



Seewiesen Colloquia

Speaker invited by: Dept. Kempenaers

Thursday, September 21, 2017, 13h, House 4, Lecture Room

A genomics perspective on selfish chromosomes of birds

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Most bird species have a diploid genome comprising around 80 chromosomes. Nearly all of these are relatively repeat-poor and gene-rich, and have been largely accessible with short-read sequencing technologies. There are, however, some chromosomes in the avian karyotype with considerable accumulation of selfish genetic elements such as transposable elements and endogenous viruses, which may imply that these chromosomes are in genetic conflict with the rest of the genome. Here I discuss ongoing research in our group focusing on two likely selfish chromosomes, the female-specific W chromosome in birds-of-paradise and the germline-specific chromosome in zebra finches. A combination of single-molecule technologies (such as long-read and linked-read sequencing) made it possible to access large parts of these highly repetitive chromosomes, showing that the birds-of-paradise W chromosome is highly enriched in endogenous retroviruses and the zebra finch germline-specific chromosome is highly enriched in tandemly repeated genes. These results raise the question of how much of the total genetic variation has previously been missed in avian genomics studies.

Who is Alexander Suh?

2016/10-present: Assistant professor, Department of Evolutionary Biology (EBC), Uppsala University, Sweden.
2014/03-04: Guest researcher, Department of Human Genetics, University of Utah, Salt Lake City, UT, USA.
2012/10-2016/09: Postdoc, Department of Evolutionary Biology (EBC), Uppsala University, Sweden.
2012/08-09: Guest researcher, Department of Biochemistry and Molecular Biology, Mississippi State University, Starkville, MS, USA.
2012/06-07: Guest researcher, Sars International Centre for Marine Molecular Biology Bergen, Norway.
2012/04-09: Postdoc, Institute of Experimental Pathology (ZMBE), University of Münster, Germany.
2009-2012: PhD student, Institute of Experimental Pathology (ZMBE), University of Münster, Germany.

Selected publications:

- Weissensteiner, M. H., Pang, A. W. C., Bunikis, I., Höijer, I., Vinnere-Petterson, O., Suh, A.*, Wolf J. B. W.* (2017) Combination of short-read, long-read and optical mapping assemblies reveals large-scale tandem repeat arrays with population genetic implications. *Genome Research* 27, 697–708. *equal contributions.
- Suh, A., Witt, C. C., Menger, J., Sadanandan, K. R., Podsiadlowski, L., Gerth, M., Weigert, A., McGuire, J. A., Mudge, J., Edwards, S. V., Rheindt, F. E. (2016) Ancient horizontal transfers of retrotransposons between birds and ancestors of human pathogenic nematodes. *Nature Communications* 7, 11396.
- Suh, A., Smeds, L., Ellegren, H. (2015) The dynamics of incomplete lineage sorting across the ancient adaptive radiation of neoavian birds. *PLoS Biology* 13, e1002224.