



UPPSALA
UNIVERSITET

PhD student in population genomics of wolves

We are looking for a highly motivated PhD student to join Hans Ellegren's lab group of about 10 PhD students, post-docs and bioinformaticians working with evolutionary and population genomic approaches to speciation, adaptation, molecular evolution and conservation genomics (<http://www.ieg.uu.se/evolutionary-biology/ellegren/>). The announced position is on an exciting project dealing population genomics and molecular evolutionary analyses of wolves.

The Scandinavian wolf population is a striking example of the impact of isolation on genetic diversity and survival. Wolves were once extinct in Scandinavia, but in the early 1980s two individuals re-entered the peninsula and successfully reproduced. Cut off from the larger Finnish-Russian metapopulation by the Reindeer husbandry area to the North, the population remained very small (less than 10 individuals) for a decade. However, in 1991 a single male immigrant entered the population and reproduced, resulting in genetic rescue through an increase in both genetic diversity and population size (Vilà et al 2003 Proc R Soc Lond B 270:91-97). To this day the population remains characterised by prolonged periods of isolation with rare immigration events. Inbreeding is extensive.

We are sequencing the genomes of hundreds of wolves from both Scandinavia and the Finnish-Russian metapopulation. This dataset provides an ideal opportunity to study the consequences of population isolation and genetic rescue, as well as providing critical conservation information for the long-term viability of the population. It also provides unique possibilities to study the distribution of fitness effects in an inbred population and the accumulation of deleterious mutations in gene sequences. We have recently demonstrated how inbreeding translates into extensive arrays of runs of homozygosity in individual wolves, with some having entire chromosome that are identical-by-descent (Kardos et al 2017 Genomic consequences of intensive inbreeding in an isolated wolf population. Nature Ecology and Evolution doi: 10.1038/s41559-017-0375-4).

There are several possible lines to pursue depending on interest and background of the successful candidate/s. These include assessment of how genomic diversity varies over time and in relation to inbreeding, identification of candidate genomic regions for inbreeding depression, assessment of gene flow between populations, and molecular evolutionary analyses of large-scale sequence data.

The venue for the position, the Evolutionary Biology Centre, is situated in central Uppsala (<http://www.ieg.uu.se>). The working atmosphere is highly international with a regular recruitment of PhD students and post-docs from abroad. The Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 300 scientists and graduate students, and with research programs in, for example, ecology, genetics, genomics and

developmental biology. Our graduate school offers a creative and stimulating environment and offers a rich variety of seminars, journal clubs, courses and possibilities to interact with other scholars and students. Local platforms for next-generation sequencing (<http://www.scilifelab.uu.se>) and high-performance computational analyses are very useful. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant college town with beautiful surroundings conveniently situated 40 minutes by train from Stockholm.

The graduate program covers four years of full-time, fully paid study. The position can be combined with teaching (maximum 20%), which prolongs the employment with the corresponding time.

Informal inquiries can be directed to Hans Ellegren (hans.ellegren@ebc.uu.se).

Applications will only be accepted when submitted through the Uppsala University web portal no later than Jan 7 2018, using this link: <http://uu.se/en/about-uu/join-us/details/?positionId=182339>