



The Leibniz Institute for Zoo and Wildlife Research (Leibniz IZW) in Berlin is Germany's premier wildlife research institute. The Leibniz IZW focuses on the life histories and mechanisms of evolutionary adaptations of mammals and birds, their limits and their conservation in natural and anthropogenically influenced environments. The institute operates within the fields of evolutionary ecology, evolutionary genetics, wildlife diseases, reproduction biology and reproduction management.

For a new interdisciplinary research initiative, entitled

“Genome invasion: understanding the evolutionary and functional roles of mutation and recombination at the earliest stages of retroviral endogenization”

the Leibniz IZW offers a **doctoral position (65 %)** in the department of wildlife diseases.

Job description:

Up to 11 % of mammalian genomes are comprised of retroviral like sequences. The processes that generated this large fraction of the genome involved an invasion of germ lines by infectious retroviruses. The process of retroviral invasion is poorly understood as most entered the germ line millions of years ago. The research project will focus on characterizing relatives of the gibbon ape leukemia virus (GALV) and the koala retrovirus (KoRV) using hybridization capture and other high throughput sequencing based approaches on rodents and bats on both sides of the Wallace Line. The Wallace Line is a faunal barrier that separates Asia from a transitional zone between Asia and Australia, and GALV has crossed this line via unknown vector species. The GALV and KoRV clades both contain infectious exogenous retroviral variants but also contain endogenous retroviruses representing very recent or ongoing germ line invasions. Inter- and intra-retroviral recombination appears to be a frequent event for GALV and KoRV. The ultimate goal of this project is to determine the role that recombination plays in the earliest stages of the genomic invasion process of retroviruses. In addition to identifying new GALV and KoRV like retroviruses in novel species on both sides of the Wallace Line, retroviruses will be tested for the functional consequences of mutation and recombination of the *gag* and *env* genes in a heterologous retroviral expression system. Part of the project will be conducted in Australia where many of the sample collections for regional species are housed.

Prerequisites:

- Completed university degree (Master of Science or Diploma) in molecular evolution, lab based evolutionary virology or related disciplines;
- Strong background in molecular virology;
- Experience generating and working with High Throughput Sequence data;
- Experience with cell culture and the production of virus or viral vector particles;
- Previous working experience in microorganism or genomics based bioinformatics would be an advantage;
- Proficiency in English (oral and written).

We offer state-of-the-art methodology and a stimulating research environment. For the successful candidate, organizational skills, high motivation and the willingness to work as part of a team within highly interdisciplinary projects are essential. The position will start **May 1st, 2018** and is limited to **three years**. Working hours comprise 25,35 hours per week (65 %) with salary and benefits according to TVöD (Bund). The place of work is the Leibniz-IZW, Alfred-Kowalke-Str. 17, 10315 Berlin.

As member of the Leibniz Association, the Leibniz-IZW is an equal opportunity employer, determined to increase the proportion of women in successful scientific careers, and particularly encourages women to apply. Preference will be given to disabled applicants with the same qualifications.

For enquiries or further questions please contact **Prof. Alex Greenwood** (Leibniz IZW) **Tel.: +49 (0)30 5158-233**, **email: assist3@izw-berlin.de**.

Please submit your application with a motivation letter, CV and copies of relevant degrees, list of publications and names and contact details of two referees before or latest **February 16, 2018** to via IZW's online-job-market (**button “Apply online”**).

We are looking forward to your application!