

## Short CV Prof Dr. Axel Janke

### Contact

Prof. Ecological Genomics

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### University Education

1995 – PhD in Zoology – LMU Munich

1991 – Diploma in Genetics – University of Hamburg

1990 – “Aufbaustudiengang” Molecular Biology – University of Hamburg

1986 – Basic studies – University of Hamburg (Genetics, Zoology, Microbiology)

### Professional Experience

2010 – Professor in Ecological Genomics – Goethe University, Frankfurt, Germany

2010 – Professor in Genetics – Lund University, Sweden

1999 – Lecturer in Genetics – Lund University, Sweden

1998 – Docent in Genetics – Lund University, Sweden

1995 – Post-doc – Lund University, Sweden

1995 – Post-doc – LMU Munich

### Academic responsibilities (selected):

2003 - 2005 – Vice-representative for genetics in the department board.

1999 - 2009 – Responsible for isotopes and ionizing radiation at the genetics group.

2004 - 2006 – Director of studies for genetics.

2001 - 2008 – Genetics representative at COB in the “integration group”.

2001 - 2008 – Genetics representative at COB for granting PhD stipends.

2010 - 2012 – Spokesperson of research area D

2010 - – Various boards of BiK-F Institute & head of the BiK-F Laboratory Center,

2012 - – Member of the Fachbereichsrat, Goethe University

2012-2016 – Spokesperson of Research Activity 6: Evolution and Climate

2018 - – Spokesperson of LOEWE TBG

### Main Research Interest

My research focuses on the analysis of vertebrate evolution, systematics, adaptation and, recently, speciation using molecular data. I was the first to use data from whole mitochondrial genomes for phylogenetic analyses (1994) and sequenced and published numerous “**first**” **mt genomes** from different vertebrate groups. In addition, I estimated divergence times from phylogenies, developed the first compensation method for rate differences, developed the first solid calibration points for a molecular clock, and set the dated phylogenies into various contexts of plate tectonics, biogeography and climate changes.

After several whole genome data became available I extended my interest 2005 to **phylogenomic** analyses, i.e. the use of whole genome data for evolutionary studies. We have been the first to make phylogenomic analysis. I discovered that the evolution of the mammalian genome is complex and phylogenetic reconstruction does not always lead to a bifurcating tree (2010). Instead some phylogenies are better depicted and understood as **networks**. This has important implications for the understanding of evolution, speciation and systematics.

Recently I got interested in recovering the signature that major environmental changes left in the mammalian genome during the last 100 million years using comparative genomics. The arctic has been one of the fastest changing and most extreme environments. It is also a rather simple biotope. This makes it an interesting region to study the influence of climate change on biodiversity. As a first step, we sequenced and analyzed the complete genomes of all **bear** species (2016), which show that bear evolution and speciation is not straight forward, but shaped by gene flow. On the other side the unexpected discovery that there is not one, but **four species of giraffe** (2016), with limited gene flow among them shows that genomic analyses are necessary to fully describe and understand biodiversity.

I am now focusing on understanding the evolution, adaptation and population genetics of mammals, using genome data, NGS sequencing techniques and multi-locus genetic analyses methods. As of July 2018 the a new LOEWE Center for **Translational Biodiversity Genomics** will be funded with about 4.5M€/year starting 2018. It is an exciting task to part of this endeavor, which will make genomics available from a broad range of taxa to a wide field of research.

#### **Number of Publications and Patents**

Total number of ISI publications: 89, h-index=46 google scholar/44 ISI, average citations 57

#### **The five most important publications since 2010**

Hallström BM and Janke A. (2010) **Mammalian evolution may not be strictly bifurcating.** *Mol Biol Evol* 27(12):2804-2816. [5+4]

Hailer F, Kutschera VE, Hallström BM, Klassert D, Fain SR, Leonard JA, Arnason U, Janke A. (2012) **Nuclear genomic sequences reveal that polar bears are an old and distinct bear lineage.** *Science* 336:344-347.

Baptiste E, van Iersel L, Janke A, Kelchner S, Kelk S, McInerney JO, Morrison DA, Nakhleh L, Steel M, Stougie L, Whitfield J (2013) **Networks: expanding evolutionary thinking.** *Trends in Genetics* 29 (8).

Fennessy J, Bidon T, Reuss F, Kumar V, Elkan P, Nilsson MA, Vamberger M, Fritz U & Janke A (2016) **Multi-locus analyses reveal four giraffe species instead of one.** *Current Biology*, 26(18), 2543-2549.

Kumar V, Lammers F, Bidon T, Pfenninger M, Kolter L, Nilsson MA & Janke A (2017) **The evolutionary history of bears is characterized by gene flow across species.** *Scientific Reports*, 7.

#### **Further qualifications**

2010 June – A professorship position in genetics was offered to me from the University of Oulu/Finland, but the position was less competitive and therefore I declined.

**External funding since 2005**

2005	Nilsson Ehle Foundation	43 kSEK	ISEV conference, Lund
2005	Carl Trygger Foundation	450 kSEK	EST of fishes
2005	Erik Philip-Sörenson Found.	220 kSEK	ISEV conference, Lund
2006	Nilsson Ehle Foundation	65 kSEK	Crocodile mitogenomics
2007	Nilsson Ehle Foundation	65 kSEK	Crocodile mitogenomics
2008	Nilsson Ehle Foundation	130 kSEK	Bovine retroposon
2008	Erik Philip-Sörenson Found	220 kSEK	Bovine EST using 454 technology
2011	Part of BiK-F/LOEWE (22M€)	3 M€	PB-D Laboratory center
2014	Part of BiK-F/LOEWE (23M€)	3.1 M€	PB-D Laboratory center
2018	Part of TBG/LOEWE	ca17 M€/4a	TBG center (with Prof Pfenninger and Pauls)