No. jar-24-154546; **Editor Assigned**: 05 October, 2024, PreQC No. P-154546; **Reviewed**: 17 October, 2024, QC No. Q-154546; **Revised**: 22 October, 2024, Manuscript No. R-154546; **Published**: 29 October, 2024, DOI: 10.37421/2155-6113.2024.15.1024

How to cite this article: Kerol, Cintori. "Mechanisms of HIV-associated Malignancies and Oncogenic Proteomics Strategies for Translational Research." *AIDS Clin Res* 15 (2024): 1024.