***Curriculum vitae***

| **NAME** | **POSITION TITLE** |
|---|---|
| Alex David Greenwood | Associate Professor & Head of Department of Wildlife Diseases |
| **DATE AND PLACE OF BIRTH**<br>February 5, 1968 Pittsburgh, Pennsylvania, USA |  |

**EDUCATION/TRAINING**

| INSTITUTION AND LOCATION | DEGREE | YY | FIELD OF STUDY |
|---|---|---|---|
| Cornell University, Ithaca, New York, USA | BA | 1986-1990 | Biology |
| University of Michigan, Ann Arbor, Michigan, USA | Ph.D. | 1990-1996 | Human Genetics |
| Ludwig Maximillian University, Munich, Germany | Postdoctoral | 1996-1999 | Ancient DNA |
| American Museum of Natural History, New York, USA | Postdoctoral | 1999-2001 | Wildlife pathogens and ancient DNA |
| Helmholzzentrum Munich, Munich, Germany | Postdoctoral | 2001-2006 | Virology |

**A. Positions and Honors**

**Positions and Employment**

2006-2009 Assistant Professor, Old Dominion University, Biological Sciences Department, Norfolk, Virginia

2009- Associate Professor (W2-S) of Wildlife Diseases, Freie Universität Berlin, Department of Veterinary Medicine, Berlin, Germany

2009- Head of Department of Wildlife Diseases, Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany

**Other Experience and Professional Memberships**

2009- Faculty of International Max Planck Research School, Berlin, Germany

2010- Associate Member of Interdisciplinary Center for Infection Biology and Immunity (ZIBI), Berlin, Germany

**Honors**

2001- Research Associate, American Museum of Natural History, Vertebrate Zoology, New York, New York, USA

2009- Research Associate, National Museum of Natural History, Smithsonian Institution, Washington, D.C., USA

**B. Professional roles and services to the scientific community**

Editorial Board for Scientific Reports
Associate Editor for BMC Research Notes
Associate Editor for Mitochondrial DNA
Associate Editor for BioMed Research International
Member, Dahlem Research School, Freie Universität Berlin
Polar Bear European Endangered Species Programme (EEP) Scientific Advisor
Co-organizer of annual International Conference on Diseases of Zoo and Wild Animals with ca 300 participants
Referee for many journals: including PLoS One, Virus Research, Journal of Virological Methods, Molecular Biology and Evolution, Journal of Virology, Scientific Reports, Current Biology
Ad hoc reviewer for National Science Foundation, various Australian funding bodies
Reviewer for tenure promotion for the Hebrew University in Jerusalem and the University of Sydney
I have served on two Habilitation committees for the Department of Veterinary Medicine at the Freie Universität Berlin
I have been invited multiple times to give presentations at national and international conferences including the Society of Molecular Biology and Evolution, The National Museum of Natural History, Smithsonian Institution, The Zoo and Wildlife Health Conference.

**C. Contributions to science**

In the following section I will outline some of my major contributions to science and in each case example publications from the area of research described.

**Unusual vectors and diseases**. Emerging infectious diseases play an increasingly important worldwide role in human and animal health (One Health) both in captivity and in the wild but their origin and emergence are not well understood. Water may be an unrecognized vector for emerging infectious mammalian viral diseases although it is essential for life. We are testing the central hypothesis that some mammalian viruses are adapted to use water as a vector (AQUAVIR) and are investigating the ecological and evolutionary factors which might favor their role as drivers of emerging infectious diseases. Specifically, we are testing five concepts derived from our central tenet: (1) AQUAVIR evolved in climatic zones with marked seasonal water shortages, where small dry season water sources concentrate both viruses and hosts, and currently may occur in any limited water source from which a large number of potential hosts drink. (2) Water transmission has a markedly different effect on virus evolution than transmission by other vectors in that it favors reduced host specificity to increase virus spread through mixed-species assemblages that drink from the same water sources. (3) Virus shedding and transmission rates are highest when water sources are scarce and hosts are physiologically stressed. (4) Viral virulence depends on the evolutionary time-span of virus-host species associations. (5) AQUAVIR adaptations are obtained at a cost to virus replication in the host e.g. investment in stability comes at a cost to replication and vice versa. Testing these ideas will enable us to accurately model viral evolutionary adaptation, emergence and the risk of transmission between distantly related species sharing water sources. Demonstrating and accurately modeling the role of water in viral emergence and spread would radically improve our understanding of emerging mammalian viral diseases and undermine the current, widely held assumption that viruses are unstable in water. This project was part

of a successful "SAW Antrag" (Greenwood PI) of the Leibniz Gemeinschaft which was awarded in 2014 to start in 2015. There were two postdoctoral and two PhD positions associated with this project and like most SAW projects, a financial support volume of over 1 million euros over three years (1.2 million). The results have been or are in the process of being published. A related Leibniz "Vebundprojekt" with a PhD position associated has examined several pathogens potentially transmitted via water in Germany (Greenwood Co-PI). The renewal process for this project is in preparation and has received personnel and consumables interim funding to continue.

Regarding unusual diseases, we were involved in characterizing a new class of wildlife diseases first described by us in the world famous polar bear Knut of the Zoological Gardens in Berlin. Originally it was generally suspected and expected that Knut died of an infectious disease having exhibited seizures prior to death and encephalitis in the post mortem. However, we discovered he suffered from an auto-immune encephalitis caused by the generation of antibodies against the N-methyl-D-aspartate receptor (NMDAR). This represents the first non-human case of this disease which in humans has overtaken viral encephalitis as the lead cause of encephalitis in humans.


a. Dayaram A, Franz M , Schattschneidera A, Damiani AM , Bischofberger S, Osterrieder N, **Greenwood AD** (2017) Long term stability and infectivity of herpesviruses in water. Sci Rep. 7:46559

b. Kampmann ML, Schnell IB, Jensen RH, Axtner J, Sander AF, Hansen AJ, Bertelsen MF, **Greenwood AD**, Gilbert MTP, Wilting A (2017) Leeches as a source of mammalian viral DNA - a case study in medicinal leeches. Eur J Wildl Res (2017) 63: 36.

c. Franz M, Goodman LB, Van de Walle GR, Osterrieder N, **Greenwood AD** (2017) A point mutation in a herpesvirus co-determines neuropathogenicity and viral shedding. Viruses. 10;9(1). pii: E6.

d. Prüss H, Leubner J, Wenke N, Czirják GA, Szentiks CA, **Greenwood AD** (2015) Anti-NMDA Receptor Encephalitis in the Polar Bear (*Ursus maritimus*) Knut. Sci Rep. 5, 12805; DOI is: 10.1038/srep12805


**High throughput viral sequence analysis methodologies**. Underpinning much of my research is method development. Whether it is trying to identify minute quantities of novel viral DNA or host ancient DNA, the challenges can be immense. Even pathogens with slow mutation rates pass through so many generations in a single infected individual, particularly for viruses, that diversification at the sequence level can be very rapid. This is extremely challenging for PCR based approaches. Given the minute quantities of DNA or specific targets that one wants to examine, shotgun sequencing next generation sequencing (NGS) approaches often fail to sufficiently sequence the target or do not sequence it at all. An added complication is that such shotgun data is hugely challenging to analyze bioinformatically. We have established several hybridization capture targeted High Throughput Sequencing (HTS) approaches for addressing these problems (see Tsangaras et al. 2014 on CapFlank attached as an example). By using PCR product baits of choice to fish out and NGS sequence specific targets, the NGS sequencing result is far more enriched for sequences of interest. The phenomenon of CapFlank we have characterized allows one to also characterized many thousands to millions of bp of bait flanking sequence. The benefit here for both host and pathogen DNA is baits to highly conserved genomic regions of any genome can then be used to determine the completely unknown and highly variable regions of the genomes by CapFlank. This is now part of a submitted patent application (DE 10 2014 105 112.2) to develop this method for pathogen diagnostics though it can be used for any type of sequence from microsatellite capture to barcoding which we have

performed on environmental DNA samples. The data obtained from such enriched sequences is also far less challenging for bioinformatics analysis as the filtering of unwanted sequences is greatly reduced which minimizes the computational and analytical effort required for processing the data.

a. Szentiks CA, Tsangaras K, Abendroth B, Scheuch M, Stenglein MD, Wohlsein P, Heeger F, Höveler R, Chen W, Sun W, Damiani A, Nikolin V, Gruber AD, Grobbel M, Kalthoff D, Höper D, Czirják GÁ, Derisi J, Mazzoni CJ, Schüle A, Aue A, East ML, Hofer H, Beer M, Osterrieder N, **Greenwood AD.** (2014) Polar bear encephalitis:establishment of a comprehensive next-generation pathogen analysis pipeline for captive and free-living wildlife. J Comp Pathol. 150(4):474-88.

b. Tsangaras K, Siracusa MC, Nikolaidis N, Ishida Y, Cui P, Vielgrader H, Helgen KM, Roca AL, **Greenwood AD**. (2014) Hybridization capture reveals evolution and conservation across the entire Koala retrovirus genome. PLoS One. 9(4):e95633

c. Tsangaras K, Wales N, Sicheritz-Pontén T, Rasmussen S, Michaux J, Ishida Y, Morand S, Kampmann ML, Gilbert MT, **Greenwood AD**. (2014) Hybridization capture using short PCR products enriches small genomes by capturing flanking sequences (CapFlank). PLoS One. 9(10):e109101

d. Seifarth, W., Frank, O., Zeilfelder, U., Spiess, B., **Greenwood, A.D.,** Hehlmann, R., and Leib-Mösch, C. (2005)Comprehensive Analysis of Human Endogenous Retrovirus (HERV) Transcriptional Activity in Human Tissues with a Retrovirus-Specific Microarray. J. Virol. 79: 341-352.

**Ancient DNA**. As a NSF/Alfred Sloan Postdoc in Munich and as a Postdoc at the American Museum of Natural History I was at the forefront of the development of pre-next generation sequencing ancient DNA development. I was the first to characterize in detail nuclear DNA sequences from Pleistocene mammals and to determine that nuclear integrations of mitochondrial DNA were as much a problem for interpretation of ancient DNA results as modern DNA results. I also characterized the first ancient retroviral sequences from ancient DNA and was one of the first scientists to examine pathogens as a potential cause of extinction. My group and many others have been involved in trying to explain the genetic dynamics of extinction at the end of the Pleistocene (ca. 10 thousand years ago) that decimated the megafaunal species such as woolly mammoths. Several studies of woolly mammoth mitochondrial diversity (species extinct) and muskox (Ovibos moschatus, extant) have thrown in question whether climate or humans played a significant role in extinction. For example, upon the arrival of humans, mammoths became extinct on the mainland but muskoxen demonstrated an increase in population. Similarly, climate change affected mainland and insular parts of Siberia equally yet mammoths survived on some Russian and Alaskan islands until about 2.5 thousand years ago. Another possible cause of population decline or fluctuation is disease. Yet identifying pathogens is exceedingly difficult from ancient DNA. As an alternative, we have begun a project to examine immunogenetic diversity of mammoths and muskoxen that have already been characterized for mitochondrial DNA diversity. The underlying hypothesis is that examining the evolution of the immunogenome over an approximately 50 thousand year interval in one species that failed to adapt and became extinct and one that survived, we will be able to determine the long term evolutionary dynamics of immunogenes, the most important defenses against pathogens in vertebrates. If there is evidence of selection of specific immunogene alleles at specific time points corresponding with increases or decreases in the population, it may provide indirect evidence of pathogen entry into the ecosystem, a likely event during a time of immense transition in the arctic which saw the movement and introduction of many species, including humans into novel geographic areas. This project was funded by the DFG (Greenwood PI) and is in the concluding stages.

a. **Greenwood, A.D.**, Capelli, C., Possnert, G., and Pääbo, S. (1999) Nuclear DNA sequences from late Pleistocene megafauna. Molecular Biology and Evolution 16(11): 1466-1473.
b. **Greenwood, A.D.**, Lee, F., Capelli, C., DeSalle, R., Tikhonov, A., Marx, P.A., and MacPhee, R.D.E. (2001) Evolution of endogenous retrovirus-like elements of the woolly mammoth (*Mammuthus primigenius*) and its relatives. Molecular Biology and Evolution 18(5): 840-847.
c. Wyatt, K., Campos, P.F., Gilbert, M.T.P., Kolokotronis, S.O., Hynes, W., DeSalle, R., Daszak, P., MacPhee, R.D.E.* and **Greenwood A.D.*** (2008) Historical Mammal Extinction on Christmas Island (Indian Ocean) Correlates with Introduced Infectious Disease. PLoS One 3(11) e3602
d. Slater G, Cui P, Forasiepi AM, Lenz D, Tsangaras K, Voirin B, de Moraes N, MacPhee RD, **Greenwood AD** (2016) Evolutionary relationships among extinct and extant sloths: the evidence of mitogenomes and retroviruses. Genome Biol Evol. 8(3):607-21

**Endogenous retrovirus molecular biology**. As a postdoc in the Institute of Virology of the Helmholtz Center Munich up through my current position, I have worked on the molecular biology of endogenous retroviruses to understand their interplay with exogenous retroviruses and their role in mammalian biology. My key contributions were examining in particular their comparative distribution and expression in non-human primates and their potential interaction with prion diseases and HIV. We uncovered several linkages between altered expression of specific endogenous retroviruses and prions and HIV in both mouse and primate model systems.

a. **Greenwood, A.D.***, Horsch, M.*, Stengel, A., Vorberg, I., Maas, E., Schädler,S., Beckers, J., Erfle, V., Schätzl, H., and Leib-Mösch, C. (2005) Cell line dependent RNA expression profiles of prion-infected mouse neuronal cells. Journal of Molecular Biology 349, 487-500. *Contributed equally
b. Stengel, A., Roos, C., Hunsmann, G., Seifarth, W., Leib-Mösch, C. and **Greenwood, A.D.** (2006) Expression profiles of endogenous retrovirus in Old World monkeys. J. Virol. 80 (9): 4415-4421.
c. **Greenwood, AD***, Vincendeau, M*, Schmädicke, AC, Montag, J, Seifarth, W, Motzkus D (2011) Bovine spongiform encephalopathy infection alters endogenous retrovirus expression in distinct brain regions of cynomolgus macaques (*Macaca fascicularis*). Molecular Neurodegeneration 6(1):44 *Co-first authors
d. Vincendeau M, Schreml JMH, Ngounou A, Mayer J, Göttesdorfer I, **Greenwood AD**, Kramer S, Seifarth S, Hadian K, Brack-Werner R, Leib-Mösch C (2015) Modulation of human endogenous retrovirus (HERV) transcription during persistent and de novo HIV-1 infection. Retrovirology. 12(1):27. doi: 10.1186/s12977-015-0156-6.

**Viral invasion of genomes**. Approximately 10% of vertebrate genomes are composed of highly variable retroviral like elements called endogenous retroviruses (ERVs). They are closely related to exogenous retroviruses such as the human immunodeficiency viruses HIV. The variability is such that even phylogenetically closely related species e.g. humans and chimpanzees, can have radically different ERV composition. However, the establishment of ERVs in the genome in most species occurred millions of years ago and thus, the process by which the genome is colonized by retroviruses are poorly understood.

Koalas (*Phascolarctos cinereus*) are the only example of a species where the process of genomic colonization is currently taking place. The koala retrovirus (KoRV) is a lymphoma/leukemia associated retrovirus that is at extremely high prevalence in northern Australia but absent in some populations in southern Australia. This means that koalas in northern Australia are genomically different from koalas in southern Australia due to an infectious process and that given that it is ongoing, it can be studied.

Using ancient DNA, genomics, epidemiology and modeling (protein and ecological) we have investigated the evolution of KoRV over space and time to examine the host and viral adaptations responsible for

endogenization and hence. Our research has shown that the process is very fast, highly dependent on recombination and that existing ERVs in the genome lower the fitness of invading retroviruses while remobilizing themselves (increasing their own fitness). The entire process is dependent on ecological factors such as koala behavior (they are sedentary) and barriers to introgression such that populations in New South Wales are completely different genomically in their content of KoRV-ancient koala ERV viruses compared to the adjacent state of Queensland. We think this demonstrates a general mechanism of endogenization and several research projects are ongoing in my laboratory to explain the details of this process mechanistically. This project has been funded for several years by the National Institutes of Health (National Institutes of General Medical Science) (Greenwood subaward).

Related to this area of research which investigates the recent changes in KoRV that allow it to endogenize, we are examining longer term viral evolutionary dynamics that have allowed KoRV like viruses to jump among taxonomically distant species. KoRV is most closely related to the gibbon ape leukemia virus (GALV) a virus identified in captive or released captive gibbons. There is no overlap of distribution of koalas and gibbons suggesting that KoRV and GALV may circulate in an unknown reservoir. We have used hybridization capture and NGS to screen Southeast Asian rodents for GALV and KoRV. KoRV was not identified but our data suggests GALV is a rodent retrovirus of several Southeast Asian Mus species. We are now screening more rodents from Southeast Asia through Papua New Guinea to attempt to identify more KoRV like viruses circulating in rodents. Comparison of the obtained sequences with GALV and KoRV would identify longer evolutionary trends in viral dynamics and potentially pinpoint mutations of interest for functional studies relevant to host specificity.

A second related project is that thus far, KoRV has been correlated with pathogenesis but this has never been conclusively established. As part of our endogenization study we have identified 17 recombinant KoRVs that are part KoRV and part ancient unrelated endogenous retrovirus. So there are currently 13 possible cancer causing agents, KoRV itself and the 17 recombinants all of which have retrotransposed and are increasing in copy number. We have collected tumor and healthy tissues from multiple animals and are testing them for novel integrations to determine if any of the 17 possible retroviral elements may be cancer causing agents. This was part of a Morris Animal Foundation funded project (Greenwood PI) with a DAAD funded postdoc working on the project. Currently, this line of research is funded by the Deutscheforschungsgemeinschaft.


a. Löber U, Hobbs M, Dayaram A, Tsangaras K, Jones K, Alquezar-Planas DE, Ishida Y, Meers J, Mayer J, Quedenau C, Chen W, Johnson RN, Timms P, Young P, Roca AL*, **Greenwood AD*** (2018) Degradation and remobilization of endogenous retroviruses by recombination during the earliest stages of a germline invasion. Proc Natl Acad Sci. 115(34):8609-8614 * corresponding authors

b. Ishida Y, Zhao K, **Greenwood AD**, Roca AL. (2015) Proliferation of Endogenous Retroviruses in the Early Stages of a Host Germ Line Invasion. Mol Biol Evol. 32(1):109-20

c. Tsangaras K, Siracusa MC, Nikolaidis N, Ishida Y, Cui P, Vielgrader H, Helgen KM, Roca AL, **Greenwood AD**. (2014) Hybridization capture reveals evolution and conservation across the entire Koala retrovirus genome. PLoS One. 9(4):e95633

d. Ávila-Arcos MC*, Ho SYW*, Ishida Y*, Nikolaidis N*, TsangarasK, Hönig K, Medina R, Rasmussen M, Fordyce SL, Calvignac-Spencer S, Willerslev E, Gilbert MTP, Helgen KM, Roca AL§, **Greenwood. AD.§** (2012) 120 years of koala retrovirus evolution determined from museum skins. Mol Biol Evol 30(2):299-304. * equal contributors, § corresponding authors

**Cross species transmission of pathogens among wildlife**. As head of the Department of Wildlife Diseases and professor for Wildlife Diseases the main focus of my research is identifying cross species transmission of pathogens among wildlife, identifying how they are transferred and the consequences on the hosts (both natural and accidental). This area of study is both at the individual level in zoos and at the population or species level in the wild. We have recently discovered a major threat in zoos as a result of the spread of recombinant zebra herpesviruses to non-African fauna which has resulted in many fatalities. I have initiated several large scale studies to understand how viruses (particularly equine herpesviruses) evolve and circulate in their natural reservoirs and the consequences of such mechanisms on captive wild animals.

a. Escalera-Zamudioa M, Rojas-Anayab E, Kolokotronis SO, Taboada B, Méndez-Ojedad ML, Loza-Rubiob E, Arias CF, Osterrieder N, **Greenwood AD** (2016). Bats, primates, and the evolutionary origins and diversification of mammalian gammaherpesviruses. mBio. 7(6). pii: e01425-16

b. Abdelgawad A, Hermes R, Damiani A, Lamglait B, Czirják GÁ, East M, Aschenborn O, Wenker C, Kasem S, Osterrieder N, **Greenwood AD** (2015) Comprehensive Serology Based on a Peptide ELISA to Assess the Prevalence of Closely Related Equine Herpesviruses in Zoo and Wild Animals. PLoS One. 10(9):e0138370

c. Escalera-Zamudio M, Mendoza ML, Heeger F, Loza-Rubio E, Rojas-Anaya E, Méndez-Ojeda ML, Taboada B, Mazzoni CJ, Arias CF, **Greenwood AD**. (2015) A novel endogenous betaretrovirus in the common vampire bat (*Desmodus rotundus*) suggests multiple independent infection and cross-species transmission events. J Virol. 89(9):5180-4.

d. Greenwood AD*, Tsangaras K*, Ho SY, Szentiks CA, Nikolin VM, Ma G, Damiani A, East ML, Lawrenz A, Hofer H, Osterrieder N. (2012) A Potentially Fatal Mix of Herpes in Zoos. Curr Biol. 22(18):1727-31 *Equal contributors

**D. Leadership**

As Head of the Department of Wildlife Diseases I have lead a group of 6 staff scientists (including my own position), 8 technical assistants and a group of doctoral and postdoctoral students that has averaged about 9 students at any given time over the last 8 years. Additionally we have hosted an almost constant but rotating group of technical assistant trainees, practical students, bachelors students and Masters students. In almost all instances, I have been the official university PI for all students seeking degrees in my department whether or not they were directly under my supervision. As Department Head, I am responsible for promoting my Departments interests within the institute regarding institute budgeting, staffing and during the evaluation our institute as a Leibniz Society institute must face every seven years. I am responsible for staff performance evaluations and for managing the allocations house positions (three half time or doctoral positions). I also set the general research direction and priorities for the department. I also regularly present the department research to the institute's advisory board (Beirat). Externally, I often represent my department at conferences such as The Zoo and Wildlife Health Conference which is organized annually with my group together with representatives of the European Association of Zoo and Wildlife Veterinarians or in commissions in Berlin, Germany and abroad. An example is short before its publication I presented the cause of Knut the polar bears death to a group of parliamentarians in the Reichstag.

**E. Teaching**

As an Assistant Professor at Old Dominion University I taught Virology, Emerging Infectious Diseases and a Seminar on Ancient DNA to undergraduates and graduate students. Undergraduate courses consisted of ca. 15 weeks of one hour lectures with regular exams and a final exam. The Ancient DNA course required students to present a paper at the end of the semester.

In Berlin, my teaching has been either split between „Wahlpflichtvorlesungen“ in the Freie Universität Berlin Faculty of Veterinary Medicine (lectures held in German) and the Dahlem Research School which includes students from all biology based fields from the Freie Universität Berlin but also students from the Humboldt University and consortium programs such as the Zentrum für Infektionsbiologie and Immunität (ZIBI). As a W2-S Professor, I have had a reduced teaching load of two “Semesterwochenstunden” connected with my duties as Department Head of Wildlife Diseases of the Leibniz Institute for Zoo and Wildlife Research.

I have regularly taught a course on Retroviruses and Retroelements and a course on Emerging Infectious Diseases in the Department of Veterinary Medicine which in addition to the basic virology of retroviruses puts a large emphasis on the molecular evolution of retroviruses and the co-evolutionary processes between pathogen and host that shapes virus and host populations. I teach a similar course for the Dahlem Research School and in addition teach a course on Ancient DNA and Next Generation Sequencing methods applied to disease and ecological questions in biology. Recently, I have taught a course on Next Generation Methods for diagnostics.

I am also supervising, co-supervising or have supervised over 20 PhD, Masters, Bachelors and Postdoctoral researchers in both the American and German academic research systems.

**F. Recent Research Support as PI or Co-PI of approximately 2.5 million total (I am showing funding obtained in Germany during my tenure at the IZW).**

2013-2015
National Institute of General Medical Sciences (National Institutes of Health) R01 grant
758.479 USD
Co-investigator Greenwood
*A singular opportunity to determine the evolutionary genetics of retroviral invasion*
This grant funded the initial modern and ancient DNA work on the koala retrovirus which has been a central theme of my research. It funded all of the historical koala DNA work we have done to date, lead to the development of our CapFlank enrichment method and initiated our work on gibbon ape leukemia virus.

2014-2016
Deutsche Forschungsgemeinschaft
25.000 €
PI Greenwood
*The Vampire Bat Virome: Evolutionary Implications in an Immunological Context*
This project funded the laboratory costs for a DAAD-CONACYT funded doctoral student project examining the co-evolution of bat viruses and host genes.
2014-2018
Deutsche Forschungsgemeinschaft
196.00 €
PI Greenwood
*Measuring immunogenetic diversity of woolly mammoths and muskoxen during the Pleistocene*

This is an example of my ongoing ancient DNA work. We are using hybridization capture on several hundred woolly mammoth and ancient muskox DNA libraries to examine long term evolutionary trends of immunogenetic loci in two species with contrasting evolutionary trajectories (extinct and extant).

2014-2017
Morris Animal Foundation, D14ZO-94
66.000 USD
PI Greenwood
*Koala retrovirus: cancer, causality and captive management*
This project is examining whether KoRV causes cancer via insertional mutagenesis. We are applying hybridization capture and long range inverse PCR-PacBio techniques to identify tumor specific integrations in paired healthy and tumor tissues we have collected.

2015-2018
SAW-2015-IZW-1, Leibniz Gemeinschaft
1.190,000 €
PI Greenwood
*AQUAVIR: Water as an aquatic viral vector for emerging infectious diseases*
In a large scale project with 2 PhD students, 2 postdocs and a dozen collaborators we are exploring whether herpesviruses have adapted to utilize water as a vector for viral transmission in ecosystems with seasonal water shortages specifically, in Tanzania in Africa and the Great Gobi desert in Mongolia.

**Ongoing support**
2015- ongoing
Leibniz Collaborative Network: Infections in the 21st Century
800.000
PI Schaible
The project involves over a dozen Liebniz Institutes and covers pathogen transmission from human to human, air, insect vectors and water. I am the PI of the water transmission group which funded a doctoral student and consumables for the project. In the interim phase before we can apply to re-fund the project, we were awarded bridge funding. We are examining water and insect vectors in urban settings for anti-microbial resistant bacteria.

2018-2021
Deutsche Forschungsgemeinschaft
267.950€
PI Greenwood
*Genome invasion: understanding the evolutionary and functional roles of mutation and recombination at the earliest stages of retroviral endogenization*
We are searching on both sides of the Wallace Line between SE Asia and Australo-Papua for relatives of the koala retrovirus and gibbon ape leukemia virus in rodents and bats to understand the biogeographical principles underlying retroviral invasion in mammals.

2019 -2022
Deutsche Forschungsgemeinschaft
246.220 €
PI Greenwood
*Purging of deleterious retroviral integrations at the earliest stages of genomic invasion*.

We are using a natural experiment of a koala population translocated to an Island 100 years ago in northern Australia to provide empirical evidence for purging of deleterious alleles (in this case koala retroviral variants).

2019-2022
ERANet-LAC
394.850 €
PI Greenwood
*WildEmerg*
In a consortium with Spain, Peru and Brazil, we are examining arboviruses and haemoparasites from Amazonian wildlife and insect vectors to understand pathogen transmission in this complex ecosystem.

**Additional Information:**

Updated projects and publications can be found at https://www.researchgate.net/profile/Alex_Greenwood