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# Partial nucleotide sequence of the avian erythroblastosis virus (AEV ES4)

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The avian erythroblastosis virus is an avian defective leukemia virus that carries and expresses two oncogenes v-erb A and v-erb B independantly. We have sequenced the non oncogenic parts of the genome. Our sequence includes the retroviral genes δ gag and δ env, the long terminal repeats (LTR) and both the 5' and the 3' untranslated regions surrounding the coding sequences.

```
...1 GCCATTTTACCTTCCACCACATTGGTGTGCACCTGGGTAGATGGACAGACCGTTGAGTCCCTAACGATTGCGAACACCTG
..81 AATGAAGCGGAAGGCTTCATTtgqtgaccccgacgtgatcgttagggaatagtggtcggccacagacggcgtggcgatcc
.161 tgccctcatccgtctcgcttaacggggagcggacgatgaccctagtagagggggctgcggcttaggaggqcagaagctga
.241 gtggcgtcggagggagctctactgcaggggccaagatacctaccgagaactcagatagtcgttggaagacgggaagga
.321 agcccgacgactgagcagtccacaccaggtgcgattccggtcacccgtggatcaagcATGGAAACCGTCATAAAGGTGAT
.401 TTCGTCCGCGTGTAAAACCTATTGGGGGAAAACCTCTCCTTCTAAGAAGGAAATAGGGGCCATGCTGTCCCTGCTACAAA
.481 AGGAAGGGTTGCTTATGTCTCCCTCAGACTTATATTCCCCGGGGTCCTGGGATCCCATTACCGCGGCGCTCTCCCAGCGG
.561 GCTATGGTACTTGGGAAATCGGGAGAGTTAAAAACCTGGGGATTGGTTTTGGCGGCATTGAAGGCGGCTCGAGAGGAACA
.641 GGTTACATCTGAGCAAGCAAAGTTTTGGTTGGGATTAGGGGGAGGGAGGGTCTCTCCCCCAGGTCCGGAGTGCATCGAGA
.721 AACCAGCAACGGAGCGGCGAATCGACAAGGGGGAGGAAATGGGAGAGACAACTGTGCAGCGAGATGCGAAGATGGCGCCG
.801 GAGAAAATGGCCACACCTAAAACCGTTGGCACATCCTGTTATCAGTGCGGAACAGCCACTGGCTGGAATTGCGTCACAGC
.881 CTCGGCTCCTCCTCCTCCTTATGTGGGGAGTGGTTTGTATCCTTCCCTGGCGGGGGCGGGAGAGCAGGGCCAGGGGGGTG
.961 ACACACCTCGGGGGGCGGAACAGCCAAAGGCGGAGCCAGGGCACGCGGGTCAGGCCCCTGGGCCGGCCCTGACTGACTGG
1041 GCAAGGATCAGGGAGGAGCTTGCGAGTACTGGTCCGCCCGTGGTAGCCATGCCTGTAGTGATTAAGACAGAGGGACCCGC
1121 CTGGACCCCTCTGGAGCCAGAGGACATC
```

A/ Sequence of 1148 nucleotides at the 5' end of the AEV genome, including R (boldface italic letters), U5 (boldface letters), the 5' untranslated region (small letters), δ gag (uppercase letters) and the beginning of v-erb A (italic letters). Noticeable stretches are also underlined : the protein binding site (position 102), the packaging signal (position 216) (3), the splice donor site (position 394), the gag consensus enhancer "core" sequence (position 910 ) (1). δ gag sequence were found to be in the same reading frame than v-erb A (2) and no terminator codons were identified as previously expected from identification of the gag-erb A fusion protein.

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...1 GAATTCCCACAGCACAGCTGTGGGCAACCCTGAGTATCTTGAGTGATCACAGTGAGTCTATACAGAAGAAGTTCCAGCTA
..81 ATGAAGGAACATGTCAATAAGATCGGCGTGGACAGCGACCCAATCGGAAGTTGGCAGCGAGGAATATTCGGAGGAATAGG
.161 AGAATGGGCCGTTCATTTGCTGAaaggactgcttttggggcttgtagttatcttgttgctagtagtgtgcctgccttgcc
.241 ttttgcagtttgtatccagtagcatccgaaagatgataaataattccatcagctaccacacggaatataagaagctgcaa
.321 aaggcctgtgggagcctgaaagcaggatagtataaggcagtacatgggtggtggtgtagcgcttcggagtcggactgtaa
.401 cggggcatggcttaactaaggggactatggcatgtataggcgtaaaggggcttcggttgtacgcggttaggagtcccct
.481 taggatatagtagacacgcttttgcataacttctttgttttgcccttagactattcaagttgcctctgtggattagggct
.561 ggaggcagctcggatggtctgatggtcaaataaggcgggcaagaaagctatgaaatacgcttttgcatagggggggggag
.641 gTGTAGTCTTATACAATAGCCTTACACAATAATGCTATGTAACGATGAAACAGCAGTATTCCATATAAGGAAAGTAAGGA
.721 CACCACACGTGTTGATTGGTGGATGTGGGGTGGTATGATGGTGGTATGATCGTACCTTATTAGGAATGTAACAGACGGGT
.801 CTCGCAAGGATTGGATAGACTACTCAGTTCCGCATAGCAGAGATATTGTATTTAAGTGCCTAGCTCGACACAATAAACGC
.881 CATTTTACCTTCCACCACA
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B/ Sequence of 899 nucleotides at the 3' end of the AEV genome, including the 3' end of v-erb B (italic letters), δ env (uppercase letters), the 3' untranslated region (small letters), U3 (boldface letters), R (boldface italic characters). The polypurine tract (position 629), the "TATA box" (position 849) and the polyadenylation signal (position 872) are underlined.

Références 1) Arrigo, S. and al.(1987) Mol. Cell Biol. 7, 388-397. 2) Debuire, B. and al. (1984) Science, 224, 1456-1459. 3) Katz, R.A. and al. (1986) J. Virol. 595, 163-167.


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