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cDNA sequence of the *env* gene of a pathogenic equine infectious anemia lentivirus variant

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We report the *env* gene nucleotide sequence from a biologically cloned, virulent variant of equine infectious anemia virus (EIAV-WSU5) (1). Dideoxynucleotide chain-termination sequencing of both strands of 2 overlapping cDNA clones isolated from cDNA libraries using cross-hybridizing EIAV-prototype *env* gene probes was done. EIAV-WSU5 *env* gene was the same length, 2,580 base pairs, as the published prototype EIAV *env* gene coding gp90 and gp45 (2). There were 13 nucleotide substitutions between the *env* gene of EIAV-WSU5 and prototype virus; 6 resulted in amino acid changes. At nucleotide 80, Cys to Tyr was in the putative signal peptide conserved in another study (3). The change at 943 resulted in Arg to Ser, adding an N-linked glycosylation site. Other changes included one polar amino acid for another (Ser to Asn, 1037), one negatively charged amino acid for a positively charged one (Lys to Glu, 1039, one hydrophobic residue for another (Val to Ile, 1276), and a single change in the gp45 coding region of Ile to Thr at 2474. One or more of these changes may alter neutralization sensitive epitopes and allow lentivirus variants to escape immune responses.

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2. Rushlow,K. *et al.* (1986) *Virology* **155**, 309-321.
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1    ATGGTCAGCATCGCATTCTATGGGGGGATCCCAGGGGGAATCTCAACCCCTATTACCCAACAGTCAGAAAAATCCAAGTATGAGGAAAAC
91   ACAATGTTTCAACCTTATTGTTATAATAATGACAGTAAGAACAGCATGGCAGAATCGAAGGAAGCAAGAGACCAAGAAATGAACCTGAAA
181  GAAGAATCTAAAGAAGAAAAAAGAAGAAATGACTGGTGGAAAATAGGTATGTTTCTGTTATGCTTAGCAGGAACTACTGGAGGAATACTT
271  TGGTGGTATGAAGGACTCCCACAGCAACATTATATAGGGTTGGTAGCGATAGGGGGAAGATTAAACGGATCTGGCCAATCAAATGCTATA
361  GAATGCTGGGGTTCCTTCCCGGGGTGTAGACCATTTCAAAATTACTTCAGTTATGAGACCAATAGAAGCATGCATATGGATAATAATACT
451  GCTACATTATTAGAAGCTTATCATAGAGAGATAACATTCATTTATAAGTCTTCTTGCACAGATAGTGATCATTGTCAAGAGTATCAATGT
541  AAAAAAGTTAATCTTAATTCCTCTGACTCCTCTAACTCTGTACGTGTTGAGGATGTAACGAACACAGCGGAATATTGGGGATTTAAATGG
631  CTAGAATGTAATCAAACAGAAAATTTTAAGACTATATTAGTACCTGAAAATGAAATGGTAAATATCAATGATACTGATACCTGGATACCT
721  AAGGGGTGTAATGAGACGTGGGCAAGAGTGAAACGTTGTCCTATAGATATTTTATATGGGATACATCCAATCAGGCTGTGTGTACAGCCA
811  CCATTTTTTCTGGTACAGGAGAAAGGGATTGCTGATACTTCTAGAATTGGCAATTGTGGGCCAACAATATTTCTTGGGGTTTTAGAAGAT
901  AATAAGGGAGTAGTACGGGGGGATTATACAGCCTGCAATGTGAGTCGCCTAAATATAAATAGAAAGGATTATACAGGGATCTATCAAGTA
991  CCTATATTTTATACATGTACTTTCACTAACATAACTTCCTGCAATAATGAGCCAATAATCAGTGTTATCATGTATGAAACAAACCAGGTA
1081 CAATATTTATTGTGTAATAATAATAATAGTAATAATTATAATTGTGTAGTACAAAGTTTTGGAGTTATAGGACAGGCACACTTAGAACTG
1171 CCTAGACCTAACAAAAGAATAAGGAATCAAAGCTTTAACCAATATAACTGCTCTATAAATAACAAAACAGAATTAGAAACATGGAAGTTA
1261 GTAAAGACTTCTGGCATAACTCCTTTACCTATTTCTTCTGAAGCTAACACTGGACTAATTAGACATAAGAGAGATTTTGGTATAAGTGCA
1351 ATAGTGGCAGCTATTGTAGCCGCTACTGCTATTGCTGCTAGCGCTACTATGTCTTATGTTGCTCTAACTGAGGTTAACAAAATAATGGAA
1441 GTACAAAATCATACTTTTGAGGTAGAAAATAGTACTCTAAATGGTATGGATTTAATAGAACGACAAATAAAGATATTATATGCTATGATT
1531 CTTCAAACACATGCAGATGTTCAACTGTTAAAGGAAAGACAACAGGTAGAGGAGACATTTAATTTAATTGGATGTATAGAAAGAACACAT
1621 GTATTTTGTCATACTGGTCATCCCTGGAATATGTCATGGGGACATTTAAATGAGTCAACACAATGGGATGACTGGGTAAGCAAAATGGAA
1711 GATTTAAATCAAGAGATACTAACTACACTTCATGGAGCCAGGAACAATTTGGCACAATCCATGATAACATTCAATACACCAGATAGTATA
1801 GCTCAATTTGGAAAAGACCTTTGGAGTCATATTGGAAATTGGATTCCTGGATTGGGAGCTTCCATTATAAAATATATAGTGATGTTTTTG
1891 CTTATTTATTTGTTACTAACCTCTTCGCCTAAGATCCTCAGGGCCCTCTGGAAAGTGACCAGTGGTGCAGGGTCCTCCGGCAGTCGTTAC
1981 CTGAAGAAAAAATTCCATCACAAACATGCATCACGAGAAGACACCTGGGACCAGGCCCAACACAACATACACCTAGCAGGCGTGACCGGT
2071 GGATCAGGGGACAAATACTACAAGCAGAAGTACTCCAGGAACGACTGGAATGGAGAATCAGAGGAGTACAACAGGCGGCCAAAGAGCTGG
2161 GTGAAGTCAATCGAGGCATTTGGAGAGAGCTATATTTCCGAGAAGACCAAAGGGGAGATTTCTCAGCCTGGGGCGGCTATCAACGAGCAC
2251 AAGAACGGCTCTGGGGGGAACAATCCTCACCAAGGGTCCTTAGACCTGGAGATTCGAAGCGAAGGAGGAAACATTTATGACTGTTGCATT
2341 AAAGCCCAAGAAGGAACTCTCGCTATCCCTTGCTGTGGATTTCCCTTATGGCTATTTTGGGGACTAGTAATTATAGTAGGACGCATAGCA
2431 GGCTATGGATTACGTGGACTCGCTGTTATAATAAGGATTTGTACTAGAGGCTTAAATTTGATATTTGAAATAATCAGAAAAATGCTTGAT
2521 TATATTGGAAGAGCTTTAAATCCTGGCACATCTCATGTATCAATGCCTCAGTATGTTTAG
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