



The 2nd Scandinavian - Baltic Symposium for Parasitology

Arctic Centre, University of Lapland

Rovaniemi, Finland

Aug 30 - Sep 1, 2007

Finnish Forest Research Institute (Metla)
Finnish Food Safety Authority (Evira)
Arctic Centre, University of Lapland

<http://www.metla.fi/tapahtumat/2007/spsb2/>

SBSP Symp. 2 Program

- All the presentations will take place in the Polarium - hall.
- Coffee and lunch (both free for the participants) will be served at the Cafeteria of the Arctic Centre.
- Remember to carry your name badge while in the Arctic Centre.
- Posters (of any size) will be displayed at the entrance to the Polarium-hall.
- Speakers are asked to strictly adhere to the program time limits in their presentations.
- **VERY IMPORTANT!!! Arctic Centre computer system is PC (Windows) based. Be sure that your Powerpoint presentation is last saved as PC (Windows) compatible, i.e. if you work with Mac, save your talk for PC. Mac-saved presentation may not show up correctly.**
- **Also very important!!! Please, give your powerpoint presentation (CD or stick) to Juha Laakkonen and/or session chairman at the computer table well in time during the break before your session, not during the session.**

Wed, Aug 29

18.00 - 21.00 Informal get-together (beer, wine and snacks) and registration at the Arctic Centre

Thu, Aug 30

8.00 - 9.00 Registration

9.00 - 9.20 Opening

9.20 - 12.00 Morning session I (chair Heikki Henttonen)

9.20 - 9.50 Stien, A., Deplazes, P., Fuglei, E., Henttonen, H., Ims, R.A., Oksanen, A., Stähler, S., Voutilainen, L. and Yoccoz, N.G.: The epidemiology of *Echinococcus multilocularis* on Svalbard

9.50 - 10.10 Moks, E., Jõgisalu, I., Valdmann, H. and Saarma, U.: Phylogenetic analysis of *Echinococcus granulosus* cervid genotypes G8 and G10 from Estonia

10.10 - 10.30 Lavikainen, A. and Oksanen, A.: Endemic human hydatidosis in Fennoscandia

10.30 - 11.00 Coffee

11.00 - 12.00 Morning session II (chair Audun Stien)

11.00 - 11.20 Borecka, A., Gawor, J., Malczewska, M. and Malczewski, A.: Occurrence of *Echinococcus multilocularis* in red foxes (*Vulpes vulpes*) in Central and Southern Poland

11.20 - 11.40 Gawor, J., Borecka, A., Basiak, W. and Bielawska, M.: Cystic echinococcosis (hydatidosis) in Central Poland - report of human cases recognised in 1998-2006

11.40 - 12.00 Laaksonen, S.: Filarioid nematodes - emerging parasites in Finnish cervids

12.00 - 13.00 Lunch

13.00 - 15.00 Afternoon session I (chair Tellervo Valtonen)

13.00 - 13.20 Valtonen, E.T., Rintamäki, P. and Karvonen, A.: Climate warming and diseases agents at fish farms - a long-term study

13.20 - 13.40 Ziętara, M., Kuusela, J., Rokicka, M. and Lumme, J.: How can a host specific *Gyrodactylus* parasite species switch host? — After good sex.

- 13.40 - 14.00 Øvstaas, O. G., Bachmann, L. and Bakke, T.A.: Host specificity and virulence differences between genetically characterized *Gyrodactylus salaris* and *G. thymalli* (Monogenea) populations
- 14.00 - 14.20 Barskaya, J.J. and Ieshko, E.P.: An attempt to experimentally determine the status of the *Gyrodactylus salaris* population in the Keret River
- 14.20 - 14.40 Novokhatskaya, O.V. and Ieshko, E.P.: Long-term trends in the fish parasite fauna in the Lake Syamozero
- 14.40 - 15.00 Sinisalo, T., Valtonen, E. T., Helle, E. and Jones, R. I.: Dietary differences between individual ringed seals (*Phoca hispida botnica*): evidence from helminth assemblages, alimentary contents and stable isotope analysis
- 15.00 - 15.30 Coffee
- 15.30 - 16.50 Afternoon session II (chair Tellervo Valtonen)
- 15.30 - 15.50 Lebedeva D. and Ieshko E.: Frequency distribution of *Diplostomum huronense* metacercariae in the roach population of the Lake Ladoga
- 15.50 - 16.10 Pulkkinen, K., Aalto, S. and Salonen K.: The effect of parasites on *Daphnia* stoichiometry
- 16.10 - 16.30 Barskaya, J.J. and Ieshko E.P.: Parasite fauna of salmon parr from the Teno and Tornio rivers
- 16.30 - 16.50 Matveeva, E.M. and Ieshko, E.P.: Experimental studies on infection dynamics: infection of potato plants by the potato cyst-forming nematode *Globodera rostochiensis* Woll.
- 17.00 - 18.00 NetVetPar network meeting

19.00 - 20.00 The reception by the City of Rovaniemi (City Hall, Hallituskatu 7)

Fri, Aug 31

- 9.00 - 10.30 Morning session I (chair Timo Soveri)
- 9.00 - 9.30 Henttonen, H., Haukisalmi, V and Hardman, L.: Comparative phylogeography of cestodes (Anoplocephalidae) of arvicoline rodents
- 9.30 - 9.50 Križanauskienė, A., Pérez-Tris, J., Gavrilo V., Zehtindjiev P., Sokolov, L., Palinauskas, V. , Hellgren O., Bensch S. and Valkiūnas G.: Phylogeography of *Haemoproteus* spp. (Haemosporida, Haemoproteidae) of blackcap *Sylvia atricapilla* in Europe
- 9.50 - 10.10 Laakkonen, J.: The hemotrophic bacteria of the genus *Bartonella* in the arctic small mammals
- 10.10 - 10.30 Ieshko, E.P. and Bugmyrin, S.: Patterns in the dynamics of the frequency distribution of the nematode abundances in bank vole (*Clethrionomys glareolus* Schreber, 1780)
- 10.30 - 11.00 Coffee
- 11.00 - 12.00 Morning session II (chair Timo Soveri)
- 11.00 - 11.20 Benesh, D.: Time to be transmitted? - Plasticity in host manipulation by a complex life cycle parasite
- 11.20 - 11.40 Isomursu, M., Rätti, O., Helle, P. and Hollmén, T.: The effect of age and sex on intestinal parasite infections of the Finnish grouse
- 11.40 - 12.00 Mlocicki, D., Swiderski, Z., Miquel, J., Eira, C.: Analysis of the cleavage pattern and blastomeres characteristic in the anoplocephalid cestode *Mosgovoyia ctenoides* (Railliet, 1890) Beveridge, 1978.
- 12.00 - 13.00 Lunch
- 13.00 - 14.00 SBSP Board meeting

- 13.00 - 14.00 Time to see the exhibitions of the Arctic Centre (free for the meeting participants)
- 14.00 - 14.30 The general assembly of SBSP (Polarium Hall)
- 14.30 - 15.00 Coffee
- 15.00 - 17.00 Afternoon session (chair Seppo Meri)
- 15.00 - 15.20 Umran, Stensvold, R., Vestergaard, L. and Nielsen, H.V.: Neospora caninum infections in man?
- 15.20 - 15.40 Traversa, D., Iorio, R., Kharchenko, V., Kuzmina, T., Paoletti, B., Gatti, A., Bartolini, R., Costanzo, F. and Klei, T.R.: Molecular identification of equine cyathostomes resistant to fenbendazole and susceptible to oxibendazole and moxidectin
- 15.40 - 16.00 Palinauskas V., Valkiūnas G., Bolshakov C. V. and Bensch S.: Effects of Plasmodium relictum (lineage P-SGS1) on experimentally infected passerine birds
- 16.00 - 16.20 Valkiūnas, G., Bensch, S., Sehgal, R. N. M. and Iezhova T. A., Križanauskienė, A., Hellgren, O. and Palinauskas, V.: Microscopic and PCR-based diagnostics of blood parasites: advantages and shortcomings of both methods
- 16.20 - 16.40 Rätti, O.: Geographical variation in avian blood parasite prevalence: the role of vectors
- 16.40 - 17.00 Babushnikova A.P., Zhurauliou D.V. and Ostrovsky O.A.: Peculiarities of the blood parasite invasion of birds of the national park "Narochansky"
- Free evening "Rovaniemi by night"

Sat, Sep 1

- 9.00 - 10.30 Morning session I (chair Osmo Rätti)
- 9.00 - 9.30 Khattab, A., Bonow, I., Schreiber, N., Petter, M., Schmetz, C., Meri, S. and Klinkert, M.-Q.: Plasmodium falciparum STEVOR proteins are located to the rhoptries and are involved in the merozoite invasion of erythrocytes
- 9.30 - 9.50 Kazemzadeh, Z., AfsharPad M., Djadid N.D., Raeisi, A., Shabani, A. and Zakeri S.: Molecular surveillance of chloroquine resistance associated mutations of Plasmodium falciparum in Iran
- 9.50 - 10.10 Djadid, N.D., Zakeri, S., Gholizadeh, S., Daneshinia, N., Bayat, N., Farhoomand, F., Mohagheghi, A. and Raeisi, A.: Twelve years of molecular studies on malaria vectors in Iran-Pakistan-Afghanistan border areas: Application in malaria control program
- 10.10 - 10.30 Stensvold, C.R. and Nielsen, H.V.: Endemic unicellular intestinal parasites (UIP) in Denmark
- 10.30 - 11.00 Coffee
- 11.00 - 12.00 Morning session II (chair Osmo Rätti)
- 11.00 - 11.20 Paulauskas, A., Ambrasiene, D., Radzijeuskaja, J., Rosef, O., Turcinaviciene, J.: Molecular ecology of Borrelia burgdorferi s. l. in ticks and rodents from Lithuania and Norway
- 11.20 - 11.40 Bugmyrin, S., Bespyatova, L., Anikanova, V. and Ieshko, E.: The abundance of taiga tick Ixodes persulcatus Schulze (Acarina, Ixodidae) on the cut-overs of different age in the middle taiga subzone of Karelia
- 11.40 - 12.00 Alekseev, A., Dubinina, H., Jääskeläinen, A., Vaheri, A. and Vapalahti, O.: Impact of environment pollution on the risk of tick-borne infection enhancements in the Baltic region.
- 12.00 - 13.00 Lunch
- 13.00 - 15.00 Afternoon session I (chair Antti Oksanen)

- 13.00 - 13.20 Oksanen, A.: Reindeer parasites
- 13.20 - 13.40 Eyðal M., Bambir S.H., Sigurdarson S., Gunnarsson E. and Fridriksson S.: Fatal infection in an Icelandic stallion caused by *Halicephalobus gingivalis* (Nematoda: Rhabditida)
- 13.40 - 14.00 Nowosad, B., Kornaś, S., Molenda, K., Skalska, M., Gawor J. and Cabaret J.: Genetic resistance to cyathostomes infection in pure blood Arabian horses
- 14.00 - 14.20 Borecka, A. and Gawor, J.: PCR method for the routine diagnostics of *Toxocara* spp. eggs from the soil
- 14.20 - 14.40 Bæk-Sørensen, L., Thamsborg, S. M. and Kristensen, T.: Liver fluke infection in dairy heifers grazing marshlands
- 14.40 - 15.00 Kornaś, S., Nowosad, B., Molenda, K., Skalska, M., Gawor, J., Cabaret, J. and Nosal P.: Differential diagnostics of cyathostomes (Cyathostominae) species on the basis of infective larvae
- 15.00 - 15.30 Coffee
- 15.30 - 16.10 Afternoon session II (chair Antti Oksanen)
- 15.30 - 15.50 Lassen, B., Talvik, H., Mägi, E. and Jarvis, T.: Preliminary study of intestinal parasites in Estonian swine herds of different management systems
- 15.50 - 16.10 Höglund, J., Engström, A. Morrison, D.A. and Mattsson J. G.: Antigenic variation in the major sperm protein gene within populations and species of the genus *Dictyocaulus*
- 16.10 Conclusions

19.00 Meet at the entrance of the Arctic Centre for the banquette bus transportation to Hirsipirtti (18 km from Rovaniemi). Menu includes traditional Lappish food (fish, reindeer, salads) and beverages (beer, wine). Late comers can buy banquette tickets at registration.

Posters

- Anikieva, L., Valtonen, E. T. and Dorovskih, G.: Polymorphism in a smelt, *Osmerus eperlanus*, specialist - cestode *Proteocephalus tetrastomus* (Rudolphi, 1810) (Proteocephalidae)
- Chomicz, L., Szubert, A., Baranowska-Korczyn, A., Stefaniak, J. and Polański, J.A.: Usefulness of morphological techniques in detection and verification of human cystic and alveolar echinococcoses
- Butautytė, G. and Mažeika, V.: Helminth community structure of small rodents in the seaside regional park in Lithuania
- Chukalova, N.N.: Trematode fauna of bream (*Abramis brama* L.) from the Curonian Lagoon (the South-East Baltic Sea)
- Eihvalde, E., Keidans, P. and Antane, V.: Serological examination of bulk milk samples to neosporosis in Latvia and comparison of cow's morphological composition of blood
- Eliseev A.: The nematode fauna of the flounder from the Russian EEZ of the south-eastern Baltic
- Keidāns, P., Krūklīte, A. and Eihvalde, E.: Enteroparasites of dogs in Latvia
- Gruzdeva, L.I., Matveeva, E.M. and Kovalenko, T.E.: Plant parasites of the soil nematode communities in natural and agrocenoses in European North
- Karbowiak, G. and Rychlik, L.: The communities of blood parasites in Mediterranean water shrew *Neomys anomalus* Cebrera, 1907
- Komisarovas, J.: Molecular study of the cestode family Dilepididae
- Malmstrøm, M., Strømnes, E., Hansen, R.R and Ugland, K.I.: The nematode *Cucullanus heterochorus*; a possible indicator species for marine xenobotics
- Monrad, J., Webster, P., Johansen, M.V. and Thamsborg, S.M.: New technique for worm burden assessment of *Angiostrongylus vasorum* in experimentally infected foxes (*Vulpes vulpes*)
- Nejsum, P., Thamsborg, S. M, Jørgensen, C., Fredholm, M. and Roepstorff, A.: Population dynamics of *Ascaris suum* in trickle infected pigs
- Nosal, P., Petryszak, A., Kornaś, S. and Eckert, R.: Efficiency of levamisole in sows under field conditions
- Näreaho, A., Saari, S., Meri, S. and Sukura, A.: Complement membrane attack complex formation and infectivity of *Trichinella spiralis* and *Trichinella nativa* in rats
- Radzijeuskaja, J., Paulauskas, A. and Rosef, O.: Detection *Anaplasma phagocytophilum* and *Babesia divergens* in Lithuania and Norway using Real time PCR method
- Thamsborg, S.M., Guillot, J., Miro, G., Epe, C., Genchi, C., Deplazes, P., van Knapen, F. and Fisher, M.: Parasite control in pets.

ABSTRACTS OF ORAL PRESENTATIONS

THE EPIDEMIOLOGY OF ECHINOCOCCUS MULTILOCULARIS ON SVALBARD

Stien, A.¹, Deplazes, P.², Fuglei, E.³, Henttonen, H.⁴, Ims, R.A.⁵, Oksanen, A.⁶, Stähler, S.², Voutilainen, L.⁴ and Yoccoz, N.G.⁵

¹ Norwegian Institute of Nature Research, Norway; ³ Norwegian Polar Institute, Norway

² Institute of Parasitology, University of Zurich, Switzerland

⁴ Finnish Forrester Research Institute, Vantaa Research Centre, Finland

⁵ Department of Biology, University of Tromsø, Norway

⁶ National Veterinary and Food Research Institute, EELA, Finland

Audun.Stien@nina.no

In 1999, the cestode *E. multilocularis* was detected in an isolated population of sibling voles (*Microtus rossiameridionalis*, syn. *M. levis*) in the high arctic islands of Svalbard. In Svalbard, the sibling vole and arctic fox are the only available intermediate and main host species for *E. multilocularis*. The sibling vole exist only in a geographically restricted area on one of the islands and long term studies has shown considerable temporal and spatial variation in vole densities within this area due to variation in winter conditions. The effect of this variation on the transmission dynamics of *E. multilocularis* has since 2002 been investigated using snap-trapping and mark-recapture studies of the vole population, estimation of scat densities and *E. multilocularis* coproantigen prevalence in the scats from the fox population. In addition, a large scale study of the prevalence of *E. multilocularis* in the fox population has been performed based on analyses of guts from trapped foxes and fox faeces collected over an extensive area. The latest results from these studies are reported.

PHYLOGENETIC ANALYSIS OF ECHINOCOCCUS GRANULOSUS CERVID GENOTYPES G8 AND G10 FROM ESTONIA

E. Moks, I. Jõgisalu, H. Valdmann and U. Saarma

Institute of Zoology and Hydrobiology, University of Tartu, Estonia

epp_m@ut.ee

Taxonomy of the genus *Echinococcus* has recently been reviewed using full mitochondrion genome sequences, but the systematic status of *E. granulosus* cervid genotypes G8 and G10 is still under question as the genotype G10 was missing from this analysis. One hypothesis proposes that G6-G10 belong to a single species, but the other suggests that cervid genotypes G8 and G10 form one and pig-camel genotypes G6-G7 another species. Until now, G10 is the only cervid genotype found from Eurasia while both G8 and G10 have been found in North-America. The aim of our study was to analyse cervid genotypes of *E. granulosus* in Estonia and evaluate their phylogenetic status. The cysts of *E. granulosus* were collected during the parasitological study of wild ungulates in 2004 and 2005. Mitochondrial gene fragments of ATP6, ND1 and CO1 were sequenced and used for phylogenetic analyses. As a result two cervid genotypes: G8 and G10 were found. The combined phylogenetic analysis of the three mitochondrial genes demonstrated with very high statistical support that the cervid genotype G10 was phylogenetically closest to the G6-G7 genotypes, while the other cervid genotype G8 was more distant. Hence, the hypothesis suggesting that cervid genotypes G8 and G10 form one and the camel-pig genotypes G6-G7 another species, receives no support. On the other hand, it is premature to say whether the genotypes G6-G10 form a single species group or not.

ENDEMIC HUMAN HYDATIDOSIS IN FENNOSCANDIA

Lavikainen, A. and Oksanen, A.
Haartman Institute, University of Helsinki, Finland
Finnish Food Safety Authority EVIRA
antti.lavikainen@helsinki.fi

The pig, camel and cervid strains of *Echinococcus granulosus* (E.g.) have been suggested to constitute an own species, *E. canadensis* (E.c.). This species causes cystic hydatid disease in humans, but it is supposed to be less virulent than *E.g. sensu stricto*. This hypothesis is mainly based on evidence from North America, where sylvatic hydatidosis caused by cervid E.c. has been found relatively benign among native peoples. In Fennoscandia, endemic human hydatidosis occurred in the reindeer herding area. To evaluate the pathogenicity of the Fennoscandian E.c. (E.g. G10), we analysed all published cases considered indigenous in origin. Between 1867 and 1977, over 170 such cases were mentioned diagnosed, of which 72 were reported in detail. Majority of the patients were Sámi reindeer herders. The Fennoscandian hydatid disease resembles North American sylvatic hydatidosis in that it involves lungs more often than liver. In addition, some asymptomatic cases and spontaneous cure by calcification or rupture of the cyst to a bronchus were described. However, most of the patients had notable symptoms, and some cases were complicated with big (up to 13 liters), multiple, atypically located (retroperitoneal, cerebral etc.) or secondarily infected cysts. Two patients died. Special eradication programs were initiated, but the main reason for the disappearance of the endemic hydatid disease from Fennoscandia was arguably the dying out of the old nomadic reindeer herding lifestyle.

OCCURENCE OF ECHINOCOCCUS MULTILOCULARIS IN RED FOXES (VULPES VULPES) IN CENTRAL AND SOUTHERN POLAND

Borecka, A., Gawor, J., Malczewska, M. and Malczewski, A.
Laboratory of Parasitoses of Domestic Animals, Institute of Parasitology of the Polish Academy of Sciences, Warsaw, Poland
ab@twarda.pan.pl

E. multilocularis is mainly transmitted in a wildlife cycle involving red foxes, wolves, coyotes, racoon dogs as final hosts and rodents (especially subfamily Arvicolinae) as intermediate hosts. Humans, domestic and wild pigs, horses, dogs and monkeys have been established as abberant, usually accidental hosts (Eckert et al. 2001). The metacestode stage of *E. multilocularis* cause human alveolar echinococcosis (AE). AE has a long incubation period about 5-15 years and clinical symptoms often occur in a rather late phase of the infection (Deplazes and Eckert 2001). The studies were carried out in central and southern part of Poland In the years 2004-2006 the intestines of 593 red foxes were examined by the intestinal scraping technique (IST) for the presence of *E. multilocularis*. 95 foxes were found infected (16.0%). The prevalence found was much higher when compare to that in the earlier studies. The increased number of infected foxes is undoubtedly a reason of growing number of AE cases in humans. Till now 49 cases were diagnosed in Poland.

Financial support was provided by the Ministry of Sciences and Higher Education, contract no. 2 PO5D10729.

CYSTIC ECHINOCOCCOSIS (HYDATIDOSIS) IN CENTRAL POLAND - REPORT OF HUMAN CASES RECOGNISED IN 1998-2006

Gawor, J.¹, Borecka, A.¹, Basiak, W.² and Bielawska, M.²

¹Laboratory of Parasitoses of Domestic Animals, Institute of Parasitology of the Polish Academy of Sciences, Warsaw, Poland

²Department of Zoonoses and Tropical Diseases of Medical University, Warsaw, Poland
gaworj@twarda.pan.pl

E. granulosus, cyclophyllidean cestode with an indirect, two-host lifecycle is one of the most important parasite species in respect of its public health importance and its geographical distribution. Hydatidosis in intermediate hosts (herbivorous or omnivorous animals including men) results from accidental ingestion of tapeworm eggs passed into environment with faeces from definitive hosts (wild or domestic carnivores). *E. granulosus* in humans develop mainly in the liver (70%) but also lungs (20%) and 10% of cysts can occur almost anywhere in the body (e.g. brain, body musculature, wall of the heart, kidneys, orbit of the eye, marrow cavity of bones). From 1998 to 2006 in Department of Zoonoses and Tropical Diseases of Medical University 96 patients from central Poland were diagnosed. Ultrasonography visualised cysts in the liver in 92 persons. Moreover 5 persons had cysts in kidneys, 2 patients in brain as well as isolated cases in spleen, thyroid gland and eye. ELISA test based on antigens of *E. granulosus* were positive for 31 persons (dilutions 1:100 - 1:400). The Hemagglutination Inhibition Test gave a positive results in serum dilution of 1:1600 for 2 patients and 1:100 - 1:800 for 27 patients. Drug treatment and/or operative treatment were used. Based on epidemiological data the main risk factors determined were dog ownership, farming and gardening.

FILARIOID NEMATODES, EMERGING PARASITES IN FINNISH CERVIDS

Laaksonen, S.¹, Solismaa, M.¹, Oksanen, A.¹, Kuusela, J.¹, Nikander, S.² and Saari, S.²

¹Finnish Food Safety Authority Evira, Oulu Research Unit (FINPAR), P.O.Box 517, FIN-90101 Oulu, Finland; ²Univ. Helsinki, Fac. Vet. Medicine
sauli.laaksonen@evira.fi

The Filarioid nematode *Setaria tundra* was first described in semi-domesticated reindeer in Arkhangelsk area, Russia, in 1928. *Setaria* sp. infections appear to have emerged in Scandinavian cervids in the late 1960's. In 1973, *S. tundra* was observed for the first time in northern Norway where there was an outbreak of peritonitis in reindeer. Also in 1973, tens of thousands of reindeer died in the northern part of the Finnish reindeer husbandry area. Severe peritonitis and large numbers of *Setaria* sp. worms were commonly found. Following this, the incidence of *Setaria* sp. in reindeer in Scandinavia diminished. According to meat inspection data and clinical reports from practising veterinarians, an outbreak of peritonitis in reindeer started in 2003 in the southern and middle part of the Finnish reindeer herding area. The outbreak was caused by *Setaria* nematodes. In the province of Oulu, the proportion of reindeer viscera condemned in meat inspection due to parasitic lesions increased from 4.9 % in 2001 to 47 % in 2004 and in Lapland from 1.4 % in 2001 to 43 % in 2005.. The focus of the outbreak moved approximately 100 km north yearly so that in the year 2005 only the reindeer in the northernmost small part of Finland were free of changes. In the same time the outbreak seems to have settled in the southern area. The present study revealed that *S. tundra* can act as a significant pathogen for reindeer, which was evident at both ante and post mortem inspection and in histological examination. Transmission dynamics of *S. tundra* will be discussed.

CLIMATE WARMING AND DISEASE AGENTS AT FISH FARMS - A LONG TERM STUDY

Valtonen, E.T., Rintamäki, P.¹ and Karvonen, A.

Department of biological and environmental science, University of Jyväskylä, Finland

¹ Department of Biology, University of Oulu, Finland

etvalto@bytl.jyu.fi

Climate warming is among the most evident threats facing the environment on the global scale. It affects the function of ecosystems and may also have indirect effects e.g. by changing the incidence of diseases and parasites. This is particularly evident in northern temperate regions where the occurrence and transmission of parasites are characterized by strong seasonality driven by temperature changes in the ambient environment. Parasites are well adapted to their environment and may quickly respond to factors influencing their transmission and growth by displaying adaptive phenotypic plasticity. We introduce the occurrence of parasites in a fish farm in Northern Finland over a period of 20 years. The farm produces salmonid smolt for stocking into the Baltic Sea. Salmonids were monitored from hatching to the age of 2 years when they were stocked. We show that the occurrence of protozoan species in particular have been highly predictable over the years; the same species occur from year to year with somewhat similar prevalences. The results presented here concern both pathogenic bacteria and protozoan ectoparasites. Disease dynamics at farms are characterised by consecutive and overlapping outbreaks from various disease agents during the summer. The yearly sum of day degrees ($\geq 5^{\circ}\text{C}$) has increased significantly over the 20 years. We describe how the occurrence of *F. columnare* infections and parasites has also increased in this environment where bath and drug treatments have been used when necessary. Global climate warming has exacerbated both bacterial and parasitic problems at fish farms and that this threat will obviously become worse in the future.

HOW CAN A HOST SPECIFIC GYRODACTYLUS PARASITE SPECIES SWITCH HOST? – AFTER GOOD SEX

Ziętara, M., Kuusela, J., Rokicka, M. and Lumme, J.

Department of Biology, University of Oulu, Finland

Jaakko.Lumme@oulu.fi

Gyrodactylus spp are considered as extremely host specific: the host fish is often the implicit basis of species recognition. On the other hand, some species are considered as generalists. The molecular species identification is leading to new insights of species and host specificity. Our major example is *G. salaris*, infamous pathogen of salmon. By DNA markers, we demonstrate that (i) the propagation of the parasite is mainly clonal, (ii) the clones are strictly host specific, (iii) *Gyrodactylus* avoids sex with clonemates, because it equals selfing, (iv) only rare hybridization may lead to host switch, and (v) hybridization may occur between surprisingly distant clones, which deserve a species rank. The examples are: (i) The Baltic salmon specific *G. salaris* is a superclone born 132 000 years ago as a hybrid between grayling parasites from the White Sea and Baltic Basins, (ii) *G. salaris* on Finnish rainbow trout is a secondary hybrid, sexual only if it meets non-self clone. (iii) *G. salaris* variant described in Denmark carried maternally inherited mitochondria from a distant species, indicating historical introgression. Every studied rainbow trout *Gyrodactylus* has been "synthetic", hybrid of local parasites. Fish farms are "parasite breeders": naive introduced species offer non-resistant testing grounds for sexual experiments leading to novel host-orientation recombinants with unpredictable pathogenic characteristics.

HOST SPECIFICITY AND VIRULENCE DIFFERENCES BETWEEN GENETICALLY CHARACTERIZED GYRODACTYLUS SALARIS AND G. THYMALLI (MONOGENA) POPULATIONS

Øvstaas, O. G., Bachmann, L. and Bakke, T.A.

Natural History Museum, University of Oslo, Department of Zoology, P.O. Box 1172 Blindern, NO-0318 Oslo, Norway
o.g.ovstaas@nhm.uio.no

Gyrodactylus salaris is a significant pathogen of East Atlantic salmon in Norway, Northern Russia, and at the west coast of Sweden. The Baltic stocks of Atlantic salmon seem to suffer from *G. salaris* infections to a lesser degree. We study the systematics and biology of gyrodactylids on salmonids, especially *G. salaris* and *G. thymalli* on grayling. *G. thymalli* hardly infects salmon but has been suggested a junior synonym of *G. salaris*. This suggestion mainly rests on molecular data. Differences in host specificity have been explained by differences in resistance and susceptibility between host species and stocks. Geographical isolates of *G. salaris* s.str. from salmon, rainbow trout and Arctic charr, have lately been found to differ in infectivity towards salmon. This highlights the need to study, beside host resistance, also level of infectivity of strains and species within this particular parasite complex to better understand the epidemiological differences. We have examined the variability in host preference and level of virulence among selected strains of *G. salaris* and *G. thymalli* that have previously been characterized with molecular markers. In laboratory tests population growth, reproductive and mortality rates have been studied by manipulations of single parasites on different salmonid species and stocks under controlled macro-environmental conditions. The results have significance for both the systematics of *G. salaris* and *G. thymalli* and for salmon management.

AN ATTEMPT TO EXPERIMENTALLY DETERMINE THE STATUS OF THE GYRODACTYLUS SALARIS POPULATION IN THE KERET RIVER

Barskaya, J.J. and Ieshko, E.P

Institute of Biology, Karelian Research Centre, Petrozavodsk, Russia

Gyrodactylus salaris was first recorded from the River Keret' in 1992. Infection of salmon parr with *G. salaris* caused the death of the fish. As the abundance of juveniles decreased, adult salmon stocks dropped more than 25 times. The epizootic and high parr infection rates of 2001 were superseded by a depression period in the parasite abundance. Neither was the parasite found during the study of juvenile salmon in 2004. In the summer of 2005 however, several specimens of the parasite were found on resident precocious males (mini-jacks) from the Sukhoi rapid (Lumme et al., in press).

In the autumn of 2005, an attempt was made to experimentally determine the status of the parasite population and its response to artificial increase in salmon population density. To this end, 2.500 individuals of 0+ salmon were stocked into each of the Sukhoi and Varatskiy rapids. Surveys carried out within a month have demonstrated that the parasite managed to restore its former abundance and yield high levels of the stocked salmon parr infection (prevalence 100%, mean intensity 61.1 specimens/fish) in the Sukhoi rapid only. Having artificially raised the host abundance we found that an infection outbreak and epizootic could develop very quickly even when the initial parasite abundance was very low.

This research was supported by the programme "Biological resources "of Fundamental Research of Biological Department, RAS № 01.0.40 001030.

LONG-TERM TRENDS IN THE FISH PARASITE FAUNA IN LAKE SYAMOZERO

Novokhatskaya, O.V. and Ieshko, E.P.

Institute of Biology, Karelian Research Centre, Petrozavodsk, Russia
novol@inbox.ru

Intensive eutrophication of freshwater bodies in central Europe began in the 1950s. The problem has now become topical also in northern countries. A vivid showcase is the transition of Lake Syamozero from the oligotrophic to the eutrophic status. Over more than 75 years of observations, the lake has undergone severe transformations telling on the productivity, abundance and structure of its fish populations and, hence, on the dynamics of the parasite fauna and occurrence of common fish parasite species. The study was carried out using to standard methods. During the period of 2003–2007, 416 specimens of 12 fish species were investigated. Fish parasite fauna includes 111 species. It is demonstrated that significant contributions to the fish parasite fauna are made by parasites specific to cyprinids – 36 species (32%), and percids – 16 species (14%), and 11 species are strict pike specialists. The proportion of salmonoid parasites is only 6% (7 species). Seven species are specific to burbot. An increase was recorded in the proportion and species richness of parasites specific to percids in the parasite fauna. The species richness of Myxosporidia has decreased compared to 1954–1956. The ratio of species restricted to specific fish families reflects the specificity of the waterbody, where an important part in the fish community belongs to cyprinids and percids.

This research was supported by the Basic Research Programme "Biological resources" of the Russian Academy of Science Biological Sciences Division №01.0.40 001030.

DIETARY DIFFERENCES BETWEEN INDIVIDUAL RINGED SEALS (PHOCA HISPIDA BOTNICA): EVIDENCE FROM HELMINTH ASSEMBLAGES, ALIMENTARY CONTENTS AND STABLE ISOTOPE ANALYSIS

Sinisalo, T.¹, Valtonen, E. T.¹, Helle, E.² and Jones, R. I.¹

¹ Department of Biological and Environmental Science, University of Jyväskylä,
P. O. Box 35, FIN-40014 University of Jyväskylä, Finland; tsinisal@bytl.jyu.fi

² Finnish Game- and Fisheries Research Institute, P. O. Box 2, FIN-00791 Helsinki, Finland

The numbers of seals in the Baltic Sea have increased rapidly over recent decades causing concern among fishermen and fishery managers. Information about temporal and spatial utilization of food resources by the seals is needed for efficient and sustainable management of endangered populations. Dietary differences between individual ringed seals were inferred by combining data from intestinal metazoan parasites, from alimentary tract contents analysis, and from stable isotope ratio analysis ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$). Food items and helminth parasites from the alimentary tract were examined from nine seals and stable carbon and nitrogen isotope ratios were determined from four different tissues (solar plexus muscle, shoulder muscle, liver and plasma) of the same individuals as well as from muscle tissue of seven fish species, and from one crustacean species. The combined approach allowed inferences of individual seal feeding behaviour in the Bothnian Bay. Some seals fed on a similar mixture of coastal and benthic fish and isopods, some foraged mainly on fourhorn sculpin, and some had mainly herring in their diets. One seal evidently fed on salmon and one seal consumed a high proportion of isopods as well as three-spined sticklebacks. The results also indicated that the breeding and moulting period imposes foraging restrictions on all seals but especially on nursing females. The differences between females may reflect variation in the onset and duration of parturition and lactation.

FREQUENCY DISTRIBUTION OF DIPLOSTOMUM HURONENSE METACERCARIAE IN THE ROACH POPULATION OF THE LAKE LADOGA

Lebedeva D. and Ieshko E.

Institute of Biology, Karelian Research Centre, Petrozavodsk, Russia

daryal78@gmail.com

Metacercariae of the fluke *Diplostomum huronense* are common parasites in the lens of roach *Rutilus rutilus* L. Infestation patterns, abundance distribution and size structure of metacercarial populations were studied in relation to fish age. Relationship between populations of the parasite and the host features spatial asymmetry with a majority of parasites found in few hosts, since the parasites are more likely to invade an already infected host than ones free of the parasites. In the roach population, *D. huronense* distribution in fish younger than 5+ is negative binomial. Aggregation of the parasites is due not only to individual differences in fish resistance to metacercarial infestation, but also to a higher mortality of heavily infected individuals. Pubertal roach (aged 5+ and older) have a higher resistance to further infestation with diplostomids, whereas the parasites that had invaded the fish previously grow in size and die, so that aggregation intensity decreases and the distribution approaches a normal one. The results of the study – distribution dynamics of the abundance and size structure of *D. huronense* metacercarial populations – prove the parasites to be a powerful factor controlling the host abundance through direct (death caused by the infection) and indirect (piscivorous birds picking out heavily infected fish) impact on the survival of juvenile fish.

THE EFFECT OF PARASITES ON DAPHNIA STOICHIOMETRY

Pulkkinen, K., Aalto, S. and Salonen K.

Dept. of Biological and Environmental Science, Univ. Jyväskylä, Finland

pukaan@bytl.jyu.fi

Ecological stoichiometry studies the balance of energy and nutrients in organisms. Generally producers contain even 10-fold lower phosphorus and nitrogen levels than their consumers. Individual growth and population dynamics in consumers can be directly constrained by their food nutrient element content. Parasites retrieve their energy and nutrients directly from their hosts, and it has been shown that they can reduce host growth, reproduction, survival and alter their nutritional status. In here we study the effect of parasites on the nutritional balance of the freshwater crustacean, *Daphnia* water flea. We grew *D. magna* populations in laboratory with green algae, and exposed half of the animals to a microsporidian parasite, which infects the epithelial cells of the gut. Half of the uninfected and infected animals were then fed with either phosphorus sufficient (HP) or P-deficient (LP) green algae for 5 days and the C:N:P stoichiometry was compared between the experimental groups. Our aim is to study the role of *Daphnia* in transferring energy in trophic cascades, and how these effects are further cascaded up and down the food web.

PARASITE FAUNA OF SALMON PARR FROM THE TENO AND TORNIO RIVERS

Barskaya, J.J. and Ieshko E.P.

Institute of Biology, Karelian Research Centre, Petrozavodsk, Russia
jbarskaya@gmail.com

The Tornio river and the Teno river are the largest salmon rivers of Northern Europe. Although their sources are close to each other, the rivers belong to different drainage basins (Tornio–Baltic Sea, Teno–Barents Sea), wherefore the parasite faunas of salmon parr from them have certain distinctions. Specificity of the relatively diversity of parr parasite fauna from the Teno river is constituted by a whole set of species (*Costia necatrix*, *Myxobolus neurobius*, *Apiosoma baueri*, *A. minimicronucleata*, *A. megamicronucleata*, *Paracoenogonimus ovatus*). Heavy infestation with infusorians, diplostomids, as well as the find of *Chloromyxum januaricus* – a species previously known from farmed salmon only, point to modifications induced by the activities of fish rearing farms in the Teno river watershed. The Tornio river parasite fauna is typical of salmon parr living in northern water-bodies. There prevail the species (*Myxidium salvelini*, *Chloromyxum truttae*, *Raphidascaris acus*, *Cystidicoloides ephemeridarum*, *Echinorhynchus salmonis*) which infect parr feeding on benthic organisms. A very common species is *Gyrodactylus salaris* – a parasite specific to the Baltic population of salmon and inciting epizootics in the Atlantic population. This species is potentially hazardous to salmon from the neighbouring system (Teno). This fact necessitates strict parasitological control, since introduction of alien species and subsequent development of epizootics is most likely for river systems located so close together.

EXPERIMENTAL STUDIES ON INFECTION DYNAMICS: INFECTION OF POTATO PLANTS BY THE POTATO CYST-FORMING NEMATODE *GLOBODERA ROSTOCHIENSIS* WOLL.

Matveeva, E.M. and Ieshko, E.P.

Institute of Biology of Karelian Research Center, Petrozavodsk, Russia

It has been experimentally demonstrated that the average number of nematodes on the roots of infected potato plants changes proportionately to the infestation dose. The frequency distribution of abundance changes from normal to aggregated as the infestation dose increases.

The experiments were carried out with sprouts of a susceptible potato variety in a controlled climate chamber, initial infestation doses being 10, 25, 50 and 100 cysts/plant (ND_10, ND_25, ND_50 and ND_100). The low-dose experiment involved also another stress factor of abiotic nature (short-term exposure to low temperature).

It is demonstrated that when the infestation dose is low (ND_10), the cysts are distributed evenly, and the plants respond to the nematode infection as to a stress factor. The degree of aggregation and heterogeneity of the plants in terms of susceptibility increase as the infestation dose is raised, and nematode abundances then follow the negative binomial distribution (NBD). The results confirm the data obtained by modeling parasite abundance (Andersen et al., 1978) indicating that presence of insignificant distinctions in susceptibility within a homogeneous sample of hosts is a prerequisite for the formation of aggregation in nematode distribution.

COMPARATIVE PHYLOGEOGRAPHY OF CESTODES (ANOPLOCEPHALIDAE) OF ARVICOLINE RODENTS

Henttonen, H., Haukisalmi, V and Hardman, L.

Finnish Forest Research Institute, Vantaa Research Unit, PO Box 18, FI-01301 Vantaa, Finland;
heikki.henttonen@metla.fi

We review the phylogenetics of anoplocephalid cestodes and their arvicoline rodent hosts (voles and lemmings) in the Holarctic. Cytochrome oxidase I (mtDNA) sequences were the basic tool, accompanied by 28S or ITS1. The host phylogenies, based mainly on *cyt b* sequences (mtDNA), were extracted from published sources. We concentrate on 1) *Paranoplocephala arctica* and *P. alternata* sister group in *Dicrostonyx* lemmings, 2) *Paranoplocephala omphalodes* group in *Microtus voles*, 3) *Anoplocephaloides dentata* group in *Microtus*- and *Chionomys*-voles, *Lemmus* spp. and *Synaptomys borealis*, and iv) *Anoplocephaloides variabilis*-like species and *P. krebsi* in *Microtus*- and *Chionomys*-voles and *Dicrostonyx* lemmings. Among arvicoline-carried anoplocephalines, colonization of new lineages has been the predominant mode of diversification. There is some evidence for allopatric divergence following host shifts, particularly in *Anoplocephaloides*. Within species or between closely related species, parasite divergence may or may not correspond to that of the hosts. High host specificity may have enhanced strict phyletic coevolution in some of the assemblages. Finally, the presence of phylogeographic structure in a parasite in the absence of corresponding host divergence may reflect "cryptic" divergence or inadequate sampling (or both) of the latter. Each anoplocephaline taxon in arvicolines shows an independent response to the host phylogeography, and there is no concerted common response.

PHYLOGEOGRAPHY OF HAEMOPROTEUS SPP. (HAEMOSPORIDA, HAEMOPROTEIDAE) OF BLACKCAP SYLVIA ATRICAPILLA IN EUROPE

Križanauskienė, A.¹, Pérez-Tris, J.², Gavrilov V.³, Zehtindjiev P.⁴, Sokolov, L.⁵, Palinauskas, V.¹, Hellgren O.⁶, Bensch S.⁶ and Valkiūnas, G.¹

¹ Institute of Ecology, Vilnius University, Vilnius, Lithuania; ² Department of Zoology and Anthropology, Madrid, Spain; ³ Lomonosov Moscow State University, Moscow, Russia; ⁴ Institute of Zoology - Bulgarian Academy of Sciences, Sofia, Bulgaria; ⁵ Institute of Zoology of Russian Academy of Sciences, St. Petersburg, Russia; ⁶ Department of Animal Ecology, Lund University, Lund, Sweden; asta@ekoi.lt

Blood samples from the Curonian Spit on the Baltic see population of juvenile blackcap (*Sylvia atricapilla*) have been investigated to determine lineages of *Haemoproteus* spp., which are transmitted at the study site. The results were compared with data from nine other local European blackcap populations. We found that blackcaps of the Curonian Spite population are infected not only with specific blackcap parasites, but also with *Haemoproteus majoris*, which is common parasite of birds belonging to the Paridae. We also found that five *Haemoproteus parabelopolskyi* mitochondrial DNA cytochrome *b* gene lineages (hSYAT1, hSYAT11, hSYAT13, hSYAT2, and hSYAT3) that are widespread in different territories of Europe (Southern Spain, Central Spain, Northern Spain, France, Belgium, Lithuania, Sweden, Russia and Bulgaria). It is probable that *H. parabelopolskyi* lineages hSYAT1, hSYAT2, hSYAT11, and hSYAT13 and *H. sp.* lineage hSYAT3 have spread to the Northern Europe from South-Western Europe and have already adapted to transmission in the Baltic region and Scandinavia, a process that took place relatively recently after the last glacial period. The *Haemoproteus majoris* lineages hPARUS1 and hWW2 parasitize blackcaps only in Northern and Middle Europe. It is possible that this parasite is of recent Northern origin in blackcaps and it may be an agent of emerging haemoproteosis in this bird in Southern Europe in the future.

THE HEMOTROPHIC BACTERIA OF THE GENUS *BARTONELLA* IN ARCTIC SMALL MAMMALS

Laakkonen, J.

Department of Basic Veterinary Sciences, FIN-00014 University of Helsinki, Finland
and Finnish Forest Research Institute, PO Box 18, FIN-01301, Vantaa, Finland
Juha.Laakkonen@helsinki.fi

The hemotrophic bacteria of the genus *Bartonella* are recognized as emerging pathogens, although they may be carried over long periods of time without causing symptoms. Arthropod vectors transmit most *Bartonella* species. Recent studies indicate that rodents may be an important reservoir for the *Bartonella* strains associated with human disease. Despite recent research on hemotrophic bacteria of small mammals in temperate and tropical areas, there is paucity of data on *Bartonella* from arctic and other northern areas. Furthermore, the few studies from northern areas are based on microscopical examination of blood smears alone. Studies assessing the effect of environmental factors on seroprevalence of *Bartonella* spp. in temperate areas indicate that increasing precipitation and climatic warmth are associated with higher seropositivity. Humid, warm areas also have the highest number of potential arthropod vectors. On spatial scale, the proximity to the coast has been shown to have a significant effect on seropositivity. The extreme temperatures, snow cover and distinct seasonality of the arctic areas provide interesting possibilities for further testing the effect of climatic factors on *Bartonella* seroprevalence. The aim of this presentation is to review the current knowledge on the diversity and distribution of *Bartonella* spp. in arctic (small) mammals, and discuss contributing factors in the ecology of *Bartonella* spp. for which future research is needed.

PATTERNS IN THE DYNAMICS OF THE FREQUENCY DISTRIBUTION OF NEMATODE ABUNDANCES IN BANK VOLE (*CLETHRIONOMYS GLAREOLUS* SCHREBER, 1780)

Ieshko, E. and Bugmyrin, S.

Institute of Biology, Karelian Research Centre RAS, Russia
ieshko@krc.karelia.ru

There exists a variety of mechanisms in the nature which form the over dispersed (aggregated) distribution of parasites (Crofton, 1971; Boswell & Patil, 1970). The two leading ones are differences in host susceptibility to infestation and variations in infestation dose due to spatial heterogeneity of the invasion agent's distribution over the host's habitats. Some published sources and our data demonstrate that insignificant individual distinctions in host susceptibility lead to the formation of aggregated distribution in the host population, and the negative binomial distribution (NBD) is the most widespread model of parasite abundance there (Crofton, 1971; Breyev, 1972; Haukisalmi, 1986; Pavlov & Ieshko, 1986; Bugmyrin et al., 2005). Long-term research in permanent sample plots showed bank vole in middle taiga to host 6 nematode species belonging to the families Capillaridae (*Capillaria murissylvatici* Diesing, 1851 (prevalence – 1.3%; abundance – 0.01 ind.)), Heligmosomatidae (*Heligmosomum mixtum* Schulz, 1954 (27.3; 0.85)), *Heligmosomoides glareoli* Baylis, 1928 (13; 0.45), *Longistriata minuta* Dujardin, 1845 (3.1; 0.14), Syphaciidae (*Syphacia petrusewiczi* Bernard, 1966 (15.9; 12.2)), Spiruroidea (*Agamospirura* sp. (0.4; 0.01)). We found the distribution of abundances of the above species in the host population in different years and seasons, in different age and sex groups of bank vole to be distinctly aggregated.

TIME TO BE TRANSMITTED? – PLASTICITY IN HOST MANIPULATION BY A COMPLEX LIFE CYCLE PARASITE

Benesh, D.

University of Jyväskylä, Department of Biological and Environmental Sciences, Finland
dabenesh@cc.jyu.fi

Complex life cycle parasites are faced with the fundamental problem of getting from one host to another. As a solution, many parasites manipulate the phenotype of their hosts in ways which seem to increase the likelihood of successful transmission. Examples of altered host phenotypes are numerous, but temporal variation in host manipulation, which could suggest changing costs and benefits associated with parasite transmission, is less well known. Freshwater isopods infected with the acanthocephalan parasite *Acanthocephalus lucii* spend less time hiding than uninfected conspecifics. I investigated whether this altered trait varies over time. Over 8 weeks of laboratory observation, the difference between the hiding behavior of infected and uninfected isopods tended to increase. Additionally, there were pronounced seasonal differences in the modification of host hiding behavior. The difference between the behavior of infected and uninfected isopods was greatest in the spring, when both hosts and parasites are presumably older. Isopods subjected to different light and temperature regimens, however, exhibited similar behavior. This could suggest that seasonal changes in host manipulation depend more on host or parasite age than changing environmental conditions. An increasing probability of host mortality, in addition to a decreasing potential for additional parasite growth, could favor increased host manipulation over time.

THE EFFECT OF SEX AND AGE ON INTESTINAL PARASITE INFECTIONS OF FINNISH GROUSE

Isomursu, M., Rätti, O., Helle, P. and Hollmén, T.

Finnish Food Safety Authority, Animal Diseases and Food Safety Research, Oulu Research Unit, Finland

Marja.Isomursu@evira.fi

Sex and age of the host may influence the distribution of parasites as they affect host behaviour, body size, diet, preferred habitat and immune defence mechanism. Physical sexual differences are particularly pronounced in polygynous grouse species. We studied the occurrence of intestinal helminth parasites of three Finnish grouse species, capercaillie *Tetrao urogallus*, black grouse *Tetrao tetrix* and hazel grouse *Bonasa bonasia*. The first two species are sexually dimorphic polygynous species while the latter is sexually monomorphic and monogamous. The grouse harboured one species of nematodes (*Ascaridia compar*) and three species of cestodes (*Skrjabinia (Raillietina) cesticillus*, *Paroniella (Raillietina) urogalli* and *Hymenolepis* sp.). We found a male-bias in the prevalence and abundance of *A. compar* which was most pronounced in the polygynous species. The male-bias was larger in juvenile than in adult grouse. In hazel grouse, there was a slight male-bias in the occurrence of ascarids, but no bias in abundance. The occurrence of cestodes was not affected by host sex, but it was strongly dependent on age class: juvenile grouse were commonly infected while infections in adult were very rare. Sexual difference in body size can be an important factor behind the sex-biased parasitism. Differences in diet explain the age-dependent distribution of cestodes: insectivorous juveniles are more exposed to cestode larvae.

ANALYSIS OF THE CLEAVAGE PATTERN AND BLASTOMERES CHARACTERISTIC IN THE ANOPELOCEPHALID CESTODE MOSGOVOYIA CTENOIDES (RAILLIET, 1890) BEVERIDGE, 1978

Mlocicki, D.^{1,2}, Swiderski, Z.^{1,3}, Miquel, J.⁴ and Eira, C.^{4,5}

¹W. Stefanski Institute of Parasitology, PAS, Warsaw, Poland; ²Dept. of Medical Biology, Medical University of Warsaw, Poland; ³Dept. of General Biology and Parasitology, Medical University of Warsaw, Poland; ⁴Laboratori de Parasitologia, Fac. de Farmàcia, Universitat de Barcelona, Spain; ⁵Dept. de Biologia, Universidade do Minho, Campus de Gualtar, Braga, Portugal; danmlo@twarda.pan.pl

The cleavage in *Mosgovoyia ctenoides* is unequal and has three types of blastomeres: 2 macromeres, 3 mesomeres and several micromeres. Macromeres, the largest of the blastomeres, contain electron-dense granules, lipid droplets and mitochondria. They also possess large nuclei with prominent nucleoli. Cell divisions during cleavage were observed only in macromeres. Mesomeres, the medium-sized blastomeres, are characterized by having lipid droplets, mitochondria and well-developed GER that is frequently adjacent to the nucleus. Their nuclei contain electron-dense, spherical nucleoli. Both macromeres and mesomeres are involved in the formation of the oncospherical envelope and are therefore excluded from further development of the haxacanth, which is produced by micromere differentiation. Micromeres are the smallest and most numerous of the blastomeres. They are free of any inclusion and are characterized by the highest N/C ratio. Their spherical nucleus contains a small nucleolus and large heterochromatine islands. Glycogen particles were most abundant in the macromere cytoplasm and lowest in micromeres. During early development, as glycogen is distributed in other parts of the embryo, there is a simultaneous increase in the number of lipid droplets. With further development, however, there is a progressive reduction of lipids, indicating that lipids may play a role as an energy source for the developing oncosphere.

NEOSPORA CANINUM INFECTION IN MAN?

Umran¹, Stensvold, R.¹, Vestergaard, L.² and Nielsen, H.V.¹

¹ Laboratory of Parasitology, ² Department for Epidemiology, Statens Serum Institut, Denmark.

Neospora caninum is a unicellular protozoan parasite that causes abortions in cattle and canines as the definitive host. *N. caninum* is closely related to *Toxoplasma gondii* with the felines as the definitive host and the cause of abortions in i.e. sheep, goat and humans. A few papers describe cases of human infected with *N. caninum*. Still is it debatable if *N. caninum* is capable of establish an infection in human. In this study app. 300 Danish and 300 Tanzanian humans were investigated for the present of antibodies against the two parasites, examined by ELISA and Western blot techniques. Comparison of possible mono- and double infected individuals will be discussed at the meeting.

MOLECULAR IDENTIFICATION OF EQUINE CYATHOSTOMES RESISTANT TO FENBENDAZOLE AND SUSCEPTIBLE TO OXIBENDAZOLE AND MOXIDECTIN

Traversa, D.¹, Iorio, R.¹, Kharchenko, V.², Kuzmina, T.², Paoletti, B.¹, Gatti, A.¹, Bartolini, R.¹, Costanzo, F.¹ and Klei, T.R.³

¹Faculty of Veterinary Medicine of Teramo, Italy; ²Schmalhausen Institute of Zoology NAS of Kyiv, Ukraine; ³School of Veterinary Medicine, Louisiana State University, Baton Rouge, USA
dtraversa@unite.it

Despite horse cyathostomes (Nematoda, Cyathostominae) resistant to anthelmintics are worldwide diffused, information on the role played at species level in the phenomenon is lacking. In the present study a diagnostic Reverse Line Blot (RLB) hybridization assay has been used to molecularly identify cyathostomes resistant to fenbendazole (FBZ) and susceptible to oxibendazole (OBZ) and moxidectin (MOX). Sixteen (Farm 1) and twenty (Farm 2) horses with a history of FBZ-resistant cyathostome infection were subjected to a Faecal Egg Count Reduction Test (FECRT) with FBZ, OBZ and MOX. Post-treatment faecal samples collected at day +14 from each groups were pooled and eggs in each pool subjected to a RLB able to simultaneously test for the presence of 13 common cyathostomes. The FECRT confirmed the presence of cyathostomin resistant to FBZ while OBZ and MOX showed an efficacy of 97.2 (Farm 1)- 100% (Farm 2), and 100% (both Farms) respectively. *Coronocylus labiatus* (Farms 1 and 2) and *Cylicostephanus goldi* (Farm 1) were detected in animals treated with FBZ, while *Cylicostephanus calicatus* and *C. labiatus* were identified in samples collected from animals treated with OBZ in Farm 1. These data report the first molecular identification of cyathostomes resistant to FBZ and susceptible to OBZ and MOX using eggs collected post-treatment. The RLB assay showed to be useful in monitoring the distribution at species level of cyathostomes susceptible/resistant to different anthelmintics.

EFFECTS OF PLASMODIUM RELICTUM (LINEAGE P-SGS1) ON EXPERIMENTALLY INFECTED PASSERINE BIRDS

Palinauskas V.¹, Valkiūnas G.¹, Bolshakov C. V.² and Bensch S.³

¹ Institute of Ecology, Vilnius University, Vilnius, Lithuania, vaidas@eko.lt.

² Biological Station of the Zoological Institute, Rybachy, Russia.

³ Ecology Building, Lund University, Lund, Sweden.

Avian malaria parasites of the genus *Plasmodium* are some of the most common haematzoa. Information about their pathogenicity and vertebrate host specificity is insufficient. *Plasmodium relictum* (lineage P-SGS1) was isolated from a naturally infected adult reed warbler on the Curonian Spit in the Baltic Sea in June 2006. This parasite was subinoculated to naive juveniles of the common crossbill, house sparrow, chaffinch, siskin and starling. Six individual birds of each species were infected. Control birds of the same species were inoculated with same amount of blood from non-infected birds. Blood was taken from all birds every third day during a month after infection. Dynamics of parasitemia, body temperature, body mass, level of haematocrit and pathological changes in internal organs were measured. The lineage P-SGS1 easily infects birds belonging to the Fringillidae and Passeridae. Starlings were resistant to this lineage. Prepatent period varied between 3 and 15 days in different bird species. Maximum parasitemia (up to 50% or red blood cells) was recorded in the crossbill. There were no effects of infection on body mass and body temperature, but significant decrease of haematocrit levels in experimentally infected birds was recorded in all experimental birds. The spleen and liver of infected birds was markedly enlarged. This study shows that European birds of different families have markedly different susceptibility to the same lineages of malaria parasites.

MICROSCOPIC AND PCR-BASED DIAGNOSTICS OF BLOOD PARASITES: ADVANTAGES AND SHORTCOMINGS OF BOTH METHODS

Valkiūnas, G.¹, Bensch, S.², Sehgal, R. N. M.³, Iezhova T. A.¹, Križanauskienė, A.¹, Hellgren, O.² and Palinauskas, V.¹

¹ Institute of Ecology, Vilnius University, Vilnius, Lithuania; gedvalk@ekoi.lt

² Department of Animal Ecology, Lund University, Lund, Sweden

³ San Francisco State University, San Francisco, USA

For a long time, microscopy was the main method in diagnosing blood parasites of vertebrates. Recently, powerful PCR-based techniques were shown to be dramatically more sensitive in determining haemosporidian infections in comparison to microscopy in some studies raising the question about value of microscopy. Using large material collected in Europe, America and Africa, we compared sensitivity of both tools in determining prevalence of avian blood parasites in the same samples. Both methods underestimate natural haemosporidian infections. The microscopy is less sensitive in determining low parasitemias, especially of *Plasmodium* spp. The differences in diagnostics of haemosporidian parasites using both these tools were minor or even insignificant when blood films of good quality were examined by well-trained specialists. PCR-based diagnostics underestimated simultaneous infections of blood haemosporidian parasites. Both methods showed the same trends in prevalence data in the same samples. PCR is a powerful tool during identification of species of parasites during light infections. The microscopy provides information about presence of all groups of haematozoa in each sample, including haemosporidians, haemococcidians, adeleid coccidians, trypanosomes, piroplasmids, microfilariae and some other parasites; that requires a set of primers and nested protocols when PCR diagnostics is used, which is expensive. Microscopy also is helpful in ‘calibrating’ quantitative PCR protocols.

GEOGRAPHICAL VARIATION IN AVIAN BLOOD PARASITE PREVALENCE: THE ROLE OF VECTORS

Rätti, O.

Arctic Centre, University of Lapland, Rovaniemi, Finland
osmo.ratti@ulapland.fi

There is a great geographical variation in the blood parasite prevalence even within one species. The pied flycatcher (*Ficedula hypoleuca*) is a small passerine species which is one of the most well studied species concerning the occurrence blood parasites. For this study we chose the two parasite genera, *Leucocytozoon* and *Trypanosoma*, which are known to be transmitted by black flies (*Simuliidae*). *Leucocytozoon* species are transmitted almost exclusively by black flies. Trypanosomes are transmitted by different haematophagous insects including black flies.

We reviewed published data to study geographical variation in the prevalence of these two blood parasite genera. The study sites ranges from Central Spain to Northern Finland. *Leucocytozoon* prevalence was clearly higher in higher latitudes in the pied flycatcher. Also, *Trypanosoma* had peak prevalence in northern Finland but rather high prevalence in Spain as well.

We also studied the abundance of potential vectors of blood parasites simultaneously in two study sites in Finland in 1995 and 1996. We exposed black grouse (*Tetrao tetrix*) for blood feeding insects in the cage. Ornithophilic black fly density was much lower in Southern than in Northern Finland. Results suggest that geographical variation in the prevalence of studied haematozoan parasites, especially *Leucocytozoon*, could be explained by variation in vector density in breeding grounds of their avian hosts.

PECULIARITIES OF BLOOD PARASITE INVASION OF BIRDS OF THE NATIONAL PARK NAROCHANSKY

Babushnikova A.P., Zhurauliou D.V. and Ostrovsky O.A.
Institute of Zoology, National Academy of Sciences, Belarus
Babushnikova@tut.by

The material was collected summer 2005-2006 at the larger lake Naroč. It is disposed in northing boreal part of Belarus. In all, 147 slides of 15 passerine birds species and 135 slides of 9 species waterfowl were investigated for blood parasites (Sporozoa: Haemosporida) during this study. The prevalence of infection from passerine was 29 %. Haemosporidian parasites belonging to the families Haemoproteus, Leucocytozoidae and Plasmodiidae were registered. Moreover Trypanosoma spp. were seen. Only 5.9 % of all infections were mixed infections with species of Plasmodium and Haemoproteus. The highest intensity 3-4 parasites per one field at the high magnification was recorded for H.sp. Only Tufted Duck of all examined water birds was recorded as a host for blood parasites. *L. simondi* in mixed infections with species of Microfilariae spp. were registered. The intensity of infection was 3-4 parasites per one field. The other 8 water bird species were not infected any hematozoan. The fact that some birds (during breeding period) harbored parasites from genus Haemoproteus and Plasmodium indicates possibility of active transmission of avian blood parasites at the study site.

PLASMODIUM FALCIPARUM STEVOR PROTEINS ARE LOCATED TO THE RHOPTRIES AND ARE INVOLVED IN THE MEROZOITE INVASION OF ERYTHROCYTES

Khatab, A.^{a,b}, Bonow, I.^b, Schreiber, N.^b, Petter, M.^b, Schmetz, C.^c, Meri S.^a and Klinkert, M.-Q.^b.

^aMalaria Research Lab, Department of Bacteriology and Immunology, Haartman Institute, University of Helsinki, Helsinki, Finland; seppo.meri@helsinki.fi

^bDepartment of Molecular Medicine, Bernhard-Nocht Institute for Tropical Medicine, Hamburg, Germany.

^cEM Laboratory, Bernhard-Nocht Institute for Tropical Medicine, Hamburg, Germany.

Antigenic variation of infectious organisms is a major factor in evasion of the host immune response. In *Plasmodium falciparum*, the most fatal etiologic agent of malaria, antigens encoded by multicopy gene families carrying a hypervariable loop region between two transmembrane domains are speculated to have roles in antigenic variation. STEVORs are encoded by one of these families and were reported in the sporozoite, trophozoite, schizont and early and mature gametocyte stages. Due to their expression in different stages, these proteins are speculated to have multiple functions, including important ones in parasite survival. Here, we present evidence for antigenic variation of STEVORs at the protein level in blood stage parasites. In addition, we show the expression of STEVORs in the merozoite, specifically at the surface as well as in rhoptries, secretory organelles at the apical end of the merozoite using IFA and immunogold electron microscopy. Most notable is our capture of a number of invading merozoites in our IFA slides, in which STEVORs were also identified as part of the “proteolytic complex” formed by the protease-mediated release of proteins at the host-parasite interface prior to or at invasion. Our first report of an involvement of multicopy variant antigens in erythrocyte invasion by the malaria parasite adds to the already complicated events surrounding the invasion process and opens up new avenues for research on blocking merozoite invasion of erythrocytes.

MOLECULAR SURVEILLANCE OF CHLOROQUINE RESISTANCE ASSOCIATED MUTATIONS OF PLASMODIUM FALCIPARUM IN IRAN

Kazemzadeh, Z.^{1,3}, AfsharPad M.^{1,2}, Djadid N.D.¹, Raeisi, A.³, Shabani, A.⁴ and Zakeri, S.¹

¹Malaria Research Group (MRG), Biotechnology Department, Pasteur Institute of Iran, Tehran, Iran; ²Biochemistry Department, Al Zahra University, Tehran, Iran; ³Biology Department, Azad University, Tehran, Iran; ⁴Center for Diseases Management and Control, Tehran, Iran; zakeris@yahoo.com; azad@institute.pasteur.ac.ir

We assessed the prevalence of polymorphisms in the Plasmodium falciparum chloroquine resistance transporter (pfcr1) and Multi Drug Resistance-1 (pfmdr1) genes before (n=158) and after treatment (n=25) with chloroquine in Iranian P. falciparum strains. Nested PCR and PCR/RFLP methods were used to detect SNPs in pfcr1 gene at positions K76T, A220S, Q271E, N326S, I356T, R371I and in pfmdr1 gene at positions N86Y, Y184F, S1034C, N1042D, D1246Y. For pfcr1 gene in pre treatment samples only 76T (97%), 220S (97%) and 326S (97%) and in pfmdr1 86Y (34.8%), 184F (7.6%) mutant allele were detected, with no mutation at other positions. To test the hypothesis that in vivo selection of mutant pfcr1 alleles occurs after chloroquine treatment, pfcr1 and pfmdr1 polymorphisms were compared among 25 post-treatment paired samples from patients' parasitologic failure. Analysis of post treatment samples showed that the high levels of CQ pressure have led to strong selection of the pfcr1 76T (100%), 220S (96%) and 326S (96%) polymorphisms in Iran. The frequency of the mutant pfmdr1 86Y allele was 40% among post treatment isolates and all also carried the mutant pfcr1 76T allele. In conclusion, these data point to high frequency of drug-resistance mutations in P. falciparum in south-eastern Iran, and strongly support that CQ as first line drug for treatment of falciparum malaria in Iran is inadequate drugs for this region.

TWELVE YEARS OF MOLECULAR STUDIES ON MALARIA VECTORS IN IRAN-PAKISTAN-AFGHANISTAN BORDER AREAS: APPLICATION IN MALARIA CONTROL PROGRAM

Djadid, N.D.¹, Zakeri, S.¹, Gholizadeh, S.¹, Daneshinia, N.^{1,2}, Bayat, N.^{1,2}, Farhoomand, F.^{1,2}, Mohagheghi, A.³ and Raeisi, A.⁴

¹Malaria Research Group (MRG), Biotechnology Dept, Pasteur Institute of Iran; ²Azad University Science and Research Branch, Tehran, Iran; ³Zahedan University of Medical Sciences, Iran; ⁴Centre for Disease Management and Control (CDMC), Tehran, Iran; ndjadid@yahoo.com; navid@institute.pasteur.ac.ir

Malaria is the most important parasitic and vector-borne diseases in southeast provinces of Iran, bordering Afghanistan and Pakistan. Eight out of 19 morphologically identified species of Anopheles in Iran incriminated as malaria vectors; Anopheles stephensi, Anopheles culicifacies, Anopheles fluviatilis, Anopheles superpictus, Anopheles dthali, Anopheles pulcherrimus, Anopheles maculipennis, and Anopheles sacharovi. However, twelve year follow-up studies of Malaria Research Group (MRG) on molecular systematics & population genetics (by rDNA-ITS, RAPD, Microsatellite), molecular mechanisms of insecticide resistance (kdr, gst, cyp450, est), host-parasite interaction related genes (lectin, actin, ...), and Wolbachia molecular systematics opened new insights in Anopheles species composition, their role in malaria transmission, and resistance status in this "Oriental" corner of WHO/EMRO territory. A regional database on genome of the main malaria vectors in this region is under construction by having submitted over 800 sequences, which in turn could act as a prerequisite for building up the "Malaria Genomic Network" in EMR. The overall results will be discussed in details for drawing the final conclusions.

ENDEMIC UNICELLULAR INTESTINAL PARASITES (UIP) IN DENMARK

Stensvold, C.R. and Nielsen, H.V.

Laboratory of Parasitology, Dept. of Bacteriology, Mycology and Parasitology, Statens Serum Institut, Artillerivej 5, DK-2300 Copenhagen S.

Unicellular intestinal parasites (UIP) are responsible for approximately 95% of intestinal parasitic infections in Denmark, where diagnostic advances and growing epidemiological knowledge contribute to the understanding of the public health significance of UIP. Whereas protozoa as e.g. *Entamoeba histolytica*, *Giardia intestinalis* and *Cryptosporidium* spp. have low prevalences in Denmark, little studied UIP such as *Dientamoeba fragilis* and *Blastocystis* sp. cause infection in 10-25% of patients suspected of intestinal parasitosis. *Blastocystis* is a parasite of unresolved clinical significance, and most patients harbouring it are only treated if co-infected with a significant pathogen. On-going studies including molecular characterisation of isolates from symptomatic and asymptomatic individuals are indicative of a potential relationship between *Blastocystis* subtype and clinical impact. In another study, *Dientamoeba fragilis* was detected in 12/103 patients by permanent staining of stool fixed in sodium acetate-acetic acid-formalin (SAF), whereas the parasite was not diagnosed by a formol ethyl-acetate concentration technique. Only in 2/12 cases *D. fragilis* was seen in co-infection with an acknowledged significant pathogen. This means that in Denmark at least 8/10 cases of curable, potentially symptomatic parasitosis go undetected using conventional diagnostic techniques. It is essential to use suitable parasitological and molecular techniques to make exhaustive characterisations of UIP parasites recovered from patients and healthy individuals.

MOLECULAR ECOLOGY OF BORRELIA BURGENDORFERI S. L. IN TICKS AND RODENTS FROM LITHUANIA AND NORWAY

Paulauskas, A.¹, Ambrasiene, D.¹, Radzijeuskaja, J.¹, Rosef, O.² and Turcinaviciene, J.³

¹ Vytautas Magnus University, Kaunas, Lithuania

² Telemark University College, Bø i Telemark, Norway

³ Vilnius University, Lithuania

a.paulauskas@gmf.vdu.lt

The northward expansion and increased density of tick populations and incidence of tick-borne diseases in Fennoscandia could be related to climate change. Ticks collected in Lithuania and Norway from different biotopes were investigated for the presence of *Borrelia*. In Lithuania, 14.0% ticks were infected with *Borrelia*, in Norway 6%. The highest prevalence was found in deciduous (20%) and mixed forests (21.2%). A lower prevalence was determined in pine forests (7.4% in Lithuania) and coastal zones (4.7% in Norway), and the least prevalence (2.4% and 0.6% respectively) was found in grasslands. Prevalence of *Borrelia* in rodents belonging to 9 species varied between species and sampling sites in both countries. In Lithuania, the prevalence of infection was higher in *M. arvalis* (range 25–57%) and in *C. glareolus* (range 14.3–71.4%) than in *A. flavicollis* (range 0–37%) and in *A. agrarius* (range 11–33%). In Norway, the prevalence in rodents was lower (range 4.9 - 6% in different rodents species). *B. afzelii* was the predominant genospecies in all studied biotopes. In Lithuania, *B. afzelii* was found in 76%, *B. garinii* in 10%, *B. burgdorferi* s.s. in 7%, and *Borrelia* spp in 6% of infected ticks. Double infections were observed in 1% of the infected ticks. In Norway, *B. afzelii* was found in 59.4%, *B. garinii* in 18.8%, and *B. burgdorferi* s.s. in 9.4% of infected ticks. All infected rodents from both countries were hosted *B. afzelii*. *Sciurus vulgaris* harbored also *B. burgdorferi* s.s.

ABUNDANCE DYNAMICS OF THE TICK *IXODES TRIANGULICEPS* BIR AND ITS HOSTS THROUGH SECONDARY POST-FELLING SUCCESSIONS OF TAIGA ECOSYSTEMS IN NORTHWEST RUSSIA

Kurhinen, J.^{1,2}, Bespyatova, L.³ and S. Bugmyrin, S.³

¹ Forest Research Institute, Karelian Research Centre, Russian Academy of Science 11 Pushkinskaya St., 185910 Petrozavodsk; ² Finnish Game and Fisheries Research Institute, Viikinkaari, 4. Box 2, Helsinki, FI-00791; ³ Institute of Biology, Karelian Research Centre, Russian Academy of Science, 11 Pushkinskaya St., 185910 Petrozavodsk

The aim of was to investigate the effect of large-scope continuous clear-cutting and subsequent forest regeneration processes on the abundance of the tick *Ixodes trianguliceps* and its hosts in the Karelian taiga zone of Northwest Russia. Three plots were selected: a site harvested 7-13 years ago, a young stand 13-18 years old, a mixed pine-deciduous forest 25-31 years old. Small mammal counts were performed in 1998-2004 (8130 trap/days, 757 animals trapped, 391 tick specimens collected) for common, pygmy and graves shrews, and bank and field voles. Common shrew, bank and field voles yielded 99.2 % of the ticks collected. Prevalence was highest in the field (31.1 %) and bank (28.4 %) voles. As the clear-cuts were regenerating, notable changes occurred in tick abundance, as well as in the species composition and abundance of the hosts. In the first year after clear-cutting, small mammal hosts leave the site, and their numbers and species diversity decrease leading to drop in tick abundance. A few *I. trianguliceps* appear only in the third year after cutting, but in 12-18 years the species abundance increases to a maximum. Tick abundance changes abruptly from zero values in the first year after harvesting, through gradual rise to maximal values in young stands, to a reduction in secondary forests. At the first stage of the secondary succession, the principal role in the tick ecology belongs to common shrew and field vole, the role of the bank vole growing later on.

THE ABUNDANCE OF TAIGA TICK *IXODES PERSULCATUS* SCHULZE (ACARINA, IXODIDAE) ON THE CUT-OVERS OF DIFFERENT AGE IN THE MIDDLE TAIGA SUBZONE OF KARELIA

Bugmyrin, S., Bespyatova, L., Anikanova, V. and Ieshko, E.

Institute of Biology, Karelian Research Centre RAS, Russia; ieshko@krc.karelia.ru

The data of long-term investigations (1998 – 2004) on abundance of the taiga tick larva and nymphs on the cut-overs of different ages (7, 12, 25 years) in the middle taiga subzone of Karelia (62 04'S; 33 55'W) are presented. Small mammals were captured by snap-traps; 8130 trap-days are completed. The host sampling was consisted of 756 specimens of small mammals belonging to 9 species: *Sorex araneus* – 522, *S. minutus* – 10, *S. isodon* – 7, *Neomys fodiens* – 1, *Sicista betulina* – 3, *Clethrionomys glareolus* – 177, *Microtus agrestis* – 33, *M. oeconomus* – 1, *Micromys minutus* – 2 spm. The total number of ticks from these hosts was equal 1415 (larva) and 281 (nymphs). In the beginning of investigation "young" cut-over was typical meadow association. The lowest tick abundance was found here. That was consequence of unfavorable abiotic conditions and low number of small mammals in the beginning of summer. "Middle" cut-over is characterized by the highest number of the tick's larva that testifies the high number of the tick's imago hosts. "Old" cut-over was the optimum conditions for development of the taiga ticks. High abundance of the tick (larva and nymphs) was marked during the whole period of investigations. It is shown, that number of ticks is much higher on cut-overs in comparison with the mixed and coniferous forests that first of all is determined by high number of small mammals. The research was supported by FTP "Integration" (638) and the grant of President of RF (MK-5496).

IMPACT OF ENVIRONMENT POLLUTION ON THE RISK OF TICK-BORNE INFECTION ENHANCEMENT IN THE BALTIC REGION

Alekseev, A.¹, Dubinina, H.¹, Jääskeläinen, A.², Vaheri, A.² and Vapalahti, O.²

¹Zoological Institute, Russian Academy of Sciences, St. Petersburg, Russia

²Haartman Institute, University of Helsinki, Helsinki, Finland

devana@HD1389.spb.edu

Monitoring of allopatric populations of Ixodes ticks (Kaliningrad and St. Petersburg vicinity, Russia; Zealand, Denmark; and Kokkola, Finland, 2004 regions) permitted to reveal the distribution and increase in the prevalence of ticks with exoskeleton anomalies (deformations of scutum, legs and body form). Increase of *I. ricinus* prevalence in Denmark 14-20% (1998-2000), in Kaliningrad vicinity 13.3-42.9%(1998-2005), of *I. persulcatus* in St. Petersburg vicinity 31.1-49.6% (2000-2004) and in Kokkola archipelago 47.7% (2004) were results of Cd accumulation in the environment and tick bodies. Within the mentioned periods the prevalences of revealed tick-borne pathogens were as follows: St. Petersburg from 33% to 63.5% (7 agents were detected), in Kokkola - 63% (6 revealed agents). In Kaliningrad vicinity within 7 years interval prevalence of ticks infected by tick-borne encephalitis virus (TBEV) increased from 0.7 to 11.5% (16-folds), and in 2005 TBEV was detected only in anomalous specimens. Number of multi-infected specimens was always greater among ticks with exoskeleton deformations (sometimes as in Kokkola ticks even in two-fold). Among detected by PCR pathogens *Borrelia afzelii*, *B. garinii*, *B. burgdorferi* s.s. and some other spirochetes of *B. burgdorferi* sensu lato group were identified, TBEV (Siberian subtype in *I. persulcatus*), *Babesia microti* and *Ehrlichia muris* were also revealed. *Anaplasma phagocytophilum* was found only in St. Petersburg vicinity.

PRELIMINARY STUDY OF INTESTINAL PARASITES IN ESTONIAN SWINE HERDS OF DIFFERENT MANAGEMENT SYSTEMS

Lassen, B., Talvik, H., Mägi, E. and Järvis, T.

Estonian University of Life Sciences, Institute of Veterinary Medicine and Animal Sciences, Tartu, Estonia

heli.talvik@emu.ee

Current study includes two industrial farms, one smaller conventional farm, one ecological farm and one biological wild boar farm. In total 283 faecal samples were collected and investigated for parasite eggs and oocysts. Helminth infections on industrial farms were limited to *Ascaris suum* (5.8 -13.1%) infection only with low (20-100) epg-s in some sow and fattener groups. The smaller conventional farm showed 100% infection of pigs with *Oesophagostomum* spp. and *Eimeria* spp. with high epg-s in all age groups (up to 10.000). Parasites found in pigs on the ecological farm: 78% *Oesophagostomum* spp., 25% *Ascaris suum*, 9.1% *Strongyloides ransomi*, 62% *Eimeria* spp., and 100% *Cryptosporidium* sp. The wild boar farm results were: *Oesophagostomum* spp. (64%), *Trichuris suis* (21%), *Metastrongylus* sp. (7%), and *Eimeria* spp. (100%) infections with low epg/opg-s. All farms had *Cryptosporidium* sp. infections, whereby “ecological” pigs were more intensively infected than industrially farmed pigs. Similar picture was seen in *Eimeria* spp. infections. The identified *Eimeria* species in domestic pigs were: *E. porci*, *E. polita*, *E. suis*, *E. neodebliecki*; wild boars had two more species: *E. crofae*, *E. guevarai*. Industrial management with regular anthelmintic treatments seems to be successfully reducing the parasite burden and variety. Biological approach to parasite control on ecological farms should be studied further.

FATAL INFECTION IN AN ICELANDIC STALLION CAUSED BY HALICEPHALOBUS GINGIVALIS (NEMATODA: RHABDITIDA)

Eydal, M.¹, Bambir, S.H.¹, Sigurdarson, S.², Gunnarsson, E.¹ and Fridriksson, S.³
meydal@hi.is

¹ Institute for Experimental Pathology, University of Iceland, Keldur, Reykjavík, Iceland

² Agricultural Authority of Iceland, Selfoss, Iceland

³ District veterinary officer

Infections by the soil nematode *Halicephalobus gingivalis* have been reported infrequently from horses worldwide. Infections are believed to be acquired after the nematode penetrates open wounds. The nematodes reproduce within the host tissues and the resulting infection is usually fatal. Following an accident, an 11 year old Icelandic stallion sustained injuries to the mouth. Several months later neurological signs were observed which gradually became more severe, the horse lost balance, and finally had to be euthanised. Symptoms observed at autopsy were broken front teeth and a loose palate. Histological examination of the brain (cerebellum) revealed severe multifocal necrotic encephalitis. In necrotic areas numerous nematodes were seen. Mature nematodes, larvae and eggs were present in the perivascular space and around blood vessels associated with inflammatory response. Mononuclear meningitis was also present. The nematode was confirmed as being the species *Halicephalobus gingivalis* based on its morphological features. Adult worms were 250 - 300µm long and 15µm wide, eggs measured approx. 45x15µm. Nematodes were not detected in other organs, but hemorrhages were seen in the liver and kidneys. The worms had presumably penetrated the wounds in the mouth of the horse as a result of the accident. In Nordic countries *Halicephalobus gingivalis* infections have been reported from Norway, but this is first case reported from Iceland.

GENETIC RESISTANCE TO CYATHOSTOMES INFECTION IN PURE BLOOD ARABIAN HORSES

Nowosad, B.¹, Kornaś, S.¹, Molenda, K.², Skalska, M.¹, Gawor J.³ and Cabaret J.⁴

¹Department of Zoology and Ecology, Agricultural University of Krakow, al. Mickiewicza 24/28, 30-059 Krakow, Poland, slawon@interia.pl

²Department of Agricultural Engineering and Informatics, Agricultural University of Krakow, ul. Balicka 104, 30-149 Kraków, Poland

³W. Stefanski Institute of Parasitology, Polish Academy of Sciences, ul. Twarda 51/55, 00-818 Warsaw, Poland

⁴Institut National de la Recherche Agronomique, IASP, 37380 Nouzilly, France

Pure Blood Arabian Horses, with complete documentation, are bred in female and male lines originating from the ancestors imported to Poland in XVIII century. During many years of breeding 14 female and 8 male lines were selected. The aim of the study was to determinate the level of cyathostomes infection and their possible genetic resistance on those nematodes in horses from different lines. From 1999-2002 and 2004-2006 4835 fecal samples from Arabian horses from southern Poland were collected during pasture seasons and examined using quantitative McMaster method. The obtained results were analyzed by ANOVA in order to determine the significance of differences of the level cyathostomes infection. The highest mean number of cyathostomes eggs occurred in 2004 - 581 EPG and the smallest in 2006 – 63 EPG. The biggest eggs output of this nematodes was found in female lines: “Mlecha” (540 EPG), “Sahara” (504), male lines: “Latif (396)”, “Kuhailan Haifi” (363), and the smallest: “Szamrajówka” (73), “Semrie” (187) and “Krzyżyk (127)”, “Ibrahim” (274) respectively. Most of these differences were statistical significant. The results of these analysis lead to the proposal that there are some susceptible and resistance genetic lines to cayahostomes infection in one breed of horses and in the scheme of deworming origin of the horses should be taken into consideration.

PCR METHOD FOR THE ROUTINE DIAGNOSTICS OF TOXOCARA SPP. EGGS FROM THE SOIL

Borecka, A. and Gawor, J.

Laboratory of Parasitoses of Domestic Animals, Institute of Parasitology of the Polish Academy of Sciences, Warsaw, Poland
ab@twarda.pan.pl

Human toxocarosis is caused by an infection with larvae of canine or feline roundworm *Toxocara* spp. The high population of dogs and cats in Europe together with high rates of *T. canis* and *T. cati* prevalence in pet animals has resulted in a widespread contamination of the soil with infective stages. The eggs are able to survive in the outer environment for many years. Identification of closely related taxa such as *T. canis* and *T. cati* is possible by applying molecular methods. DNA techniques utilizing genetic markers in ribosomal DNA have been employed to resolve taxonomic problems relating to various parasitic groups including nematodes (Jacobs et al. 1997; Zhu et al. 2001). The present study was undertaken to develop a routine PCR technique for differentiation to the species level of *Toxocara* eggs isolated from the soil. The naturally contaminated soil samples were incubated at 65°C with proteinase K for 12h (Paquet-Durand 2001). PCR amplification of ITS2 with species specific primers were performed according to Jacobs et al. (1997). This method alone makes possible to distinguish *T. canis* and *T. cati* eggs from the soil samples.

LIVER FLUKE INFECTIONS IN DAIRY HEIFERS GRAZING MARSHLANDS

Bæk-Sørensen, L., Thamsborg, S. M. and Kristensen, T.

Department of Veterinary Pathobiology, Faculty of Life Sciences, University of Copenhagen

In recent years water levels of the marshlands of Tønder in Denmark have been raised in order to improve the nesting conditions of wading birds. These areas serve as pastures for cattle, and a survey was performed with the objective of assessing the influence of water level on transmission of the liver fluke, *Fasciola hepatica*. 232 heifers were sampled in early 2005 after a first grazing season on either wet pastures (n=126) or normal, dry pastures (n=106). Faeces were examined for eggs by sedimentation and serum was analysed for specific antibodies. The prevalence of infection determined by sedimentation was 16% and 22% on wet and dry pastures (NS; Chi-square test). By antibody detection the corresponding figures were 31% and 34% (NS). The mean intensity of infection was low (1-19 eggs per 5 g of faeces). The density of the intermediate host, *Lymnaea truncatula*, on six wet and six dry pastures was determined by a 30 minutes visual scan of the sides of ditches in 2005. In June, the mean number of snails detected was 64 and 20 on wet and dry pastures (P<0.01). In August, the corresponding figures were 70 and 19 (P<0.01). It is concluded that no difference in prevalence could actually be detected in the heifers but there were clear indications that *L. truncatula* was more prevalent on wet pastures.

DIFFERENTIAL DIAGNOSTICS OF CYATHOSTOMES (CYATHOSTOMINAE) SPECIES ON THE BASIS OF INFECTIVE LARVAE

Kornaś, S.¹, Nowosad, B.¹, Molenda, K.², Skalska, M.¹, Gawor, J.³, Cabaret, J.⁴ and Nosal P.¹

¹Department of Zoology and Ecology, Agricultural University of Krakow, al. Mickiewicza 24/28, 30-059 Krakow, Poland: slawon@interia.pl

²Department of Agricultural Engineering and Informatics, Agricultural University of Krakow, ul. Balicka 104, 30-149 Kraków, Poland

³W. Stefanski Institute of Parasitology, Polish Academy of Sciences, ul. Twarda 51/55, 00-818 Warsaw, Poland

⁴Institut National de la Recherche Agronomique, IASP, 37380 Nouzilly, France

Cyathostomes are the most common parasites of alimentary tract in horses in different climatic zones. The aim of the study was to evaluate the cyathostomes species on the basis of their infective larvae cultured from eggs obtained from nematode mature females. Mature strongyles were collected from horses autopsied at the abattoir and classified to the species. The uterus with eggs were placed on the culture media to obtain infective L₃ larvae. Morphological parameters of individual species cyathostomes larvae, i.e. the total skin length with the tail, the larvae body length comprising: esophagus length, alimentary tract length, the length from the end of alimentary tract to the end of the body and finally the body breadth were determined. Checked was also the arrangement of 8 cells forming the alimentary tract of the larvae. Morphological parameters of the infective larvae were determined in nine cyathostomes species: *Cylicocyclus nassatus*, *C. ashworti*, *C. insigne*, *Cylicostephanus goldi*, *C. longibursatus*, *C. calicatus*, *Cyathostomum catinatum*, *C. pateratum* and *Coronocyclus coronatus*.

Morphological parameters of infective larvae showed statistically significant differences between species. Statistical analyzes were used to develop a key for identification of larvae based on a mathematical function classification, which gives maximal probability to the individual species. This key may be useful for intravital diagnostic of cyathosomes infection of horses.

ANTIGENIC VARIATION IN THE MAJOR SPERM PROTEIN GENE WITHIN POPULATIONS AND SPECIES OF THE GENUS DICTYOCAULUS

Höglund, J., Engström, A. Morrison, D.A. and Mattsson J. G.

Department of Parasitology (SWEPAR), National Veterinary Institute and Swedish University of Agricultural Sciences, SE-751 89 Uppsala, Sweden.

The aim of this study was to investigate antigenic variation in the bovine lungworm *Dictyocaulus viviparus*. We decided to focus on the Major Sperm Protein (MSP1), because this is an abundant protein used in diagnostic immunoassays, and a reasonably small cytoskeletal protein (≈15 kDa) that can be studied by direct sequencing. Thus, MSP is an ideal model protein to test the hypothesis of whether and to what extent the variation previously observed using mtDNA and AFLP data, also is reflected in a protein involved in immune recognition. MSP was sequenced with standard methods using worm DNA from eight adult worms from each of nine populations that had been defined as genetically structured. For comparison we also analysed MSP sequences of *D. eckerti* and *D. capreolus* as well as from nematodes deposited in GenBank. The MSP1 of *D. viviparus* is similar to that of other nematodes. Almost no sequence variation, and thus no antigenic variability, was detected in MSP1 between worms from different sub-populations, or in the other *Dictyocaulus* species investigated. A functional test of a recombinant variant of the MSP showed that the expressed protein was recognised by antibodies in sera from infected cattle. This has practical implications for the development of recombinant vaccines and immunodiagnosics.

POSTER ABSTRACTS

POLYMORPHISM IN A SMELT, OSMERUS EPERLANUS, SPECIALIST – CESTODE PROTEOCEPHALUS TETRASTOMUS (RUDOLPHI, 1810) (PROTEOCEPHALIDAE)

Anikieva, L.¹, Valtonen, E. T.² and Dorovskih, G.³

¹Institute of Biology, Karelian Research Centre, Russian Academy of Science, 185910 Petrozavodsk, Russia; ²University of Jyväskylä, P.O. Box 35 (YA), Fin-40014 Finland

³University of Syktyvkar, Russia anikieva@krc.karelia.ru

Morphological variability was studied in *P. tetrastomus* from smelt from the Gulf of Bothnia and Lake Ladoga (Baltic Sea catchment), as well as from Lake Goluboye (Pechora River watershed). Two forms were distinguished by proglottid structural types and two – by discrete variations of the ovary. Slightly craspedote individuals with a dump-bell-shaped ovary were included in the first group. The second group is made up of distinctly craspedote individuals. It comprises two variations by the ovary shape – dump-bell-shaped and triangular. Both forms are present in the Gulf of Bothnia and Lake Ladoga. The slightly craspedote form dominates, whereas the other form is rare. In Lake Goluboye, *P. tetrastomus* is represented by one form only – distinctly craspedote individuals with a triangular ovary. Differences in the morphometric parameters of the forms, as well as geographic and habitat distinctions were determined. Compared to other studied cestode species of genus *Proteocephalus* – *P. torulosus*, *P. longicollis*, *P. percae* the smelt parasite *P. tetrastomus* has fewer polymorphic traits and their variations, and a much narrower range of variability of measurable, countable and relative traits. Analysis of published sources and our own data suggest that the species is host-specific and relatively stable. It can be concluded from the studies that *P. tetrastomus* is a polymorphic, complex-structured species.

HELMINTH COMMUNITY STRUCTURE OF SMALL RODENTS IN THE SEASIDE REGIONAL PARK IN LITHUANIA

Butautytė, G. and Mažeika, V.

Klaipėda University, Lithuania

vytautas.mazeika@ku.lt

Rodents were caught in the Seaside Regional Park in three habitats in 2004 – 2006: sandy meadow, forest and bushed meadow. 62 yellow-necked mice (*Apodemus flavicollis*), 15 striped field mice (*Apodemus agrarius*), 1 harvest mouse (*Micromys minutus*), 35 bank voles (*Clethrionomys glareolus*), 14 common voles (*Microtus arvalis*) and 5 short-tailed voles (*Microtus agrestis*) were studied helminthologically. 12 species and other taxa of helminthes were found in 132 rodents: 7 – in the yellow – necked mice (*Capillaria* sp., *Heligmosomoides polygyrus*, *Hydatigera taeniaeformis*, *Longistriata* sp., *Syphacia stroma*, *Syphacia* sp., *Brachylaima* sp.), 2 – in the striped field mice (*Syphacia stroma*, *Syphacia* sp.) 1 – in harvest mouse (*Syphacia vandenbruei*), 5 – in the bank voles (*Capillaria* sp., *Longistriata* sp., *Syphacia petruszewiczi*, *Syphacia stroma*, *Syphacia* sp.), 6 – in the common voles (*Capillaria* sp., *Heligmosomum costellatum*, *Syphacia stroma*, *Syphacia* sp., *Cestoda* g. sp., *Trichocephalus muris*), 1 – in the field vole (*Cestoda* g. sp.). In most cases helminthes are overdispersed in the population of the rodents.

USEFULNESS OF MORPHOLOGICAL TECHNIQUES IN DETECTION AND VERIFICATION OF HUMAN CYSTIC AND ALVEOLAR ECHINOCOCCOSES

Chomicz, L.¹, Szubert, A.¹, Baranowska-Korczyn, A.¹, Stefaniak, J.² and Polański, J.A.¹.
 Dept. of Medical Biology, ¹Dept. of General and Transplantation Surgery, Medical University of Warsaw, Poland; ²Clinic of Tropical and Parasitological Diseases, University of Medical Sciences, Poznań

In the human echinococcoses, metacestodes of *Echinococcus multilocularis* or *E. granulosus* develop primarily in liver, although lung, kidney, brain may be also involved. Prolonged latency period (5 to 15 years) and, particularly, cancer-like growth of *E. multilocularis* cause diagnostic difficulties. Epidemiological data indicate that distribution of echinococcoses in the central Europe is wider than it was previously anticipated. In this report, we present several cases of alveococcosis in which surgical treatment was included. In all patients with severe liver dysfunction the hepatic localization of lesions was visualized by the US and CT techniques. Liver tissue samples were taken during surgery; then, the material was verified by parasitological, histopathological as well as transmission electron microscope techniques. No protoscolices were detected. In one patient, results of the microscopic examinations revealed appearance of Pass-positive fragments of the laminated layer of the larval cestode stage not only in the liver but also inside bile ducts and blood vessels, indicating on a risk to spread of the infection. Our studies confirm that final diagnosis should always be based on several procedures. Morphological techniques are usefulness both for verification of the suspect cases and assessment of risk of involvement of neighbouring organs.

TREMATODE FAUNA OF BREAM (*ABRAMIS BRAMA L.*) FROM THE CURONIAN LAGOON (THE SOUTH - EAST BALTIC SEA)

Chukalova, N.N.

Atlantic Research Institute of Fisheries and Oceanography (AtlantNIRO), Russia
 chuk_nn@rambler.ru

Investigations were carried out in different seasons of 2004- 2006. 206 specimens of bream (length 17,0 – 60,0 cm) caught in the Russian EEZ of the Curonian Lagoon were examined. Identification of trematodes was provided with standard methods. Eight species of trematodes were found out in bream. Most of them (7 species) parasitized the fish in larval stage. Metacercariae of *Tylodelphys clavata* (P= 6,76%, A= 0,21 sp.) and *Diplostomum spathaceum* (P= 5,31%, A= 0,22 sp.) were detected in vitreous humor of eyes, *Paracoenogonimus ovata* (P= 4,35%, A= 0,22 sp.), *Apophalus mühlingi* (P= 0,97%, A= 0,18 sp.) and *Bucephalus polymorphus* (P=2,9%, A= 0,05 sp.)- in skeletal muscle, *Ichthyocotylurus plathycephalus* (P= 39,10%, A= 2,79 sp.)- in heart muscles and in mesentery, *Posthodiplostomum cuticola* (P= 20,29%, A= 0,97 sp.)- in pharynx, gills, skin and fins of bream. Mature trematodes *Sphaerostomum bramae* (P= 0,97 %, A= 0,01 sp.) were found in fish intestine. Seasonal and ontogenic variability of bream infestation with trematodes were revealed. Prevalence of infected fish was the lowest (56,2%)- in autumn, and the highest (64.7%) in summer. Ontogenic variability showed the increasing of prevalence and abundance indices from P= 9,0%, A=0,36sp. (in fish 0- 1 years old) to P= 100%, A= 12,9 sp. (in fish more than 15 years old). Detected peculiarities of age variability connected with accumulation of helminths in fish organism.

SEROLOGICAL EXAMINATION OF BULK MILK SAMPLES TO NEOSPOROSIS IN LATVIA AND COMPARISON OF COW'S MORPHOLOGICAL COMPOSITION OF BLOOD

Eihvalde, E., Keidans, P. and Antane, V.

Faculty of Veterinary Medicine, Latvian University of Agriculture, Latvia

Serological examination of bulk milk samples to neosporosis with ELISA test were carried out in the State Veterinary Diagnostic Centre (from 1st January 2006. – National Diagnostic Centre) in 2005. Positive tests to neosporosis were obtained in 10 (7.4%) bulk milk samples from 136 randomly selected dairy herds. The numbers of lactating cows in 7 herds (70%) were till 20. In positive herds the bulk milk optical densities ranged between 31.00 and 87.04. All female animals (> 3 months) in 4 herds (142 cows and heifers) in 2006 were serologically investigated to neosporosis with ELISA test (SVANOVIR[®] Neospora-Ab iscom ELISA, Svanova Biotech AB, Uppsala, Sweden). There were 22 seropositive animals (15.5 %). The blood serum samples were taken from 28 animals (20 cows and 8 heifers) for examination of morphological composition of blood. The animals groups were ordered after serological examination – serologically positive (10 cows and 4 heifers) and negative cows (10 cows and 4 heifers). The analysis of morphological composition showed the increase of total leucocytes count in both animals groups. Between seropositive and seronegative to neosporosis animals' groups' relevant differences between morphological compositions of blood unascertained.

THE NEMATODE FAUNA OF THE FLOUNDER FROM THE RUSSIAN EEZ OF THE SOUTH-EASTERN BALTIC

Eliseev A.

Atlantic Scientific Research Institute of Marine Fisheries and Oceanography, Kaliningrad, Russia.

alex-elyssey@rambler.ru

A total of 472 flounders (length 16.2-40.5 cm) from the Russian EEZ of the South-Eastern Baltic were studied during 2002-2006. The nematode fauna of fish were presented by 8 species: *Cucullanus heterochrous* (l., ad.), *Hysterothylacium aduncum* (l., ad.), *Dichelyne minutus* (l., ad.), *Contraecum osculatum* l., *Cucullanus cirratus* (l., ad.), *Anisakis simplex* l., *Raphidascaris acus* l., *Ascarophis* sp.l. The parasites of marine origin dominated. Specific nematodes for the pleuronectid fishes-*D. minutus* and *C. heterochrous* were marked. *C. heterochrous* (P=58,1 %; A=2,72 sp.), *C. heterochrous* l. (P=48,5 %; A=1,9 sp.) and *H. aduncum* l. (P=26,9 %; A=0,66 sp.) were found the most frequently. Larvae (P=5.1 %; A=0.06 sp.) and adults (P=6.14 %; A=0.08 sp.) of *C. cirratus* were found rare. Larvae both of *R. acus* (P=0.42 %; A=0.004 sp.) and *Ascarophis* sp. (P=3.8 %; A=0.06 sp.) were marked very rare. The positive correlation between flounder's infestation with *C. heterochrous* (adults and larvae) and *H. aduncum* l. and fish length was revealed. The highest indices of prevalence were marked in fish length 30.0-40.0 cm (31 %, 50.3 %, 47.7 % accordingly).

Two nematodes species, *C. osculatum* l. and *A. simplex* l., dangerous for the human health were found occasionally. Nematodes *Camallanus lacustris*, *C. truncatus*, *Pseudoterranova decipiens*, *Paracuaria* sp.l. and *Cosmocephalus* sp.l. found in other Baltic areas (Fagerholm, Kjøie, 1994 et al.), were absent in our study region.

PLANT PARASITES OF THE SOIL NEMATODE COMMUNITIES IN NATURAL AND AGROCENOSSES IN EUROPEAN NORTH

Gruzdeva, L.I., Matveeva, E.M. and Kovalenko, T.E.

Institute of Biology, Karelian Research Centre, Russian Academy of Sciences, Petrozavodsk, Russia
gruzdeva@krc.karelia.ru

Plant parasitic nematode complexes are usually formed from the natural communities existing in local areas. In Karelia the basis of this complex consists of 7 root parasite genera: Paratylenchus, Pratylenchus, Tylenchorhynchus, Helicotylenchus, Merlinius, Globodera, Heterodera. Among stem parasites species Aphelenchoides fragaria, Ditylenchus destructor are observed. Agroecosystems are characterized with monoculture that enhances a distribution of specialized plant parasites, for example, potato cyst forming nematode (PCN). Diversity of nematode fauna was low: 15-17 genera were revealed on the infested fields and 21-24 genera – on health fields. Index of the maturity of nematode communities MI accounted for 2.0-2.4, plant parasite index *PPI* – 2.8-3.2. Nematode fauna of agrocenoses was characterized by the high number of bacterial and fungal feeders that indicated the presence of large amount of organic residuals in the soil. Plant parasites were observed as subdominant group. Nematode community structure has been changed after fields were excluded from agriculture: a share of plant parasites was lowered, the number of nematodes of other eco-trophic groups increased and MI rose up to 2.9.

THE COMMUNITIES OF BLOOD PARASITES IN MEDITERRANEAN WATER SHREW NEOMYS ANOMALUS CEBRERA, 1907

Karbowiak, G.¹ and Rychlik, L.²

1 W.Stefański Institute of Parasitology PAS, Warszawa, Poland, grzgrz@twarda.pan.pl

2. Present address: Department of Systematic Zoology, Adam Mickiewicz University, Poznań, Poland

Blood parasites of small insectivores are not very well known groups of pathogens due to the difficulties to investigate the blood parasites, by the technical problems with the material collection and status of the protected animal. Mediterranean water shrews *Neomys anomalus* living in Białowieża Forest (eastern Poland) were investigated in 2006. The shrews were caught in live-traps placed at permanent trap stations. Blood samples taken from the tip of the tail were examined for the presence of trypanosomes using the microhaematocrit centrifugation technique (8 minutes, 6200 g). The flagellates accumulated above the WBCs fraction, and their movements were observed under a light microscope, using magnifications of 100 and 200. The intracellular blood parasites were investigated using standard Giemsa-stained blood smears. Infection with *Trypanosoma* sp. n. was discovered in the blood of 3 out of 12 shrews examined, prevalence of infection was 27.3 %. The trypanosomes occurred as pleomorphic trypomastigote forms only. The density of infection was low; only single parasites were observed in the haematocrit capillary and stained blood films. Some non-identified *Bartonella* species were found in the erythrocytes in 2 shrews (prevalence about 45.4%). There were no mixed infections. The prevalence and diversity of blood parasites were lower in mediterranean water shrews than in water and common shrews, investigated in this same areas earlier.

ENTEROPARASITES OF DOGS IN LATVIA

Keidāns, P., Krūklīte, A. and Eihvalde, E.

Faculty of Veterinary Medicine, Latvian University of Agriculture, Latvia

During the period of time from 1991 till 2006, in the Republic of Latvia, material was collected from different regions and coprological examinations of 2413 dogs (*Canis familiaris*) were performed by Fuelleborn and Berman's methods.

Helminthological necropsies were carried out by random according to the method of the academician K. I. Skrjabin. In Riga region, enteroparasitoses distribution in dogs also has been investigated in connection with their lifestyle, age, sex and seasonality.

It was stated that totally 27.3 % of the examined dogs were infected with some of enteroparasites. The prevailing species of parasites *Toxocara canis* Werner, 1782 was found in 520 dogs (21.5 %). The stray dogs at the age till 1 year were more often infected with toxocarosis in the summer months. The bitches were infected more intensively. *Dypilidium caninum* Linnaeus, 1758 (8.78 %) and *Uncinaria stenocephala* Railliet, 1884 (3.14 %) helminths were found in comparatively many animals. *Coccidia Isospora* spp. Schneider, 1881 (1.86 %) and *Sarcocystis* spp. Lankester, 1882 (0.33 %), trematodes *Alaria alata* Goeze, 1782 (0.12 %) and *Opisthorchis felinus* Rudolphi, 1819 (0.08 %), cestodes *Taenia* spp. Linnaeus, 1758 (0.87 %), *Echinococcus granulosus* Batsch, 1786 (0.04 %), *Diphyllobothrium latum* Linnaeus, 1758 (0.04 %) and *Mesocestoides lineatus*, Goeze, 1782 (0.04 %), as well as nematodes *Toxascaris leonina* Linstow, 1902 (0.82 %), *Strongyloides stercoralis* Bavay, 1876 (0.41 %) and *Trichuris vulpis* Fröhlich, 1789 (0.45 %) were found more rarely.

MOLECULAR STUDY OF THE CESTODE FAMILY DILEPIDIDAE

Komisarovas, J.

Institute of Ecology of Vilnius University, Lithuania

jurijus@ekoi.lt

Earlier caryological and morphological investigations (Freeman, 1973; Bona, 1994; Petkevičiūtė, Binkienė and Komisarovas, 2006) provided grounds to assume that cestodes of family Dilepididae do not form a monophyletic group. Therefore, the author carried out molecular research into nine species of the family deposited in his collection – *Dilepis undula* (Schrank, 1788), *Monopylidium exiguum* (Dujardin, 1845), *Monosertum mariae* (Mettrick, 1958), *M. parinum* (Dujardin, 1845), *Emberizotaenia raymondi* (Gigon et Beuret, 1991), *Sobolevitaenia spinoscapite* (Joyeux et Baer, 1955), *Sobolevitaenia moldavica* (Schumilo et Spasskaja, 1975), *S. verulamii* (Mettrick, 1958), *Molluscotaenia crassiscolex* (von Linstow, 1890).

This study showed that *Dilepis undula*, a type species of type genus of the family, reliably differs from other cestode species included. This supports the morphological and developmental particularity of this widespread species, documented by many authors. This molecular study on cestodes of the family Dilepididae is the beginning only. It cannot serve as the basis for the phylogeny of the whole family. In our opinion, solely taxonomic and molecular features are not sufficient for the explanation of taxonomy and phylogeny of such taxonomically complicated family as Dilepididae. Deeper complex investigations are necessary, supplemented with knowledge about life cycles. So far it is clear that cestodes of family Dilepididae form group with still not finally explained taxonomic structure.

THE NEMATODE CUCULLANUS HETEROCHROUS; A POSSIBLE INDICATOR SPECIES FOR MARINE XENOBIOTICS

Malmstrøm, M.¹, Strømnes, E.², Hansen, R.R.¹ and Ugland, K.I.¹

¹ Marine Biodiversity Research Group, Department of Biology, University of Oslo, Norway, ² Natural History Museum, University of Oslo, Norway
einar.stromnes@nhm.uio.no

For several decades parasites have been used as biological tags for studying marine organisms, mainly as a tool in identifying and separating fish stocks. Lately, they also have been used as biomarkers for marine pollution. *Cucullanus heterochrous* is an intestine parasite found mainly flatfish. The parasite may, according to Schmidt et al (2003a), serve as an important biological marker in monitoring of both PCB and dissolved heavy metals in marine environments. This nematode has never before been reported from the inner region of the Oslo fjord. During the last twelve years, there has been a pronounced reduction in xenobiotics, particularly PCB, in this area. If a marine nematode like *C. heterochrous* as described is applicable as a biological tag, it is reasonable to assume that the species would now be detected there, due to the prevailing low levels of marine pollution. Thus, the purpose of this pilot study was to investigate the presence of *C. heterochrous* in the region mentioned. The gut and intestine of 47 flatfish from 5 different flatfish species were examined. For the first time *C. heterochrous* was detected in this area: Of the 47 fish examined, 5 were found to be infected with a total of 56 specimens. This indicates that the nematode is now able to thrive in the Oslo fjord, and that *C. heterochrous* may be used as a biomarker for the Norwegian fjords, and presumably in other waters

NEW TECHNIQUE FOR WORM BURDEN ASSESSMENT OF ANGIOSTRONGYLUS VASORUM IN EXPERIMENTALLY INFECTED FOXES (VULPES VULPES)

Monrad, J.¹, Webster, P.¹, Johansen, M.V.² and Thamsborg, S.M.¹

¹Department of Veterinary Pathobiology, Faculty of Life Sciences, University of Copenhagen.

²DBL Centre for Health Research and Development, Jægersborg Allé 1D, Charlottenlund, Denmark

Assessing the *Angiostrongylus vasorum* worm burden of a final host based on lung tissue dissection, is very complicated and approximate, resulting in high level worm damage. In a large-scale study on experimental angiostrongylosis in foxes, a novel technique for reverse perfusion of the cardio-pulmonary vascular system was developed in order to recover as many intact worms as possible. Anaesthetized foxes were given heparin i.v. (350 IU/kg) in order to prevent blood clotting during *post mortem*. Three minutes later a lethal pentobarbital dose (100 mg/kg) was given, thorax opened and the thoracic organs were perfused *in situ*. The aorta, vena azygos and the both venae cavae were clamped off. About three litres of isotonic perfusion liquid (normal saline with sodium citrate) were pumped into the left auricle, through the pulmonary veins, the lung capillaries and the pulmonary arteries to the pulmonary trunc from which it was led via a plast pipe onto a sieve (200 µm aperture) for collection of worms. After removal of the lungs, dissection of the pulmonary arteries and subsequent baermannization of the dissected lung tissue in normal saline the total worm burden was estimated as the sum of recoveries made by perfusion, dissection and baermannization, respectively, 49%, 40% and 11% of the total worm burden were recovered by each of these three methods, respectively. In contrast to dissection / baermannization, however, close to 100% of the worms recovered by perfusion were intact.

POPULATION DYNAMICS OF ASCARIS SUUM IN TRICKEL INFECTED PIGS

Nejsum, P.^{1,2}, Thamsborg, S. M.¹, Jørgensen, C.², Fredholm, M.² and Roepstorff, A.¹

¹Danish Centre for Experimental Parasitology, Department of Veterinary Pathobiology

²Genetics and Bioinformatic, Department of Animal and Veterinary Basic Sciences, Faculty of Life Sciences, Copenhagen University, Denmark; .pn@life.ku.dk

We studied the population dynamics of *Ascaris suum* and *Trichuris suis* in trickle infected pigs during long term exposure. Pigs 10 weeks of age were experimental infected with 25 *Ascaris* and 5 *Trichuris* eggs/kg/day, respectively (only observations on *Ascaris* are reported here). At week 4, 8 and 14 post infection (p.i.), 7, 8 and 8 pigs, respectively were slaughtered. Liver ‘white spots’ (due to migrating *Ascaris*) was enumerated and worms in the lungs and small intestine were isolated using an agar method. The mean number of white spots was 272 by week four and was considerably diminished to 22 and 10 spots by week 8 and 14 p.i., respectively. Likewise, a dramatic reduction in numbers *Ascaris* in the lungs were observed with a mean number of 48 larvae by week 4 p.i. and only 1 on both week 8 and 14 p.i. At the three slaughtering days the mean numbers of worm in the small intestine were 376 (range; 39-913), 39 (range: 12-89), 15 (range: 2-40), respectively. In contrast to a previous singel infection study we have here found high numbers of *Ascaris* in the small intestine by week 4 p.i. suggesting a ‘delay’ in the main expulsion of worms suggesting different population dynamic in trickle infected pigs. The high reduction of white spots and numbers of larvae within the lungs between week 4 and 8 p.i. suggest a ‘prehepatic’ barrier which makes the establishment of new incoming *Ascaris* less successful. This observation is supported by the length of the worms at week 8 and 14 p.i.

EFFICIENCY OF LEVAMISOLE IN SOWS UNDER FIELD CONDITIONS

Nosal, P.¹, Petryszak, A.¹, Kornaś, S.¹ and Eckert, R.²

¹ Department of Zoology and Ecology, Agricultural University of Cracow, Kraków, Poland,

² Department of Animal Genetics and Breeding, National Research Institute of Animal

Production, Balice near Kraków, Poland

rznosal@cyf-kr.edu.pl

The study was carried out during 2006-2007 to assess the therapeutic effect of levamisole against naturally acquired gastrointestinal helminths in two pig herds from southern Poland, where the sole medication was used for years. The sows examined had not been dewormed for at least 12 weeks prior to the research. Anthelmintic was administered orally with water at the manufacturer’s recommended dose. To determine the parasite burden, faecal samples were collected on Day -7, Day 0 (the day of treatment) and Day 10 from a group of animals in each farm and processed according to a modified concentration McMaster method (Roepstorff & Nansen 1998). Since no control group was used, the individual faecal egg count reductions (iFECRs) were calculated for each treated swine and then the mean reduction for the treatment group in every farm was estimated (Cabaret & Berrag 2004). In herd A, consisting of 950 breeding sows, a group of 40 sows was sampled one week before treatment, and for 7 animals having on Day 0 the *Oesophagostomum* spp. output of over 300 eggs per gram of faeces (epg), mean iFECR was found to be 77.4%. In herd B, rearing 8 sows and 7 dewormed (except one lactating), 6 had over 300 epg on Day 0, mean iFECR being 77,1%, respectively. Considering sows with the egg output of over 150 epg for counting FECR (Coles et al. 1992), the efficacy could be estimated at the level of 65.6% for 11 sows in herd A, and 80.4% for 7 sow in herd B. Resistance could be suspected in both herds.

COMPLEMENT MEMBRANE ATTACK COMPLEX FORMATION AND INFECTIVITY OF TRICHINELLA SPIRALIS AND TRICHINELLA NATIVA IN RATS

Näreaho, A.¹, Saari, S.¹, Meri, S.² and Sukura, A.¹

¹Department of Basic Veterinary Sciences, Faculty of Veterinary Medicine, ²Department of Bacteriology and Immunology, Haartman Institute, University of Helsinki, Finland
anu.nareaho@helsinki.fi

Rats readily become infected with *Trichinella spiralis* but are more resistant to *T. nativa*. We infected complement factor C6-deficient (C6-) rats and control (C6+) rats with *T. spiralis* and *T. nativa* to compare the effects of membrane attack complex on these parasites in vivo. The 2000 larvae infection dose per rat (equivalent to 7-8 larvae per gram, lpg) yielded 652 lpg in the C6- group and 608 lpg in the C6+ group with *T. spiralis*, whereas with *T. nativa* the corresponding figures were only 1.05 and 1.87 lpg. The difference between the *Trichinella* species was evident, but the infection intensity was unaffected by the C6 deficiency. When newborn larvae were incubated in C6-deficient and control rat sera for 24h in vitro, no changes in viability were observed. Immunohistochemistry revealed that the musculature of cross-sectioned adults and certain stichocytes bound human complement factors C3, C8 and C9, but not C1q. Interestingly, the outermost layer of the cuticle and the newborn larvae did not show any binding activity. Similar findings were obtained with immunofluorescence microscopy of intact newborn larvae. These results indicate that both *T. spiralis* and *T. nativa* have efficient mechanisms to protect themselves against complement attack. The difference in infectivity for rats between the two species, however, is not due to a differential resistance to complement membrane attack complex.

DETECTION ANAPLASMA PHAGOCYTOPHILUM AND BABESIA DIVERGENS IN LITHUANIA AND NORWAY USING REAL TIME PCR METHOD

Radzijeuskaja¹, J., Paulauskas¹, A. and Rosef, O.²

¹Vytautas Magnus University, Kaunas, Lithuania

²Telemark University College, Bø i Telemark, Norway

a.paulauskas@gmf.vdu.lt

The prevalence of *Anaplasma phagocytophilum* and *Babesia divergens* in 364 *Ixodes ricinus* ticks collected from different locations in Lithuania and Norway was detected by Taq Man based Real time PCR method. The *msp2* gene of *A. phagocytophilum* and 18srRNA gene of *B. divergens* have been chosen as amplification targets in analysis. The overall infection level of *A. phagocytophilum* in Norwegian ticks was higher (10/224; 4.5%) than in Lithuanian (4/140; 2.9%). Prevalence rates varied in different collection sites between 0 and 9.1% in Lithuania, and between 0 and 8.7% in Norway. A total 3 of 140 (2.1%) ticks were infected with *B. divergens* in Lithuania and 2 of 224 (0.9%) were infected in Norway. Prevalence of infection varied from 0 to 2.8% and from 0 to 4.3% in different collection sites in Lithuania and Norway respectively. The detected presence of *A. phagocytophilum* and *B. divergens* in *I. ricinus* ticks in Lithuania and Norway demonstrated the possibility of transmitting these infections. Taq Man based Real time PCR method was also used for investigation of small rodents as potential reservoirs of *A. phagocytophilum*. 212 small rodents belonging to 5 species were captured in the ticks sampling sites. Tissue samples (ears and spleens) and engorged nymphal ticks collected on rodents were analysed. The *A. phagocytophilum* infection was not found in any of tested samples.

PARASITE CONTROL IN PETS

Thamsborg^{1,2}, S. M., Guillot, J.², Miro, G.², Epe, C.², Genchi, C.², Deplazes, P.², van Knapen, F.² and Fisher, M.²

¹Danish Centre for Experimental Parasitology, Department of Veterinary Pathobiology, Faculty of Life Sciences, Copenhagen University,

²ESCCAP

European Scientific Counsel Companion Animal Parasites (ESCCAP) was formed in 2005 with the objective of developing guidelines for the control of major parasitic infections in companion animals in order to protect the health of pets, enhance the safety of the public and preserve the bond between pets and people. The guidelines will be subject to regular revision in dialogue with practitioners and researchers across Europe, as the great diversity in parasites and their importance is recognised. Guidelines and other news for vets and pet owners will be presented on the website (www.esccap.org) and by other means. Guideline No.1: Worm control in dogs and cats, was launched on the website 2006. The first guideline identifies three “key” parasite groups that cause severe disease and/or pose a zoonotic risk and have high prevalence in some or all areas of Europe: *Toxocara* spp. and hookworm, *Echinococcus* spp. and *Dirofilaria immitis*. The guideline deals with geographical distribution and prevention by environmental control of parasite transmission, animal management and treatment. ESCCAP is an independent, non-profit making organisation registered in UK, expecting to get charitable status in 2007.

List of participants

Alekseev, Andrey	Zoological Inst., Sankt Peterburg, RAS	Russia
Babushnikova, Alena	National Academy of Sciences of Belarus	Belarus
Bachmann, Lutz	Univ. of Oslo	Norway
Bakke, Tor	Univ. of Oslo	Norway
Baranowska-Korczyn, Anna	Medical Univ. of Warsaw	Poland
Barskaya, Julija	Karelian Res. Centre, RAS	Russia
Benesh, Daniel	Univ. of Jyväskylä	Finland
Borecka, Anna	Polish Academy of Sciences	Poland
Bugmyrim, Sergey	Karelian Res. Center, RAS	Russia
Chukalova, Natalia	Atlantic Scientific Res. Inst.	Russia
Djadid, N. D.	Malaria Research Group (MRG)	Iran
Eihvalde, Evija	Latvian Univ. of Agriculture	Latvia
Eliseev, Alexander	Atlantic Scientific Res. Inst.	Russia
Eydal, Matthias	University of Iceland	Iceland
Gawor, Jakub	Polish Academy of Sciences	Poland
Hamnes, Inger	National Veterinary Institute	Norway
Henttonen, Heikki	Finnish For. Res. Institute	Finland
Höglund, Johan	Swedish Univ. of Agricultural Sciences	Sweden
Ieshko, Evgeny	Karelian Res. Center, RAS	Russia
Isomursu, Marja	Finnish Food Safety Authority Evira	Finland
Jortikka, Sinikka	Finnish For. Res. Institute	Finland
Karbowiak, Grzegorz	Polish Academy of Sciences	Poland
Kirjusina, Muza	National Diagnostic Centre	Latvia
Kivilahti, Raija	Univ. of Lapland, Arctic Centre	Finland
Komisarovas, Jurius	Vilnius University	Lithuania
Kornaś, Sławomir	Agricultural University	Poland
Križanauskienė, Asta	Vilnius University	Lithuania
Laakkonen, Juha	Univ. Helsinki	Finland
Laaksonen, Sauli	Finnish Food Safety Authority Evira	Finland
Lavikainen, Antti	Univ. of Helsinki	Finland
Lebedeva, Dariya	Karelian Res. Center, RAS	Russia
Lumme, Jaakko	Univ. of Oulu	Finland
Maddox-Hyttel, Charlotte	National Veterinary Institute	Denmark
Marcinkute, Audrone	Vilnius University	Lithuania
Matveeva, Elizaveta	Karelian Res. Center, RAS	Russia
Mažeika, Vytautas	Klaipeda University	Lithuania
Meri, Seppo	Univ. of Helsinki	Finland
Mlocicki, Daniel	Medical Univ. of Warsaw	Poland
Moks, Epp	University of Tartu	Estonia
Monrad, Jesper	Danish Centre of Experimental Parasitology	Denmark
Näreaho, Anu	Univ. of Helsinki	Finland
Nielsen, Henrik	Statens Serum Institut	Denmark
Novokhatskaya, Olga	Karelian Science Centre, RAS	Russia
Oksanen, Antti	Finnish Food Safety Authority Evira	Finland
Øvstaas, Ole	Univ. of Oslo	Norway
Palinauskas, Vaidas	Vilnius University	Lithuania
Paulauskas, Algimantas	Vytautas Magnus University	Lithuania
Pulkkinen, Katja	Univ. of Jyväskylä	Finland

Radzijeuskaja, Jana	Vytautas Magnus University	Lithuania
Rätti, Osmo	Univ. of Lapland, Arctic Centre	Finland
Rintamäki, Päivi	Univ. of Oulu	Finland
Roepstorff, Allan	Danish Centre of Experimental Parasitology	Denmark
Sinisalo, Tuula	Univ. of Jyväskylä	Finland
Soveri, Timo	Univ. Helsinki	Finland
Stensvold, Rune	Statens Serum Institut	Denmark
Stien, Audun	NINA	Norway
Strømnes, Einar	Univ. of Oslo	Norway
Talvik, Heli	Estonian Univ. of Life Sciences	Estonia
Thamsborg, Stig	Danish Centre of Experimental Parasitology	Denmark
Traversa, Donato	Univ. of Teramo	Italy
Turunen, Tuula	Åbo Akademi	Finland
Valkiūnas, Gediminas	Vilnius University	Lithuania
Valtonen, Tellervo	Univ. of Jyväskylä	Finland
Zakeri, Sedigheh	Malaria Research Group (MRG)	Iran