

Nucleotide sequence of an intermediate filament cDNA from *Torpedo californica*

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We report the nucleotide and deduced amino acid sequence for an intermediate filament (IF) gene from the elasmobranch *Torpedo californica*. The clone was isolated from a λgt11 cDNA expression library encoding transcripts from the electric organ and the sequence was obtained from both DNA strands. The deduced protein sequence is highly homologous to other IF proteins in the rod and coil demains, especially desmin and vimentin (1). Western blotting showed that a monoclonal antibody that recognizes all classes of IFs (2) recognizes a β-galactosidase fusion protein that encodes the sequences of the full length clone (data not shown). The relationship between our clone and other electric organ antigens (3), including a frog postsynaptic antigen that is recognized by the IF monoclonal antibody (4), has not been determined.

REFERENCES

1. Weber,K. and Geisler,N. (1985) *Annals New York Academy of Sciences* **455**, 126–143.
2. Pruss *et al.* (1981) *Cell* **27**, 419–428.
3. Froehner,S. (1984) *J. Cell Biol.* **99**, 88–96.
4. Burden,S. (1982) *J. Cell Biol.* **94**, 521–530.

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   1 GCACAGCATCTAACTATGGAAAAGGGATACAAAATGAACAGATCCAGTGTCTACCGCAATATGTTTTCAGAGAAACCGGTTCGAGTTTCAAGC
                     M  E  K  G  Y  K  M  N  R  S  S  V  Y  R  N  M  F  S  E  K  P  V  R  V  S  S
  94 ATCCGGCGCAGCTACACGGCTCGCGGGAATCCGCAGGGCAGTTTGATCATCCCTTCTTCCAGCCGTTCCAGGGTTAGTTACGTGACGCCGATC
      I  R  R  S  Y  T  A  R  G  N  P  Q  G  S  L  I  I  P  S  S  S  R  S  R  V  S  Y  V  T  P  I
 187 AGTTCGCGAAGTGTGAGGCTTGTGAGGAGCAGTGCTCCTGTAGTTGCCTCGAGCAGCAACTTGGACTTTACCTTGGTGGATGCCATGAACTCG
      S  S  R  S  V  R  L  V  R  S  S  A  P  V  V  A  S  S  S  N  L  D  F  T  L  V  D  A  M  N  S
 280 GAGTTCAAGGTGAACCGCACCAATGAGAAGGCTGAGATGATTGAGCTGAATGATCGCCTCGCCAACTTCCTCGACAAGGTGAGGTCGCTGGAG
      E  F  K  V  N  R  T  N  E  K  A  E  M  I  E  L  N  D  R  L  A  N  F  L  D  K  V  R  S  L  E
 373 CAACAGAACAAGATGCTCCTGGCCGAACTGGAGCAAGTGAAGGGTAAACGCCCGTCCAAAATAGGGGACCTGTACGAACAGGAGCTGAGGGAG
      Q  Q  N  K  M  L  L  A  E  L  E  Q  V  K  G  K  R  P  S  K  I  G  D  L  Y  E  Q  E  L  R  E
 466 CTACGTCTCCAGATTGACCAGATAAGCAACGAGAAGTCGAGGGTTGAAGTGGAAAGGGATAACCTGGCCGATGATCTTCAGAAGCTGAGAGAG
      L  R  L  Q  I  D  Q  I  S  N  E  K  S  R  V  E  V  E  R  D  N  L  A  D  D  L  Q  K  L  R  E
 559 AAATTGCAAGATGAAGTTATTCAGCGGGAGGATGCTGAAAACAATCTGGCAGCTTTCAGACAGGATGTGGATGATGCCTGTCTGGCACGCTTA
      K  L  Q  D  E  V  I  Q  R  E  D  A  E  N  N  L  A  A  F  R  Q  D  V  D  D  A  C  L  A  R  L
 652 GATTTGGAGCGTAAAGTTGAGACACTACAAGAAGAAATTATGTTCCTGAAGAAACTTCATGAAGAGGAAATTATAGAATTGCAAGCTCAAATC
      D  L  E  R  K  V  E  T  L  Q  E  E  I  M  F  L  K  K  L  H  E  E  E  I  I  E  L  Q  A  Q  I
 745 CGGGATTCGCAGTTCAAGGTTGAGATGGATGTTGTCAGACCTGACCTGACTGCAGCACTTCAAGACGTTCGTTCTCAGTTTGATAAACTTGCT
      R  D  S  Q  F  K  V  E  M  D  V  V  R  P  D  L  T  A  A  L  Q  D  V  R  S  Q  F  D  K  L  A
 838 TCCAAGAACATAGCTGAGACTGAGGAATTGTACAAGTCCAAGCTGGCCGATATAACTGATTCTGCTTCTCGTAACAATGATGCTCTTCGTTTG
      S  K  N  I  A  E  T  E  E  L  Y  K  S  K  L  A  D  I  T  D  S  A  S  R  N  N  D  A  L  R  L
 931 GCAAAACAAGAAAATAATGAGTACCGCAGGCAAGTCCAGTCACTGACCTGTGAAATTGATGCACTGAAGGGAACGAATGAATCCCTTGAGCGC
      A  K  Q  E  N  N  E  Y  R  R  Q  V  Q  S  L  T  C  E  I  D  A  L  K  G  T  N  E  S  L  E  R
1024 CAGATGCAAGATGTGGAAGATCGGTATAATATGGAGACCACTAATGCCCAGGACACCATTTCCCATCTTGAAGATGAAATCAGTCATTTGAAG
      Q  M  Q  D  V  E  D  R  Y  N  M  E  T  T  N  A  Q  D  T  I  S  H  L  E  D  E  I  S  H  L  K
1117 GATGAGATGACTCGCCATTTGCAAGAATATCAGGAGCTATTGACAGTTAAGATGGCTTTAGATGTTGAGATTGCAACTTACAGGAAATTACTG
      D  E  M  T  R  H  L  Q  E  Y  Q  E  L  L  T  V  K  M  A  L  D  V  E  I  A  T  Y  R  K  L  L
1210 GAAGGTGAAGAAAACAGGATTTCTATGCCATTGCCCTCATTTGGATCTATGAGCCTCTCTGATGCCATGTTTGAGCAGCAGCCATTTGAAAAT
      E  G  E  E  N  R  I  S  M  P  L  P  S  F  G  S  M  S  L  S  D  A  M  F  E  Q  Q  P  F  E  N
1303 CGAACATCAAAGAAGAAAATTGTCATTAAAACTGTTGAGACCAGTGGTGGAGATGTAATCAGTGAAACTACCCAGAAAATTGAAGACTAAACC
      R  T  S  K  K  K  I  V  I  K  T  V  E  T  S  G  G  D  V  I  S  E  T  T  Q  K  I  E  D  *
1396 TGGTCAGCAGCCTAAAAATATGCATTGAAGCTGAAGTTCTTCAAAAATAAAGTGCTAGACAAGAATATTGCTCCTTCTCTTAATCAAGAAGAA
1489 TACTGTGGCTTTGAAGTGCCTTTCTGCATCTAATTGAAGAGTGCTAGATTCAATAAAGTTTAGTTGTAAGCTTTATAGAATAGTAAAAATACA
1582 GTAAATGGCTTTACTGAAGTTATACTACACTCTGTTTATGAAGACAGTCACTAGTTTACAACTAGTTTACAATTGCACAGTGACAACTAGCAA
1675 TACTTCACCAGTTCTGAATCTTTATTTACATTCAGAATCACAATTGCTTTTTTCCCCCAGTAAGTACCTGTAAACAAGCTCTAATAAAACATC
1768 TGCCCGAA
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