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HIV-1 diversity and challenges toward development of effective vaccines

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Human immunodeficiency viruses (HIVs) are characterized by extremely high genetic variability. This extensive heterogeneity resulted from high error rate of reverse transcriptase in combination fast turnover of virions among HIV-infected individuals. Generation of recombinant strains is most obvious among members of different subtypes and is also likely to occur among members of the same subtypes. Human beings are very dynamic and sexual activities are even complex. With geographical distribution of subtypes its dynamic and unpredictable process and intermixing of HIV-1 variants is inevitable. Recombinant viruses contribute already substantially to the global pandemic. This has been obvious especially in western and eastern Africa which is situated in devastated area of sub-Saharan Africa. The forefront reasons for the difficulties towards HIV vaccine development can be summarized below. First, nobody has ever recovered from HIV infection therefore no natural mechanism to imitate and produce vaccine, which will be potent across subtypes and all recombinant forms. Secondly no good animal models to use in experiments, because monkeys are mostly similar but no identical to human beings. Thirdly, HIV destroys the immune system cells that are responsible to fight against it. Lastly, HIV is highly variable and constantly changing therefore it is difficult to find a vaccine which will have the same effects across changing strains. Therefore for the effective vaccine, it is important to determine how and when super infection occurs during the course of infection. It is crucial to understand at what extend humoral and cellular immune response is efficient against divergent strains.

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