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Mechanism of Nucleic Acid Chaperone Function of Retroviral Nucleocapsid (NC) Proteins IOULIA ROUZINA, MY-NUONG VO, KRISTEN STEWART, KARIN MUSIER-FORSYTH, MARGARETA CRUCEANU, MARK WILLIAMS, Northeastern University, U OF M TEAM, NORTHEASTERN TEAM — Recent studies have highlighted two main activities of HIV-1 NC protein contributing to its function as a universal nucleic acid chaperone. Firstly, it is the ability of NC to weakly destabilize all nucleic acid,(NA), secondary structures, thus resolving the kinetic traps for NA refolding, while leaving the annealed state stable. Secondly, it is the ability of NC to aggregate NA, facilitating the nucleation step of bi-molecular annealing by increasing the local NA concentration. In this work we use single molecule DNA stretching and gel-based annealing assays to characterize these two chaperone activities of NC by using various HIV-1 NC mutants and several other retroviral NC proteins. Our results suggest that two NC functions are associated with its zinc fingers and cationic residues, respectively. NC proteins from other retroviruses have similar activities, although expressed to a different degree. Thus, NA aggregating ability improves, and NA duplex destabilizing activity decreases in the sequence: MLV NC, HIV NC, RSV NC. In contrast, HTLV NC protein works very differently from other NC proteins, and similarly to typical single stranded NA binding proteins. These features of retroviral NCs co-evolved with the structure of their genomes.

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