Project outline

1. Project outline describing the scientific rationale of the project (max 4,000 characters incl. spaces and returns)

Genome structure, including the number and arrangement of chromosomes (called the karyotype), is relatively stable across evolutionary time, with only a few small changes between human and gorilla karyotypes, for example. Gibbons, including the Hylobates, Nomascus and Siamang genera, are exceptional, in that there has been a very high level of genomic structural rearrangements over a relatively short evolutionary timescale. This has resulted in species that are closely related at the taxonomic and DNA sequence level being dramatically different in their genome structure.

The reason for this burst of genomic rearrangement is not clear, although it may be due to activity of retrotransposons. We wish to investigate whether such genomic rearrangement is ongoing, and how the gibbon manages to tolerate such a high degree of genomic plasticity. This will provide important fundamental insights into chromosomal evolution, in particular the role of genome rearrangement in speciation and how genome integrity and gene expression is maintained.

We have assembled, in collaboration with Twycross Zoo, a gibbon DNA biobank which is unique in the UK and, to our knowledge, in Europe. We will sequence a selection of samples from this Biobank using short read (Illumina) and long-read (10xChromium) technology and use these sequences to infer copy number variation and inversion across the whole genome, using well-established software. A subset of copy number variable genes will be validated using wet-lab techniques, selected based on predicted functional consequences of the CNV.

Techniques that will be undertaken during the project

10x chromium sequencing

Genome analysis of copy number variation using a variety of tools, such as LUMPY, cnMOPs and GenomeSTRIP.

Comparison of call rates of different approaches.

Validation of copy number variants using digital droplet PCR