

A close-up photograph of a small, light-colored mouse with dark eyes and whiskers, peeking out from a nest made of sticks and twigs. The mouse is positioned in the lower center of the frame, looking directly at the camera. The nest is constructed from a dense pile of dry, brown sticks and twigs, with some green leaves visible at the top left. The lighting is natural, highlighting the texture of the mouse's fur and the surrounding environment.

Conservation of Adaptive Potential & Functional Diversity

Durham, Sept. 14-15, 2017

Conservation of Adaptive Potential and Functional Diversity

14-15 September 2017, Durham University, UK

A discussion meeting to explore the potential for new paradigms and next generation sequencing to facilitate the more effective conservation of adaptive potential and functional diversity. Natural selection at functional loci together with gene-environment interactions and phenotypic plasticity (including epigenetic effects) allows a population to respond to changing environments, and current advances are improving our ability to integrate this important information into conservation strategies.

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Program (all talks in L50):

Day 1:

08:20 – *registration in Atrium*

08:50 – Opening remarks

✓ 09:00 – Bob Wayne - Measuring adaptive and deleterious variation in threatened populations and its importance for conservation management.

09:40 – Chris Funk - Incorporating information on adaptation into conservation policy: integrating genomics into Endangered Species Act decisions.

10:20 – *Tea break in the Atrium & registration*

10:40 – Rob Fleischer - Genomic and transcriptomic assessments of host response to invasive pathogens.

11:20 – Simone Sommer - Does low diversity influence MHC immune gene expression level in endangered wild cheetahs?

12:00 – Paul Hohenlohe - Evaluating the potential for a genetic marker panel of susceptibility to Tasmanian devil facial tumor disease.

12:40 – *Lunch in the Atrium & posters*

14:00 – Violeta Fuentes - The International Mouse Phenotyping Consortium (IMPC): a functional catalogue of the mammalian genome that informs conservation.

14:40 – Cock van Oosterhout - The Red Queen paradox of the MHC.

15:00 – Rebecca Pawluk - Could individual transcriptomic responses to parasite infection compensate for the absence of genetic diversity in naturally inbred fish?

15:20 – Heidi Haufler - Conserve the germs: the gut microbiome and adaptive potential.

15:40 – *Tea & posters in the Atrium*

16:00 – Menno de Jong - Searching for genomic signals of selection in bottlenecked founder populations.

16:20 – Deborah Leigh - Bottlenecks, evolution and the detection of selected variation.

16:40 – Sonya Eynard - Genetic diversity in the barn. Updates in livestock genetic diversity conservation and its potential use for wildlife conservation.

17:00 – Patrícia Pečnerová - Temporal change in genome-wide and functional diversity in the woolly mammoth.

17:20 – Roundtable Discussion

18:30 – *Conference Dinner (Collingwood)*

Day 2:

09:00 – Rasmus Nielsen - Genetic rescue from inbreeding depression and its evolutionary limits.

09:40 – Oscar Gaggiotti - Understanding associations between species and genetic diversity requires the use of consistent measures of biodiversity across levels of organisation.

10:20 – *Tea break in the Atrium*

10:40 – Barbara Mable - Changing environments and genetic variation: does inbreeding compromise short-term adaptive potential?

11:20 – Victor Soria-Carrasco - Demographic patterns and processes in *Timema* stick insects.

12:00 – Mike Bruford - Population Transcriptomics, demographic history and high altitude adaptation in a predatory bird.

12:40 – *Lunch in the Atrium*

14:00 – Rus Hoelzel - Next generation fisheries management – detecting and conserving functional diversity.

14:40 – Chris Jiggins - The origins of diversity in *Heliconius* wing patterns: Re-use of ancient variants and its implications for conservation.

15:20 – Henri Thomassen - Modeling intraspecific genetic variation for multi-taxa conservation prioritization.

15:40 – *Tea in the Atrium*

16:00 – Joe Colgan - Signatures of selection revealed by population analyses of bumblebee genomes across the United Kingdom.

16:20 – Malgorzata Pilot - Functional genetic diversity in grey wolves and domestic dogs, and adaptive potential of hybridisation.

16:40 – Kristina Ramstad - Signatures of positive selection in a basal avian lineage (*Apteryx* spp.).

17:00 – Roundtable Discussion

Conserve the germs: the gut microbiome and adaptive potential [Talk]

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Although the diversity of microbial communities inhabiting the gastrointestinal tract (microbiota) are of proven importance to health in both humans and non-human animals, the functional importance of these collective genomes (microbiome) to the adaptive potential of their hosts has only recently been considered within a conservation framework. If loss of gut genome diversity threatens the health (and therefore the fitness of individuals), and indices of such diversity can be correlated with the adaptive potential of a species in changing environments, measuring functional composition of the metagenome from non-invasive fecal samples could provide a useful and practical tool for determining conservation priorities. Since habitat quality plays a crucial role in determining the diet ingested by the host, one of the most plausible drivers of gut microbiomes, testing species and populations living in contrasting environments, such as degraded habitats versus uncontaminated and continuous forests, is of primary interest. One of our focal species includes the Udzungwa red colobus monkey (*Procolobus gordonorum*), among the most threatened primate species in Africa. Primarily arboreal and highly sensitive to hunting and habitat destruction, they provide a useful model for understanding whether anthropogenic disturbance impacts gut functional diversity. Analysis of genus composition of the fecal microbiota using metataxonomics showed a marked diversification across habitats, with gut microbiota α -diversity significantly higher in undisturbed forest. Functional analysis of the metagenome also suggests that such variation may be associated with food plant diversity in natural versus human-modified habitats, requiring metabolic pathways to digest xenobiotics. We discuss how such changes have implications for future adaptive potential of the species.