48. Jahrestagung der Österreichischen Gesellschaft für Tropenmedizin, Parasitologie und Migrationsmedizin

48th Annual Meeting of the Austrian Society of Tropical Medicine, Parasitology and Migration Medicine

"Emerging Diseases & Migration"

Programm
Programme

Kurzfassungen
Abstracts

ÖGTPM

Meerscheinschlössl
Graz, Austria
20. – 22. November 2014

www.ögtpm.at

Umschlagbild: Christkindlmarkt vor dem Rathaus am Hauptplatz
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Dear Colleagues and Friends,

Hereby I would like to cordially welcome you to the 48th Annual Meeting of the Austrian Society of Tropical Medicine, Parasitology and Migration Medicine, which will be held from November 20-22, 2014 at the beautiful Meerscheinschlössl in Graz. This year's conference is entitled "Emerging Diseases and Migration" and again we have tried to compile an exciting programme, embracing the manifold activities of our society in the areas of tropical medicine, parasitology and migration medicine.

The scientific programme will cover a diversity of topics, including basic, translational and clinical research, as well as case reports and skill enhancements.
Also this year we have been able to invite renowned researchers from Austria and abroad to present their cutting-edge research. We hope that the variety of topics provide a "healthy mix" of molecular biology, epidemiology and clinical research and will attract participants from a wide range of fields. There was scope for submission of presentations in any aspect of tropical medicine, parasitology and migration medicine. Besides oral presentations we will again also have a chaired poster session giving the authors the opportunity to present and discuss their work.

We would like to particularly welcome also young scientists who attend the meeting, competitive travel grants, poster and junior awards will again be provided.
On this occasion I would like to express again my sincere thanks to our sponsors, who support us once again in the organisation and the funding of the meeting.
I am looking forward to a thrilling, informative and rewarding conference and to seeing you all in Graz!

On behalf of the conference committee and the board of the ÖGTPM,

Sincerely yours,

Julia Walochnik
President of the ÖGTPM

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KURZFASSUNGEN DER VORTRÄGE/*ABSTRACTS OF LECTURES*

(in chronologischer Reihenfolge, fett: Plenarvorträge, Stern: Bewerb um Junior Award)
(*in chronological order, bold: plenary lectures, asterisk: applicant for Junior Award*)

20.11.2014

21.11.2014

22.11.2014

KURZFASSUNGEN DER POSTER/*ABSTRACTS OF POSTERS*

(in chronologischer Reihenfolge, Stern: Bewerb um Posterpreis)
(*in chronological order, asterisk: applicant for Poster Award*)

THURSDAY, NOVEMBER 20th

9:00 – 10:00 Registration

10:00 – 10:15 **WELCOME ADDRESS**
Julia WALOCHNIK (President of the ÖGTPM)

10:15 – 11:00 **KEYNOTE LECTURE**
Chair: Angelika Wagner

Marylyn M. ADDO: Research on Emerging Infectious Disease Agents
Division of Infectious Diseases, Universitätsklinikum Hamburg-Eppendorf, Germany

11:00 – 11:30 *Coffee break*

11:30 – 12:50 **VETERINARY PARASITOLOGY**
Chairs: Anja Joachim & Georg Duscher

11:30 – 11:50 Elick O. Otachi, S. A. Locke**, Franz JIRSA**, C. Fellner-Frank, D. J. Marcogliese: Morphometrics vs. Genetics: *Tylodelphis* sp. from four fish species in Lake Naivasha, Kenya

11:50 – 12:10 **Martina ONDROVICS**, K. Silbermayr, N. D. Young, M. Mitreva, E. Razzazi-Fazeli, R. B. Gasser, A. Joachim: Elucidating the moulting process in *Oesophagostomum dentatum* using -OMIC technologies

12:10 – 12:30 **Walter GLAWISCHNIG**, E. Vanek, A. Wunsch, P. Pless: First reports of *Trichinella pseudospiralis* in wild boars (*Sus scrofa*) in Austria

12:30 – 12:50 **Georg DUSCHER**, H.-P. Fuehrer, A. Kübber-Heiss: Unexpected findings of tick-borne pathogens: *Hepatozoon canis* and *Babesia microti*-like pathogens in red foxes from Austria

12:50 – 14:20 *Lunch break*

14:20 – 15:40 **EXPERIMENTAL/MOLECULAR PARASITOLOGY**
Chairs: Michael Duchêne & Irma Schabussova

14:20 – 14:40 **Lucie ŠKORPÍKOVÁ**, B. Koudela, J. Ilgová, E. Šrámová, M. Gelnar, M. Kašný: Cystatins of the parasitic Nematodes -*Trichinella spiralis, T. britovi* and *T. pseudospiralis*

14:40 – 15:00 **Ursula FÜRNKRANZ**, B. Henrich, J. Walochnik: Stable co-cultivation of *Mycoplasma hominis* and *Trichomonas vaginalis* does not depend on the P50/Vaa architecture

15:00 – 15:20 **Ute SCHEIKL**, A. Tsao, M. Horn, A. Indra, J. Walochnik: Free-living amoebae (FLA) and their intracellular bacteria in Austrian cooling towers and tap waters

15:20 – 15:40 **Elisabeth DIETERSDORFER**, B. Schrammel, A. Kirschner, J. Walochnik: From amoebae to macrophages: Testing the infectivity of viable but non-culturable *Legionellae*

15:40 – 16:15 *Coffee break*

16:15 – 18:00 **HOT TOPICS: EMERGING PATHOGENS & THEIR VECTORS**
Section planned by the "Network for Young Parasitologists Austria (NYP@)
Chairs: Ursula Fürnkranz & Hans-Peter Fuehrer

16:15 – 17:00 **Colin SUTHERLAND**: Biological observations on the persistent human parasites *Plasmodium malariae, P. ovale curtisi* & *P. ovale wallikeri*
London School of Hygiene & Tropical Medicine, London, UK

17:00 – 17:20 **Carina ZITTRA**, B. Eigner, G. G. Duscher, K. Lebl, A. G. Obwaller, T. Zechmeister, C. Baumgartner, J. Waringer, H-P. Fuehrer: Invasive mosquitoes in Austria – an overview of the mosquito fauna in Eastern Austria

17:20 – 17:40 **Hans-Peter FUEHRER**, H. Auer, M. Leschnik, K. Silbermayr, G. Duscher, A. Joachim: *Dirofilaria repens* and *Dirofilaria immitis* in Austria

17:40 – 18:00 **Adelheid G. OBWALLER**, W. Poeppl, A. Graf-Langheinz, G. Mooseder, A. Faas, J. Walochnik: Seroprevalence and asymptomatic carriage of *Leishmania* spp. in Austrian soldiers returning from missions in the Lebanon, Syria and Bosnia

18:30 GET TOGETHER at the Meerscheinschlössl

FRIDAY, NOVEMBER 21st

8:30 – 9:00 Registration

9:00 – 9:45 **KEYNOTE LECTURE**
Chair: Julia Walochnik

Toni AEBISCHER: *Leishmania* infections: Towards understanding the intracellular life style of the parasites
Agents of Mycoses, Parasitoses and Mycobacterioses, Robert Koch Institute, Berlin, Germany

9:45 – 10:10 *Coffee break*

10:10 – 11:40 **CLINICAL TROPICAL MEDICINE**
Chairs: Martin Haditsch & Harald Nödl

10:10 – 10:40 **Martin HADITSCH**: The Good, the Bad and the Ugly

10:40 – 11:00 **John WACHIRA**: Percutaneous treatment for cystic *Echinococcus* in Kenya - is pair treatment of CE a sound alternative in low-income countries?

11:00 – 11:20 **Maria KITCHEN**, S. Strickner, G. Leierer, M. Rappold, M. Geit, A. Steuer, A. Rieger, N. Taylor, B. Haas, M. Kanatschnig, M. Sarcletti, R. Zangerle' for the AHIVCOS Study Group: Travel and migration shape the distribution of HIV-1 subtypes in the Austrian HIV Cohort: an epidemiological update

11:20 – 11:40 **Aline LAMIEN-MEDA**, K. König, M. Mischka, R. Meda, M. Compaoré, M. Kiendrebeogo, H.-P. Fuehrer, H. Noedl, J. Novak: In vitro antiplasmodial activity of *Cochlospermum planchonii* and its phytomedicine N'dribala

12:00 – 14:00 **LUNCH SYMPOSIUM I: SELTENE PARASITOSEN** (in **German**)
(in collaboration with INSTAND & ÖQUASTA)

Chairs: Herbert Auer & Klaus Janitschke

Gabriele SCHÖNIAN:	Leishmaniose
Martina KÖHSLER:	Akanthamöben-Keratitis
Marija STOJKOVIC:	Alveoläre Echinokokkose
Herbert AUER:	Toxokarose – eine vielgestaltige und weithin unbekannte Helminthose in Mitteleuropa

14:00 – 15:20 **PARASITOLOGY**
Chairs: Martin Kasny & Franz Jirsa

14:00 – 14:20 **Nikol RESLOVÁ**, M. Slaný, M. Kašný, P. Králík: Detection of parasitic helminths in final meat products

14:20 – 14:40 **Martin WEILER**, G. Duscher, P. Hufnagl, J. Walochnik: Tick screening and risk assessment at military training sites in Austria

14:40 – 15:00 Julia Matt & **Michael DUCHÊNE:** *Entamoeba histolytica* – the ways to eat simple sugars

15:00 – 15:20 Andreas Trobisch, K. Pfurtscheller, I. Knez, F. Reinthaler, A. Gamillscheg, A. Pilhatsch, W. Klepetko, G. Zobel, C. Urban, **Werner ZENZ**: Management of a 16 year old patient with cardiac and pulmonary cystic echinococcosis

15:20 – 16:00 *Coffee break*

16:00 – 18:00 Guided **POSTER SESSIONS**

SESSION I
Chair: Erich Schmutzhard

1. **Gebeyaw GETNET**, A. Alemu, S. Getie, M. Srivastava, H.-P. Führer, S. Duparc, H. Noedl: Relapses in *Plasmodium vivax* malaria in Ethiopia from a clinical and microscopy perspective
2. **Josef HARL**, H.-P. Fuehrer, A. Joachim: DNA-Barcoding of helminth parasites in Austria within the framework of the Austrian Barcode of Life initiative (ABOL)
3. **Adnan HODŽIĆ**, M. S. Latrofa, G. Annoscia, A. Alić, R. Beck, R. P. Lia, F. Dantas-Torres, D. Otranto: The spread of zoonotic *Thelazia callipeda* in the Balkan area
4. **Jana ILGOVÁ**, M. Gelnar, M. Kašný: Cysteine peptidase inhibitors from blood-feeding fish parasite *Eudiploozoon nipponicum* (Monogenea)
5. **Verena MÜNDLER**, I. Häfeli, I. Steinmetz, J. Walochnik: *Acanthamoeba* - possible host for *Burkholderia pseudomallei*
6. **Nicola PALMIERI**, H. L. Worliczek, D. Blake, A. Joachim: Identification of vaccine candidates protective against *Cystoisospora suis* using reverse vaccinology

SESSION II
Chair: Julia Walochnik

7. **Alireza SAZMAND**, B. Eigner, M. Mirzaei, S. Hekmatimoghaddam, A. Joachim, H.-P. Fuehrer: Molecular identification of blood parasites in camels (*Camelus dromedarius*) of Iran
8. **Aruna SHRESTHA**, L. R. Norup, H. R. Juul-Madsen, R. M. Engberg: Influence of chicken serum mannose-binding lectin levels and feed on the immune response towards *Ascaridia galli* in organic layers: Preliminary results
9. **Mitaly SRIVASTAVA**, A. Alemu, S. Getie, G. Getnet, H.-P. Führer, S. Duparc, H. Noedl: Molecular analysis of reemergence of parasitemia in *Plasmodium vivax* malaria in Ethiopia. Preliminary data.
10. **Thomas STREBINGER**, I. Häfeli, H. Auer, A. Obiltschnig, H. Aspöck, J. Walochnik: Babesiosis in Austria

11. **Sarah ÜBLEIS**, D. Berer, B. Eigner, C. Zittra, K. Lebl, H.-P. Fuehrer: Filarioid helminths and avian malaria in mosquitoes in metropolitan Vienna
12. **Carina ZITTRA**, Z. Kocziha, S. Pinnyei, J. Harl, K. Kieser, A. Laciny, B. Eigner, K. Silbermayr, G. G. Duscher, E. Fok, H.-P. Fuehrer: The use of screening blood-fed mosquitoes for the diagnosis of filarioid helminths and avian malaria

EVENING EVENT
Mayors Reception at the Graz City Hall from 19:30
Hauptplatz 1, 8010 Graz (Gemeinderatssitzungssaal)

HANDING OVER of the TRAVEL GRANTS *(courtesy of ÖGTPM)*
HANDING OVER of the JUNIOR-AWARD *(sponsored by Pfizer)*
HANDING OVER of the POSTER-PRIZE *(sponsored by Pfizer)*

Jazzkeller in der Gartengasse 11 (Uli Hahn-Quintett **)**

SATURDAY, NOVEMBER 22nd

FORTBILDUNG ÄRZTE/APOTHEKER (in **German** language)

8:30 – 9:00 Registrierung

9:00 – 10:30 **VIRUSINFEKTIONEN**
Chairs: Herwig Kollaritsch & Angelika Wagner

09:00 – 09:30 **Franz X. HEINZ:** Die Entstehung neuer Viren des Menschen
Department of Virology, Medical University Vienna, Austria

09:30 – 10:00 **Kilian STOECKER**, E. Fleischmann, S. Mely, E. Newman, S. Meschi, B. Becker-Zjaja, M. Gabriel, A. DiCaro, S. Günther, R. Wölfel: First deployment of the European mobile laboratory in the course of the Guinea Ebola outbreak

10:00 – 10:30 **Maria PAULKE-KORINEK**: Impfungen gegen Tollwut und Japanische Enzephalitis: Neue klinische Daten

10:30 –11:00 *Kaffeepause*

11:00 – 12:00 **REISE- & TROPENMEDIZIN: QUIZ mit VOTING**
(mit Unterstützung durch MSD)
Moderation*:* **Herwig KOLLARITSCH & Martin HADITSCH**

12:00 – 13:00 **LUNCH SYMPOSIUM II: DURCHFALL**
(in collaboration with Gilead Sciences & Astellas Pharma)

Chairs: Horst Aspöck & Wolfgang Graninger

Wolfgang GRANINGER: Durchfall durch Viren und Bakterien
Horst ASPÖCK: Durchfall durch Parasiten

Research on Emerging Infectious Disease Agents

Marylyn M. Addo

Division of Infectious Diseases, Universitätsklinikum Hamburg-Eppendorf, Germany
E-mail: m.addo@uke.de

Leishmania infections: Towards understanding the intracellular life style of the parasites

Toni Aebischer

Robert Koch-Institute, Berlin, Germany
E-mail: AebischerA@rki.de

Intracellular protozoan parasites of the genus *Leishmania* are the causative agents of a spectrum of diseases in humans. Their outcome ranges from self healing to fatal. Visceral leishmaniasis alone contributes some 500 000 infections and an estimated 50 000 deaths annually to the burden of these infections. Drugs are available but costly and resistance to several first line treatments is of concern. The development of new therapies and vaccines is therefore a high priority. Current treatment options and the status of vaccine development will be briefly reviewed before presenting a selective overview over available –omics data sets in this field that hold the promise of boosting process and efforts of vaccine development and new drug target identification. The process will be illustrated with our own examples of vaccine development, by a variation of reverse vaccinology, and of drug target identification starting from a proteomic description of the intracellular form of the parasites. With respect to vaccine development, we will discuss the relative importance of criteria for the selection of candidate vaccine antigens from large data sets. In regard to drug target identification, data on the relevance of particular enzymes of the beta-oxidation of fatty acids in the parasites will be presented and discussed in the context of a model of the parasites' intracellular habitat.

Durchfall durch Parasiten

Horst Aspöck

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Akute Durchfallerkrankungen sind nicht nur in den gemäßigten Zonen, sondern auch in den Tropen fast immer viral oder bakteriell und nur selten durch parasitäre Erreger bedingt. Unter den Ausnahmen steht an erster Stelle *Giardia duodenalis* (= *Giardia intestinalis = Lamblia intestinalis*), ein weltweit verbreitetes Protozoon, mit dem man sich durch orale Aufnahme von Zysten (mit kontaminiertem Trinkwasser, mit verunreinigten Lebensmitteln oder auch durch Kontakt mit infizierten Personen) infizieret. Der weitaus gefährlichste Erreger ist *Entamoeba histolytica*: Amöbenruhr ist eine lebensbedrohende Krankheit. Zudem können viele andere Protozoen und Helminthen zu unterschiedlich schweren Durchfällen mit unterschiedlichen Inkubationszeiten führen.
Erfolgreiche Parasiten sind dadurch ausgezeichnet, dass sie ihren Wirt möglichst wenig schädigen und möglichst keine Verkürzung seiner Lebenserwartung bedingen. Das gilt für Protozoen und Helminthen gleichermaßen, und das gilt natürlich auch für die Parasiten des Menschen, allerdings nur, wenn der Mensch einen essentiellen Wirt im Zyklus des Parasiten darstellt, wenn also der Parasit den Wirt *Homo sapiens* für sein Überleben braucht. Wenn der Mensch ein zufälliger, gelegentlicher Wirt ist (und er ist es bei einer großen Zahl von Parasiten), erübrigt sich eine „Rücksichtnahme“ auf die Lebensqualität und Lebenserwartung des Wirts. All dies gilt auch für die Darmparasiten des Menschen. Tatsächlich fungiert der Mensch als essentieller Wirt für nicht wenige Darmparasiten (einige sind sogar streng anthropostenoxen): *Giardia duodenalis, Cryptosporidium hominis, Sarcocystis suihominis und S. bovihominis, Isospora belli, Cyclospora cayetanensis, Entamoeba histolytica, Entamoeba dispar; Taenia saginata, T. solium, T. asiatica, Trichuris trichiura, Enterobius vermicularis, Strongyloides stercoralis, S. fuelleborni, Ancylostoma duodenale, Necator americanus, Ascaris lumbricoides* u.a.
Alle diese Parasiten können zu Durchfällen führen, aber – wenn man von *Entamoeba histolytica* absieht – sind die durch diese bedingten Diarrhoen selten akut und schon gar nicht lebensbedrohend, sondern eher chronisch mit wechselnder Intensität, oft auch selbstlimitierend. Aus der Sicht der Evolution sind leichtere Formen von Durchfällen für die Parasiten durchaus vorteilhaft, weil durch sie die Beförderung der für die Verbreitung wichtigen Stadien (v.a. Zysten, Oozysten; Eier) nach außen gefördert wird, was der Ausbreitung der Parasiten zugute kommt.
All dies gilt für den immunkompetenten Menschen. Bei einer Immunsuppression ist alles ganz anders. Bei diesen Menschen können sonst harmlose Durchfälle zu einer tödlichen Gefahr werden. Dies ist besonders bei HIV-Positiven zu bedenken.
Die Diagnose der Darmparasiten ist für den Parasitologen in der Regel eine sehr einfache Angelegenheit mit verlässlichem Ergebnis. Der Nachweis einer Infektion oder Infestation mit Darmparasiten ist eine Conditio sine qua non für eine adäquate Therapie, wofür uns eine Reihe hochwirksamer Medikamente zur Verfügung steht.
Natürlich gibt es keine Impfungen gegen irgendwelche Darmparasiten, und auch eine Chemoprophylaxe ist keinesfalls gerechtfertigt. Hingegen können einfache Verhaltesweisen im Sinne einer Expositionsprophylaxe zu einem erheblichen Teil Durchfallerkrankungen durch Parasiten verhindern.

Toxokarose – eine vielgestaltige und weithin unbekannte Helminthose in Mitteleuropa

Herbert Auer & R. Schneider

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Unter dem Begriff „Toxokarose“ werden verschiedene Krankheitssyndrome des Menschen zusammengefasst, die durch Infestationen mit dem Hundespulwurm (*Toxocara canis*) und dem Katzenspulwurm (*T. cati*) verursacht werden. Die natürlichen Wirte von *T. canis* und *T. cati* stellen Hunde und Füchse bzw. Katzen dar, in deren Darm sie als erwachsene weibliche und männliche Würmer leben. Der Mensch ist für beide Spezies ein Fehlwirt, der die Infestation durch orale Aufnahme von mit infektionstüchtigen Eiern kontaminiertem Wasser, kontaminierter Erde oder kontaminierten Hände erwirbt. Im Dünndarm des Menschen schlüpfen aus den Eiern Larven, die über den Pfortaderkreislauf und den großen Blutkreislauf in alle Organe transportiert werden können. Die *Toxocara*-Larven können sich im Fehlwirt Mensch nicht zu erwachsenen Würmern entwickeln, sondern bleiben im Menschen lebenslang eine Larve; ihre Lebenserwartung kann mehrere Jahre betragen. In Abhängigkeit von ihrer Organ- oder Gewebslokalisation können die Larven durch ihre „Wandertätigkeit“ und ihren Stoffwechsel einerseits und die Reaktivität des Immunsystems andererseits beachtliche Zell- und Gewebeschäden verursachen, die sich auch klinisch manifestieren. Auch wenn die meisten *Toxocara*-Infestationen des Menschen klinisch unauffällig verlaufen, so müssen wir heute dennoch davon ausgehen, dass in Österreich pro Jahr mehrere hundert Menschen an einer Toxokarose leiden. Die Toxokarose kann sich als „viszerales Larva migrans-Syndrom (VLM), als „okuläres Larva migrans-Syndrom (OLM)“, als „covert toxocarosis“, als „common toxocarosis“ oder als „zerebrale Toxokarose“ manifestieren. Darüber hinaus werden aber auch immer wieder Assoziationen von Toxocara-Infestationen zu den Symptomkomplexen „Rheuma“, „Epilepsie“ und „Asthma“ vermutet. Dieses Referat gibt einen Überblick über die Toxokarose in Österreich.

From amoebae to macrophages: testing the infectivity of viable but non-culturable *Legionellae*

Elisabeth Dietersdorfer[1], Barbara Schrammel[2], Alexander Kirschner[2], Julia Walochnik[1]

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The abundance of medically relevant legionellae in anthropogenic water systems may be underestimated, mainly due to the non-culturability of a considerable percentage of the *Legionella* populations. *Legionella pneumophila* can infect the human lung, replicate within alveolar macrophages and cause, besides milder forms, Legionaires' disease. Under poor nutrient conditions, legionellae can enter the viable but non-culturable (VBNC) state. Free-living amoebae are known to be reservoirs and vehicles for *L. pneumophila.*If a formerly non-culturable *Legionella* strain enters an amoebae, it may become resuscitated and culturable again.The aim of this project is to investigate the infectious potential of *VBNC* legionellae from environmental water samples. To achieve this, different infection models were installed: Amoeba models *(Acanthamoeba* and *Vermamoeba vermiformis)* are used as "training grounds" for the legionellae to test their survival and resuscitation potential. As intracellular replication in amoebae may trigger the ability of VBNC legionellae to infect human cells, a macrophage model was established to test infectivity. For setting up the models, optimal bacteria:amoeba ratios as well as environmental conditions were evaluated. In the *Acanthamoeba* host model it was shown that laboratory-induced VBNC legionellae are able to infect amoebae, replicate intercellulary and lyse their hosts. The progression of infection was observed by microscopy and FISH. Current work focuses on testing if VBNCs may become resuscitated, be converted into a culturable state by passages through amoebae and their ability to start an infectious cycle in human macrophages before and after passage through amoebae.

Unexpected findings of tick-borne pathogens: *Hepatozoon canis* and *Babesia microti*-like pathogens in red foxes from Austria

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The red fox (*Vulpes vulpes*) has been described as carrier of many human and pet relevant pathogens such as fox tapeworm, rabies and scabies. In the recent past it was also assumed in the spreading and transmission of several tick-borne pathogens like *Anaplasma phagocytophilum*, *Hepatozoon canis*, *Babesia* spp., *Ehrlichia canis* and *Rickettsia* spp.
Due to the close vicinity of fox habitats and human settlements, an interface between ticks, wildlife and urban areas is built, which may contributes transmission of pathogens from wildlife to pets and humans.
During a molecular screening for several tick-borne pathogens of spleens and blood originating from 36 Austrian foxes, a high amount of *Babesia microti*-like and *Hepatozoon canis* positive animals was found. Twenty-one out of 36 foxes, 58.3 %, turned out to be positive for *H. canis*. Since the main vector species of *H. canis*, *Rhipicephalus sanguineus*, is not endemic in Austria and no autochthonous reports of this pathogen in dogs have been reported so far, this raises new questions. Other tick species might act as vectors as well. Furthermore vertical transmission in the foxes or transmission via preyed tissue could also occur. Concerning *B. microti*-like pathogens, we identified 50 % (18 out of 36) positive foxes. For this pathogen, only scarce information is available. The tick *Ixodes hexagonus* is considered to be involved in the transmission cycle. In some countries dogs are affected. Until now cases of dogs in Austria were not reported. Information about the zoonotic potential is not available.
In conclusion, foxes are carriers of human and pet relevant tick-borne pathogens. Further efforts are needed to investigate their role as reservoir and spreader of several diseases.

Dirofilaria repens and *Dirofilaria immitis* in Austria

Hans-Peter Fuehrer[1], Herbert Auer[2], Michael Leschnik[3], Katja Silbermayr[1], Georg Duscher[1], Anja Joachim[1]

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Dirofilaria immitis and *D. repens* are filarioid helminths with domestic and wild canids as main hosts and mosquitoes as vectors. Both species are known to cause zoonotic diseases, namely ocular (*D. repens*) and subcutaneous (*D. repens*) as well as pulmonary (*D. immitis*) dirofilariosis. Both *D. repens* and *D. immitis* are known as invasive species and their distribution is associated with climate change. Until very recently both species were known not to be endemic in Austria.
In Austria most cases of *Dirofilaria* sp. in humans and dogs are introduced. However, rarely infections with *D. repens* were discussed to be autochthonous. The introduction of *D. repens* to Austria was confirmed only very recently. Within a mosquito surveillance the parasite was detected in Burgenland (Eastern Austria) for the first time in its vector.
We summarize introduced and possible autochthonous cases of *Dirofilaria* sp. in humans, dogs and vectors in Austria.

Parts of this study were supported by the Austrian Science Fund (FWF): I1437.

Stable co-cultivation of *Mycoplasma hominis* and *Trichomonas vaginalis* does not depend on the P50/VAA architecture

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Trichomonas vaginalis, the most common non-viral sexually transmitted pathogen, can provoke several clinical symptoms and infection during pregnancy can seriously affect the foetus. *Mycoplasma hominis*, another potential pathogen of the urogenital tract, can survive and replicate within *T. vaginalis* and is assumed to enhance its pathogenicity and drug resistance.
The overall goal of this project is to elucidate impacts of this interaction on several patho-physiological features, as well as benefit(s) for the respective microorganism. In a first step, conditions for creation of a stable co-culture of *T. vaginalis* with *M. hominis* were elucidated and the requirements for perpetuation characterized. On the one hand this was performed by characterising naturally infected *T. vaginalis* and their symbionts in terms of the properties mentioned below. On the other hand, *in vitro* co-cultivation of four *M. hominis*-free isolates of *T. vaginalis* with four isolates of *M. hominis* was investigated. *M. hominis* was isolated from vaginal mucosa of healthy and symptomatic individuals and from one *T. vaginalis*. All eight isolates of pathogens were characterized concerning their growth kinetics, drug susceptibility, ecto-ATPase activity and cytotoxicity. *M. hominis* was further characterized by the architecture of the main P50/Vaa adhesin and further adhesive membrane proteins, for *T. vaginalis* RAPD analyses are ongoing. Co-cultivation was performed and the survival of both microorganisms as well as the presence of adherent *M. hominis* was proven. The co-cultivation experiments showed significant isolate-to-isolate differences in the ability of establishing a stable co-culture, which could not be related to the kind of P50 architecture.

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Relapses in *Plasmodium vivax* malaria in Ethiopia from a clinical and microscopy perspective.

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In spite of significantly reduced mortality, malaria due to *Plasmodium falciparum* and in certain regions also due to P. vivax remains a major health threat in Africa. Although *P. vivax* is generally considered to be rare in sub-Saharan Africa, with an estimated 665,000 annual cases (WHO 2012) Ethiopia has recently been reporting more cases of *P. vivax* than any other country in the world. A major challenge in controlling and ultimately eliminating vivax malaria is the fact that *P. vivax* can lead to reemergence of parasitemia from dormant liver stage parasites sometimes even years after the initial infection. New treatments for a radical cure of vivax malaria are therefore urgently needed but the pattern of recurrence of parasitemia shows major geographical differences and remains poorly understood.
The goal of the current study has therefore been to establish patterns in recurrence of parasitemia (i.e. the time to and the frequency of recurrence) in patients with *P. vivax* malaria in Ethiopia using a retrospective and a prospective approach. Subjects diagnosed with *P. vivax* monoinfections were followed for 6 months with bi-monthly follow-ups to assess recurrence of parasitemia after treatment with chloroquine following the national treatment guidelines. A total number of 50 study participants were identified at two health centers within the catchment area of the University of Gondar Hospital. Participants were asked to return for regular follow-ups every two months during the 6 month follow-up period. During these visits a slide was taken and examined for malaria parasites as well as blood spots on filter paper for molecular analysis and genotyping.
For all participants the initial diagnosis was done at the HC by microscopy. The geometric mean parasitemias at both enrollment sites were 6230 and 7571/uL, respectively. All participants were febrile (with a duration of fever before enrollment of 2-4 days), had signs and symptoms consistent with malaria, and received chloroquine for their case of vivax malaria. Based on microscopic examination 11 participants (22%) had at least one reemergence of parasitemia during follow-up either during scheduled (4) or unscheduled (7) visits. One subject tested positive on more than one occasion. The survival probability estimates (i.e. the chances of not experiencing a reemergence of parasitemia) for Day 60, 120, and 180 based on microscopy were 0.75, 0.65, and 0.65, respectively at Kola Diba Health Center and 0.92, 0.87, and 0.79 at Maksegnet HC.
A better understanding of the relapse patterns in Ethiopia will be vital for improving current treatment paradigms and for controlling and ultimately eliminating vivax malaria in the country. Microscopical data suggest a relatively low relapse rate among *P. vivax* patients in Ethiopia. This may have major implications for the future treatment of *P. vivax* malaria.

First reports of *Trichinella pseudospiralis* in wild boars (*Sus scrofa*) in Austria

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In Austria more than 5 million slaughtered fattening and breeding swine are examined every year for the presence of *Trichinella* larvae. Since decades no positive finding was detected in domestic pigs. In wildlife the population of wild boars (*Sus scrofa*) is increasing, at present the hunting bag counts about 30.000 animals per year. About 80% of the hunted wild boars originate from the two eastern provinces Upper Austria and Burgenland. When entering the food chain, every carcass of wild boars has to be examined for *Trichinella* by either digestion ore trichinoscopic methods.
We report for the first time the finding of *Trichinella pseudospiralis* in two wild boars in Austria. The first case was found in the year 2011 in the political district Hartberg in the federal province of Styria. The positive animal was a two year old female and showed a larval density of 10 larvae per gram muscle tissue. The second case originated from the political district Neusiedl in the province of Burgenland and was detected in the year 2014. This animal was also a two year old female with a larval density of 19 larvae per gram muscle tissue. Both infections in wild boars were identified by artificial digestion method. In both cases it could be prevented that no meat products entered the food chain.
Trichinella pseudospiralis is a cosmopolitan species belonging to the non-encapsulated clade of the genus *Trichinella*. The larva is lacking a thick collagen capsule as it is observed in the other species found in Europe (*Trichinella spiralis*, *Trichinella britovi*, *Trichinella nativa*). Therefore *Trichinella pseudospiralis* can be missed when applying the trichinoscopic method. For this reason it is highly recommended that the digestion methods should be generally used when examining wild boars for human consumption.

Durchfall durch Viren und Bakterien

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The Good, the Bad and the Ugly

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DNA-Barcoding of helminth parasites in Austria within the framework of the Austrian Barcode of Life initiative (ABOL)

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DNA-barcoding describes the technique of identifying organisms based on species-specific DNA sequences. Specimens investigated have to be examined by taxonomists specialized on the particular groups and are deposited in collections of scientific institutions such as museums and universities. The aim of the International Barcode of Life Project (iBOL) is to establish a public database providing reference sequences of all organisms. In its current applications, DNA barcoding cannot entirely replace species identification based on morphological characters, but it is especially useful when morphometrics are difficult or impossible. This is the case in many parasite species which are small, develop through multi-host life cycles or are found in host tissues or blood. Thereby, the specific identities of the parasites are crucial for understanding host-parasite interactions that underlie parasitic diseases afflicting humans, domesticated animals and wildlife. In 2012, the Austrian Barcode of Life initiative (ABOL) was founded with the goal to record Austrian biodiversity by the use of DNA barcoding. In 2014, the Federal Ministry of Science, Research and Economy (BMWFW) granted funding for a three-year kick-off project in order to establish DNA barcoding in four selected animal groups, including vertebrates, mollusks, butterflies and parasitic worms (helminths). DNA barcoding of helminths is conducted at the University of Veterinary Medicine, Vienna (Institute of Parasitology), in cooperation with the Natural History Museum, Vienna (3rd Zoological Department) and other institutions. Owing to the vast number of helminth species, we will mainly focus on DNA barcoding of vertebrate parasites in the initial stage of the ABOL project.

Die Entstehung neuer Viren des Menschen

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Der Mensch ist durch vielfältige Kontakte mit Tieren ständig einem ‚Schauer' von Viren ausgesetzt, die jedoch in den meisten Fällen aufgrund von Speziesbarrieren sowie unspezifischen und spezifischen Abwehrmechanismen keine Gefahr darstellen. In seltenen Fällen kann es jedoch trotz dieser Hindernisse nach ursprünglicher zoonotischer Übertragung zu Infektionsketten im Menschen kommen und damit zur Entstehung einer Viruserkrankung, die unabhängig vom ehemaligen tierischen Reservoir von Mensch zu Mensch übertragen wird. Die besten Beispiele aus der jüngeren Vergangenheit sind HIV/AIDS (ursprüngliches Reservoir nichthumane Primaten in Afrika), SARS (Fledermäuse in China), MERS (Dromedare sowie Fledermäuse in Afrika und der Arabischen Halbinsel), Influenza (Entstehung neuer Pandemie-Viren aus dem Influenza Virus-Pool in Wildvögeln) sowie Filoviren (Marburg- und Ebola-Viren aus Fledermäusen in Äquatorialafrika). Die der Adaptierung an den Menschen zu Grunde liegenden Mechanismen werden diskutiert und anhand von Beispielen erläutert.

The spread of zoonotic *Thelazia callipaeda* in the Balkan area

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Thelazia callipaeda (Spirurida, Thelaziidae), also known as "oriental eyeworm", is a small nematode parasite that lives in the conjunctival sac of domestic and wild carnivores, rabbits and even humans, causing mild (e.g., conjunctivitis, epiphora, and ocular discharge) to severe (e.g., keratitis, and corneal ulcers) ocular disease. This study reports the occurrence of *T. callipaeda* infection in the Balkan regions for the first time and it provides genetic evidence on the origin of the infection in that area.

The survey was conducted in two Western Balkan countries, Bosnia-Herzegovina (B&H) and Croatia. At necropsy, from January 2011 to April 2014, a total of 184 carcasses of red foxes were examined throughout B&H and worms were collected from the conjunctival sac. In the same period, worms were also collected during clinical examination from the conjunctival sac of four dogs and a cat from B&H and two dogs from Croatia. All nematodes collected were morphologically identified and molecularly characterized by sequencing of partial *cox*1 gene.

T. callipaeda was observed in 51 (27.7%) foxes and the highest prevalence (50.0%) was in the region of East Bosnia. Beside the 4 cases of hyperemia (7.8%), most of the infected animals had no signs of ocular infection (n = 47, 92.1%). A total of 417 adult nematodes collected (364 from foxes, 51 from dogs, 2 from cat) were morphologically and molecularly identified as *T. callipaeda* haplotype 1.

This is the first report of autochthonous cases of *T. callipaeda* infection in red foxes, dogs and cat in B&H and Croatia. The data presented here suggest that reports of thelaziosis in other Balkan areas are, as yet, not diagnosed most likely due to the lack of awareness of practitioners. In addition, data regarding the spread of the infection in Europe over the last ten years suggests that an increasing pattern in the distribution of this disease in domestic and wild animals should be expected in the future.

Cysteine peptidase inhibitors from blood-feeding fish parasite *Eudiploozoon nipponicum* (Monogenea).

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Blood-feeding monogenean *Eudiplozoon nipponicum* parasitizing the gills of common carp (*Cyprinus carpio*) is widely distributed Euroasian ectoparasite from Diplozooidae family. The foregoing research has been oriented toward understanding the morphology and ecology of particular species from this taxonomic group. Currently only a little is known about the mechanisms of host-parasite interactions associated with the functional molecules produced by this parasites.
Among these molecules appear also the cystatins - inhibitors of cysteine peptidases. These were previously proven to play a substantial role in manipulation of the host immune response by various parasitic species and thus maximizing the parasite success.
By revealing the function of cystatin of *Eudiplozoon nipponicum* we would like to fill the gap in the present knowledge concerning the molecules from diplozoid parasites.
By using the data based on *Eudiplozoon nipponicum* transcriptome we identified cystatine gene sequence homologous to cystatins of other related platyhelminth species. We designed specific primers, amplified, cloned and sequenced the gene coding cystatin. Currently we are optimizing the recombinant protein expression in *E. coli* expression system (pET19b vector plasmid, *E. coli* BL21 strain). Recombinant form of *E. nipponicum* cystatin will be characterized in detail.

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Travel and migration shape the distribution of HIV-1 subtypes in the Austrian HIV Cohort: an epidemiological update

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The majority of HIV-infected persons living in Austria are being cared for in the 7 clinical centres of the Austrian HIV Cohort Study (AHIVCOS). Since the beginning of the epidemic a total of 8097 patients have been followed and their virological, clinical and epidemiological data systematically recorded. While Subtype B viruses were predominant in the early years of the epidemic, Non B Subtypes were introduced in subsequent years. Currently, 4147 HIV infected individuals are on regular follow-up in the AHIVCOS centres. Their median age is 45 years and 27.3% are female. 41.4% have acquired the HIV infection through heterosexual contact, 39.0% are MSM (men who have sex with men) and 13.8% intravenous drug users (IVDU).

While in MSM und IVDU the great majority of infections are still due to HIV Subtype B, the viruses transmitted in the heterosexual community have changed over the years. The spectrum of Non-B Subtypes appearing in Austria was shaped by movements of travel and migration. 27.6% of the heterosexually infected patients in the current cohort come from high-prevalence countries (i.e. countries with HIV prevalence in adults > 1%) and further 17.6% acquired the HIV infection through sexual contact with persons originating from high prevalence countries (either in the respective countries or in Austria). With the majority of immigrants in the cohort coming from sub-Saharan Africa (about 70%), the most commonly isolated Non-B Subtypes are the African Subtypes C and AG. Austrian tourists to South East Asia brought the HIV subtype CRF_AE back to Austria and caused pockets of transmission of “Thailand viruses” among the Austrian heterosexual community. In the Tyrol Subtype CRF_AE is the most common Non-B Subtype, accounting for over a quarter of the heterosexually transmitted viruses. In Vienna the various African subtypes dominate (50% in the heterosexual community), reflecting the high number of refugees/immigrants from (West) Africa. However, in the past years the number of HIV infections diagnosed in immigrants from all foreign countries has decreased (to less than 30%) and currently most HIV transmissions seem to occur in the homosexual community.

Acanthamoeba keratitis

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Acanthamoebae are primarily free-living, ubiquitously spread organisms that are able inhabit a wide range of habitats. However, under certain circumstances they can act as facultative pathogens being the causative agents of several disseminating infections, mostly in immunocompromised individuals, and more importantly they are the causative agents of an often seriously progressing keratitis occurring predominantly in contact lens wearers.

Acanthamoeba keratitis (AK) is usually a very painful, sight-threatening inflammation of the cornea. Most commonly AK is associated with considerable production of tears, epithelial defects, conjunctiva congestion, photophobia and massive pain. As the infection progresses corneal infiltration and clouding, scleritis and marked loss of vision are typical symptoms. Eventually, AK can even result in blindness if not treated early enough.
Clinical diagnosis is usually based on phase contrast microscopy and culture of amoebae in combination with a highly sensitive PCR, specific for the genus *Acanthamoeba*. For accurate diagnosis of AK the investigation of adequate clinical material is crucial.
Therapy of AK is still problematic and no specific agent against *Acanthamoeba* is currently available. The recommended treatment regimen includes a combination of polyhexa-methylene biguanide or chlorhexidine digluconate with propamidine isethionate. However, another problematic aspect of therapy is the high resistance of *Acanthamoeba* cysts, which often leads to recurrent infections.
For more than twenty years now, *Acanthamoeba* diagnostics is performed at our institution, which is the Austrian reference laboratory for *Acanthamoeba* infections. More than 160 AK cases have been diagnosed to date.
The current presentation will give an overview on the most relevant facts about *Acanthamoeba* keratitis, including the most important aspects of diagnosis and therapy and some interesting cases from the recent past.

In vitro antiplasmodial activity of *Cochlospermum planchonii* and its phytomedicine N'dribala

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The rhizome of *Cochlospermum planchonii* Hook. f. ex Planch. (Bixaceae) is traditionally used in West African countries as a decoction for the treatment of fevers and malaria. In Burkina Faso, this phytomedicine is called 'N'Dribala. It has been proven by clinical trials to be efficacious as chloroquine for the treatment of uncomplicated *Plasmodium falciparum* malaria (Benoit-Vical, 2003). Different in vitro studies have proven the antimalarial activity of
C. planchonii roots extracts, but the active compounds of the plant still remain unknown.
The aim of our study was to comparatively screen the antiplasmodial activity of extracts obtained with different solvents and fractions of *C. planchonii* using the chloroquine sensitive strain 3D7 of *P. falciparum* and the histidine-rich protein II (HRP2) assay.
The results showed similar IC50 values (> 40 µg/ml) for both methanolic and decoction extracts of *C. planchonii*. An interesting increase in activity was obtained with the successive liquid-liquid partition of the methanolic extract of *C. planchonii* ethyl acetate and dichloromethane, respectively (methanolic extract: 46 µg/ml, ethyl acetate fraction: 11 µg/ml, dichloromethane fraction: 0.8-4 µg/ml). The main compounds of the dichloromethane fraction have been isolated and antiplasmodial testing of these pure compounds is actually ongoing.
This study is presenting interesting comparative data regarding the antimalarial activity of *C. planchonii*, and is showing the potential of initially poorly active target extract of an antimalarial medicinal plant.

Entamoeba histolytica - the ways to eat simple sugars

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The human protozoan parasite *Entamoeba histolytica* causes amoebic colitis and amoebic liver abscess. For the treatment of *E. histolytica* infections, the nitroimidazole drug metronidazole is used. The medium for axenic culture of the parasite contains glucose as energy source, which can readily be phosphorylated by both hexokinase isoforms to enter glycolysis. Through the widespread use of high-fructose corn syrup, human food and beverages often contain more fructose than glucose. In this study we addressed the question whether *E. histolytica* can use fructose as an alternative energy source. As the amoebic hexokinases do not use fructose as substrate, a separate fructokinase is essential. The genome project had revealed a single candidate gene coding for an *E. histolytica* homolog of bacterial fructokinases. This gene was cloned, and the recombinant enzyme was purified and examined. The enzyme had a magnesium-dependent fructose 6-kinase activity with a K_m for fructose of 0.156 mM and a V_{max} of 131 U / mg protein and a much weaker mannokinase activity. No activity was observed with glucose or galactose. The amoebae could be switched from glucose to fructose medium without any problem. Fructokinase mRNA was modestly, but significantly up-regulated in amoebae switched abruptly to fructose medium as well as in fructose-adapted amoebae. Confocal immunofluorescence microscopy revealed a cytoplasmic distribution of fructokinase in the amoebae. Taken together, this product of a laterally acquired gene has become very useful for *E. histolytica* metabolism.

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Acanthamoeba – possible host for *Burkholderia pseudomallei*

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Burkholderia pseudomallei is a gram negative bacterium and the causative agent of melioidosis. The disease is associated with different symptoms including severe pneumonia and septicemia, diagnosis can be very complex. Although an antibiotic therapy e.g. with Ceftazidime is possible, the mortality rate is rather high with up to 50%. Early detection and adequate treatment can reduce lethality significantly. The disease can be acquired by inoculation of the pathogen through skin lesions, by bacteria-containing aerosols from contaminated soil and water and also by ingestion. Until recently, melioidosis was mainly known from northeast Thailand and northern Australia, more and more cases from Africa are being reported. *Burkholderia pseudomallei* are intracellular bacteria and therefore need host cells for replication. *Acanthamoeba spp.* are found in almost every soil and water sample and as they produce extremely resistant cysts they are known to be reservoirs for many other bacterial pathogens, e.g. *Legionella pneumophila*. This ability of the amoebae to survive under extreme conditions like high temperatures and desiccation is one of the main reasons why they seem to be the optimal host of *Burkholderia pseudomallei*. To verify this theory different molecular methods like PCR, gel electrophoresis and sequencing are used. The aim of the current study is to verify the hypothesis that free-living amoeba function as host cells for survival and multiplication of *Burkholderia pseudomallei* in the environment. This project will lead to a better understanding of the global epidemiology of melioidosis and can help undertaking preventive measures.

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Seroprevalence and asymptomatic carriage of *Leishmania* spp. in Austrian soldiers returning from missions in the Lebanon, Syria and Bosnia

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Leishmaniases are caused by the protozoan parasites of the genus *Leishmania*, ranging from cutaneous lesions to visceral disease. Humanitarian assistance or peace-keeping missions allow extensive contact with the local population and environment which increases the chance of getting in contact with endemic infectious diseases.
The aim of this study was to assess the risk factors and exposure to *Leishmania* spp. in Austrian soldiers serving in peace-keeping missions in Syria, Lebanon and Bosnia-Herzegovina.
In June and July 2013, serum, EDTA whole blood samples and epidemiological data were collected from 225 healthy soldiers. Antibodies were tested using a commercial ELISA (RIDASCREEN Leishmania AB ELISA kit, R-Biopharm). All seropositive and borderline subjects were then tested for the presence of *Leishmania* DNA with an established PCR and *Leishmania* species were identified using DNA sequencing.
In total, 18 out of 225 individuals (8%) tested positive and 12 (5%) showed borderline results in the serological screening. Broken down to the operation areas, the data showed an expected higher seroprevalence in soldiers serving in Syria (12% positive, 6% borderline) and Lebanon (7% positive, 5% borderline). Individuals returning from Bosnia showed a seroprevalence of 3%. Ten samples from Syria tested seropositive/borderline by ELISA were PCR positive. The positive PCR results were identified as *Leishmania donovani/infantum* complex.
The present study indicates that the risk of being exposed to *Leishmania* spp. is highest in Syria and lowest in Bosnia.

Elucidating the moulting process in *Oesophagostomum dentatum* using -OMIC technologies

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Parasitic nematode infections of humans and livestock impose a significant burden on public health and economy worldwide. Ecdysis (moulting of the cuticle) constitutes a critical developmental process in this phylum which is absent from the host and might provide a new target for intervention strategies. By combining *in vitro* assays with transcriptomic, proteomic and bioinformatic analyses, we aimed to elucidate the moulting process of the porcine nodule worm *Oesophagostomum dentatum*, a model organism for parasitic nematodes of socio-economic importance. Molecules inferred to be involved in the *in vitro* moult from third-stage larvae (L3s) to fourth-stage larvae (L4s) and in the *in vitro* exsheathment of L3s of *O. dentatum* were identified by gel electrophoresis and subsequent MALDI-TOF/TOF mass spectrometric and bioinformatic analyses. The proteins identified were annotated to different biological processes including energy metabolism, interaction with the host, structure and motility, signalling and interaction and/or development and growth. For specific proteins, reported roles in the moulting process in related nematode species were confirmed (e.g. peptidyl-prolyl *cis-trans* isomerase, cuticlin-1, intermediate filament protein B and tropomyosin), predicted roles in the moulting process were further supported (e.g. fructose-bisphosphate aldolase, propionyl-CoA carboxylase and phosphoenolpyruvate carboxykinase [GTP]) and, new molecules were identified and proposed to play key roles during moulting/exsheathment (e.g. aspartyl protease inhibitor and transthyretin-like protein 5). Some proteins were inferred to be involved both in the *in vitro* moult from L3s to L4s and the *in vitro* exsheathment of L3s of *O. dentatum*, and nine protein homologues could be linked to dauer formation in the free-living nematode *Caenorhabditis elegans*, indicating that these molecules might act on all four moults in *O. dentatum* and thus be part of a conserved pathway or mechanism of moulting generally. This study improves our understanding of moulting in *O. dentatum*, might have implications for other parasitic and free-living nematodes and provides a foundation for investigations on a range of basic and applied aspects of developmental parasitology and new intervention strategies.

Morphometrics vs. Genetics: *Tylodelphis* sp. from four fish species in Lake Naivasha, Kenya

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The species discrimination of metacercariae of Diplostomidae using morphology, infection site or host, has been a challenging task over the last decades and has provoked a lively debate on this issue in the scientific community. During parasitological investigations in fish from lake Naviasha, Kenya, a well-established population of *Tylodelphis sp*. metacercariae was recorded from the vitrous humour of 4 fish species. The parasites were collected from 221 fish comprising one species within the Cyprinidae (*Cyprinus carpio*, n = 145), two Cichlidae (*Oreochromis leucostictus*, n = 56, and *Tilapia zillii*, n = 18) and one Centrarchidae (*Micropterus salmoides*, n = 2). First morphological analyses, mainly based on different size, suggested at least two different species of parasites were present. Quantitative morphometric analyses of 14 characters and 8 indices in 111 specimens gave intermediate support of this distinction into two morphotypes. The subsequent molecular analyses using sequences from the barcode region of the cytochrome c oxidase 1 gene in 11 specimens revealed that both morphotypes were conspecific. All the specimens therefore are inferred to belong to a single unidentified species of *Tylodelphys*, which is not conspecific with any other diplostomid for which comparable molecular data are available, including four diplostomid species known from siluriform fish in Nigeria and Tanzania.

Identification of vaccine candidates protective against *Cystoisospora suis* using reverse vaccinology

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Coccidiosis is a widespread disease of suckling piglets caused mainly by the eukaryotic parasite *Cystoisospora suis* (Phylum: Apicomplexa), which induces profuse diarrhea and growth retardation and results in severe economic losses. Unfortunately, no vaccine is currently available. In this study we evaluate the potential for reverse vaccinology to identify vaccine candidates protective against *C. suis*. Our approach consists of *in silico* screening of the putative parasite proteome to predict proteins likely to induce an appropriate immune response, building on comparable screens applied previously with many bacterial species. Since no genomic resources were available for *C. suis*, we constructed a first genomic reference by *de novo* assembly of 80M Illumina paired-end reads, resulting in ~14000 contigs with a total length of 84Mb. To annotate putative protein-coding genes we combined *ab initio* gene predictions with orthology alignments derived from other apicomplexan species and identified more than 7000 putative protein-coding genes. We plan to validate these predictions and detect additional genes using RNA-Sequencing. Finally, we will screen for vaccine candidates using the recently developed program Vacceed, which is especially suitable for eukaryotic pathogens.

Impfungen gegen Tollwut und Japanische Enzephalitis: Neue klinische Daten

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Japanische Encephalitis (JE) ist eine virale Gehirnhautentzündung und wird durch Stechmücken hauptsächlich der Gattung Culex übertragen. Infektionen mit dem JE-Virus verursachen in Endemiegebieten Asiens jährlich um die 68,000 klinische Fälle (1/3 der Fälle tödlich), welche nur symptomatisch behandelt werden können.
Das Tollwutvirus wird meistens durch den Biss infizierter Tiere übertragen. Treten klinische Symptome von Tollwut auf, so ist die Erkrankung praktisch immer tödlich und verursacht somit weltweit jährlich über 66,000 Todesfälle.
Sowohl JE als auch Tollwut können durch sichere, effektive, inaktivierte Impfstoffe vermieden werden. In beiden Fällen ist eine mehrteilige Grundimmunisierung erforderlich: Für JE sind im Rahmen der Grundimmunisierung 2 Impfungen im Abstand von 4 Wochen vorgesehen bzw. für Tollwut 3 Impfungen innerhalb von 3-4 Wochen.
Das stellt in der täglichen Praxis der Reisemedizin ein Problem dar, da sich viele Reisende mit Indikation zur prophylaktischen Impfung kurzfristig vorstellen und vor Reiseantritt oftmals wenige Tage für erforderliche Reiseimpfungen verbleiben.
Es werden neue Daten aus einer Studie an ca. 660 Testpersonen zu Schnellimpfschemata präsentiert, welche die Immunogenität und Sicherheit von Impfstoffen gegen JE und Tollwut bis zum Tag 56 nach der ersten Impfung zeigen. Impfstoffe gegen JE wurden im Schema 0-7 Tage verabreicht, Tollwut-Impfstoffe im Schema 0-3-7 Tage. Eine Gruppe von Testpersonen erhielt beide Impfstoffe gleichzeitig. Es konnte gezeigt werden, dass beide Impfstoffe auch im Schnellschema bis zum Tag 56 hoch immunogen sind und es zu keiner erhöhten Rate von Nebenwirkungen im Vergleich zu einzeln in konventionellen Schemata verabreichten Impfungen kommt.
In einer weiteren Studie an ca. 350 Probanden wurde die Verabreichung von Impfstoffen gegen JE und Tollwut gemeinsam mit einem quadrivalenten, konjugierten Impfstoff gegen Meningokokken untersucht. Es konnte keine nachteilige Auswirkung auf Immunogenität oder Verträglichkeit der Impfstoffe im Vergleich zu den einzeln verabreichten Impfstoffen beobachtet werden.
Die Untersuchungen zeigen, dass Impfstoffe gegen JE, Tollwut und Meningokokken (konjugierter, quadrivalenter Impfstoff) gleichzeitig und in verkürzten Impfschemata (derzeit keine Zulassung) verabreicht hoch immunogen sind, ohne dass es zu einer erhöhten Rate an Nebenwirkungen kommt.

Detection of parasitic helminths in final meat products

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The changes in farming practices toward to bio-production, globalised food market with increasing transportation of animals and also global climate change facilitate the widespread dissemination of food-borne diseases, including the pathogens such as zoonotic multicellular parasites. These facts consequently induce the improvement of various diagnostic methods of food-borne agents in the final products such as meat.
Our work is in this context focused on development of reliable comprehensive molecular diagnostic method useful for rapid control of final meat products designated for European and Czech market.
We adopted high sensitive multiplex oligonucleotide ligation-PCR technique (MOL-PCR), representing the novel diagnostic platform based on magnetic microspheres and detection realized via instrument for qualitative and quantitative analysis (MAGPIX). This modern approach enables simultaneous direct screen of complex samples potentially containing the DNA from number of different parasitic organisms.
Up to now, the molecular probes allowing the detection of targeted DNA, the further amplification of this probes and capturing system for generated products were designed for two parasitic worms - *Trichinella spiralis* (partial sequence of 18S rRNA gene) and *Taenia saginata* (partial sequence of *COX1* gene). The calibration of the system and optimization of method is in process.

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Molecular identification of blood parasites in camels (*Camelus dromedarius*) of Iran

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This study aimed to investigate the infection rate of parasites (e.g. filarioid helminths) in Iranian camels by molecular techniques.
In this pilot study a total of 200 apparently healthy one-humped camels (*Camelus dromedarius*) of both sexes and different ages were sampled randomly. Animals were kept by local farmers in central and south-eastern of Iran. Jugular vein blood samples were taken and drops of blood were spotted on Whatman FTA Elute® cards. Genomic DNA was purified according to the filter papers manufacturers' instructions. Polymerase chain reaction was applied for detection of filarioid worms and other pathogens.
Primary results have shown that filarioid helminths are present in camels in the studied area. However, further examinations are needed to investigate the parasite fauna of camels in Iran.

Free-living amoebae (FLA) and their intracellular bacteria in Austrian cooling towers and tap waters

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Free-living amoebae (FLA) are widely spread in the environment and also known to cause rare but often serious infections. Besides this, FLA have an indirect public health significance as they may serve as vehicles of dispersal and replication for bacterial pathogens. In particular, *Legionella pneumophila*, the causative agent of Legionnaires´ disease, replicates within FLA. Intracellular replication in amoebae seems to trigger the ability of the legionellae to infect human alveolar macrophages and besides, intracellular legionellae are protected against disinfection. As in environmental samples intracellular legionellae might not be detected by standard screening methods, the aim of the current study was to evaluate the diversity of FLA in water samples routinely screened for legionellae and to investigate all amoebal isolates for intracellular bacteria. To achieve this, a new screening system for FLA including real-time PCR assays specific for *Acanthamoeba*, Vahlkampfiidae and *Vermamoeba*, was established. From three cooling towers of public buildings and various tap water facilities an overall of 82 samples were taken periodically over the period of 18 months and investigated by culture and molecular methods in parallel. Altogether, 29/44 samples were positive for *Acanthamoeba* spp. and 16 were positive for Vahlkampfiidae, whereas *Vermamoeba* was not detected. Further amoebic genera, including *Cochliopodium* were isolated by culture. Interestingly, five of the amoeba isolates revealed intracellular bacteria by fluorescence in situ hybridization (FISH) and sequencing. Six samples were positive for *Legionella* and *Pseudomonas aeruginosa* was detected in 15 samples by standard cultivation techniques.

Leishmaniose

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Leishmaniases are sand fly-borne diseases caused by protozoan parasites of the genus *Leishmania* that affect people in 98 countries of the Old and New Worlds leading to different forms of the disease, visceral (VL), cutaneous (CL) and muco-cutaneous (MCL) leishmaniasis. Leishmaniases are not endemic in Central Europe, but imported cases are becoming increasingly important due to intensive human travelling. It also feared that the parasites and their vectors could spread from sub-tropic areas to Central Europe as a consequence of global warming.
The current classification systems of the genus *Leishmania* proposes up to 30-35 species that differ in their geographical distribution, transmission systems and virulence in mammalian hosts. Species identification should be included in the diagnostic procedure for making conclusions about the prognosis and the therapy. For this purpose, different reliable molecular methods exist, however interlaboratory standardization is mostly absent, complicating comparisons among different studies.
The current gold standard for differentiating *Leishmania* parasites at the strain level, multilocus enzyme typing (MLEE), needs cultured parasites and lacks discriminatory power. Multilocus sequence typing (MLST) is potentially the most powerful phylogenetic approach and will, most probably, replace MLEE in the future. Multilocus microsatellite typing (MLMT) is able to discriminate below the zymodeme level and seems to be the best candidate for becoming the gold standard for distinction of strains. It has demonstrated substantial intra-species diversity and the existence of geographically and genetically isolated populations in all *Leishmania* species tested so far but failed to correlate the genotype of parasite to its virulence or drug resistance phenotypes.
However, typing and analytical tools need to be further improved. New high-throughput and cheaper sequencing technologies will probably be available in near future for genome-wide multilocus genotyping. Accessible databases should be created and sustained for integrating data obtained by different researchers. This would allow for global analyses and help to avoid biases in analyses due to small sample sizes.
(The presentation will be given in German).

Influence of chicken serum mannose-binding lectin levels and feed on the immune response towards *Ascaridia galli* in organic layers: Preliminary results

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The study aimed to investigate the effect of mannose binding lectin (MBL) serum concentrations and feed on susceptibility to *Ascaridia galli* (*A. galli*) infections in organic chickens. A group of Hisex layers were raised organically until 46 weeks of age and fed either a control diet or a control diet supplemented with maize silage. All the chickens were genotyped for serum MBL as homozygous for allele A1, A3 or as heterozygote A2/A3 using Taqman SNP genotyping assay. Chickens homozygous for allele A1 have significantly lower serum MBL concentrations compared to chickens homozygous for allele A3 and heterozygote A2/A3. Forty-eight chickens from each dietary group exhibiting the highest (alleles A3/A3 or A2/A3) and the lowest (allele A1/A1) MBL serum concentrations, respectively, were selected and challenged with *A. galli*. At 7, 10 and 14 weeks post infection (pi) fecal egg counts (EPG) and body weight were measured. The chickens were slaughtered at 14 weeks pi and adult worm counts were enumerated. *A. galli* specific IgG and whole blood cell counts were measured in blood samples taken at 2, 7, 10 and 14 weeks pi. The MBL genotype alone did not show any specific effect on EPG and adult worm counts ($P>0.05$) but a tendency towards an interaction between the genotypes and the feeding groups could be observed ($P=0.06$). However, in chickens supplemented with maize silage, adult worm counts were higher compared to chickens fed with control diet. For all chickens, *A. galli* specific IgG titers peaked at week 2 pi followed by a rapid decrease at week 7 pi ($P < 0.001$). Absolute lymphocyte, monocyte and heterophil counts peaked at week 2 pi followed by a gradual decrease at week 7 and week 14 pi irrespective of the experimental groups. In conclusion, our results suggest that maize silage supplementation tends to increase incidence of *A. galli* infection in organic layers. Serum IgG concentration did not prevent infection as all the chickens remain to be infected until the termination of the experiment. Furthermore, no consistent correlation was found between the MBL genotypes, specific IgG titers and level of *A. galli* infection indicating that MBL might be of little importance for future selection of more robust chickens for organic farming.

Cystatins of the parasitic Nematodes -*Trichinella spiralis*, *T. britovi* and *T. pseudospiralis*

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The nematodes of the genus *Trichinella* are intracellular parasites which invade the cells of small intestine and skeletal muscles. They infect a broad range of worldwide distributed hosts, like mammals, birds and reptiles. All *Trichinella* spp. are zoonotic; six of twelve genotypes have been detected in humans. The serious human disease is called trichinellosis and it has been documented in 55 countries.

Our work is focused on cystatins -a reversible inhibitors of cystein peptidases of three trichinella species -*Trichinella spiralis*, *T. britovi* and *T. pseudospiralis*. Cystatins are compounds of excretory-secretory products (ESP) which are released by muscle larvae (L1) into the external environment. They are involved in many essential biological processes like growth, development, digestion and migration and also in manipulation of the host immunne system by parasite.

Up to now, the specific primers were designed for "multi cystatin-like domain" gene of *T. spiralis*, *T. britovi* and *T. pseudospiralis*; this gene was amplified, cloned and sequenced. The comparison of sequential data showed that cystatin genes of *T. spiralis* and *T. britovi* are significantly homologous but differs to gene conserved motifs of *T. pseudospiralis* cystatin and in number of domains. The recombinant forms of cystatins of mentioned trichinella species will be prepared and their biochemical properties will be compared.

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Molecular analysis of reemergence of parasitemia in *Plasmodium vivax* malaria in Ethiopia. Preliminary data.

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Although microscopy remains the gold standard in diagnosing malaria in clinical and field settings, molecular analysis has previously proven to be considerably more sensitive in identifying low-level parasitemia and mixed malaria infections. This particularly applies to non-falciparum malaria, which frequently leads to parasitemia below detection levels and therefore frequently remains underdiagnosed, particularly in sub-Saharan Africa where *P. vivax* transmission is focal and other species are rarely diagnosed. Molecular analysis therefore provides a superior tool for assessing low-level parasitemia as frequently seen during P. vivax relapses and chronic infections. However, molecular tools do not allow for a distinction of recrudescence, reinfection, and relapses in *P. vivax* infections.

In the current study molecular analysis was used to support microscopy and RDT data in establishing patterns in recurrence of parasitemia (i.e. the time to and the frequency of recurrence) in patients with *P. vivax* malaria in Ethiopia. Subjects diagnosed with *P. vivax* monoinfections were followed for 6 months with bi-monthly follow-ups to assess recurrence of parasitemia after treatment with chloroquine. A total number of 50 study participants were identified at two health centers within the catchment area of the University of Gondar Hospital. During these visits a slide was taken and examined for malaria parasites as well as blood spots on filter paper for molecular analysis and genotyping. Filter papers were dried and individually packed, shipped to the laboratory and analyzed. Parasite detection and species classification by nested PCR assay was performed for all samples using techniques previously established at our laboratory.

As compared to malaria microscopy a significantly higher proportion of study subjects was identified as having a reemergence of parasitemia during the 180-day follow up. Preliminary analysis suggests that based on genus-level PCR, at least seven subjects developed parasitemia during follow-up at Kola Diba Health Center and another 12 subjects at Maksegnet HC resulting in survival probability estimates (i.e. the chances of not experiencing a reemergence of parasitemia) for Day 60, 120, and 180 based of 0.46, 0.46, and 0.38, respectively at Kola Diba Health Center and 0.70, 0.52, and 0.48 at Maksegnet HC.

A better understanding of the relapse patterns in Ethiopia will be vital for improving current treatment paradigms and for controlling and ultimately eliminating vivax malaria in the country. As compared to standard microscopy our molecular data suggest a significantly higher rate of reemergence of parasitemia (and potentially relapses) among *P. vivax* patients in this part of Ethiopia. This may have major implications for the future treatment of malaria and would suggest an urgent need for a change in the current treatment paradigms to include anti-relapse treatment in order to ultimately reduce the *P. vivax* burden in Ethiopia.

First deployment of the European mobile laboratory in the course of the Guinea Ebola outbreak

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Over the last 30 years Filovirus outbreaks repeatedly occurred in the sub-Saharan African region. However, until recently the western African sub-region was spared from this burden. On the 10th of March 2014 local health authorities in Guéckédou and Macenta, Guinea, reported the outbreak of a deadly disease characterized by severe diarrhea, fever and vomiting. After confirmation of an Ebola Zaire strain as the causative agent of the disease, the Global Outbreak and Response Network of the World Health Organisation (GOARN/WHO) asked the European Mobile Laboratory (EMLab) Consortium on the 23rd of March to support the outbreak response mission by the deployment of the EMLab. Three days later the lab equipment was deployed, accompanied by a team of the EMLab consortium. Upon arrival at the Médecins Sans Frontières isolation ward in Guéckédou, the epicentre of the outbreak, the lab was set into operational readiness, and started to run diagnostic tests on patient samples. Since then, more than 3.800 samples have been analysed and 11 team rotations took place (as of end of October). Moreover, two further European mobile lab units have been deployed to Liberia and Nigeria, respectively, in the course of the ongoing outbreak response. Here, we introduce the concept of the EMLab, which has been developed at the Bundeswehr Institute of Microbiology. Furthermore, lessons learned so far from this first deployment of the EMLab, including logistics, laboratory concept, differential diagnosis, case load and daily routine will be presented. The EMLab consortium consists of partners from the Bernhard-Nocht-Institute, Bundeswehr Institute of Microbiology, Instituto Nazionale per le Malattie Infettive, Irrua-Specialist-Teaching-Hospital, Public health England, Institute of Virology Marburg, Laboratoire P4 INSERM, Robert Koch Institute and Spiez Laboratory.

Alveoläre Echinokokkose

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Die alveoläre Echinokokkose ist auf der Nordhalbkugel verbreitet. Sie ist durch infiltrierend-nekrotisierende Leberläsionen charakterisiert. Die Patienten haben über lange Zeit lediglich keine oder geringfügige Oberbauchbeschwerden. Hilusnahe Läsionen machen sich mit einem schmerzloser Ikterus bemerkbar. Zufallsbefunde im Ultraschall sind häufig. CT und MRT werden ergänzend hinzugezogen. Sehr seltene extrahepatische Manifestationen werden durch Bildgebung von Lunge und ZNS im Rahmen des Stagings erfasst. Die Verdachtsdiagnose AE kann in vielen Fällen serologisch gesichert werden. Gelingt dies nicht, wird die histopathologische Beurteilung hinzugezogen. Die Therapie erfolgt chirurgisch mit 2-jähriger postchirurgischer Albendazoltherapie und 10-jähriger Nachbeobachtungszeit, sofern kurativ reseziert werden kann. Ist dies nicht möglich, bietet die lebenslange medikamentöse Suppressionstherapie mit Benzimidazolen (Albendazol) eine sehr gute Langzeitprognose. Zentral wachsenden Läsionen mit Stenosierung der Gallenwege werden erfolgreich mit Dilatationen und Stenting behandelt.

Babesiosis in Austria

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Babesiosis is an emerging, tick-transmitted disease caused by protozoan hemoparasites of the genus *Babesia*. *Babesia* spp. are known to infect mammals, birds and facultatively also humans. Up to now several cases of human babesiosis have been published, 3 of them occurred in Austria. The causative agents of two of these cases were identified as *B. venatorum* and the third as *B. microti* (Herwaldt et al. 2003, Ramharter et al. 2010, Blum et al. 2011). The prevalence of *Babesia* spp. in Austrian ticks has been shown to be highly variable depending on the region where the ticks had been collected, with a mean infection rate of 51% (Blaschitz et al. 2008).
With this background the aim of this diploma thesis was to evaluate the infection rates in humans in Austria and identify the *Babesia* spp. that are involved in human infections. To achieve this, samples investigated for *Babesia* spp. by routine diagnostics (serology) in 2013 were reevaluated and serologically positive patients were then investigated by a commercial PCR. All PCR-positive patients were further investigated by a second PCR that allows species identification after DNA sequencing of the amplicon.
Among the 414 patients screened for antibodies against *Babesia* spp. 35 were positive and 10 borderline with serological titers ranging between 1:16 and 1:256. Of these 26 could be recruited for follow-up. EDTA blood was screened by PCR resulting in 7 positive samples. Sequences obtained showed highest identity to *B. bovis*, *B. microti* and *Theileria* sp.

Biological observations on the persistent human parasites *Plasmodium malariae, P. ovale curtisi* & *P. ovale wallikeri*

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Recent studies of *P. malariae* and *P. ovale* spp. infections in travellers returning to non-endemic countries from Africa have identified novel aspects of the biology of each of these parasites which enhance their persistence in the human host. At the same time, application of sensitive molecular detection methods in field studies have shown these three species to be far more common in Africa, Asia and the SW Pacific than previously acknowledged. Worryingly, there is some evidence that artemisinin combination therapy is not completely effective at eradicating the low density, sub-microscopic infections that are characteristic of all three species. Recent data on parasite biology and drug response patterns in vivo will be presented for each of these parasites.

Management of a 16 year old patient with cardiac and pulmonary cystic echinococcosis

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A 16 year old girl was admitted to our hospital with mild cough, mild symptoms of dyspnoea, weight loss and the diagnosis of a cardiac cyst. She originated from Romania, had moved to Austria 2 years ago, and had had close contact to dogs in Romania.
ELISA and Western blot were positive for both *E. granulosus* and *E. multilocularis*. Additionally to the 3,3 x 3,4 cm cystic lesion in the apex of the right ventricle, diagnostic imaging showed multiple cystic lesions up to 4 cm in diameter in lung-tissue and an occluding process in both pulmonary arteries, causing absent perfusion of the whole right and the left lower lobe of the lung.
She first underwent cardiac surgery, in which the cardiac cysts were removed, and treatment with Albendazole was then administered, since rupture of cardiac cysts with possible anaphylactic shock and/or pericardial tamponade had been reported if such patients were solely treated with antihelmintic drugs.
She was transferred to Vienna to have the echinococcal cysts removed from the pulmonary vasculature by pulmonary thrombendarteriectomy. After this operation the right upper and middle lobe became re-perfused, but not the right and left lower lobes. The pulmonary arterial pressure, however, had returned to normal levels. At her last visit she described feeling better, since much of the dyspnoea had resolved.

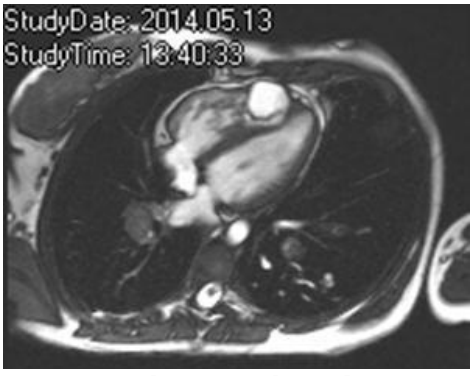

Fig.1 MR Thorax with cardiac cyst

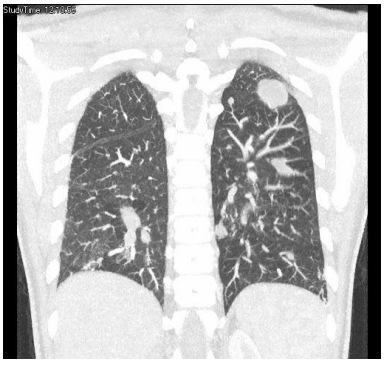
Fig.2 Cysts in Thorax-CT

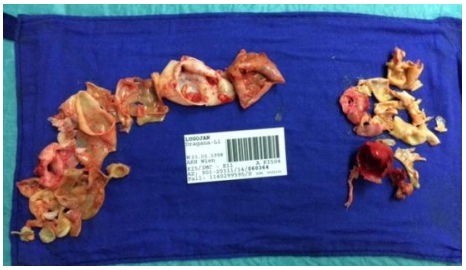
Fig.3 Thromendarteriectomy material

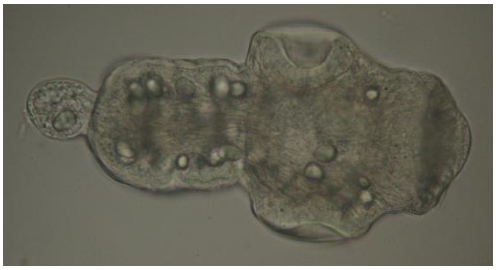
Fig.4 Protoscolices

Filarioid helminths and avian malaria in mosquitoes in metropolitan Vienna

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A range of factors (e.g. climate change, trade, and people/pet animal movement) have major impacts on the distribution of invasive pathogens (e.g. *Dirofilaria repens*), their invertebrate vectors (e.g. mosquitoes), and vertebrate hosts (humans, pet animals, livestock, and wild animals), leading to an emergence and spread of vector-borne infections. First findings of *D. repens* in mosquitoes in Burgenland indicate that this parasite has invaded Austria. However, there is virtually no information about the parasite fauna transmitted by mosquitoes in metropolitan Vienna.
Within this study over 7,000 mosquitoes were caught in 2013 at three different sampling sites in Vienna (e.g. at the University of Veterinary Medicine of Vienna), using special carbon dioxide traps. Mosquitoes were specified according to morphological characteristics. Mosquitoes were pooled and homogenized. After DNA extraction each pool was screened for the presence of DNA of filarioid helminths and *Plasmodium* sp. using molecular tools.
DNA of several vector-borne parasitic pathogens was examined within this study, for example *Setaria tundra* and avian malaria. On the other hand neither *D. repens* nor *D. immitis* were found in mosquitoes in metropolitan Vienna, indicating that these parasites were not present in the examined area during the investigation period in 2013.

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Percutaneous treatment (P.A, I.R) for cystic *Echinococcus* (CE) in Kenya – is pair treatment of CE a sound alternative in low-income countries?

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BACKGROUND
CE is a significant public health concern in Turkana County in Kenya. It is a zoonotic disease caused by the larvae stage of dog tapeworm, *Echinocuccus granulosus.* Humans become immediate hosts by accidental ingestion of E.granulous eggs directly through contact with dogs or indirectly via contaminated food or water. This leads to the development of cysts which cause the morbidity associated with CE.

OBJECTIVES
To document the outcome of PAIR treatment for CE in Turkana and propose guidelines for its management as a neglected tropical disease in a low income country.

STUDY DESIGN
A descriptive study on data that was collected prospectively; sampling was selective.

RESULTS
PAIR was used as a percutaneous treatment of CE by Amref surgical team in Kakuma Hospital, Turkana County in Kenya. Between 1993 to 2013 a total of 219 cysts in 168 Patients aged between 3-65 years were treated and majority (70%) were females.
In the follow up period of 6months-10 years, 82% of the followed up patients showed good results as indicated by the marked reduction in the cyst size or its disappearance, and the sub sequent solidification of the contents. Complications, including Anaphylaxis, were few and minor, except 1 death (0.6%); and only 5 cases (2.5%) of recurrence.

CONCLUSION
P.A.I.R is safe, efficient, and inexpensive and offers cure in selected patients and is thus am alternative option in treatment of CE especially in developing countries with limited resources.

Tick screening and medical risk assessment at military training sites in Austria

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Ticks are the most relevant vectors of pathogens in Austria. As military training is conducted primarily in the field tick exposure cannot be prevented entirely. For this reason an evidence-based medical risk management is crucial for preventive measures. The goal of this study is to collect baseline data for a follow-on risk assessment for various training activities at different seasons at the training sites.
Ticks were collected from all 54 active training sites in Austria. On two locations ticks are sampled on a weekly basis to track the tick activity during the year. Species and life cycle stage of all ticks were determined by morphology. Until now, more than 5000 ticks have been collected. Ticks were found at all training sites, even at an altitude of 1,450 m a.s.l. *Ixodes ricinus* was the predominant species (92%), but also *Haemaphysalis concinna* (7%) and *Dermacentor reticulatus* (<1%) were found. The spectrum of pathogens carried by the collected ticks will be evaluated by PCR. The following pathogens are included in the screening: TBE-virus, *Borrelia burgdorferi*, *Brucella* spp., *Coxiella burnetii*, *Francisella tularensis*, and *Babesia* spp. First screenings (86 pools of 10 *Ixodes ricinus* nymphs each) were negative for TBE-virus, *Francisella tularensis* and *Coxiella burnetii*, but a high percentage (66%) of ticks positive for *Borrelia burgdorferi* was found.

The use of screening blood-fed mosquitoes for the diagnosis of filarioid helminths and avian malaria

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As a result of the fatal case of a dog infested with *Dirofilaria immitis* in the city of Szeged, Southern Hungary, in 2013, mosquitoes were caught in the corresponding habitat to screen for filarioid helminths and avian malaria using molecular tools. At the same time, some other dogs also proved to be positive for *D. immitis* in this area, using different rapid antigen tests. Therefor we were eager to know more about the potential intermediate host role of mosquitoes.

Blood-fed mosquitoes were caught in July 2013 in the garden were the dog was kept using a M-360 electric mosquito trap. Mosquitoes were stored in 70% ethanol until further processing. Female mosquitoes were identified to genus level by morphological characteristics. Afterwards each single mosquito was homogenized and screened for filarioid helminths and avian malaria using molecular techniques. Mosquitoes positive for filarioid helminths or *Plasmodium* sp. were further classified to the species level with barcoding of the COI gene.

In total 267 blood-fed female mosquitoes were caught in the garden in Szeged. Molecular screening revealed DNA of several pathogens (e.g. *D. immitis, D. repens* and *Plasmodium* sp.). This method can only be used for screening if a pathogen is present, because the role of the mosquito as vector cannot clearly be verified due to blood of the bitten hosts in the sample. However, the analysis of blood-fed mosquitoes seems to be an adequate technique to evaluate if filarioid helminths and avian malaria are present in a certain area.

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Invasive mosquitoes in Austria – an overview of the mosquito fauna in Eastern Austria

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In Austria, 42 mosquito species belonging to six genera (*Aedes*, *Anopheles*, *Culex*, *Coquillettidia*, *Culiseta* and *Uranotaenia*) have been specified using morphological standard characteristics, but the information concerning the genetic diversity is still scarce. Since global change favours the establishment of invasive mosquito species and new emerging vector-borne diseases, distribution patterns of mosquito species and their ecology are re-gaining importance in Europe. However there is still insufficient information on the current mosquito species inventory and seasonal and spatial distribution patterns in Austria.
In our study 27 permanent sampling sites distributed across Vienna, Lower Austria and the Burgenland are monitored using specialized mosquito traps equipped with carbon dioxide as attractant. Adult mosquitoes were sampled twice a month from April to October 2014.
The aim of the study is to update information on the current mosquito species inventory, to identify ecological habitat parameters influencing the spatial and seasonal distribution of mosquito species and to screen them for mosquito-borne pathogens (e.g. filarioid helminths and avian malaria). We will present the preliminary results of the mosquito species inventory and the seasonal occurrence of the mosquitoes of Vienna, Lower Austria and Burgenland.

This study is supported by the Austrian Science Fund (FWF): I1437

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