Non-structural protein 1 of parvoviruses: homology to purine nucleotide using proteins and early proteins of papovaviruses

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The role of the non-structural protein 1 (NS1) of parvoviruses is obscure and prior efforts to find homology with other proteins have failed (1). We note here that NS1's have a sequence pattern seen in many proteins which use purine nucleotides: the A-type of Walker et al. (2). Compilations of this pattern exist (3). The large T antigens (T's) of polyoma viruses and the E1 proteins (E1's) of papillomaviruses are weakly homologous in parts and both have the A-type pattern (4). The T's are ATPases and the part around the A-type sequence is implicated in this activity from other work (5). Papovavirus genomes are DS circular DNA but parvoviruses have SS linear DNA. Surprisingly, the bit of NS1's with the A-type pattern may be more homologous to the analogous bits of T's and E1's than expected from the A-type consensus alone. We predict that NS1's will show ATPase (or GTPase) activity. Below: top 4 rows - polyoma T's; centre 3 rows - parvovirus NS1's; lower 3 rows - papillomavirus E1's. Sequences are from the NBRF database (Protein Identification Resource) and (1). On the left: no. of first a.a. in each bit. At the bottom: A-type consensus. Identical or similar a.a.'s are boxed to mark homologies between the NS1's and T/E1's.

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418  KKRYWLFKGPIDSGKTTLAAALLELCGGKA  SV40
565  KRRNILFRGPVNSGKTGLAAALISLLGGKS  mouse polyoma
420  KRRYWLFKGPIDSGKTTLAAGLLDLCGGKA  BK
540  KKRNVLFRGPVNSGKTSLAAAIMNLVGGVA  hamster polyoma

391  KRNTVLFHGPASTGKSIIAQAIAQAVGNVG  MVM
320  KKNTLWFYGPPSTGKTNLAMAIAKSVPVYG  B19
326  KRNTIWLFGPATTGKTNIAEAIAHTVPFYG  AAV2

425  KKNCLAFIGPPNTGKSMLCNSLIHFLGGSV  bovine
432  KKNCLLIFGPPNTGKSMFCTSLLKLLGGKV  human 1a
423  KKNCMVFYGPPNSGKSYFCMSLIRLLAGRV  rabbit

          GXXg(t/s)GK(T/S)XXXXXX(I/V)   A-type consensus
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