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Structural analysis of peptides that interact with Newcastle disease virus

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A peptide with the sequence CTLTTKLYC has been identified to inhibit the propagation of Newcastle disease virus (NDV) in embryonated chicken eggs. Oligonucleotide-directed mutagenesis was used to mutate the peptide displayed on the pIII protein of filamentous M13 phage and identify the amino acid residues that are involved in the interaction with NDV. Mutations of Y8 to A severely disrupted the interaction suggesting that Y8 plays an important role in the interaction whereas other mutations did not significantly affect the interaction. The two- and three-dimensional conformations of the peptides were determined by using CD, NMR, and molecular modelling. The three-dimensional conformation of the linear peptide could not be determined due to the mixture of beta-turn and beta-sheet. The cyclic peptide, on the other hand, exhibited only beta-turn structure. Two models on the peptide structure are presented.