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AI and Genotype Testing on HIV patients for better prediction rates of drug resistance

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Abstract

Through the use and support of other peer-reviewed evidence and sources, this paper aims to characterize, explore, and feature strategies for monitoring and managing drug resistance among different methods of HIV treatment more effectively. Utilizing a comprehensive review of current methodologies, including genotypic and phenotypic resistance testing, we identified important impacting factors contributing to resistance developments over recent years of different Mutations and strands of HIV (human immunodeficiency virus) and AIDS (acquired immunodeficiency syndrome). Commonly patients for HIV-2 have shown signs of resistance toward many popular forms of antiretroviral medications aimed to target different organelles of infected leukocytes. Combined with the lack of current testing of patients for this commonly developed resistance many patients have been left taking expensive treatments without knowledge of the lack of efficiency it has on them. With the use of modern artificial intelligence and new methods of DNA Genotyping patients, such as the use of INSTI's testing as highlighted through the peer-reviewed journal "Clinical Outcomes of Integrase Strand Transfer Inhibitors Containing Antiretroviral Therapy in HIV-2," the large heterogeneity pool of patients with higher risk factors for developing this resistance could be mitigated. These findings suggest an approach that combines regular resistance testing, personalized treatment regimens, and patient education programs on Retroviral drug immunities can significantly enhance the management of drug resistance as well. Implementing these strategies, HIV treatment programs can improve patient outcomes and sustain the long-term effectiveness of antiretroviral therapy for many years to come.

Keywords: Antiretroviral Therapy, HIV, Efficiency, Treatment, Risk factors

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