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Nucleotide sequence of the mouse *hck* gene

Michael J.Klemsz, Scott R.McKercher and Richard A.Maki

Cancer Research Center, La Jolla Cancer Research Foundation, La Jolla, CA 92037, USA

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A cDNA clone coding for the mouse hck gene was identified. The clone was isolated from a mouse macrophage cDNA library (Clontech Laboratories, Inc., Palo Alto, CA, catalogue number ML 1005) using a 1.7 Kb cDNA insert from the mouse lck gene as a hybridization probe (1). Clone 13.5, containing the largest insert was characterized in detail. The nucleotide sequence revealed an open reading frame of 503 amino acids (M.W. = 55,300 daltons). The nucleotide sequence is identical with the nucleotide sequence of a genomic clone containing part of the mouse hck gene (underlined) (2). Four differences at nucleotide positions 1103, 1104, 1107, and 1108 in the genomic sequence have recently been corrected to agree with the cDNA sequence (R. Perlmutter, personal communication). The mouse hck protein sequence has 90% homology with human hck (2,3), 65% with mouse lck (1), 65% with v-yes (4) and 57% with chicken c-src (5). Based on this homology, it is likely that the mouse hck cDNA identified is a member of the src family of related tyrosine kinases.

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                                                                GAATTCCGGCCCGTGAAGGGGGCTCTGACCCGTTCCGAGCGCCAACGCAGCC     52

TCTGTAGCCCGCAAGTCTTCGTCGCTTGCTCCGGGCTCTGAAGTCCGGGGCCACCAGGGGCCGCAGCGCTGGGGGGTCGGTCTAGCTGCGAGGATCCGGGCTGCCCACGAAGCGAAGGGCGGGCGCCCAGG    183

 M   G   C   V   K   S   R   F   L   R   D   G   S   K   A   S   K   T   E   P   S   A   N   Q   K   G   P   V   Y   V   P   D   P      33
ATG GGA TGC GTG AAG TCC AGG TTC CTC CGA GAT GGA AGC AAG GCC TCA AAA ACA GAG CCA AGT GCC AAT CAG AAG GGC CCT GTG TAT GTG CCG GAT CCC    282

 T   S   S   S   K   L   G   P   N   N   S   N   S   M   P   P   G   F   V   E   G   S   E   D   T   I   V   V   A   L   Y   D   Y      66
ACG TCC TCC AGC AAG CTG GGA CCA AAC AAC AGC AAC AGC ATG CCC CCA GGG TTT GTG GAG GGC TCT GAG GAT ACC ATT GTG GTC GCA CTG TAC GAC TAT    381

 E   A   I   H   R   E   D   L   S   F   Q   K   G   D   Q   M   V   V   L   E   E   A   G   E   W   W   K   A   R   S   L   A   T      99
GAG GCT ATT CAC CGT GAA GAC CTC AGC TTC CAG AAG GGA GAC CAG ATG GTG GTT CTG GAG GAG GCT GGG GAG TGG TGG AAG GCA CGG TCC CTG GCT ACC    480

 K   K   E   G   Y   I   P   S   N   Y   V   A   R   V   N   S   L   E   T   E   E   W   F   F   K   G   I   S   R   K   D   A   E     132
AAG AAG GAA GGC TAC ATC CCA AGC AAC TAT GTG GCT CGA GTT AAC TCT TTG GAG ACA GAA GAG TGG TTC TTC AAG GGG ATC AGC CGG AAG GAT GCA GAG    579

 R   H   L   L   A   P   G   N   M   L   G   S   F   M   I   R   D   S   E   T   T   K   G   S   Y   S   L   S   V   R   D   F   D     165
CGC CAC CTC CTG GCT CCA GGC AAC ATG CTG GGC TCC TTC ATG ATC CGG GAC AGT GAG ACC ACC AAA GGG AGC TAC TCG TTG TCT GTT CGA GAC TTT GAC    678

 P   Q   H   G   D   T   V   K   H   Y   K   I   R   T   L   D   S   G   G   F   Y   I   S   P   R   S   T   F   S   S   L   Q   E     198
CCC CAG CAC GGA GAC ACC GTG AAG CAC TAT AAG ATC CGG ACG CTG GAC AGT GGA GGC TTC TAC ATC TCT CCA AGG AGC ACC TTC AGC AGC CTG CAG GAA    777

 L   V   L   H   Y   K   K   G   K   D   G   L   C   Q   K   L   S   V   P   C   V   S   P   K   P   Q   K   P   W   E   K   D   A     231
CTC GTG CTC CAC TAC AAG AAG GGG AAG GAT GGG CTC TGC CAG AAG CTG TCA GTG CCC TGT GTG TCT CCC AAA CCC CAG AAG CCA TGG GAG AAA GAT GCT    876

 W   E   I   P   R   E   S   L   Q   M   E   K   K   L   G   A   G   Q   F   G   E   V   W   M   A   T   Y   N   K   H   T   K   V     264
TGG GAG ATT CCT CGA GAA TCC CTC CAG ATG GAG AAG AAA CTT GGA GCT GGG CAG TTT GGA GAA GTG TGG ATG GCC ACC TAC AAC AAG CAC ACC AAA GTG    975

 A   V   K   T   M   K   P   G   S   M   S   V   E   A   F   L   A   E   A   N   L   M   K   S   L   Q   H   D   K   L   V   K   L     297
GCG GTG AAG ACA ATG AAG CCA GGG AGC ATG TCC GTG GAG GCC TTC CTG GCT GAG GCC AAC CTG ATG AAG TCG CTG CAG CAT GAC AAA CTG GTG AAG CTA   1074

 H   A   V   V   S   Q   E   P   I   F   I   V   T   E   F   M   A   K   G   S   L   L   D   F   L   K   S   E   E   G   S   K   Q     330
CAC GCT GTG GTC TCT CAG GAG CCC ATC TTT ATT GTC ACG GAG TTC ATG GCC AAA GGA AGC CTG CTG GAC TTT CTC AAG AGT GAA GAA GGC AGC AAG CAG   1173

 P   L   P   K   L   I   D   F   S   A   Q   I   S   E   G   M   A   F   I   E   Q   R   N   Y   I   H   R   D   L   R   A   A   N     363
CCA CTG CCA AAA CTC ATT GAC TTC TCA GCC CAG ATC TCA GAA GGC ATG GCC TTC ATT GAG CAG AGG AAC TAC ATC CAC CGA GAC CTG AGG GCT GCC AAC   1272

 I   L   V   S   A   S   L   V   C   K   I   A   D   F   G   L   A   R   I   I   E   D   N   E   Y   T   A   R   E   G   A   K   F     396
ATC TTA GTC TCT GCA TCA CTG GTG TGT AAG ATT GCT GAC TTT GGA CTG GCA CGA ATC ATC GAG GAC AAT GAG TAC ACA GCT CGG GAA GGA GCC AAG TTC   1371

 P   I   K   W   T   A   P   E   A   I   N   F   G   S   F   T   I   K   S   D   V   W   S   F   G   I   L   L   M   E   I   V   T     429
CCC ATC AAG TGG ACA GCT CCT GAA GCC ATC AAC TTT GGT TCC TTC ACC ATC AAG TCA GAT GTC TGG TCC TTT GGT ATC CTG CTG ATG GAA ATT GTC ACC   1470

 Y   G   R   I   P   Y   P   G   M   S   N   P   E   V   I   R   A   L   E   H   G   Y   R   M   P   R   P   D   N   C   P   E   E     462
TAT GGC CGG ATC CCT TAC CCA GGT ATG TCA AAC CCA GAG GTG ATT CGG GCA CTA GAG CAT GGG TAC CGT ATG CCT CGA CCA GAT AAC TGT CCA GAA GAG   1569

 L   Y   N   I   M   I   R   C   W   K   N   R   P   E   E   R   P   T   F   E   Y   I   Q   S   V   L   D   D   F   Y   T   A   T     495
CTC TAC AAT ATC ATG ATC CGC TGC TGG AAG AAC CGC CCC GAG GAA CGG CCC ACC TTT GAA TAC ATC CAG AGT GTG CTG GAT GAC TTC TAC ACG GCC ACT   1668

 E   S   Q   Y   Q   Q   Q   P  End                                                                                                    503
GAG AGC CAG TAT CAG CAG CAG CCT TGA CAGCAGTAAGGACATGAGCAGAGCCAGAAGCCCCATCAGTGCCTTGACACGCCCAACTTGCTGGGCCCACTCTCAGACACCACACCACACACACT   1790

GCAGCTGTTGAGTGGGTGGGAGGACTTCACAATCTCTTTCTGACTCTAGTCATCTGCAATCCGCCACTCTCAGGGCCTCCAAGTTGGTATGTCTCATTTGCCTGGAATGACTGAATTC               1908
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