Conclusion In the Arkharinsky district of the Amur region the main carriers of trichinelae are raccoon dogs which as animals with compound type of nutrition are highly susceptible to trichinosis and play, probably, an important role in its spreading in nature. Inhabitants use sometimes meat of raccoon dogs as medicinal products of nutrition. Foxes as mass species also play an important role in keeping up a reservoir of trichinosis in this region.

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GENETIC POLYMORPHISM. METHODS OF STUDY

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More than 99% of people's genes are almost identical. A relatively small difference in the genes of any of us is of fundamental importance, since it determines our individuality. Genetic polymorphism or genetic diversity is a different variation of genes (poly - many, morpho - form). The presence of polymorphism of genes explains the structure and properties of those proteins that are produced in the body, i.e. changes in the proteome. Genetic polymorphism can be caused by: substitution of nucleotides, duplication, insertions, prolapses, nucleotide repeats. Genetic polymorphism can be of a quantitative or qualitative nature. Some of the polymorphisms occur quite often, others are very rare. Changes in the function of genetic polymorphism may be beneficial to the body, neutral or slightly negative, negative, • beneficial in a certain environment and negative in another. A classic example of gene polymorphism is the four blood groups. Under certain conditions, some genetic polymorphisms can either predispose or inhibit the manifestation of various diseases.

A single nucleotide polymorphism (SNP) sequence differences in the DNA of one nucleotide (A, T, G or C) in the genome cospecifics or between homologous regions of individual homologous chromosomes. SNPs arise as a result of point mutations and are especially important for the molecular diagnosis of diseases. To detect genetic polymorphism, DNA sequencing is used-the determination of the sequence of nucleotides in the polynucleotide chain. With full genomic sequencing, the whole DNA molecule consisting of 3 ml of man is sequenced. 200 million nucleotides. To solve such a grandiose task, methods of indirect sequencing have been developed (methods of sequencing a new generation). Partial sequencing determines the nucleotide sequence of selected DNA loci and this kind of sequencing finds application in clinical laboratory diagnostics. In particular, in the Amur Regional Children's Clinical Hospital a pyro-sequencer has been installed, which makes it possible to detect some genetic diseases.

Restriction fragment length polymorphism (RFLP) is a method for studying DNA by cutting it with endonucleases and determining the size of the fragments (restriction) formed by gel electrophoresis. An analysis of the diversity of the resulting restriction is an important tool in mapping the genome, localizing genes responsible for genetic diseases, determining the risk of the disease, obtaining genetic fingerprints and determining the relationship. The latter direction was called DNA fingerprinting.

Short tandem repeats - varying portions (loci) in the nuclear and mitochondrial DNA consisting of tandemly repeating monomer length less than 9 base pairs. They are widely distributed molecular markers in genetic and genomic studies. Increasing the number of repeating units of microsatellites in exons or regulatory genes associated with the development of neurological disease - Huntington's disease, spinal-bulbar amyotrophy, spinocerebellar ataxia syndrome, Fragile X-chromosome, ataxia, myotonic dystrophy, are associated with changes in properties of the proteins of the nervous tissue, accompanied by aggregation and precipitation. One of the most important proteins of the nervous tissue is gentingtin (Htt). A unique feature of this protein is the presence of a recurring sequence of glutamine residues near the N-terminus of the polypeptide chain. The number of glutamine repeats in Htt healthy people varies, but does not exceed 35. The development of Huntington's chorea is a consequence of a mutation in the first exon (EX1) by the type of short tandem repeats, resulting in an increase in the number of recurring glutamine residues, the number of which can reach 250 or more. The time of onset of the disease and its severity directly depend on the number of repetitions [1].

It is assumed that in the mutant protein mHtt, the polyglutamine region acquires a toxic conformation in the form of the ß-structure, as a result of which the protein aggregates and precipitates as amyloid fibrils. At least ten neurodegenerative diseases are caused by polyglutamine expansions, including Huntington's chorea, spinal and bulbar muscular atrophies, and polyglutamine spinocerebellar ataxia. In connection with the foregoing, Htt represents a target in the development of new effective medicines created with the help of computer design. To create such tools, it is absolutely necessary to know the tertiary structure of the protein (3D structure), which is established traditionally with the help of physicochemical methods (NMR spectroscopy, Rg-structural analysis, electronic cryomicroscopy), which require expensive equipment and absorb a lot of time. To date, the 3D structure of Htt has not been investigated. More precisely, only the structure of the initial N-terminal fragment of 430 amino acids is established, which includes a repeat of 17 glutamine residues [2]. To solve the above problem, computer simulation methods are used. Their essence is simple. In the database of 3D structures of proteins (RCSB PDB, etc.) using the BLAST algorithm, a

template is found with a physico-chemical 3D-structure, whose amino acid sequence (primary structure) coincides with the primary structure of the protein, The 3D structure of which you want to model. In the future, the computer models the 3D structure of the protein of interest to the researcher (query). In the case of Htt, the main difficulty is the uniquely long length of its polypeptide chain, comprising 3142 amino acids. For such a long chain, it is impossible to find pattern proteins. Therefore, to solve the problem, we proposed an approach consisting in modeling 3D structures of individual sections of the Htt polypeptide chain, combining the latter into a single molecule eventually.

We used UniProt database http://www.uniprot.org/ and NCBI Protein http://www.ncbi.nlm.nih.gov/protein to search for primary Htt sequence in FASTA format. The primary sequence was conditionally divided into 11 plots of ~ 300 AMC (142 AMC in 11 sites) in each. For each site, we searched for a template protein with a known tertiary structure using the BLAST algorithm and based on the 3D model template on the SWISS-MODEL server https://swissmodel.expasy.org/. It is noteworthy that the template proteins for each site belonged respectively to different groups according to their pharmacological properties (Table 1). Consequently, it is possible to assume the polyfunctionality of the physiological role of Htt. The obtained 11 models were loaded into Chimera 1.11.2, where peptide bonds were formed between them to form the 3D model of Htt. The results are presented in the .pdb file format, available for further use in any software for bioinformatic work with proteins.

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CATGUT IMPLANTATION IN ACUPOINT IN THE TREATMENT OF SHOULDER-HAND SYNDROME AFTER CEREBRAL APOPLEXY:A RANDOMIZED TRAIL

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ABSTRACT Shoulder-hand syndrome is a common complication after stroke and often occurs within 1-3 months. Stroke patients may cause shoulder pain, movement limitations, hand swelling, even hand muscles atrophy and other symptomsif improper care. For strokepatients, shoulder hand syndrome severely hinders the recovery of upper limb function, delays the rehabilitation process and course disability. Based of routine treatment and rehabilitation training, the patients were treated with catgut implantation at acupoint and compared with ordinary acupuncture group. The upper limb movement, pain score and edema changes were observed.

Material and Method Material:0.35*4.0cmAndy acpuncture needle;Andy electric acupuncture;Disposable catgut implantation needle (Zhenjiang high crown Medical Instrument Co., Ltd.); PGLA 90cm (surgical suture in Shanghai Pudong gold medical supplies Limited by Share Ltd); Disposable dental package;Sterile scissors.

Method:60 patients were divided into the treatment group and the control group.

The treatment group was treated with catgut implantation at acupoint on the basis of conventional treatment and rehabilitation. After hand disinfection, the PGLA line is cut into a 2cm standard with the sterile scissors. Asking the patient to be supine and then doing routine disinfection with iodophor. Using sterile forceps to put the catgut into the catgut implantation needle. Tightening the skin around the acupuncture point with the left hand, the right hand quickly into the needle. After the emergence of the needle response, twisting out needle. With sterile cotton swab pressed for a moment to prevent bleeding. Ten days at a time and three times a course for treatment. To observe the curative effect of 30 days.

The control groupwas treated with common acupuncture treatment on the basis of routine treatment and rehabilitation.Acupointselection:Jianliao,Jianyu,Jianzhen,Quchi,Shousanli,Waigua

n,Hegu,Baxie,Houxi.Operation:Choosing0.35*4.0cmAndy acpuncture needle and disinfecting.

Acupuncture with reinforcing reducing method. When the needle response ,retaining 30 minutes and supplement electric acupuncture (dilatational wave). Semel in die,.Observeafter30 days.

The data were analyzed by spss 17.0 statistical software

Result and Conclusion: Result:There was no significant difference in pain score, FMA score and hand swelling be-