

Name	PONTUS SKOGLUND	
Position	Group Leader (1 st 6)	
Year joined (Crick or founder institute)	2017	

Career History

2003- 2007: BSc Biology, Umeå University, Sweden
 2007- 2009: MSc Biology, Uppsala University, Sweden
 2009- 2013: PhD, Uppsala University, Sweden
 2013- 2014: Postdoctoral researcher, Uppsala University, Sweden
 2014- 2017: Postdoctoral research fellow, Harvard Medical School, USA

Major Awards, Honours and Prizes

Vallee Scholar 2020, Bert and Kuggie Vallee Foundation
 Bjurzon prize 2015, Faculty of Science & Technology, Uppsala University
 Linnaeus prize 2014, Royal Society of Sciences, Sweden.

Membership of external committees, editorial boards, review panels, SABs etc

Lab Name	<i>Ancient Genomics Laboratory</i>
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Research programme and achievements

All human biology and disease is the outcome of evolution, and many current health challenges have appeared or radically changed their dynamics recently with changes such as agriculture, urbanisation, and industrialisation. But how does human biology adapt to such challenges? The Ancient Genomics Lab uses ancient DNA as a direct source of information from the past to understand the evolutionary processes that shaped human genome variation. The goal is to link evolution and population history to historical factors such as epidemics, environmental and societal changes, and thus uncover new insights about human biology and its mechanisms.

Our three main research directions are currently:

Fine-scale reconstruction of evolution in the ancestry of the UK Biobank

We are sequencing 1,000 ancient British genomes to add a third dimension to the world-leading resource in human medical genomics that is the UK BioBank, and the future NHS 100,000 genomes. We aim to reconstruct evolutionary processes in the genome across the past few thousand years, in response to past epidemics, and societal changes.

Adaptation of human biology and societies during worldwide transitions to agriculture. We are studying human adaptation to one of the key evolutionary transitions in the human past: that to agricultural societies. Questions surround dietary shifts, and infectious disease. We are also studying domestic dogs as a separate organism that went through the same transition.

Co-evolution of human, pathogen, and domestic animal genomes. Zoonoses are a major source of current global health challenges for infectious disease. We are retrieving ancient pathogen genomes from past individuals to directly study their past genomic diversity, and in parallel reconstruct the evolutionary history of the link between humans and domestic animals.

Since the founding of the lab, we have reconstructed the evolutionary history of domestic dog and human populations over the past 11,000 years, revealing an ancient origin of the dog. In addition, we find that adaptation to diet, such as the expansion in amylase family copy numbers also seen in humans, was more recent. We have also provided a synthesis of our understanding of human origins, which is critical of previous simplistic concepts and ideas, and contributed to collaborative projects on present-day human genomic diversity with the Sanger Institute, and early modern humans in Europe with the Max Planck Institute of Evolutionary Anthropology. Other new finds still in preparation include preliminary detection of syphilis and leprosy genomes in ancient skeletons, and finds of previously unknown adaptations to agriculture in ancient Europe.

As a postdoc at Harvard Medical School during the period of the quinquennium that spans April 2015-November 2017, my research revealed complex founding of population structure in the Americas, the origins of population structure in the Pacific, and adaptations and past genomic diversity in Africa. I also studied the origin of dogs, the early history of Easter Island, and ancestry of archaic humans in Eurasia.

Research outputs

A Bergström, C Stringer, M Hajdinjak, E Scerri, P Skoglund. (2021) *Origins of modern human ancestry*. Nature 590(7845): 229-237. DOI: [10.1038/s41586-021-03244-5](https://doi.org/10.1038/s41586-021-03244-5)

This is a review paper that addresses the question on the origins of the ancestry of modern humans, *Homo sapiens*. Together with experts in the fossil and archaeological records, we synthesize recent evidence in those fields as well as genetics to conclude that there is currently no support for often-cited simple narratives of the origin of human ancestry. We currently can't identify a specific time or place of origin with a larger period and the region of Africa.

Bergström A et al. (2020) *Origins and genetic legacy of prehistoric dogs*. Science 370 (6516), 557 – 564. DOI: [10.1126/science.aba9572](https://doi.org/10.1126/science.aba9572)

This first research paper led by our lab presents the first large-scale study of ancient genomes from early domestic dogs. We show that dogs were domesticated prior to the agricultural transition, with a dynamic history that includes collapse of early genetic diversity of dogs in Europe, and a complex evolution of genetic adaptation to starch rich diets.

A Bergström, S A McCarthy, R Hui, MA Almarri, Q Ayub, P Danecek, Y Chen, Sabine Felkel, P Hallast, J Kamm, H Blanché, J-F Deleuze, H Cann, S Mallick, D Reich, MS Sandhu, P Skoglund, A Scally, Y Xue, R Durbin, C Tyler-Smith. (2020) *Insights into human genetic variation and population history from 929 diverse genomes*, *Science*, 367(6484):eaay5012. DOI: [10.1126/science.aay5012](https://doi.org/10.1126/science.aay5012)

In this paper, led by the Sanger Institute, we characterised global human genetic diversity in whole-genomes at a greater scale and with broader diversity than before. We documented complex divergence between modern humans and archaic groups such as Neanderthals. Lead author Anders Bergström started work on the project during PhD studies at the Sanger, and continued it with my input as a Crick postdoc from April 2018 until publication in 2020.

P Skoglund, J Thompson, ME Prendergast, A Mittnik*, K Sirak*, M Hajdinjak*, T Salie*, N Rohland, S Mallick, A Peltzer, A Heinze, I Olalde, M Ferry, E Harney, M Michel, K Stewardson, J Cerezo-Roman, C Chiumia, A Crowther, E Gomani-Chindebvu, AO Gidna, KM Grillo, G Hellenthal, R Helm, M Horton, S Lopez, AZP Mabulla, J Parkington, C Shipton, R Tibesasa, M Welling, V Hayes, DJ Kennett, R Ramesar, M Meyer, S Pääbo, N Patterson, A Morris, N Boivin, R Pinhasi, J Krause, D Reich (2017) *Reconstructing prehistoric African population structure*. *Cell*, 171:59-71. DOI: [10.1016/j.cell.2017.08.049](https://doi.org/10.1016/j.cell.2017.08.049)

The first population genomic study of prehistoric Africa. We developed new methods for studying selective sweeps and polygenic selection using ancient genome data, revealing previously unknown diversity and adaptation in Africa during the past 8,000 years.

P Skoglund, C Posth, K Sirak, M Spriggs, F Valentin, S Bedford, GA Clark, C Reepmeyer, D Fernandes, Q Fu, E Harney, M Lipson, S Mallick, M Novak, N Rohland, K Stewardson, S Abdullah, MP Cox, FR Friedlaender, JS Friedlaender, T Kivisild, G Koki, P Kusuma, DA Merriwether, F-X Ricaut, JTS Wee, N Patterson, J Krause, R Pinhasi*, D Reich*. (2016) *Genomic insights into the peopling of the Southwest Pacific*. *Nature*, 538:510–513. DOI: [10.1038/nature19844](https://doi.org/10.1038/nature19844)

In this study of the first tropical ancient DNA, we revealed how the first people in Remote Oceania had an ancestry that contributed to groups across the region today.
