

Update section

Sequence

An alfalfa cDNA encodes a protein with homology to translationally controlled human tumor protein

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In mouse tumor cell lines, an abundant mRNA species was found to occur largely as untranslated mRNP particle. The corresponding cDNA sequence was isolated from a cDNA library derived from mouse cells [1] and subsequently from human mammary carcinomas [2]. The two putative proteins are highly identical (96%) and encode proteins of 21 kDa.

Here, we report the isolation and characterization of an alfalfa cDNA clone which has considerable homology to these proteins. The alfalfa clone was isolated from an alfalfa cDNA library prepared from suspension culture cells which were induced to form somatic embryos [3]. The probe used for screening was a PCR fragment with homology to phosphoprotein phosphatases (unpublished results). The complete nucleotide sequence with the predicted amino acid sequence is shown in Fig. 1. Comparison of the predicted protein sequence with the SWISS PROT data bank revealed homology over the entire length of 157 amino acids to mouse and human translationally controlled tumor proteins (42.7% and 40.8% identities, respectively). When conserved amino acid exchanges were taken into consider-

ation a similarity score of 78.3% was obtained for both mammalian proteins. Figure 2 shows the sequence alignment of the putative alfalfa and mouse proteins. Although the plant sequence appears to lack the first ten amino acids, the two proteins are highly similar over the whole sequence, including the very carboxyl end.

Taken together, the data suggest that the alfalfa and the mammalian proteins could be either homologues of each other or belong to a family of closely related proteins. Unfortunately, nothing is known about the function of the translationally controlled human tumor proteins. Since this protein appears to be highly conserved during evolution, it can be expected to be also found in yeast cells. Here, a genetic approach might reveal some unexpected scientific treasures.

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                                30                                60
GAT GAG CTT CTG TCA GAC TCT TAC CCA TAC AAG GAA ATT GAG AAT GGA ATG TTG TGG GAG
D  E  L  L  S  D  S  Y  P  Y  K  E  I  E  N  G  M  L  W  E

                                90                                120
GTT GAG GGA AAG TGG GTT ACT AAG GGA GTT GTT GAA GTA GAC ATT GGT GCT AAC GCT TCT
V  E  G  K  W  V  T  K  G  V  V  E  V  D  I  G  A  N  A  S

                                150                                180
GCT GAA GGT GGA GAA GAT GAG GGT GTT GAT GAC ACA GCT GTT AAG GTT GTC GAC ATT GTT
A  E  G  G  E  D  E  G  V  D  D  T  A  V  K  V  V  D  I  V

                                210                                240
GAC GTA TTC AGA CTT CAG GAA CAA CCT GCT TTT GAC AAG AAG CAG TTT CTT GGC TTT GTT
D  V  F  R  L  Q  E  Q  P  A  F  D  K  K  Q  F  L  G  F  V

                                270                                300
AAG AGG TAT ATC AAG TTG CTG ACA CCC AAA CTA GAT GCA GAG AAA CAA GAG CTG TTT AAG
K  R  Y  I  K  L  L  T  P  K  L  D  A  E  K  Q  E  L  F  K

                                330                                360
AAG CAC ATT GAG GGA GCA ACC AAA TAC TTG CTC GGC AAG CTC AAG GAC CTT CAA TTC TTT
K  H  I  E  G  A  T  K  Y  L  L  G  K  L  K  D  L  Q  F  F

                                390                                420
GTT GGT GAG AGC ATG CAT GAT GAT GGT AGC TTG GTC TTT GCC TAC TAC AAG GAT GGT GCT
V  G  E  S  M  H  D  D  G  S  L  V  F  A  Y  Y  K  D  G  A

                                450                                480
GCT GAT CCA ACA TTT CTC TAC TTT GCT TAT GCT TTG AAG GAA ATC AAG TGT TAA GTG TTG
A  D  P  T  F  L  Y  F  A  Y  A  L  K  E  I  K  C

TAC TAC ACT AGT TGT TCT GCC CCT AAT TTA TCA TGT TTT TGT TCT ACA ATG TCT TCT AAG
TTA CTC GAG AGT TGA GAC TAT GAT TTG GTA TTT TTG ATA ATG ATG TGA TGA TTT GAA CTT
AAT TAT CAT TCC CAT TAA ATT TAA TCA GGT TGG ATA GAA TTC ATA AAT ATA TGA TTT TTC
TTG TGT TTC ATA AGG AAT GTC AGT TGT CTG GTT TGA AGA TTT GTT TTG TGA ACT GAA ATA
GTT CG
    
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Fig. 1. Nucleotide sequence and predicted amino acid sequence of alfalfa cDNA.

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                                10          20          30          40
TCTP.Ms          DELLSDSYPYKEIENGMLWEVEGKWVTKGVVEVD---IGANASAEGGEDE
                ..... : ..... : ..... : ..... : ..... : ..... : ..... : ..... :
TCTP.Mm          MIIYRDLISHDELFSDIYKIREIADGLCLEVEGKMVSRTEGAIDDSLIGGNASAEGPEGE
                10          20          30          40          50          60

                50          60          70          80          90          100
TCTP.Ms          GVDDTAVKVVDIVDVFRLQEQPAFDKKQFLGFVKRYIKLLTPKLDAEKQELFKKHIEGAT
                ..... : ..... : ..... : ..... : ..... : ..... : ..... : ..... :
TCTP.Mm          GTESTVVTGVDIVMNHHLQE-TSFTKEAYKKYIKDYMKSLKGLKLEEQKPERVVKPFMTGAA
                70          80          90          100          110

                110          120          130          140          150
TCTP.Ms          ---KYLGLKLDLQFFVGESMHDDGSLVFAYYK-DGAADPTFLYFAYALKEIKC
                ..... : ..... : ..... : ..... : ..... : ..... : ..... : ..... :
TCTP.Mm          EQIKHILANFNFYQFFIGENMNPDGMVALLDYREDGVT-PFMIFFKDGLEMEKC
                120          130          140          150          160          170
    
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Fig. 2. Sequence alignment of putative alfalfa protein (TCTP.Ms) and mouse translationally controlled tumor protein (TCTP.Mm). Gaps, introduced for improved alignment, are denoted by dashes. Identical amino acids are indicated by two dots, structurally similar amino acids by single dots.

References

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