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DNA sequence analysis of the inverted terminal repeats of a non-oncogenic avian adenovirus

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In all adenoviruses (AV) studied to date the DNA possesses a unique inverted terminal repeat (ITR) of the form abc ... c'b'a'.Although the repeat sequences are thought to have a role in DNA replication their exact function is unknown(1).Terminal DNA fragments of fowl adenovirus type 10 were identified by limited Bal 31 digestion of genomic DNA prior to restriction enzyme cleavage and gel electrophoresis.The terminal fragments identified were further confirmed by extracting the viral DNA with the terminal protein intact, as previously described (2).The sequence of the non-oncogenic fowl adenovirus type 10 ITR is presented (Fig. 1), comparison with other AV ITRs reveals several interesting features.Firstly the length of the ITR of this non-oncogenic avian AV is no less than that of the ITR from the highly oncogenic fowl AV type 1(CELO).This is in direct contrast to results reported for human AV where the length of the ITR increases with the increasing oncogenicity of the virus type (1).This result suggests that, at least in avian AV, the length of the ITR is not related to oncogenicity.Secondly, unlike CELO and mammalian AV, this virus does not possess the sequence ATAATA at position 9-14 within the ITR.This sequence is thought to be a recognition sequence for the precursor of the terminal repeat protein which is involved in the initiation of DNA replication (3).However, the ITR of this type 10 avian AV does possess the sequence ATATA at position 10-14, suggesting that this abbreviated form may be sufficient for recognition by the terminal protein precursor.Thirdly the left and right ITR of the type 10 avian AV, unlike CELO virus, end with the sequence ACGT an abbreviated form of the TGACGT sequence found in the same or similar position in human AV types 2, 3, 5, 7 and 12(1).

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                    10        20        30        40        50        60        70
Type 10 5' CATCATCTTATATAACCGCGTCTTTTGACACACTTACAACCGCCGCGCGCACGT
CELO    5' C-TCATCTATAATAACCTCAAAAACTAACGCAGTCATAACCGACCATAACCGCA
FL      5' CATCATCAATAATATACAGTTAGCAAAAAATGGCGCCTTTGTTTGGCTTTGTTCCAACTGTTTTTGGCCC
SA7     5' ----ATCAATAATATACCTTATTTGGGAACGGTGCCAATATGCTAATGAGGTGGGCGGAGTTTGGTGACG
7       5' CTATCTATATAATATACCTTATAGATGGAATGGTGCCAATATGTAAATGAGGTAATTTAAAAAAGTGCGC
                    80        90        100       110       120       130
FL          GAGTTGGGTTTCGTTTTCCCGGG
SA7         TATGCGGAAATGGGCGGAGTAGG
7           GCTGTGTGGTGATTGGCTGTGGGGTGAACGGCTAAAATGGGCGGGGCGGCCGTGGGAAAATGACGT
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Fig.1 Sequence data of the ITR of fowl AV type 10, a non-oncogenic virus. Sequence data for CELO (Avian), FL(Murine), SA7(Simian) and 7(Human) AV are taken from (2).

References: (1) Shinagawa, M. and Padmanbhan, R. (1980) Proc. Natl. Acad. Sci., USA 77, 3831-3835.(2) Zsak, L. and Kisary, J. (1981) J. Gen. Virol., 56, 87-95. (3) Shinagawa, M., et al., (1983) Virology 125, 491-495.