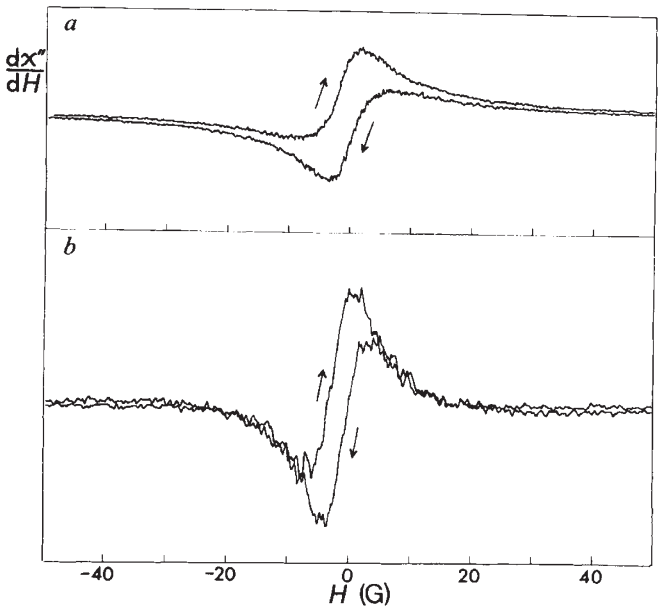


Low-field ESR spectra of $YBa_2Cu_3O_{7-x}$: *a*, at 77 K, obtained with an X-band spectrometer (microwave frequency 9.45 GHz); *b*, at 60 K, at S-band (2.40 GHz). The measured signal is the field derivative of the imaginary part of the magnetic susceptibility ($\chi''$), as a function of the external magnetic field.

spin states with a zero-field splitting of the order of 0.3 $cm^{-1}$, as proposed in ref. 1.

Insight into this non-resonant microwave absorption is obtained from one additional measurement, which demonstrates that the amplitude of the absorption is insensitive to whether the $H_1$ field of the microwave radiation is parallel or perpendicular to the external magentic field. These observations are consistent with the studies of Blazey *et al.*[2] and of Khachaturyan *et al.*[3], and support the proposed mechanism of non-resonant absorption. Blazey *et al.*[2] used low-field microwave absorption data to argue that the material is a superconducting glass which consists of weakly coupled superconducting clusters.

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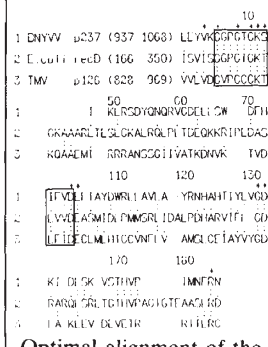
# A conserved NTP-motif in putative helicases

Sir—*Escherichia coli recBCD* enzyme is a multifunctional protein involved in general recombination which possesses, among other functions, an ATP-dependent DNA helicase activity[1]. Inspection of the amino-acid sequences of the complex subunits reveals that two of them, *recB* and *recD*, contain a consensus pattern of residues characteristic of the catalytic sites of many enzymes that use nucleoside triphosphates (NTPs), the socalled NTP-motif[2]. This prompted us to perform a more detailed computer-assisted comparison of the sequences of these two proteins with those of other enzymes of this class.

This comparison reveals an unexpected similarity between *recD* and the NTP-motif-containing domain of a non-structural protein of beet necrotic yellow vein virus (BNYVV), a positive-strand RNA plant virus. This domain belongs to a recently identified family of homologous viral proteins (domains) involved in virus RNA replications[3,4]. In these proteins the NTP-motif is one of the most strictly conserved stretches of sequence.

For one of them, tobacco mosaic virus (TMV) protein p126, the NTP-binding capacity has been demonstrated experimentally[5]. The optimal alignment of the NTP-motif-containing domains of *recD* and of the BNYVV and TMV proteins is shown in the figure. The similarity is high enough to suggest a monophyletic origin for the compared domains (see table).



Optimal alignment of the NTP-motif-containing domains of *recD* and the presumptive NTPases of BNYVV and TMV. Sequences from refs 1 (*recD*), 7 (BNYVV) and 8 (TMV). Alignment generated by the program OPTAL, based on the original algorithm of Sankoff[9]. Identical residues (:) and conservative replacements (.) are highlighted. Asterisks, residues constituting the putative viral NTP-motif consensus[4,11] The residues constituting the NTP-motif proper are boxed.

Summary of the alignments

| | *recD* | BNYVV | TMV |
|---|---|---|---|
| *recD* | — | 28.8(51.5) | 16.2(35.2) |
| BNYVV | 5.9 | — | 20.5(31.8) |
| TMV | 3.7 | 3.2 | — |

Below the diagonal: Alignment scores calculated in standard deviation (s.d.) units for the three alignments. Note that the similarity between the *recD* and BNYVV segments is the highest and exceeds the threshold of 5 s.d. thought to be indicative of a true evolutionary relationship[10]. Above the diagonal: per cent similarity expressed as strict coincidence and, in parentheses, coincidence including conservative replacements.

Strikingly, the similarity betwen the *recD* and BNYVV sequences is even higher than that between the two viral sequences. Such a pronounced sequence similarity could be due to conservation of a specific NTP-requiring function. Thus, viral NTP-motif-containing proteins may be subunits of RNA helicases involved in the unwinding of double-stranded replication forms during viral RNA replication, and in recombination between RNA genomes, a process recently described for plant viruses[6].

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# A new superfamily of replicative proteins

Sir—I report a set of 21 related proteins, identified by computer searches, which are all involved in nucleic-acid replication and/or recombination. These include two *Escherichia coli* ATP-dependent helicases, four essential human herpesvirus proteins (probably also helicases), two exonuclease V (ExoV) subunits, and the yeast PIF protein (involved in mitochondrial DNA recombination). These helicases and nucleases are structurally related to a set of conserved domains (20–70% amino-acid identity) that are common in RNA viruses[1], and which I used as the starting point for the search.

The *uvrD* and *rep* helicases are both