

Research

I am interested in the evolution of vertebrates in general, including marsupials, birds, almost every placental mammalian order, lizards, snakes, crocodiles and fishes. Besides reconstructing and dating their evolutionary tree, placing the events into larger contexts of e.g. biogeography, plate tectonics and climate is exciting. Currently - as of January 2017 - I am interested and working on the following topics for which PhD, master or project students are welcome.

Evolution of Giraffe - Developing markers for some simple population study for the Giraffe Conservation Foundation turned out to be an exciting project about cryptic biodiversity. Instead of one there seems to be four species of giraffe. Currently we genome sequence a number of individuals from each former subspecies to determine the degree of genetic separation and gene flow.

Bear Genomics - We have sequenced a number of bear genomes to study their evolution. Surprisingly there is a substantial of gene flow not only between polar and brown bear, but also among other bears. We continue to study the extent and the consequences of this level of gene flow between species.

Mammalian phylogenomics - The analysis of nuclear genome data for resolving the mammalian tree is currently a rapidly changing and competitive field. To date our group has analyzed the largest available data set to resolve the basal placental mammal divergences (Hallström et al. 2007, Janke and Hallström 2008, 2010) and the basal mammalian divergences (Kullberg et. al. 2008). The data matrices comprised some 3300 genes, equivalent to about 3 million nucleotides of coding genome sequences from today 31 mammalian species. This comprises about 10 % of all coding data of a vertebrate genome and represents the largest hitherto assembled, analyzed, and published data set. We have revised some of the erroneous results from mitogenomic and nuclear gene data by analyzing these comprehensive genome data sets. New genome data from placental mammals are currently being released into the databases can be studied for new phylogenetic information. In particular, we focus on non-bifurcating branches in the placental mammalian tree using sequence data and rare genomic changes.

Tools for phylogenomic studies - The enormous amount of sequence data from ongoing and future genome sequencing projects makes it necessary to develop tools for data handling. We develop bioinformatical tools and pipelines for phylogenomic studies. Such programs involve automatic retrieval of sequences data, filtering at different levels, alignment and alignment quality check routines. The first programs, "EST-e-mate" and "recursive BLAST", will soon be published (Hallström and Janke 2010 in preparation). EST-e-mate is an interface for the semi-automated analysis of EST sequence data and has been used in Kullberg et. al. (2007, 2008). Currently Maria Nilsson and Fritjof Lammers work on TeddyPi a program for TE detection and discovery for Phylogenetic Inference).

Genomics and speciation - Our recent phylogenomic analyses, indicated a major obstacle in even deep phylogenetic analyses that needs to be further understood and quantified - speciation. The divergence times among many mammalian groups are very short. Most splits are only a few million years apart and thus within the time frame of mammalian speciation and species duration. This leads to problems in the phylogenetic reconstruction even of ancient branches due to incomplete lineage sorting and hybridization. We suggested that mammalian evolution, and thus evolution in general, may not be strictly bifurcating and that therefore evolutionary processes may better be depicted by networks instead of bifurcating trees (Hallström and Janke 2010). (Besides genome analyses of placental mammals in general, we focus on the evolution and speciation within order, which underwent recent radiations.

Genomics and climate (environmental) change - Evolution is influenced by many abiotic factors, one major cause certainly is climate. Our phylogenomic and mitogenomic studies suggest that some mammalian radiations occurred during drastic changes of the paleoclimate such as during the mid-Cretaceous warming (some 100 Ma), the K/T boundary (65 Ma) or the Eocene-Oligocene transition cooling (some 33 Ma). We try to figure out, if this is a chance correlation or if it has a significant signal and natural cause. Currently, we are trying to understand the impact of recent changes on the evolution of the polar bear and brown bear using next generation sequencing approaches for genome and transcriptome analyses. Another project focuses on the evolution of Artiodactyla during different climatic phases.

The basic divergences of crocodiles - We have sequenced the mt genomes for most crocodilian species and for the first time found statistical significant evidence that the gharial (*Gavialis gangeticus*) is not basal in the crocodilian tree as has been expected by morphological data. The data also allowed dating major crocodilian divergences with high confidence. Now that major branches of the crocodilian tree are resolved we are investigating why morphological and paleontological data gave strong support for an erroneous topology.((

The evolution of marsupials - The relationship among marsupials is fascinating, because it shows many parallels to the evolution of their cousins - the placental mammals. Yet, marsupialian phylogeny is still not well understood, despite recent efforts to produce mitogenomic and nuclear gene data. Only few genome data have been produced and therefore additional nuclear gene and mitogenomic data will still provide valuable insights into the evolution of marsupials, in particular within species-rich orders such as: Dasyuromorphia (carnivorous marsupials), Diprotodontia (kangaroos and allies) and Didelphimorphia ("opossums").