

Abstract

Integration and provirus establishment are the key steps of retroviral life cycle. Genome-wide studies show that the integration is not a random process and that groups of related retroviruses display distinguishable patterns of integration preferences. The most rated genomic features forming the integration preferences of retroviruses are transcription units, transcription start sites and CpG islands. Whereas extending knowledge of genome structure, new, mainly epigenetic marks, which have a relationship to retroviral preferences are being defined. The integration into a specific genome region has a straight influence on the provirus expression and therefore on the production of virus progeny. While integration into some regions results in provirus silencing which is managed and maintained by variety of factors, some other genomic regions are *vice-versa* capable of stable provirus expression maintenance. These findings have implications for construction of safe and efficient retroviral vectors as well as for use of modified retroviruses as markers for an epigenetic and expression profile determination of genome regions.