

Abstracts of the "Second symposium on tropical medicine and infectious diseases in an international military context 2019"



27th and 28th June 2019

**Laufende Nummer:** TropMedSymp-01

**Eingereicht am:** 09.01.2019

**Abstractsprache:** Englisch

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## Inhalt

<b>Titel:</b>	<b>Borrelia persica</b> - the agent of tick borne relapsing fever in Israel and the Palestinian Authority
<b>Fragestellung:</b>	Even though tick-borne relapsing fever (TBRF) is endemic in the Middle East, data on its infectious agent, vector, animal reservoir(s) or pathogenesis are fragmentary. We established a research network between Israeli, Palestinian and German research groups, with logistics for the collection and exchange of data, protocols, ticks and tissue samples.
<b>Methodik:</b>	We used PCR with subsequent sequencing of the 16S rRNA-gene, the 16S-23S intergenic spacer, partial <i>flaB</i> genes and partial <i>glpQ</i> genes for identification of the causative spirochete <i>Borrelia persica</i> . For classification of the vector we used 12S rRNA gene sequencing. DNA extracted from gorged ticks was submitted to mitochondrial DNA typing to identify the potential host reservoir. To study the pathogenesis of <i>B. persica</i> infections we established a mouse infection model.
<b>Ergebnisse und Schlussfolgerung:</b>	The 16S rRNA gene sequences obtained were identical in patient samples and ticks, proving that <i>B. persica</i> is the etiological agent of TBRF in Middle East. Sequences of the flagellin- and <i>glpQ</i> -gene allowed further sub-typing of <i>B. persica</i> strains. The soft tick <i>Ornithodoros tholozani</i> was ascertained as the vector of TBRF. DNA extracted from naturally <i>B. persica</i> infected gorged ticks was submitted to mitochondrial DNA typing and identified dogs, sheep, hyrax and goats as the ticks' hosts. This is the first time that potential reservoir animals were characterized from gorged ticks in a field study of TBRF in this region. Whereas <i>B. persica</i> is very difficult to culture in vitro, we succeeded in infecting immunocompromized mice: <i>B. persica</i> was successfully passaged in mice and the time course of the amplification and tissue invasion of the borreliae was visualized by Fluorescence in situ Hybridization (FISH). Similar to <i>B. hermsii</i> , <i>B. persica</i> showed intercellular invasion into different organs including kidney, heart, and brain, possibly organotropism in the white pulp of the spleen and surrounding of blood cells and cell nuclei. Discussion We definitively characterized <i>B. persica</i> as the etiological agent of TBRF in the Middle East which is prevalent in Israeli and in the Palestinian territories. It is transmitted to human by <i>Ornithodoros tholozani</i> possibly from a reservoir comprising dogs, sheep, goat and hyrax. FISH proved to be a valuable tool for the observation of fastidious microorganisms in ex vivo samples.

Bearbeitet am: 28.01.2019

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**Abstractsprache:** Englisch

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## Inhalt

<b>Titel:</b>	Mass-spectrometry based Proteotyping – A Novel Subtyping Method for Bacteria
<b>Fragestellung:</b>	Intact cell mass spectrometry is the recent standard method in clinical routine diagnostics to identify microbes based on masses of high abundant low molecular weight proteins. Variation in biomarker genes result in varying allelic isoforms of these proteins. These variations give rise to a novel sub-typing method for bacteria named mass spectrometry-based proteotyping (MSPT).
<b>Methodik:</b>	To establish MSPT-schemes for <i>Campylobacter jejuni</i> , <i>Campylobacter coli</i> and <i>Clostridioides difficile</i> , we analyzed and evaluated a MLST-typed, and in the case of <i>C. difficile</i> ribotyped cohort of each microbial biospecies representative for clinically relevant clades by mass spectrometry. Genome sequenced reference strains were used for biomarker identification and genome sequences deposited in the IMG and NCBI databases were used to set up a biomarker isoform database. Concatenated amino acid sequences of biomarkers of each tested isolate were used to infer phylogeny using the UPGMA-algorithm.
<b>Ergebnisse und Schlussfolgerung:</b>	We were able to associate 19 <i>Campylobacter</i> -specific but only 9 <i>C. difficile</i> -specific biomarkers with their encoding genes and include them in the corresponding MSPT-scheme. Using MSPT we were able to distinguish all <i>C. jejuni</i> ssp. <i>jejuni</i> , <i>C. jejuni</i> ssp. <i>doylei</i> and all three <i>C. coli</i> clades. Regarding <i>C. difficile</i> the most important finding was that one of the MSPT-clades only contained, isolates of the hypervirulent ribotype 027. In specific cases, the MSPT method is able to distinguish clinically relevant pathogen groups at the below-species level. Integrated in a sub-typing module, MSPT can be used with existing mass spectrometric equipment as a fast and cost-effective method.

Bearbeitet am:	28.01.2019
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**Laufende Nummer:** TropMedSymp-03

**Eingereicht am:** 08.02.2019

**Abstractsprache:** Englisch

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## **Inhalt**

**Titel:** Patient placement under various hygienic conditions

**Fragestellung:** Placement of potentially infectious patients is not trivial when maximum hygiene precautions on one hand and space constraints in highly efficient medical institutions on the other hand have to be observed. Official and binding hygiene rules from several countries give clear recommendations for separation of patients with infectious risks, but little help concerning the problem which patients can be placed in one room at acceptable risk levels.

**Methodik:** In this presentation, suggestions for solving this problem are made with respect to the transmissible infectious agent, the route of transmission and the risk of the exposed persons

**Ergebnisse und Schlussfolgerung:** Overall, infectious and non-infected persons can be placed in one room, if the infectious agent is transferred by direct or indirect contacts, as long as some specific hygiene rules are constantly observed. For patients colonized or infected by droplet or air-borne transmissible agents, only cohortation with patients carrying similar agents is an acceptable option.

<b>Bearbeitet am:</b>	12.02.2019
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**Laufende Nummer:** TropMedSymp-04

Eingereicht am: 23.01.2019  
Abstractsprache: Englisch  
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## **Inhalt**

**Titel:** Beyond the pill and the scalpel – Pastoral aspects of international infectious disease crises  
**Fragestellung:** In addition to the medical matters which occur on missions, religious matters require an increasing level of expertise, especially in non-typical Christian countries. For example, in Liberia, medical staff were recently confronted with problems when dealing with inhabitants who refused to incinerate the corpses of Ebola victims. Intercultural advisors and international chaplains can help to sensitize commanding officers to the challenges posed by such religious and cultural aspects during missions.

Bearbeitet am:	02.05.2019
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**Laufende Nummer:** TropMedSymp-05

**Eingereicht am:** 28.02.2019

**Abstractsprache:** Englisch

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## Inhalt

**Titel:** Zoonotic and Infectious Disease Pathogen Surveillance in Multiple Canine Populations from Varying Regions of South America

**Fragestellung:** Zoonotic and infectious diseases, more specifically vector-borne diseases, continue to increase over time in global distribution and emergence<sup>1</sup> and increasingly continue to be described as primary causes of zoonotic and infectious diseases.<sup>2</sup> Ongoing surveillance for exposure to vector-borne pathogens provides critical information for protecting public and animal health, deployed U.S. service members, host nation and allied service members, working dog handlers, and working dogs globally. The objective was to survey multiple canine populations from varying regions of Colombia, South America to determine seroprevalence of *Ehrlichia* spp., *Anaplasma* spp., *Dirofilaria immitis*, and *Borrelia burgdorferi*.

**Methodik:** Canine (n=270) blood samples from shelter and stray canines (n=122), Police working canines (n=69), Army working canines (n=42), security canines (n=29), and pets (n=8) were tested using SNAP<sup>®</sup> 4Dx<sup>®</sup> Test Kits.

**Ergebnisse und Schlussfolgerung:** The overall zoonotic and infectious vector-borne disease prevalence was 70% in shelter and stray canines, 52% in Police working canines, 7% in Army working canines, 0% in security canines, and 12% in pets. Five canines tested positive for Leishmania along with one Lyme positive.

This data indicate exposure to vector-borne pathogens in the newly surveyed regions of Colombian is extremely high. For the first time, Leishmania positives were discovered in canines from these regions of South America. Exposures to the overall very high level of zoonotic and infectious vector-borne diseases is significant and warrants aggressive and immediate precautionary measures for working dogs, working dog handlers, deployed U.S. service members, and the public living and working in these areas.

Bearbeitet am:	03.03.2019
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**Laufende Nummer:** TropMedSymp-06

**Eingereicht am:** 28.02.2019

**Abstractsprache:** Englisch

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## Inhalt

**Titel:** Screening of 1003 whole blood samples from febrile patients in Mbeya, Tanzania for the presence of Relapsing Fever Borrelia using real-time PCR

**Fragestellung:** Relapsing fevers are vector borne diseases caused by bacteria of the genus *Borrelia*. The clinical course is characterized by recurrent episodes of fever. Epidemiologically relapsing fevers are more common in resource limited settings and rarely occur in central Europe. There are two main relapsing fever groups, Louse borne relapsing fever (LBRF) caused by *Borrelia recurrentis* is transmitted by the body louse and is characterized by high mortality rates and epidemic occurrences. Tick borne relapsing fever (TBRF) is transmitted mainly by soft ticks and caused by different related *Borrelia* species. TBRF can be found in certain geographical areas epidemically and occurs sporadically in patients. The clinical course is most often less severe, lethality is low [1, 2]. Reports about the prevalence of TBRF vary considerably in the literature. It is generally assumed that the burden of disease is underestimated due to the lack of sensitive detection in patient material.

**Methodik:** In this study, 1003 blood samples from the Mbeya region (Tanzania), which were collected during the HOMA trial were investigated for the prevalence of *Borrelia* DNA. Therefore, freshly frozen whole blood samples of acute febrile patients were extracted using a robotic platform and investigated for the presence of *Borrelia* DNA with two different and newly validated real-time PCR protocols. The protocols were validated with enumerated *Borrelia* cultures, as well as extracted positive blood samples to have a sensitivity of 102-101 DNA copies/5µl. Controls included T/L-BRF strains *B. miyamotoi*, *B. hermsii* and *B. recurrentis*. Lyme group *Borrelia* were also detected. One protocol was based on SYBR green, the second on TaqMan probes, both using a different set of primers. Similar studies used this approach successfully to detect *Borrelia* in the blood of patients [3]. Within this study however, no *Borrelia* could be detected. This may be due to regional peculiarities. It may be a highly unlikely sporadically occurring disease which is of less importance given the overall disease burden. The patient cohort was selected to be regionally as well as socio-economically diverse. A significant proportion of the study participants were rural inhabitants with livestock keeping.

**Ergebnisse und Schlussfolgerung:** This is the first cohort of acute febrile patients in the Mbeya region, which has been screened for relapsing fever *Borrelia*. Within the sample, no relapsing fever cases could be found. Thus, the disease seems to be absent or present only in very small numbers in the population.

Bearbeitet am: 28.03.2019

**Laufende Nummer:** TropMedSymp-07

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Abstractsprache: Englisch

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Erstautor: Sudeck, H

Präsentierender Autor: Sudeck, H

Institut/e: -

## **Inhalt**

**Titel:** The History of Plague

**Fragestellung:** In ancient descriptions the plague was associated with Apollo, the "fever-arrow-shooting god". After Christ's birth the plague broke out violently: her consequences were aggravated by the Byzantine emperors, because they persecuted doctors and philosophers who were not considered Christians. In Europe started around 1350 a massive outbreak of the plague with 25 million dead. This was mainly caused by the unhygienic conditions in the cities which provided ideal conditions for disease with open sewers, pig husbandry, half-timbered buildings with rats in abundance and lack of personal hygiene. Because the plague first broke out in the ghettos the Jewish population was considered the culprit: the compulsion to trade with used clothes and filth, led to a heavy exposure of the Jews, as well as the obligation for the Jews to catch rats. The further spread in Europe from the 15th to the 18th century led to isolation and quarantine concepts; the first "protective suits" appeared around 1500 in contemporary illustrations. Venice is regarded as a pioneer of modern disease control concepts which G.F. Ingrassia used successfully 1575 in Palermo. In 1720, Professor Deidier from Montpellier carried out the first animal studies on the spread of the plague by intravenous, oral and subcutaneous route. With the identification of *Yersinia pestis* and Yersin's demonstration of the link between plague and rat, systematic research into the transmissibility, prevention and treatment of this disease began.

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**Laufende Nummer:** TropMedSymp-08

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**Abstractsprache:** Englisch

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**Erstautor:** Siedenburg, J

**Präsentierender Autor:** Siedenburg, J

**Institut/e:** 1: German Foreign Ministry – Medical Department

## Inhalt

<b>Titel:</b>	Contagious Diseases in Aviation: challenges and countermeasures
<b>Fragestellung:</b>	The more the speed of international traffic increases, the quicker contagious diseases may travel. The duration of travel has been minimised and is much shorter than the incubation period of most contagious diseases. Diseases are not yet apparent during travel, but only some time after arrival. Nevertheless, passengers may be infectious before and infect fellow travellers as primary contacts.
<b>Methodik:</b>	Cabin pressurisation and climatisation, highly efficient filtering of cabin air, frequent exchange of air and low humidity reduce survival of germs. The chance for transmission of infectious agents on board is almost remote and would require direct contact. However, IHR preclude transport of contagious passengers by aeroplanes or ships. If infectious passengers are detected in-flight, an isolation of the patient will be commenced. Relevant equipment is included in the emergency equipment of major air carriers. If infectious diseases are diagnosed after a flight a meticulous follow-up is required to tackle further spread in the area of destination.
<b>Ergebnisse und Schlussfolgerung:</b>	The risk of sudden decompression has long prevented transport of contagious patients by air within isolation equipment. The CDC spearheaded the development of a transport aircraft. Germany went a step further during the Ebola outbreak in West Africa 2014 - 2016. A tent construction within the Airbus A 340 "Robert Koch" even allowed access of medical personnel in protective garments to the patient. However, a practical mission was never necessary and the aircraft was dismantled afterwards. The good news is that a new European project is under way.

Bearbeitet am:	20.03.2019
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**Laufende Nummer:** TropMedSymp-09

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**Abstractsprache:** Englisch

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**Erstautor:** Niemeyer,B

**Präsentierender Autor:** Horn, H

**Institut/e:** 1: Helmut-Schmidt-University Hamburg

## Inhalt

<b>Titel:</b>	Automatized Aerosol Disinfection Processes
<b>Fragestellung:</b>	In order to prevent the spread of pathogens, automatic aerosol processes can be of high value for the disinfection of equipment and rooms, as high amounts and large spaces can be covered at once while minimizing the risks for personal. A suitable disinfectant is sprayed inside the application room or area and deposits onto the potentially contaminated surfaces. For providing reproducible and safe routines, these processes have been investigated focusing on the reachability of surfaces in complex geometries and higher positions in the application room as well as onto different materials and surfaces.
<b>Methodik:</b>	In order to provide highest applicability, especially if the potential pathogens are unknown, peracetic acid (PAA) was used as main active ingredient, as PAA is effective against a broad range of microorganisms and viruses. The PAA solutions were modified applying several additives to provide suitable fluid characteristics for creating a stable aerosol and enhanced material compatibility. As test germs, spores of the <i>Geobacillus stearothermophilus</i> have been utilized. Process parameters as needed amounts of disinfectant and exposure time were investigated.
<b>Ergebnisse und Schlussfolgerung:</b>	It could be shown, that a reduction of $10^6$ spores is possible even in smaller slits (down to 10 mm width) and at higher positions (up to 3 m relative to the aerosol generator) when a suitable additive combination is used. The reduction of 6 log-levels was also demonstrated on several metal and non-metal materials e.g. stainless steel, aluminium, copper, wood and ceramics.

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**Abstractsprache:** Englisch

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## Inhalt

<b>Titel:</b>	Once is not enough – Lessons learned from a schistosomiasis control project in a high transmission setting
<b>Fragestellung:</b>	Schistosomiasis still causes a high burden of disease in Sub-Saharan Africa despite the availability of efficient treatment. Currently the only large scale intervention is Praziquantel (PZQ) mass drug administration (MDA) for School aged children (SAC). In a pilot project we attempt to control schistosomiasis in a high transmission setting with a combination of interventions.
<b>Methodik:</b>	Study site: Ijinga, an island in Lake Victoria, 45 km northwest of Mwanza. Population: 2500 inhabitants, among them 600 SAC, living mainly on subsistence farming and fishing. No water supply apart from lake water, no electricity. A baseline study on the prevalence of schistosomiasis (Kato-Katz technique (KK) plus urine-antigen-rapid test (CCA)) and morbidity (ultrasound) was conducted. After intensive counselling 5 rounds of PZQ for the entire population were provided. In addition WASH interventions (construction of wells) were started. After each MDA a sentinel group of 250 SAC was followed up.
<b>Ergebnisse und Schlussfolgerung:</b>	The predominant type of schistosomiasis was <i>Schistosoma mansoni</i> . Initial prevalence in 931 inhabitants (50% adults, 50% SAC) was 94,5% (CCA) and 69% (KK). Prevalence in SAC was 98,9% and 87,4%, respectively. Participation in MDA was 70-95%. After 3 MDA rounds 4-6 weeks apart prevalence in a sentinel group dropped to 12,6% / 3,6%. Spacing the following MDA by 3 and 6 months caused an increase in the prevalence: 85,7% (CCA) / 22% (KK) prior to 5th MDA. In a high transmission setting it will be unlikely to control schistosomiasis by MDA alone. Community based interventions plus WASH are equally important.

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Abstractsprache: Englisch

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## Inhalt

**Titel:** The destructive power of creation - Growth and innovation as underlying principles leading to mass dying and potential extinction

**Fragestellung:** Percentage growth looks harmless if numbers are low however percentage growth is (counter intuitively) not linear, but exponential making human population growth resemble bacterial growth.

With a rule of thumb one can calculate the doubling time as  $70/\text{growth in \%}$  (70 arises from  $\ln 2 * 100$ ). A population that grows by 2% per year will double after  $70/2=35$  years.

Growth, of populations or economies, leads to depletion of resources with potentially violent global and local competition for remaining resources. With "depletion of resources" we think of resources to keep up our civilisation such as oil and gas. However we also have to consider the depletion of resources essential for the pure survival of human beings, such as water. While human populations grow exponentially, ground water levels shrink nearly everywhere. It won't be long before the first mega city runs dry.

Where cities rise, natural habitats must go. The currently on-going mass extinction of animal species is caused by *Homo sapiens*. Despite its current large population, *Homo sapiens* may also go extinct if the biosphere becomes incompatible with human survival as some post nuclear-war or runaway climate change scenarios suggest. The discovery of fossil fuels as energy resource around 250 years ago has lead to the great acceleration of the anthropocene reflected by exponential curves.

If not near term human extinction, we will at least face enormous challenges in the coming years with potential mass dying in some regions of the world, most of them probably poor developing countries of the tropics.

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3: Instituto Militar de Engenharia, Brazil

## Inhalt

**Titel:** Easing up on Quality Control of Active Principles

**Fragestellung:** Traditionally, the majority of methods for quality control of pharmaceutical products use chromatography, either liquid or gas. These methods have been well established and improved over many decades, thus are considered very trustworthy. Unfortunately, chromatographic methods require expensive equipment, consumables and reference materials, turning it into a complex setup.

**Methodik:** We are currently establishing Nuclear Magnetic Resonance (NMR) methods for some of the most common active principles, that are under continuous surveillance in Brazil. The methods are being developed for high and low field NMR, allowing qualitative and quantitative analysis. Today, low field NMR equipment is available as benchtop setup and needs a single power outlet to work. The consumables comprise small quantities of deuterated solvents per sample and (reusable) tubes, no standards are needed; combined with the relatively low cost of equipment acquisition, the total cost of operation tends to be lower than for chromatography.

**Ergebnisse und Schlussfolgerung:** Besides the costs, there are additional arguments in favor of NMR. The complete process, from sample preparation to identification of the compound is very fast and can be fully automated, thus allowing short turn over times. Additionally, as NMR is a nuclear method, unexpected contaminants can be detected as well, and, if known, identified.

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**Autorenliste:** Savini H<sup>1</sup>, Christen, J<sup>1</sup>, Delaval, F<sup>2</sup>, Simon, F<sup>1</sup>

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## Inhalt

<b>Titel:</b>	An outbreak of 107 cases of acute Schistosomiasis in a French detachment returning from Centrafrican Republic.
<b>Fragestellung:</b>	French army deploys about 5000 militaries in Sahel area, where schistosomiasis is endemic. An outbreak of acute <i>Schistosoma mansoni</i> Schistosomiasis occurred in 2012 among a French detachment of 265 militaries returning from Centrafrican Republic.
<b>Methodik:</b>	All the French militaries of the detachment were included in the study. Clinical examination, biological screening (hemogram, total Ig E, serologies against Schistosomia, Polymerase Chain Reaction (PCR) schistosomia in stool and sera, stool examination) were performed once they returned to France and one, three and six months later. Schistosomiasis infection was confirmed when stool examination, serology or PCR were positive. Infected people were treated by praziquantel at the posology of 60mg/kg at least two months after exposure.
<b>Ergebnisse und Schlussfolgerung:</b>	A total of 173 militaries bathed in a river among the 223 investigated militaries. We diagnosed 107 infected cases (attack rate of 62%) and 58 were symptomatic (58%). Two severe forms were described. Eosinophilia was present in 87% (n=90), increased total IgE in 43% (n=45 patients), ELISA serology was positive in 87% (n=94), IHA serology in 73% (n=77), sera PCR in 59% (n=63), stool PCR in 86% (n=90). Eggs of <i>Schistosoma mansoni</i> in stool were present in only 3% (n=3). All the infected people were treated. Among them, 25 necessitated a second cure and 13 a third because of persisting eosinophilia. Schistosomiasis management is a strong challenge for the military health Service because this infection can significantly impact the mission. This outbreak enhances the difficulty of diagnosing and preventing this disease.

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## Inhalt

<b>Titel:</b>	Experience of the Healthcare workers Treatment Center of Conakry during Ebola virus (EBOV) outbreak, 2015.
<b>Fragestellung:</b>	In January 2015, the French Armed Forces opened a Healthcare workers treatment Center (HTC) near Conakry. The goal of this HTC was to provide intensive medical care to EBOV-infected healthcare workers.
<b>Methodik:</b>	This modular and under-tents HTC was composed of a 10-bed unit for patients with confirmed EBOV infection and a transit ward for probable cases. We deployed a biosafety level 3 field laboratory, in which EBOV-specific reverse transcription polymerase chain reaction (RT-PCR) analysis can be performed, as well as a wide panel of biological tests for guiding treatment, resuscitation, and discharge decisions. Baseline clinical data were noted at admission and twice a day during follow-up; laboratory analyses were studied between 23 January and 15th March 2015.
<b>Ergebnisse und Schlussfolgerung:</b>	A total of 14 EBOV-patients (13 males; mean age $30 \pm 7$ years) and 13 non-confirmed patients were hospitalized at the HTC Treatment Center. We described the different phases of the disease and atypical forms (meningitis, myocarditis and arthritis). The disease was fatal in 5 cases (36%). All fatal cases were characterized by an increasing viral load, but also elevated AST, elevated C-reactive protein levels, hypoalbuminemia, hypocoagulation and kidney failure. No secondary transmission occurred. This experience showed that the deployment of an Ebola treatment center by armed forces is feasible. Our data confirmed that viral load at admission is associated with death but also AST secondary to rhabdomyolysis. We described for the first time atypical forms of the disease.

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**Abstractsprache:** Englisch

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## Inhalt

<b>Titel:</b>	Q Fever Outbreak in the Amazon Rainforest in French Guiana: Involvement of <i>Hydrochoerus hydrochaeris</i> and a Brush Cutter
<b>Fragestellung:</b>	Q fever is a cosmopolitan zoonosis caused by <i>Coxiella burnetii</i> . Its transmission to humans occurs mainly through inhalation of contaminated particles present in the environment. Cattle, sheep, and goats constitute the main reservoirs worldwide. Q fever in French Guiana is caused by a unique genotype, <i>C. burnetii</i> multispacer sequence type (MST) 17. We describe here an outbreak investigation that improved our knowledge about Q fever transmission and a potential reservoir.
<b>Methodik:</b>	A retrospective case-control study was performed, including 3 controls per case. We assessed possible exposures to <i>C. burnetii</i> . We sampled several possible environmental sources of <i>C. burnetii</i> .
<b>Ergebnisse und Schlussfolgerung:</b>	From late August to mid-September 2014, five Q fever cases were diagnosed among 12 French Navy service members who were deployed in mid-August for three days to a <i>carbet</i> (an open-sided wooden shelter surrounded by forest). Symptoms began between 12 to 23 days after the stay, with elevated fever and pneumonia for four patients. Fresh feces identified as belonging to a capybara ( <i>Hydrochoerus hydrochaeris</i> , the world's largest rodent), which lay a few meters from the <i>carbet</i> , were positive for <i>C. burnetii</i> MST17. This was the first Q fever outbreak described outside Cayenne and suburban areas, in the Amazon rainforest. These results confirm wildlife exposure and a sylvatic transmission cycle of <i>C. burnetii</i> MST17. The role of the capybara as a putative reservoir has to be confirmed. We cannot control the transmission chain due to the sylvatic cycle, but protective measures implemented during risky activities can prevent human cases.

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**Eingereicht am:** 12.04.2019

**Abstractsprache:** Englisch

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## Inhalt

<b>Titel:</b>	Efficacy and safety of methylene blue-based combination therapy in the treatment of falciparum malaria: Expert review
<b>Fragestellung:</b>	Previous success in malaria control was largely attributed to artemisinin-based combination therapy (ACT), but resistance against ACTs has emerged in Asia. Methylene blue (MB) is a promising candidate to be added to ACT.
<b>Methodik:</b>	A literature review on MB and malaria has identified 474 reports. MB is a dye which has been used for a long time in medicine and is registered in many countries for several indications. MB is the oldest synthetic antimalarial and has first been used in a German hospital in the year 1891. Cure rates with MB monotherapy were around 90%, MB was shown to act synergistically with ACT and to be highly effective against the gametocytes of <i>P. falciparum</i> . MB side effects were a green-blue discoloration of the urine, gastro-intestinal side effects, and urethritis symptoms; no serious adverse events were reported, and a meta-analysis showed no clinically relevant hemolysis in G6PD-normal and G6PD deficient African patients with malaria. The strong effects of MB on the gametocytes of <i>P. falciparum</i> have recently been confirmed in phase II studies in Mali and Burkina Faso.
<b>Ergebnisse und Schlussfolgerung:</b>	MB is an alternative to primaquine in the combination therapy of falciparum malaria, in particular where the goal of malaria programmes is elimination. Moreover, adding MB to existing ACTs will reduce <i>P. falciparum</i> transmission intensity, increase treatment efficacy, and reduce the risk for development and spread of resistant malaria parasites. However, there is a need to improve the taste and acceptability of MB formulations.

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**Eingereicht am:** 16.04.2019

**Abstractsprache:** Englisch

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**Erstautor:** Kann, S

**Präsentierender Autor:** Kann, S

**Institut/e:** 1: Medical Mission Institute Würzburg

## Inhalt

<b>Titel:</b>	Neglected Tropical Diseases: Problems and Challenges on the example of Chagas Disease
<b>Fragestellung:</b>	Neglected Tropical Diseases (NTDs) affect about 149 tropical and subtropical countries and consist out of a diverse group of communicable diseases. Most of them could be avoided or diminished by public health approaches, including the improvement of living conditions, health structures, diagnostic and therapeutic tools. Chagas Disease (CD) is the second highest illness burden among NTDs and is the third most common parasitic disease worldwide. The Chagas causing parasite <i>Trypanosoma cruzi</i> ( <i>T. cruzi</i> ) is mainly transmitted by vectors called Triatomines and from mother to child. According to WHO about 6 Mio individuals are infected and 25 Mio live with the daily risk of infection, but many experts fear higher numbers. However, only less than 1% has access to diagnostics, causing high mortality and morbidity rates especially in young adults. CD is difficult to diagnose, therefore there is up to date no gold-standard available. WHO recommends serologic tests, but they have limitations, e.g. the detection of acute cases, where therapy outcomes are most promising.
<b>Methodik:</b>	To overcome these problems, hence, a new, highly specific Real Time Polymerase Chain Reaction (PCR) for the detection of <i>T. cruzi</i> was developed. Serum samples from 352 individuals living in high endemic CD areas were analyzed and compared to leading PCRs and conventional tests. Further 87 PCR-products were verified by sequence analysis after plasmid vector preparation.
<b>Ergebnisse und Schlussfolgerung:</b>	We could prove, that the new developed PCR showed superior data compared to commonly used PCRs, especially in regard to sensitivity (92,3%), specificity (100%) and accuracy (98,4%). In combination with serologic tests, it can improve diagnostic safety significantly and can be used for therapy, vector and surveillance control as well as for public health purposes.

<b>Bearbeitet am:</b>	26.04.2019
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**Abstractsprache:** Englisch

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**Erstautor:** Becker, S

**Präsentierender Autor:** Becker, S

**Institut/e:** 1: Institute of Medical Microbiology and Hygiene, Saarland University

## Inhalt

<b>Titel:</b>	Imported cases of histoplasmosis and coccidioidomycosis: implications for differential diagnosis and management in non-endemic areas
<b>Fragestellung:</b>	Endemic mycoses are caused by dimorphic fungi and mainly occur in geographically restricted areas outside Europe. While they may give rise to severe, life-threatening infections, the initial clinical symptomatology may also be mild and the awareness of these infections is usually low among clinicians and laboratory staff outside endemic areas. Culture-grown agents of endemic mycoses are biosafety level 3 pathogens and are thus highly contagious in the clinical microbiology laboratory. Here, we describe two cases of imported histoplasmosis and coccidioidomycosis to highlight challenges pertaining to adequate diagnosis and clinical management.
<b>Methodik:</b>	A 57-year-old patient was admitted with nausea, weight loss, eosinophilia and hyperkalemia. He had lived in Thailand until 2003, but denied any international travel ever since. Imaging studies revealed a tumor in his left adrenal gland. Adrenalectomy was performed and histopathological and molecular analysis revealed chronic <i>Histoplasma capsulatum</i> infection. A soldier was admitted with signs of chronic meningitis. Imaging studies showed an infiltrative mass that led to compression of the cervical myelon. Surgical hemilaminectomy was performed and intraoperative tissue samples grew a mould, which was further identified by nucleic acid sequencing as <i>Coccidioides</i> spp. Both patients were treated with liposomal amphotericin B, followed by oral itraconazole, and made a full recovery.
<b>Ergebnisse und Schlussfolgerung:</b>	There is a need to consider endemic mycoses in patients with a travel history to endemic areas who suffer from aetiologically unclear disorders. Accurate communication between the treating physicians and the microbiology laboratory is crucial to reduce the risk of laboratory-acquired infections.

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**Abstractsprache:** Englisch

**Autorenliste:** Muigg, V<sup>1,2</sup>, Poppert, S<sup>1,2</sup>, Neumayr, A<sup>1,2</sup>

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## **Inhalt**

<b>Titel:</b>	Case Reports: The challenges of diagnosing tissue invasive parasites
<b>Fragestellung:</b>	The diagnosis of tissue invasive helminth infections is often challenging, since these infections are rare, especially in non-endemic regions where they are not widely known, and the availability of diagnostic tests is limited and mainly restricted to indirect methods such as serology.
<b>Methodik:</b>	Using the example of three cases of tissue invasive helminth infections, from the three main families of helminths (nematodes, cestodes, trematodes), we exemplarily demonstrate the challenges and pitfalls linked to diagnosing tissue invasive parasite infections.
<b>Ergebnisse und Schlussfolgerung:</b>	The options for diagnosing tissue invasive parasites are limited and mainly restricted to serology, since direct detection in and removal of the parasite from body tissues is often impossible. Due to the cross-reactivity of most serological assays, interpretation of serological results remains challenging. In cases where the parasite is removed and available for investigation, molecular methods are valuable and increasingly applied tools for the identification of helminths to species level.

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**Abstractsprache:** Englisch

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## Inhalt

<b>Titel:</b>	Dual Seroreactivity to Chikungunya and O'nyong'nyong viruses, and to West Nile and Tick-borne Encephalitis viruses from Sera of Rwandan and Swedish Blood donors
<b>Fragestellung:</b>	Seroprevalence of Chikungunya virus (CHIKV) and West Nile virus (WNV) have recently been conducted on blood donors from Rwanda and Sweden. CHIKV seroprevalence was found to be very high in Rwanda (63%), while no significant difference of seroprevalence of WNV among donors from both countries (10.4% for Rwanda and 14.1% for Sweden) was observed. These unexpected results, especially for CHIKV in Rwanda and WNV in Sweden raised the suspicion of cross-reactivity of O'nyong'nyong virus (ONNV) with CHIKV in Rwanda, and of tick-borne encephalitis virus (TBEV) with WNV in Sweden.
<b>Methodik:</b>	Samples (n=40, ten CHIKV ELISA negatives and ten CHIKV ELISA positives from both Rwandan and Swedish donors) were subjected to CHIKV and ONNV plaque reduction neutralization test (PRNT) as confirmatory test. All Swedish blood donors (n=199), but only those Rwandan donors who tested positive for WNV IgG (n=91), were tested for TBEV IgG antibodies. Moreover, PRNT to TBEV was performed on all WNV positive (n=28) Swedish blood donors.
<b>Ergebnisse und Schlussfolgerung:</b>	Of these 28 Swedish donors and the 91 Rwandan donors who were IgG seropositive for WNV, 22 (78.6%) and 64 (70.3%) were also IgG seropositive for TBEV, respectively. Furthermore, of these Swedish donors, nine tested negative and 19 positive for TBEV-NT. For CHIKV and ONNV cross-reactivity, all samples from Sweden and all of the CHIKV ELISA negative samples from Rwanda were found to be PRNT negative for both CHIKV and ONNV. Out of ten CHIKV ELISA IgG positive Rwandan plasma samples, two were double-negative, and eight samples were double-positive against both viruses in PRNT. CHIKV and WNV are both circulating in Rwanda, as shown by the seroreactivity to both viruses. Moreover, the serological cross-reactivity among alphaviruses and flaviviruses in Rwanda and in Sweden should be further elucidated.

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Abstractsprache: Englisch

Autorenliste: Plenge-Bönig, A<sup>1</sup>

Erstautor: Plenge-Bönig, A

Präsentierender Autor: Plenge-Bönig, A

Institut/e: 1: Head Infectious Diseases Surveillance Unit, Institute for Hygiene and Environment, Free and Hanseatic City of Hamburg

## **Inhalt**

**Titel:** Infectious disease epidemiology: Surveillance of infectious diseases and outbreak investigations with methods of field epidemiology

**Fragestellung:** According to the definition of the World Health Organization, surveillance is the systematic ongoing collection, collation and analysis of data and the timely dissemination of information to those who need to know so that action can be taken. In charge of the action are the public health structures at local, national or international level. The final objective of surveillance is prevention. The methods of systematic surveillance in Germany are explained presenting the different modules and steps of epidemiological assessment and their ability to support public health action be based on valid data and statistical evidence. Additionall epidemiological surveillance tools and the systematics of field epidemiological investigations of outbreaks are presented. Finally, an overview on infectious diseases in Germany is given.

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**Abstractsprache:** Englisch

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**Erstautor:** Beji, M

**Präsentierender Autor:** Beji, M

**Institut/e:** 1: Military Hospital of Bizerte, Tunisian General Directorate of Military Health. Tunisia

## Inhalt

**Titel:** Respiratory infection risk in the pilgrim, experience of the Tunisian Medical Assistance

**Fragestellung:** Muslims from all over the world travels every year to Mecca for one month to realize pilgrimage rituals. This gathering exposes the pilgrims to several risks, traumatic accidents, acute decompensation of chronic illness, chest stroke and specially epidemics' infectious diseases.

**Methodik:** From Tunisia, about 10,000 people, nearly one per thousand of all citizens, participate to Haj. Middle age is about 65 years. In 30% of all cases, pilgrims suffer from chronic diseases. They are mostly treated for diabetes, hypertension, osteoporosis, arthrosis and chronic obstructive pulmonary diseases. This travel is characterized by promiscuity, important mobility and exposure to heat particularly in summer season.

**Ergebnisse und Schlussfolgerung:** A cohort observational study was conducted from 2015 to 2017. The follow-up and emergencies prehospital cares were done by a mobile team of health physicians and nurses. They took care of resuscitated cases in the health care center, out of Saoudian hospitals. Shortness of breathiness was the main cause of consultation (29%) associated to fever, cough and modified mucus expectorations. In the second place was heart stroke (21%). Dehydration and exhaustion were about 15%. Acute complications of diabetes represented 13%. Chest pain and palpitation were 11%. Traumatic accidents represented about 8%, falls were main lesions cause. Acute abdominal pain was registered in 3%. About half of pilgrims referred were hospitalized. Respiratory tract infections werethe main cause to hospitalization, about 80%. In 2009, a questionnaire of pilgrims was done at their arrival and after their departure (a week). A nasal swab and an examination of the throat were done on the arrival for 519 pilgrims and before the departure for 2699 pilgrims. Influenza, rhinovirus and parainfluenza were the most common viruses detected among pilgrims. Streptococcus pneumoniae was found to be the leading Gram positive organism isolated.

In this context of infectious challenge, health authorities developed recommendations of pilgrim's vaccinations. Vaccination against seasonal influenza is mandatory and vaccination against pneumococcal infections is recommended especially for those aged > 65 years and with chronic diseases. In the reported studies, influenza vaccines appear to decrease the development of influenza illness among pilgrims. Pneumococcal vaccination is not mandatory because of the modest rate of pneumococcal infection comparatively to viral infections. In addition, the available pneumococcal 13-valent and 10-valent polysaccharide conjugate vaccines cover only 37 (18%) of serotypes identified during Hajj.

Pilgrimage is a mass gathering in witch acquisition and transmission of respiratory viruses and bacteria is frequent and associated with a high risk of morbidity and may cause mortality. Effective preventive measures include recommendations for widespread vaccination of attendees before arrival to Mecca.

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**Abstractsprache:** Englisch

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**Institut/e:** 1: BG Klinikum Hamburg, Department for septic bone and joint surgery

## Inhalt

**Titel:** Results of Stage-Adapted Therapy of shoulder-joint-infections in 139 cases

**Fragestellung:** Arthroscopy is gold standard in therapy of acute joint Empyema of the shoulder. Nevertheless there's no standardized approach to manage chronic shoulder joint empyema.

**Methodik:** From 11/1999 to 1/2016 139 patients were treated because of shoulder-joint-infections in our hospital.

**Ergebnisse und Schlussfolgerung:** The reason of infection was in most cases iatrogenic. Hematogenous bloodstream infections were causative just in 4 cases. The time until we were engaged in the treatment of these patients was in average 2 month. Most of patients had severe comorbidities. Until we assumed the treatment 108 patients underwent up to twenty infect-caused surgical procedures. In 66% we found pathogenic germs. In the run of the study we noticed a change to difficult to treat bacteria. Our management of infection-treatment depends on the infectious stadium of the empyema. Here we use the Gächter-classification. In 4 cases we could treat by arthroscopy, in all other cases we had to do open surgery. In 63 cases we could preserve the joint. There were 72 patients who underwent a resection arthroplasty. 3 Patients got a shoulder-prosthesis later on. In one case we had to do a thoraco-scapular exarticulation of the shoulder joint caused by a necrotizing soft tissue infection. We lost one patient after long-term treatment in another hospital with extraordinary comorbidities. 122 of 139 patients underwent a follow-up-examination in a retrospective study. The clinical and radiological check-up was in average 21.8 months after end of treatment. We also asked about the DASH-Score to evaluate the subjective outcome. Surgical treatment of fractures with plate or prosthesis was the main reason of shoulder joint infections between 1999 and 2005. Afterward's the surgical treatment of degenerative shoulder lesions became main reason. The spectrum of germs in chronic shoulder infections also changed. We mostly found multisensible staph. aureus first, later the multiresistant difficult to treat bacteria. In every patient, who underwent follow up examination, the infection was calmed down, in 4 cases via arthroscopy, in 63 cases open surgery with joint-saving, in 72 cases with joint-resection. We now found late-infection-recurrence in 3 Cases. The best results in ROM and DASH-Score had the acute infections within the first 7 days which could be calmed down by arthroscopy. But also some patients with resection-arthroplasty reached a good ROM and DASH-Score < 50. Overall the results of patients with infection after treatment of degenerative diseases are poorer than those with infections after treatment of fractures. We accomplished good results with our stage-adapted therapy-regimen in treatment of mostly long-lasting chronic shoulder-joint infections. All infections could be calmed down. Although resection-arthroplasty must be done in 72 cases the results are convincing.

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**Abstractsprache:** Englisch

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**Präsentierender Autor:** Habiba, N

**Institut/e:** 1: Department of microbiology, Military Hospital of Tunis; Tunisia

## Inhalt

**Titel:** West Nile virus: Tunisian epidemiological situation

**Fragestellung:** West Nile (WN) virus is a mosquito-transmitted flavivirus that was first isolated in 1937 from the blood of a febrile woman in the WN province of Uganda. It is one of the most widely distributed arboviruses in the world, and a pathogen of public health significance in both humans and animals. The virus is maintained in nature by an enzootic transmission cycle between mosquitoes and avian hosts. Humans and horses are considered incidental or "dead-end" hosts. Most human WN virus infections are asymptomatic or present a mild influenza-like illness including fever, malaise, headache, myalgia, vomiting or diarrhea. Less than 1% of infected patients develop neuroinvasive diseases, including meningitis or meningo-encephalitis with some fatalities occurring in immunocompromised or elderly person. All these non-specific symptoms of the WN virus infection highlights the need for laboratory testing of suspected human cases. Like all arboviruses, WN virus outbreaks are generally occurred in areas where the reservoir and the vector coexist and when ecological, biotic or abiotic conditions are favorable.

**Methodik:**

**Ergebnisse und Schlussfolgerung:** In Tunisia, WNV is circulating these last decades and this virus has been associated with 4 epidemic peaks that have affected particularly humans in 1997 (111 cases, 8 deaths), 2003 (112 cases, 9 deaths), 2012 (86 cases, 12 deaths) and 2018. Following the second Tunisian outbreak, a national surveillance system was initiated in 2004 to detect early viral circulation and implement appropriate prevention and control actions. However the occurrence of outbreaks of WN fever remains unpredictable. In the absence of vaccine and effective treatment, more efforts are needed to monitor the infection in birds, vectors, animals, and humans.

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**Eingereicht am:** 29.04.2019

**Abstractsprache:** Englisch

**Autorenliste:** Sumenko, A<sup>1</sup>, Fischer, M<sup>1</sup>

**Erstautor:** Sumenko, A

**Präsentierender Autor:** Sumenko, A

**Institut/e:** 1: BwK Hamburg, Abteilung f. Dermatologie

## **Inhalt**

<b>Titel:</b>	Dermatologists of German armed forces on the Amazon
<b>Fragestellung:</b>	For years, the Brazilian Navy has carried out missions with the help of hospital ships in the remotest regions of the Amazon on behalf of their government. This has created an ambitious, regularly operating and functioning infrastructure for the supply of the disadvantaged and usually under the simplest conditions living river population.
<b>Methodik:</b>	In 2018, the Brazilian Navy invited a German medical officer to participate in one of the missions.
<b>Ergebnisse und Schlussfolgerung:</b>	The following report will summarize the structure and organization of the deployment, the disease spectrum and dermatological care in simple conditions with limited diagnostic and therapeutic possibilities.

<b>Bearbeitet am:</b>	29.04.2019
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**Laufende Nummer:** TropMedSymp-26

**Eingereicht am:** 29.04.2019

**Abstractsprache:** Englisch

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**Erstautor:** Fischer, M

**Präsentierender Autor:** Fischer, M

**Institut/e:** 1: BwK Hamburg, Abteilung f. Dermatologie

## Inhalt

<b>Titel:</b>	History and presence of Chagas disease
<b>Fragestellung:</b>	Chagas disease or American trypanosomiasis identified in 1909 by Carlos Chagas and its causative agent <i>Trypanosoma cruzi</i> are endemic in almost all countries in South and Middle America. Currently more than 10 million people are affected. Due to permanent migration from Latin America to Europe, United States, Canada and Japan Chagas disease has become over the last decades a global health concern.
<b>Methodik:</b>	In Europe, most migrants from CD-endemic areas are concentrated in Spain, Italy, France, United Kingdom and Switzerland. Pooled seroprevalence studies, conducted in Europe, show an overall 4.2% prevalence in migrants with the highest infection rates observed among individuals from Bolivia (18.1%). However, in most European countries the disease is neglected with absence of screening programmes and low access to diagnosis and treatment.
<b>Ergebnisse und Schlussfolgerung:</b>	The goal of this presentation is to make the audience familiar with the causative agent of Chagas disease, the different forms of transmission, the variety of clinical signs and symptoms in acute and chronic stages, namely cardiomyopathy, megacolon and megaesophagus. Besides diagnostic and therapy also the efforts of the Brazilian ministry of health concerning control, prevention and early detection are pointed out. This overview review should raise the awareness of internists, general practitioners and also dermatologists in order to diagnose affected patients in their routine daily activities.

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**Eingereicht am:** 29.04.2019

**Abstractsprache:** Englisch

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**Präsentierender Autor:** Demchyshyna, I

**Institut/e:** 1: State Institution Public Health Center of the Ministry of Health of Ukraine (PHC MOH)

## Inhalt

<b>Titel:</b>	Measles and Rubella Laboratory network of Ukraine
<b>Fragestellung:</b>	The support of epidemic well-being of the country is guaranteed by high-quality and timely laboratory diagnostics at the early stages of outbreaks of measles disease. The constant surveillance of the circulating genotypes of viruses being the pathogens of the specified infections on all of the administrative territories allows determining the source of importation and spread of infection.
<b>Methodik:</b>	Virological method was used for urine samples: 29 viruses were isolated for 2017 – 2018. The polymerase chain reaction method was used in order to identify the nucleic acid fragments of the measles virus in clinical specimens from patients with measles. The genotype identification was carried out by sequencing method at the WHO's Regional Reference Laboratory at Luxemburg.
<b>Ergebnisse und Schlussfolgerung:</b>	At the beginning of the rise of morbidity during December 2016 – February 2017, from patients with measles registered in the territories of the Ivano-Frankivsk, Dnipropetrovsk regions and Kyiv, the circulating D8 measles virus genotype was identified, which was similar to the two genetic lines. During March – June 2017, the circulation of several genotypes of different genetic lines, referring both to the D8 genotype and to the B3 and D9 genotypes, were on the territory of Ukraine. In 2018, 631 samples were collected from 4805 persons with measles infection for further study, the definition of the genotype. The identified strains were similar to strains originating from the United Kingdom, Malaysia, India, Ireland, Afghanistan, and Singapore. Thus, we can conclude concerning the sources of the measles import to Ukraine.

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**Abstractsprache:** Englisch

**Autorenliste:** Pfefferle, S<sup>1</sup>, Christner, M<sup>1</sup>, Aepfelbacher, M<sup>1</sup>, Lütgehetmann, M<sup>1</sup>, Rohde, H<sup>1</sup>

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**Präsentierender Autor:** Pfefferle, S

**Institut/e:** 1: Institute of Medical Microbiology, Virology and Hygiene, University Medical Center Hamburg-Eppendorf

## Inhalt

<b>Titel:</b>	Implementation of the BioFire FilmArray ME in laboratory routine: a real-life experience
<b>Fragestellung:</b>	Infectious Meningitis is a serious disease with high morbidity and mortality rates. Optimal patient outcome relies on fast and reliable diagnostic, especially in bacterial meningitis. The FilmArray ME panel offers a syndromic panel testing approach including bacterial, viral and fungal pathogens. We report our experience of the implementation of the assay into routine diagnostic in a university hospital setting, particularly with regard to application of a pragmatic risk assessment-driven sample selection method.
<b>Methodik:</b>	Over a period of 18 months we received n=4.623 CSF samples (n=2.338 hospitalizations, n=1.601 individuals). N=171 samples matched to our risk criteria and were subjected to FilmArray ME analysis. Samples were also tested by reference methods: culture only (n=45), PCR only (n=20) or both methods (n=106).
<b>Ergebnisse und Schlussfolgerung:</b>	: 56/171 (32.75 %) were FilmArray ME positive. Bacterial pathogens were detected in 30/56 (53.57 %) and viral pathogens were detected in 27/56 (48.21 %) of positive samples. 52/56 FilmArray ME results could be confirmed by the reference assays. We provide data on the clinical performance of the system and indicate an easy and efficient way to implement rapid and reliable molecular testing to improve patients care in the modern diagnostic microbiological laboratory without creating unmanageable cost burden. The FilmArray ME is a useful tool for fast and reliable diagnostic of infectious meningitis and can be easily implemented in routine diagnostic workflows. However, considering the need for antimicrobial susceptibility testing, the use of molecular tests as stand-alone diagnostic cannot be recommended.

Bearbeitet am:	29.04.2019
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**Laufende Nummer:** TropMedSymp-29

**Eingereicht am:** 29.04.2019

**Abstractsprache:** Englisch

**Autorenliste:** Elsner, E<sup>1</sup>, Hartmann, R<sup>2</sup>

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## Inhalt

<b>Titel:</b>	Increase of scabies among German military personnel – a seven year survey in the skin clinic of the Bundeswehr Hospital Berlin
<b>Fragestellung:</b>	Diagnosis of scabies has become surprisingly frequent in Germany in recent years and the use of scabicides has risen significantly. Present figures indicate an increase in prevalence and incidence of scabies, but only scarce valid data are available. The aim of our survey was to figure out, whether this trend can also be displayed among military personnel of the Bundeswehr.
<b>Methodik:</b>	The study was conducted as a retrospective single center survey over seven years (2012 - 2018) in the skin clinic of the Bundeswehr Hospital Berlin, Germany. Data was generated from the hospital information system (KIS) searching for all scabies-coded diagnoses according to ICD10 Code B86. All scabies-diagnoses have been confirmed by dermatoscopy by a dermatologist or microscopy. Inpatient treatment was carried out if an outpatient was not cured after at least one anti-scabies treatment.
<b>Ergebnisse und Schlussfolgerung:</b>	The data show that there has been a steady increase from 16 patients in 2012 to 40 patients in 2018 (in absolute terms); when looking at percentages of diagnoses of all referred soldiers it rose from 0.28% (2,8 /1000) in 2012 to 0.74% (7,4 /1000) in 2018. Moreover our data show that the number of unsuccessfully treated outpatients rose from 1-2 patients per year in 2012, 2013 and 2014 to 9 patients in 2018 (from <0,2% to 1,5% of all admitted patients). We could show an increase of scabies among German military personnel over the last seven years with the highest number in 2018. This result supports the observations of an increased incidence of scabies in Germany in the general population but also emphasizes the low overall prevalence of scabies with <1%. All diagnoses in our survey were confirmed by dermatoscopy and/or microscopy ruling out the bias of overreporting by false-positive cases diagnosed only by clinical examination.

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**Abstractsprache:** Englisch

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## Inhalt

**Titel:** The role of the moth fly, *Clogmia albipunctata*, as a new mechanical vector in transmission of bacterial pathogens in hospitals

**Fragestellung:** The moth fly species *Clogmia albipunctata* is now present in Germany and has developed a synanthropic behaviour allowing frequent, year-round infestations in hospital buildings. Aim of this study was to investigate its potential to transport and transmit bacterial pathogens in infested German hospitals.

**Methodik:** 271 *C. albipunctata* were collected from four hospitals and qualitatively and quantitatively investigated for bacterial colonization of the outer body surface as well as of the gastrointestinal tract/inner body. The bacterial spectrum in water samples from identified breeding places were analyzed and compared with the bacterial colonization pattern on, and in the flies. For identification of bacteria, routine media and tests for differentiation were employed. Species confirmation and resistance patterns were obtained using the automated Phoenix system.

**Ergebnisse und Schlussfolgerung:** 271 *C. albipunctata* were individually analyzed qualitatively and, in part, quantitatively, for bacterial colonization. Overall, 45 bacterial species representing 40 genera were found colonizing this moth fly species. Among the bacteria isolated were the nosocomial pathogens *Acinetobacter baumannii*-complex, *Aeromonas hydrophila*, *Alcaligenes faecalis*, *Bacillus cereus*, *Escherichia coli*, *Klebsiella pneumoniae* ssp. *pneumoniae*, *Pseudomonas aeruginosa*, *P. fluorescens*, and *Stenotrophomonas maltophilia*, with colonization rates of 0–17.5%, 0–16.7%, 0–12.5%, 0–62.1%, 0–2.5%, 0–4.1%, 0–12.5%, 0–7.6%, and 0–10%, respectively, per inspection trial. Additionally, one strain of both *Yersinia fredericksonii* and *Nocardia* sp. was detected. Unlike the 11 strains of multidrug-resistant (MDR) *S. maltophilia* collected from one hospital, no MDR Enterobacteriaceae were isolated. *Acinetobacter* sp. colonized *C. albipunctata* at rates from 2.9% to 36.8%, and revealed a high affinity for the exoskeleton, with up to 2,080 colony-forming units per moth fly for *A. baumannii*-complex. Results obtained clearly demonstrate that *C. albipunctata* should be considered a potential mechanical vector of bacterial pathogens associated with nosocomial infections while infestation indicates that enhanced sanitation efforts concerning hospital water and pest management are necessary.

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**Eingereicht am:** 30.04.2019

**Abstractsprache:** Deutsch

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**Erstautor:** Fajta, J

**Präsentierender Autor:** Fajta, J

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- 4: Tropical Health Foundation, St. Marta, Kolumbien
- 5: Institute for Parasitology - Dept. of Infectious Diseases, University of Veterinary Medicine Hannover, Foundation
- 6: Institute for Biometry, Epidemiology and Information Processing, University for Veterinary Medicine, Hannover, Germany
- 7: Medical Mission Institute Würzburg, Germany

## Inhalt

<b>Titel:</b>	Occurrence of bacterial and parasitological pathogens in canine faeces and blood samples from rural settlements in Northern Colombia
<b>Fragestellung:</b>	Wide Areas of Colombia have rural landscapes with indigenous villages, which have very limited access to modern civilization. There is just simple infrastructure with rare access to safe drinking water or health care. People are living in close contact to their animals including pets.
<b>Methodik:</b>	During a health care project, supported by the Else Kröner-Fresenius-Foundation, besides medical care for the indigenous people, blood and fecal samples were taken from nearby living dogs (n= 50). The fecal samples were tested for 12 medical relevant tropical pathogens (bacteria, protozoan and helminths) using three different multiplex-realtime-PCR assays. The blood samples were tested for antibodies against <i>Ehrlichia</i> , <i>Anaplasma</i> , <i>Borrelia</i> and <i>Leishmania</i> by Indirect Immunofluorescence, and in addition for <i>Babesia</i> and <i>Hepatozoon</i> DNA by realtime-PCR.
<b>Ergebnisse und Schlussfolgerung:</b>	Similar to the findings from human stool samples (data not shown), from canine fecal samples high rates of <i>Giardia intestinalis</i> were detected. From eight positive samples the genotyping was possible, five dogs were positive for the zoonotic genotype A and B. The Multiplex PCR, designed to specifically detect human pathogens, gave positive results for <i>Ancylostoma</i> sp., <i>Campylobacter jejuni</i> , <i>Strongyloides stercoralis</i> and surprisingly <i>Cyclospora cayetanensis</i> in the canine feces. Initial screening of the blood samples by realtime-PCR detected 10 samples positive for <i>Hepatozoon</i> sp. and/or <i>Babesia</i> sp.. Subsequent sequencing verified <i>Babesia canis vogeli</i> in two samples and <i>Hepatozoon canis</i> in samples from four dogs. More than half of the dogs were serologically positive for <i>Anaplasma phagocytophilum</i> and <i>Ehrlichia canis</i> . <i>Leishmania</i> sp. specific antibodies have been detected with IFT in one case.

Bearbeitet am:	11.05.2019
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**Laufende Nummer:** TropMedSymp-32

**Eingereicht am:** 30.04.2019

**Abstractsprache:** Englisch

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## Inhalt

<b>Titel:</b>	Development and application of a core genome-based multilocus sequence typing system for <i>C. perfringens</i>
<b>Fragestellung:</b>	Whole genome sequencing can provide a comprehensive overview of the genetic information of a pathogen and also represents a powerful molecular epidemiological tool for subtyping and outbreak investigations. In this study, we describe a cgMLST scheme for the Gram-positive anaerobic bacterium <i>C. perfringens</i> , which is based on the allelic profiling of the core genes.
<b>Methodik:</b>	A core genome of 1510 genes was initially identified in 38 genomes that represent different phylogroups of <i>C. perfringens</i> . We evaluated these genes via performing allele typing in a data set of 80 <i>C. perfringens</i> strains.
<b>Ergebnisse und Schlussfolgerung:</b>	As a result, 60 genes were discarded because no allele number was assigned to them in more than 5% of the genomes. Thus, the final cgMLST scheme comprises 1450 genes which were found typeable in a collection of 160 genomes by an average of 99.5% (range 95.3% to 100%) per each genome. The developed cgMLST scheme has superior discriminatory power compared to classical MLSTs. We applied the developed cgMLST scheme to analyze a set of 87 <i>C. perfringens</i> genomes from poultry with regard to the country of isolation, NetB toxin gene presence and clinical disease. The data set also included 50 epidemiologically related isolates derived from diseased and non-diseased poultry in Egypt. Based on the cgMLST results, we discovered a limited diversity among the suspected necrotic enteritis isolates compared to the isolates obtained from healthy birds and meat samples.

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Eingereicht am: 30.04.2019

Abstractsprache: Englisch

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Präsentierender Autor: Oltmanns, K

Institut/e: BwK Westerstede, Abteilung f. Innere Medizin

## **Inhalt**

**Titel:** A case of leptospirosis in a forest ranger in Germany

**Fragestellung:** A forest ranger felt increasingly tired with myalgia and diffuse pain. On admission to our hospital he presented with a hepatitis with slight jaundice. Investigations showed no viral hepatitis, therefore we performed a further workup with additional emphasis on the patient's history and laboratory investigations. The patient admitted eating sorrel salad from a fenced forest conservation zone regularly. He reported that mice were present in this protected zone. The patient's exposition and history, symptoms and positive antibodies led us to the diagnosis of a leptospirosis.

**Ergebnisse und Schlussfolgerung:** Leptospirosis is a rare cause of a hepatitis in Germany. However, more frequent infections could not be found, there was no suspicion for an autoimmune disorder in laboratory or from patients history and the patient did not take any medication recently. Leptospirosis is an important infection in countries with low standards of housing and hygiene, nevertheless it also has a link to travel-related and military medicine. These infections can occur in most parts of the world and are mostly related to exposition to infected water and infected animals.

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**Abstractsprache:** Englisch

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**Institut/e:** 1: Analyticon instruments gmbh  
2: Biofire Defense

## Inhalt

**Titel:** Detection of pathogens of global fever diseases - direct, easy, fast, on-site

**Fragestellung:** Acute feverish diseases can be triggered by a variety of different pathogens, including bacteria, viruses and parasites. Currently BioFire Defense - partner of the German analyticon instruments gmbh- is developing a kit to quickly detect global Acute Febrile Illness (AFI).

**Methodik:** The kit can be used with the semi-stationary PCR system Filmarray. The development is being carried out in cooperation with the US authorities "Department of Defense"<sup>a</sup> and "National Institute of Allergy and Infectious Diseases"<sup>b</sup>. The FilmArray itself is an in vitro diagnostic platform that performs both nucleic acid purification and multiplex PCR for the simultaneous identification of many infectious agents in less than an hour.

The kits are closed systems in which all steps of a PCR are performed directly. GF Kit detects and identifies the following viruses Chikungunya, CCHF, Dengue (Sterotype 1-4), Ebola, Lassa, Marburg, West Nile, Yellow Fever, Zika as well as Bacillus anthracis, Francisella tularensis, Leptospira spp. Salmonella enterica serovar Typhi and Paratyphi A, Yersinia pestis, Leishmania donovani complex and Plasmodium spp. in samples of venous blood from individuals who have or have had signs and/or symptoms of febrile illnesses, and knowingly or potentially come into contact with pathogens.

Expected studies on the limits of quantification show clinically relevant detection limits, in addition exclusivity tests show the high specificity. Preliminary off-panel exclusivity studies assess specificity against closely related organisms or organisms that could be found in whole blood and show no significant cross-reactions.

**Ergebnisse und Schlussfolgerung:** The lecture will present the semistationary PCR instrument Filmarray for the rapid diagnosis of diseases, the detection limits of the individual pathogens and further information on the test results of the new GF kit for the detection of global fever diseases.

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**Eingereicht am:** 03.05.2019

**Abstractsprache:** Englisch

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**Präsentierender Autor:** Bogreau, H

**Institut/e:** 1: Biomedical Research Institute of the French Army (I.R.B.A.) / Microbiology and infectious Diseases department / Parasitology and Entomology Unit.

## Inhalt

<b>Titel:</b>	Molecular study of therapeutic failures in the treatment of <i>Plasmodium falciparum</i> infections with artesunate-amodiaquine combination (ASAQ).
<b>Fragestellung:</b>	<i>Plasmodium falciparum</i> 's resistance to Artemisinin-based combination therapies (ACT) and the risk of its spread in Africa remains a major public health problem. This molecular study aims to assess the effect of Artesunate-Amodiaquine (ASAQ), one of the two main ACTs used in Africa, on <i>P. falciparum</i> populations.
<b>Methodik:</b>	Samples were collected during a clinical trial evaluating the efficacy of ASAQ at the beginning of its implementation in south-eastern Côte d'Ivoire and 24 months later. Parasites from treatment failure were genotyped at molecular markers previously associated with resistance to artemisinin derivatives, amodiaquine and Sulfadoxine-Pyrimethamine.
<b>Ergebnisse und Schlussfolgerung:</b>	Out of 62 therapeutic failures, 5 were recrudescences (2/25 in 2010 and 3/34 in 2013). Taking ASAQ is associated with an increase in the prevalence of the pfcr1 K76T mutation in 2010 ( $p=0.0025$ ) and 2013 ( $p=4.6 \times 10^{-9}$ ) despite a decrease in its prevalence between 2010 and 2013. A similar trend can be observed for the pfmdr1 marker N86Y. Markers associated with resistance to artemisinin derivatives are not selected by the ASAQ and remain stable between 2010 and 2013 despite the rare observations in 2013 of two mutations PF3D7-0311000 I103V and PF3D7-0104300 k874R. The prevalence of mutations in the pfdhfr gene is high (>57%) and remains stable. Pfcrt 76T and pfmdr1 86Y mutations provide a selective advantage to the parasite responsible for new infections after treatment with ASAQ and remain the most informative markers about the risk of treatment failure. However, the situation in the field and in particular the effectiveness of Artesunate does not allow their dissemination in Côte d'Ivoire.

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**Abstractsprache:** Englisch

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## Inhalt

**Titel:** Hantavirus Infection in Ukraine

**Fragestellung:** Hantavirus infection is a widespread viral infection. The main clinical forms of Hantavirus disease are Hemorrhagic fever with renal syndrome (HFRS), Hantavirus cardiopulmonary syndrome and Epidemic nephropathy. In Ukraine, Hantavirus infection is registered in the form of sporadic cases with a predominantly benign course.

**Methodik:** We observed 12 cases of Hantavirus infection at Infectious Diseases Department of O.O. Bogomolets National Medical University during 2016-2018.

**Ergebnisse und Schlussfolgerung:** All patients are residents of Ukraine. Age of patients is from 27 to 44 years. Most of the patients were infected on the territory of Ukraine. Only one case was imported - the patient traveled in the wooded areas of Indonesia and in Thailand. The disease occurred during the typical season - late April - May, November, imported case from countries with subtropical climates, and one case of infection in - December-January in Kyiv. The typical clinical manifestations were acute onset, fever, impaired vision, nephritis (with acute renal syndrome in two cases), normocytosis with a left shift and thrombocytopenia in CBC. The diagnosis was verified retrospectively serologically: specific IgM and IgG to Hantaviruses were detected in serum. Thus, our observations indicate the presence of hantavirus infection in Ukraine. Along with the benign course, like epidemic nephropathy, the disease can be severe, with the development of acute renal failure. The absence of hemorrhagic syndrome, severe renal failure does not exclude the diagnosis of HFRS. The availability of timely specific diagnostics is a decisive factor in making the final diagnosis of Hantavirus infection.

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