BiRC Seminar – open to all

Ludovic Orlando and Hákon Jónsson
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University of Copenhagen

Time: Friday 10 October, 2014, 14:00 — 15:25
Venue: BiRC, C. F. Møllers Allé 8, Building 1110-223

Program for the Seminar:
14:00 – 14:30 Hákon Jónsson
14:30 – 14:40 Short break
14:40 – 15:25 Ludovic Orlando

Abstracts:

Hákon Jónsson: Evolutionary genomics of the equine radiation

The extant species in the Equus genus are solely composed of horses, asses and zebras, which share a common ancestor 4.0-4.5 myr ago (mya). Despite the iconic fossil record of the rapid species diversification in Equidae, little is known about the evolutionary trajectory that resulted in the panel of modern equine species. Here, we sequenced 6 genomes of asses and zebras, completing the whole-genome characterization of extant species in Equus. In addition, we sequenced the extinct Quagga zebra, a recently extinct variant of the plains zebra. This extensive genome dataset allowed us to screen for linage specific adaptations, resulting in the discovery of 48 positively selected genes associated with olfaction, immune response, development, locomotion and behavior. Furthermore, the whole genome sequences allowed us to decipher the complex history of equids and speciation, with synchronous population size changes for different species in line with past variations in climate. The equine speciation is generally characterized with gene-flow, starting with the split of the ancestor of asses and zebras from the horses in the New-world 4.0-4.5 mya and the subsequent dispersion to the Old World 2.1-3.4 mya. We also found genetic signatures of ancestral gene-flow between three contemporary equine species with extremely divergent karyotype structures. This is in stark contrast with the previously proposed role of karyotype differences in complete reproductive isolation for equids.

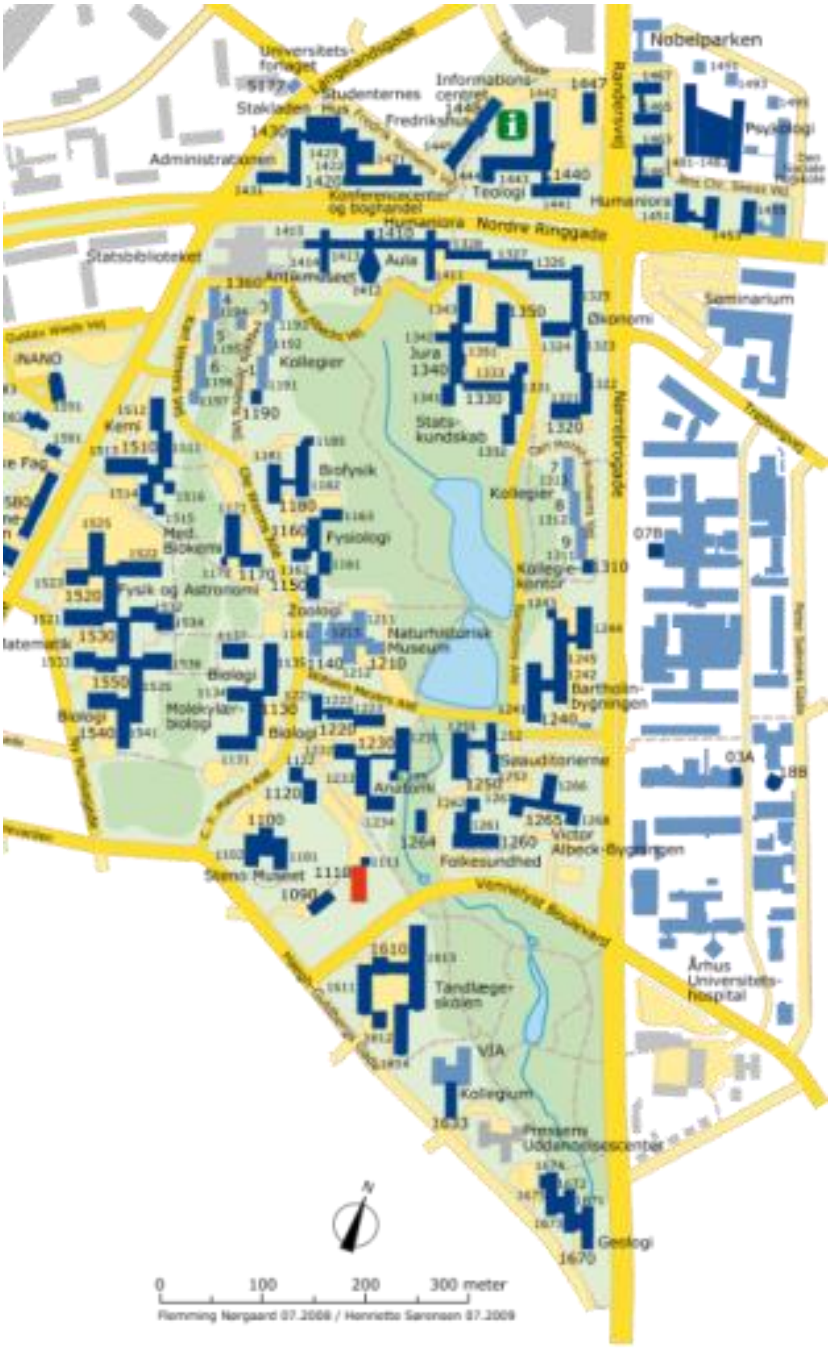
Ludovic Orlando: Characterizing really old genomes, proteomes and epigenomes

Traces of DNA and other biomolecules can survive up to hundreds of thousands of years in a wide range of fossils, such a bones, teeth, hairs, coprolithes and even in soils. Sequencing these molecules literally catch evolution red-handed, providing precious sources of information about past populations and communities, ancient epidemics and extinct species. Such templates, however, are extensively damaged over time and present specific biochemical features, including extensive fragmentation, deamination and deamidation. Additionally, ancient DNA extracts most often consist of a mixture of DNA from different sources, as fossils get colonized by environmental microbes soon after death. These features have long restricted the amount of genetic information that one could resurrect from the past. The advent of Next-Generation Sequencing technologies has been a game changer, unlocking access to the first complete genomes from the past. Brute-force sequencing of ancient genomes, however, is most often cost-ineffective due to the metagenomic nature of ancient extracts. Our lab took advantage of high-resolution tandem mass

spectrometry, second and third-generation sequencing technologies to illuminate the biochemical structure of ancient DNA molecules and ancient proteins. With this information in hand, we developed novel molecular tools and bioinformatic approaches that improve our ability to access ancient genetic information. These approaches enabled us to characterize a first draft of the oldest genome ever characterized, that of a horse that lived in Yukon, Canada some 700 thousands years (kyr) ago. Direct comparison with a 43 kyr-old horse genome and a handful of modern horse breeds revealed the demographic dynamics, admixture and selective forces that shaped the horse genome over time, including in the early stages of their domestication. This work illustrates how state-of-the-art high-throughput approaches tailored to the specificities of ancient biomolecules now enable the characterization of whole genomes from really old material, even for non-model organisms. This opens the full Middle Pleistocene period (ca. 125-780 kyr) to genomics and proteomics. We also developed new approaches that exploit the way ancient DNA molecules are degraded for reconstructing ancient epigenomes from fossil material. Those approaches have enabled us to reconstruct and make use of the first genome-wide nucleosome and methylation maps ever characterized in order to predict ancient gene expression levels and thereby recover phenotypic information that is not accessible from the sole analysis of the gene sequences. This work adds epigenomics to the list of –omics that one can now access from fossil material.

After the seminar there will be beer/soda/coffee and chips in the coffee room on the 4th floor.

http://birc.au.dk/activities/seminar-series/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Flemming Nørgaard 07.2008 / Henriette Sørensen 07.2009