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Vector-Borne Diseases:
Impact of Climate Change on Vectors and Rodent Reservoirs

Berlin, 27 & 28 September 2007

PROGRAMME AND ABSTRACTS

Organization

Umweltbundesamt – Federal Environment Agency
FG IV1.4
B. Habedank, J. Klasen, E. Schmolz
Postbox 33 00 22
D-14191 Berlin
Germany

Conference Venue

Botanical Museum Berlin
Königin-Luise-Str. 6 – 8
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Vector-Borne Diseases: Impact of Climate Change on Vectors and Rodent Reservoirs
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PROGRAMME

Thursday, 27 September

8:15 h **Registration**

9:00 h **Welcome notes**

Prof. Dr. A. Troge, President of the Federal Environment Agency (DE)

MBA J. Küllmer, Federal Ministry for the Environment, Nature Conservation and Nuclear Safety (DE)

Dr. J. Strobel, Federal Ministry of Health (DE)

Vector-borne diseases and influencing factors

Moderator: P. Greiner (Federal Environment Agency, Berlin, DE)

9:40 h **Vector-borne diseases and their control: An introduction**
J. Klasen, B. Habedank (Federal Environment Agency, Berlin, DE)

10:00 h **Climate modelling: Global and regional scenarios**
D. Jacob (Max-Planck-Institute for Meteorology, Hamburg, DE)

10:30 h Coffee break

11:00 h **Postglacial formations and fluctuations of the biodiversity of Central Europe in the light of climate change**
H. Aspöck (Medical University of Vienna, AT)

11:30 h **Epidemiology of vector- borne diseases in Germany**
K. Stark (Robert-Koch-Institute, Berlin, DE)

Vectors of vector-borne diseases I:

Mosquitoes and mosquito-borne diseases

Moderator: J. Klasen (Federal Environment Agency, Berlin, DE)

12:00 h **Influence of climate change on mosquito development and mosquito-borne diseases in Europe**
N. Becker and B. Pluskota (KABS, Waldsee, DE)

12:30 h **Mosquito-borne viruses in Europe**
Z. Hubalek (Academy of Sciences, Brno, CZ)

13:00 h **Lunch break**

14:00 h **Yellow fever to Chikungunya - the globalization of vectors and vector-borne diseases**
P. Reiter (Institut Pasteur, Paris, FR)

14:30 h **Epidemiology of West Nile infection in Volgograd, Russia, in relation to climate change and mosquito bionomics**
A.E. Platonov, Fedorova M.V., Karan L.S. S., Shopenskaya T.A., Platonova O.V., Zhuravlev V.I. (Central Institute of Epidemiology, Moscow, RU)

15:00 h **Circulation of West Nile Virus in Germany ?**
S. Linke, M. Niedrig and G. Pauli (Robert-Koch-Institute, Berlin, DE)

15:30 h **Modelling of temperature-dependent Malaria risk in Lower Saxony, Germany**
W. Schröder and G. Schmidt (University of Vechta, DE)

16:00 h **Coffee break and Poster Session**

Sand flies and transmitted diseases

Moderator: E. Schmolz (Federal Environment Agency, Berlin, DE)

17:00 h **Sand flies and leishmaniasis in Germany**
T. Naucke (University Hohenheim / Parasitus Ex e.V. Niederkassel, DE)

Biting midges and transmitted diseases

17:20 h **Bluetongue: Vectors, epidemiology and climate change**
P.S. Mellor, A. Wilson (Institute for Animal Health, Surrey, GB)

17:50 h **Biting midges as vectors of blue tongue virus inGermany**
H. Mehlhorn (University Düsseldorf, DE)

Evening program

Guided tour through the “Large Glass House” of the Botanic Garden

19: 30 h **Dinner and Come Together in the “New Glass House” of the Botanic Garden**

Friday, 28 September

Rodent-borne diseases

Moderator: E. Schmolz (Federal Environment Agency, Berlin, DE)

9:00 h **Rodent-borne diseases in a changing European environment**
H.Henttonen (Finnish Forest Research Institute, Vantaa, FI)

9:30 h **Network „Rodent-borne pathogens" in Germany: Longitudinal studies on the geographical distribution and prevalence of hantavirus infections**

R.G. Ulrich[1], J. Schmidt-Chanasit, M. Schlegel, M. Wenk, M. Mertens, J. Jacob, H.-J. Pelz, T. Büchner, D. Masur, K. Sevke, S. Mikolajczak, H.W. Gerstengarbe, M. Pfeffer, R. Oehme, U. Hartelt, S. Pluta, W. Wegener, G. Heckel, S. Brockmann, S.S. Essbauer and members of the Network „Rodent-borne pathogens"
([1]Friedrich-Loeffler-Institute, Riems, DE)

9:45 h **Emergence of Hantavirus in Germany: Rodents, climate and human infections**
I. Piechotowski [1], S.O. Brockmann, C.H. Winter, C. Schwarz, U. Ranft, E. Göhring-Zwacka, G. Pfaf
([1]Baden-Wuerttemberg State Health Office, Stuttgart, DE)

Vectors of vector-borne diseases II:

Ticks and tick borne diseases

Moderator: B. Habedank (Federal Environment Agency, Berlin, DE)

10:00 h **Tick ecology and climate: Mechanisms regulating the distribution and life cycle of *I. ricinus***
J.-L. Perret (Novartis AG / University Neuchatel, CH)

10:30 h **What makes ticks tick? Climate changes, ticks and tick borne diseases**
J. Süss (Friedrich-Loeffler-Institute, Jena, DE) and F.-W. Gerstengarbe (Potsdam Institute for Climate Impact Research, DE)

11:00 h Coffee break

11:30 h **Modelling and prediction of habitat suitability for ticks**
A. Estrada-Pena (University of Zaragoza, ES)

12:00 h **Influence of meteorological conditions on the occurrence of ticks and TBD in the Czech Republic**
B. Križ, V. Danielova and M. Daniel (National Institute of Public Health, Prague, CZ)

12:30 h **Ticks and tick-borne diseases in Southern Germany**
P. Kimmig, K. Hartelt and R. Oehme (Baden-Wuerttemberg State Health Office, Stuttgart, DE)

13:00 h **Lyme borreliosis in Germany: Data and Trends**
G. Poggensee (Robert-Koch-Institute, Berlin, DE)

13:20 h **Lunch break**

Surveillance of vectors and vector-borne diseases: Programs, Concerted Actions, Networks

Moderator: G. Mücke (Federal Environment Agency, Berlin, DE)

14:20 h **WHO Europe: IPCC, the cChash-Projekt (Climate Change and Adaptation strategies for human health) and ECDC/WHO/JRC/EEA: Surveillance of vector-borne diseases in several countries**
B. Menne (WHO Europe, Rom, IT)

14:50 h **The EDEN – project (Emerging Diseases in a changing European Environment)**
P.G. de Mendonca (Ludwig-Maximilian-University, Munich, DE)

15:10 h **Climate change and adaptation needs**
P. Mahrenholz (Federal Environment Agency, Berlin, DE)

15:30 h **Closing discussion and conclusions**

16:15 h **End of the Conference**

Poster session

P 01 **Climatic extremes and mosquito occurrence in the Czech Republic**
F. Rettich (Prague, CZ)

P 02 **Chikungunya fever – a threat for Europeans**
R. Eitrem and S. Vene (Karlskrona, Stockholm, SE)

P 03 **Quest for novel viruses in mosquitoes collected in the area of the Taï National Park, Côte d'Ivoire**
S. Junglen, A. Kurth, F. Leendertz, A. Nitsche, G. Pauli and H. Ellerbrok
(Berlin, DE)

P 04 **IRM in a Multi-Resistant Malaria Vector Scenario Mexico Trial**
IRAC

P 05 **Insecticides Mode of Action Classification: A Key to Effective Insecticide Resistance Management in Mosquitoes**
IRAC

P 06 **Entomological and epidemiological surveys for monitoring bluetongue disease**
S. Bartsch, A. Stephan, P. Hoffmann-Köhler, B. Bauer, E. Schein, P.-H. Clausen, G. Liebisch, A. Liebisch, E. Kiel, D. Werner, C. Bauer, M. Geier, G. A. Schaub, F.J. Conraths, H.-J. Bätza and H. Mehlhorn
(Berlin, Burgwedel, Oldenburg, Giessen, Regensburg, Bochum, Jena, Bonn, Düsseldorf, DE)

P 07 **Monitoring of Ceratopogonidae in the German federal states Rheinland-Pfalz and Saarland**
B. Vorsprach and G.A. Schaub (Bochum, DE)

P 08 **Potential impacts of climate change on stable flies, investigated along an altitudinal gradient**
J. Gilles, J.-F. David, E. Tilard, G. Duvallet, K. Pfister (Munich, DE)

P 09 **A study of the sylvatic rodent reservoir for *Bartonella* spp. in NE Poland: prevalence and the diversity of infection**
Renata Welc-Falęciak, Anna Paziewska, Anna Bajer, Edward Siński
(Warsaw, PL)

P10 **RatMap: a digital geodata supported monitoring project of urban rat populations in Hamburg, Germany**
A. Plenge-Bönig, K. Baumgardt, F. Ukena and A. Sammann
(Hamburg, DE)

P11 **Winter acitivy of Ixodes ricinus in a Berlin forest area**
H. Dautel, C. Dippel, D. Kämmer, A. Werkhaus and O. Kahl
(Berlin, DE)

P12 **Seasonality of Ixodes ricinus in Germany: Preliminary results from the EDEN project**
A. Kupča, J. Raczynski, P. G. de Mendonça, M. Rinder and K. Pfister
(Munich, DE)

P13 **Seasonal and geographic variation in the epidemiology of *Anaplasma phagocytophilum* and *Rickettsia spp.* in the hard tick *Ixodes ricinus* in Bavaria**
C. Silaghi, J. Gilles and K. Pfister K. (Munich, DE)

P14 **Ticks, rodents and tick-born diseases in Lithuania and Norway**
A. Paulauskas, D. Ambrasiene, J.Radzijevskaja, O. Rosef, J. Turcinaviciene (Kaunas, Vilnius, LT; Telemark, NO)

P15 **Genetic heterogenity of *Borrelia burgdorferi s*ensu lato in the Kemerovo region (West Siberia) of Russia based on restriction fragment length polymorphism and sequence analysis**
M. Filipenko, O.Yatsenko, E.Khrapov, E.Voronina, A.Shabaldin, T. Poponnikova, L. Galaganova (Novosibirsk, Kemerovo, RU)

P16 **Climate Change: More vector transmitted plant pests?**
H. Kehlenbeck, G. Schrader and J.-G. Unger (Kleinmachnow, Braunschweig, DE)

P17 **Incidence and epidemiology of gramineous viruses transmitted by insects and eriophyid mites in Germany**
F. Rabenstein, F. Ehrig, J. Schubert, A. Habekuß, E. Schliephake, W. Huth, R. Götz (Quedlinburg, Braunschweig, DE)

P18 **Impact of climate change on insect vector populations and the occurrence and prevalence of insect-transmitted plant viruses in major crop plants of Germany**
K. R. Richert-Pöggeler, R. Götz, K. Lindner, V. Zahn, H.-J. Vetten, S. Busche, U. Heimbach and G. Deml (Braunschweig, Hannover, DE)

P19 **Climate change as a potential cause of the occurrence of potato stolbur in Germany**
K. Lindner, M. Maixner and M. Roman (Braunschweig, Bernkastel-Kues, DE; Timisoara, RO)

ABSTRACTS OF ORAL PRESENTATIONS

Vector borne diseases and their control: An introduction

Jutta Klasen and Birgit Habedank

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In the view of climate change, vector-borne diseases of man and animals with vectors and reservoirs developing in natural habitats are of special interest. Vector density, spread of vectors into new geographical areas and the prevalence of infectious agents in the vectors are strongly influenced by micro- and macroclimatic and other environmental conditions. However, climate is only one factor among others: travelling and transportation, human behaviour, socioeconomic conditions, land use and immunity have to be considered for the evaluation of changes in the occurrence of vector-borne diseases. In the recent discussion concerning the impact of climate change on the occurrence of tick-borne diseases in Europe, some studies (e.g. Randolph and Rogers 2000, Randolph 2004, Sumilo et al. 2007) pronounced the importance to include these factors into the analysis.

Nevertheless, in awareness of forthcoming significant climate change it is necessary to work out the impact to be able to make predictions. Vector and reservoir surveillances are important components of such a strategy.
In 2003 the Federal Environment Agency (FEA) published a report on the *'Possible impact of climate change on distribution of pathogens primarily relevant to humans through animal vectors and to human parasites in Germany'.*
The study compiled all available data on occurrence and distribution of human parasites and disease vectors in Germany until 2001. The overall conclusions were:

- Many of the relationships concerning climate and vector-borne diseases remain postulated ones. Quantitative data are lacking.
- We need studies to close the information gaps about distribution and occurrence of vectors which already exist in Germany and its neighbouring countries.

Since then, studies form neighbouring countries have also been published which contributed to our current state of knowledge.

In contrast to the great vector-control campaigns on other continents to fight major human infections like malaria, leishmaniasis, trypanosomiasis and onchocerciasis, vector control programs are not yet common and necessary in Europe. The WHO has reviewed in its reports on vector-borne human infections of Europe (WHO 2004) and on cCASH (Menne et Ebi 2006) that chemical vector control measures should be limited to application in indoor conditions. Public education and preventive advices are more likely to be effective measures to reduce transmission of VBD in Europe than massive outdoor use of biocides. Ecological soundness and sustainability of chemical control measures are even more mandatory for Europe than for African or Asian areas suffering under lethal vector-borne diseases. Lack of effective drugs or emergence of resistance to drugs makes vector control the most important preventive measure in many areas of the world. Since 1998 the WHO proposes the Integrated Vector Management (Townson et al. 2005). Multiple interventions that target different points of the disease circle lead to significant decrease in disease transmission, e.g. the consequent destruction and avoidance of breeding places for mosquitoes can reduce transmission rates of mosqito borne diseases significantly. A prerequisite for this strategy is excellent knowledge about biology and ecology of all stages of vector development and the transmission circle.

In many European countries we are far away from systematic knowledge even about the regional presence of potential disease vectors. The first outbreak of blue-tongue disease in ruminants in Germany in 2006 triggered a first large Midge-Monitoring-System established in March 2007 at 90 German farms, funded by the German Federal Ministry of Food, Agriculture, and Consumer Protection. Shall we wait until an epidemic outbreak of a severe human infection like leishmaniasis or dengue before we start looking for competent vectors systematically?

Although the vector-borne diseases in Europe do not cause approximately as many deaths than in other continents, we must be prepared for the occurrence of new emerging diseases which can become more likely in a changing environment.

International networking, interdisciplinary cooperation in research and public education are key words to be discussed during the conference.

References:

Maier W.A., Grunewald J., Habedank B. et al (2003): Possible impact of climate change on distribution of pathogens primarily relevant to humans through animal vectors and to human parasites in Germany. UFOPLAN-Bericht 200 61 218/11. Climate Change 05/03. Umweltbundesamt, Berlin. 341pp.

Menne B. and Ebi K.L. (Eds.) 2006): Climate change and adaptation strategies for human health. Springer Verlag, Steinkopf Verlag Darmstadt, 449 p.

Randolph S.E. (2004): Evidence that climate change has caused “emergence” of tick-borne diseases in Europe? Int. J. Med. Microbiol. 293, Suppl. 37: 5-15.

Randolph S.E. and Rogers D.J. (2000): Fragile transmission cycles of tick-borne encephalitis virus may be disrupted by predicted climate change. Pros. R. Soc. Lond. B , 267: 1741-1744.

Sumilo D., Asokliene L., Bormane A. et al. (2007): Climate change cannot explain the upsurge of tick-borne encephalitis in the Baltics. PLoS ONE 2 (6), e500.

Townson H., Nathan M.B., Zaim M. et al. (2005): Exploiting the potential of vector control for disease prevention. Bull World Health Organ. 83: 942-946.

WHO (2004): The vector-borne human infections of Europe – their distribution and burden on public health. WHO Regional Office for Europe, 144p.

Climate Modelling: global and regional scenarios

Daniela Jacob, Max-Planck-Institute for Meteorology, Hamburg, Germany

Meteorological and hydrological observations demonstrate that during the last decade the climate has changed. As reported by the *Intergovernmental Panel on Climate Change* (IPCC, 2001), a mean increase of temperature by 0.09 K per decade was observed globally from 1951 to 1989. Up to now, 2006, this trend has continued. Europe experienced an extraordinary heat wave in summer 2003, with daily mean temperatures being about 10° warmer than the long term mean. The increase of temperature varies depending on the region and season. If the temperature of the atmosphere increases, it should be assumed that the water cycle is intensified. However, it has not been possible until now to present clear statements on changes in the water cycle as a consequence of climate change.

Global climate models (GCM) have been developed to study the Earths climate system in the past and future, for which assumptions of green house gases are needed. Theses models are mathematical images of the Earth system, in which physical and biogeochemical processes are described numerically to simulate the climate system as realistically as possible. The model quality, however, can only be judge on in comparison with independent observations. Therefore, time periods of the past are simulated and the model results are compared against measurements before the models are used for climate change studies.

Even today global climate models provide information only at a relatively coarse spatial scale. Therefore high resolution regional climate models (RCM) are nested into global calculations to investigate the impact of potential global climate change on specific regions. The results of these investigations depend on both the quality of the global and regional models and the choice of the climate scenario.

In order to achieve information about the probability, e.g. for the intensification of the hydrological cycle over Europe, several models from different European climate research institutes are used, such as it was done in the EU project PRUDENCE (prudence.dmi.dk).

Following the climate change scenario A2 projecting a relatively strong future increase of greenhouse gases until the year 2100 (IPCC, 2001) and a subsequent global mean temperature increase of about 3.5°, numerous simulations were conducted within PRUDENCE. An analysis of their results for different river catchments shows significant differences between the projected changes over northern and central Europe for the time period 2070 – 2100 compared to the current climate (1961-1990). For the Baltic Sea catchment, a precipitation increase of about +10% for the annual mean is projected, with the largest increase of up to +40 % in winter, while a slight reduction of precipitation is calculated for the late summer. Evapotranspiration will increase during the entire year with a maximum increase in winter. These rises in precipitation and evapotranspiration may lead to an increase of river discharge into the Baltic Sea of more than 20% in winter and early spring.

Here, the seasonal distribution of discharge is largely influenced by the onset of spring snowmelt.

For the catchments of Rhine, Elbe and Danube, a different change in the water balance components is yielded. While the annual mean precipitation will remain almost unchanged, it will increase in late winter (January-March) and decrease significantly in summer. The evapotranspiration will rise during the entire year, except for the summer, with a maximum increase in winter. These changes lead to a large reduction of 10 to 20% in the annual mean discharge. Especially for the Danube, the projected summer drying has a strong impact on the discharge that is reduced up to 20% throughout the year except for the late winter (February/March) when the increased winter precipitation causes a discharge increase of about 10%. These projected changes in the mean discharge will have significant impacts on water availability and usability in the affected regions.

Under climate change conditions not only the absolute amounts of precipitation may change but also the precipitation intensities, i.e. the amount of precipitation within a certain time period. The simulation of precipitation intensities or extreme precipitation events requires however a considerably higher resolution than the A2 results presented above so that for example the influence of the topographically largely varying Alps on the formation of precipitation over the Rhine catchment could be adequately calculated. High resolution RCM results show that the global warming until 2050 will lead to an increase of high precipitation events over the Alpine part of the Rhine catchment, especially in summer. This climate change signal becomes clearly visible in the Pre-Alps, but a similar trend is seen in the high resolution simulations over large parts of Europe.

An overview over existing regional climate change simulations for Europe will be presented together with results achieved within several EU-funded projects like MERCURE, PRUDENCE and ENSEMBLES.

A major break through was possible with the regional climate change simulations on 10 km grid scale. Within a co-operation with the national environmental agency, REMO was used for a control simulation from 1950 to 2000 and three transient run for the IPCC SRES scenarios A2, A1B and B1. The simulation domain covers Germany, Austria and Switzerland. As an example the most important results for Germany at the end of this century are summarized as follows:

- Increase of the annual mean temperature by 4°C (depends on emission amount and region)
- South and Southeast warm more than the other areas
- Decrease of precipitation amount in wide areas of Germany during the summer
- Increase of precipitation amount in South and Southeast during the winter
- Less precipitation as snow

The simulations results offer a variety of follow-up analyses, like extreme value statistics, which is currently in progress, or impact studies. All data are stored in the CERA data base and are open for commercial and non-commercial use.

Postglacial formation and fluctuations of the biodiversity of Central Europe in the light of climate change

Horst Aspöck, Medical University of Vienna (MUW), Vienna, Austria

We are living in an interglacial period, in one of the several cycles of glacial formation and melting that have occurred since the continuous decrease of the average temperature during the Pliocene beginning about 2.5 million years ago. Glacial periods usually last about 90,000-100,000 years, interglacial periods are much shorter, usually 15,000-20,000 years or less. (There is, however, some variation, and the length of these cycles was distinctly shorter at the beginning of the ice age.)

The present biodiversity of Central Europe, including animals, plants, fungi, but also (with some restriction) eukaryotic and prokaryotic unicellular organisms and, thus, also at least many parasitic organisms s.l. and even, to some respect, viruses, particularly those transmitted by arthropods, is largely the result of a deep climate change and, moreover, of various climatic fluctuations during the past – roughly spoken – 15,000 years. At that time the latest (certainly not the last!) glacial period (i.e. the Würm period = Weichsel period) came rather rapidly to an end. The annual average temperature increased gradually and finally reached values up to 12°C (average annual temperature) higher than a few thousand years before. 20,000 years ago the northern and, moreover, larger parts of Central Europe were covered by huge ice sheets, partly of a thickness of several hundred metres up to more than three kilometres. At the maximum of glaciation in the most recent glacial period (about 18,000 years ago) the southern border of the huge area covered by ice ran through the northern parts of Germany. (The Saale-Riß glacial period, which lasted from 230,000 to 130,000 B.P., was accompanied even by a larger glaciation, which included larger parts of Germany.) Also the Alps were straddled by huge glaciers, of course. (The area of Innsbruck e.g. lay under a glacier with a thickness of more than 1.5 kilometres.) The parts of Central Europe between the northern glaciers and those covering the Alps were of a tundra-like character without forests and with an extremely reduced number of species of animals, plants and other organisms, however, inhabited by several spectacular mammals (homoiothermic animals!) like mammoths, woolly rhinoceros, musk oxen, sable-tooth cats, and others like roe deer. The South European peninsulas, largely covered by forests of various kinds, represented, however, huge refugial areas with distinctly different inventories of biodiversity. These refugial centres, particularly the Atlantomediterranean, the Adriatomediterranean, the Balkanopontomediterranean subcentre and several others as parts of a big Holomediterranean centre were of utmost importance for the biological recolonisation of Central Europe. However, another important corridor became increasingly significant for the growing biodiversity of Central Europe after the end of the latest (in principle, however, of each) glacial period, namely the broad area in the east. From the Palaearctic parts of Asia numerous species could invade the central parts of Europe; these are called Siberian faunal elements, usually adapted to ecosystems in cooler climates. (The animals associated with spruce forests are typical examples, but also many mosquito species occurring in Central Europe are Siberian faunal elements.)

Mediterranean faunal elements in Central Europe are characterised by distributional patterns including at least refugial centres in one of the South European peninsulas and covering smaller or larger parts of Central Europe, in many cases also of Northern Europe. These species migrated northwards, when the increasing temperature led to markedly improved ecological conditions. Several *Anopheles* species (*A. algeriensis*, *A. hyrcanus*, *A. plumbeus* …) are examples for Mediterranean faunal elements.

The Siberian faunal elements (with refugial centres as far as Mongolia in the east) are usually characterised by distributional patterns covering large Palaearctic parts of Asia as well as northern and central parts of Europe, but not the Mediterranean parts of Europe (except in higher mountains). Moreover, extramediterranean European faunal elements have contributed to some extent; these are organisms which have survived the latest glacial period in refugial centres in various southern parts of Central Europe (particularly south of the Alps). In addition, there are few other centres (e.g. the Pontocaspian centre) which have also contributed – although to a very small extent – to the biodiversity of Central Europe. Moreover, due to polycentricity and various degrees of expansivity, the situation may become rather complex in many cases.

The concept of formation of the postglacial biodiversity of Central Europe by invasion of Mediterranean faunal elements, on one hand, and of Siberian elements, on the other hand, is particularly valid for animals inhabiting the arboreal biomes (i.e. areas in which natural forests can develop), thus also for all vectors for infectious diseases in Central Europe. The show horses among the animals following these biogeographical mechanisms are the arthropods as ectothermic animals, and from the standpoint of medical entomology and acarology the arthropod vectors. Several other mechanisms of distribution exist, which are of high significance particularly for plants and free-living micro-organisms, but need not be discussed in this context.

At the beginning of our interglacial – about 12,000 years ago – the average temperature increased rapidly, it reached a first peak about 10,000 years ago, and after a period of about 1,000 years it increased again continuously until it attained values higher than or approximate to present ones. This period marked by two peaks about 6,500 and about 4,500 years B.P. is known as the Holocene climatic optimum (or Atlanticum), and these 2,000 years were of utmost significance for the immigration of organisms, in particular also arthropods and thus also potential vectors of infectious micro-organisms into Central Europe. The arthropod fauna of Central Europe harbours many species of Mediterranean origin, which show a more or less continuous distribution pattern in the south, but gradually becoming scattered northwards. Several species occur for example in few isolated spots in Northern Germany, and if they had not been detected many decades ago, but were to be discovered today, one might conclude that they are recent immigrants due to global warming. They are, however, not newcomers, but the remains of the intensive and extensive immigration of Mediterranean faunal elements during the Holocene climatic optimum – or in some cases of later immigrations during warmer periods, a particularly marked one occurring about 2,000 years ago.

A good example for vectors which have only recently been found to occur in Germany are the Phlebotominae/sandflies (*Phlebotomus mascittii*). It was claimed that they demonstrate global warming, but we know that the species was found several decades earlier in adjacent regions outside Germany. It is a reasonable assumption that sandflies had immigrated from the south of Europe in the Atlanticum, that they were widely distributed in Central Europe during that time, that they died out during the following colder periods, but remained in a few xerothermic places like the southwestern parts of Germany, where there are many other insects of Mediterranean origin (e.g. *Mantis religiosa*, *Libelloides longicornis* and *L. coccajus*, *Mantispa styriaca*,…). *Uranotaenia unguiculata* is another good example among mosquitoes. Usually it is believed that the present Alpine glaciers are the remnants of the huge glaciers of the latest glacial period; however, most probably this is not true, since most probably the glaciers in the Alps had totally disappeared during the Atlanticum, and we definitely know that the timber-line in the Alps was considerably higher 6,000 years ago.

The fluctuations of the post-Pleistocenic climate demonstrate that considerable fluctuations of the biodiversity of Central Europe must have occurred and continue to occur. Every year new species are detected, while others seem to have disappeared. One should keep this in mind when concluding hastily that a new record of a Mediterranean species so far unknown in Central Europe is the result of global warming. It cannot be questioned that 6,000 years ago, and probably also (again) during the height of the Roman Empire, Central Europe harboured considerably more Mediterranean faunal elements, and among these also potential vectors of infectious diseases, than today. Nevertheless, this does not discharge us from being aware of possibly new immigrating – emerging – vectors and thus also emerging diseases. The increase of the temperature has now reached values which are comparable to those of the warmest postglacial periods, i.e. the Atlanticum, or which are about to exceed them gradually. Ten years ago it was argued that the climate change lies entirely within the postglacial fluctuation and can thus be neglected. Today we must confess that it would be irresponsible to neglect the present trend which will inevitably lead to further increase of the temperature and thus to considerable ecological and chorological consequences including the possible immigration and dispersion and spread of vectors of micro-organisms causing serious infectious diseases in humans.

The present day molecular biological methods have opened new ways of studying the provenance of migrating organisms so that we can trace the origin of newly detected populations. Phylogeography has become a very important new field not only in biogeography, but also in the epidemiology of infectious diseases.

For further reading:

Aspöck, H. (1979): Biogeographie der Arboviren Europas. – Beiträge zur Geoökologie des Menschen, Vorträge des 3. Geomedizinischen Symposiums, Schloß Reisensburg, 1977. Geographische Zeitschrift, Beiheft 51: 11 - 28.

Aspöck, H., U. Aspöck & H. Rausch (1991): Die Raphidiopteren der Erde. Eine monographische Darstellung der Systematik, Taxonomie, Biologie, Ökologie und Chorologie der rezenten Raphidiopteren der Erde, mit einer zusammenfassenden Übersicht der fossilen Raphidiopteren (Insecta: Neuropteroidea). Biogeographisches Glossarium. – 2 Bände: 730pp; 550pp. Goecke & Evers, Krefeld.

Aspöck, U. & H. Aspöck (2005): Verbreitungsgrenzen von Neuropterida in Mitteleuropa. – Linzer biologische Beiträge (Verhandlungen des XVIII. Internationalen Symposiums über Entomofaunistik Mitteleuropas [SIEEC]) 37/1: 29-38.

De Lattin, G. (1967): Grundriß der Zoogeographie. – Fischer, Stuttgart. 602 pp.

Hewitt, G.M. (1993): Postglacial distribution and species substructure: lessons from pollen, insects and hybrid zones. – Linnean Society Symposium Series 14: 97-123.

Hewitt, G.M. (1996): Some genetic consequences of ice ages, and their role in divergence and speciation. – Biological Journal of the Linnean Society 58: 247-276.

Hewitt, G.M. (1999): Post-glacial re-colonization of European biota. - Biological Journal of the Linnean Society 68: 87-112.

Hewitt, G.M. (2000): The genetic legacy of the Quaternary ice ages. – Nature 405: 907-913.

Hewitt, G.M. (2001): Speciation, hybrid zones and phylogeography – or seeing genes in space and time. – Molecular Ecology 10: 537-549.

Schmitt T. & A. Seitz (2001): Intraspecific allozymatic differentiation reveals the glacial refugia and the postglacial expansions of European Erebia medusa (Lepidoptera: Nymphalidae). – Biological Journal of the Linnean Society 74: 429-458.

Schmitt T. & A. Seitz (2002): Postglacial distribution area expansion of Polyommatus coridon (Lepidoptera: Lycaenidae) from its Ponto-Mediterranean glacial refugium. – Heredity 89: 20-26.

Sudhaus, W., K. Kiontke, A. Fürst von Lieven, A. Manegold & V. Seitz (1997): Speziation in Mitteleuropa im Gefolge der Eiszeiten. – Sitzungsberichte der Gesellschaft Naturforschender Freunde zu Berlin (N.F.) 36: 1-175.

Varga, Z. (1977): Das Prinzip der areal-analytischen Methode in der Zoogeographie und die Faunenelements-Einteilung der europäischen Tagschmetterlinge/Lepidoptera: Diurna. – Acta Biologica Debrecina 14: 223-285.

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Epidemiology of vector-borne diseases in Germany

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Surveillance of notifiable infectious diseases in Germany covers locally-endemic infections as well as imported infections. Tick-borne encephalitis (TBE) and lyme borreliosis are the major tick-borne infections endemic to Germany. The incidence of both infections has increased since 2001. Apart from environmental and climatic factors influencing vector and reservoir populations and human exposure (eg, outdoor activities), factors such as immunisation coverage (TBE) and raised diagnostic awareness may also contribute to these trends in the surveillance data. Notifiable imported mosquito-borne infections include malaria, dengue virus, and other viruses which may cause haemorrhagic fever. Under the current entomologic and climatic situation in Germany the risk of authochthonous transmission of pathogens imported from tropical countries is negligible. However, the recent chikungunya virus outbreak in Northern Italy demonstrates that distinct pathogens may also emerge in other European countries under certain conditions. In addition to routine surveillance, epidemiological and entomological studies are needed in order to monitor the geographical spread of endemic pathogens and the distribution of relevant vectors in Germany, and to enable early detection of any new vector-borne pathogens and/or their vectors.

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Influence of climatic change on mosquito development and mosquito-borne diseases in Europe

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In Europe mosquitoes have a strong impact on life quality of humans, tourism and economic development and can also threaten by transmitting mosquito born diseases. In this paper the consequences of climatic change on the development of mosquitoes and their control as well on emerging diseases are discussed. The comparison of temperature development in three time periods as 1952-1966, 1967 to 1981, 1982-2006 in Central Europe and West-Africa will serve as basis for the changing scenario related to population dynamics, abundance and phenology of mosquitoes. Furthermore, the risk for mosquito borne diseases such as West-Nile-Fever will be discussed based on the adaptation capacity of *Aedes albopictus* to climatic change. *Aedes albopictus* has been spreading world-wide since decades due to its high adaptation capacity to various climatic conditions it has been spreading world wide since decades. The mosquito invaded Italy in 1990 and a rapid spreading in most parts of southern Europe seems only a question of time. Also an immigration of the species further north is possible when we consider the changing climatic conditions during the last decades. Potential invasion places for *Ae. albopictus* have been investigated such as plant markets which offer lucky bamboo, stock piles of imported scrap tires, cargo harbour, railway stations and service areas along tourist routes and cargo traffic from countries where *Ae. albopictus* occurs. The vector capacity of anophelines in Central Europe for the transmission of *Plasmodium falciparum* causing Malaria tropica will be highlighted.

Keywords: Climatic change, mosquito development, mosquito-borne diseases in Europe, West-Nile-Virus.

Mosquito-borne viruses in Europe

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We can distinguish three categories of mosquito-borne viruses in Europe: (i) human pathogenic and autochthonous; (ii) human pathogenic and imported; (iii) pathogenic for other vertebrates than humans.

1. Mosquito-borne human pathogenic viruses autochthonous in Europe

Sindbis virus (*Alphavirus, Togaviridae*); synonyms Ockelbo, Pogosta and Karelian fever viruses

History: first isolated 1952 by R. M. Taylor & al. from *Culex univittatus* mosquitoes collected in Sindbis village, Nile Delta (Egypt). In Europe, first isolated by E. Ernek & al. from a Reed Warbler (*Acrocephalus scirpaceus*) caught in Western Slovakia, July 1971. SINV is very widely distributed, it occurs in Africa, Eurasia and Australia.

Human disease: fever 3-4 d. with headache, myalgia, arthralgia (polyarthritis), malaise, conjunctivitis, pharyngitis and rash (skin vesicles on the trunk and limbs while the face remains usually unaffected). Acute illness lasts up to 10 d., but fatigue and tendon pains may persist for several weeks or months, and chronic arthritis may develop in some patients. No lethality. An extensive epidemic in Fennoscandia since 1981.

Distribution in Europe (a map). In Czechland, SINV has not yet been isolated, but antibodies are present in some birds and domestic and wild mammals though at a relatively low frequency.

Vectors in Europe: *Culex pipiens, Cx. torrentium, Culiseta morsitans, Mansonia richiardii, Aedes communis, Ae. cinereus, Ae. cinereus, Ae. excrucians, Anopheles hyrcanus*.

Hosts: largely wild passeriform birds (e.g. *Turdidae*), less often rodents and amphibians.

Natural foci: mainly wetland ecosystems in diverse biomes.

West Nile virus *(Flavivirus*, *Flaviviridae*); synonym Rabensburg virus

History: First isolated 1937 from a patient's blood by K. C. Smithburn & al. in Uganda. First recorded epidemics in Israel in 1950's, then in South Africa at least 3000 cases in 1974. Soon recognized as one of the most widespread flaviviruses, distributed through Africa, Asia, Europe, and Australia; since 1999 also present in America.

Human disease: moderate to high fever, headache, sore throat, backache, myalgia, arthralgia, fatigue, anorexia, nausea (vomiting), rash, lymphadenopathy, acute aseptic meningitis or encephalitis; less often myocarditis, pancreatitis, hepatitis; lethality 5-10% (majority of fatal cases recorded in persons aged >60 years).

Distribution in Europe (a map). In Czechland, WNV was isolated in 1997 and 1999 from *Cx. pipiens* mosquitoes, and five human cases of WNF were described in South Moravia (Hubálek & al. 1999). The two virus strains were later sequenced and found to represent either a new, 3rd genomic lineage of WNV, or possibly even a new flavivirus (Rabensburg) within the Japanese encephalitis group of flaviviruses (Bakonyi & al. 2005).

European vectors: WNV was isolated from *Culex pipiens, Cx. modestus, Mansonia richiardii, Aedes cantans, Ae. caspius*, *Ae. excrucians, Ae. vexans,* and *Anopheles maculipennis* group.

Hosts: largely wild birds. In Europe, WNV was isolated from a number of wild birds, part of them being migratory.

Natural foci: wetland ecosystems.

Ťahyňa virus (California group, *Orthobunyavirus, Bunyaviridae*); synonym Lumbo virus

History: first isolated 1958 from *Aedes vexans* and *Ae. caspius* mosquitoes in Ťahyňa and Križany villages, E. Slovakia (V. Bárdoš & V. Danielová). This is the first mosquito-borne virus of vertebrates isolated in Europe. An antigenically identical virus Lumbo was later reported from Africa. TAHV occurs in Eurasia and Africa.

Human disease: 'Valtice fever', an influenza-like illness occurring in summer and early autumn mainly in children, with sudden onset of fever (3-5 d.), headache, malaise, conjunctivitis, pharyngitis, myalgia, nausea, gastrointestinal disorders, anorexia, occasional arthralgia, stiff neck or other signs of the CNS involvement, sometimes bronchopneumonia. No lethality (contrary to the N.-American La Crosse virus).

Distribution in Europe (a map). In Czechland, it occurs in southern Moravia, much less frequently in northern Moravia, Silesia, southern, central and western Bohemia.

Vectors: mainly culicine mosquitoes *Aedes vexans, Ae. caspius, Ae. cinereus, Ae. cantans, Ae. communis* (N. Europe), *Culiseta annulata, Culex modestus,* sporadically *Anopheles hyrcanus.*

Hosts: European hare, hedgehog, rodents.

Natural foci: inundated lowland habitats (floodplain forest ecosystem) including periurban areas, in diverse biomes.

Snowshoe hare virus (California group, *Orthobunyavirus, Bunyaviridae*)

History: first isolated 1959 by W. Burgdorfer from an emaciated snowshoe hare (*Lepus americanus*) in Montana, U.S.A. In Europe, first isolated 1986 by A.M. Butenko, S.D. Lvov et al. from *Aedes communis* in N. European Russia. Closely related to Tahyna and LaCrosse viruses.

Human disease: fever, headache, vomiting, sometimes CNS affection.

Distribution in Europe: Northern Europe.

Vectors: *Aedes canadensis, Ae. communis, Ae. cinereus, Ae. punctor, Ae. cataphylla, Culiseta inornata,* etc.

Hosts: snowshoe hare; lemmings and other rodents.

Natural foci: tundra and taiga biomes.

Inkoo virus (California group, *Orthobunyavirus, Bunyaviridae*)

History: first isolated 1964 by M. Brummer-Korvenkontio & al. from *Aedes communis/punctor* mosquitoes collected in South Finland, 1964.

Human disease: influenza-like illness or aseptic meningitis characterized by sudden onset of fever, weakness, headache, retrobulbar pain, conjunctivitis, pharyngitis, and occasional rash. The closely related Jamestown Canyon virus causes CNS infections among adults in North America.

Distribution in Europe (a map). The virus is obviously restricted to northern Europe, including Russia. In Czechland, the virus has not been detected, and probably is absent.

Vectors: *Aedes communis, Ae. punctor, Ae. hexodontus*.

Hosts: *Lepus timidus, Alces alces* (?).

Natural foci: open farmland with water pools at northern latitudes.

Batai virus (*Orthobunyavirus, Bunyaviridae*); synonyms Čalovo and Chittoor viruses

History: first isolated 1955 by B. Elisberg & E. L. Buescher from *Culex gelidus* collected on Kuala Lumpur (Malaysia) grazing grounds. Antigenically identical Čalovo virus was isolated in Europe later (1960) by V. Bárdoš & E. Čupková from *Anopheles maculipennis* s.l. mosquitoes near Čalovo, South Slovakia.

Human disease: serological data have indicated an association with influenza-like illness accompanied by malaise, myalgia and anorexia (F. Sluka & V. Bárdoš). BATV was also isolated from the blood of febrile patients in Thailand and Sudan, and antigenically similar African Ilesha virus was described as the cause of human febrile illness with rash or even haemorrhagic fever including one fatal case.

Distribution in Europe (a map). In Czechland, the virus was isolated by A. Smetana & al. from *Anopheles maculipennis* s.l. mosquitoes in South Moravia in 1966, and antibodies occur at a low frequency in domestic and some wild mammals, especially ruminants, less often in birds.

Vectors: *Anopheles maculipennis* s.l., *An. claviger.*

Hosts: domestic pig, ruminants, birds.

Natural foci: agroecosystems (farms, villages); domestic animal–zoophilic mosquito cycle.

2. Exotic (imported) mosquito-borne human pathogenic viruses in Europe

In 2006-2007, tens of **chikungunya** fever cases have been imported from the islands of Indian Ocean (Reunion, etc.) and Indian subcontinent to many European countries: France, U.K., Germany, Italy, Czechland, etc.

Dengue human cases in Europe: several tens are introduced each year from tropical regions, as reported by many European countries.

Occasionally, also **yellow fever** cases are being imported in Europe.

Epidemics of imported exotic mosquito-borne virus infections in Europe:

- Yellow fever: Portugal, Spain, XVIII-XIX century (the largest outbreaks in 1741 and 1802-1821: about 100,000 victims); France (Saint Nazaire), 1860s; England (Swansea), 1865.
- Dengue: a focus in Athens, 1927-28 (650,000 patients, 1060 died).
- Chikungunuya: an Italian focus Ravenna province (Castiglione di Cervia) of Emilia-Romagna, September 2007 (≥80 confirmed human cases).

Such mosquito-borne virus outbreaks are determined by the import and presence of competent vectors of the particular disease, i.e. *Aedes aegypti* in the past (YFV, DENV), and *Ae. albopictus* recently (CHIKV) in Europe.

In general, the mosquito-borne virus importation to Europe is possible *via:* viraemic travellers; introduction of infected mosquitoes (incl. larvae, puppae, eggs: *Ae. albopictus* etc.) on planes, ships, cars (international traffic and trade); trade in domestic, pet and ZOO infected vertebrates; infected migratory birds (WNV).

3. Mosquito-borne viruses not pathogenic to man in Europe

Lednice bunyavirus (Turlock group) and **Usutu** flavivirus (Japanese encephalitis goup) are associated with wild birds, and occur in Central Europe, though they are of African origin. USUV is pathogenic largely for passeriform birds and raptors (Weissenböck & al. 2002).

Favourable ecological factors for (autochthonous and imported) mosquito-borne viruses: abundance of wild vertebrates and vectors; intense summer precipitations, floods; summer temperatures and drought; appropriate habitats, e.g., humid building basements.

Virus perpetuation is possible: in overwintering mosquitoes (*Culex, Culiseta* or *Anopheles* females); by transovarial transmission in mosquitoes; during chronic infection of vertebrates.

Weather and climate effects on mosquito-borne viruses (under climate warming scenario):

- higher virus replication rate in vector mosquitoes (a shortened extrinsic incubation period)
- increased vector populations
- expanding range of vectors – northwards (e.g. *Culex modestus*)
- but: higher mortality rate of the vector population.

Epidemiological surveillance = an approach combining epidemiology with ecology, consisting of: routine diagnosis of human disease; reporting incidence of human disease; monitoring animal disease (if it exists); monitoring mosquito vector populations; testing mosquito vector infection rates; domestic+wild vertebrate serosurveys; monitoring ecological factors.

Conclusions

Eleven mosquito-borne viruses have been reported in Europe to date: six of them are autochthonous and cause human infections (Sindbis, West Nile, Ťahyňa, Snowshoe hare, Inkoo, and Batai viruses); three of the viruses are exotic, being occasionally imported to Europe (Chikungunya, dengue and yellow fever); and two of the viruses are associated with birds and are not pathogenic to humans (Lednice, Usutu). Mosquito-borne virus outbreaks are strictly determined by the presence and/or import of particular competent vectors of the disease. Ecological variables affect mosquito-borne viruses considerably, the main factors are: presence of appropriate habitats for mosquitoes, e.g., wetlands, small water pools, or humid building basements; abundance of mosquito vectors and their vertebrate hosts; intense summer precipitations, floods; summer temperatures and drought;. A surveillance for mosquito-borne viruses, the diseases they cause, and their vectors in Europe is highly recommendable.

REFERENCES

Bakonyi T., Hubálek Z., Rudolf I., Nowotny N. 2005. Novel flavivirus or new lineage of West Nile virus, Central Europe. Emerg. Infect. Dis. 11: 225-231.

Gratz N. 2006. Vector- and Rodent-borne Diseases in Europe and North America: their Distribution and Public Health. Cambridge Univ. Press. 393 pp.

Hubálek Z., Halouzka J. 1996. Arthropod-borne viruses of vertebrates in Europe. Acta Sci. Nat. Brno 30(4-5): 1-95.

Lundström J.O. 1999. Mosquito-borne viruses in western Europe: a review. J. Vector Ecol. 24:1-39.

Weissenböck H., Kolodziejek J., Url A., Lussy H., Rebel-Bauder B., Nowotny N. 2002. Emergence of Usutu virus, an African mosquito-borne flavivirus of the Japanese encephalitis virus group, central Europe. Emerg. Infect. Dis. 8: 652-656.

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Yellow fever to Chikungunya – the globalization of vectors and vector borne diseases

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Yellow fever epidemics were once a dreaded feature of life in many parts of the Americas, with devastating epidemics as far north as Boston. The vector, *Aedes aegypti*, and the virus were both introduced from Africa during the slave trade. *Ae. aegypti* is present, often common, in urban areas from South Carolina to Argentina, and responsible for endemic and epidemic transmission of another Old World virus, dengue. Yellow fever virus is now enzootic in the rainforests of South America, and may well cause devastating urban epidemics in the future. Another Old World pathogen, West Nile virus, appeared in New York in 1999, probably introduced in an infected bird imported from the Middle East. It is now enzootic from Canada to Venezuela. In addition to its public health and veterinary significance, it has caused a major wildlife catastrophe that will probably continue for centuries to come. The Asian mosquito, *Ae. albopictus*, has conquered the world in the past 30 years. Most infestations can be traced directly or indirectly to Japan, disseminated by a world-wide commerce in used tyres. The species is well adapted to cold climates, and can survive sub-zero winter temperatures. In Europe, it is now established as far north as Holland. Infestations are particularly high in Italy, predominantly in the northern half of the peninsula, where the species first appeared in the early 1990s. Its future range could well extend southward, to warmer climes, and northward into Scandinavia. Lastly, chikungunya, another African virus known for frequent pandemics throughout Asia, has now appeared in northern Italy, apparently introduced by an infected person who arrived from India. A small epidemic began in late June, 2007, in a village just south of the Po river, an area once notorious for malaria transmission. It is quite possible that further outbreaks will occur further north in Europe, as may dengue, which caused a massive epidemic in Greece in 1927-28 and is rampant throughout the tropics. It is clear that all these events are the result of human activities—transportation of goods and people—and will continue with increasing globalization of trade. Recent statements that they are the result of climate change are ill-informed, misleading and irresponsible.

Epidemiology of West Nile infection in Volgograd, Russia, in relation to climate change and mosquito bionomics.

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Background. West Nile fever (WNF) is endemic disease in Southern Russia. Human clinical WNF cases were occasionally registered in Astrakhan Province from the sixties as well as the WNF virus findings in environmental samples took place. In 1999 there was the large outbreak of WNF in Southern Russia (> 500 cases in Volgograd Province that is about 25 cases per 100,000 of population). In 2000-2003 the WNF incidence rate decreased steadily from 2 cases/100,000 to zero, but the new outbreak occured in 2007 (38 WNF cases).

Methods. The weather data were obtained by local daily observation in 1996-2007 and from the database of the International Research Institute for Climate Prediction. The entomological results were obtained during the own field studies in Volgograd Province in 2001-2007.

Results. The analysis of climatic dataset in Volgograd from 1900 showed that the years 1999 and 2007 were the hottest year. This was due to very mild "winter" (Dec-Mar) and hot third quarter (Jul-Sep). We hypothesized that the high temperature in winter supported the survival of overwintering mosquito vectors and the high temperature in third quarter facilitated the growth of virus in mosquitoes, as well as propagation of mosquitoes themselves. There are up to 15 potential WNF vectors in Volgorad, but only *Cx.pipiens* (both autogenous and anautogenous populations) and *Cx.modestus* are abundant in late summer, when a peak of WNF incidence is observed, both in urban and rural conditions. Only these species are naturally attracted to and feed on both humans and birds. When more then 20,000 mosquitoes were studied by RT-PCR, the RNA of pathogenic WN virus genovariant were found only in Culex mosquitoes with infection rate of about 0.04%. So these species may be considered as a potential WNF "bridge vector" between birds and humans as well as main vector in sylvatic avain cycle. Their abudnance in an epidemic season was higher in the years with mild winter and hot summer, so this phenomenon may serve as a connection link between a climate and WNF epidemiology.

Conclusions. These findings give some hints on the predisposing factors for WNF epidemic as well as the possibility of weather surveillance and prediction of WNF outbreaks in temperate climatic zones such as Southern Russia. Entomological studies stress the need of vector control, first of all, the control of Culex mosquitoes both in their breeding and resting sites indoor and outdoor.

Circulation of West Nile Virus in Germany?

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The natural reservoir for *West Nile virus* (WNV), a mosquito-borne *Flavivirus,* are birds. Humans and a variety of other vertebrates can be infected by mosquitoes which are blood feeding on birds and mammalians. WNV gained world wide attention when the first cases of WNV infections were reported in 1999 in North America, a region where WNV was not present before. The infection spreads rapidly all over the USA and also to Canada and to Middle and South America. WNV was most probably imported by migrating birds from WNV-endemic regions (Isreal or Africa).

Although the viremic phase in humans is short with comparatively low virus titers transmission of WNV by transfusions, transplantation and from mother-to-child in the United States were observed. Taking these observations into account the question arose, whether WNV is prevalent in Germany.

To estimate the risk to acquire an infection with *West Nile virus* (WNV) in Germany, studies on the prevalence and incidence of WNV infections in migrating birds were initiated. In addition human patients with neurological symptoms compatible with WNV induced diseases as well as horses with clinical signs of an encephalitis/meningoencephalitis were included. Serological (immune fluorescence assay, ELISA, neutralisation assay) as well as molecular methods (species specific and lineage 1 and 2 specific) were established for the detection and differentiation. Between 2000 and 2005 blood samples from birds (n= 3399) belonging to 87 species were collected and analysed for WNV specific antibodies and for WNV genomes. Only 53 birds belonging to 5 species had WNV specific antibodies.

None of the birds investigated by WNV specific PCR was positive. Humans (n = 144) or horses (n=169) with neurological symptoms showed no markers of a WNV infection (negative for antibodies and in PCR).

In addition to the investigation of humans with neurological symptoms bird ringers from Germany and Austria who have a close contact to birds during bird-ringing were included as risk group. Several serological test systems were used to study WNV the antibody prevalence among 137 bird ringers. Neutralizing antibodies were detected in three of the bird ringers. This seropositivity could be explained by alternative factors such as traveling to endemic areas. The application of different serological methods showed that WNV IgG ELISAs were less specific than WNV IgG immunofluorescence tests (IFT). The neutralization test (NT) appears to be the gold standard for *flavivirus* differentiation. From these data it was concluded that at present no evidence for the circulation of WNV could be found.

Modelling of temperature-dependent Malaria risk in Lower Saxony, Germany

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Abstract

One of the effects of climate change can be the change in geographic distribution and intensity of transmission of vector-borne diseases such as malaria. Given the most conservative estimate of change, these diseases are expected to occur, compared with the past and present, at higher latitudes or altitudes. A slight rise in ambient temperature and rainfall can extend the duration of the season in which mosquito vectors are transmitting malaria. The parasites that they transmit usually benefit from increased temperatures, as both their reproduction and development are then increased, too. Thus, it seems prudent to examine potential effects on the transmission length due to the predicted climate changes. Lower Saxony (Northwest Germany) is a former malaria region with highest incidences of *Anopheles atroparvus* and malaria tertiana along the coastal zones before malaria had finally become extinct in the early 1950s. Nevertheless, the Anopheles mosquitoes which transmit the malaria pathogens have still been present in Lower Saxony up to now. This together with the climate change related implications gave reason to investigate whether a new autochthon transmission could take place if the malaria pathogen is introduced again in Lower Saxony. Thus, the spatial and temporal structure of temperature driven malaria transmissions was investigated using the basic reproduction rate (R_0) to model and geostatistically map areas at risk for an outbreak of malaria tertiana due to measured (1947-1960, 1961-1990, 1985-2004) and predicted (2020, 2060, 2100, each best case and worst case scenario) air temperatures. The respective risk maps show that the period of potential malaria tertiana transmissions in terms of R_0 could be expected to increase from two months in the past to six months in the future in Lower Saxony. Past and recent findings of *Anopheles atroparvus* coincide with those regions where the potential malaria transmission length accounts for 4 months in 2060 (best case scenario) and for 6 months in 2100 (worst case), respectively, and, in addition, where malaria tertiana occurred up to the 1950's. The geostatistically estimated malaria risk maps were intersected by a map on ecological land units. This approach made an ecoregionalisation of the risk estimation possible.

Keywords: Climate Change; Ecoregionalisation; Malaria; Predictive mapping; Reproduction rate

Leishmaniasis – entering Germany

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This study has provided evidence for the natural occurrence of sand flies in Germany. Two species belonging to the genus *Phlebotomus* were detected. *Ph. perniciosus*, a proven vector of leishmaniasis, was found associated with an autochthonous case of canine leishmaniasis near Kaiserslautern. One hundred and twenty-one specimens of *Ph. mascittii* were caught in twelve different locations in Baden-Wurttemberg. The most northerly town in which *Ph. mascittii* was detected was Baden-Baden. *Ph. mascittii* has not yet been confirmed as a vector of leishmaniasis but its competence is strongly suspected. In addition to the detection of the vector, since 1991 there have been eleven cases of leishmaniasis in Germany, in which an autochthonous origin was confirmed or which was highly likely to have been of an indigenous origin. Current data from the German meteorological service indicates that Germany currently has a Mediterranean climate with the yearly average temperature exceeding 10 °C having been reached or exceeded in several regions. This type of climate is also appropriate for the living conditions of sand flies. Therefore it is assumed, that sand flies have a greater geographical distribution in Germany than the first investigations indicated, which were restricted to the southern region of Baden-Württemberg. The risk of an autochthonous canine infection in Germany occurring is very low. With the rapidly increasing number of imported cases of leishmaniasis in dogs, veterinary advice to dog owners on prophylaxis requires special attention. The results indicate that the use of repellents and preventive behavioural measures are vital.

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BLUETONGUE: VECTORS, EPIDEMIOLOGY AND CLIMATE-CHANGE

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Key words: Bluetongue, *Culicoides*, Vectors, Epidemiology, Climate-change

Summary

The presentation will begin with a brief discussion of those climatic variables that are likely to influence the distribution and incidence of vector-borne diseases such as bluetongue. An explanation of how these variables may induce their own particular effects will be included.

The talk will then move on to describe recent changes in the world distribution of bluetongue virus and its vectors focussing on Europe from 1998 until 2006. It will be argued that the recent changes, both in terms of virus distribution and the species of vectors transmitting the virus can be linked to climate-change.

Suggestions of what this might mean for the future, in a time of on-going climate-change will be set out.

Biting midges as vectors of blue tongue virus in Germany

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In August 2006 an outbreak of Blue-tongue-disease (BTD) occurred in Germany along the border to Belgium and the Netherlands spreading constantly eastwards reaching in September 2007 rather East regions in Germany.

The virus was described by the Friedrich Löffler Institute (FLI) as serotype 8, which is one of the twenty other types found in South Africa, where the midges of the species *Culicoides imicola* were known as (main) vector.

Thus from the early beginning it was needed to find out the vectors in Germany. Was it also *C.imicola*, which is only found in rare cases at the Northern border of the Mediterranean Sea- having migrated undercover to the north or were other *Culicoides* species involved?

Catches at two farms- a convential one and a biofarm- using ultraviolet light traps, showed that mainly (>90%) *C.obsoletus* occurred joined by a few specimens of *C.pulicaris* and even fewer *C.nubeculosus* and *C. festivipennis*. The caught female specimens of the midges were separated according to their species relations and the status of feeding- fed or unfed. Then they were sent to FLI for PCR investigations with respect to the occurrence of the BT-virus and its serotype. It turned out- beginning after 3 weeks of daily catching midges, that pooled (20-50 specimens) *C. culicoides* were proven positive for BTV-virus type 8. The virus was found in both fed and unfed groups. *C.pulicaris* pools were never positive, even when coming from a third farm, where huge numbers of *C. pulicaris* were caught due to the presence of many horses.

Thus it is concluded that the African vector *C. imicola* has not migrated to the North (as follower of global warming), but that the most common species (*C. obsoletus*)

is apparently able to act as vector. They are perhaps supported by related species, of which 8-10 were caught in very small numbers during the Midges-Monitoring-System established in March 2007 at 90 German farms by the German Ministery of Agriculture, Food and User Protection. Although the number of BTD-involved farms increased more than sevenfold (1000 in 2006/ 7000 until Sept. 2007) the Monitoring in 2007 confirmed the species spectrum (as in 2006), but did not detect any BTV infected pool in 2007. However, at present only pools until July had been PCR-checked, while in 2006 the main findings of the virus were obtained at the end of September and at the beginning of October. Thus there is apparently a still open frame.

Evaluating the findings until now- September 2007- the import of the Blue Tongue Virus is apparently based on the globalisation with an intensive , world wide animal transportation, while the local spread, however was facilitated of course by a warm, long summer 2006 and a short, warm winter in 2006/2007.

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Network „Rodent-borne pathogens“ in Germany: Longitudinal studies on the geographical distribution and prevalence of hantavirus infections

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Human hantavirus infections have been reported in Germany since the 1980s. These infections can cause haemorrhagic fever with renal syndrome (HFRS), usually representing with renal failure. *Puumala virus* (PUUV) causes the majority of HFRS cases in Germany which are characterized by mild to moderate courses. The geographical distribution and frequency of hantavirus infections in humans is well documented by large seroprevalence studies and recording of clinically apparent infections according to the "Infektionsschutzgesetz". Endemic regions have been known for long time in Baden-Wuerttemberg (Suebian Alb) and Bavaria (Lower Franconia). Whereas in 2001-2004 and 2006 about 70-240 human cases were recorded annually in Germany, in 2005 and 2007 a large increase in the number of cases was observed, reaching 448 and 1339 cases, respectively (Robert Koch-Institut: SurvStat, http://www3.rki.de/SurvStat, Data from 19.09. 2007). The majority of cases was recorded in Bavaria (2004, 2007), Lower Saxony, North Rhine Westphalia (2005) and Baden-Wuerttemberg (2007).

Potential reservoirs for hantaviruses in Germany are bank vole (*Myodes glareolus*, formerly *Clethrionomys glareolus*), common vole (*Microtus arvalis*) and striped field mouse and yellow-necked mouse (*Apodemus agrarius* and *A. flavicollis*). PUUV and *Tula virus* (TULV) were indeed detected in bank voles and common voles, respectively. However, the reservoir for *Dobrava-Belgrade virus* (DOBV) in Germany remains obscure. The similarity of a patient DOBV sequence to other *A. agrarius*-derived DOBV sequences suggested an *A. agrarius* origin of the infection. Other rodents, e.g. Norway rat (*Rattus norvegicus*) and house mouse (*Mus musculus*), as well as shrews might represent reservoirs for other hantaviruses as well.

In contrast to the well-documented distribution of human hantavirus cases the geographical distribution and prevalence of hantavirus infections in rodent reservoirs is poorly studied. Moreover, there is little known about oscillations of the prevalence and sequence variation of the hantaviruses and the underlying molecular processes driven by rodent population dynamics as well as by transmission and migration processes. The influence of climate change on these processes is also unknown. Therefore, the network ”Rodent-borne pathogens” was initiated representing a platform for an interdisciplinary collaboration of research groups dealing with rodent reservoirs themselves, i.e. their biology, population genetics, distribution and population dynamics, and studies dealing with pathogens of different nature (i.e. viruses, bacteria, parasites).

The investigations in the first ”descriptive” phase of the network were focussed on the following objectives: (i) establishment of a monitoring program of hantaviruses and other rodent-associated pathogens, (ii) identification of causative hantaviruses in outbreak regions during 2004, 2005 and 2007, (iii) promotion of population dynamics studies including potential influences of climate conditions and (iv) search for novel rodent viruses which may represent model viruses for human pathogens.

In a pilot study in Brandenburg, a serological and RT-PCR screening of about 1,700 rodents trapped during 1994 - 2005 demonstrated for the first time a continuous presence of TULV in common vole (*Microtus arvalis)* and field vole (*M. agrestis*) populations at certain trapping sites throughout the study period. A serological screening of 341 bank voles, common voles and field voles trapped during 2004-2007 in Brandenburg, Saxony-Anhalt, Saxony and Mecklenburg-Western-Pomerania was performed by ELISA using recombinant nucleocapsid proteins of PUUV and TULV. These investigations revealed a low number of samples with specific antibodies against PUUV and TULV from Brandenburg (1/66), Mecklenburg-Western-Pomerania (2/39) and Saxony-Anhalt (3/150).

During hantavirus outbreaks, investigations were focused on rodents from different parts of Bavaria (Lower Bavaria 2004, Lower Franconia 2007), North Rhine Westphalia (city of Cologne, 2005, and rural region close to Muenster, 2007), Lower Saxony (a rural region close to Osnabrück, 2005) and different regions in Baden-Wuerttemberg (2007). In all investigated regions a high PUUV prevalence of 10-90% was observed in bank voles. RT-PCR amplification and subsequent phylogenetic analysis of S and M genome sequences demonstrated significant differences between PUUV strains originating from the different regions. Initial longitudinal studies in rural regions of Lower Bavaria and close to Osnabrueck as well as in the city of Cologne demonstrated a continuing presence of PUUV in the local bank vole populations.

The distribution and prevalence of rodent-associated diseases is mainly driven by oscillations in demographic structure and density of rodent populations but also by habitat properties. A study about the fluctuations in population density of common voles was initiated. Time-series of population abundance of 12-125 years duration were obtained from >20 locations in Germany. Initial analyses suggest that there was no change in outbreak frequency since the late 1800s. There seems to be no consistent pattern in changes in amplitudes of peak densities of common voles across Germany. However, reports from West Germany and Central Spain suggest that common vole outbreaks recently occurred in historically unaffected regions. Time series data will be used to develop spatially-explicit pattern-oriented models that link population dynamics to environmental parameters. These parameters will include climate variables to identify potential effects of climate change on the population dynamics of common voles. This work will be extended in the network ”Rodent-borne pathogens” to include interactions of rodent population dynamics, epidemiology and evolution of viral and bacterial diseases in the rodent host, and prevalence of zoonoses in humans.

In conclusion, the network will enable synergistic effects by a close collaboration of zoologists, veterinarians, physicians, epidemiologists, virologists, geneticists, microbiologists, parasitologists and evolutionary biologists. The centralized facility for rodent necropsy, sample storage and documentation and a standard scheme for necropsy will allow a coordinated study on rodent biology and rodent-associated viral and bacterial pathogens. A network database will be established to help to identify potential interactions of the various pathogens in rodents and to link these aspects to population genetic markers. The longitudinal studies will allow conclusions about the evolution of rodent-borne pathogens and changes in their distribution which might result in a risk assessment for human infections. This may become very important in order to evaluate changes in the epidemiology of rodent-borne pathogens in the light of expected global climate changes in the future.

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Emergence of Hantavirus in Germany: Rodents, climate and human infections

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Puumala Hantavirus (PUUV) is the prevalent serotype in central and northern Europe with bank vole (*Myodes glareolus*) as main reservoir. PUUV is transmitted to humans by infected rodents through urine, droppings, or saliva. While 80 % of infected humans reportedly are asymptomatic or develop mild symptoms, PUUV can cause Nephropathia epidemica, a renal disease of sudden onset with fever, headache, backpain and gastrointestinal symptoms, in rare events leading to internal haemorrhaging and death.

Between 2001 and 2006 the incidence of PUUV infections in Germany ranged from 0.1 - 0.5 per 100.000 inhabitants and year. Approximately 75 % of infections were reported from the State of Baden-Württemberg, with between 24 and 169 infections annually. In 2007, a PUUV epidemic with early seasonal onset was observed in Baden-Württemberg: Based on 925 laboratory-confirmed infections, the 8month incidence of 8.4/100.000 represents an eight-fold increase over the statewide median incidence of the same period in the years 2001 to 2006 (1.04/100.000). Patients were predominantly male (71.3 %) and aged 20 - 60 years (81.5 %). 48.6 % required hospital treatment. Most cases were reported from districts with large areas of beech forest, which is the main habitat of bank vole.

To further investigate potential routes of infection and risk factors as well as possible causes of the early seasonal onset and high number of cases several studies were initiated by the state health department: A case control study, enlargement of laboratory analysis, investigation of bank vole population (in cooperation with Friedrich-Löffler-Institute and others), and an analysis of the association of PUUV incidence with habitat factors, climate and other potential risk factors.

The case control study comprised cases with clinical onset between 1 April and 30 June 2007 and randomly recruited controls, matched for sex, age group (+/- 10 years) and place of residence. Interviews covered socio-demographic factors and exposure in the four weeks before clinical onset. 191 matched pairs were included in the analysis. Multivariate analysis confirmed the known risk factors noticing small rodents and cleaning of utility rooms. Primarily visiting forest shelters was detected as new source of human PUUV infection.

Spatial and temporal incidence of PUUV infections between 2001 and 2006 was analysed with regard to bank vole habitat, climatic factors and human population density by using Poisson-regression. A regression model which included data on beech forest, seed plants, beech-nut crop, human population density, winter and spring temperature above long-term average and year of investigation showed a fit of R^2= 35 %. The model indicated a positive association with the year of investigation, suggesting that the disease might spread out. Furthermore, increasing winter and spring temperature were significantly associated with an increase in PUUV incidence. This result highlights the possible impact of climate change.

The results so far gave hints to some aspects of the present epidemic. Causal aspects of rodent population dynamics and spread of PUUV infection remain however poorly understood and need to be further investigated.

Tick ecology and climate: Mechanisms regulating the distribution and life cycle of *I. ricinus*

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Abstract

The population dynamics of the tick *Ixodes ricnus* is complex and difficult to measure. Key factors affecting the population dynamics of this tick are: 1) its huge reproduction potential, 2) its development and moulting speed, 3) its host-finding behavior, 4) host species relative and absolute densities as well as their behaviour, 5) predator species relative and absolute densities as well as their behaviour and 6) tick pathogens.

In this talk I will present experimental as well as field results regarding factors 1) to 3) and demonstrate how the climate is influencing these factors. Finally given this knowledge we will have a retrospective look on a long term record of *I. ricinus* questing densities collected in Switzerland.

What makes ticks tick? Climate change, ticks and tick-borne diseases*

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In Europe 90 – 95 percent of all tick bite incidences in humans are caused by *Ixodes ricinus* (in Eastern Europe by *I. persulcatus*). Without considering a large number of unreported cases, of these incidences 100,000 to 150,000 become manifest as Lyme Borreliosis (LB) and between 10,000 to 15,000 as tick-borne encephalitis (TBE).

As you all know, there is no TBE in the new world and between 17.000 – 23.000 cases of LB per year in the United States.

A humidity rate of >85 percent, air temperature of >6 to 7°C and a large number of blood delivering hosts are the basic requirements to make ticks 'happy'. Unfortunately, these three basic requirements necessary for the well-being of ticks is changing to the worst in many areas in Europe and in Germany as well. In TBE risk areas in Germany the average temperature increased by >0.6 to 1.5°C between 1951 and 2000. According to prognosis there will be a further increase in temperature by >1.2°C in the period 2001 to 2055. The number of days with temperatures >25°C has increased while the number of days with temperatures <0°C decreased and rainfall has increased annually by 9 percent (90mm). Ticks have moved northwards and can be found in mountainous areas above 1000 metres above sea level. The northward movement of *Dermacentor reticulates* is an additional sign for ecological changes in the environment. Agricultural land set aside because of EU subsidies leads to fallow and scrublands which in turn increases the amount of hosts for ticks.

A distinct sign of these changes in the environment is the fact that host searching *I. ricinus* have frequently been found on open land in Germany in November and December 2006 and again in January 2007, a fact which had not been noted in former years. It is believed that the number of life cycles of ticks will increase within the next few years, and as a result of this the geographical distributions of ticks will expand and population density will rise. The epidemiological development of TBE is accordingly. On average, the TBE incidence rate of all European 'TBE-countries' with the exception of Austria (vaccination rate of 90 percent) increased by approx. 400 percent in the years 1974 to 2002. Most surprisingly, however, was the fact that in the Czech Republic, in Switzerland, in Poland and in Germany anew an increase in TBE by 137.5 percent was found in the relatively short period between 2002 and 2006. The Czech Republic reported on an entirely different epidemiological situation. About

500 incidences out of more than 1000 reported cases in 2006 have been acquired in the last third of the year 2006, representing a completely different state yet again.

It can be stated for certain that global warming causes some of these dramatic changes. However, there are additional factors to be considered such as social and political changes in agricultural production and in leisure time,and increase in travelling (in TBE areas) which in turn leads to a higher exposition rate.

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Modeling and prediction of habitat suitability for ticks.

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Ticks are a serious pest of domestic animals, and a threat for human health. Efforts continue at global, regional, and local scales to understand the major factors governing tick distribution, as a necessary step in the development of sound, ecologically based, control measures. The need for models in tick research arose from the problems associated with the use of acaricides in Australia, because of the development of resistance by the cattle tick. With the arrival of the computer age and the use of robust statistical methods to test the feasibility of the model's output, we have at hand a new set of tools devoted to understanding the effect of environmental factors on the tick's ability to colonize a site. This article is not a review of the different models built around the ticks and tick-borne diseases, but a personal insight into the main developments in this field, and how these models could help to protect humans by providing information about the "hot spots" by ticks.

In the last few years, models built around the main features of the life cycle of ticks have been produced, which not only provided information about the main demographic processes of ticks at a given site, but also allowed new insights into the sometimes complex regulation of the tick populations. At geographical scales beyond experimentation, empirical models provide one of the only ways to develop and test hypotheses about ecological features affecting tick distribution. It is a central premise of biogeography that climate exerts a dominant control over the natural distribution of species. Like many other arthropods, ticks are sensitive to climate features, these climate variables promoting, enhancing, or even stopping different and more or less critical parts of their life cycle. Models exploring the relationships between species occurrence and sets of predictor variables produce two kinds of useful outputs: (1) estimates of the probability that a species of tick might occur at given unrecorded locations and (2) an area's suitability for the species. Probabilities of occurrence could be interpreted as estimates of the probability that the species might find a suitable habitat in a given area.

A number of modeling strategies for predicting the impacts of climate on tick distribution have been developed. These have focused on the identification of the "bioclimate envelope" (alternatively termed climate space) through methods that correlate current species distribution with climate variables. The bioclimate envelope modeling approach has its foundations in the ecological niche theory, defined as the fundamental ecological niche as comprising those environmental conditions within which a species can survive and grow. The fundamental niche would completely define the ecological properties of a species: a conceptual space whose axes include all of the environmental variables affecting that species. Bioclimate envelopes can be defined as constituting the climatic component of the fundamental ecological niche. The validity of the bioclimatic envelope approach has been questioned by pointing to many other factors that play an important part in determining tick species distribution and their dynamics over time such as hosts, landscape patterns of vegetation, or even the competition between tick species for resources (hosts in this case). It has been proposed that continental-scale distributions of ticks are principally determined by climate, and it is therefore suggested that many species distributions can in fact be considered to be in equilibrium with the current climate at the macroscale.

Genetic adaptation of species is rarely considered, being range shifts frequently seen as the expected response to the climate. It is usually expected that evolutionary change occurs only on long time scales and that the tolerance range of a species remains the same as it shifts its geographical range. However, studies have shown that climate-induced range shifts can involve not only migration into newly suitable areas, but also selection against phenotypes that are poorly adapted to local conditions. The potential impact of rapid evolutionary change means that the climatic tolerances of a tick may alter from the original founders, making the fundamental niche unstable over time. It has been reported that tick species distributed over large areas display very different climate preferences. Therefore, the development of models for the whole distributional range would produce biased predictions. The erection of models applied on partial ranges (population-derived models) seems to be a better approach to this trouble.

However, the predictive mapping of the so called “climate suitability” (rather than the widely used habitat suitability, as commonly only climate is involved in calculations) is not necessarily a straightforward door to the understanding of ticks dynamics. Nor is the better way to discern the somewhat complex patterns behind epidemic processes of tick-borne diseases. These diseases are commonly the result of complex transmission patterns, the presence and abundance of important reservoir hosts, and, perhaps most important, the dynamics, social changes and behavior of humans in the vicinity of tick foci. At high resolution, vegetation, landscape pattern, and connectivity between patches of suitable vegetation and climate are the major determinants of tick distribution and abundance. Ticks spent most of their life cycles in sheltered microhabitats in the ground, and only a small part feeding on hosts. Acquisition and transmission of pathogens are therefore separated by long periods of free-living existence during which the tick develops from one stage to the next.

Much concern exists currently about the possibility of spread of some prominent tick species, restricted to the Mediterranean region because climate limiting factors into northern latitudes. The rational behind is that warmer winters could provide a more adequate environment for those species. However, as explained before, climate is not the only limiting factor in the spread of a tick population, as barriers to dispersion, lack of adequate hosts, or inadequate temporal synchrony between hosts and parasites would make the invasive event unlikely. Efforts should be addressed towards the evaluation of process-based models. Such an effort must to be based on the knowledge of microclimatic requirements for tick survival and development, in terms of temperature and moisture conditions, obtained from laboratory experiments under controlled conditions or long-term field work must to be obtained and applied to the development of models describing the different patterns of life cycles. These models should be aimed to understand the development and mortality processes behind the observed pattern of tick dynamics. The most important feature to obtain from these models should be the determination of R0, the basic reproduction rate of a disease. This is a pivotal feature in the understanding of the dynamics of any tick-borne disease and the best way to determine the potential impact of the many factors (and not only climate) involved on the transmission rates of such a disease.

Influence of meteorological conditions on the occurrence of ticks and TBD in the Czech Republic.

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Background:

In the second half of the twentieth century there have been two markedly warm periods in the Czech Republic. There was a smaller one in the years 1948-55 and a longer one since 1990 lasting up to now. It certainly was not just by chance that the tick-borne encephalitis (TBE) virus had been discovered in Europe in that first warmer period and Lyme borreliosis (LB) agents become a significant thread during the second period.

In the year 1993, there was a great increase of TBE and LB cases in the Czech Republic and this high level (with certain fluctuations) persists.

Material and methods:

The influence of weather condition on day-to-day changes of *I. ricinus* host-seeking activity was studied in 2001-2006. *I. ricinus* activity was investigated by flagging method on 3 plots (200 m^2 each) in weekly intervals (March-November). The instruments for micrometeorological observations were installed between the experimental plots. Macrometeorological data were used from the nearby Czech Hydrometeorological Institute meteorological observatory. Simple and multiple linear regression and quadratic regression were used to test the relation between the weather modification and *I. ricinus* host-seeking activity.

Presence of TBD infectious agents in ticks were investigated by PCR and cultivation methods.

Data of human TBE and LB cases were obtained from the National mandatory ID reporting system EPIDAT and analyzed by conventional statistical methods.

Results:

Since 1990, increasing Tick–borne encephalitis (TBE) occurrence trends in the Czech Republic were associated with higher numbers of cases in areas well-known for TBE occurrence in humans; re-emergence in areas where TBE cases were not observed, or only sporadically, for a long time; emergence of TBE in sites previously unknown as TBE foci (including mountainous areas newly colonized by ticks e.g. the Šumava and Krkonoše Mts.) and a significant shift of TBE incidence towards spring and autumn months (together with an analogous shift of *I. ricinus* activities). Both TBE and LB trends were significantly associated during this period.

Discussion:

Human Tick-borne diseases (TBD) incidence is largely influenced by temperature as a leading climatological factor with at least a triple effect

1.upon tick *I. ricinus* biology and distribution,

2.upon TBD infectious agents replication in ticks (demonstrated in laboratory experiments),

3. upon human behaviour. TBD are exclusively recreational diseases in the Czech Republic and these outdoor activities are also influenced by climate factors.

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Ticks and tick-borne diseases in Southern Germany

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During the last years, we could observe additional tick borne infections beside TBE and Lyme Borreliosis. Special investigations in South-West-Germany offered ticks, affected with Coxiella, Rickettsia, Anaplasma and Babesia.

Q-fever was imported into Germany after the second world war from endemic areas in all probability together with the vector species *Dermacentor marginatus*. The course of the infection mostly presents subclinical or mild symptoms, but chronification and infection can be very dangerous, especially for pregnant women. The infection can be transmitted by two infective cycles, a haploxenic which includes *Dermacentor marginatus* as vector and wild animals as hosts and a hemixenic, where infections are transmitted from domestic animals by the aerogenic route. To localize natural foci of the haploxenic cycle in Baden-Wuerttemberg (BW), 1066 ticks and 49 samples of tick feces were examined for *Coxiella burnetii* by PCR. Only one tick and one feces sample from an area near Basel were positive for *Coxiella burnetii*. An investigation of 450 *Dermacentor* ticks collected in the Rhine and Kinzig valleys gave no positive results for *Coxiella*. Therefore it is to be presumed, that the endemic foci in theses areas are very small. On the other hand, human infections are rather frequent: In a cross sectional survey in Leutkirch 7,4% of the population was found seropositive for *Coxiella burnetii*, 47% of the soldiers on a military training area were infected with Q-fever within 3 years following an outbreak.

Tick borne rickettsial diseases are mainly found in warm, dry regions.Rickettsial species are also found in Middle and Eastern Europe, –but the two species *R. helvetica and R. slovaca* seem to be apathogenic. To clarify the endemic situation in BW, 1026 ticks (*Ixodes ricinus*) of 3 different areas were investigated for *Rickettsia*. An average infection rate of 8,9% was found , exclusively *R. helvetica* was diagnosed by sequencing. *Dermacentor* spp. from the Rhine and Kinzig valley showed an average infection rate of 14% for *Rickettsia* as well. The exact species is not identified yet, but *R. conorii* could be excluded.

The only known Ehrlichiosis in Europe is Anaplasmosis caused by *A. phagocytophilum*. . The infection appears mostly asymptomatic, only a few cases with symptoms of a summer flu are described. To determine the prevalence in BW 5424 ticks (*Ixodes ricinus*) of different areas were tested for *Anaplasma*. The infection rates differed from 0% to 3%, with an average rate of 1%. To find out the animal reservoir 512 rodents were tested for *Anaplasma*. Among 253 rodents of Arvicolidae the infection rate was 10,2%, whereas from 259 Muridae only 0,4% of the animals were infected. So Arviculidae may represent the main reservoir for *Anaplasma phagocytophilum*. These data correspond with the results of a seroepidemiological survey: In the sera of 4332 forestry workers of all districts of BW seroprevalences for *Anaplasma* ssp. up to15% were found, with an average of 11%.

Among the *Babesia* genus *B. divergens* and *B. microti* are also pathogenic for man. In Europe cases of Babesiosis are known mainly in splenectomized persons, in the USA however also immunocompetent persons are affected. To investigate the epidemiology of *Babesia* in Southern Germany, 3113 ticks (*Ixodes ricinus*) were tested for *Babesia*. They originated from 2 areas of BW and 1 from Northern Bavaria. The average prevalence rate was 1%. By sequencing 90% were identified as *B. divergens*, 10% as *B. microti*. Investigating the animal reservoir 508 rodents of the families Arvicolidae and Muridae were tested. In 1,6% of the Arvicolidae (n=253) *B. microti* was found, species of Muridae were not infected.

It cannot be excluded the climate change may increase the problem of tick borne diseases in Southern Germany. By an increased population of rodents following mild winters the number of *Ixodes ricinus* will rise as well; in the consequence the infective cycles could be intensified. *Dermacentor* is a thermophilic tick, at a global warming, this vector and the haplogenic cycles of Q-fever may be further distributed. *Rhipicephalus sanguineus* is often imported from the mediterranean area to Germany by dogs. It could form here natural foci, a prerequisite for establishing mediterranean spotted fever. Therefore it is necessary to control these processes investigating the status quo and the further development.

Lyme borreliosis: Data and trends

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Introduction

Lyme borreliosis (LB) is the most prevalent human tick-borne illness of the northern hemisphere and is caused by the spirochete *Borrelia burgdorferi*. LB is a multisystem infection affecting skin, nervous system, joints and heart. LB is a curable disease; however, if early disease manifestations are overlooked or misdiagnosed, LB may lead to severe neurological complications and chronic arthritis. In Europe, all known human pathogenic genospecies are prevalent and there is evidence for varying clinical presentations of Lyme borreliosis caused by these different genospecies.

Data bases

In many European countries LB is not a mandatory reportable disease. In the majority of countries, data is collected through diagnostic laboratory reporting. Other sources of incidence estimates include voluntary reporting, GP/physician surveys, and hospital in- and out-patient diagnoses (1).

In Germany, LB is not a notifiable disease; however, the six eastern German states (Berlin, Brandenburg, Mecklenburg-Western Pomerania, Saxony, Saxony-Anhalt and Thuringia) have extended notifications systems including Lyme borreliosis. Cases fulfilling the case definition are transmitted electronically from the local health authorities via the intermediate health authorities to the Robert-Koch-Institute (clinical picture of erythema migrans or early neuroborreliosis laboratory confirmed by the presence of lymphocytic pleocytosis in cerebrospinal fluid and detection of intrathecally produced specific antibodies or detection of nucleid acids or detection of *B. burgdorferi* by culture).

Data and Trends

Since the 1990s the number of reported cases has increased in Europe and the geographical regions have expanded. The highest incidences within Europe are seen in the Baltic States and Sweden, Austria, the Czech Republic, Germany, Slovenia, and central Europe. In Southern Europe, incidences appear to be much lower. However, focal areas of higher incidences can occur in countries where the incidence is generally low (1).

In Germany, between 2002 and 2006 a total of 23.170 cases has been reported; the majority presenting the clinical picture of erythema migrans (n = 20.787). The incidence increased from 17.8 cases per 100.000 inhabitants in 2002 to 37.3 cases per 100.000 inhabitants in 2006. The highest incidences were seen in counties in Brandenburg (especially in the eastern part), Saxony (Erz Mountains, Upper Lusatia Region) and Thuringia (Thuringian forest) and Mecklenburg-Western Pomerania (island of Rügen). The patients' ages were bimodally distributed, with a first incidence peak among children and a second peak among adults starting in the fourth decade with a maximum in the 60 to 65 years age group. A total of 92% of the reports had data on the onset of symptoms. Illness started in the majority of cases between the months of June to September (2). In 2005 and 2006 the proportion of reported onset in the months September to November increased, in these years tick activities were prolonged due to a warm autumn as well as a mild winter (3).

Conclusion

The surveillance systems of Lyme borreliose differ largely between the European countries; therefore comparisons of epidemiological data on LB are notoriously difficult. The available data indicate that the incidence of LB may have increased markedly in various European countries assuming that the surveillance systems have been stable. An array of factors possibly leading to the increased incidences have been identified including ecological and climatic changes, changes in human settlements, recreational behaviour, but also increasing awareness of the general population and physicians resulting in an increased number of notified cases. To what extent the different factors contribute to the increased incidences is not known. The time-series data available from the European countries cover only a relatively short time interval and might not reflect long-term trends.

1. Smith R et al. (2006) Lyme borreliosis: Europe-wide coordinated surveillance and action needed? Eurosurveillance 11(5).
2. RKI (2007): Zur Situation der Lyme-Borreliose in den sechs östlichen Bundesländern: Analyse der Meldedaten aus dem 5-Jahreszeitraum von 2002 bis 2006. Im Druck.
3. Dautel H et al. Winter activity of Ixodes ricinus in a Berlin forest area. IX International Jena Symposium on Tick-Borne Diseases, Jena, 15.-17. März 2007.

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WHO Europe: IPCC, the cChash-Projekt (Climate Change and Adaptation Strategies for human health) and ECDC/WHO/JRC/EEA: Surveillance of vector-borne diseases in several countries

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Will be given a brief summary on the chapter on human health of the IPCC, the results of the results of the research project “Climate change and adaptation strategies for human health in Europe” (cCASHh) (May 2001-July 2004), coordinated by WHO and supported by the Energy, Environment and Sustainable Development Programme in the frame of the Fifth European Union Framework Programme for Research and Development.

Current climate trends point to the likelihood that southern Europe will become drier in the future, while northern Europe is likely to become warmer and wetter. Extreme events are expected to increase in frequency and severity, particularly heat-waves, droughts and intense rainfall events. The range of infectious diseases could be changing

cCASHh identified a range of options that have been taken or could be taken by European policy-makers to prevent, prepare and respond to the effects of weather and climate variability on people’s health. These measures are classified into strengthening existing measures and developing new measures. Cooperation between health and climate institutions, building capacity for action now and communication needs to be strengthened. The specific measures include information for the prevention of health effects from heat stress, floods, vector, rodent and food borne diseases.

Ref.:

Confalonieri et al. Human health in IPCC

WHO (2005): HEALTH AND CLIMATE CHANGE: the “now and how” A policy action guide. WHO Regional Office for Europe, 33S.

B. Menne and K.L. Ebi (2006): Climate change and adaptation strategies for human health. Springer Verlag, Steinkopf Verlag Darmstadt, 449 p.

The EDEN project

P. G. de Mendonça, Ludwig-Maximilian-University, Munich, Germany

The EDEN project (Emerging Diseases in a changing European eNvironment) is a Europe-wide research project involving 47 institutions in 24 countries. It includes six sub-projects investigating either one disease or a group of diseases. These are:

- Tick-borne Diseases,
- Rodent-borne Viruses (hanta, arena, cowpox),
- Leishmaniasis,
- West Nile Virus,
- Malaria,
- “African Platform” (new pathogens imported from Africa).

Most of the selected diseases are zoonoses involving both domestic and wild animals as hosts for vectors and /or reservoirs for pathogens. The EDEN project aims at quantifying the epidemiological role of wild and domestic animals in the amplification and the endemisation of selected emerging disease. Therefore, the specific composition and abundance of wild reservoir populations in contact with vector population must be studied. Spatial distribution, local displacements and seasonal dynamics of host populations must be compared to disease patterns. The risk of introducing new pathogens through active transport by wild (e.g. migrating birds) or domestic animals must also be investigated.

EDEN deals with emerging diseases linked to a changing environment. One must therefore identify environmental changes likely to favour (re-)emergence and spread of pathogens. This is achieved with predictive emergence and spread models. Such models, however, must be fully parameterized. A catalogue of ecosystems and environmental conditions likely to harbour “emerging disease hot-spots” is thus required. This will allow the development of a monitoring and early warning system. This should then contribute to decision support and policy making.

The environment is a combination of various components including hosts, reservoirs, vectors and pathogens. It is therefore necessary to consider each of these in an epidemiological model taking into account the interactions between them and their environment in terms of co–adaptation and selection. One ought to characterise the infectious agents most likely to (re–)emerge or spread in Europe, as well as the capacity of potential vectors, hosts and reservoirs to perpetuate or spread new disease cycles.

In order to forecast the future, one must examine current and expected future changes in the European environment likely to favour the emergence or re-emergence of vector-borne diseases. One may then develop statistical models and “risk maps” of vector and disease distribution and abundance or prevalence.

Such “risk maps” include the description of biotopes suitable for selected diseases, and imply monitoring and describing changes occurring there which are likely to affect transmission cycles by influencing vectors, hosts, or reservoirs.

The sub-project investigating tick-borne diseases (TBD) is precisely doing so on a most suitable ground. Indeed, it covers a wide geographic area, with partners in 14 different countries (Czech Republic, Estonia, Germany, Hungary, Italy, Latvia, Lithuania, Poland, Romania, Slovakia, Slovenia, Spain, Switzerland and United Kingdom). Between them, these countries have experienced a large range of socio-economic, agricultural and environmental changes in the recent past (from the collapse of communism to the first signs of global warming).

A particular emphasis has been put on woodland habitats, which are thought to be optimal habitats for ticks. It was then realised that additional attention ought to be paid to reduction in agricultural land and reversion to shrub, a more suitable habitat for some rodent species. Indeed, rodents play a major role as hosts and reservoirs for ticks. This point has led to the creation of a joint database on rodent populations in collaboration with members of the rodent-borne viruses (ROBO) sub-project.

Tick-borne diseases have recently shown considerable increases in incidence, at least partly due to changes in human behaviour in relation to the environment. Tick-borne pathogens are already present in Europe. Some are widespread (e.g. Lyme disease) whereas others display a focal distribution (e.g. tick-borne encephalitis). This is thought to be due to varying interactions between pathogens, ticks, vertebrate hosts, and environmental conditions.

Therefore, the general objective of EDEN-TBD is to identify which socio-economical and environmental factors govern the currently observed upsurge of tick-borne diseases in Europe. In particular, one wishes to establish if local socio-political factors have altered human behaviour and agriculture, causing greater contact with tick-infested habitats during work, food harvest, and leisure activities. In addition, TBD incidence may be influenced by changes in public health activities (e.g. vaccination, improved diagnostic or reporting).

More precisely, the EDEN-TBD sub-project wishes:

- to explore and model the relationship between climate and landscape changes and incidence of tick-borne diseases,
- to describe the impact of environmental changes or human intervention on host availability (e.g. rodents and deer),
- to describe the impact of environmental changes or human intervention on abundance and seasonal dynamics of ticks,
- to establish the present relationship between tick abundance and seasonal dynamics, host availability and infection prevalence in tick populations with selected pathogens.

Pathogens selected for this study are: Tick-borne encephalitis virus, *Borrelia* spp, *Babesia* spp and *Anaplasma phagocytophilum*. These are diagnosed by molecular biology methods based on the amplification of nucleic acids by PCR. The University of Munich (LMU) is responsible for molecular diagnostic quality control.

Furthermore, LMU is in charge of collecting and analysing data for Germany. Ticks have been collected since 2006 on a monthly basis by dragging a $1m^2$ white flag over soil and vegetation over a $100m^2$ transect at various field sites in Bavaria. These field and laboratory data shall be integrated in a Pan-European data-bank and analysed in this wider framework. At Munich, these local data shall further be included as parameters in a computer model exploring the relationships between ticks, tick-borne pathogens, and reservoir hosts (e.g. rodents and deer) in Bavaria.

Source: This presentation is mainly based on Annex 1 of the EDEN integrated project.

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ABTRACTS OF POSTER PRESENTATIONS

Climatic extremes and mosquito occurrence in the Czech Republic

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At the Intergovernmental Panel on Climate Changes (IPCC) in Paris in February 2007 important conclusions were approved. One of them stated: At continental, regional and ocean basin scales, numerous long-term changes in climate have been observed. These include changes in arctic temperatures and ice, widespread changes in precipitation amounts, ocean salinity, wind patterns and aspects of extreme weather including droughts, heavy precipitations, heat waves and intensity of tropical cyclones. Over the last 10 years we have witnessed such extremes of weather patterns on the territory of the Czech Republic. Since 1997 the country has suffered catastrophic floods. In July 1997 and August 2002 floods were caused by intensive precipitations. Each of these floods resulted in a massive **occurrence of mosquitoes - potential vectors of mosquito-born diseases -** of *flood water* species *Aedes vexans* (in flooded meadows) and *Ochlerotatus sticticus* (in flooded forests). In April 2006 the flood was caused by rapid thaw of unusually large quantities of snow in the end of extreme severe winter. *Snow melt* species *Oc.cantans* and *Oc.cataphylla* prevailed (especially in the Labe Lowland, in the Morava /Dyje basin *flood water* species developed as well). To control larval populations around larger human settlements Vectobac G (in a dosage of 10-15 kg/ha) applied aerially and Vectobac 12AS applied by ground were used.

On the contrary the last winter was extremely warm which resulted in unusual early hatching of *Ochlerotatus* larvae. In the Labe Lowland on February 2, 2007 we recorded the occurrence of 2nd instar *Oc.cantans* and *Oc.cataphylla* larvae (usual time for hatching of those species is mid-March). Moreover, and for the first time in the Czech Republic, hibernating larvae of *Culiseta annulata* (4th instar) were found in the Melnik area (50°N,15°E) at the same time.

During almost forty years of mosquito studies the following changes which might be attributed to the local climate warming, were observed by the author. In the last few years *Oc. sticticus* hatched in March - April in some breeding sites of the Melník and Podebrady areas in the Labe Lowland (approx. 50°10´N). This species did not occur so early in spring in over the last 35 years here, in contrast to its regular appearance in the early spring in the southern and warmer parts of the Morava and Dyje basins (approx. 48°40´N). On the other hand the disappearance of *Culiseta alaskaensis* and a very low percentage of *Oc.communis* in this region was recorded. Quite recently occasional anthropophily (in August-October) of unautogenous biotype of Culex pipiens has been observed in Prague (the biotype regularly bites men in warmer parts of Moravia).

More observations will be needed in future years to consider the permanence of our findings of local mosquito fauna due to the climate change.

Chikungunya fever – a threat for Europeans

A review of the recent literature

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Background: Chikungunya fever (CHIKF), is a self-limiting illness characterised by fever, headache, weakness, rash and arthralgia. Sometimes the course of the disease is more severe. The virus is transmitted to humans by various *Aedes* species.

Material and methods: Events during the last 2½ years have been dramatic. We were asked by the organizers of this conference to review the recent literature. The majority of the papers were only available on the Internet.

Results: In 2004, Gratz (1)* noted that *Aedes albopictus* (*Aea*) had spread from Asia to Africa, Europe and the Americas. *Aea* is a competent vector for 22 arboviruses incl. chikungunya. According to ECDC (2), *Aea* is now present in several European countries; including Albania, Italy, France, Belgium, Montenegro, Switzerland, Greece, Spain, Croatia, the Netherlands, Slovenia and Bosnia and Herzegovina. A CHIKF epidemic started on Reunion and Mayotte in April and in May there were three autochthonous cases. The epidemic peaked in February 2006 and altogether 266,000 people contracted clinical CHIKF and 254 patients died. The epidemic was over in May 2006. Nine cases were imported to the French territories in West India but they did not lead to any secondary transmission. Through tourism 783 cases were imported to France (3).

Since the start of the Indian Ocean outbreak in 2005, CHIKF has been imported to several European countries, e.g. France (3), Germany (4), Switzerland (5), U.K. (6), Italy (7,8), Norway and Sweden (our unpublished observations).

Beltrame (7) and Fusco (8) described several cases imported to Italy and noted that the ongoing epidemic abroad was a risk for introducing the virus to Italy as the vector *Aea* is widespread there. This was what happened recently (9). A person from a CHIKF endemic area fell ill with a CHIKF compatible disease after arriving in a village in Italy June 21. In August 2007 there was an unusually high number of cases of febrile illness in the village. Investigations confirmed the diagnosis of CHIKF. The virus was also detected in *Aea*. As at 4 Sept a total of 197 cases had been reported.

Discussion

CHIKF is a threat for Europeans travelling to endemic areas, which is a nuisance that may be managed. Even worse is that CHIKF may have established a bridgehead in Italy, which may add a new disease of public health concern in Europe.

* The reference list may be obtained by request or at the poster in the congress.

Quest for novel viruses in mosquitoes collected in the area of the Taï National Park, Côte d'Ivoire

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Vector-borne pathogens are among the most important emerging and re-emerging viruses that cause epidemics in the human population. As part of a comprehensive study on the distribution of arboviruses and their vectors in different ecological habitats, 7,067 mosquitoes were collected along a straight transect from the inside of the Taï National Park to surrounding fields and villages. From a total of 437 female mosquito pools, 98 (22.4%) caused a cytopathic effect in cell culture. 30 pools were analysed by electron microscopy. Three rhabdoviruses, one flavivirus, one bunyavirus, one orbivirus, one corona-like virus and 10 pools with uncharacterised viral particles were found. From 7 morphologically pre-characterized pools viral sequence information was retrieved by random PCR amplification. Sequence homology to known viruses was low, and relationships were mostly found only on amino acid level. Our system of vector analysis is a powerful tool for routine screening and for the identification of novel viruses. In our screen only new viruses were found, demonstrating that viral diversity in tropical rainforests is still far from being understood.

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* The reference list may be obtained by request or at the poster in the congress.

IRAC (Insecticide Resistance Action Committee) and its Aims

The dispersal of mosquitoes and associated mosquito born diseases are challenges caused among other things by global warming. The introduction of suitable insecticides and the prevention of resistance build up are therefore important tasks.

The Insecticide Resistance Action Committee IRAC was formed in 1984 to provide a co-ordinated crop protection industry response to prevent or delay the development of resistance in insect and mite pests. The main aims of IRAC are firstly to facilitate communication and education on insecticide resistance and secondly to promote the development of resistance management strategies in crop protection and vector control so as to maintain efficacy and support sustainable agriculture and improved public health. It is IRAC's view that such activities are the best way to preserve or regain the susceptibility to insecticides that is so vital to effective pest management. In general, it is usually easier to proactively prevent resistance occurring than it is to reactively regain susceptibility (McCaffery & Nauen 2007).

Two posters with selected topics in mosquito control of the IRAC are presented:

IRAC (2007): IRM in a Multi-Resistant Malaria Vector Scenario Mexico Trial. Designed and produced by the IRAC Public Health Team, July 2007

IRAC (2007): Insecticides Mode of Action Classification: A Key to Effective Insecticide Resistance Management in Mosquitoes. Designed and produced by the IRAC Public Health Team, July 2007

Ref.:

McCaffery, A. & Nauen R. (2006): The Insecticide Resistance Action Committee (IRAC): Public responsibility and enlightened industrial self-interest. Outlooks on Pest Management, February 2006: 11-14.

Entomological and epidemiological surveys for monitoring bluetongue disease

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The agent of bluetongue disease (BTD), a notifiable viral disease affecting domestic and wild ruminants, belongs to the genus orbivirus. It is transmitted by biting midges of the family Ceratopogonidae, genus Culicoides. In Germany, BTD (serotype 8) was detected for the first time on 21 August 2006 in the vicinity of Aachen, North Rhine-Westphalia. Culicoides species belonging to the obsoletus and pulicaris complexes were caught in this area during the outbreak and found infected (Mehlhorn et al., 2007).

Based on the decision 2007/20/EU of 22 December 2006 and funded by BLE through BMELV, a large-scale serological, entomological and virological surveillance programme was initiated in selected regions. Data on the autochthonous biting midges and their potential infection with BTD virus are collected.

Further emphasis is placed on an assessment of the occurrence and dispersal of the midges in different regions. In addition, it is intended to appraise their seasonal abundance and to define optimal methods for the reliable identification of the indigenous species of biting midges. At the same time, BTD-free cattle were monitored to detect a re-appearance of the disease in the current year as early as possible. Based on the knowledge acquired, appropriate strategies will be developed to help contain the further spread of BTD.

Monitoring of Ceratopogonidae in the German federal states Rheinland-Pfalz and Saarland

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In August 2006, the bluetongue disease arose for the first time in northwestern Germany. It came from the Netherlands/Belgium, although thus far the distribution had been restricted to Africa and the Mediterranean countries. The disease is caused by the bluetongue virus – an RNA virus – which infects ruminants, above all cattle and sheep. Vectors of the virus are midges belonging the family Ceratopogonidae, all of the genus *Culicoides*. The main vector in Africa is *Culicoides imicola,* which does not occur in Germany. The Federal Ministry of Food, Agriculture and Consumer Protection initiated a monitoring of the ceratopogonids in nearly all federal states of Germany lasting from the end of March 2007 until January 2008 and encompassing ninety quadrants (45 x 45 km). The group Zoology/Parasitology evaluated twelve uv-light traps located at cattlefarms, two in the Saarland – at Merzig-Wadern and St. Wendel – and ten in different districts of Rheinland-Pfalz (Ahrweiler, Altenkirchen, Alzey-Worms, Bad Dürkheim, Germersheim, Kusel, Mayen-Koblenz, Rhein Hunsrück-Kreis, Trier-Saarburg and the Vulkaneifel). Starting at the end of March, 2007, traps were used - always for seven nights at the beginning of each month. The insects were attracted by uv-light and sucked by a ventilator into a beaker filled with 70% ethanol. A mesh excluded the capture of bigger insects.

Most of the captured *Culicoides* spec. were *C. obsoletus s.l.* (92%), 3% *C. pulicaris s.l.* and 5% other *Culicoides* species. The number of all *Culicoides* found increased from May to June up to 54,703, was reduced in July (46,884), increased to a maximum in August (177,303) and was reduced again in September (28,171). On the average 4,700 *Culicoides*/week/farm were captured. This pattern of abundance changes occurred in Ahrweiler, Alzey-Worms, Kusel, Mayen-Koblenz, Merzig-Wadern, Trier-Saarburg, and in the Vulkaneifel. In the districts Altenkirchen and Bad Dürkheim, the abundance increased from March to August and was reduced in September. In the district Rhein-Hunsrück, the abundance was reduced in August for the first time and the decrease continued in September. In St. Wendel and in Germersheim, in some months no *Culicoides* were captured, but an increase in August was also evident. The most midges were trapped in the Vulkaneifel (90,727 in total from March-September). There the maximum was also reached in August with 54,912 *Culicoides* species. In the district Trier-Saarburg, only 1,509 *Culicoides* spec. were counted in this month, the minimum in comparison to the other eleven districts at the same period.

Potential impacts of climate change on stable flies, investigated along an altitudinal gradient

Gilles J, David J-F, Tilard E, Duvallet G, Pfister K.

Abstract

Adult populations of two species of stable flies were sampled along an altitudinal transect to determine whether higher temperatures resulted in (i) increased fly numbers, (ii) a longer season of infestation, and (iii) different responses in the cosmopolitan Stomoxys calcitrans and the tropical Stomoxys niger niger. Flies of both species were trapped at seven farms located at four altitudes (from 1600 to 100 m a.s.l.) in Reunion island. Trapping occurred once weekly over a 90-week period.

In either species, there were no relationships between the maximum or mean fly abundance and altitude. Only minimum abundance in winter increased significantly with decreasing altitude. Maximum and mean abundances differed significantly between nearby farms under similar climatic conditions. S. calcitrans was overall the most abundant species, but the proportion of S. niger significantly increased with decreasing altitude and became predominant at 100 m a.s.l. In both species, there were marked seasonal fluctuations in abundance, which changed along the gradient. When altitude decreased, population growth started earlier in winter but abundance declined earlier in summer, which resulted in a shift, not a lengthening of the season of infestation. Seasonal fluctuations of both species were strongly related to climate variables at high altitude, mainly temperature (positive relationship) and relative humidity (negative relationship). However, climate variables explained a decreasing proportion of the variations in abundance with decreasing altitude.

Synthesis and applications. The results indicate that (i) the maximum abundance of stable flies is limited by local factors, probably larval resources, and should not increase in response to climate warming; (ii) relationships between stable fly abundance and climate variables deteriorate when climate changes, which does not permit accurate predictions of population changes using climatic models; (iii) the tropical species tends to be the predominant pest at elevated temperatures, and it is recommended not to introduce S. niger in areas where climate is changing and where its other habitat requirements are met.

A study of the sylvatic rodent reservoir for *Bartonella* spp. in NE Poland: prevalence and the diversity of infection

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Bartonella spp., are vector-borne bacteria associated with numerous emerging infections in humans and animals. Human specific *Bartonella* species are responsible for diseases like Carrion's disease, cat scratch disease, endocarditis and neuroretinitis. A wide range of animals, including wild rodents, plays role as a reservoir host for these pathogens. Additionally, these intraerythrocytic parasites are easily transmitted by vectors among certain populations of hosts and this results in the significant genetic diversity of *Bartonella*. The purpose of these longitudinal environmental studies was to investigate the prevalence of bacteremia and the diversity of *Bartonella* isolated from wild rodents trapped during three years (2004-2006) in the Mazury Lakes District, near Mikołajki ($53^0$47.745'N, $21^0$39.640'E), north-eastern Poland. DNAs were obtained from the blood of four species of rodents (*Apodemus flavicollis*, *Myodes glareolus*, *Microtus arvalis* and *Microtus oeconomus*). Using PCR *Bartonella* spp. DNA was detected in 313 of 1022 (30.6%) rodents, particulary 31% of 583 *M. glareolus*, 42% of 161 *A. flavicollis*, 33% of 152 *M. arvalis* and 11% of 126 *M. oeconomus*. Based on sequence analyses of the *Bartonella* citrate synthase gene (*gltA*), the amplicons were divided into six genogrups. The level of sequence homology between the genogrups varied from 88% to 99%. Importantly, a few of studied isolates were identical (100% homology) to *B. grahamii*, a species associated with human illness. The prevalence and bacteremia of *Bartonella* spp. in rodents are likely to be affected by climate change. This is significantly related to a combination of milder winters and extended autumns (temperatures of 4-9^0C), thus influencing the springtime development of vectors for *Bartonella*, predominantly the tick *Ixodes ricinus*.

RatMap: a digital geodata supported monitoring project of urban rat populations in Hamburg, Germany

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Background:

Hamburg is a large seaport with ideal living conditions for rattus norvegicus as are mild climate and abundant waterways. On public properties rodent control is performed by governmental pest controllers. Lack of information on the outcome of control measures and on rodenticide resistance as well as short public funds asked for a modernised concept of urban rat control.

Methods:

A digital rat monitoring system using a MySql data-base linked to a geographical information programme was implemented. Data on notification of urban rats and governmental control procedures are regularely entered into the database and linked to different types of maps.

Results:

Hot spots for rats, changes in rat densities and control actions can be analysed over space and time. Areas with rat populations and their neighbouring streets, buildings and sites can be inseen at the same time to follow up previous finds and control actions as well as rodenticide resistance areas. Close cooperation with the City Water Company makes a three dimensional analysis possible, for maps used for pipes and manholes are based on the same digital city maps. The investigation of correlations of rodent findings to several ecological and geological as well as technical data will allow descriptive and analytical analysis of conditions relating to the frequency, distribution and dynamics of rat populations.

Conclusions:

A systematic and continued monitoring of populations and rat control measures is a useful tool to accomplish a scientific approach to urban rat control. Modern rodent control should follow methods of integrated pest control. This makes a controlled and moderate use of pesticides mandatory, which is strongly ameliorated through our data supported systems.

This abstract has been recently published at the 6th European Vertebrate Pest Management Conference 2007.

Winter acitivy of Ixodes ricinus in a Berlin forest area

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The seasonal activity of Ixodes ricinus has been the subject of many field studies. It is well-known that nymphs and adults of this important vector tick of numerous human pathogenic agents usually quest in Central Europe from March/April to October/early November depending on the weather situation in early spring and late autumn, respectively. Having in mind the warm autumn and very mild early winter in 2005/6, the present study aimed at following the host-seeking activity of I. ricinus from early autumn 2006 into the following winter months up to early March 2007.

Field-collected larval and nymphal ticks were allowed to take a full blood meal in the laboratory on Mongolian gerbils and to moult to the next life-stage in early summer 2006. The resultant unfed nymphs (n=204) and adults (n=196) were released onto 4 field plots in a Berlin forest area in September 2006. Each plot was covered by an approximately 10 cm thick layer of leaf litter (mostly from oak and beech) to provide a microclimatic humid refuge and shelter for non-active ticks. Forty-eight 60 cm wooden rods, arranged in a 6 x 8 grid, were placed at an approximately 75–80° angle on each of the plots.

Active ticks, both nymphs and adults, climbed these rods and usually quested close to the top approximately 35–40 cm above the leaf litter. Active ticks were observed on each observation date from early September 2006 to early March 2007 (14 observations from early September to late October and another 19 observations from early November to early March). These data were confirmed through flagging for ticks on two occasions in January and February 2007.

This might be the first time that extended winter activities of I. ricinus nymphs and adults have been demonstrated in Central Europe. The fact that I. ricinus can be active during the whole winter, a time of the year when these ticks are usually dormant, is relevant to the public because people who enter forest areas should be well aware of the risk of getting tick bites and tick-borne infections in very mild winter periods.

The study has been supported by Baxter Deutschland GmbH.

Seasonality of Ixodes ricinus in Germany: Preliminary results from the EDEN project

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Many pathogens are transmitted by ticks from wild reservoir hosts to Humans and/or domestic animals. Such pathogens are being investigated as part of the EDEN project (Emerging Diseases in a changing European environment). The University of Munich (LMU) is in charge of collecting and analysing data for Germany. Data on tick seasonality have been collected since 2006 on a monthly basis by dragging a $1m^2$ white flag over soil and vegetation over a $100m^2$ transect at various field sites in Bavaria. These data shall be integrated in a pan-European data-bank and analysed in this wider framework. At Munich, these local data shall further be included as parameters in a computer model exploring the relationships between ticks, tick-borne pathogens, and reservoir hosts (e.g. rodents and deer) in Bavaria.

Seasonal and geographic variation in the epidemiology of Anaplasma phagocytophilum and Rickettsia spp. in the hard tick Ixodes ricinus in Bavaria.

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The presence of tick-borne pathogens like Borrelia spp. and Babesia spp. in Germany has long been known. In recent years, also A. phagocytophilum and Rickettsia spp. have been detected in I. ricinus in Germany and thereby, a focal distribution has been suggested for A. phagocytophilum. This study investigates the prevalence of A. phagocytophilum and Rickettsia spp. in DNA-Extracts of 2862 unfed ticks (adults and nymphs) from 8 sites in Munich, collected regularly over 5 months, by PCR and Real-Time PCR.

The overall prevalence was 3.60% and 6.34% for A. phagocytophilum and Rickettsia spp. respectively, 0.35% were coinfected. The prevalence varied between 0 % and 11.77%, regarding the different pathogens, areas and months under investigation. The prevalence of A. phagocytophilum in a recreational park in the centre of Munich, highly frequented by people and dogs, was higher than in a natural forest outside of Munich, whereas the prevalence of Rickettsia spp. was opposite. For both pathogens, the prevalence in adults was higher than in nymphs. 16S rDNA nested-PCR products of A. phagocytophilum and gltA/ompA PCR products of Rickettsia spp. were sequenced. The majority belonged to Ehrlichia sp. “Frankonia 2” and R. helvetica, the presence of other species or variants of A. phagocytophilum and Rickettsia spp. was also detected.

This study manifests clearly a strong seasonal and geographic variation of A. phagocytophilum and Rickettsia spp. and shows that a big city park is an area of accumulation for A. phagocytophilum. Further studies will be needed to evaluate risk areas of these pathogens.

Ticks, rodents and tick-born diseases in Lithuania and Norway

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The northward expansion and increased density of *I. ricinus* tick populations in Fennoscandia and increasing incidence of tick-borne diseases could be related to climate change. The prevalence of *Borrelia* genospecies in 2221 *I. ricinus* ticks and 398 rodents collected in different landscapes of Lithuania and Norway were detected. Ticks and rodents tissue were tested for the presence of the *Borrelia* spirochetes DNA using PCR. As targets for DNA amplification of pathogens were used *fla* and *OspA* genes of *B. burgdorferi* s.l. genome. In ticks, the overall prevalence of *B. burgdorferi* s.l. infection was 14% in Lithuania, and 5.6% in Norway. The highest prevalence of *B. burgdorferi* s.l (20% in Lithuania; 21.2% in Norway) was found in deciduous and mixed forests. A lower prevalence (7.4% in Lithuania) was determined in pine forests and in the coastal zone coastal (4.7% in Norway), and the least prevalence (2.4% in Lithuania; 0.6% in Norway) was found in grasslands. In Lithuania, *B. afzelii* genotype was found in 76% of infected ticks, *B.garinii* in 10%, and *B. burgdorferi* s.s. in 7%. Double infections were observed in 1% of the infected ticks, 6% of the *Borrelia* infections were not typed. In Norway, *B. afzelii* was found in 59.4%, *B.garinii* - in 18.8%, and *B. burgdorferi* s.s. - in 9.4% of infected ticks.

The 23.4% (58 out of 248) rodents from Lithuania and 6.7% (10 out of 150) rodents from Norway were infected with *B. afzelii.* In Lithuanian samples, 53% of *M. arvalis*, 22.2 % of *M. agrestis*, 21% of *C. glareolus*, 10.5% of *A. flavicolis* and 6.7% of *A. agrarius* were positive according PCR, in Norway, 4.9 % of *A. sylvaticus* and 5.9%of *A. flavicolis* were infected with *B .afzelii*. *Sciurus vulgaris* harbored both, *B. afzelii* and *B. burgdorferi* s.s. genotypes.

The prevalence of *A. phagocytophilum* and *Babesia divergens* in 364 *I. ricinus* ticks collected in Lithuania and Norway was detected by Taq Man based Real time PCR method. The *msp2* gene of *A.phagocytophilum* and *18sr* RNA gene of *B.divergens* have been chosen as amplification targets in analysis. The overall infection level of *A.phagocytophilum* in Norwegian ticks was 4.5% (rates from 0 to 8.7%), in Lithuanian - 2.9% (rates from 0 to 9.1%). A total of 2.1% ticks were infected with *B. divergens* in Lithuania and 0.9% in Norway. The *A. phagocytophilum* was not found in any of tested ear and spleen samples of 164 small rodents and engorged nymphal ticks collected on rodents.

Genetic Heterogeneity of *Borrelia burgdorferi* Sensu Lato in the Kemerovo region (West Siberia) of Russia Based on Restriction Fragment Length Polymorphism and Sequence Analysis.

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In West Siberia, landscape–geographic conditions proved to be favorable for the formation of large TBE foci with a high epidemiological potential, and the values of TBE and borreliosis morbidity annually recorded in all administrative units of this region are many times higher than the average indications for Russia as a whole. The climate is sharp continental. The summer t balances from +11 up to +36, the winter one from 0 up to minus 50. Mountain snow reaches 5m oh height, taiga snow goes up to 3 m. Statistically proved dependence of tick activity and frequency of unfavourable outcomes on climate isn't discovered.

In this study the genetic diversity of *B. burgdorferi* sensu lato in local tick populations from Kemerovo region of Russia was analyzed. Ticks were collected by blanket dragging from different forestry in region. One hundred twenty *Ixodes persulcatus* adult ticks were selected for analysis. DNA was prepared from ticks by alkali extraction and was used for nested PCR that targeted the *rrf* (5S)-*rrl* (23S) intergenic spacer of *B.burgdorferi* sensu lato. *B. burgdorferi* sensu lato DNA was detected in 26 of 108 adult ticks (24%). *B.burgdorferi* genotypes were characterized by PCR-restriction fragment length polymorphism (RFLP) analysis of 5S-23S intergenic spacer amplicons. On the basis of both the *Tru9I* and the *Dra*I restriction patterns, the 26 isolates were separated into two genospecies that had 4 different restriction patterns.*B. garinii* was found in 11 ticks, 14 ticks carried *B. afzelii*. Double infections with *B. afzelii* and *B. garinii* were found in one case.

To confirm the results of PCR-RFLP analysis and to assess the DNA relatedness within and between genospecies, the complete sequences of the *rrf-rrl* intergenic spacers from 9 positive DNA samples were determined. The DNA sequence analyses of *rrf-rrl* intergenic spacers confirmed our PCR-RFLP results. These sequences were then aligned against each other and the reference sequences downloaded from GenBank by using Clustal W. The 9 strains clustered into two separate lineages. One was more close to B. *afzelii* ticks from Czech Republic and the second one was close to *B.garinii* strains from Portugal.

Climate Change: More vector transmitted plant pests?

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A number of plant pests like viruses, bacteria and nematodes are transmitted by vectors. Many of them are not able to establish at current climate conditions. However, climate change is expected to have effects on their establishment, spread and reproduction potential as well as on the pest transmission. Vectors established in greenhouses up to now only may be able to escape from these and may now establish and damage plants outdoors.

Traditional Pest Risk Analysis used to decide on the necessity of phytosanitary measures to prevent introduction and spread of those harmful plant pests and their vectors does not take into account climate change.

Existing studies of climate change on organisms suggest that direct effects of temperature are likely to be larger and more important than any other factor. The main effect of temperature in temperate regions is to influence winter survival of vectors. Natural spread of vectors, pests and diseases is accelerated towards the North, as former climate barriers are no longer effective. This results in more severe outbreaks of plant-disease vectors like aphids, white flies, thrips or beetles, an extension of the period of disease infection further into the growing season and also introduction and establishment of new vector species. More vectors survive from one vegetation period to the next leading to earlier and faster development of the transmitted disease.

Examples relevant for plant health are: *Bemisia tabaci* and *Thrips palmi*, both vectoring several viruses relevant for vegetable crops, and *Monochamus* spp., vectoring nematodes harmful to pines.

The described effects on vectors can have severe negative effects on food production or result in an increased use of plant protection products to control the vectors. Phytosanitary measures, that are currently effective, need to be adapted. Therefore

1. Pest Risk Analysis has to take climate change effects into account,

2. Phytosanitary regulations need to be adapted to climate change effects in order to prevent or limit the negative effects on plants and

3. more specific research on climate change and effects on introduction and spread of plant pests and their vectors is necessary.

Incidence and epidemiology of gramineous viruses transmitted by insects and eriophyid mites in Germany

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Approximately 90 different viruses of *Poaceae* are described of which about 60 are present in Europe. In Germany almost 23 viruses of grasses and cereals are known of which only some are of economic importance. Besides the soil-borne viruses economically important yield losses are caused by several other vector borne viruses as the luteoviruses *Barley yellow dwarf virus* (BYDV) and *Cereal yellow dwarf virus,* which are transmitted in a persistent manner by different aphid species and the geminivirus *Wheat dwarf virus* (WDV), which is transmitted persistently by a leafhopper. An infection of wheat and barley in autumn by these viruses reduces frost hardiness and yield losses can be decreased up to 95%.

Analyses have shown that the infection of winter cereals by BYDV and WDV is varying considerably between years. In 2001, 2002 and 2005 members of the BYDV group dominated while in 1998, 1999 und 2000 WDV was detected more frequently. In 2006 and 2007 both viruses appeared in similar frequencies. The strain BYDV-PAV and mixed infections with BYDV-MAV were dominating. Concerning the WDV complex, phylogenetic analyses have revealed that the “wheat”-, “barley”- and “oat”-strains may be considered as different viruses of the genus *Mastrevirus*. In Germany the “barley strain” is most frequent.

The epidemiology of these viruses is mainly influenced by climatic conditions and agricultural practice. The prolongation of the growing period in autumn stimulates the activity of aphids and leaf hoppers. Therefore, in years with a high incidence of BYDV and WDV temperatures are normally $>$ 10 °C for a longer period. With respect to the transmission efficiency of luteoviruses, differences between aphid clones were detected. The minimum temperature for an efficient transmission is 10 °C and transmission efficiency rises with growing temperature.

Wheat streak mosaic virus, which in the US causes periodically losses up to 100%, is not yet found in Germany. However, this virus transmitted by the mite species *Aceria tosichella* has been detected in south east Europe and was recently isolated by us from wheat in France. The impact of climate change on further gramineous viruses will be discussed.

Impact of climate change on insect vector populations and the occurrence and prevalence of insect-transmitted plant viruses in major crop plants of Germany

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In recent years the impact of climate change on our ecosystem and all its participants has become obvious. The average temperature has increased by 0.7 °C within the last hundred years globally and an average temperature rise of 6.3 °C by the year 2100 has been predicted (Randall et al., 2007). This will dramatically affect both mobile (fauna) and immobile (flora) organisms, resulting in both altered and novel forms of interactions between host plants, plant pathogens and their vectors. Unlike animal viruses, many of which can depend upon host mobility for transmission, most plant viruses are transmitted by vectors, the majority by insects (Power, 2000). Particularly aphids are expected to react strongly to environmental changes because of their short generation time, low developmental threshold temperatures (Harrington et al., 2007) and ability to survive mild winters without winter forms. An increase in the numbers of insect vectors will inevitably lead to a higher risk for viral infection of plants.

The aphid transmissible complex of barley yellow dwarf viruses (BYDV, Luteoviridae) in cereals and potato virus Y (PVY, Potyvirus) in potato were selected to illustrate a climate dependent scenario for vector-borne diseases in plants and its potential effects on the prevalence (incidence) of virus infection and yields. Both viruses cause severe yield and quality losses in their respective host plants and are transmitted by a number of different aphid species. However, the vector-virus interactions are distinct: BYDV is transmitted by aphids in the persistent (circulative) manner, whereas PVY is transmitted non-persistently.

A correlation between mild winters, high intensity of aphid movement during spring and a high frequency of PVY-infected potatoes will be discussed. Studies are in progress to investigate the observed climatic conditions and their impact on BYDV epidemiology in cereals.

Power AG (2000). Insect transmission of plant viruses: a constraint on virus variability. Curr. Op. Plant Biol. 3, 336-340.

Harrington R et al. (2007). Global Change Biology 13, 1550-1564.

Randall DA et al. (2007): Climate Models and Their Evaluation. In: Climate Change 2007: The Physical Science Basis. Contribution of Working Group I to the Fourth Assessment Report of the Intergovernmental Panel on Climate Change [Solomon S, D Qin, M Manning, Z Chen, M Marquis, KB Averyt, M Tignor and HL Miller (eds.)]. Cambridge University Press, Cambridge, United Kingdom and NewYork, NY, USA.

Climate change as a potential cause of the occurrence of potato stolbur in Germany

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Phytoplasmas are wall-less and non-helical bacteria of the class Mollicutes. Bois noir in grapevine and potato stolbur are caused by phytoplasmas of the stolbur (16Sr-XII-A) group and transmitted by the planthopper *Hyalesthes obsoletus,* a southern European, xerothermic species. In Germany it was long restricted to viticultural sites on the steep slopes of the river valleys of Rhine and Mosel until it spread recently to climatically less favorable areas. Since average temperature increased significantly, e.g. by 1.7 °C within the last 40 years in the Mosel valley, this range expansion is thought to be related to changing climatic conditions. The capability of *H. obsoletus* to inoculate potato plants with stolbur has been confirmed by transmission experiments.

The potato stolbur phytoplasma has quarantine status in the European Union (Status: EPPO A2 list, Nr. 100, EU Annex designation II/A2). Germany was considered to be free from potato stolbur even though the vector and the pathogen appeared in vineyards. The disease was first detected in Hesse in 2006 and occurred in Rhineland-Palatinate and Lower Saxony in 2007. *H. obsoletus* was found on some of the affected sites. A noteworthy loss of yields due to potato stolbur is not to be expected in the near future. However, because of the quarantine status of potato stolbur and its adverse affects on tuber quality growers should keep an eye on the further development of the disease

The fact that stolbur phytoplasma and its vector were present for a long time at viticultural sites but occurred just recently in potatoes appears contradictory. However, potatoes are grown in areas where ambient temperatures were not sufficient for the vector to complete its life cycle. Changing climatic conditions could have allowed *H. obsoletus* not only to spread to new viticultural sites but also to potato growing areas with a rather mild climate. Since early maturing varieties are grown there, stolbur symptoms might become visible only in years when high spring temperatures lead to an exceptionally early flight of *H. obsoletus* and an inoculation of the potato plants ahead of the normal time in July. This could allow symptoms to develop before harvest. Symptoms of potato stolbur closely resemble that of *Verticillium*- and *Colletotrichum*-wilt or of black scurf caused by *Rhizoctonia solani* (common diseases for local potato production). Therefore, a confusion of the three diseases with stolbur by growers is quite imaginable.