mational and post-translational modifications are identical with the ones synthesized in the course of the infection [Whitton, 1996].

The aim of our study was a construction and subsequent cloning (within a plasmid vector) of a gene encoding RVFV immunodominant protein epitopes promising with respect to development of recombinant and DNA vaccines.

Based on the literature data and computer analysis of the amino acid sequences of glycoproteins Gn, Gc and nucleoprotein N, sequences of predicted protein protective epitopes were determined [EpitPred, Imatdinov IR, 2012]. The selected sites were used in a computer designing of an artificial polyepitopic protein [RaptorX, http://raptorx.uchicago.edu; I-TASSER, http://zhanglab.ccmb.med.umich.edu/I-TASSER]. As a result, an amino acid sequence of a polypeptide variant «S73» which includes T -and B – epitopes was arranged. To assemble an artificial gene, some primers flanking the respective sites of the nucleotide sequences were designed. The plasmids from a gene library of a RVF virus strain "1974 VNIIVViM" were used as templates. In the sequences of glycoprotein Gn, some 3 sites of 192, 291 and 153 bps, of glycoprotein Gc one site of 216 bps, and of nucleoprotein N sites of 134 and 149 bps were selected. Also, a site-directed mutagenesis of the two amino acid sequences of two glycoprotein Gn epitopes inducing the formation of neutralizing antibody resulted in the amino acid sequences of epitopes of endemic strains.

The artificial gene encoding the polyepitope polypeptide (NpEpt2-GnEpt2-GnEpt1-GcEpt-GnEpt3-NpEpt1) was cloned within a plasmid pJET1.2. The carried out sequencing showed the identity of the nucleotide sequence with the one theoretically predicted. The length of the insertion containing the incorporated restriction sites XhoI and StuI was 1099 bps, and the encoded protein comprised 363 amino acids.

The predicted conformational structure of the recombinant protein indicates its promising use in the development of recombinant or DNA vaccines against Rift Valley fever. The further step will be the cloning of this gene under control of a cytomegalovirus promoter for evaluation of an immune response to recombinant plasmid inoculation.

ГЕНЫ ТРАНСКРИПЦИОННЫХ ФАКТОРОВ MYB *A. THALIANA* — МИШЕНИ MIRNA

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Семейство транскрипционных факторов MYB влияет на развитие, метаболизм и ответ на стресс растений. Установление регулирующей роли miRNA в экспрессии генов открыло новые возможности влиять на продуктивность и устойчивость растений. О влиянии miRNA на экспрессию генов MYB имеется мало сведений. Нами были определены сайты связывания 337 miRNA *A. thaliana* в mRNA 144 генов MYB. Все выявленные сайты связывания miRNA локализованы в белок кодирующей области mRNA генов-мишеней. Сайты связывания семейства miR156 выявлены в mRNA генов AT3G06490 и AT5G17800. miRNA семейства miR159 и miR319 имели общие гены-мишени: AT2G26290, AT2G32460, AT3G11440, AT5G06100 и AT5G55020. Все сайты связывания кодировали гептапептиды, гомологичные LELPSFQ. Для miR414 найдены сайты связывания в mRNA восьми генов, которые кодировали олигопептиды, гомологичные DDDDDD. miR828 имела сайты связывания в mRNA 14 генов MYB. Нуклеотидные последовательности всех сайтов связывания miR828 кодировали олигопептиды, гомологичные WNTHLKK. miR856a,b связывались с mRNA 18 генов и сайты связывания кодировали поли-

пептиды, гомологичные PGRTDNE. Для miR5021 найдены сайты связывания в mRNA генов AT1G56160, AT2G32460, AT3G12820, AT4G18770, AT5G25560 и AT5G62470. Сайты связывания кодировали гексапептид SSSSSS. miR5658 имела сайты связывания в mRNA генов AT1G79180, AT2G32460, AT3G12820, AT3G13890, AT4G18770, AT4G25560, AT5G26660 и AT5G62470, которые кодировали консервативный пентапептид SSSSS. mRNA одиннадцати других генов связывали miR5658 в сайтах, кодирующих олигопептиды, гомологичные HHHHH. То есть, высоко гомологичные нуклеотиды в сайтах связывания miR5658 кодировали олигопептиды в разных открытых рамках считывания. mRNA пяти генов, кодировавших олигосерин, были общими мишенями для miR5021 и miR5658. Для miR414, miR5021 и miR5658 выявлены множественные сайты связывания, начала которых локализованы последовательно через 1-3 нуклеотида.

MYB TRANSCRIPTION FACTOR GENES OF *A. THALIANA* AS TARGETS FOR MIRNAS

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MYB transcription factors family affects plant development, metabolism and response to stress. Establishing the regulatory role of miRNA in gene expression had opened up new opportunities to influence on plant productivity and stability. There is a little information about the impact of miRNAs on MYB genes expression. The binding sites for 337 miRNAs in mRNAs of 144 MYB genes in *A. thaliana* were determined. All identified miRNA binding sites were located in the protein coding region of target mRNAs. The binding sites for miR156 family were identified in mRNAs of AT3G06490 and AT5G17800 genes. miR159 and miR319 families had common target genes: AT2G26290, AT2G32460, AT3G11440, AT5G06100 and AT5G55020. All binding sites encoded heptapeptides homologous to LELPSFQ. miR414 targeted eight genes that encoded oligopeptides homologous to DDDDDD. mRNAs of 14 MYB genes were shown to have binding sites for miR828. The nucleotide sequences of all miR828 binding sites encoded oligopeptides homologous to WNTHLKK. miR856a,b bound to mRNAs of 18 genes and binding sites encoded polypeptides homologous to PGRTDNE. It was found that miR5021 targeted mRNAs of AT1G56160, AT2G32460, AT3G12820, AT4G18770, AT5G25560 and AT5G62470 genes. Its binding sites encoded SSSSSS hexapeptide. miR5658 had binding sites in mRNAs of AT1G79180, AT2G32460, AT3G12820, AT3G13890, AT4G18770, AT4G25560, AT5G26660 and AT5G62470 genes that encoded conservative SSSSS pentapeptide. mRNA of other eleven genes bound to miR5658 in sites encoding oligopeptides homologous to NNNNN. That is, a highly homologous nucleotides of miR5658 binding sites encoded oligopeptides in different reading frames. mRNA of five genes encoding oligoserine were targets for miR5021 and miR5658. For miR414, miR5021 and miR5658 were revealed multiple binding sites, the beginning of which are localized consistently in 1-3 nucleotides.

ИСТОЧНИКИ ГЕНЕТИЧЕСКОЙ ГЕТЕРОГЕННОСТИ ЭМБРИОНАЛЬНЫХ КЛЕТОК

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Выполнены исследования эпи- и генетической гетерогенности герминативных клеточных линий мышей. Клеточные линии G1 и G4 получены независимо друг от друга из половых бугорков 12,5 дневных эмбрионов мышей линии BALB/c и любезно предоставлены для цитогенети-