Nucleotide sequence of the quail *c-jun* protooncogene

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The *c-jun* protooncogene is a member of a multigene family of transcription factors with leucine zipper which also includes *jun B* and *jun D/S*^{1,2}. The protein complex *c-jun/c-fos* has been shown to be responsible for the so-called AP1(human)/PEA1(murine) transcription factor activity³. Several evidences show that *c-jun* is involved in mediating cellular responses to growth factors as well as to tumor promoters⁴. The nucleotide sequence determination of human, rodent and chicken *c-jun* genes indicates that they are devoid of intron and encode proteins with a highly basic 3' conserved domain⁴⁻⁶. In order to study the regulation of *c-jun* expression in connection with the transforming and mitogenic effects of the RSV *src* oncoprotein in quail neuroretina cells, we have determined the nucleotide sequence of the quail gene. When compared to the chicken gene, the coding region shows high amino acid conservation; however, the quail gene appears 1 amino acid shorter and only two amino acid changes occur in the modulatory region of the protein. By contrast, the nucleotide sequences diverge strongly in the 5' and 3' untranslated regions.

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1  gccgcgcgtgagaagcttctagggcggggtgtccatggcgaccggtgccatgcaacgcgcggggccagcgcccaagcctccccgggac
91  ggccggcgagccaatgggagcgccgggtgacatcatgggctattttagcgggctccgggtcgctgataagtgaagggtcgcaaggag
181  cgagcgggtctcagagcggcgccggcgaggaatcagccgccacagcgccagcgagcgagcgagggtacaagcgcg
271  aacggcgccgagcgccggccggcgacagcgcgagagcgccggcgagcagcagcagagtagcagagtagcagcgtagcag
361  cgcacagcgcagcagctagggccggcgccggcgagcgagcgccgtgtgtcccgccgagaaagtaaggaaagcctccggcttgcct
451  ttcccccaagccgcttggccgggagcggtgtgtggcgccctccccggcccaattttgggctctgtct  ATG AGT GCA AAG ATG
535  GAG CCT ACT TTC TAC GAG GAT GCA CTG AAC GCC AGC TTC GCG CCG CCG GAG AGC GCT TAT GGA TAT AAT
AAC GCG AAG GTG CTG AAG CAG AGC ATG ACG CTG AAC CTG TCC GAC CCG GCC AGC AGC CTG AAG CCG CAC
673  CTG CGG AAC AAG AAC GCC GAC ATC CTC ACC TCC CCC GAC GTG GGG CTG CTG AAA TTG GCC TCC CCG GAG
CTG GAG CGG CTC ATC ATC CAG TCC AGC AAC GGG TTA ATC ACC ACC ACG CCG AGC CCG ACG CAG TTC CTG
811  TGC CCC AAG AAC GTT ACC GAC GAA CAA GAG GGG TTT GCC GAA GGC TTC GTG AGA GCG CTG GCG GAA CTG
CAC AAC CAG AAC ACG CTG CCC AGC GTC ACC TCG GCC GCG CAA CCT GTT AGC GGT GGC ATG GCA CCT GTG
949  TCC TCC ATG GCC GGC GGC AGC TTC AAC ACG AGT TTG CAC AGC GAG CCC CCG GTG TAC GCC AAC CTC
AGC AAC TTT AAC CCC AAC GCG CTC AAT TCC GCA CCC AAC TAC AAT GCC AAC GGC ATG GGC TAC GCG CCG
1087  CAG CAT CAC ATA AAC CCC CAG ATG CCA GTG CAG CAT CCC AGG CTT CAG GCT GTG AAA GAA GAG CCT CAG
ACT GTA CCT GAA ATG CCG GGG GAA ACC CCT CCC CTG TCC CCT ATT GAC ATG GAG TCG CAG GAG AGA ATC
1225  AAA GCC GAG AGA AAA GCG ATG AGA AAC AGA ATC GCG GCG TCC AAA TGC CGG AAA AGG AAG TTG GAA AGG
ATT GCC AGG TTG GAA GAA AAA GTG AAA ACT TTG AAA GCC CAG AAC TCA GAG CTG GCA TCC ACT GCC AAC
1363  ATG CTC AGA GAA CAG GTT GCA CAG CTT AAG CAG AAG GTC ATG AAC CAT GTC AAC AGC GGG TGC CAG CTA
ATG CTA ACA CAA CAG TTG CAA ACG TTT  tgaagagactgacttcaataggaactgtgattgttgggtataactaaacgaca
1512  aaccaaaaagcggcgagcgcgttaagctcagcgttagaagctgggaggtgctgagtcctgctcgtgtgcgaagcacatgtgtgcaaaag
ctggggcagctcagctcgaggtgtgtggaagcagcgccgcgcctccgaggtgctgatcctgctccatgagggcgtcagatcttcgtttaa
1692  cattgaccaagacgtcggaactcaacattcagatgatcattcagtagtataaagggttaaaactgcaataagaactgtagattgttcattgta
gtattccttaagaacaaacaaacaaacaaagcggggaggggtttgtgggaggtgataaacaacaaagactgtgttctcctgctt
1872  cagtaaatggtgtatgtacatctcttttttattttttatgaaagttgattaatgtcaataaactactcatgacttttgtaagtta
tttttatgttgtttatttgggtactgccagtagttgtttgtaataagaggtcttttttagcagcgtgagttaccatttgaataaag
2052  tataatttttttaagtgttctgtttctggaaaa 2085

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Capital letters correspond to the reading frame. This sequence was determined from two *c-jun* overlapping cDNAs clones isolated from a quail neuroretina cells cDNA library and from a genomic quail DNA clone ending at an *Sau3a*I site (arrowhead). Since the mRNA size is about 2 kb long the above sequence covers the whole transcribed region and part of the proximal promoter of the gene.

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