UiO : Natural History Museum

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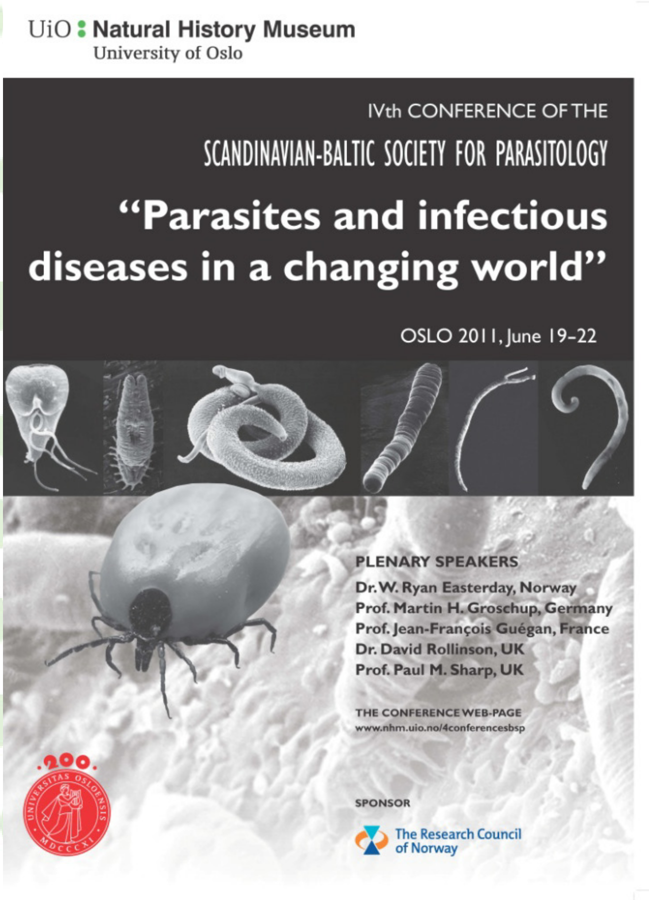
“Parasites and infectious diseases in a changing world”

The 4th Conference of the
Scandinavian-Baltic Society for Parasitology (SBSP)



UiO : Natural History Museum
University of Oslo

IVth CONFERENCE OF THE
SCANDINAVIAN-BALTIC SOCIETY FOR PARASITOLOGY

“Parasites and infectious diseases in a changing world”

OSLO 2011, June 19–22

PLENARY SPEAKERS
Dr. W. Ryan Easterday, Norway
Prof. Martin H. Groschup, Germany
Prof. Jean-François Guégan, France
Dr. David Rollinson, UK
Prof. Paul M. Sharp, UK

THE CONFERENCE WEB-PAGE
www.nhm.uio.no/4conferencesbsp

SPONSOR
The Research Council of Norway

UiO : Natural History Museum
University of Oslo

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Front picture: The official poster of the 4th SBSP Conference

UiO Natural History Museum
University of Oslo

Parasites and infectious diseases in a changing world

Christoph Hahn and Bastian Fromm (eds.)

Programme and Proceedings from the 4th Conference of the Scandinavian-Baltic Society for Parasitology, June 19th-22nd 2011

sponsors:

The Research Council of Norway

ARTSDATABANKEN

UiO : **Natural History Museum**
University of Oslo

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Summary:

The 4th Scandinavian Baltic Conference of Parasitology was held in Oslo from the 19th to the 22nd June 2011, as part of the bicentenary celebrations of the University of Oslo. The theme of the conference was '*Parasites and infectious diseases in a changing world*', and attracted an international audience from 17 countries, including delegates from Pakistan, Iran, Taiwan, Russia, Greece, France, Poland, UK and Germany, as well as the more traditional Denmark, Norway, Sweden, Iceland, Finland, Latvia, Lithuania and Estonia. A total of 48 talks (including 3 plenary addresses) and 38 posters addressed a range of issues in contemporary parasitology, with a strong focus on parasite ecology and systematics, and of the role of museums in parasite species discovery. The conference included a workshop sponsored by the Norwegian Artsdatabanken (www.artsdatabanken.no) addressing the prospects for parasite species discovery in future, which was open to all.

Oslo June 10th 2011

Christoph Hahn and Bastian Fromm

Editors

UiO : Natural History Museum
University of Oslo

Foreword

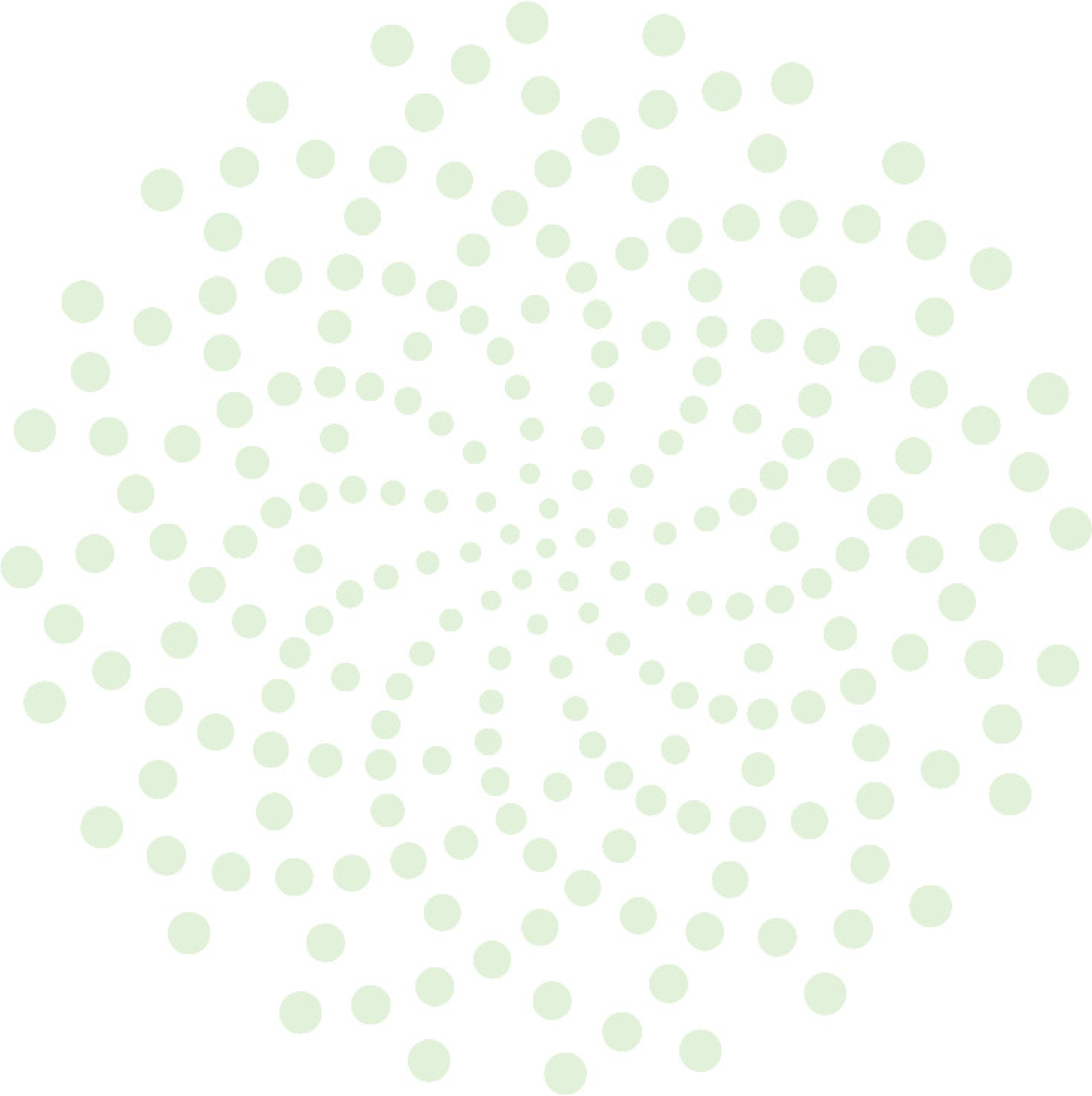
It is our pleasure to invite you to take part in the biennial conference of the Scandinavian-Baltic Society for Parasitology (SBSP) at Georg Sverdrup's House, University of Oslo (UiO), June 19th to 22nd 2011 under the auspices of the local arrangement committee at Natural History Museum (NHM), Oslo, and the SBSP. The Welcome reception will take place at NHM's Geological Museum situated in the Botanical Garden, Tøyen, and the Opening ceremony will be held in Georg Sverdrup's House on the Blindern campus of the UiO. UiO celebrates its 200th anniversary this year which also marks the bicentenary of the establishment of universities in general in Norway. Several important conferences, international, European and Nordic, will be held in Oslo this year, and we are pleased to be your hosts for this 4th SBSP Conference marking the 200th anniversary of the University. The program will include keynote lectures, oral communications and posters on the theme of “Parasites and infectious diseases in a changing world” and will be an important forum for the dissemination and discussion of new findings in this rapidly expanding field. Parasites have an enormous impact on animal and human health, and the conference will focus our attention on the dynamic and integrated nature of interactions between wildlife, domestic animals, humans and the environment. We hope that the diversity of themes covered at this conference will encourage positive discussions and new collaborations between the delegates.

Oslo is the largest city in Norway, and has been the country's capital since 1814 although the history of the city extends back to the year 1000 AD. Since the Middle Ages Oslo has undergone great changes, even the name of the town being changed a few times. The Government and Parliament of Norway are located in Oslo, and at the end of the main street, Karl Johan's gate, you will find the Royal Palace. Oslo's beautiful location at the head of Oslo Fjord surrounded by forested ridges gives the city qualities that you do not normally expect from a capital. Oslo has a rich and varied cultural life with many attractions not least those exhibited at Bygdøy where we will enjoy the Conference dinner at the *Kon-Tiki* museum celebrating Thor Heyerdahl's famous expeditions. Heyerdahl is best known for his *Kon-Tiki* expedition, and later with the *Ra* expeditions when he crossed the Atlantic Ocean; his last great raft expedition was when he sailed around the Arabian peninsula in the reed boat *Tigris*. He also conducted scientific expeditions to Easter Island, Galapagos, and the Maldives and to the ancient pyramids of Tucume in Peru, among other places.

The Research Council of Norway has kindly sponsored the conference, and the Norwegian Artsdatabanken has sponsored the workshop “Modern methods for species discovery amongst poorly studied parasite groups”.

Oslo June 10th 2011,

Tor A. Bakke, Chair 4th SBSP Conference,



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1. GENERAL CONFERENCE INFORMATIONS

1.1. Local Arrangement Committee

The local arrangement committee have worked hard to ensure that the 4th Scandinavian-Baltic Society for Parasitology (SBSP) Conference will provide a scientifically interesting and appealing program for both SBSP members and non-members worldwide. The local organizing committee consists of the members of the Evolutionary Parasitology Group (EPG) at Natural History Museum, University of Oslo: Tor A. Bakke (chair of the conference), Lutz Bachmann, Phil D. Harris, Einar Strømnes, Bastian Fromm, Christoph Hahn, Raul Ramirez, Ann-Helén Rønning, Eve Zeyl, Susanna Lybæk and Odd Halvorsen. The professors: Harris, Bakke and Bachmann constituted the scientific committee with Harris as chair. During the conference the local arrangement committee will carry a large red UiO anniversary button next to their name plates.


Tor A. Bakke


Lutz Bachmann


Philip D. Harris


Bastian Fromm


Christoph Hahn

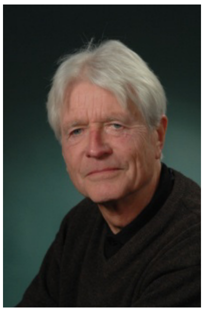

Raul Ramirez


Ann-Helén Rønning


Eve Zeyl


Susanna Lybæk

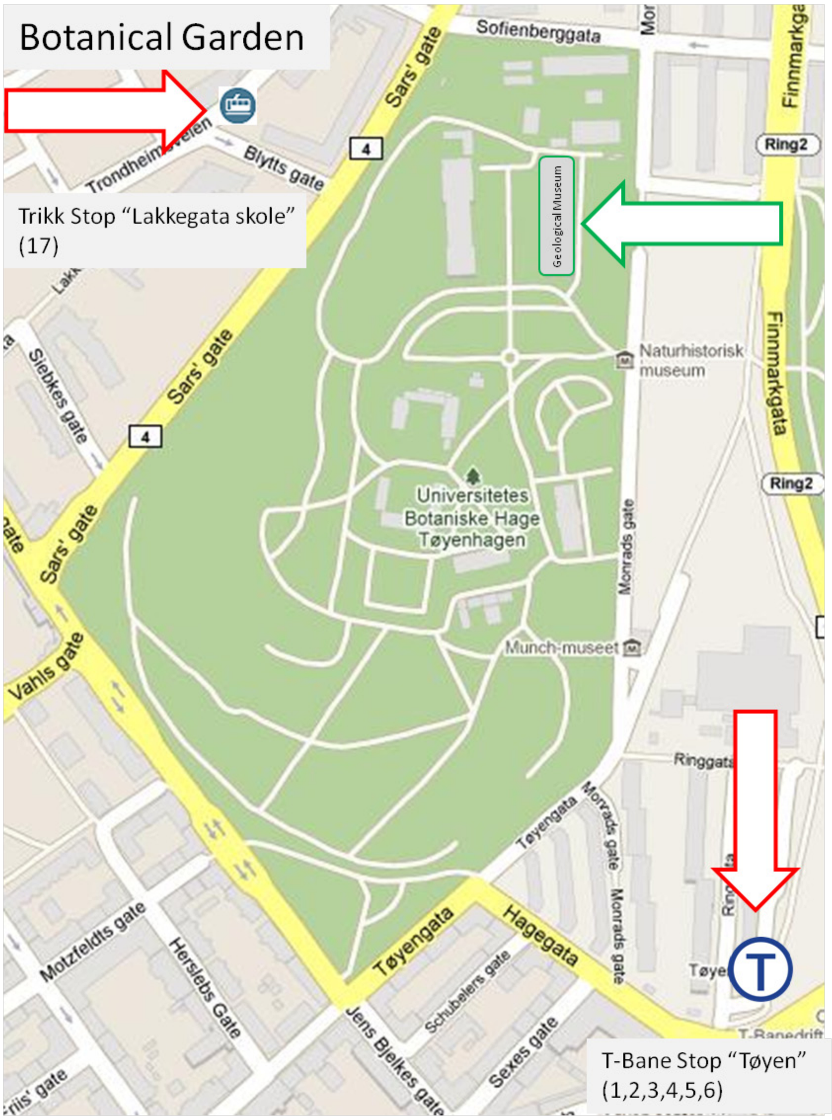

Einar J. Strømnes


Odd Halvorsen

1.2. Conference venues, local transport and maps

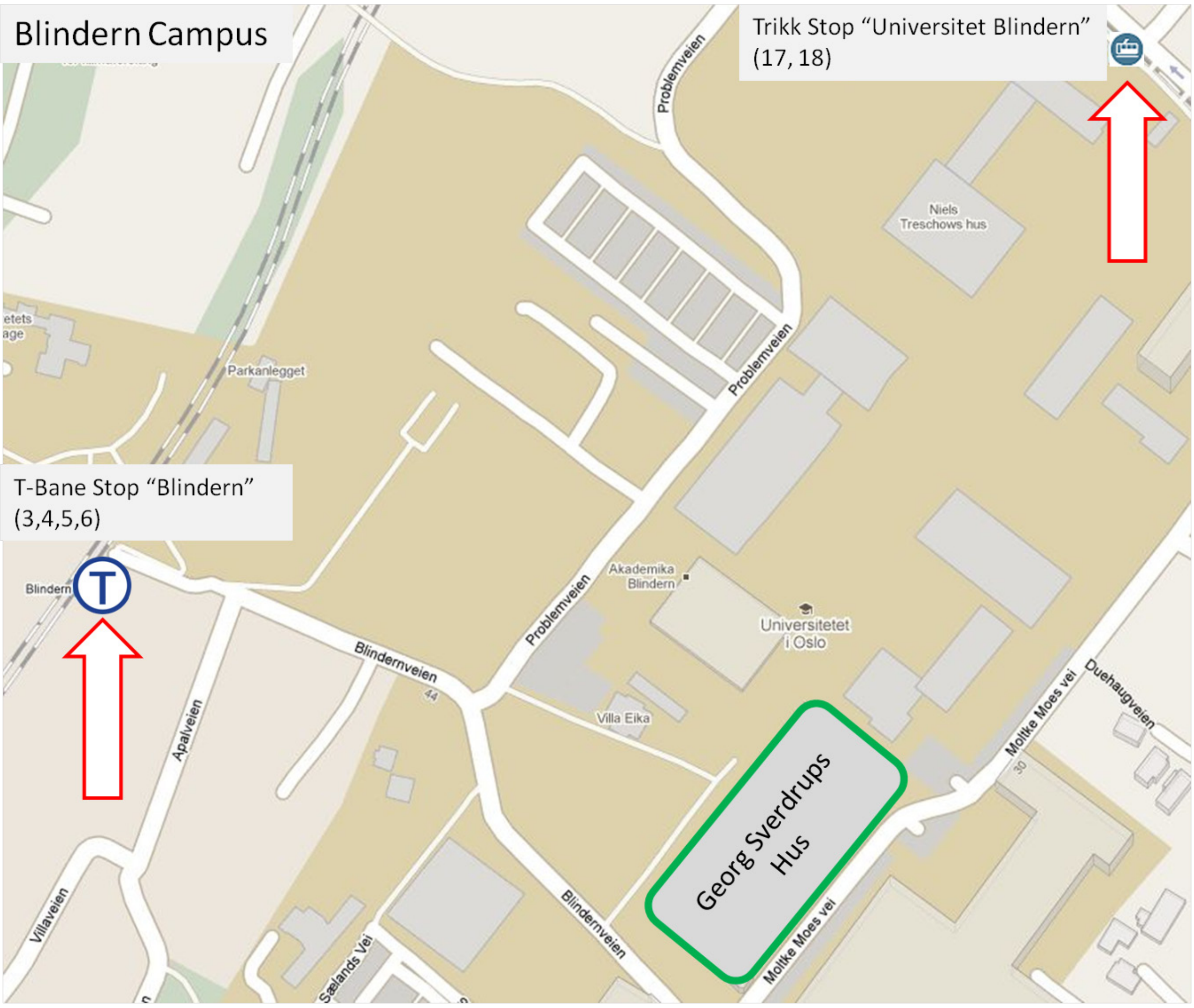
Welcome reception

The welcome reception will take place June 19th at the Geological Museum which is located in the beautiful Botanical Garden at Tøyen, east of Oslo city centre. The garden is popular for recreation but is a scientific collection in itself. The Geological museum together with the Zoological and Botanical museums were established in the early 20th century for exhibitions and research in natural sciences. NHM has Norway's most comprehensive natural history collection going back almost 200 years. A selection of the specimens are on display for the general public. The Geological museum is marked with a green arrow on the map. **Metro:** all eastbound lines to Tøyen station; Tram no. 17 to "Lakkegata skole", Bus no. 20 to "Munch-museet", Bus no. 31 to "Lakkegata skole", Bus no. 60 to "Tøyen kirke" or "Tøyen skole". **Street address:** Monrads gate / Botanical garden.



Conference venue

All oral and poster presentations will take place June 20th and 22nd in Georg Sverdrup's House (green square) at Blindern Campus. The building was opened in 1999 as one of the landmarks at the Campus. **Metro:** westbound lines 3, 4 and 5 to Blindern station. **Tram:** westbound lines 17, 18 to Universitetet Blindern stop. **Street address venue:** Moltke Moes vei 39.



Conference dinner

The conference dinner will take place at the Kon-Tiki Museum, which is situated at Bygdøynes, just outside the centre of Oslo. It can be reached by bus or boat. **Bus** number 30 departs from the National Theatre and the Central Station at 10 minute intervals and the journey to Bygdøynes takes approximately 25 minutes. **Boat:** The ferry number 91 sails frequently from the quayside near the City Hall and takes only 15 minutes to reach Bygdøynes, which is the second stop.The ferry ride is recommended **Street address venue:** Bygdøynesveien 36

1.3. Storage of luggage

If there is a need for storage of luggage etc. at Blindern Campus during the conference or especially on Tuesday if not staying at the hotel to Wednesday, Grupperom 2 will be available. Please take contact to a member of the local arrangemnet committee if you need to store luggage.

1.4. Identification and insurance.

We would like to remind the delegates to wear the name plates (badges) at all time during the conference to identify themselves to the University staff at the venues and during tea breakes and at lunch time which will both be held in the cafeteria in Georg Sverdrups's House. Only badge holders will be admittted to the scientific sessions and social events, except for the Artsprojekt sponsored workshop on Tuesday afternoon. The local arrangement committee will in addition to a name plate wear a large red button for easy recognition. Photos of the members can be found at page 7 and the conference web page <www.nhm.uio.no/4conferencesbsp>. The local organization committee does not assume any responsibility for individual medical, travel or personal insurance. The delegates are advised to arrange their own personal insurance.

1.5. Currency, delegate registration and payment

Currency situation June 8th 2011:

1 € = 7.88577 NOK.

1 $ = 5.37694 NOK

(http://www.xe.com/ucc/)

The conference registration desk will be open for registration on Sunday 19th at the Welcome reception, Geological Museum, Botanical garden, Tøyen, from 5:00 to 9:00 pm, and on Monday 20th and Tuesday 21st from 8:00 am to 5:00 pm at the entrance hall in Georg Sverdrup's House, Blindern campus. The desk will be staffed during the conference if you require assistance; if temporarily closed a sign will indicate when it will next be open. When you register you will receive your conference bag, including an information pack, this abstract and program book, your badge, your receipt and other goodies. Delegates who have not yet paid the fee are kindly requested to pay at the registration desk in Norwegian currency (NOK) before receiving the conference bag.

1.6. Conference fee and refund policy

The 4th SBSP Conference fees are:

non members	NOK 2500
SBSP members	NOK 2000
student non members	NOK 1500
student SBSP members	NOK 1000
accompanying person	NOK 1000
conference dinner	NOK 800
post-conference tour	NOK 700

Early registration enclosure is June 1st, after June 1st the fee increases with NOK 400, final deadline for registration, June 15th, 2011. Cancellations before June 1st, 2011 will be refunded in full, minus a processing fee of NOK 400 for professionals and NOK 200 for students and attendees. No refund of any kind will be given for cancellations occurring after June 1st, 2011.

1.7. Internet facilities

Delegates can access the internet via wireless networks at Georg Sverdrup's House. The guest password <uio200uio> will be valid for the duration of the conference. A few desktop computers with internet access will also be available during daytime in the library in Georg Sverdrup's House.

1.8. Student presentation awards

Prizes for the best oral and poster presentations by student delegates have been generously provided by the Scandinavian-Baltic Society for Parasitology. All student presentations will be evaluated. The awards will be presented during the conference dinner.

1.9. Food and refreshment

With the exception of the Welcome reception at the Geological Museum, Tøyen, and the conference dinner in the Kon-Tiki Museum, Bygdøynes, all refreshment-, coffee and tea breaks, and the lunches on June 20th and 21st will be provided in the cafeteria ("*Café Sverdrup*") in Georg Sverdrup's house - close to the lecture halls.

1.10. Social programme

1.10.1. Welcome reception

The Welcome reception at NHM, University of Oslo, Sunday June 19th.

10:00 –21:00	Garden open to the public	Botanical Garden
16:00	Geological Museum closes for the public and opens for the delegates	Monrads gate
17:00 – 21:00	Open registration desk	Geological Museum
18:00 – 21:00	Finger buffet served	
19:00 - 19:15	Welcome address by head of the National Centre of Biosystematics (NCB), Prof.Jan Lifjeld	
20:00 - 21:00	Optional garden tour	Botanical Garden

1.10.2. Conference dinner

The conference dinner will be held on Tuesday June 21st 2011 at the Kon-Tiki Museum, Bygdøynesveien 36. The museum will be open for guests from 19:00, and dinner will be served at 20:00. At 19:15 there will be a guided tour in the museum by a member of the museum staff, Halfdan Tangen jr. The conference dinner will close at 23:00 when it will be necessary to return to the city by bus. The Kon-Tiki Museum is situated next to the museum where Fridtjof Nansen's ship Fram is exhibited. At walking distance from the Kon-Tiki Museum (ca. 1500 m) you will find the famous Viking Ship Museum with the Oseberg, Gokstad and Tune ships from ca. 800-900 A.D. and the Norsk Folkemuseum giving a broad representation of the Norwegian and Sámi culture from the 16th century onwards. A three-course dinner consisting of Kon-Tiki fish casserole, lamb and the Kon-Tiki exotic fruit arrangement will be served. Three glasses of wine are included, and extra wine can be bought at the table.

1.10.3. Post-conference tour

The post-conference tour to Blaafarveværket Wednesday 22nd will be by car not bus.

08:30	Departure from the back of Oslo City Hall	Oslo, Fridtjof Nansens Plass
08:30 - 10:30	Trip through scenic country west of Oslo	Oslo - Åmot via Sollihøgda and lake Tyrifjorden
10:30 - 10:50	Stop at Haugfoss waterfall	Haugfoss waterfall
10:50 - 11:00	Walk Haugfosstråkka to Blaafarveværket (10 minutes)	Haugfosstråkka
11:00 - 12:00	Cobalt works' history and exhibitions (guided tour)	Blaafarveværket
12:00 - 12:45	Break	
12:45 - 12:50	Coach trip to the Cobalt mines	The Ore Road
13:15 - 14:15	Lunch	The Miners' Inn
14:15 - 15:00	Visit the Th. Kittelsen art museum	Skuterudhøgda
15:00 - 16:15	Guided tour into the mines	The Clara Stoll drifts
16:15 - 18:00	Return coach trip to Oslo via Drammen along river Drammenselva	Åmot - Oslo

2. SCIENTIFIC PROGRAMME

2.1. Oral and poster presentations

Presentations can be delivered to the registration desk at any time or to the AV assistants in the session-rooms during breaks before your session. Each room will be manned by an AV assistant in case of problems with the equipment. Please ensure that you keep to the timeslots so that delegates who wish to move between sessions can do so. NB! Please use USB sticks, as it will not be possible to read from CDs. If your presentation is on CD please contact the Registration desk in good time to transfer the presentation to USB stick.
The plenary and invited lectures will be limited to 60 or 40 minutes including discussions; oral presentations are limited to 20 minutes including discussion.
Posters may be put up from 8:00 am on Monday 20th and must be removed by 5:00 pm Tuesday 21st. You will be provided with a number for your poster corresponding to a particular poster board. All boards are located in the hall below the entrance hall in Georg Sverdrup's house. All posters should be displayed in time for the poster sessions.

2.2. Workshop:

ARTSDATABANKEN

"Modern methods for species discovery amongst poorly studied parasite groups"

This workshop is sponsored by Artsprosjektet, a program established by the Norwegian government to improve knowledge of Norwegian biodiversity andmanaged by The Norwegian Biodiversity Information Centre (NBIC, www.artsdatabanken.no). NBIC is a national source of information on biodiversity. The main function of the organisation is to supply updated and accessible information on Norwegian species and ecosystems.

"*Modern methods for species discovery amongst poorly studied parasite groups*" will address methodologies for species discovery among the principal groups of parasitic invertebrates which remain poorly known in Norway. The workshop will focus on training methodologies, especially for morphological species assignation.

The session will feature the following speakers: Matthias Vignon, University of Perpignan, France; Egil Karlsbakk, University of Bergen, Norway; Lutz Bachmann and Øyvind Hammer, Natural History Museum, University of Oslo, Norway. They will address morphometric analysis, Principal Components Analysis, and the use of natural history collections for species discovery.

2.3. Plenary and invited speakers

The local arrangement committee is pleased to be able to announce that the following experts will give eleven lectures on various aspects under the theme “Parasites and infectious diseases in a changing world.”

Martin Groschup is head of the Institute of Novel and Emerging Infectious Diseases (INEID) at the Friedrich Loeffler Institute, Island of Riems, Germany. His primary research interest is in the evolution and transmission to humans of Transmissible Spongiform Encephalopathies (TSEs) of domestic and wild ruminants, cats and mink. However, he leads an institute with a much wider mission, with research covering the full spectrum of emerging pathogens, in particular vector-borne and other viral zoonoses of importance, such as West Nile Virus, and hantavirus. As such his research yields clues about the spread of infectious disease agents through a susceptible host population, and is of interest to all involved in wildlife disease epidemiology

David Rollinson is a senior researcher within the Natural History Museum, London, where he is head of the Biomedical Research Group. He has worked on schistosome parasites of man and animals for more than 30 years, and is best known for his work on the evolutionary biology of this group, in relation to the evolution of both the snail and vertebrate hosts. He is currently involved with EU funded control and surveillance projects in sub-saharan Africa, and in studies of the interactions between the genomes of *Schistosoma mansoni* and its host *Biomphalaria glabrata*. He is, however also based in a museum setting, and has appreciation of the uses and limitations of helminthological collections for biomedical research.

Paul Sharp has been professor of genetics at the University of Edinburgh, UK, since 2007. He was one of the first population geneticists to take an evolutionary perspective in studying the molecular variation of bacteria and viruses, and is best known for his work on HIV evolution. However, he has wider interests in co-evolution and the transfer of pathogens from wild animals to humans, and most recently has turned his attention to the evolution of *Plasmodium falciparum* from ancestral lineages infecting gorillas. His work on codon usage in an evolutionary context will be of interest to all concerned with parasite phylogenetic research.

Additionally we are happy to announce 8 other invited speakers, which will address particular conference sessions. These include:

Dr. Ryan Easterday
CEES, University of Oslo, Norway

Professor Arne Skorping,
Department of Biology, University of Bergen, Norway

Dr. Audun Stien,
Norwegian Institute for Nature Research (NINA), Tromsø, Norway

Professor Kurt Buchmann,
Department of Veterinary Disease Biology, University of Copenhagen, Denmark

Dr. Solveig Haukeland,
Bioforsk, Ås, Norway

Magister Christoph Hahn,
Natural History Museum, University of Oslo, Norway

Dr Matthias Vignon
University of Perpignan, France

Dr Egil Karlsbakk
Institute of Marine Research, Bergen, Norway

2.4. Scientific programme overview

MONDAY MORNING		
8:00	Registration desk opens, Georg Sverdrup’s House, UiO, Blindern.	
9:00	Opening ceremony (Auditorium 2) Prof. John P. Collett (UiO, Head of Forum for University History)	
9:45	Plenary Lecture (Auditorium 2): Prof. Martin H. Groschup *"Prions - lessons from BSE and Scrapie"*	
10:45	Coffee break,Café Sverdrup Posters up	
Parallel Sessions	**1 A (Auditorium 2) Artsdatabanken sponsored workshop: Species discovery amongst parasitic groups**	**1 B (Teaching Room 1): Ectoparasitic arthropods and their transmitted pathogens**
11:15	M. Vignon (University of Perpignan) *The use of geometric morphometrics in disentangling sources of shape/size variation in monogenean haptoral hard parts. Insights into modularity* Invited Talk	W. R. Easterday (CEES, Oslo) *The flea, the plague and friends (From the perspective of a microbiologist)* Invited Talk
11:55	L. Bachmann (NCB, NHM Oslo) *Mining natural history collections for gyrodactylid flatworms*	A. Paziewska (NCB, NHM Oslo) *Bartonella infections in fleas – does prevalence reflect vector competence?*
12:15	Ø. Hammer (NHM Oslo) *Introduction to morphometrics with Past*	H. Vatandoost (University of Medical Sciences, Tehran) *Current situation of arthropod-borne disease in Iran*
12:35	E. Karlsbakk (University of Bergen) *Species discovery in the Myxosporea*	Å. Andreassen (Norwegian Institute of Public Health, Oslo) *Prevalence of Tick-born encephalitis virus (TBEV) in Southern Norway*
12:55	P. D. Harris (NCB, NHM Oslo) *Prospects for parasite species discovery*	S. A. Qamar (GDG College, Karachi) *Human Health problems and zoonotic disease*
13:15	Lunch, Café Sverdrup	

MONDAY AFTERNOON		
14:15	Plenary lecture (Auditorium 2): Dr. David Rollinson “*Museomics - parasites and collections*”	
15:15	Coffee break, Café Sverdrup	
Parallel Sessions	**2 A (Auditorium 2): Parasite Epidemiology, modelling and control**	**2 B (Teaching Room 1): Terrestrial wildlife parasitology**
15:45	S. Haukeland (Bioforsk, Ås) *Use of bacterial infected nematodes to combat insects and slugs* Invited Talk	A. Stien (University of Tromsø) *Host-parasite dynamics in the terrestrial high Arctic ecosystem of Svalbard* Invited Talk
16:25	K. Pulkinnen (University of Jyväskylä) *Impacts of introduced predatory crayfish on parasites of native perch*	E. Osterman Lind (Veterinary Institute Uppsala) *The first findings of Echinococcus multilocularis in Sweden*
16:45	R. Ramirez (NCB, NHM Oslo) *Error estimation in gyrodactylid population studies*	J. Hildebrand (University of Wrocław) *Ecological analysis of occurrence of Brachylecithum glareoli in bank voles Myodes glareolus*
17:05	K. Olstad (NINA Lillehammer) *Acidic aluminum reducing and eradicating infections of Gyrodactylus salaris (Monogenea: Gyrodactylidae) from Atlantic salmon (Salmo salar): treatment strategy and impact on population dynamics*	R. Davidson (Veterinary Institute Oslo) *Echinococcus multilocularis surveillance in Norway*
17:25	D. Hendrichsen (NINA Lillehammer) *Modelling the effects of temperature on Gyrodactylus salaris on Atlantic salmon in Norway*	P. Jokelainen (University of Helsinki) *Farmed wild boar are exposed to Toxoplasma gondii and Trichinella spp. in Finland*
18:00	Coffee break, Café Sverdrup, Poster session OPEN END	

TUESDAY MORNING

9:00	Plenary lecture (Auditorium 2): Prof. Paul M. Sharp *“Genomics and the evolution of Plasmodium”*	
10:00	Coffee break, Café Sverdrup	
Parallel Sessions	**3 A (Auditorium 2): Museomics and Parasite Systematics**	**3 B (Teaching Room 1): Ecology of aquatic parasites**
10:30	C. Hahn (NCB, NHM, Oslo) *Museomics of ectoparasites – chasing the origin of Gyrodactylus salaris* Invited Talk	K. V. Galaktionov (Russian Academy of Sciences, St Petersburg) *Transmission patterns, phylogeny and historical biogeography of the “pygmaeus” microphallids (Digenea: Microphallidae): widespread parasites of marine and coastal birds in the Holarctic*
10:50		D. Jouet (UFR de Pharmacie, Reims) *Parasites as markers and tracers of the populations of aquatic birds in France and Iceland*
11:10	L. G. Podubnaya (Russian Academy of Sciences, Borok) *Ultrastructure as an aid to understanding of the phylogenetic relationships of the Gyrocotylidea*	K.E. Nikolaev (Russian Academy of Sciences, St. Petersburg) *Transmission patterns of seabird trematodes Himasthla elongata and Cercaria parvicaudata (Renicola sp.) in coastal communities of the White Sea*
11:30	A. Križanauskienė (Nature Reserve Centre, Vilnius) *Haemoproteids (Haemosporida, Haemoproteidae) of doves (Columbidae) belong to Haemoproteus and Parahaemoproteus subgenera: call for vector studies*	R. Petkevičiūtė (University of Vilnius) *Studies on chromosome sets and DNA sequences of Phyllodistomum spp. (Digenea): taxonomic and phylogenetic implications*
11:50	P. Prakas (Nature Reserve Centre, Vilnius) *Investigations of Sarcocystis spp. in birds of the order Anseriformes*	M. Yakhchali (Faculty of Vet. Med. Urmia) *Pathology changes in gastrointestinal tract infected with Neoechinorhynchus spp. (Neoacanthocephala: Neoechinorhynchidae) in Barbus capito of Zarine-Roud River, Iran*
12:10	G. Zalesny (University of Environmental and Life Sciences, Wrocław) *The occurrence of larval form of cestodes in free living rodents from Lower Silesia*	S.M. Sadjjadi (University of Shiraz) *Parasitological and molecular investigations of snails for cercariae in Fars province, Iran*
12:30	R. Holgado (Bioforsk, Ås) *Cyst nematodes on grasses in Norway.*	K. Skirnisson (University of Iceland) *The avian schistosome fauna of Iceland and its biogeographical position*
12:50	Lunch, Café Sverdrup	

TUESDAY AFTERNOON

Parallel Sessions	**4 A (Auditorium 2): Gyrodactylus genomics**	**4 B (Teaching Room 1): Parasites in artificial ecosystem**
13:50	K. Buchmann (University of Copenhagen) *Susceptibility and resistance of Atlantic salmon Salmo salar L. to Gyrodactylus salaris infections: which molecules are involved?* Invited Talk	A. Skorping (University of Bergen) *Evolutionary effects of intensive farming on parasite life histories and virulence* Invited Talk
14:30	J. Lumme (University of Oulu) *The motivation to conduct whole genome sequencing in Gyrodactylus (reasoned after first glimpse on the data)*	B. Lassen (Estonian University) *Simple survival assay for determining environmental and chemical effects on Eimeria bovis*
14:50	B. Fromm (NCB, NHM Oslo) *MicroRNA preparations from individual monogenean Gyrodactylus salaris – comparison of six commercially available “totalRNA” extraction kits*	A. Mennerat (Oxford University) *Life history and virulence are linked in an ectoparasite, the salmon louse Lepeophtheirus salmonis*
15:10	M. Zietara (University of Gdansk) *Detecting species hybrids in Gyrodactylus is possible by few molecular markers: nuclear ITS of rDNA and mitochondrial cox1*	O. Moberg (University of Bergen) *Immunisation impairs cognitive and neural development in fish*
15:30	H. Aisala (University of Oulu) *Molecular ecology in the era of next generation sequencing: Examples from the early phases of the Gyrodactylus salaris genome project*	A.V.M. Domke (Norwegian School of Veterinary Science) *An overview of anthelmintic resistance in Norwegian sheep and goat flocks*
15:50	S. Hietala (University of Oulu) *Uniform evolution rate in mitochondrial CO1-gene in Gyrodactylus*	T. Lepik (Estonian University) *Haptoglobin levels in blood from calves in response to experimental infections with Eimeria zuernii*
16:30	Coffee break, Café Sverdrup	
17:00	SBSP Annual General Meeting (Auditorium 2)	
19:00	Conference Dinner at the Kon-Tiki-museum	

3. ABSTRACTS

3.1. Submitted abstracts for oral presentation

ABSTRACT No. 1 – Session 4A

Molecular ecology in the era of next generation sequencing: examples from the early phases of the *Gyrodactylus salaris* genome project

Aisala, H. & **Lumme, J.**

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Genetic studies in parasitic species have usually been limited to a few conservative loci, as marker design for non-model organisms is often both laborious and time-consuming. Next-generation sequencing (NGS) technologies offer the potential for fast and cost-effective development of genetic resources, even without prior genomic information. We used Roche 454 sequencing of amplified genomic DNA to facilitate the discovery of molecular tools for genome wide studies in *Gyrodactylus salaris*. Already the first sequencing phase covering only 1 % of the genome has yielded a good selection of nuclear markers that have been tested in different *G. salaris* strains and in some closely related species. The preliminary study provided many interesting findings about *Gyrodactylus* population biology and evolutionary genetics. This proves that even a very low coverage genome survey is an effective method to generate useful information about species currently lacking genomic sequence data.

ABSTRACT No. 2 – Session 4A

The motivation to conduct whole genome sequencing in *Gyrodactylus* (reasoned after first glimpse on the data)

Aisala, H. & Lumme, J.

Department of Biology, University of Oulu, P.O. Box 3000, 90014 University of Oulu, Finland

We have approached the biology of *Gyrodactylus* by utilizing two next generation sequencing methods, 454 (Roche) and SOLiD (Applied Biosystems), on a strain of *G. salaris* collected from a Karelian salmon stock in river Suna, Russia. Why? What do we expect to learn from it? The ready or next to ready genomes of flatworms include the important parasites *Schistosoma mansoni* and *S. japonicum*, *Echinococcus multilocularis* and *Fasciola hepatica.* The genome of free-living *Schmidtea mediterranea,* the model organism of tissue regeneration, will be published soon. In this framework, the monogenean *Gyrodactylus* is an interesting missing link. It is rather like a predator, freely moving and autonomously selecting her specific host. Thus, it needs a strict system to synchronize with and to recognize the host. We don't find many components of the circadian system. *Gyrodactylus* has no obvious eyes, yet many genes associated with optic systems in other organisms are present, among them the fundamental *Pax6*, perhaps inducing the protonephridium. Osmoregulation is one of the important aspects of their life in freshwater and marine environments, and there are indeed channels available for saving and wasting ions, and multiple proteins to store calcium and iron. The repertoire of putative chemosensory receptors is less wide than in *Schmidtea*, but wider than in passively transmitted *Echinococcus*. Two classes of digestive enzymes (*elastases*, *cathepsins*) are much expanded. A candidate family for the unique proteins for haptoral hooks has been found, called *hamulins*. The control of parthenogenesis and sexuality is very important in *Gyrodactylus*. We may not expect to find any 'key genes' for such purposes; yet three separate genes related to *gynecophoral canal protein* of *Schistosoma* have been detected, perhaps associated with the occasional male sexual functions of these hermaphrodites.

ABSTRACT No. 3 – Session 1B

Prevalence of Tick-born encephalitis virus (TBEV) in Southern Norway

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Tick-borne encephalitis (TBE) is a viral infection of the central nervous system caused by TBE virus (TBEV), a member of the Flaviviridae. TBE is endemic in many European countries, and the prevalence has increased over the past three decades in Europe. In Norway, the annual number of reported cases of TBE has increased during the last ten years (MSIS). The knowledge of distribution and prevalence of TBEV in ticks in Norway is limited to one study area where it was estimated to be 0.2-0.3 %. The aim of this study was to estimate the distribution and prevalence of TBEV along the southern coast of South Norway. We wanted to compare prevalence between the different areas to see whether these corresponded with the Norwegian government advices for vaccination against TBE.

The ticks were collected at different locations according to registrations of human cases of TBE in MSIS. The ticks were pooled in groups of ten. A positive patient sample was used as a positive control in each PCR assay. Two methods were used, one real-time PCR designed for this study, and one nested PCR. All positive pools were verified by sequencing. In total 5630 ticks, all nymphs, from seven different locations, were collected during June 2009. The MIR of TBEV in pools were 5.15% (29/563) by real-time PCR and 15 of 29 (52%) were verified. The real-time PCR detected 10^{-6} dilution of the standard ($5x10^4$ copies/ul), and appeared to be ten times more sensitive when compared to the nested PCR. The prevalence of TBEV in tick pools varied from 1.1-12% between the different locations. The rate of TBEV in tick pools in Norway has increased from 2.0-3.0% in 2003/2004 to 5.15% in 2009. We detected TBEV in tick pools from all seven locations by real-time PCR with large variations. This indicates that TBEV is distributed over a larger area in Norway than previously suspected. The real-time PCR assay designed for this study was shown to be a suitable method for rapid screening of tick pools.

ABSTRACT No. 4 – Session 1A

Mining natural history collections for gyrodactylid flatworms

Bachmann, L., Zeyl, E. & Harris, P.D.

Natural History Museum, University of Oslo, 0318 Oslo, Norway

The biodiversity of invertebrate parasites is an important factor in ecosystem health. Gyrodactylid ectoparasites of fish and cephalopod molluscs include the relatively well known "salmon killer" *Gyrodactylus salaris* on Atlantic salmon and the emerging pathogen *Gyrodactylus marinus* on cod. Nevertheless, the biodiversity of the genus *Gyrodactylus* is poorly known and many species and parasite strains await proper description. When it comes to Norwegian gyrodactylids perhaps up to 50 species remain to be described and catalogued. Several species new to science can also be expected. We have just begun a project funded by The Norwegian Biodiversity Information Centre (www.artsdatabanken.no) aiming to develop a comprehensive picture of the Norwegian gyrodactylid fauna of both freshwater and marine fishes, predominantly using the museum fish collection as a resource. We plan to describe these parasites using advanced morphometric and molecular approaches.

Until now we have focused on estuarine and marine fish from various Norwegian sampling localities have been checked for parasites. Gyrodactylid parasites were found on almost all fish even those which have been in the collection for more than 100 years. We will present examples of gyrodactylids found during our survey for parasites. This includes gyrodactylids new to Norway but also some species that may turn out new to science.

ABSTRACT No. 5 – Session 4A

Susceptibility and resistance of Atlantic salmon *Salmo salar* L. to *Gyrodactylus salaris* infections: which molecules are involved?

Buchmann, K.

Section of Biomedicine, Faculty of Life Sciences, University of Copenhagen, Denmark

The devastating epidemics in Norwegian salmon rivers which followed the introduction of *Gyrodactylus salaris* Malmberg, 1957 paved the way for considerable research efforts within parasite taxonomy, ecology and pathology. It was indicated that East-Atlantic salmon, including the Norwegian salmon, possesses no effective response mechanism which can limit parasite population growth on its skin. In contrast, most strains of Baltic salmon tested showed a low susceptibility towards infection. These relatively resistant salmon types were able to limit growth of the parasite population on the skin a few weeks post-infection. The mechanisms behind these differential reaction patterns have been elucidated in several investigations. The first contact between host and parasite may include recognition of host molecules (including certain carbohydrate epitopes). The susceptibility/resistance pattern is seen following two to three weeks at which time the parasite numbers decrease on resistant salmon. Corticosteroids may interfere with the response which suggests that immune-related factors, at least partly, may be involved in this reaction. The relatively resistant fish do not respond with a fast expression of the pro-inflammatory cytokine IL-1 beta but rather with significant expression of genes expressing effector molecules, such as SAA (Serum Amyloid Protein A), MHCII, TCR and cytokines IL-10 and IFN-gamma during the response phase when the parasite population decrease. This response pattern suggests that cellular elements including macrophages and lymphocytes take part in the effective reactions against the parasite. SAA may bind to the parasite and interfere with various functions including feeding and food uptake. Complement activity may contribute to protection. The involvement of adaptive humoral elements such as antibodies is unclear. Up-regulation of IgM genes in the skin of resistant salmon has been observed during the response phase but Western blot analyses did not demonstrate binding of specific antibodies to *G. salaris* antigens.

ABSTRACT No. 6 – Session 2B

Echinococcus multilocularis surveillance in Norway

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Dogs and cats currently wishing to enter Norway from the European Union (including Sweden as of March 2011), with the exception of animals from Finland, the United Kingdom and Ireland, must be treated for the zoonotic tapeworm *Echinococcus multilocularis* (E.m.). Norwegian authorities were required by the EU to provide documentation to support this requirement for tapeworm treatment. So the Food Health Safety Authority commissioned the Norwegian Veterinary Institute (NVI) in Oslo to carry out a surveillance program in foxes (*Vulpes vulpes*) in 2006.

The aim of the program was to examine around 500 red foxes annually for this parasite. Frozen faecal material from foxes, that had been sampled at the NVI during 2002-2005, was also examined. The faecal samples from 2002-2005 were screened using a copro-ELISA at the University of Zürich, Switzerland, and those that tested copro-antigen positive were further examined using egg-isolation and multiplex-PCR. Sampling for the active surveillance program was carried out in the 2006-2007, 2007-2008, 2008-2009 and the 2010-2011 hunting seasons. The faecal samples were examined using the same egg-isolation and multiplex-PCR technique as had been carried out in Switzerland.

Since 2002, a total of 1840 red fox faecal samples have been examined. None of these have tested positive by PCR for *E. multilocularis*. Additionally 12 wolves, 2 racoon dogs and 2 dogs have also been examined during the same period (2002-2011) for this parasite with negative findings. These results therefore would seem to indicate that either *E. multilocularis* is absent from mainland Norway or is at such a low prevalence as to be undetectable with the sampling methods used. Continued annual surveillance will be necessary to ensure the absence of this zoonotic parasite from all regions of the country, especially given the recent findings in Sweden.

ABSTRACT No. 7– Session 4 B

An overview of anthelmintic resistance in Norwegian sheep and goat flocks

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Faecal egg count reduction test (FECRT) and larval culture for L_3 larvae identification from pooled faeces was performed in 28 sheep and 12 dairy goat flocks. All the flocks were randomly selected from either coastal, mountain or northern areas of Norway. In each flock, two groups of twelve animals each were treated with anthelmintics (Benzimidazole (BZ) or Macrocyclic lactones (ML)) and one group of twelve animals was used as untreated controls. In sheep flocks only lambs and in goat flocks only adult animals were included. The FECRT were successfully completed in 19 of the 28 sheep flocks and 4 out of 12 goat flocks. BZ resistant nematodes were detected in 2 of the 19 (10.5 %) sheep flocks. The flocks resistant to BZ were all located in the same county in the coastal area of south-western Norway. In addition, nematodes from two more sheep flocks showed a reduced susceptibility for BZ. Nematodes resistant to BZ were detected in one of the four goat flocks. In sheep, L_3 larvae of *Teladorsagia*/*Trichostrongylus* or *Haemonchus* were detected in the post-treatment samples from the groups with anthelmintic resistant nematodes. In the resistant goat flock only L_3 larvae of *Teladorsagia*/*Trichostrongylus* occurred in the post-treatment samples. This study indicates that anthelmintic resistant nematodes are present at a low level in small ruminant flocks in Norway. However, there are indications that some areas of Norway have a higher prevalence of anthelmintic resistant nematodes in sheep than recorded in the present study.

ABSTRACT No. 8 – Session 1B

The flea, the plague and friends (From the perspective of a microbiologist)

Easterday, W.R.

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The emergence and evolution of *Yersinia pestis* as a flea-borne pathogen has honed its genome to association with fleas, mammals and possibly other microbes found in the flea gut. This talk will be focused on the interaction between the flea life-cycle and strategy of *Y. pestis* to persist and the co-evolution of the flea, host and pathogen. Many of these strategies have been played out on the gene repertoire and immune system; we will look at some of these in detail to elucidate major trends we find within this co-evolution. Along with a guide of what not do while doing field work in foreign countries.

ABSTRACT No. 9 – Session 4 B

MicroRNA preparations from individual monogenean *Gyrodactylus salaris* – comparison of six commercially available “totalRNA” extraction kits

Fromm, B., Bachmann, L. & Harris, P.D.

Natural History Museum, University of Oslo, 0318 Oslo, Norway

MiRNAs are single-stranded, 22 nucleotide long, noncoding RNA transcripts derived from different genome-encoded hairpin precursors. They represent the most recently discovered gene regulators and regulate gene expression in many different ways. Therefore the expressed miRNA inventories of organisms attract particular attention. Application of next generation sequencing strategies is common but requires high yield extraction protocols that deliver RNA of high purity and quality. Samples should not only contain abundant ribosomal RNA species but also the miRNAs, i.e. real total RNA. This is of particular importance if only small amounts of material are available.

Gyrodactylus salaris is an important monogenean pathogen on Norwegian salmon, and just a small (500µm in length) parasite offering only very limited amounts of nucleic acids per individual. We compared the performance of six commercially available totalRNA extraction methods on 1, 10 and 100 *Gyrodactylus salaris* individuals.

The quality of the obtained RNA was assessed in terms of totalRNA yield, RNA integrity, small RNA and miRNA yield, and A260/280 ratio. The 6 RNA extraction methods that yielded considerably different total RNA extracts yield with striking differences in low molecular weight RNA recovery.
We will present an optimized picking and RNA extraction protocol for single *Gyrodactylus salaris* individuals from infected salmon (*Salmo salar*) delivering a yield of real total RNA suitable for downstream next generation sequencing analyses of miRNA.

ABSTRACT No. 10 – Session 3 B

Transmission patterns, phylogeny and historical biogeography of the "*pygmaeus*" microphallids (Digenea: Microphallidae): widespread parasites of marine and coastal birds in the Holarctic

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The "*pygmaeus*" microphallids (MPG) are a closely related group of six *Microphallus* species that share a two-host life cycle in which metacercariae develop inside daughter sporocysts in the intermediate host (intertidal and subtidal gastropods, mostly of the genus *Littorina*) and are infective to marine birds (ducks, gulls and sandpipers). In this study we investigated MPG transmission patterns in coastal ecosystems and their diversification with respect to historical events, host switching and host-parasite co-evolution. Species phylogenies and phylogeographic reconstructions are estimated based on 28S, ITS1 and ITS2 rDNA data and we use a combination of analyses to test the robustness and stability of the results, and the likelihood of alternative biogeographic scenarios.

Results demonstrate that speciation within the MPG was not associated with co-speciation with either the first intermediate or final hosts, but rather by host-switching events. Their radiation appears to have been coincident with the dramatic environmental changes in late Pliocene/Pleistocene, caused by glaciation cycles in the Northern Hemisphere. These resulted in the expansion of Pacific biota into the Arctic-North Atlantic, periodic isolation of Atlantic and Pacific populations of speciating MPG and their hosts, fragmentation of populations and species of parasites and hosts in regional refugia in stadials, and their subsequent range expansion from refugial centers in interstadials.

The study was supported by the grants of RFBR (10-04-00430), St. Petersburg State University (1.37.80.2011) and PIOF-GA-2009-252124 within the FP7/2007-2013.

ABSTRACT No. 11 – Plenary Monday morning

Prions – lessons learned from BSE and scrapie

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Transmissible spongiform encephalopathies have received considerable attention because of the huge BSE epidemic which affected more than 185 000 clinically and fatally diseased bovines. Roughly 3 million infected animals that were still in the preclinical state were slaughtered and entered the human food chain in the United Kingdom and elsewhere. Transmission of BSE prions to man has eventually caused a variant form of Creutzfeldt-Jakob disease in about 200 humans primarily in the UK, but also in France, Italy, Japan and elsewhere. As a preventive measure in the European Union the risk of human BSE exposure was minimized by BSE rapid testing of all cattle and by the removal of specified risk materials from slaughter cattle which are considered to possibly contain BSE infectivity in incubating animals. During the BSE epidemic, bovines were most likely infected by the oral uptake of infectious feed. However, although several approaches addressing the pathogenesis of BSE have been undertaken, the route and time course of the infectious agent from the gastrointestinal tract (GIT) to the central nervous system (CNS) was an enigma for a long time.

To elucidate this pathogenesis, we have carried out an oral BSE challenge and sequential kill study on 56 calves (plus 18 control animals). Relevant tissues belonging to the peripheral and central nervous system as well as to the lymphoreticular tract from necropsied animals were analysed by highly sensitive immunohistochemistry and immunoblotting techniques to reveal the presence of BSE associated pathological prion protein (PrP^{Sc}) depositions. Our results demonstrate three routes involving the spinal cord as well as the autonomic nervous system through which BSE prions spread by anterograde pathways from the gastrointestinal tract (GIT) to the central nervous system (CNS): a) via the Ganglion coeliacum and mesentericum caudale complex, splanchnic nerves and the lumbal/caudal thoracic spinal cord (representing the sympathetic GIT innervation) and b) via the Nervus vagus (parasympathetic GIT inervation). The dorsal root ganglia seem to be subsequently affected. Therefore it is likely that the BSE prion invasion of the non-autonomic peripheral nervous system (e.g. sciatic nerve) is a secondary retrograde event following the prion replication in the CNS. Moreover, BSE associated PrP^{Sc} was already detected in the brainstem of an animal 24 months post infection. These findings are important for the understanding of the BSE pathogenesis and for the development of new diagnostic strategies for this infectious disease.

Classical scrapie (first described around 1732) occurs as a “natural” infection in sheep and goats. Clinical cases have been reported from most countries worldwide. The introduction of a surveillance program has resulted in a massive increase of notified TSE cases in small ruminants throughout Europe. In sheep, the majority of classical scrapie cases was observed in genotype categories considered moderately to highly susceptible to classical scrapie. These genotypes were targeted in the selective culling and breeding-for-resistance programs throughout the EU, and the further reduction of these genotypes intends to significantly reduce the future scrapie incidence. However, in 2003, for the first time a number of sheep with an atypical form of small ruminant TSE with special clinical, histological, immunohistochemical and rapid test properties were described by Norway researchers, terming these isolates Nor98. The intensified epidemiosurveillance after 2002 revealed a high number of similar atypical scrapie cases in almost all European countries.

ABSTRACT No. 12 – Session 3 A

Museomics of ectoparasites – chasing the origin of *Gyrodactylus salaris*

Hahn, C., Zeyl, E., Bakke, T.A., Harris, P.D. & Bachmann, L.

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Gyrodactylus v. Nordmann, 1832 (Platyhelminthes; Monogenea) is a genus of viviparous ectoparasites infecting teleost fish species throughout the world, but the ~450 described species are expected to only represent about 2% of the worldwide diversity. The salmon killer *Gyrodactylus salaris* is a major pathogen of Atlantic salmon (*Salmo salar*) in Norway which, apart from its economic importance, has imposed significant ecological burdens upon freshwater ecosystems. *G. salaris* may have evolved by a host shift from the related *G. thymalli* on grayling. Despite extensive research neither morphological nor molecular analyses have yet unambiguously identified the origin of the host shift. Salmonids are, due to the nature of their habitats, highly affected by geographical fragmentation, causing isolation and rather complex phylogenetic patterns. To reconcile the host patterns with the complex *Gyrodactylus* phylogenies and to disentangle host-switches from co-evolutionary events is an ambitious task, particularly as human impacts caused regional extinction of former abundant freshwater fish species. The impact of stocking on autochtonous fish populations is also an important issue in conservation biology.

Historical changes in fish diversity are well documented in ichtyological collections, but so far very few attempts have been made to explore the ectoparasites unwittingly collected together with their hosts. We apply museomics approaches to add a temporal dimension to the understanding of the current distribution of *Gyrodactylus salaris* and *G. thymalli* in European watercourses. Until now gyrodactylids could be identified from fish material from the Natural History Museums Vienna (Austria), Paris (France) and Oslo (Norway) including parasites from historical fish collected in the late 19th century. Most of the recovered parasites still allow for morphological species identification, e.g., *Gyrodactylus* specimens from salmon collected in 1876 and grayling in 1880 were identified as *G. derjavinoides* and *G. thymalli*, respectively. Furthermore, we have successfully amplified and sequenced the intergenic spacers of the nuclear ribosomal gene cluster and the mitochondrial cytochrome oxidase I gene from this material.

ABSTRACT No. 13 – Session 1 A

Introduction to morphometrics with Past

Hammer, Ø.

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Morphometrics is the quantitative study of variation in continuous characters. The tools of morphometrics are indispensable for investigating e.g. ontogeny and ecophenotypy, but also for taxonomy and systematics, especially in combination with genetic information. I will give a short, practical introduction to both classical and modern (geometric) morphometrics, with emphasis on visualization methods. Key concepts include data collection, landmarks, outlines, Procrustes fitting, thin-plate splines, Fourier analysis, PCA, MANOVA, discriminant analysis and regression. In the demonstrations I will use the free software package "Past", developed at the Natural History Museum in Oslo, but the techniques are common to all morphometric packages, including available modules in R.

ABSTRACT No. 14 – Session 1A

Prospects for species discovery in parasite groups

Harris, P.D.

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Although the distribution and diversity of some groups (plants, butterflies, birds) is extraordinarily well known, most parasitic organisms fall into ‘poorly known groups’ where discovery of species new to science remains a strong possibility. Parasitology began in Europe, but there remain lacunae in our knowledge where a modest investment in research can yield a big return. We have heard about a number of such groups – plant parasitic nematodes, myxosporea and monogeneans offer great opportunities for species discovery. What of others? The Acari represent the biggest gap in knowledge. Literature is rudimentary, fragmented and much dates from the soviet era and remains inaccessible in the west. The animals themselves are cryptic, rare and discovered accidentally. The situation with Acari is so severe that family level groups were omitted from Fauna Europea. The other great lacuna lies with the parasites of invertebrates, especially of marine invertebrates, with groups such as orthonectids or mesozoans known mainly from pictures. Finally, the age of some taxonomic descriptions (from the late 18th Century) makes assignation difficult, and the taxonomist must be more historian than scientist. Many important collections have been destroyed (especially Berlin and Konigsberg) and old soviet material is fragmented and possibly threatened. There is a case for ‘rescue taxonomy’, ensuring the preservation of key collections, specimens and literature before they are irretrievably lost.

ABSTRACT No. 15 – Session 2 A

Use of bacterial infected nematodes to combat insects and slugs

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Nematodes associated with bacteria have life cycles that can be useful for controlling invertebrate pest species. Several species of one particular group of nematodes, Entomopathogenic nematodes (*Steinernema* & *Heterorhabditis* spp.), and a slug parasitic species (*Phasmarhabditis* spp.) have been commercialized for this purpose. Entomopathogenic nematodes are mutualistically associated with specific bacteria, a unique association whereby bacterial cells, never found free in soil, are carried by the free-living nematode infective stage into an insect host. Inside the host, bacteria are released by the nematodes and start the process of septicaemia and host death. The bacteria also produce toxins and antibiotic substances ensuring favourable conditions for nematode and bacterial reproduction. When resources are depleted a new generation of free-living infective juveniles leaves the host cadaver carrying bacterial cells in their intestine ready for the next round of infection.

The slug parasitic nematodes are facultative parasites and are associated with several bacterial species. These nematodes have 3 possible life cycles, saprobic, parasitic and necromantic. The parasitic life cycle is somewhat similar to that described for entomopathogenic nematodes, but involves more than one bacterial species. The necromenic life-cycle is often observed in large slugs where nematodes are present as infective juveniles usually in the shell cavity having no (obvious) effect on the slug. Once the slug dies naturally the nematodes and bacteria recover and reproduce on the slug cadaver. The mechanisms regulating pathogenicity (necromantic or parasitic life-cycle) are not understood. Saprobic life-cycles have been observed in laboratory studies only, but are likely to occur in nature due to the ability of the nematodes to feed on a wide range of bacteria.

ABSTRACT No. 16 – Session 2 A

Modelling the effects of temperature on *Gyrodactylus salaris* on Atlantic salmon in Norway

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The parasite *Gyrodactylus salaris* (Platyhelminthes: Monogenea) was introduced to Norway 30-40 years ago, and since then, local populations of wild salmon (*Salmo salar*) in affected rivers have declined considerably. Atlantic salmon populations seemingly have little resistance against the parasite and many juvenile fish in affected rivers die as a result of the infection.

The population dynamics of *G. salaris* parasites is influenced by a variety of environmental factors. For example, water temperature has been shown to strongly influence the survival and reproduction of *G.salaris* under experimental conditions. Spatial and temporal variations in water temperature in different salmon rivers may consequently affect the interspecific interactions between, and long term population dynamics of *G. salaris* and salmon, as well as potentially influencing their interactions with other fishes in the river ecosystem, such as the brown trout (*Salmo trutta*) and trout-x-salmon hybrids.

Here, we present ongoing work on modelling the population dynamics of salmon and *G. salaris* in relation to seasonal variations in water temperature. We also discuss how the combination of environmental variation and ecosystem interactions may jointly influence population dynamics of the salmon in *G. salaris* affected rivers.

ABSTRACT No. 17 – Session 4 A

Uniform evolution rate in mitochondrial *CO1*-gene in *Gyrodactylus*

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Parasite speciation by adaptation to new hosts and new habitats depends on genetic modifications of key factors. In the case of *Gyrodactylus,* the genetic factors presumably under strong selection after host switch deal with host recognition, digestion and toleration of host antigens, as well as those adaptive in the temperature, oxygen pressure, salinity or pH of the new environment. In this study we have concentrated on variation found in the mitochondrial *cytochrome c oxidase subunit 1* -gene, which has a key role in aerobic metabolism. Our study material consists of several species of *Gyrodactylus* hosted by Eurasian minnow, whitefish, sticklebacks, Northern pike and by salmonids like Atlantic salmon, brown trout and rainbow trout. Analysis of the mitochondrial *CO1* suggests that allopatric differentiation (up to speciation) in geographically isolated populations on the same host has maintained a high and uniform level of purifying selection. On the contrary, the phylogenetic lineages which have switched to new hosts, have in several cases evolved *slightly more* also with respect of protein sequence, even if the signal of purifying selection is the main message from the sequence comparison. The PAML-analysis of the d_N/d_S ratios shows similar results for the selection. The host switch may be effectively associated with e.g. the oxygen saturation level (pike vs. salmon), and thus it might affect the mitochondrial genes. However, the selection signal was weak, and the mtDNA seems to serve well as a calibration for the rate of evolution in other genes.

ABSTRACT No. 18 – Session 2 B

Ecological analysis of occurrence of *Brachylecithum glareoli* in bank voles *Myodes glareolus*

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Brachylecithum glareoli Hildebrand et al. 2007 is a recently described member of the genus *Brachylecithum* Shtrom, 1940, one of the most species rich genera of the Dicrocoeliidae, which includes many bird parasites. Small mammals are hosts to a few species only. Besides *B. glareoli,* the species found in Palaearctic rodents were *B. rodentini* Agapova, 1955, described from gray-sided voles and *B. eliomydis* Jourdane & Mas-Coma, 1977 from dormouse. In the present study we have made an attempt to describe the pattern of occurrence of *B. glareoli* and associations with other helminths within the population of rodents in the context of intrinsic and extrinsic factors. Our investigation was carried out in three ecologically similar sites for eight years. Overall 863 individuals belonging to 7 species were examined. Aside from two accidental cases *B. glareoli* was reported only in bank voles collected from one site. The prevalence of *B. glareoli* was 16.7% and there was no statistically significant differences in relation to host sex and year of study. But a strong seasonal effect was observed, the prevalence of *B. glareoli* being three times higher in autumn (36.7%) than in summer (11.8%) while during the spring no voles were found infected with this parasite. Additionally we observed that in rodents infected with *B. glareoli* mean helminth species richness (1,95) was almost 1,5 times higher than in voles uninfected with this trematode (1,35). Since the information on the life cycles of dicrocoeliids are scarce our results may be a contribution to knowledge of biology of this group.

Study is supported by Polish Ministry of Science and Higher Education grant N303580939.

ABSTRACT No. 19 – Session 3 A

Cyst nematodes on grasses in Norway

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Cyst nematodes, *Heterodera* spp. are known world-wide as parasites of cereals and grasses. Norwegian surveys have revealed that nematodes belonging to the *H. avenae* complex occur throughout the country; our studies have combined morphology, protein variability (IEF), bio-tests and internal transcribed spacer sequences for the species identification of *Heterodera* populations. Our results showed some divergences in species identity between techniques. In Norway *H. avenae* is the most common species followed by *H. filipjevi* (Holgado *et al.,* 2009). Several populations identified by ITS as *H. filipjevi* did not reproduce in oat differentials. In this case the morphology and protein patterns were indicative of *H. pratensis*. A population from Brekstad was close to *H. mani* in morphology and protein pattern, while ITS studies indicated *H. avenae*. It seems urgent to revise the current *H. avenae* gene library. The least degree of divergent results on species identity was between morphology and IEF, which indicates the importance of combining several techniques in species identification. Observed variations in morphology and host preferences suggest a potentially high diversity of cyst nematode species on grass in Norway. Studies on the occurrence of cyst nematodes in natural habitats could add important information on below ground biodiversity.

ABSTRACT No. 20 – Session 2 B

Farmed wild boar are exposed to *Toxoplasma gondii* and *Trichinella* spp. in Finland

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Undercooked meat of wild boar (*Sus scrofa* L.) can be a source of human infections with zoonotic parasites *Toxoplasma gondii* and *Trichinella* spp. The aim of our study was to estimate the exposure of Finnish farmed wild boar population to these parasites. We screened 197 farmed wild boar sera, collected from 25 Finnish farms in 2007-2008, for serological evidence of *T. gondii* and *Trichinella* spp. infections. We used a direct agglutination test at dilution 1:40 and detected *T. gondii*-specific IgG antibodies in 65 (33.0%) of the samples. Four (2.0%) of the wild boar tested *Trichinella* seropositive with an in-house enzyme-linked immunosorbent assay with a conservative cut-off for seropositivity. No animals had a mixed infection with the two parasites. Taken together, 69 (35.0%) of the 197 farmed wild boar raised and used for human consumption showed specific serological evidence of exposure to a zoonotic parasite. Reduction of exposure of farmed wild boar to these parasites is possible and has food safety in addition to animal health and welfare implications. The results of this study emphasise that preventive measures are also needed: currently, Finnish farmed wild boar are commonly exposed to zoonotic parasites.

ABSTRACT No. 21 – Session 3 B

Parasites as markers and tracers of the populations of aquatic birds in France and Iceland

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A parasitic control of various potential hosts (aquatic birds) under natural conditions in France and Iceland enabled us to highlight different parasites belonging to the avian schistosome group. The nasal parasite *Trichobilharzia regenti* was found under natural conditions in 6 species of water birds: Mallard (*Anas platyrhynchos*), Mute swan (*Cygnus olor*), Tufted duck (*Aythya fuligula*), Pochard (*Aythya ferina*), Goosander (*Mergus merganser*) and Greylag goose (*Anser anser*). In spite of the confirmation of these parasites as *T. regenti* by molecular analysis of eggs and adults, we would highlight the presence of morphological variations for this parasite under natural conditions compared to species described under experimental conditions by Horák et al. in 1998. By a molecular approach, we also clarified the situation of a visceral species, *Trichobilharzia franki* Müller and Kimmig, 1994, showing the presence of two clades depending on the specificity of the parasites for their intermediate hosts, thus allowing us to separate the parasites belonging to the previously described species *T. franki*, from another probable new species. Finally, we have started evaluating parasites as markers or tracers of migrating and sedentary final hosts (birds), by studying parasite of the family Notocotylidea isolated from aquatic birds in different regions of the Palaearctic.

ABSTRACT No. 22 – Session 1 A

Marine Myxosporea (Myxozoa) in Scandinavian waters: An update

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Myxosporea (phylum Myxozoa) are metazoan but microscopic parasites that usually infect aquatic vertebrates and annelids. Few marine life cycles have been elucidated, these involve a fish and a polychaete worm. Life cycles involve asexual proliferation and sporogony in the fish resulting in the production of myxospores, infective for the annelid. In the annelid a second cycle of sporogony culminates in the production of actinospores, which are infective for the fish host. Myxosporean species descriptions have been recommended to be based on the myxosporean stage, which is the basis for the current classifications. These classifications do not reflect phylogeny (e.g. rDNA), and many genera are polyphyletic. There are few characters in the myxosporean spores, and dimensions, on which species identification often relies, may vary both within and between host species. Together with poor species descriptions and differing methodology, this has caused much taxonomic confusion.
It is therefore important to redescribe many 'old' species from type hosts in type localities, and include DNA sequences. Scandinavian coastal waters contain type localities for several species, including types of genera. The known diversity, life cycles, and problems faced in the revision of this group are presented.

ABSTRACT No. 23 – Session 3 A

Haemoproteids (Haemosporida, Haemoproteidae) of doves (Columbidae) belong to *Haemoproteus* and *Parahaemoproteus* subgenera: call for vector studies

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Taxonomy and systematics of protists have never been easy issues. Over the last twenty years, fast development of molecular techniques has revealed much unexpected diversity of these organisms. *Haemoproteus* is a largest genus of avian haemosporidian parasites including a large number of described species. Following widely accepted subgeneric classification of malaria parasites of mammals and birds, Levine and Campbell (1971) suggested a subgeneric classification of avian haemoproteids. They attributed subgeneric status to two formerly described genera *Parahaemoproteus* and *Haemoproteus.* Avian haemoproteids, which are transmitted by hippoboscid flies (Hippoboscidae), were placed in the subgenus *Haemoproteus* (parasites of columbiform birds exclusively) and haemoproteids transmitted by biting midges (Ceratopagonidae) – in the subgenus *Parahaemoproteus.* In our study we applied microscopy and PCR based protocols and used sequences of 5 species, which formerly were attributed to the subgenus *Haemoproteus*. Our study shows that the majority of *Parahaemoproteus* and *Haemoproteus* species might be distinguished due to their position on phylogenetic trees which are constructed using mitochondrial gene sequences. Constructed phylogeny showed that *H. turtur* and *H. sacharovi*, common parasites of doves, are placed in subgenus *Parahaemoproteus*, the parasites being transmitted by biting midges. The presence of two species of haemoproteids from columbiform birds, which are readily distinguishable by gametocyte morphology, within the clade of *Parahaemoproteus* species indicates that these species can also be transmitted by biting midges too. This study shows that subgenera *Haemoproteus* and *Parahaemoproteus* are probably monophyletic and subgeneric classification of avian haemoproteids is worth using, but the position of some species in certain subgenera need clarification. Lack of vector information on the majority of species of avian haemoproteids is an obstacle for taxonomy and ecology research.

ABSTRACT No. 24 – Session 4 B

Simple survival assay for determining environmental and chemical effects on *Eimeria bovis*

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Eimeria oocysts can survive in the environment under various stresses and most disinfectants meant to control new infections. The gold standard for testing whether oocysts are alive is by reinfecting animals with treated oocysts, but a simpler and faster method would allow testing of control measures prior to animal trials. Here such a method is described, and used in a pilot study on the survival of *E. bovis* afterultra violet (UV) light and formaldehyde (FORM) treatment. The control (N=9), UV (N=5), and FORM (N=3) groups were 40 µl sporulated *E. bovis* oocysts in phosphate buffered saline pretreated with: nothing, 64 mWs/cm^2 295 nm UV light, or 10 minutes in 30% FORM, respectively. Fluorescent dyes 4',6-diamidino-2-phenylindole (DAPI) and Acridine Orange (AO) were then added to a final concentration of 0.005% and 0.2 mM respectively. After adding a cover glass, the oocysts were mechanically opened by lowering the microscope ocular on the glass. The samples were incubated for 10 minutes before reading with DAPI and FITC filters in a fluorescent microscope. A minimum of 50 sporocysts were counted in 5 different areas per sample. Sporocysts showing positive stainings for both DAPI and AO were considered living sporocysts. After both UV ($p=0.001$) and FORM treatment ($p<0.001$), less living sporocysts were seen compared with the control. This method may serve as a tool for testing the effect of chemical control on *Eimeria*, and could be adapted to study oocysts survival in the environment.

Thanks to Berit Bangoura, University of Leipzig, Germany for providing fresh oocysts for the experiment, and Estonian funding from Project 8-2/T9001VLVL and SF0170165s08.

ABSTRACT No. 25 – Session 4 B

Haptoglobin levels in blood from calves in response to experimental infections with *Eimeria zuernii*

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Eimeria zuernii is a parasite causing disease (coccidiosis) in calves often observed as diarrhoea. Haptoglobin (Hp) is an acute phase protein that can be use as an indicator of calves' systemic inflammatory response. In this study we tested whether there was a rise in Hp in blood from the time of an experimental infection with *E. zuernii*'s to the end of the patent period Calves (10 days to 4 weeks old) were divided into groups according to infection dose of *E. zuernii*: control group 0 (n=13), group 1 (n=11) 150 000 oocysts, and group 2 (n=13) 250 000 oocysts. Blood and faecal samples were collected on days: -1, 0, 1, 3, 7, 9, 12, and 14-28. The Hp data was calculated for the periods: -1 to 17th days (I, prepatent period) and 18-28th days (II, patent period) respectively. The area under the curve (AUC) were calculated for each calf for both periods and adjusted for days in the period. Differences between the groups were compared using a t-test. In the patent period there was a tendency for higher Hp production in group 2 compared with the control (p=0.06). There may be an association between Hp production and the shedding of *E. zuernii* oocysts following a single high infection indicating activation of the calves´ systemic inflammatory reaction. However, further experiments with larger group sizes will be needed.

ABSTRACT No. 26 – Session 4 B

Life history and virulence are linked in an ectoparasite, the salmon louse *Lepeophtheirus salmonis*

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A vast majority of models of virulence evolution are based on the assumption that virulence and transmission are linked by a genetic trade-off. For certain shapes of such trade-offs, models predict the evolution of an intermediate optimal level of virulence that can be modulated by ecological factors, such as parasite independent mortality, host population density and the rate of multiple infections (Alizon et al. 2009. *Journal of Evolutionary Biology* 22, 245-259). However, empirical support for a relationship between parasite transmission and virulence is scant and mostly limited to microparasites. In this study we explored the relationship between parasite age at reproduction, fecundity (as a proxy for transmission) and disease severity (virulence), using the salmon louse, *Lepeophtheirus salmonis*, a crustacean copepod ectoparasitic on Atlantic salmon *Salmo salar* L. Repeated measures on fish maintained separately in laboratory conditions allowed us to quantify disease severity both as the direct effects of lice on their hosts (skin damage) and as the indirect costs of infection in terms of fish growth. We found that earlier onset of reproduction is associated with higher fecundity in individual lice. Higher average fecundity of lice was not significantly related to skin damage on the fish, which decreased over the course of the experiment due to the host's immune defence but was however associated with lower specific weight gain of the fish. This result is particularly relevant in the context of increasing intensive salmon farming, where frequent drug use, increasing host population size and density may have selected for faster production of transmission stages – and hence earlier reproduction and increased early fecundity of salmon lice (Mennerat at al. 2010. *Evolutionary Biology* 37, 59-67). Salmon lice therefore appear as a good model for studying how human activity may affect the evolution of parasite virulence.

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ABSTRACT No. 27 – Session 4 B

Immunisation impairs cognitive and neural development in fish

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Vertebrates are equipped with complex and highly sophisticated immune and neural systems, both considered costly in terms of energy and material requirements. Since resources are not unlimited, we might therefore expect a conflict between these two systems, and while both are important for survival, we expect them to operate on different time scales. While neural development and cognition is a prerequisite for developing several behavioural traits important through life, functioning immune-responses gives immediate, short-term benefits in the presence of potential lethal pathogens. We suggest that in a potential conflict between immunity and cognitive development, the long-term benefits of cognition should be traded off against the short-term benefits of immunity.

In this study, juvenile Atlantic salmon (*Salmo salar L.*) were challenged with vaccines combined with environmental enrichment, known to stimulate cognitive development, and tested for spatial learning and memory skills in a maze.

We found that an up-regulated specific immune system was followed by a decreased expression of genes associated with synaptic plasticity and neuronal differentiation, and that this decrease was correlated with poorer performance in learning a novel, spatial task.

If a resource conflict between immune and neural systems is a general phenomenon within vertebrates, and if such a conflict leads to a down regulation of neural growth, this could have wide-ranging consequences both for current vaccination schedules and for our interpretation of the apparent variation in cognitive ability among human as well as animal populations.

ABSTRACT No. 28 – Session 3 B

Transmission patterns of seabird trematodes *Himasthla elongata* and *Cercaria parvicaudata* (*Renicola* sp.) in coastal communities of the White Sea

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Trematodes *Himasthla elongata* and *Cercaria parvicaudata* (*Renicola* sp.) are common and widespread parasites of marine and coastal birds of the White Sea. Both species use periwinkles (*Littorina* spp.) and blue mussels (*Mytilus edulis*) as the first and the second intermediate hosts correspondingly. Seasonal monitoring in selected intertidal sites in the Chupa Inlet (White Sea) in 1999-2008 showed that mature infrapopulations of *H. elongata* and *C. parvicaudata* parthenitae emitting cercariae occurred in populations of *Littorina saxatilis* and *L. obtusata* in May-October. Hence, the cercariae in coastal waters are especially abundant in the time period which is optimal for infection of mussels. During the cold season (November-April) production of cercariae by parthenitae is ceased and resumed during the next warm season. These data coincided with observed seasonal changes in metacercariae component populations in the blue mussel settlements. The metacercariae occur in mussels all year round but the highest values of mean abundance were recorded in July-September. During this season the White Sea intertidal is visited by gulls, marine ducks and shorebirds, which promote transmission of *H. elongata* and *C. parvicaudata*. Transmission success of cercariae *H. elongata* and *C. parvicaudata* was studied in a selected sheltered intertidal site. Our approach was based on comparison of numbers of cercariae of both species emitted during the period of our study (May-October) from infected periwinkles and the values of seasonal increase in numbers of metacercariae in the blue mussel settlement. Results showed that ca. 25% of *H. elongata* and ca. 47% of *C. parvicaudata* cercariae emitted from *Littorina* spp. during the warm season encysted in mussels. Such significant transmission success can be conditioned by high density of blue mussels (ca. 5500 individuals per sq. m) in the intertidal site and high water pumping activity of these bivalves.

ABSTRACT No. 29 – Session 2 A

Acidic aluminum reducing and eradicating infections of *Gyrodactylus salaris* (Monogenea: Gyrodactylidae) from Atlantic salmon (*Salmo salar*): treatment strategy and impact on population dynamics

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One of the main threats against populations of eastern Atlantic salmon (*Salmo salar*) is the monogenean ectoparasite *Gyrodactylus salaris*. Experiments during the late 1990s showed that acidic solutions of aluminium (Al) have the potential to reduce and remove infections of *Gyrodactylus salaris* from Atlantic salmon (Soleng *et al.* 1999. *Parasitology* 119, 19-25). Results from these laboratory experiments have led to the development of a method were acidic Al solutions are used in treatment of entire river systems in Norway. Today, the method is established, but still under development. The understanding of the mechanisms and effects of Al on *G. salaris* is crucial in this context. Additionally, varying levels of episodic and chronic acidification in salmon rivers also makes this knowledge relevant in a parasite population dynamics perspective. Here, we present the results from experiments focusing on numerical *G. salaris* infection responses to Al-exposure at different water temperatures. The results are interpreted in context of the potential mechanisms through which Al removes *G. salaris* from Atlantic salmon. It is argued that Al seem to have a direct effect on *G. salaris,* influencing the parasite through binding to its surface and disturbing physiological processes such as for example cross-tegument gas exchange.

ABSTRACT No. 30 – Session 2 B

The first findings of *Echinococcus multilocularis* in Sweden

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Echinococcus multilocularis is endemic in many parts of Europe and has been increasingly reported from countries near Sweden. Due to detection of the parasite in foxes in Denmark in 2000, a monitoring programme was initiated in Sweden. From 2000 to 2009, a total of 2 962 red foxes (*Vulpes vulpes*), 68 raccoon dogs (*Nyctereutes procyonoides*) and 35 wolves (*Canis lupus*) were screened for *Echinococcus* spp at the National Veterinary Institute (SVA). They were all negative. At examination of 304 foxes shot in 2010, the first case of *E. multilocularis* was found. After the positive finding in February 2011, 3 300 foxes were submitted by hunters to the National Veterinary Institute (SVA). This sample size is sufficient to detect a prevalence of 0.1% on a country basis, with approximately 95% confidence. In the south-western part of Sweden, hunters were requested to submit 10 foxes per municipality in 93 municipalities, whereas in other parts of Sweden, 4 foxes were requested from each of the remaining 197 municipalities. The intestines of the foxes were examined by the segmental sedimentation and counting technique. In the region where the infected fox had been shot, faecal samples from hunting dogs were collected and examined by egg flotation and PCR.

By May 31st 2011, intestines of 2 646 foxes have been examined and additionally three *E. multilocularis* infected foxes have been found. One originated from the same spot as the first positive fox but the other two had been shot 300 km and 400 km, respectively, north-east of this place. A total of 110 dog fecal samples were examined and they were negative for *Echinococcus* sp. In conclusion, *Echinococcus multilocularis* appears to be spread in Sweden although the prevalence is very low; it is estimated to be 0.1-0.2% in the fox population.

ABSTRACT No. 31 – Session 1 B

Bartonella infections in fleas; does prevalence reflect vector competence?

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Identification of vectors of *Bartonella*, the alpha proteobacterium responsible for significant human disease, has typically been *via* PCR amplification of *Bartonella* sequences from the presumed vector organism, and Koch's postulates have never been completely fulfilled; in only a few experiments has transmission been shown to occur in the presence of fleas, but not when they are absent. This study presents data from a 2-year field study of *Bartonella* epidemiology in woodland rodents in NE Poland. Form all of the captured and re-captured rodents blood samples and ectoparasites were collected for PCR analysis for *Bartonella* prevalence using citrate synthase (*gltA*) primers. Primers for a 340bp *gltA* fragment amplified poorly, but primers for 150bp fragment revealed prevalences of up to 100% in some months. Prevalence in fleas was weakly correlated with prevalence in rodents (r^2= 0.56 for *A. flavicollis*, 0.21 for *M. glareolus*). However, in all specimens tested, there was a strong reduction in the amplification signal using the largest *gltA* fragment (340bp) relative to an intermediate length (250bp) or a short fragment (150bp). This signal reduction was not due to preparation method (the ammonium technique), neither due to storage, and truncation of product was not noted with flea 18S rDNA (controlling for integrity of flea DNA), bacterial 16S rDNA (controlling for integrity of symbiotic bacteria apart from *Bartonella*), or mammalian cytB gene fragments (controlling for integrity of host DNA in gut contents). We conclude therefore that much of the *Bartonella* signal in natural populations of fleas comes from short, partially degraded DNA. It is possible that amplification from fleas greatly overestimates prevalance, and successful transmission is dependent on the parasites being passaged mechanically on the mouthparts of the insect vector.

ABSTRACT No. 32 – Session 3 B

Studies on chromosome sets and DNA sequences of *Phyllodistomum* spp. (Digenea): taxonomic and phylogenetic implications

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Considerable variation in life-history patterns occurs in closely related species within the genus *Phyllodistomum*. It was supposed that species with different cercarial anatomy, developing in different intermediate hosts, reflected distinct phylogenetic units. On the other hand, the use of cercariae as phylogenetic tools is questionable.

Chromosome sets and ITS2 and 28S RNA sequences of adult and larval stages of *Phyllodistomum* spp. and larval *Gorgogerina vitelliloba* were studied. Four different types of cercariae, obtained from bivalves of three families, were studied: microcercous *P. folium* sensu Sinitsin 1905 from Dreissenidae, macrocercous and macrocercous-cystocercous *Phyllodistomum* spp. and *G. vitelliloba* from Sphaeriidae and rhopalocercous *Cercaria duplicata* from Unionidae.

A high degree of similarity was noted between the karyotypes of *Phyllodistomum* spp. The same chromosome number, $2n = 18$, and close values of relative length of chromosomes were revealed for different species. Interspecific differences were observed in centromeric index values of corresponding chromosomes; such variation is most easily explained by pericentric inversions. From a karyological point of view the phyllodistomes studied form a phylogenetically closely related group. The karyotype of *G. vitelliloba*, $2n = 14$, differs more significantly.

Molecular phylogenetic trees all provided evidence that gorgoderines studied are monophyletic compared to the outgroups and can be divided into three well supported clades. The first comprised solely cystocercous species developing in sphaeriid clams. Intriguingly, *Gorgodera* and *Gorgoderina* spp. cluster with cystocercous *Phyllodistomum* spp. The second clade was made up of rhopalocercous cercariae from unionids, and the final clade contained microcercous *Phyllodistomum* from *D. polymorpha* and macrocercous cercariae from *Pisidium amnicum*.

In general, karyological and molecular markers revealed different patterns of differentiation of species within Gorgoderinae.

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ABSTRACT No. 33 – Session 3 A

Ultrastructure as an aid to understanding of the phylogenetic relationships of the Gyrocotylidea

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The phylogenetic relationships between monozoic Gyrocotylidea and other parasitic Platyhelminthes are analysed. Specimens of *Gyrocotyle urna* Wagener, 1852 were removed from the spiral valve of *Chimaera monstrosa* L. caught in the North Sea off Bergen, Norway. Ultrastructural investigations on *G. urna* have highlighted some ultrastructural characters which may be useful for phylogenetic analyses of the Gyrocotylidea. These include: laminate neodermal sclerites resembling the calcareous corpuscles of eucestodes; microthrix-like structures on the body surface; the similarity between the secretory glands of the posterior rosette of *G. urna* and those in the anterior attachment glands of monogeneans; the structural arrangement of the protonephridial terminal organ and the apical structures of protonephridial canal walls; the cellular nature of the protonephridial ducts in *Gyrocotyle*, monogeneans and trematodes; the similarity in the degree of division of the ovary and arrangement of associated ducts in *G. urna* and the basal monogenean genus *Chimaericola*; a common pattern in the relationships of the different cell components within the ovary of *Gyrocotyle*, monogeneans, trematodes and eucestodes; and the unique ultrastructural pattern of the uterus in *Gyrocotyle*. The above-mentioned features tend to support the opinion that the Gyrocotylidea are basal to Eucestoda, indicate an unrelatedness between Gyrocotylidea and Amphilinidea, and add weight to suggestions of a close relationship between Gyrocotylidea and Monogenea.

We greatly appreciate to Drs G. Bristow and H.E. Karlsen for help with the collection of gyrocotylids, to Drs W. Xylander, R. Kuchta and T. Scholz, co-authors of published papers. The present study is supported by the Russian Foundation for Basic Research project No. 09-04-00342a.

ABSTRACT No. 34 – Session 3 A

Investigations of *Sarcocystis* spp. in birds of the order Anseriformes

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The genus *Sarcocystis* are apicomplexan parasites with an obligatory prey-predator two-host life cycle. In the muscle tissues of the intermediate host asexual reproduction of sarcocysts occurs, and the sexual phase with formation of oocysts/sporocysts takes place in the small intestine of the definitive host. Birds may serve as intermediate or definitive hosts for many *Sarcocystis* species. Investigations of *Sarcocystis* in birds of the order Anseriformes are mainly restricted to prevalence of infection and morphology of sarcocysts. In the period of 2007-2011, muscle tissues of 3 barnacle geese (*Branta leucopsis*), 81 white-fronted geese (*Anser albifrons*) and 124 mallards (*Anas platyrhynchos*) were examined. Cysts of *Sarcocystis* spp. were investigated using light microscopy, transmission electron microscopy and DNA analysis (18S rDNA, 28S rDNA, ITS–1 region). Prevalence of infection was 30.7%. By light microscopy 3 types of microcysts and one type of macrocysts were determined. According to the ultrastucture and DNA analysis, macrocysts extracted from two mallards belongs to *S. rileyi*. This result is the first conclusive demonstration of *S. rileyi* in Europe. On the grounds of genetic and morphological studies *S. wobeseri* sp. nov. from the barnacle goose, which parasitizes in the mallard duck too, were described. *Sarcocystis* sp. (cyst type II) ex *Anas platyrhynchos* and *Sarcocystis* sp. (cyst type III) ex *Anser albifrons* are also characterized for the first time in detail and new specific species names would be proposed in the near future. In the phylogenetic tree constructed from data of 18S rRNA and 28S rRNA gene sequences, examined *Sarcocystis* species are grouped together with other *Sarcocystis* species parasitizing in birds.

ABSTRACT No. 35 – Session 3 B

Impacts of introduced predatory crayfish on parasites of native perch

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Introduced species form a threat to native biodiversity and function of ecosystems e.g. through predation, competition or habitat alteration. Introduced species may also affect native species by causing changes in their parasite burden. The simplest way by which introduced predatory species can have an impact on parasites, is consuming the hosts needed for the completion of parasite´s life cycle. We show that the native parasite fauna of perch, *Perca fluviatilis* L., is affected by the presence of introduced predatory crayfish species, *Pacifastacus leniusculus* Dana, in two large boreal lakes in Finland. In crayfish impacted areas, the mean abundance of trematode parasites transmitted from snails or mussels, as well as an acanthocephalan transmitted from aquatic isopod, was significantly reduced as compared to sites free from crayfish. However, no changes in the mean abundance of parasites transmitted from planktonic copepods were detected between the sites. Preliminary analyses from one of the lakes imply that the changes are associated with a marked decrease in the abundance of benthic invertebrates, especially snails, in crayfish impacted sites as compared to sites free from crayfish. Our data demonstrates that introduced predators can have profound effects on parasite composition of native species via predation on the invertebrate hosts of parasites. Thus, the indirect effects of species introductions can be more far-reaching than generally anticipated.

ABSTRACT No. 36 – Session 1 B

Human Health Problems and Zoonotic Diseases

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Zoonotic diseases spread from animals to humans and cause acute or severe health problems in humans. In most industrialized countries, traditional pets have become an integral part of modern life. These family pets not only bring happiness, psychological support and friendship, and reduce tension but they also act as a source of direct or indirect contact with viral, bacterial, fungal and parasitic infections and they also injured to protect themselves from bites and scratches. Those people who are more susceptible to pets due to their immune status including pregnant women, diabetics or allergic patients and young children should be discouraged from sharing their bed with their pets or regularly kissing their pets. Some common diseases are brucellosis, cat scratch fever and cat biting fever, psittacosis (bacterial) cryptococcosis (fungal), cryptosporidiosis, giardiasis, hookworm infection, roundworm infection, tapeworm infection and toxoplasmosis (parasitic).

Detailed clinical study and routine fecal examination of patients was done and complete history was taken through questionnaires. A proforma was provided to each family member of pet owners. The research was documented during 2009 in Karachi. A total of 450 pet owners were examined for diseases, including 150 males and 300 females of different age groups.

Result showed that cat scratch fever 35%, cat bite fever 20%, giardiasis 24%, round worm infection and toxoplasmosis was 10% each respectively. In case of infection, take proper personal hygiene, completing regular vaccination that will help lessen the chances of spreading these diseases.

(Chomel, B. B.and Sun, B Infectious emerging disease Volume 17, Number 2–February 2011;Overgaauw PA, van Zutphen L, Hoek D, Yaya FO, Roelfsema J, Pinelli E, et al Vet Parasitol. 2009;163:115–22; Low SC, Greenwood JE. J Med Microbiol. 2008;57:901–3)

ABSTRACT No. 37 – Session 2 A

Error estimation in gyrodactylid population studies

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Comparative studies of the performance of gyrodactylid monogeneans on different host species or strains, typically rely upon observation of growth on individual fishes maintained within a common garden environment. Performance is then typically summarized using maximum likelihood statistics – mean and estimate of variance based upon population growth on individual fish. We argue here that such measures are invalid and insensitive. The methodology is invalid because the assumption of independence of observations is violated; population size at time point $n+1$ is entirely dependent on population size at time point n. Maximum likelihood estimates based on a number of host replicates are also insensitive because of the magnitude of stochastic variation in reproduction and survivorship early in the infection (when population size is less than 10 worms per fish) and because they entirely mask the importance of genetic variation in hosts, which the studies are often designed to test in the first place. What is needed is a method of evaluating error in the performance of gyrodactylid populations on individual hosts. Here we present an agent-based simulation model of single infections based on described gyrodactylid life histories in order to examine the error structures of *Gyrodactylus salaris* infections on different salmonids.

ABSTRACT No. 38 – Plenary Monday afternoon

Museomics: developing schistosome collections and contributing to control

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Considerable opportunities are being provided by new and emerging molecular technologies for the study of parasites and their hosts. Higher molecular resolution and increased output promise to open up Museum collections in an unprecedented way. At the same time it is necessary to ensure that new field-derived collections are appropriate and suitable for future molecular analysis. In this talk, I will discuss developments in terms of molecular research associated with parasite collections, drawing on examples from schistosomiasis research in Africa, and highlight the importance of understanding parasite diversity in relation to control and elimination activities.

A new repository for schistosomiasis research is under development, and aims to incorporate the extensive collections of schistosome specimens held at the Natural History Museum into a new Molecular Collections Facility. Further development of the collections is planned with new material suitable for population genetic analysis and other molecular biological research. Participation in the Schistosomiasis Consortium of Operational Research and Evaluation (SCORE) will provide a unique opportunity to collect specimens and datasets and facilitate research on the effect that disease control programmes have on schistosome populations. The breadth of the SCORE programme will allow comparisons of parasites and snails collected from a number of African countries. Large-scale studies will identify infection prevalence of schistosomiasis in school-aged children and the impact of different control intervention strategies will be monitored. In Zanzibar, a new programme is being initiated to eliminate urinary schistosomiasis. Parasite samples submitted to the repository will provide an invaluable resource for retrospective analysis.

Sampling individual schistosome larval stages from endemic areas has enabled multi-loci molecular analysis of parasites directly from infected individual people or snails and is providing fresh insights into host-parasite interactions. For example, in West Africa, four species of *Schistosoma* are known to occur. *S. mansoni* and *S. haematobium* are common parasites of people while *S. bovis* and *S. curassoni* are associated with cattle, sheep and goats. Each parasite has a preference for development in particular species of *Bulinus* or *Biomphalaria*, freshwater snails commonly found across the sub-Saharan zone. The distribution of the schistosome species mirrors to some extent the distribution of the appropriate intermediate snail hosts. Following the construction of the Diama Dam in the Senegal River Basin major changes in the epidemiology of disease occurred, with initially high levels of intestinal schistosomiasis associated with the spread of *Biomphalaria pfeifferi*. The situation is extremely dynamic in that urinary schistosomiasis is now commonly observed and mixed infections of *S. mansoni* and *S. haematobium* are also common in school children in many areas. Concerns have been raised concerning the response of *S. mansoni* to treatment with praziquantel and further investigations are needed. In addition, new hybrid strains of schistosomes have been found in Senegalese children and livestock, resulting from introgressive hybridization between ruminant (*S. bovis* and *S. curassoni*) and human parasites. Analysis of new samples from other countries together with comparative material form the collections is now needed to confirm the extent and consequences of these parasite interactions across West Africa.

ABSTRACT No. 39 – Session 3 B

Parasitological and molecular investigations of snails for cercariae in Fars province, Iran

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A wide variety of animal Schistosomes can penetrate into human skin to create cercarial dermatitis or swimmers itch. One of these parasites in the Fars province, *Orientobilharzia* in animals, has been reported before. However, no study has so far been carried out on determining the host specificity of the snails and the rate of their infection. A study was made in order to investigate the snails and their infection to different cercariae in this province. A total of 2252 snails were collected from agriculture canals, rivers, swamps and drains in different regions of Fars province, with priority in the range of habitats of migratory birds. The locality of collected snails were determined by Global Positioning System (GPS).The snails were collected by hand and a handle paddle, transferred to the laboratory and investigated for cercariae using crushing method as well as shedding cercariae in light. The following snails were collected: *Melanopsis* (1735*), Physa acuta (*87) *Planorbis* (52) and *Lymnaea spp.* (378). Shedding method as well as crushing snails were applied for study of cercariae. Different morphological study using formalin-alcohol- Azocarmine and lactophenol (FAAL) as well as molecular techniques were applied. Of 2252 snails, one snail (0.04%) was infected with furcocercariae. Molecular studies revealed that this furcocercaria belongs to the family *Cyathocotylidae* with accession number of HQ219207.1. A total of 35 (1.6%) snails were infected with simple tailed cercariae. The infected snails were all *Melanopsis spp.* Their geographical distributions and their importance are discussed.

ABSTRACT No. 40– Plenary Tuesday morning

The origins of human malaria

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Until recently, very little has been known about the evolutionary history of the *Plasmodium* species infecting humans. The only known close relative of *P. falciparum* was (a single isolate of) *P. reichenowi*, from a chimpanzee. The consensus view has been that these two species co-diverged with the ancestors of their hosts, implying that humans (and their ancestors) have been infected with *P. falciparum* (and its ancestors) for at least 5-7 Myr. The closest known relatives of *P. vivax* have been found infecting monkeys in SE Asia. The consensus view has been that a human ancestor acquired *P. vivax*, perhaps around 2 Myr ago. However, alternative views exist. For *P. falciparum*, various lines of evidence have been taken to suggest that it is unlikely that it could have been maintained in human populations prior to the spread of agriculture, less than 10,000 years ago. For *P. vivax*, the near fixation of the Duffy negative mutation, conferring resistance to infection, in west and central Africa, is not simply consistent with an origin of the human parasite in SE Asia.

For the past decade, we have been conducting non-invasive sampling of wild African great apes, initially to trace the evolutionary origins of AIDS viruses. We have around 3,000 faecal samples from more than 50 field sites across central Africa. We have now detected *Plasmodium* DNA in these same samples. *Plasmodium* sequences were amplified from samples from three different subspecies of chimpanzee (*Pan troglodytes ellioti*, *P. t. troglodytes* and *P. t. schweinfurthii*) and from western gorillas (*Gorilla gorilla*), but no evidence of *Plasmodium* was found in samples from bonobos (*Pan paniscus*) or from eastern gorillas (*G. beringei*). Many samples show evidence of multiple infection.
Sequence data from three genomes (mitochondrial DNA, apicoplast DNA and nuclear DNA) are consistent in providing evidence of multiple previously unknown species of *Plasmodium* infecting chimpanzees and gorillas. Comparative analyses provide strong evidence that humans acquired *P. falciparum* from gorillas, comparatively recently, while African apes are also infected by parasites very closely related to *P. vivax*.

My colleagues in this work include: Beatrice H. Hahn and Weimin Liu (University of Alabama at Birmingham), Julian C. Rayner (Sanger Institute, Cambridge) and Martine Peeters (University of Montpellier I).

ABSTRACT No. 41 – Session 3 B

The avian schistosome fauna of Iceland and its biogeographical position

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Research on avian schistosomes started in Iceland in 1997 when maculopapular eruptions were noted on legs of children after wading in a shallow pond in Reykjavík. Studies were intensified when thousands of bathers developed swimmer's itch in a thermally heated area (the natural bathing site in Landmannalaugar) and in some oligotrophic lakes. So far, 15.191 *Radix peregra*, the only snail actually reported as intermediate host for ocellate furcocercariae in Iceland, have been examined; 213 (1.4%) shed these cercariae. Also, 160 water birds of the orders Gaviiformes, Podicipediformes and Anseriformes have been examined for the presence of nasal or visceral eggs and adults of avian schistosomes. Six schistosomes were detected in four anseriform birds; *Allobilharzia visceralis* in whooper swan *Cygnus cygnus*; *Trichobilharzia* sp., *T. regenti* and *Dendritobilharzia* sp. in grey-lag goose *Anser anser; T. regenti* and *T. franki* “form *peregra*” in mallards *Anas platyrhynchos* and *T. franki* “form *peregra*” and *Trichobilharzia* sp. in red-breasted merganser *Mergus serrator.* All are visceral species except *T. regenti* which is a nasal schistosome. For each species, except *A. visceralis* and *Dendritobilharzia* sp., larval stages and adults were isolated, thus confirming their complete parasitic life-cycle in Iceland. Morphological features were examined and all have been confirmed by a molecular approach, using markers as ITS, D2 and COX1. The seventh species detected in Iceland is a cercaria that seems to have a new position within the phylogenetic tree of bird schistosomes. In recent years, molecular systematic work has added several additional lineages to the list of bird schistosomes, especially from Europe and N-America. Attempt is made, in particular by the study of the various flyways of water birds, to explain those factors that determine the great diversity of the bird schistosome fauna of Iceland, an isolated island situated at the western limits of the Palaearctic.

ABSTRACT No. 42 – Session 4 B

Evolutionary effects of intensive farming on parasite life histories and virulence

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Intensive farming is one important aspect of human activity that might affect the evolution of parasites and pathogens. Farmed host populations are usually of high local densities, which could affect the transmission success of parasites. Moreover, such host populations are regularly treated with drugs, designed to either increase parasite mortality rate og reduce their fecundity. Intensive farming, therefore, substitutes an important alteration of the environment that most parasites are adapted to, and could therefore lead to evolutionary changes. Evolutionary theory suggests that both increased transmission opportunities and a lower life expectancy should select for a higher developmental rate and higher within-host growth. Such a life-history change could also lead to increased virulence. In this talk I will review any empirical evidence for the effects of intensive farming on parasite evolution, using examples from farmed mammals and fish farming.

ABSTRACT No. 43 – Session 2 B

Host-parasite dynamics in the terrestrial high Arctic ecosystem of Svalbard

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Svalbard is a high Arctic archipelago situated 600 km north of Norway and 500 km east of Greenland. The terrestrial ecosystem of the archipelago is characterised by a low number of resident host and parasite species. Only three terrestrial mammalian species have established themselves on the islands; the Svalbard reindeer (*Rangifer tarandus platyrhynchus*) , the Arctic fox (*Vulpes lagopus*), and the Sibling vole (*Microtus levis*). In addition, only one terrestrial bird species live year round on the islands; the Svalbard rock ptarmigan (*Lagopus muta hyperborea*), while a large number of migrating birds breed on the archipelago in the spring and summer months. I will present the result of 15 years of work on population dynamics of the mammalian species on Svalbard and how the climate, host population biology, trophic interactions, and parasite life histories determine the host-parasite population dynamics in the system. Focal parasite species will be cestodes using the Arctic fox as their main host, including *Echinococcus multilocularis*, and the gastrointestinal nematodes of the Svalbard reindeer.

ABSTRACT No. 44 – Session 1 B

Current situation of arthropod-borne disease in Iran

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Iran with different epidemiological and climatological characteristics has several arthropods which play an important role for disease agent transmission as well as nuisance. Malaria, with different types of *Plasmodium* is one of the most important diseases, transmitted by different *Anopheles* mosquitoes. Various types of leishmaniasis including cutaneaous, (ACL, ZCL) and visceral leishmaniasis are the main *Phlebotomus*-borne diseases in 50% of the provinces. The two important tick-borne diseases are; Crimean Congo Hemorrhagic Fever (CCHF) and tick-borne relapsing fever. Different flies cause myiais on humans and livestock. Stable fly, horsefly, black flies and fire ants bite people around their breeding places. There are several *Aedes* and *Culex* mosquito species which are the main nuisance and probable arbovirus vectors such as dengue, rift valley fever and West Nile. Papatasi fever has also been reported from some parts of the country where there is the vector and gerbil reservoir of ZCL. Nuisance caused by different species of fleas is reported for animals and humans. The plague agent may circulate among wild rodents in some parts of the country. Pediculosis and sarcoptosis are common among school children and populated communities. Bedbugs and cockroaches are the main pests in the urban areas. Scorpion and spider stings (latrodectism) are also a main concern of public health in tropical areas of the southern parts. Rove and blister beetles are considered the main causative insects for blister on the skin. Rodents are the main reservoir of some agents and host of ectoparasites.

Different methods for prevention and control are employed by the community and governmental authorities. These measure depend on the targets and include: environmental management, environmental sanitation, house design, health education, bed nets, screens, protective cloths, insect-repellent, tent-treated, vapor mats, coils ,dispenser, electric buzzer, traps, catching, Ultra Violet light (UV), proofing, physical method, polystyrene beads, biological control, chemical control, vaccination, drug treatment, site selection, ultra sonic device, chemoprophylaxis, bait, zoopyrophilaxy, collar, ear tags.

ABSTRACT No. 45 – Session 1 A

The use of geometric morphometrics in disentangling sources of shape/size variation in monogenean haptoral hard parts. Insights into modularity

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Among monogeneans (Platyhelminthes), haptoral hard parts provide prominent morphological characters upon which identifications are largely based. Traditionally, morphometric approaches are based on the use of arbitrary collections of linear distance measurements between landmarks. However, a significant proportion of diagnoses using such traditional approach do not maximize the amount of information available from morphological features, and traditional linear measurements mainly provide information on the size of haptoral hard parts but provide very little information on their shape. Given this prominent bias, I suggest the use of alternative methods in systematic parasitology that fully take into consideration the shape and size of morphological features. This presentation aims to both highlight the limitations that may arise when using traditional morphometric techniques and illustrate the use of geometric morphometrics in disentangling the specific sources of shape and size variation in monogenean haptoral hard parts. In addition, a move toward placing shape at the centre of species descriptions may provides new insights into the modularity of attachment organs that may be mutually beneficial for both taxonomists and non-taxonomists.

ABSTRACT No. 46 – Session 3 B

Pathology changes in gastrointestinal tract infected with *Neoechinorhynchus* spp. (Neoacanthocephala: Neoechinorhynchidae) in *Barbus capito* of Zarine-Roud River, Iran

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This study was undertaken to determine pathological changes in the gastrointestinal tract (GI) of *Barbus capito* due to *Neoechinorhynchus* spp. Over a one year period, a total of 89 fish (*B. capito*) were collected from the Zarrine-Roud River of Bokan, Iran. Intestines were removed and investigated for infection (Szalai and Dick, 1987; Vosughi and Mostajir, 1992). Histopathological sections were prepared and stained routinely with Hematoxylin & Eosin (H&E) (Sastry and Rao, 2001). Overall prevalence of infection was 16%. Histopathological findings indicated epithelial thickness and folding. Fibrinous enteritis with epithelial hyperplasia as a result of mechanical irritation was observed. In the lamina properia and mucosa of the intestine, the vessels were dilated and congested. In the mucosa folding sections, hyperemia and inflammatory cell infiltration including eosinophil, lymphocyte and fibrinous secretion were observed as well. These results illustrate the traumatic and irritating actions of *Neoechinorhynchus* spp. on the GI of *B. capito* and show that the *Neoechinorhynchus* spp. infection is relatively frequent in *B. capito* in the region.

ABSTRACT No. 47 – Session 3 A

The occurrence of larval form of cestodes in free living rodents from Lower Silesia (Poland)

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Rodents may play a role as intermediate or paratenic hosts for many species of cestodes, mainly from the families Taeniidae (*Taenia* sp. and *Echinococcus* sp.), Paruterinidae (*Cladotaenia* sp.) and Mesocestoididae (*Mesocestoides* sp.). During long-term (2001-2008) studies on the helminth fauna of rodents in Lower Silesia a total of 1068 individual hosts belonging to seven species were examined. The overall prevalence of infection with helminths amounted to 74.0% while the infection with larval forms of cestodes was observed in 10%. In our studies 5 species of metacestodes were identified, i.e. *Taenia taeniaeformis*, *T. martis*, *T. mustelae*, *C. globifera* and *Mesocestoides* sp. The morphometric identification of representatives of Taenidae and *Cladotaenia* sp. allowed us to determine metacestodes to the species level. The main features in this identification was the size and shape of hooks and cysts. In relation to *Mesocestoides* sp. the techniques of molecular biology was applied. The results showed that tetrathyridia found in rodents in Poland belong to *Mesocestoides litteratus*.

ABSTRACT No. 48 – Session 4 A

Detecting species hybrids in *Gyrodactylus* is possible by few molecular markers: nuclear ITS of rDNA and mitochondrial *cox1*

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Gyrodactylus species are very numerous and highly host specific. At least in some groups, evolution has led to speciation via host switching. A good example is the *G. wageneri* species group consisting of more than 25 molecularly identified species, including the infamous *G. salaris*. The evolutionary host switch should be based on genetic adaptation. A possible fast process enabling the genomic reorganization is hybridization. An example of an ‘ancient’ case of hybridization is the suggested creation of Atlantic salmon specific strain of *G. salaris* by crossing of grayling specific strains some hundred thousand years ago. Illustrative ‘modern’ cases are associated with rainbow trout farming. (1) *G. pomeraniae* x *G. lavareti* hybrid is a clone specific for rainbow trout created by crossing of two species – one from roach (*Rutilus*) and the other from whitefish (*Coregonus*). (2) An unknown *G. sp.* x *G. salaris* hybrid with alien 'non-salaris' mitochondria has been found on rainbow trout in Denmark, Poland and Macedonia. (3) A good complementation to the story is an assemblage of four *pannonicus*-like species parasitizing the Eurasian minnow (*Phoxinus*). The four species are allopatric, but hybrids between two of them were found in the less than 8400 years old postglacial contact zone of the Baltic and White Sea basins, in northern Finland. The hybrids were evidently sexual to some degree, but the mixed population was still not panmictic.

3.2. Submitted abstracts for poster presentation

POSTER No. 1

The G protein-coupled receptor repertoires in sequenced Flatworm genomes

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The G protein-coupled receptors (GPCRs) are transmembrane proteins that constitute a large and diverse superfamily in eukaryotes. Different receptors are involved in various types of signalling pathways triggered by ions, hormones, odorants, amines, peptides, proteins, and other types of ligands. Being acoelomates, flatworms lack the capacity of endocrine signalling and must rely entirely on the nervous system to control essential physiological functions. Thus, many important adaptations should be regulated by GPCRs expressed in specialised neurons, and the receptor repertoires should correlate with different life histories and niches. We took advantage of the available genomic data to identify the GPCR genes in the parasitic flatworms *Schistosoma mansoni, S. japonicum, Echinococcus multilocularis* and *Gyrodactylus salaris* as well as in the free-living *Schmidtea mediterranea*. All genomes contained sequences belonging to each of the major GPCR classes: *Glutamate, Rhodopsin, Adhesion, Frizzled* and *Secretin*. However, the receptor repertoires in parasitic species were remarkably different from that of the free-living *Schmidtea*. There were also numerous novel genes that didn't have any sequence similarities to known receptor proteins. These include also the potential flatworm chemosensory receptors that may have an important role in adaptation to different environments and, in parasitic species, orientation to host.

POSTER No. 2

Infestation rate of sheep and goats with ticks during winter 2011 in Jiroft of Kerman propvince, Iran

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Ticks play a significant role as a vector of pathogens of domestic animals and they are considered as the main vectors for transmission of various diseases to human beings. Kerman province, including Jiroft city, is one of the most important husbandry regions of south Iran. This study was conducted to determine tick infection rate of sheep and goats in Jiroft. Sampling was performed in 4 villages during winter only. Sheep and goats were selected and tested for tick infection. After collection ticks were identified by morphological characteristics using a stereomicroscope device.Tick infection was detected in 33 sheep and also 84 goats. Infection rate in sheep was 17/33 (51.5%) and also in the goat 29/84 (34.5%). In this study 265 ticks were collected on the sheep and goats which were classified in Ixodidae ticks family. They belong to three genera , *Hyalomm*a (2%) , *Rhipicephalus* (96.5 %) and *Haemaphysalis* (1.5%). *Rhipicaphalus* was the most abundant genus in this search. In this survey we could find several tick genera which are important in causing diseases in sheep, goat and humans.

POSTER No. 3

Helminth fauna of Moose (*Alces alces*) in Lithuania

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The moose (*Alces alces*) is one of the game animals in Lithuania. Their population density is 2.1 animals in 1000 ha in the investigated region. To date, however, there has been no data about the parasites of moose in Lithuania. The aim of this study has been to identify the eggs of helminths in the faeces of moose by mean of ovoscopic analyses. A modified McMaster method was applied for qualitative and quantitative testing of the presence of helminth eggs. The sedimentation technique was used to separate helminth eggs from faeces. When the data obtained during 2007-2010 were taken into consideration, 100% of the samples studied showed roundworm and/or flatworm eggs and the number of eggs per gram faeces (EPG) varied between 19 – 1680, the mean being 82.1±26.5. The presence of flatworm eggs was more frequent (209.2±97.7) than the nematode eggs (38.3±6.3). The obtained eggs of flatworms were identified as belonging to the worms of the *Paramphistomum* spp. (47.3±21.9) and *Moniezia* spp. (816.6±328.4). The eggs of five nematode species were identified. They belong to *Cooperia* spp. (32.7±5.4), *Nematodirus* spp. (27.3±4.0), *Chabertia* spp. (47.4±11.8), *Strongyloides* spp. (16.0±2.5) and *Trichuris* spp. (53.6±19.9). *Paramphistomum* spp. and *Trichuris* spp. eggs were the most prevalent helminth eggs in moose faeces and have been identified in more than half samples, but most abundant were *Moniezia* spp. eggs, there were 1600 eggs of this cestode in few samples. The necropsy of one moose showed *Cysticercus tenuicollis* (*Taenia hydatigena*) in the liver. The influence of other species of wild cervids, domestic ruminants and carnivores on the helminth fauna of moose is further discussed.

POSTER No 4

Investigation of *Sarcocystis* in domestic pigeons (*Columba livia* f. *domestica*) and woodpigeons (*Columba palumbus*) in Lithuania

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Protists of the genus *Sarcocystis* are parasites of mammals, birds and reptiles and have an obligatory prey-predator two-host life cycle. Birds of the family Columbidae serve as intermediate host for these parasites. In 2010 two new *Sarcocystis* species parasitizing in pigeons were described in Germany, *S. calchasi* causing several neurologic disorders in feral pigeons and *S. columbae* from woodpigeons. In the period of 2008-2011, leg, neck and breast muscles of 18 woodpigeons and 54 domestic pigeons from Lithuania were examined for sarcocysts. *Sarcocystis* cysts were found in only two woodpigeons and infected birds did not show any clinical signs of the disease. The morphologically investigated *Sarcocystis* sp. had a type-1 tissue cyst wall and was not distinguishable from *S. calchasi*, *S. columbae* and *S. wobeseri*, parasitizing birds. According to DNA analysis, *Sarcocystis* sp. from the woodpigeon was identified as *S. columbae*. According to the phylogenetic and ecological data, predatory birds are expected to be definitive hosts of *S. columbae*. This is the first report of *Sarcocystis* in birds of the family Columbidae in Lithuania. The reasons, why domestic pigeons were negative for *Sarcocystis* are discussed.

POSTER No. 5

Preliminary studies on ticks (Acari: Ixodida) collected from game animals in Silesian Province, Poland

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Ticks are ectoparasites of different species of vertebrates, including game mammals. Among 19 species of ticks recorded in Poland, the castor bean tick *Ixodes ricinus* (Linnaeus, 1758) is the most common and widely distributed species. Its distribution and activity are mainly correlated with mean air humidity level and activity of its hosts. The aims of presented studies were to investigate the presence of correlation between tick infestation level and host age, sex and size, as well as study which species of ticks infest wild game in the area of Silesian Province. Ticks were collected from game in cooperation with wild-game animal purchasing agencies. The total number of 1595 ticks of *Ixodes ricinus* (Linnaeus, 1758) species was collected in 2008 and 2009 from 49 individuals of roe deer *Capreolus capreolus* (Linnaeus, 1758). The highest mean number of ticks was observed for females and the lowest for larvae. All individuals of roe deer were infested with ticks. There were no correlations recorded between intensity of infestation and sex and age of the host. There was however a correlation between size of the host and total number of ticks, especially tick females. Presented preliminary studies show that in the area of Silesian Province 100% prevalence of roe deer invasion by *I. ricinus* is observed. Studied animals are hosts mostly for females of *I. ricinus*, which was the only tick developmental stage present on all roe deer.

POSTER No. 6

Intestinal parasites of the Eurasian lynx (*Lynx lynx*) in Finland

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Despite the increase in the Finnish lynx (*Lynx lynx*) population in recent years, there is little information on helminth diversity and of its epidemiological importance. In this study, the prevalence of Eurasian lynx intestinal parasites in Finland was investigated by coprological examination and by visual examination of the gastrointestinal tract for adult helminths (n = 332). The samples were collected during hunting season 2010/2011 from all over the Finland. The method used for faecal samples was quantitative $MgSO_4$ flotation (FLOTAC® technique) and 5 grams of faeces were analysed. Parasite species identification was based on egg morphology. Identification of adult forms was also based on morphological key characteristics. Parasitological analysis of the faecal samples revealed eggs and oocysts of 6 different endoparasites and reached prevalence of 91.9%. *Toxocara cati* eggs were present in 72.0% of samples (mean intensity 883.7 eggs per gram (epg)), *Capillaria* sp. eggs were present in 45.8% of samples (115.9 epg), *Taenia* sp. eggs were present in 27.1% of samples (123.3 epg) and *Diphyllobothrium latum* eggs were present in 5.1% of samples (588.4 epg). *Isospora* sp. oocysts were detected only in one sample (0.3%) and *Uncinaria stenocephala* eggs were detected in two samples (0.6%). Visual examination of the gastrointestinal tract revealed adult helminths in 145 animals. The highest prevalence in these samples was for *T. cati* (95.7%) and *Taenia* sp. (57.2%). Two adult cestodes of *Mesocestoides* sp. were detected in one sample and part of *D. latum* in one sample. There were seven samples with low worm intensity (*T. cati* – 2.4 worms per sample and *Taenia* sp. – 5 worms per sample) which were negative in coprological examination. The overall prevalence and diversity of intestinal parasites in lynx was high in Finland.

POSTER No. 7

High prevalence of *Eimeria* spp. Infection in European ground squirrel (*Spermophilus citellus*) in Northern Greece

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The European ground squirrel (*Spermophilus citellus*) is distributed in Southeastern Europe in two main basins: Pannonian and Balkan. It is a small mammal categorized as vulnerable according to the International Union for Conservation of Nature (IUCN). Greek populations can be especially important, as they are found at the periphery of the southern border of the range of this species. Parasites can, under certain circumstances, become a serious, even life threatening problem. The aim of the present study is to investigate the parasite fauna of this animal species and its monthly variation in different areas of Northern Greece. Our preliminary results reveal a particularly high prevalence (92.59%) of *Eimeria* spp. infection, in animals originating from two different populations. The species found were *Eimeria callospermophili*, *E. citelli* and *E. cynomysis*. *Eimeria* is a protozoan parasite that can cause enteritis of the small and large intestine. The significance of these findings in the health and conservation status of the European ground squirrel is discussed.

POSTER No. 8

Toxoplasma gondii infection in wild and domestic pigeons (*Columba livia*)

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Toxoplasma gondii is a protozoan parasite of great medical and veterinary importance with a worldwide distribution. There is evidence that birds, and especially pigeons, may be a good indicator of soil contamination, since they feed from the ground. In Greece, there is no information available on the infection of birds with *T. gondii*. Therefore, a study to assess the prevalence of *T. gondii* in wild and domestic pigeons (*Columba livia*) from different parts of the country is currently underway and the preliminary results are presented here: 379 domestic pigeons from 97 flocks originated from 6 different areas of the mainland were examined. An Enzyme Linked Immunosorbent Assay (ELISA) was performed for the detection of specific *T. gondii*- IgG. Twenty two of the pigeons (5.8%) were seropositive. However in a wild population of pigeons (n=50) living in the area of Thessaloniki, no seropositive birds were found. The correlation of the area and the management of the pigeons with the seroprevalence, as well as the significance of the findings to the domestic animals and Public health are discussed.

POSTER No. 9

Age determination of malaria vector *Anopheles stephensi* by liquid chromatography

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The objective of this study was to determine the daily age of *Anopheles stephensi* based on changes in pteridine concentration in cuticles by liquid chromatography. Females were raised in an insectary. At 1, 5, 10, 15, 25, 30 days post-emergence they were divided into groups of 10 mosquitoes each. The mosquitoes in each age group were further divided into 3 subgroups of 10 each for chromatographic (HPLC, emission = 355 nm and excitation= 465 nm) pteridine extraction..Four types of pteridines were detected in the cuticle of *A. stephensi*, including isoxanthopteridine, pteridine-6-carboxylic acid, biopteridine, and xanthopteridine. They were all present in all the cuticle of the mosquitoes; however, no biopteridine in the head or xanthopteridine in the thorax were found. Generally, as the age of the mosquitoes increased, pteridine concentrations kept declining, such that after 30 days the total concentration reached 10% of the original. The findings indicate that there is a negative correlation between the concentration of pteridines in the cuticle and daily age of female mosquitoes. The method described can be used as a standard method to determine the daily age of *Anopheles*, since it is fast and precise and needs small samples. Its major limitation is non-availability of HPLC in many parts of the country, although it is possible to freeze dead mosquitoes and transfer them to centers where HPLC is available.

POSTER No.10

Scientific productivity in the field of Leishmaniasis 2000-2009

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A bibliometric study was carried out to analyze and visualize the scientific production of countries in the field of *Leishmania* during a period of 10 years. Only scientific profiles published in the journals which indexed in Medline through 2000-2009 were taken under consideration. All data was extracted from PubMed online. The study focused on the scientific production and productivity of Iranian institutes in the field of *Leishmania*. Analysis of data showed that English consisting 96.3% of total publications' language is the dominate dominant language of publications. Brazilian authors with contributing 18.2% of total pubications in the field are the most prolific authors during the period of study, followed by authors from USA (16.1%), India (13%), UK (8.4%), Spain (5.6%), France (4.4%), Germany (3.9%), Canada (3.5%), and Iran (2.7%) respectiviely. The journal of "*Molecular and biochemical parasitology"* is the most productive journal regarding to distributing the great number of publications in the field of *Leishmania* followed by "*Infection and immunity*" and ""*Experimental parasitology*". Among Iranian institutes "Pasteur Institute of Tehran" with contributing 30.1% of total publications from Iranian institute is the most productive institute in Iran followed by "*Tehran University of,Medical Sciences*" and *"Shiraz University of Medical Sciences"* contributing 20.3% and 18.7% of total publications from Iran respectively.

POSTER No. 11

Species identification in Notocotylidae (Digenea): morphology and molecules

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Notocotylids are widely spread parasites of birds, including those in coastal ecosystems. Their only intermediate host is a mollusk: metacercariae encyst in the external environment and become invasive for the definitive host. Classification is based on adults while it is not always clear which species cercariae belong to. Even simple discrimination among these cercariae by morphology is not particularly easy. Molecular research on notocotylids has been very limited so far and there is a lack of sequence data. The purpose of this study is to compare morphological and molecular markers and to define more exactly the number of cercariae species we are dealing with. Further work includes linking the discovered cercariae species to defined adult species from birds. Samples were collected from infected intertidal snails *Hydrobia ventrosa* (Kandalaksha Bay, White Sea) and *Littorina saxatilis* (southeastern Barents Sea). Basing on morphometrics and excretory system structure, several cercariae morphotypes were marked out, but no certain species identification was possible. Cercariae from *L. saxatilis* appeared to form a separate species. ITS1 sequence analysis has shown that “Imbricata” morphotype cercariae represent one species while “Monostomi” are heterogenic group and include at least two species. There is also evidence supporting that cercariae from *L. saxatilis* (Barents Sea) belong to a species significantly different compared to those from *H. ventrosa.* Discussion concerns possible systematic position of cercariae; and transmission routes in coastal ecosystems.

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POSTER No. 12

GIT parasite infections elucidated by coprology in alpacas from the Peruvian Andes

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Peru has the largest population of alpacas in the world. Alpacas are primarily kept for their fleece, but they are also harvested for meat and leather. This study was conducted in order to determine the effect of ivermectin and levamisole on faecal parasite egg counts and on the post-treatment strongyle reinfection rates in the transitional period between dry and rainy weather. One hundred and twenty one-year-old male alpacas were randomly divided into three groups and marked with ear tags, as they were herded freely in the Andes. On day 0 faecal samples were collected from the rectum, and animals from the two treated groups were injected subcutaneously with either ivermectin or levamisole, while the control group was left untreated. Faecal samples were subsequently taken on days 17, 32 and 49 post treatment. Later on the number of animals was reduced to 90 due to lack of time. Faecal samples were processed with McMaster and sedimentation techniques, and larval cultures were made from every sample with a positive McMaster result. Samples from day 0 were also processed with a Baermann technique, but since these were all negative, no further lungworm examinations were performed. Initially, 75 % of the animals [67;83=$CI_{95\%}$] were found to be infected with strongyles (EPG ranging from 50 to 350, with a mean of 95). On day 17 we detected a significant reduction ($p<0.05$) of the number of strongyle eggs shed in faeces by the two treated groups in comparison with the control group. For the ivermectin-treated group the treatment efficacy was 96 % [84;99]. The corresponding value was 92 % [78;97] for the levamisole-treated group. The rela-tively low treatment efficacy could be due to the relatively low egg counts found initially. On day 32 we detected 26 % [9;42] of the alpacas in the levamisole group and 6 % [0;13] of the ivermectin group to have strongyle EPG ≥ 50. On day 49 it was 29 % [11;47] for the levamisole group and 19 % [0;33] for the ivermectin group.

POSTER No. 13

The hidden cost of import – an emerging parasitic disease in dogs in Norway

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People and their pets are on the move. We have become more cosmopolitan in our travel tastes and no longer like leaving our pets at home or at the kennels when we go on holiday. The ease of travel for pets within the EU means that many owners do not think twice before taking their four-legged friends along with them on vacation. Additionally the demand for many of the fashionable dog breeds can outstrip supply and puppies and breeding stock are imported both legally and illegally from other countries. We report here two cases of the potentially zoonotic parasite *Strongyloides stercoralis* in young dogs in Norway.

POSTER No. 14

Host-parasite interface: Secreted digestive enzymes in *Gyrodactylus salaris*

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As ectoparasites, *Gyrodactylus* species are rather superficial feeders on the fish skin. They most probably secrete digestive enzymes from the glands near the mouth and pharynx, or from the gut, and then swallow the fluidy or slimy product. The gut of the parasite seldom contains fish skin pigments, showing that the primary damage is shallow. Field observations suggest that in the wild, the host-parasite contact is in evolutionary balance and rather harmless for the fish, indicating that the digestive substance is not eliciting any strong immunological reactions. We used a bioinformatic approach to identify putative secreted digestive enzymes from the draft genome of *Gyrodactylus salaris*. The genes were annotated using similarity searches and protein structural domain predictions. Then, we compared the genes phylogenetically with free-living (*Schmidtea*) and endoparasitic (*Schistosoma*, *Echinococcus*, *Fasciola*) flatworms, as well with different blood-sucking insects. There are several promising candidate gene families to be tested and characterized. These include four *A*, two *D* and 13 *L cathepsins*. The *L cathepsins* allow *Fasciola* to digest its way to invade into the host tissue. *Elastases* serve the *Schistosoma* cercariae to penetrate the host skin without eliciting immunoreaction: there are 13 potentially functional secreted elastase-like genes in *G. salaris*.

POSTER No. 15

Emergence, spread, persistence and fade-out of sylvatic plague in Kazakhstan

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Predicting the dynamics of zoonoses in wildlife is important not only for prevention of transmission to humans, but also for improving the general understanding of epidemiological processes. A rare opportunity for detailed statistical modelling of an infectious disease is provided by a large dataset on sylvatic plague, caused by *Yersinia pestis*, in the Pre-Balkhash area in Kazakhstan, where the main host is the great gerbil (*Rhombomys opimus*) and the vector is various species of *Xenopsylla* fleas. Previous work using these data (collected for surveillance purposes) has revealed a host abundance threshold for epizootics, and climatic influences on plague prevalence. Here, we present a model describing the local space–time dynamics of the disease at a spatial scale of 20×20 km^2 and a biannual temporal scale, distinguishing between invasion and persistence events. We used a Bayesian imputation method to account for uncertainties resulting from poor data in explanatory variables and the response variable. Spatial autocorrelation in the data was accounted for in imputations and analyses through random effects. The results show (i) a clear effect of spatial transmission, (ii) a high probability of persistence compared with invasion, and (iii) a stronger influence of rodent abundance on invasion than on persistence. In particular, there was a substantial probability of persistence also at low host abundance.

POSTER No. 16

The parasite *Syngamus trachea* in a metapopulation of House sparrows (*Passer domesticus*)

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Syngamus trachea is a nematode parasite species found in many terrestrial bird species all over the world. It is also known as “Gapeworm” because of the gaping behaviour infected individuals often exhibit due to reduced respiration function. Despite the Gapeworm being a fairly common parasite in the poultry industry its fitness consequences on populations in the wild are poorly known. Here we focus on whether the prevalence of *Syngamus trachea* differs spatially and temporally and between sexes and ages. We also investigate whether *Syngamus trachea* can result in reduced survival probability on its host.
The study system consists of a metapopulation of House sparrows which include 18 island populations in the archipelago of Helgeland in northern Norway that covers 1600km^2 in total. The study populations have been closely monitored since 1993 using capture-recapture methods. Since 2007 we have collected data on parasites, mainly through counting eggs in collected faeces-samples. The study populations are relatively small (10-120 adults), and since the house sparrow is a sedentary bird species this enables us to sample a high proportion of the individuals annually. Individual variation in reproductive success was recorded from nests during the breeding season. In the present study we demonstrate significant seasonal changes in prevalence of the parasite over the course of a year and differences in prevalence between islands, sexes and age-classes. We also demonstrate that Gapeworm infection resulted in higher annual mortality in house sparrows exhibiting severe symptoms of the parasite. Accordingly, there is reason to believe that the presence of Gapeworm may influence the population dynamics in time and space of a spatially distributed Passerine species.

POSTER No. 17

Genetic polymorphism at the C-terminal domain (region III) of knob-associated histidine-rich protein (KAHRP) of *Plasmodium falciparum* in isolates from Iran

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The knob-associated histidine-rich protein (KAHRP) plays a major role in the virulence of *Plasmodium falciparum*, and is one of the targets for molecular therapy. The primary structure of KAHRP of *P. falciparum* consists of three domains (regions I-III), of which the C-terminal domain (region III) is the most polymorphic segment of this protein. One of the main obstacles is genetic diversity in designing and developing of malaria control strategies such as molecular therapy and vaccines. The primary objective of the present study was to investigate and analyze the extent of genetic polymorphism at the region III of KAHRP of *P. falciparum* in isolates from Iran. A fragment of the *kahrp* gene spanning the C-terminal domain was amplified by nested PCR from 50 *P. falciparum* isolates collected from two malaria endemic areas of Iran during 2009 to August 2010 and sequenced. In this study, three allelic types were observed at the C-terminal domain of KAHRP on the basis of the molecular weight of nested PCR products and the obtained sequencing data. The presence of multiple alleles of the *kahrp* gene indicates that several *P. falciparum* strains exist in the malaria endemic areas of Iran. Our findings will be valuable in the design and the development of the molecular therapeutic reagents for *falciparum* malaria.

POSTER No. 18

Preliminary study on the efficacy of single-PCR for diagnosis of *Strongyloides stercoralis* in stool samples

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Strongyloides stercoralis is an intestinal parasitic nematode. Due to autoinfection in humans, it causes infections lasting for decades. In immunocompromised patients, infection leads to life threatening disease. Early diagnosis of infection is crucial to prevent complicated syndromes. This study was performed to have a preliminary evaluation on the efficacy of single-PCR for diagnosis of *S. stercoralis* compared with agar-plate culture of stool samples. For this purpose, 16 confirmed stool samples infected with the agent were used to set up the method, using two primer sets designing to amplify partial ribosomal DNA of *S. stercoralis* genome. Then, 30 stool samples which were negative for *S. stercoralis* by agar plate culture were examined by single-PCR, resulting in amplifications of *S. stercoralis* extracted DNA in 5 samples. Statistically single-PCR detected more positive cases of infections compared to agar plate culture ($P<0.05$). Further evaluation considering times of stool sampling is recommended.

POSTER No. 19

Paediatric hydatidosis in Iran

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Hydatidosis is one of the major zoonotic diseases that cause considerable public health problems in Iran. The present study was designed to investigate paediatric hydatidosis in Iran. Data were collected from the records of 17 patients referred to the Children Medical Centre Hospital in Tehran, Iran, with hydatidosis from 2005 to 2010. Collected data included demographic data, and information on clinical manifestations, type and site of cysts, laboratory results, and therapeutic procedures employed. Nine patients were boys (52.9 %), and eight patients (47.1%) were girls. Most patients lived in the central areas of Iran (52.9%). Thirteen patients had cysts in the lungs (76.5%) and eight cases in the liver (52.9%). Six cases (35.3%) had simultaneous lung and liver cysts, 3 patients had brain cysts and 2 patients showed multi-organ involvement. All patients underwent surgery and treatment with albendazole, recurrence was seen in only 1 (5.9%) of the cases and one case, because of a torn cyst and anaphylactic shock, died. Hydatid cyst has high prevalence in human and domesticated animals of Iran and causes great hygienic and economic damage in this country. So, to reduce this problem, individuals especially parents should be trained to observe the hygiene, and design a controller hygienic plan all over the country.

POSTER No. 20

First report of *Crenosoma striatum* and *Haemonchus contortus* in the long-eared hedgehogs, *(Hemiechinus auritus)* in Iran

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Crenosoma striatum is a common lungworm of hedgehogs, in various parts of the world. The infection with *C. striatum* can cause loss of weight, dry cough, bronchitis with ulcerous reactions based on secondary bacterial infections, pulmonary damage, thickening of the tracheal wall, pulmonary emphysema and even cardiovascular failure. In this survey, six long-eared hedgehogs *Hemiechinus auritus*, have been examined for the presence of pulmonary nematodes. All the hedgehogs had *C. striatum* in their lungs; L1-stages were also detected in the bronchial tubes. There were a large number of *Haemonchus contortus* in affected stomachs. The worms were removed from of the stomachs and cleared in lactophenol. This is the first report of *C. striatum* and *H. contortus* in Iran. Keywords: *Crenosoma striatum, Haemonchus contortus,* long-eared hedgehog, Iran

POSTER No. 21

Occurrence of *Dipetalonema evansi* in camels (*Camelus dromedarius*) in Mashhad area, North East of Iran

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This research was conducted to determine the prevalence and seasonal fluctuation of *Dipetalonema evansi* in dromedaries in the North eastern part of Iran. A total of 200 male camels of different ages slaughtered at Mashhad slaughterhouse were inspected for infection with *D. evansi*. In the study, the testicles, epididymises and spermatic cords of 200 male camels were examined, and 47 (23.50%) were infected with adult forms of *D. evansi*. The prevalence was highest in aged 5-10 years (33.33%), ($P< 0.05$). Also the prevalence rate of infection with *D. evansi* was highest in summer ($P> 0.05$). *D. evansi* is highly endemic and constitutes an important health problem to camels in this area, resulting in high morbidity, impaired working capacity, and lowered productivity.

POSTER No. 22

Trichosomoides crassicauda the most prevalent helminthes of rats in Iran

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Urinary bladders in rats harbor a threadworm nematode, *Trichosomoides crassicauda* (Bellingham, 1840) which is known to be prevalent throughout the world. Infection has also been reported amongst laboratory albino rats in animal houses under conventional regulations. The transmission route, which may be direct for this parasite, allows the easy spread of infection within a colony. *T.crassicauda* is a relatively nonpathogenic hair-like worm with an unusual behavior for the male individuals that spend their life inside the female uterus. Physiopathological traits of rat bladder worm such as migration through visceral organs during the course of development and induction of bladder tumor in rats have rarely been seen and are of experimental research interest. In this study we examined 50 infested rat bladders histopathologically. The main object was to determine the grade of epithelial damage in accordance with worm burden. Observations are encouraging to conduct other fundamental experiments which can assist researchers to understand more about *T.crassicauda* life cycle and host parasite relationships in general.

POSTER No. 23

Urban rats by their parasitic worms as available environmental indicators for harmful elements

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Rats have a cosmopolitan distribution. Although they are judged as pests, they might have key roles in the natural environment. A variety of parasites which can be important in public health are harboured by rats. According to recorded high levels of pollution in last decades, their ability as bioindicators regardless of their consequence in the nature must be considered seriously. Heavy metal pollution is one of the most important risk factors facing to environment which has hazardous effects on animals and human beings. Based on high level of contamination for some elements in populated areas, ecosystem monitoring must performed more intensively. By the means of bioindicator assessment duration of pollution in the given problematic cities can be clarified. Recent studies have shown the significant role of some parasites, specifically those worms with tegumental absorption which can indicate environmental pollution with heavy metals such as Cadmium and Chromium. During the Present research we have analysed rat parasites with these capabilities to describe Cadmium and Chromium pollution in metropolitan Tehran. Comparison of concentrations of these two elements in host tissues and the worms have elaborated this issue clearly. The helminths which have been candidate in this research are *Hymenolepis diminuta* and *Moniliformis moniliformis.*

POSTER No. 24

The first report of *Hartmannella vermiformis* & *Vannella persistens* isolation from public areas of Tehran by molecular methods

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Free-living amoebae are unicellular protozoa that have a worldwide distribution and inhabit a wide variety of soil and aquatic environments. The free-living amoebae *Acanthamoeba* spp., *Hartmanella vermoformis* and *Vannella* spp., have been recognized as etiological agents of meningoencephalitis and keratitis. A comprehensive survey to document the presence of these free-living amoeba and to identify their different genus was conducted in public areas related to human environments in parks and squares in Tehran, Iran. From April to October 2008, 50 water samples were randomly collected from 26 public squares and 24 park ponds from the 22 municipal districts of Tehran and transported to the Department of Medical Parasitology and Mycology, School of Medicine, Shahid Beheshti University of Medical Sciences. Water samples were filtered through a 0.45 µm diameter cellulose nitrate filter. The filters were inverted on heat inactivated, *E. coli* treated, 1.5% non-nutrient agar plates. Genomic DNA was extracted from positive samples and PCR was performed to amplify the SSU-rRNA gene and they were sequenced to determine the genus and species of isolates. All of them were analyzed with BLAST.

Out of the 50 samples, 27 isolates (54%) were positive on culture, with the usage of molecular methods and sequencing analysis, 6 (28.6%) *Hartmannella vermiformis* and 2 (9.5%) *Vannella persistens* were recognized. The other positive isolates were determined as *Acanthamoeba*. The results described here suggest that PCR is a sensitive and powerful analytical tool that allows effective genus discrimination. We have shown for the first time, the presence of *Hartmannella vermiformis* and *Vannella persistens* in waters of Iran.

Due to opportunistic features of these two amoebae serious attention to control the problem of ree-living amoebae in public areas is recommended.

ACKNOWLEDGEMENTS

The authors are indebted to Dr Keshavarz for expert technical assistance and and Dr. Bandepour from Cellular and Molecular Biology Research Center, Shahid Beheshti University of Medical Sciences for her kind cooperation.

POSTER No. 25

Red deer (*Cervus elaphus* L.) – a new host for *Eimeria virginianus* Anderson and Samuel, 1969 (Protozoa: Apicomplexa)

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Eimeria virginianus is a coccidian of white-tailed deer, however it is probably able to infect other deer species. It is believed to have been brought to Poland with introduced American wapiti, at the end of the 19th century. 3g taken from 229 individual faecal samples from free-roaming red deer were examined using the direct flotation method and the McMaster quantitative method. The sample with the highest OPG was mixed with 20x its volume in an aqueous 2.5% potassium dichromate solution and kept at a temperature of 23C to determine the sporulation time. Oocysts were identified at 1000x magnification and the morphological structures were measured using the Cell^{D} computer program. The direct flotation method revealed 5 positive samples (4 with 1, and 1 with 16 oocysts), whereas only 1 was positive in the McMaster method (OPG=50). Dimensions were taken and the results in µm are: 34 oocysts: 45.8±3.3 x 31.8±2.1; 8 sporocysts: 22.9±1.2 x 9.8±0.3. All oocysts were brown, elongate ovoid with a micropyle, and ~3µm thick wall. The sporulation time was 12 days, and no residuum or polar body was observed. A Stieda body was found at the pointed end of sporocysts. All of the investigated features suggest *E. virginianus* infection, however the prevalence and OPG's were very low.

POSTER No. 26

Plasmodium vivax Infection during pregnancy In Karachi-Pakistan

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Plasmodium vivax, is a widespread protozoan parasite and the most common agent causing malaria in Asia and other continents. Malaria is risky to both the mother and fetus. *P. falciparum* infection is a well known cause of maternal and fetal morbidity and mortality during pregnancy. *P. vivax* infected women are more commonly anemic and deliver lower birth weight neonates, as compared to healthy women.

Detailed clinical and personal history was taken by interviews and questionnaires. A proforma was provided to the pregnant women before the blood sampling. Blood samples were obtained from the finger pricks and parasitological studies was done under the microscope. Blood was also tested for blood groups, Hb%, ESR/mm, TLC/cmm, and DLC.

Of 750 women were examined, who visited different hospitals of Karachi. 15.4% were parasitoid at the time of delivery of whom 66% and 22% had *P.vivax* and *P. falciparum* infections respectively and the remainder had mixed infections of both species. The primigravidae or women having 1st to 3 rd month's pregnancy had 30% infection of *P. vivax* and the women living in lower middle class areas had highest rate of infection i.e. 54%. *P. vivax* infected women also delivered children with lower birth weights.

It is concluded that this problem has long been neglected, and that there is a need to educate and inform pregnant women and their family members about the severity and risk of malaria during pregnancy. Clinical visits, use of insecticides treated bed nets, and preventive measures with the advice of doctors may decreases the chance of malaria and also hope for reducing the burden of malaria in pregnancy and improving the health of mothers and newborns.

POSTER No. 27

Giardia duodenalis prevalence and associated risk factors in school-age children of Gorgan, Iran

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This study was designed to describe prevalence of *Giardia duodenalis* infections in school-age children from Gorgan city and its possible association with socio-economic variables. A cross-sectional epidemiological study was carried out on school children from 18 primary schools in Gorgan city during the years from 2010-2011. Data were collected from 801 children from 7 to 12 years of age of both genders from urban areas using structured questionnaires and laboratory analysis of fecal samples. The parasites were detected using a single-stool sample by direct wet and formalin-ether sedimentation examination under a light microscope.One hundred and thirty-five (33.7%) of 801 children were positive for giardiasis. *Giardia* cysts were positive in 93% and trophozoites in 7%. No correlation was found between giardiasis and age, gender, residence in urban or rural areas, availability of piped water or sewage system. In contrast, both mother's and father's levels of education were found significant predictors of giardiasis (P-value ≤ 0.05). Some infected samples (48.8%) showed double or triple infections and *G. lamblia* was found with *Entamoeba histolytica/Entamoeba dispar, Hymenolepis nana, Blastocystis hominis*, and *Iodamoeba butschlii*. Giardiasis is a continuing public health problem in Gorgan. As long as the environmental and socio-economic factors associated with infection persist, this intestinal protozoan infection will not be controlled. Thus, the local administrators need to pay more attention to the prevention of parasitic infections along with improvement in education, environmental, and sanitary conditions.

POSTER No. 28

Survey of prevalence of *Theileria annulata* and *Anaplasma marginale* in cattle in Kerman, southeast of Iran

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This study was conducted in the Kerman area to investigate the prevalence of *Theileria* spp. and *Anaplasma* spp. in cattle during different seasons. For this purpose, cattle of different sex and age were examined. The study was conducted during April 2009 and February. Examination of 200 cattle revealed that 63 (31. 5%) and 6 (3%) of cattle were infected with *Theileria annulata* and *Anaplasma marginale*, respectively. Mixed infections were observed in 4 (2%) cattle. *T. annulata* was the prevalent blood parasite among cattle while *A. marginale* was scarcely encountered. The parasitaemia of *Theileria annulata* infection was higher than *Anaplasma marginale* infection. In addition,the highest rate of infection was in cattle under one year old (35.33%) and this difference was statistically significant ($P<0.05$). Additionally, no significant difference was observed between male and female ($p>0.05$). Comparison of results in different seasons indicated that the lowest and highest rate of *Theileria annulata* infection were observed in cool and warm months respectively. The prevalence of *Anaplasma marginale* infection in relation to age, sex and season was not statistically significant.

POSTER No. 29

Genetic characterization of *Trichostrongylus* isolates from some domestic livestock in Iran

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Infection of herbivores with *Trichostrongylus* nematodes is widespread in many countries, and has a major economic impact on breeding, survivability and productivity of domestic livestock (Hoste, H., *et al.* 1995. *International Journal for Parasitology* **25;** 75-80). This study was carried out on genetic characterization of *Trichostrongylus* species isolated from domestic livestock in Iran, in order to develop an easy-to-perform method for species identification. *Trichostrongylus* isolates were collected from sheep, goat, cattle and buffaloes in Khuzestan Province, southwest Iran. Primary species identification was carried out based on morphological characterization of male worms. PCR amplification of ITS2 rDNA region was performed on genomic DNA and the products were sequenced. Phylogenetic analysis of the nucleotide sequence data was conducted employing Bayesian Inference approach. A restriction fragment length polymorphism (RFLP) profile was designed to differentiate *Trichostrongylus* species. A consensus sequence of 238 nucleotides was deposited in the GenBank for Iranian isolates of *Trichostrongylus* species including *T. colubriformis*, *T. capricola*, *T. probolurus* and *T. vitrinus*. The designated RFLP using restriction enzyme *Tas*I could readily differentiate among species, having different ITS2 sequence. The molecular analysis was in concordance with morphological findings. Phylogenetic analysis indicated a close relationship among the sequences obtained in this study and reference sequence of relevant species, with a high statistical support.

POSTER No. 30

Disruption, a major phenomenon for *Trichomonas vaginalis* growing with human cervical epithelium *in vitro*

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Trichomonas vaginalis, a protozoan parasite of the urogenital-vaginal tract, is the causative agent of trichomoniasis, the most common non-viral sexually transmitted disease (STD) in human. In male, the trichomoniais is usually asymptomatic, although it may cause irritating urethritis or prostatitis. In female, trichominiasis is associated with a wide spectrum of clinical signs ranging from a relatively asymptomatic state to severe vaginitis with a foul-smelling vaginal discharge. *T. vaginalis* may act as a potential catalyst in the acquisition of secondary infection such as that caused by human papilloma virus, the organism responsible for the pathogenesis of cervical cancer. The adherent clump of this protozoan will destruct the epithelial cell and induce pathogenesis by contact-dependent cytotoxicty. A co-culture system of *T. vaginalis* and human cervical epithelium cancer cell line (Z172 cell) has been established in this study. Both of the protozoan and host cell grow well in the same culture condition and atmosphere. When Z172 cell exposure under *T. vaginalis* attack, the morphology of the host cells become round shape, shrinkage, detach, and part of the cells are died. The single Z172 cell is easier attacked by *T. vaginalis* then colonial cells. The more co-culture time and the more adhesion rate were observed in this study. After 12 hours' co-culture, the adhesion between protozoan and cell become the most significantly than other time points observation. RT-PCR results showed that, the expression of adhesion protein 65 of protozoa were increasing after the interaction between host and parasite. Time-lapse recording and flow cytometry were used for the studies of the host and parasite relationship. Z172 attacked by *T. vaginalis*, there are 70% of cell with disruption, 8% with apoptosis-like and 18% with necrosis-like after 10 hours. Cell activity was decreased after 6 hours interaction but raised after 10 hours Does the pathological changes of the Z172 cell are derived by the physical or chemical after the adhesion of *T. vaginalis* are needed to more studies in the future.

POSTER No. 31

Parasite diversity of the Rock ptarmigan in Iceland

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The rock ptarmigan *Lagopus muta* in Iceland shows cyclic population changes with peak numbers c. every 11 years. This project focuses on the relationship of rock ptarmigan population change and health related parameters, including parasite infections. Here we focus on the diversity and microhabitat use of the parasite fauna. From 2006 to 2009, every year 100 ptarmigans were collected in Þingeyjarsýsla, in total 400 birds. The plumage and skin of every bird was examined for ectoparasites and signs of disease; intestines and tissues were examined for endoparasites. Blood parasites were searched for in 2006, but not found. The ptarmigan body is habitat for a diverse ensemble of parasite species. Sixteen parasite species were found. Seven were new to science* and three were new host records#. The endoparasites are the coccidians **Eimeria muta* and **Eimeria rjupa*; #*Blastocystis* sp.; the cestode #*Passerilepis serpentulus* and the nematodes *Capillaria caudinflata* and *Trichostrongylus tenuis*. The ten ectoparsites include the astigmatan mites **Metamicrolichus islandicus*, **Strelkoviacarus holoaspis*, **Tetraolichus lagopi* and **Myialges borealis*; the prostigmatan mite **Mirinovia lagopus;* the mallophagans *Goniodes lagopi*, *Lagopoecus affinis* and #*Amyrsidea lagopi*; the louse fly *Ornithomya chloropus* and the flea *Ceratophyllus garei*. Each of these species has its specific niche with respect to where to live, what to feed on, and how to disperse – a clear example of biodiversity on the micro scale. The astigmatan mites, e.g. live in or on the skin, between vanes on wing feathers or in the down or plumage; the prostigmatan mite lives inside shafts of feathers. Regarding nourishment most species feed on various host tissues (including keratin and blood); one of the mites consumes wax originating from the sebaceous gland. Most of the life cycles are direct. The louse fly is used to transport some of the ectoparasites to uninfected hosts (phoresy).

POSTER No. 32

Comparative studies on European freshwater bucephalid digeneans based on karyotypes and sequences of 28S and ITS2 rDNA

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The cosmopolitan family Bucephalidae represents parasites that occur in bivalves as first intermediate hosts. Only three species of bucephalid digeneans are known in European freshwater bivalves: *Bucephalus polymorphus*, developing in *Dreissena polymorpha*, and two species of the genus *Rhipidocotyle* – *R. campanula* (= *R. illense*) and *R. fennica,* developing in Unionid mussels.

In this study parthenitae of *R. campanula* and *R. fennica* infecting *Anodonta anatina,* gathered from the lake Saravesi (Finland) and *R. campanula* from *A. anatina*, gathered from the water reservoir of the dammed up river Nemunas in Lithuania, were investigated using karyological analysis and DNA sequencing. The data obtained were compared with previous data on *B. polymorphus* from Belarus. ITS2 and 28S DNA sequences were used to estimate the phylogenetic affinities of three bucephalid species via Neighbour-joining (NJ) phylogenetic analysis. Very close phylogenetic affinity between investigated species was revealed; sequence difference between two *Rhipidocotyle* spp. (3.8 % based on 28S) was comparable with intergeneric differences between *Rhipidocotyle* spp. and *B. polymorphus* (3.48% and 4.13 % based on 28S). A high degree of similarity was noted in karyotype structure; the diploid chromosome sets consist of 14 biarmed chromosomes with the 1st pair of metacentric elements markedly larger than the remaining chromosomes. One specimen of *A. anatina* was infected with tetraploid *R. fennica*, 4n=28. On the basis of karyotypic characters, as well as with molecular data, species of the genus *Rhipidocotyle* can't be recognised to be more closely related to each other than to *B. polymorphus.*

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POSTER No. 33

Molecular and karyological evidences for the systematic position of *Cercariaeum crassum* among Allocreadiidae (Trematoda: Digenea)

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Cercariaeum crassum Wesenberg-Lund, 1934 is among the fairly common and widely distributed larval digeneans parasitizing the sphaeriid bivalve, *Pisidium amnicum*. The systematic position of *C. crassum* has been obscured for many years. It was ascribed to the Monorchidae or Lissorchiidae by different authors, and has previously been reported as *Cercaria* (=*Cercariaeum*) *crassa* in Ukraine, *Palaeorchis* sp. in Russia or *Palaeorchis crassus* in Finland. After comparative study of morphology and development of intramolluscan stages of *C. crassum,* Niewiadomska and Valtonen suggested its allocation to the family Allocreadiidae (Niewiadomska, Valtonen 2007. *Systematic Parasitology* 68, 147). In our study *C. crassum* was obtained from *P. amnicum*, collected in Lithuanian and Finnish rivers. A karyotype and two regions of rDNR (ITS2 and partial 28S) were used for comparative phylogenetic analysis. In phylogenetic trees, based on ITS2 and 28S sequences, *C. crassum* clusters into one clade with *Allocreadium* spp., together with *A. isoporum* as a closest sister species; the level of rDNA sequence divergence between them (2.67% for ITS2 and 1.16% for 28S) is consistent with the level expected for intrageneric variation. Allocreadiid species possess comparatively large chromosomes (up to 13-14 μm) and low haploid numbers of six, seven or eight. Karyotype of *C. crassum* consists of 5 pairs (2n = 10) of large, up to 14 μm, bi-armed chromosomes. One or two small, metacentric, mitotically stable B chromosomes were detected in the cells of parthenitae isolated from some host individuals.

This research was funded by a grant (No. MIP-84/2010) from the Research Council of Lithuania.

POSTER No. 34

Regulation of fibronectin-mediated adherence in *Trichomonas vaginalis*

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Trichomoniasis is the most common nonviral sexually transmitted disease, caused by the parasitic flagellate *Trichomonas vaginalis.* This parasite attaches to vaginal epithelial cells (VEC) in females and causes contact-dependent cytotoxicity which leads to erosion of the epithelium. Previous studies showed that fibronectin genes, the major extracellular matrix component of VEC, were overexpressed in *T. vaginalis* attached cells. In the present study, we used fibronectin-induced cytoadherence as a model to investigate the effects of cell density and pH on cytoadherence in *T. vaginalis*. The cytoadherence assay revealed that the maximum fibronectin-mediated cytoadherence occurred at a cell density of 10 million cells/ml and pH 7.0. It implies that during the menstruation cycle, which is usually accompanied by an increase in vaginal pH, will induced the adherence of *T. vaginalis* to VEC. We also followed the gene and protein expression levels of the actin-depolymerizing factor (ADF)/cofilins, a family of actin-binding proteins, which disassembles actin filaments, in the trophozoite and adherent stages of *T. vaginalis*. Bioinformatics analysis of the *Trichomonas* genome identified two ADF/Cofilin homologous genes (Tv_ADF1 and TvADF2) based on the conserved actin-depolymerizing protein signature. The gene expression levels of both Tv_ADFs were up-regulated in adherent cells while Tv_ADF1 was expressed higher than Tv_ADF2. We also determined the gene expression profiles of 8 cytoskeleton-related genes. Our experimental data showed actin-related protein (arp) 2/3 complex, gelsolin, fimbrin and coronin genes were up-regulated in adherent cells but not formin, capping protein, kinesin, profilin and 14-3-3. Based on the experimental results obtained, we suggested that the clinical symptom of Trichomoniasis is related to the increased binding ability of *T. vaginalis* to the surface fibronectin of vaginal epithelial cells at pH 7 during menstruation.

POSTER No. 35

Survey on the ectoparasites (Flea) of *Rattus norvegicus* captured in Tehran, Iran

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Rodents play an important role as host of ectoparasites and as a reservoir of different zoonotic diseases. The aim of this study was the morphological identification of ectoparasites (fleas) of *Rattus norvegicus* captured in different areas of Tehran.
Rodents were captured using live traps during the study period in year 2009-2010. After transferring the rodents to the laboratory, they were identified and *R. norvegicus* were selected and their ectoparasites were collected and mounted for species identification using appropriate systematic keys. A total of 150 rodents were identified including *R. norvegicus* (83%), *Rattus rattus* (11.7%) and *Mus musculus* (5.3%). *R. norvegicus* were selected for this study; 92% of them were infested with ectoparasites. A total of 628 ectoparasites were collected, comprising mites (320), lice (214) and fleas (93). Among all ectoparasites the lice were selected as case to morphologically. Two species of flea; *Xenopsylla cheopis* and *Nosopsylla fasciatus* were identified with higher index of *X. cheopis*. Among all arthropods collected, mites and fleas had the greatest and the least frequency, respectively. The data showed that the ectoparasites on some rodent hosts tend to prefer particular host body sites, and that some ectoparasite species sites may overlap owing to their inaccessibility to the host. These arthropods are important due to their role in plague, CCHF and typhus transmission. Monitoring of ectoparasite infestation is important for preparedness and early warning preparation for possible control of arthropod-borne diseases.

POSTER No. 36

Biotransformation study of anthelmintic drugs in *Hymenolepis diminuta*

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Biotransformation enzymes and transport proteins can, to a certain extent, protect the parasitic worms against the toxic effects of anthelmintics and contribute to resistance development. Obtained information can also be applied in development of new drugs or modification of the old ones. The objective of our work was to find and identify phase I and phase II metabolites of anthelmintic drugs formed by the rat tapeworm (*Hymenolepis diminuta*), a species often used for the study of tapeworm life and metabolism. For characterization of metabolites liquid chromatography/mass spectrometry methods were used. For *ex vivo* and *in vitro* biotransformation studies with *H. diminuta* several drugs from benzimidazole group - albendazole, flubendazole, and mebendazole, and from pyrazino-isoquinoline group - praziquantel, were selected. These drugs are often used all around the world for treatment of parasitoses and in some cases the resistance of parasites to them was described. Our study proved the ability of *H. diminuta* to metabolize some benzimidazole drugs, especially flubendazole and mebendazole, where phase I and II metabolites with probably lower anthelmintic activity were observed. On the contrary, no metabolites were found in experiments with praziquantel and albendazole. These facts show that tapeworms are not able to metabolize some drugs but are able to metabolize and deactivate other drugs which can lead to resistance development.

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POSTER No. 37

Evolutionary immunogenetics: host-parasite interactions in Atlantic salmon (*Salmo salar* L.)

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Human activities and climate change are rapidly altering natural environment, resulting in many organisms being exposed to new pathogens. Different populations of the same species may exhibit unequal levels of susceptibility to pathogens, and evolutionary approaches aimed at understanding the immunological reasons behind these differences in susceptibility may help to predict future immunological consequences of climate change. In my recently started PhD project, I study the interactions of Atlantic salmon and its parasite *Gyrodactylus salaris* (Monogenea). Together, they form an ideal model to study the evolution of host-parasite resistance as there is a pronounced susceptibility gradient: Barents Sea and Atlantic Ocean salmon populations are highly susceptible to *G. salaris*, Baltic Sea — moderately susceptible and Karelian landlocked populations are resistant. Three projects will be conducted: 1) identification of genomic regions under natural selection in salmon 2) population genomics of *G. salaris* and 3) identification of enzymes the parasite uses for digesting salmon skin. Modern genetic methods and bioinformatics tools will be applied to find immune-relevant genes explaining the adaptation gradient existing in salmon populations. Also I will sequence several strains of the parasite in order to assess *G. salaris* strain diversity. Thus the geological history of host-parasite association and evolution of parasite resistance in salmon will be reconstructed. Transcriptomics techniques will be applied to find a transcribed parasitic enzyme involved in salmon mucus digestion, which is the first step towards detecting the cause of inflammation and syndrome of gyrodactylosis in salmonids.

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