```
Motif              I                 II            III             IV                  V                  VI    Source
                                                                                                                  ref.
uvrD     26 VLAGAGSGKTRVLV_174_NILVDEFQNTN_16_VMIVGDDDQSIY_26_QNYRSTSNI_267_LMTLHS-AKGL-EFPQVFIVG_23_LAYVGVTRA (20)
rep      19 VLAGAGSGKTRVIT_175_YLLVDEYQDTN_16_FTVVGDDDQSIY_26_QNYRSSGRI_271_LMTLHA-SKGL-EFPYVYMVG_22_LAYVGITRA ( 2)
recB     20 IEASAGTGKTFTIA_345_VAMIDEFQDTD_18_LLLIGDPKQAIY_24_TNWRSAPGM_286_IVTIHK-SKGL-EYPLVWLPF_44_LLYVALTRS ( 4)
recD    164 ISGGPGTGKTTTVA_ 82_VLVVDEASMID_16_VIFLGDRDQLAS_24_QLSRLTGTH_198_AMTVHK-SQGS-EFDHAALIL_11_LVYTAVTRA (21)

EBV      69 ITGTAGAGKSTSVS_113_VIVVDEAGTLS_26_IVCVGSPTQTDA_44_NNKRCTDVQ_426_AMTIAK-AQGL-SLNKVAICF_ 9_HVYVALSRA (22)
HCMV    117 VTGTAGAGKTSSIQ_125_IIVIDECGLML_26_IICVGSPTQTEA_44_HNKRCTDLD_513_AMTIAK-SQGL-SLEKVAVDF_10_HIYVAMSRV
HSV      94 ITGNAGSGKSTCVQ_136_VIVIDEAGLLG_26_LVCVGSPTQTAS_44_NNKRCVEHE-442_AMTITR-SQGL-SLDKVAICF_ 8_SAYVAMSRT ( 6)
VZV      87 ISGNAGSGKSTCIQ_135_VIVIDEAGLLG_26_IVCVGSPTQTDS_44_NNKRCQEDD_447_AMTIAR-SQGL-SLEKVAICF_ 8_SVYVAMSRT (23)

PIF     255 YTGSAGTGKSILLR_ 46_ALVVDEISMLD_25_LIFCGDFFQLPP_29_KVFRQRGDV_219_MQTIHQNSAGKRRLPLVRFKA_33_QAYVALSRA (10)

AlMV    821 VDGVAGCGKTTNIK_ 55_RLIFDECFLQH_15_VIGFGDTEQIPF_22_ITWRSPADA_ 66_IFTTHE-AQGK-TFDNVYFCR_19_NGLVALSRH ( 1)
BMV     687 VDGVAGCGKTTAIK_ 54_RLLVDEAGLLH_15_VLAFGDTEQISF_22_KTYRCPQDV_ 78_IKTVHE-AQGI-SVDNVTLVR_13_YCLVALTRH ( 1)
CMV     709 VDGVAGCGKTTAIK_ 54_RVLVDEVVLLH_15_ALCFGDSEQIAF_22_TTFRSPQDV_ 79_IKTVHE-SQGI-SEDHVTLVR_13_YCLVAVTRH ( 1)
TMV     829 VDGVPGCGKTKEIL_ 57_RLFIDEGLMLH_15_AYVYGDTQQIPY_24_TTLRCPADV_ 62_VHTVHE-VQGE-TYSDVSLVR_14_HVLVALSRH ( 1)
ToMV    829 VDGVPGCGKTKEIL_ 57_RLFIDEGLMLH_15_AYVYGDTQQIPY_24_TTLRCPADV_ 62_VHTVHE-VQGE-TYADVSLVR_14_HVLVSLSRH (24)
TRV     901 VDGVPGCGKSTMIV_ 56_VLHFDEALMAH_15_CICQGDQNQISF_24_ETYRSPADV_ 64_VSTVHE-SQGE-TFKDVVLVR_13_YLIVALSRH ( 1)
SFV     183 VFGVPGSGKSAIIK_ 50_ILYVDEAFACH_16_VVLCGDPKQCGF_21_ISRRCTRPV_ 58_VMTAAA-SQGL-TRKGVYAVR_14_HVNVLLTRT ( 1)
SV      183 VIGTPGSGKSAIIK_ 50_VLYVDEAFACH_16_VVLCGDPMQCGF_24_ISRRCTQPV_ 58_VMTAAA-SQGL-TRKGVYAVR_14_HVNVLLTRT ( 1)

IBV    1209 VQGPPGSGKSHFAI_ 54_ILLVDEVSMLT_15_VVYVGDPAQLPA_30_KCYRCPKEI_ 82_VQTVDS-SQGS-EYDYVIFCV_11_RFNVALTRA (25)

BNYVV1  893 VKGGPGTGKSFLIR_ 48_IIFVDEFTAYD_11_IYLVGDEQQTGI_25_MNFRNPVHD_ 72_KTTVRA-NQGS-TYDNVVLPV_12_LNLVALSRH (26)
BNYVV2  121 VLGAPGVGKSTSIK_ 49_TMLVDEVTRVH_11_VICFGDPAQGLN_18_ASRRFGKAT_ 67_SILYSD-AHGQ-TYDVVTIIL_13_VRAVLLTRA (26)
BSMV2   267 ISGVPGSGKSTIVR_ 41_LLIIDEYTLAE_11_VLLVGDVAQGKA_18_TTYRLGQET_ 62_CALAID-VQGK-EFDSVTLFL_12_LRLVALSRH (27)
              *  * ***         ******        ***** *       *****         ***  ***  *   * * *    *******
            V G AG GKS         VDE           GD  Q           R           T    SQG  E   V         VALSR
            I A P    T         I              S                          L    AK   S   A         TLVT
            Y                  F                                              VH   T              GM
                                                                              NA   R              SI
```

Alignment of conserved motifs from six protein families (single-letter code). Hyphens, gaps introduced during alignment. The number of residues between each motif is shown. At the base of alignment, characteristic residues have been shown where there are less than five alternatives. The main RNA virus family includes: AlMV, alfalfa mosaic virus 1a; BMV, brome mosaic virus 1a; CMV, cucumber mosaic virus 1a; TMV, tobacco mosaic virus (common strain) p126; ToMV, tobacco mosaic virus (tomato strain) p126; TRV, tobacco rattle virus p134; SVF, Semliki Forest virus nsP2; SV, Sindbis virus nsP2. The last two are alphaviruses infecting animals. Conserved regions in this protein family were used to construct motifs for the program TPT[14], which extracted uvrD from the Protein Information Resource database. A general database search using FASTP[15] then matched a region from recD with Epstein–Barr virus (EBV) BBLF4. Related genes in other herpesvirus: human cytomegalovirus (HCMV) PS3 (J.A. Martignetti, personal communication), herpes simplex virus (HSV) UL5, and varicella-zoster virus (VZV) gene 55, are strongly conserved. Similarities between the yeast PIF sequence[5] and uvrD, and between infectious bronchitis virus (IBV) F2, beet necrotic yellow vein virus (BNYVV1) 237K protein and the alphavirus nsP2 family were noted by the original authors. The relationship between the (BNYVV2) 42K and barley stripe mosaic virus (BSMV2) 58K proteins was also noted, but their similarity to all the other proteins was not. Asterisks, positions used for statistical analysis[16]. The probability of each motif occurring by chance was $\sim 10^{-6}$, and for the six- and seven-member patterns 1.9×10^{-33} and 1.6×10^{-39}, respectively.

DNA-dependent ATPases sharing 37% amino-acid identity[2]. The recB and recD are subunits of ExoV. The former probably carries out the helicase activity of the ExoV holoenzyme because it has been shown to bind ATP[3] and single-stranded DNA[4]; also, it has 20% amino-acid identity with the above helicases. Its extra sequences presumably carry out ExoV-specific functions. The recD does not have a demonstrated helicase function, binds ATP only in the presence of the other subunits[3], and has diverged further than the others. The structural resemblances between these proteins strongly suggest that they belong to a DNA helicase family that is distinct in evolutionary terms from other *E. coli* helicases, although they are related to PIF, a yeast nuclear gene product involved in mitochondrial DNA repair and recombination[5].

Genetic data in herpes simplex virus[6] show that UL5 is essential for DNA replication, a finding that is consistent with its stringent conservation among other herpesviruses. UL5 could also be a helicase[6], a function possibly common to all groups within the superfamily, although the level of similarity between the groups is too low to allow a direct functional comparison. The available evidence shows that the RNA viral protein domains containing these conserved motifs are involved in replication[7], but are distinct from the suspected polymerase domain[8].

The very broad occurrence of these motifs in otherwise unrelated proteins strongly suggests that they all carry out crucial nucleoside triphosphate-dependent steps in nucleic acid replication. Motif I is well-known[9], and is found almost exclusively in ATP and GTP binding proteins. Where the crystal structure is known[10–12], the motif forms a loop which binds one of the phosphates, another being bound by an aspartate via a magnesium ion. There is a suitably located, strictly conserved aspartate in motif II. Motif III was previously noted[13] to resemble a conserved region from viral DNA polymerases. This study shows that the proteins have no overall relationship, though it remains possible that they have similar local folds. Note also that only the presumed DNA binding proteins have tyrosine at position 3 of motif VI and another motif between motifs I and II.

These motifs probably represent common secondary structures that make up functional sites for pyrophosphate, magnesium or nucleic acid binding, while the rest of the sequence provides the structural framework, the specificity and any supplementary functions. The resolution of the exact structure, function, and evolutionary significance of these motifs is still awaiting further crystallographic analysis.

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Lifting heavy loads not just by the Egyptians

SIR—The astute suggestion made by John Cunningham (*Nature* **332**, 22–23; 1988) that certain old Egyptian art work illustrates a method of raising heavy weights prompted me to look into that compendium of primitive clever invention, Francis Galton's *Art of Travel* (5th edn, David and Charles, Newton Abbot, 1971).

Sure enough, two related systems, which make use of this principle of successive small forces being applied to a series of springy supports, are mentioned under the heading "Accumulation of Efforts".

To lift and swing forward a heavy log in a tropical forest, "the labourer gets hold of one of these creepers that runs from the top of the boughs of a tree in the direction in which he wants to move his log, and pulling this creeper home with all his force, bending down the bough, he attaches it to the log; then he goes to another creeper and does the same with that; and so on until he has accumulated strain of many bent boughs, urging the log forward and of sufficient power to move it". The other example concerns a commercially available 'accumulator', consisting of cords of india-rubber each hooked to a fixed ring at one end, the other ends being then hooked one by one to the object to be moved.

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