

1. Demko I.V., Chubarova S.V., Gordeeva N.V. et al. Algorithms of diagnostics and records of proceedings of medical help in pneumonia. Methodic recommendations for physicians. - M. 2015. 49 c.
2. Intensive therapy in pulmonology (S.N. Avdeeva). V. 1. – 2014 – M. – “Atmosfera” - Serious community-acquired pneumonia – 249 – 270.
3. The use of discriminative analysis in the development of diagnostic (prognostic) important rule / N.V. Ulyanychev, V.F. Ulyanycheva, V.P. Kolosov, Yu. M. Perelman// Informatics and systems of management. - 2009. – 4 – 13-15.
4. Kolosov V.P., Perelman Yu.M, Ulyanychev N.V. Methodological approaches to the development of technologies of prognosis in pulmonology // Bul. Physiol. and pathol of respiration 2006. 22. – 20 – 23.
5. Kruglyakova L.V., Naryshkina S.V., Orlova T.S., Vjunova E.V. Hospital medical help and outcomes of community-acquired pneumonia in Blagoveshchensk- Materials of the VI Committee of physicians-pulmonologists of Siberia and Far East. Blagoveshchensk. - 2015 – 110 – 114.
6. Kruglyakova L.V., Naryshkina S.V., Sulima M.V. Peculiarities of community –acquired pneumonia in Blagoveshchensk.- XXVI National Congress on the diseases of organs of respiration.- M. - 2016 – 96.
7. Kruglyakova L.V., Markova E.G., Vjunova E.V., Pogorelova E.L. Criteria of diagnose of community-acquired pneumonia. XXVI National Congress on the diseases of organs of respiration –M. 2016. 97 – 98.

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SPREADING OF TRICHINOSIS IN THE ARKHARINSKY DISTRICT OF THE AMUR REGION

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Introduction The Arkharinsky district in the area of 14,6 thousand square kilometers occupies the far south-east of the Amur region in the river basin of Arkhara. In the north-west and west it borders on the Bureisky district, in the east and south-east – on the Khabarovsk territory, in the south-west and south the frontier passes through the Amur river. Warm, temperate and damp climate prevails. An average temperature of January is – 26,7° C, of July + 20,7° C. Deciduous or larch woods and flood-lands are situated in the valley of the Amur river. Difficult to traverse, dense, deciduous and cedar deciduous woods with underbrush and lianas sometimes pine forests are typical for low mountains.

Fauna is presented by brown bear, black bear, wolf, Manchurian deer, Japanese wild boar, lynx, otter, Manchurian hare, common field mouse, mandarin duck, white-naped and Japanese cranes, grey larva-eating bird, Indian cuckoo, tree wagtail, black wild duck, Amur and patterned sledge runners, Far-Eastern tree frog and many species of insects are typical. A family of carps prevails in rivers and lakes.

Agriculture is an economic profile of the district.

Key words: trichinella, infection, raccoon dogs

The objective: to study epizootology, epidemiology, diagnostics and prophylaxis of trichinosis in the Arkharinsky district.

Materials and methods Researches were carried out by methods of a compressor trichinelloscopy and digestion of muscles tests in an artificial gastric juice. 24 cuts from a masseter, a tongue, crura of diaphragm, gastrocnemius muscles were taken. Each cut was as large as an oat grain. The cuts were placed on the glass bottom of a compressor, covered with the upper glass and examined under the microscope MBS-10. The muscles, examined by digestion with gastric juice, were crushed in a meat grinder or with scissors. The received forcemeat was placed on the mill sieve № 23, being in the device of Berman, and filled with warm fresh artificial gastric juice in the ratio 100 ml of artificial gastric juice per 1g of forcemeat. Gastric juice was prepared according to: 3% - pepsin per 0,5% solution of hydrochloric acid. Berman's filled device was placed in the thermostat adjusted to the temperature 38-39° C. In half an hour the sieve in the device was stirred up. In an hour necessary amount of liquid was taken from the device, placed into the Petri's dish and examined under the microscope BMS-1.

Material for research was received from hunters, sanitary-and-epidemiologic establishments and individuals.

Results and discussion Larvae of trichinellae were revealed in a raccoon dog, a red fox, a sable and a lynx. The maximum contamination in raccoon dogs makes up 33%, in foxes – 27% and in sables – 12%. The average intensity of invasion in raccoon dogs makes up 93 larvae in 1g of gastrocnemius muscles, in red foxes – 88 larvae in 1g of gastrocnemius muscles, in a sable – 176 larvae in 1g of masseter, in a lynx – 1112 larvae in 1 g of masseter

Species of *Trichinella* native was revealed in all cases by using the method of keeping exposed to frost in deep freezer at the temperature - 18° C during a week. High frost-resistance of this trichinellae species may prove the fact that invasion in nature comes from corpse to an animal.

Corpses of animals contaminated with trichinella may be used as a food in the frozen form only. According to V.A. Britov it is observed in winter.

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.

References

1. Schul'man N.K. Amur region. Experience of the encyclopedic dictionary. Blagoveshchensk. Khabarovsk book publishing house, 1989. – 415 p.
2. Bessonov A.S.// Theory and practice of fight against parasitic diseases. – M: Rosselkhozakademiya, 2004. – P.71-72.
3. Britov V.A. Causative agents of trichinosis. – Moscow: Science, 1982. – 270 p.

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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 gelelectrophoresis. 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 huntingtin (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 β -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