

Postdoc:

Population genetic studies of the origin and early history of the dog

A 2-year Postdoc position is available in the research group of “Evolutionary biology and forensics” at the Department of Biotechnology, Royal Institute of Technology, Stockholm, Sweden (www.biotech.kth.se/genetech/info/savolainen.html).

We are a small research group (Assistant professor Peter Savolainen and two PhD-students) performing world-leading research about the origin and early history of the domestic dog. We have in earlier studies of mtDNA shown that the dog probably has a single origin from wolf somewhere in East Asia (Savolainen *et al*, 2002, *Science*: 298,1610-1613), and that the Australian dingo originates from this population of East Asian domestic dogs (Savolainen *et al*, 2004, *Proc Natl Acad Sci U S A*: 101,12387-12390).

Our studies are based on a unique sample collection from more than 2,000 dogs representing all major populations worldwide. This collection is, to our knowledge, the most comprehensive for any domestic animal, most other collections consisting mostly of European breeds. This puts us in a very good position for our further studies.

The over all aim for our work is to describe in detail the first origin and early history of the domestic dog. First we want to study in more detail the exact geographic origin and time for the origin of dogs, the number of founder animals (wolves), and the extent of subsequent interbreeding between dog and wolf. In the next step we will describe the spread around the world (routes and time points) from East Asia to Europe, America, Africa and Island Southeast Asia/Australia, and the first steps in the development of morphological variation leading to today’s types and breeds of dog. Thus, the rather bold goal is to describe more or less everything about the genetic origin and history of the dog, leaving few fundamental questions unanswered.

Our earlier studies have been based on sequencing of the mtDNA control region, but we are now analysing also entire mtDNA genomes as well as Y-chromosome sequence and microsatellites. Since we have very powerful large-scale systems for DNA analysis, but have been understaffed for the population genetic analyses, we have at the moment a large amount of genetic data just waiting to be analysed. This is therefore a good chance for a Postdoc with a good knowledge in population genetics to rapidly generate a number of papers.

We are looking for a Postdoc with a good knowledge and experience in population genetics, phylogenetics and statistics, to help us analyse our large data set. Some practical lab skills would be preferable, but the important thing is a good knowledge in population genetic and phylogenetic methods and ability in manuscript writing. The applicant should, at the start of appointment, have obtained a PhD-degree not more than five years earlier.

The Postdoc would receive a stipend (tax free) of 17,000-19,000 Swedish crowns per month (exact sum not fixed at this point), equivalent to 1,800-2,000 euros per month.

There is no exact deadline for applications, the position is supposed to be started during the autumn 2006.

If interested in applying for this position, send an email to Peter Savolainen (savo@biotech.kth.se), containing a letter describing your previous research experience (including a description of your skills in for example population genetics, phylogenetics, statistics, computer programming and molecular genetics lab work), a CV and publication list.