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**Relationship between amino acid polymorphism of  
hemagglutinin and its domains  
composition in influenza virus.**

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**Abstract:** The relationship between amino acid polymorphism of hemagglutinin and its domains composition in *Influenzavirus* was shown

**Key words:** *Influenzavirus*, polymorphism, hemagglutinin, domains, relationship.

Influenza viruses (types A, B and C) cause highly contagious respiratory tract infections associated with high mortality rates. Complications, hospitalization and death occasions are most common for people with low immunity.

One of the most important antigenic and pathogenic factors is hemagglutinin (HA). HA is a classical type I membrane glycoprotein which functions as a sialic acid binding and membrane fusion protein during virus entry into target cells. Different strains of Influenza viruses have different virulent properties.

**The aim** of this work was to detect relationship between amino acid polymorphism of HA and domains of this protein.

**Material and methods.** Domains of 154 different amino acid sequences from National Centre of Biotechnology Information were detected by DELTA-BLAST program.

**Results and discussion.** All of studied HA samples contained pfam00509 domain (Fig. 1).



**Figure 1. Structure of pfam00509 domain of HA.**

This domain causes membrane fusion of the viral membrane with the host membrane. Fusion occurs after the host cell internalizes the virus by endocytosis. The drop of pH causes release of a hydrophobic fusion peptide and a large conformational change leading to membrane fusion.

As **result**, there was shown the absence of HA amino acid polymorphism in its domain composition.