



Seewiesen Colloquia

Speaker invited by: Küpper Research Group

Thursday, February 16, 2017, 13h, in House 4, Lecture

Recombination hotspots vs. coldspots: Examples from two lekking bird species

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Genomes vary in diversity within and among species. Even within diploid individuals, there are parts of the genomes that are characterized by high diversity (heterozygosity) and others that are more homozygous. It is the aim of this talk to discuss how such differences come about and are maintained in natural free-living populations. I will give a brief background on recombination and linkage disequilibrium. I will then describe a genomic region described as a recombination 'hotspot' with examples of our studies of the MHC-region in the black grouse (*Tetrao tetrix*). Next I will discuss a recombination 'coldspot': an inversion polymorphism (so called supergene) recently discovered in the ruff (*Philomachus pugnax*) which may explain the maintenance of the extraordinary behavioural polymorphism found in males of this species. I will end by relating our findings to other studies of supergenes and the maintenance of complex phenotypic traits.

Who is Jacob Höglund?

- 1989 PhD Uppsala University, Sweden
- 1989 Royal Society postdoctoral fellowship University of East Anglia, UK
- 1990 NFR Assistant professor Uppsala University with extended periods at Univ. of Leicester UK, Queen's Univ., Kingston, Ontario, Canada and University of Jyväskylä, Finland
- 1994 Senior Lecturer Uppsala University
- 1999 Professor of Animal Conservation Biology, Uppsala University

Selected publications:

- Strand T Wang B Meyer-Lucht Y Höglund J 2013 Evolutionary history of black grouse major histocompatibility complex class II B genes revealed through single locus sequence-based genotyping. *BMC Genetics* 14: e29
- Wang B Ekblom R Bunikis I Siitari H Höglund J 2014 Whole genome sequencing of the black grouse (*Tetrao tetrix*): reference guided assembly suggests faster-Z and MHC evolution. *BMC Genomics* 15: e180
- McMahon BJ Teeling EC Höglund J 2014 How and why should we implement genomics in conservation? *Evol Appl* 7: 999-1007
- Lamichhaney S Fan G Widemo F Gunnarsson U Schwochow Thalmann Hoepfner MP Kerje S Gustafsson U Shi C Zhang H Chen W Liang X Huang L Wang J Liang E Wu Q Ming-Yuen Lee S Xu X Höglund J Liu X Andersson L 2016 Structural genomic changes underlie alternative reproductive strategies in the ruff (*Philomachus pugnax*). *Nature Genetics* 48: 84-88